

4th Crossing the Palaeontological-Ecological Gap (CPEG)

3rd Conservation Paleobiology Symposium

27 July - 1 August 2025 | University of Zurich

Program and Abstracts



Universität
Zürich UZH

CONTENTS

CONTENTS	2
Program Availability	2
ABOUT THE MEETING	3
Format	3
Sustainability and justice	3
The venue	4
Getting Around	5
Wifi on Campus	7
Socials and Contact info	7
Organising committee	7
Keynotes	8
Workshops	9
Field Excursion	11
Student events	12
SPONSORS	14
PROGRAM	15
Schedule of presentations and other activities	15
Poster presentations	26
ABSTRACTS	31
Invited Keynote Speakers	31
Oral presentations	35
Posters	113

Program Availability

In an effort to minimize waste, hard copies of the program and abstracts will not be provided. Instead, it will be available as a digital file on the conference website and accessible with a QRcode at the venue.

This abstract booklet is archived and freely available on Zenodo,

DOI: [10.5281/zenodo.16443650](https://doi.org/10.5281/zenodo.16443650)

ABOUT THE MEETING

The CPEG meeting aims to bring palaeontologists and ecologists together to share ideas, data and methods in research areas that are studied by both, but typically independently (e.g., community and population ecology, food web dynamics, extinction mechanisms and conservation). On this occasion, the meeting will be merged with the 3rd Conservation Paleobiology Symposium to promote the application of palaeobiological and ecological records to the conservation, management, and restoration of biodiversity.

Format

Our meeting is **hybrid**. Virtual participants are able to deliver pre-recorded talks with questions from the audience, and all talks will be streamed and accessible to accommodate participants who cannot attend in-person due to geo-political, financial, or other logistical constraints.

We are planning a six-day (Sunday to Friday) meeting without parallel sessions. We will offer two **in-person workshops** on Sunday, July 27th and a **field trip** on Friday, August 1st. Two additional **virtual workshops** will be offered prior to the meeting. From Monday to Thursday, we will host **keynote** addresses, **oral presentations** and **lightning talks**. During these days, lunch and coffee breaks will be provided for attendees. A **welcoming reception** and a **poster session** will take place on Monday at the Natural History Museum. Awards will be given for the best student oral and poster presentations and for travelers' lowest carbon footprint (corrected for distance). There will also be two students events, including a **Roundtable lunch** and an **Informal dinner**.

We aim to ensure a balanced program that includes a wide range of topics and perspectives, as well as equal opportunities in terms of gender, underrepresented backgrounds, and career-stages.

Sustainability and justice

We aimed to ensure a balanced program that includes a wide range of topics and perspectives, as well as equal opportunities in terms of gender, underrepresented backgrounds, and career-stages. We also sought ways to keep our carbon emissions as low as possible in the planning and delivery of this meeting, and to provide options for students and other attendees from low-income countries to participate. Accordingly, we took the following actions:

- We invited keynote speakers who can/are willing to reach Zurich by train (and additional virtual keynote speakers)
- We ensured gender and career-stage balance in our contributors
- We provided exclusively vegetarian, locally sourced and seasonal food
- We sought funding to make the registration fee as affordable as possible for all participants.

- We provided financial support to 3 students or postdocs currently residing in low-income countries (middle HDI and developing countries with a HDI index < 0.85 as defined [here](#)) to attend in person.

The venue

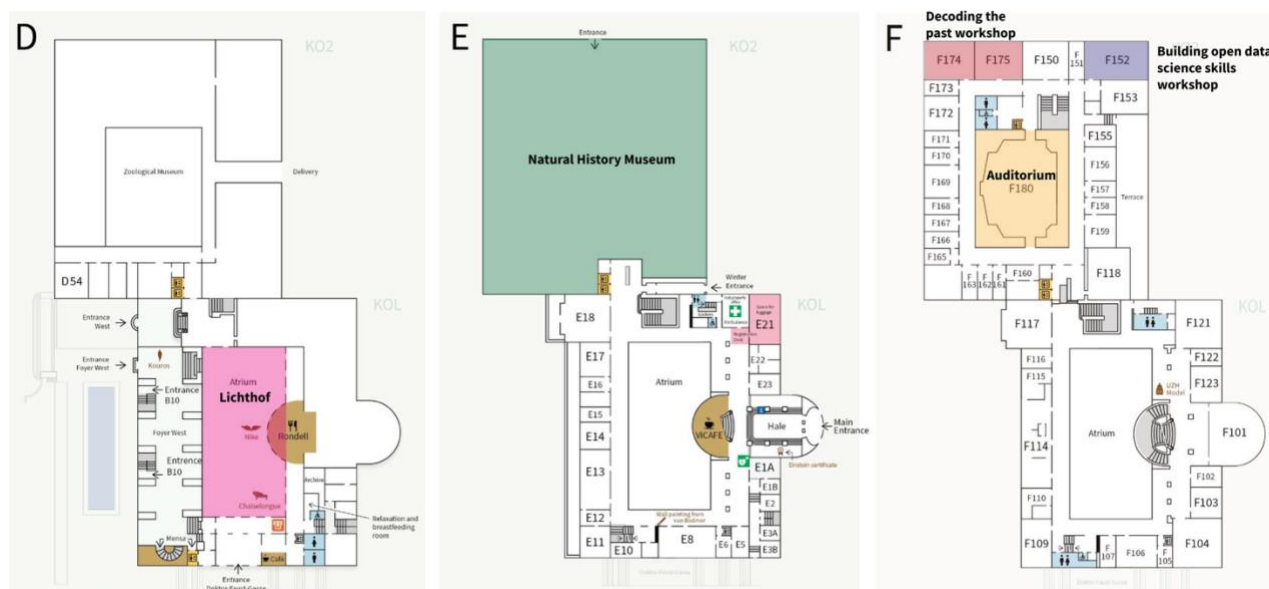
The meeting will take place at the University of Zurich, in Zurich, Switzerland. Specifically, it will be held at the Universität Zentrum - Central Campus. The Central Campus is comprised of multiple buildings, the meeting will primarily take place in building K02, which also houses the Natural History Museum (see on Google [map](#)). The best way of accessing this building is through the entrance from [Karl-Schmid-Strasse](#), where the registration desk will be set up.



Photo: <https://www.llm.uzh.ch/en.html>

- Oral sessions will be held in the auditorium **K02-F-180**, marked with yellow on the map below.
- The *Building open data science skills* workshop will be held in room **K02-F-152**, marked in blue on the map below.
- The *Decoding the past* workshop will be held in rooms **K02-F-174** and **175**, marked in red on the map below.
- The poster session and the Icebreaker will be held in the Natural History Museum, situated on floor E, marked in green on the map below.
- Coffee breaks and lunches will be served in the **Natural History Museum** on Monday July 28 only. All subsequent breaks and lunches will take place in **Lichthof Nord**, situated on floor D, marked with pink on the map below.
- The student roundtable lunch will be held in **Lichthof Süd**.

Entering the Buildings: we kindly ask attendees to only use the entrance from Karl-Schmid-Strasse for all events taking place in these buildings. This is the entrance to the museum and all session rooms can be accessed from here (follow signs posted). Registration will also be at this entrance.



Getting Around

Public Transit

The public transit system in Zurich is one of the most efficient in the world.

Zones: **110** is the main zone that both the **Main Station (Zurich HB)**, the **Natural History Museum** and the **University** are located in. To travel around any zone, we recommend you buy a one-day ticket (12,80 CHF) and you can use any train, tram, bus or even boat within that zone for 24 hours.

Buying tickets: you can do this from the main station, some transit stops have ticketing machines, but it is much easier to download the SBB app and use that the app is downloadable on both iPhone and Android. Alternatively, you can use the [SBB website](https://www.sbb.ch) itself, although we recommend the app. With the app you can also take advantage of the **"Easy Ride"** option - simply switch it on when you get on a tram/bus, switch it off when you hop off, and it will automatically calculate the cheapest cost for the route you took. This way you do not need to worry about looking up the names of the specific stops and buying specific tickets. You can use Easy Ride even when travelling through multiple zones or even between different cities!

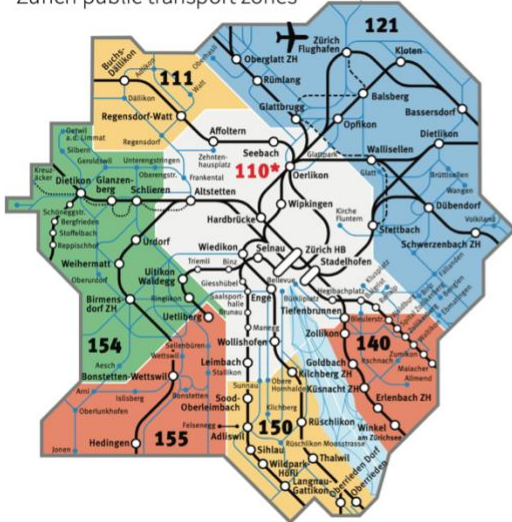
Getting to the event: the event is held at the university and the Natural History Museum in the KO2 and KOL buildings (see map of campus below). The closest transit stop to these buildings is **ETH/Universitätspital**. The trams number T10*, T9 and T6 (the direction that the tram will be going will be displayed on the app) will stop here. Alternatively, you can take the **Polybahn** (a cute little funicular railway that is also included in the day ticket, highlighted with yellow dots on

the Central Campus map below) up to the ETH campus and walk from there. This starts next to the Starbucks at the tram stop **Zurich, Central** (stop for trams T3, T4, T6, T7, T10, T15).

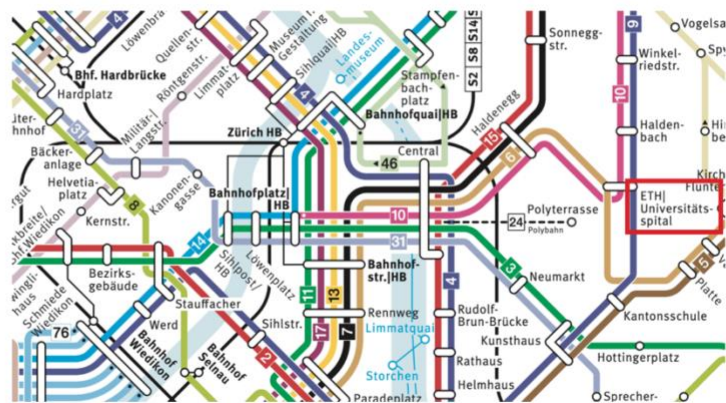
*T stands for tram and will be displayed in the app but not on the tram itself

Public transport maps

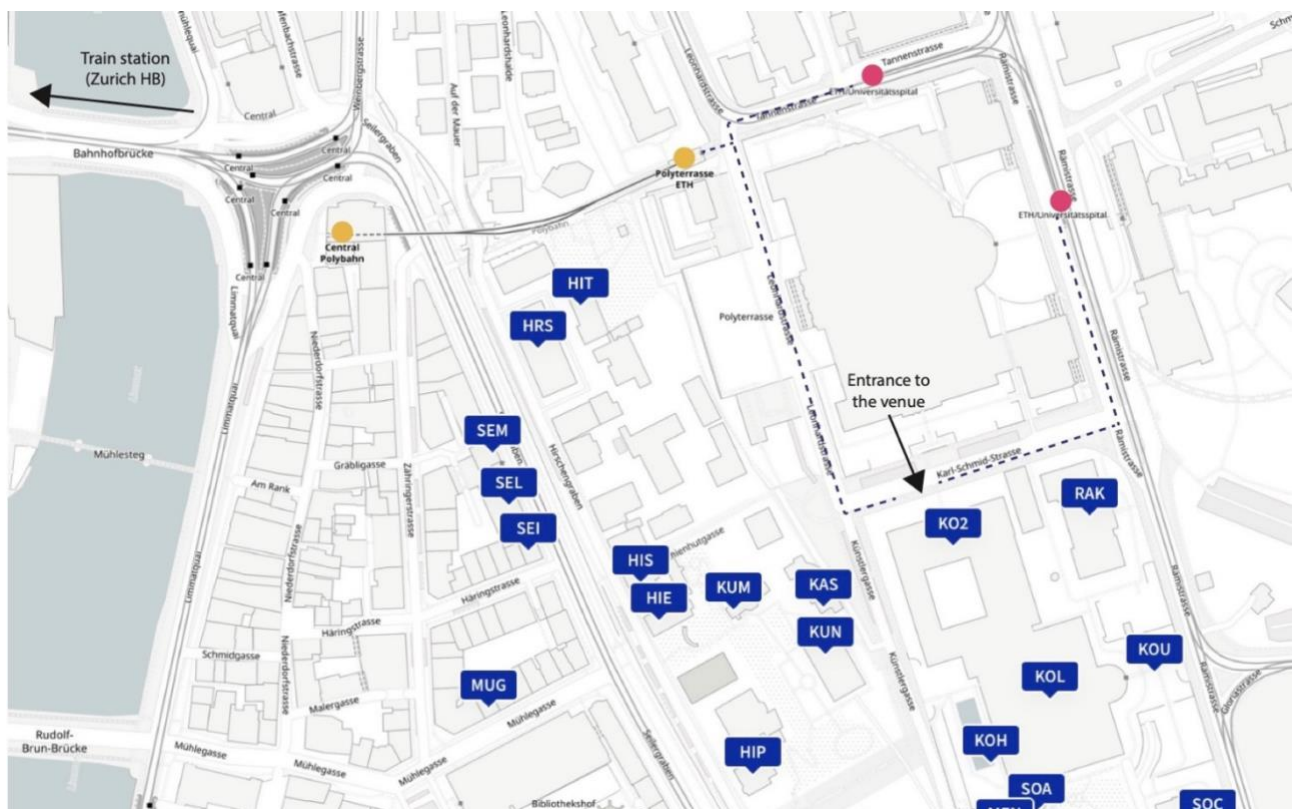
Zurich public transport zones



Tram and bus lines leading to the central campus



Central campus map



Wifi on Campus

The guest wifi is **uzh-guest**. You will need to accept the terms and conditions and out in your phone number (for text confirmation). You will need to login like this every day, as the session times out after 24 hours.

Socials and Contact info

X (formerly Twitter): @CPEG_CPB25

Bluesky: @cpeg-cpb25.bsky.social

E-mail: cpeg-cpb25@pim.uzh.ch

Organising committee

Conveners

Catalina Pimiento and Kristína Kocáková, Department of Paleontology, University of Zurich

Scientific committee

Erin Dillon, Smithsonian Tropical Research Institute, Panama; Juan David Carrillo, Department of Biology, University of Fribourg; Lewis Williams, Biosciences Department, Swansea University; Fernando Blanco, Department of Biological and Environmental Sciences, University of Gothenburg; and Juan Cantalapiedra, Museo Nacional de Ciencias Naturales, Madrid.

Logistics & Event Coordination

Morgane Brosse and Taylor Norris, Department of Paleontology, University of Zurich.

Volunteer Team

Efe Arman, Jordan Bestwick, Amin El Fassi El Fehri, Merle Greif, Stefanie Herter, Yiwei Hu, Mathilde Le Pallec, Kévin Le Verger and Jack Norton, Department of Paleontology, University of Zurich.

Keynotes



Ruth Thurstan

Senior Lecturer | Centre for Ecology and Conservation | University of Exeter
marine historical ecology | biogenic ecosystems | mixed-methods | local ecological knowledge | archives

Emily Mitchell

Assistant Professor | University of Cambridge
|| Curator of Invertebrates incorporating the Watson Curator of Malacology

ediacaran life | community ecology | marine ecology | origins of animals | networks



Emma Dunne

Lecturer and Researcher | Palaeontology, FAU Erlangen-Nürnberg

climate change | terrestrial tetrapods | biogeography | biodiversity | deep-time



Daniele Silvestro

Staff of Professorship for Computational Evolution | ETH Zurich

computational paleobiology | conservation | artificial intelligence | evolution | bayesian statistics



Oskar Hagen

PostDoc | German Centre for Integrative Biodiversity Research (iDiv)

biogeography | macroecology | eco-evolutionary dynamics | process-based modelling



Julia Tejada (virtual)

Assistant Professor | Division of Geological and Planetary Sciences | California Institute of Technology

paleoecology | stable isotopes | evolutionary biology | trophic dynamics | Amazonia



Mónica Carvalho (virtual)

Assistant Professor and Curator | Museum of Paleontology | Department of Earth and Environmental Sciences | University of Michigan

terrestrial ecosystems | plant ecology | climate change | deep-time | tropical ecosystems



Workshops

Workshop 1: Building open data science skills in paleobiology and ecology

Led by: Erin Dillon, Lewis Jones, Bethany Allen, William Gearty

Date: July 27th 2025, 09:00-17:00

Location: University of Zurich, Central campus, room KO2-F-152

Description

R is one of the most popular languages in the world of data science and has been widely adopted by the paleobiological and ecological communities for data analysis. General familiarity with R allows users to automate routine tasks, create reproducible analytical workflows, and expand the potential of their research. This workshop aims to introduce participants to the versatility of R for cleaning, analyzing, and visualizing paleobiological and ecological data. It will cover topics including: data acquisition from biodiversity databases such as the Paleobiology Database, Neotoma Paleoecology Database, and Global Biodiversity Information Facility; building workflows in R to clean and analyze data; data visualization and synthesis; and guidelines (e.g., FAIR and CARE principles) and tools (e.g., GitHub) for creating more reproducible code and accessible documentation. In doing so, this workshop will introduce attendees to palaeoverse, an R package that supports data preparation and exploration for paleobiological analysis. Participants will also become familiar with additional packages developed by the Palaeoverse Community (www.palaeoverse.org), such as rphylopic. More broadly, this event aims to connect participants working in different fields who share a common interest in data science and provide a platform for participants to gain experience working collaboratively in R to generate reproducible interdisciplinary research. Participation will be capped at 30 individuals.

Scope of topics:

- Acquisition of modern and fossil biological datasets from biodiversity databases, including a discussion of data harmonization and synthesis;
- Data preparation and exploration using the palaeoverse R package, focusing on a worked example that integrates modern and fossil biodiversity data (e.g., using BioDeepTime, GBIF, or iDigBio) in an analysis to cross the gap;
- Data visualization Open and collaborative data science practices, including the FAIR and CARE principles as well as data science tools like GitHub, Quarto, Zenodo, etc.
- Computational paleobiology and programming resources
- Hands-on coding practicum

As we cover each of these topics, we will discuss the integration and visualization of different paleobiological and ecological data types to promote CPEG's interdisciplinary goals.

Workshop 2: Decoding the past: Deep learning for macroevolutionary analyses

Led by: Daniele Silvestro, Torsten Hauße, Juan L. Cantalapiedra, Fernando Blanco, Rebecca Cooper

Date: July 27th 2025, 09:00-17:00

Location: University of Zurich, Central campus, rooms KO2-F-174 and KO2-F-175

Description

Understanding how biodiversity has changed through geologic time and which mechanisms mediate the uneven extinction and diversification of species are central challenges in paleobiology, particularly due to the incomplete nature of the fossil record. Deep learning is a powerful tool that can assist paleontologists in estimating past biodiversity and exploring the different factors that could drive dynamics. In this workshop, we present two new methods based on deep learning: (1) Deep Dive for estimating past biodiversity from fossil occurrence data incorporating spatial, taxonomic, and temporal biases, and (2) birth-death neural networks (BDNN) in PyRate for exploring the differential effects of abiotic and biotic variables on the diversification rates of extinct species without the necessity to include phylogenies in the model. At the end of the workshop, participants will understand the theoretical background of the approaches and be able to run fossil biodiversity analysis, diversification (extinction and speciation) rate estimations, and variable testing over diversification rates using both software packages and will have the necessary tools to customize analyses.

Workshop 3: Improving your communication skills with storytelling

Led by: Soledad De Esteban-Trivigno

Date: July 21st 2025, 10:00 AM (CEST)

Location: Virtual

Description

We have evolved as social mammals with spoken language, and stories appeal to our feelings, which in turn help us to learn. Understanding this is key to improving our communication skills. In this workshop, we will discuss different aspects of presenting your science using different tools drawn from the field of storytelling.

Workshop 4: The individual career: beyond the “job for life” model

Led by: Haris Saslis

Date: July 23rd 2025, 10:00 AM (CEST)

Location: Virtual

Description

Many people think of a career as a linear progression within a field, but careers can be a lot more flexible and diverse than that. We evolve as individuals, and so do our needs, life commitments, priorities, and passions. In this workshop, we will investigate how to build a career that caters to our needs. We will discuss different career models that consider –among others– our values, life-work balance, self-expression, and passions. We will explore how to tune in with ourselves to identify key life and work priorities, and how to align our careers with these evolving priorities.

Field Excursion

The Argovian Middle and Late Jurassic in the quarry Jakobsberg (Jura Cement) at Holderbank.

Led by: Christian Klug, Kristína Kocáková

Date: August 1st 2025, ~08:00 – ~16:00

Program

- 08:00 - Meeting at Platform 32 at Zurich HB (Main station)
- 08:10 – 08:49 - Transport by train to Holderbank AG
- 09:00 – 11:45 - Holderbank fossil collection
- 12:15 – 12:37 - Transport to Lenzburg
- 13:00 – Onwards - Lunch at [Hotel Krone](#)
- Optional: Tour of the [Lenzburg castle](#)
- Transport by train to Zurich

What to bring

Snack for the morning, water or other drinks

Sturdy shoes, hat, sunglasses, sunscreen

Optional: Hand lense, geologic hammer, materials to store collected fossils (zip-lock bags, newspaper, tissue paper)

Important tips

This trip will include a lot of walking, including walking uphill for long periods of time, potentially in quite hot weather. Please make sure you have adequate clothing and bring plenty of fluids.

Description

The former Schümel Quarry near Holderbank, nested in the Jura mountains of Aargau canton, offers a unique insight into the geological history of this mountain range and is often described

as a geological open-air museum. The site exposes a well-preserved sequence of Jurassic marine sediments, deposited in an epicontinental marine basin of moderate depth probably ranging from fair weather wave base to 300 meters depth. These strata, ranging from the Bajocian to the Oxfordian, show clear temporal facies changes, from cross-bedded condensed limestones with ooids to marl-rich limestones, reflecting shifting depositional environments over time. Bathonian and Callovian marl layers are particularly rich in ammonites, while the Oxfordian marls and limestones contain diverse assemblages of cephalopods, including both ammonites and belemnites, along with other macrofossils. The Birmensdorf Member particularly contains abundant calcareous sponges, brachiopods, and ammonites. Sea urchins and shark teeth may also be found. This site provides an excellent opportunity to study Jurassic sponge meadow development, faunal diversity, and sedimentary facies variation in a relatively small geographic area.



Photo: Amin El Fassi El Fehri

Student events

Led by: Lucia Snyderman

Roundtable Lunch

Date: July 29th 2025, 12:30 - 13:30

Location: University, KOL building, Lichthof Süd

Description

Students, postdocs, and professionals working in or interested in conservation palaeobiology are encouraged to network during a formal roundtable lunch organised by the [CPN](#) student panel. Professionals will introduce themselves and their research and postdocs and students will rotate tables to engage in a variety of discussions.

Informal dinner

Date: 30th of July 2025

Time: 18:00

Description

There will be an informal picnic at the [Polyterrasse](#), a relaxed outdoor space perfect for casual chats and connecting with fellow students and postdocs. This is a BYO (Bring Your Own) event—please bring your own food and drinks. It's a great opportunity to unwind and meet new people in the CPB community. No registration is required—just show up and enjoy the evening.

SPONSORS



**Universität
Zürich**^{UZH}

UZH
science

UZH
Graduate
Campus



**Schweizerischer
Nationalfonds**

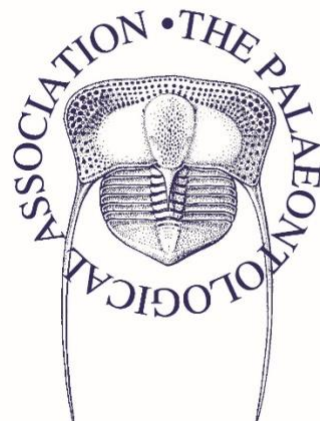
UZH alumni



**Kanton Zürich
Baudirektion**



Stadt Zürich



PROGRAM

Schedule of presentations and other activities

*Presentations eligible for the Student/Postdoc Best Oral Talk Award

**Presentations eligible for the Student/Postdoc Best Lightning Talk Award

Sunday, July 27, 2025

08:00-09:00	Registrations <i>Natural History Museum</i>	
09:00-17:00	Workshop 1: Building open data science skills in paleobiology and ecology <i>KO2-F-152</i>	9
09:00-17:00	Workshop 2: Decoding the past: deep learning for macroevolutionary analyses <i>KO2-F-174, KO2-F-175</i>	10
10:30-11:00	Coffee Break <i>Lichthof Nord</i>	12:30-13:30 Lunch Break <i>Lichthof Nord</i>
		15:30-16:00 Coffee Break <i>Lichthof Nord</i>

Monday, July 28, 2025

08:00-09:00	Registrations, poster set up, tea and coffee <i>Natural History Museum</i> Presentation upload <i>KO2-F-180</i>	
09:00-09:05	Welcome address and opening remarks Kocáková Kristína <i>KO2-F-180</i>	
Session 1	Evolutionary Dynamics and Diversification Patterns Session Chairs: Blanco Fernando and Godoy Pedro <i>KO2-F-180</i>	Page number ↓
09:05	Keynote: Leveraging AI to understand past and present biodiversity dynamics Silvestro Daniele	31
09:50	*Addressing cryptic diversity in crocodylian diversification dynamics analysis Darlim Gustavo & Höhna Sebastian	49

10:05	*Breaking the code of diversification: deciphering 60 million years of large herbivore evolution through unsupervised neural networks Blanco Fernando et al.	40
10:20	**Regional and Global Drivers of Mesozoic Dinosaur Diversification Heath Joel A. et al.	65
10:25	**Rise, demise, and replacement: The evolutionary history of Cenozoic South American mammals Pino Kateryn et al.	90
10:30	Coffee Break and Poster Session <i>Natural History Museum</i>	
11:00	*Invasion and Interaction: Diversity shifts in the Nashville Basin during the Late Ordovician Richmondian Invasion Kundladi Shymah Beegam et al.	73
11:15	*Ontogeny and Population Structure of the Early Jawless Fish <i>Protaspis</i> (Heterostracan) from the Devonian Period Okabe Nanako et al.	87
11:30	Occupancy and extinction dynamics in Phanerozoic bivalves Hauffe Torsten et al.	65
11:45	*Evaluation of the third law of paleobiology in large herbivorous mammals Anjos Samuel A. A. et al.	36
12:00	*Extinction patterns in sloths are explained by life history traits, not phylogeny Landim Fernanda D. P. et al.	74
12:15	**The Impact of Tip Age Distribution on Reconstructing Trait Evolution Using Phylogenetic Comparative Methods Gearty William et al.	62
12:20	**Are ecological and dental traits conserved along the shark tree of life? Williams Lewis et al.	109
12:25	Low diversity in semicircular canal shape mirrors the reduced genetic variation of Late Pleistocene Neandertals. Urciuoli Alessandro et al.	106
12:30-13:30	Lunch Break and Poster Session <i>Natural History Museum</i>	
Session 2	Trophic Ecology and Ecological Interactions Session Chairs: Sánchez-Villagra Marcelo R. and Shipley Amy E. K02-F-180	Page number ↓

13:30	*The Lost World: Building Food Webs for Paleo Communities Strydom Tanya et al.	103
13:45	*Dietary partitioning and ecosystem structural shifts revealed by dental microwear in faunivorous megatheropod dinosaurs during the Cretaceous Morrison Cassius et al.	83
14:00	Ecological dynamics and conservation paleobiology implications of <i>Thylacoleo carnifex</i> extinction in Australia DeSantis Larisa et al.	52
14:15	Prehistoric archives provide evidence for a cascading effect of predator loss in Caribbean reef fish communities O'Dea Aaron et al.	86
14:30	*From extirpation to reintroduction: investigating the trophic ecology of the Dalmatian pelican (<i>Pelecanus crispus</i>) in England using stable isotopes Snyderman Lucia S. et al.	102
14:45	The evolution of ecosystem and Earth system engineering Lyons Kathleen S. et al.	77
15:00	*Are introduced species appropriate ecological substitutes for Pleistocene megafauna? (virtual) Carrasco Thayara S. et al.	44
15:15	Coffee Break and Poster Session <i>Natural History Museum</i>	
16:00	**Small fossils, big insights: mites and ecological interactions preserved in amber Arce Sofía I. et al.	37
16:05	**264 North American Trophic Networks through the Cenozoic and the Future of the World's Food Chains Bateman Louis-Philippe et al.	39
16:10	Compound-specific stable isotopes of amino acids reveal ecology of planktic foraminifera species (virtual) Doherty Shannon C. et al.	57
16:15	Keynote: Deep-time ecology and evolution of dietary adaptations through chemical fingerprints (virtual) Tejada Julia	34
17:30- 20:30	Icebreaker and poster session <i>Natural History Museum</i>	

Tuesday, July 29, 2025

08:00- **Tea and coffee**
09:00 *Lichthof Nord*
Presentation upload
KO2-F-180

Session 3 **Extinctions and Recovery**
Session Chairs: Kocáková Kristína and Williams Lewis
KO2-F-180

Page
number
↓

09:00	Keynote: Using ecology to unlock the secrets of early animal evolution Mitchell Emily	33
09:45	*Causes and consequences of a marine megafaunal extinction Shipley Amy E. et al.	98
10:00	The differing response of carnivores to the terminal Pleistocene extinction Smith Felisa A. et al.	101
10:15	Pathologies, Inbreeding, and Extinction: On the dwindling populations of <i>Smilodon fatalis</i> of the La Brea Tar Pits Schmökel Hugo et al.	97
10:20	Neotropical freshwater fish faunal extinction and diversification in the Neogene Sánchez-Villagra Marcelo R. et al.	94
10:25	Neotropical lungfish and bonytongues: the fossil record of geologically resilient and currently endangered clades Carrillo-Briceño Jorge D. et al.	45
10:30	Coffee Break <i>Lichthof Nord</i>	
11:00	*Snake diversification rates estimated from occurrence data reveal a significant impact of the K-Pg extinction event on the group Karam Gama Gabriela et al.	71
11:15	A Tale of Two Paleocommunities: Functional variation after the Permo-Triassic mass extinction Dineen Ashley A. & Roopnarine Peter D.	56
11:30	*The impact of Permian–Triassic mass extinction on marine trophic web structure Karapınar Baran et al.	71
11:45	*Ecosystem Recovery Following the Permo-Triassic Mass Extinction Nicholls Annabel L. et al.	86

12:00	**A Taxonomic Distinctness Approach to Macroevolutionary Dynamics of Bivalve Recovery in the Triassic Suarez M. Gabriela & Hautmann Michael	103
12:05	Spatial restructuring of bivalve diversity through the last mass extinction at the Cretaceous-Palaeogene boundary Cooper Rebecca B. et al.	47
12:10	Remarks and Invitation (virtual) Transmitting Science	
12:15- 13:30	Lunch Break <i>Lichthof Nord</i> Student Roundtable Lunch <i>Lichthof Süd</i>	12
Session 4	Biodiversity Patterns and Biogeography Session Chairs: Hauffe Torsten and Carrillo Juan D. <i>K02-F-180</i>	Page number ↓
13:30	Keynote: Climate impacts on terrestrial tetrapods in deep time Dunne Emma	31
14:15	*Future paleontologists will detect current mammal Latitudinal Biodiversity Gradient (virtual) Galván Sofia et al.	61
14:30	*Occupancy modelling as a novel approach for conservation palaeobiology Dean Christopher D. et al.	50
14:45	*Geographical patterns in the diversity of small mammal species in mainland Spain related to contemporary climate and its potential use for palaeoecological inferences. Pacheco-Scarpitta Rachel V. et al.	88
15:00	Climate velocity and extinction in ancient and modern communities Shipley Benjamin R. et al.	99
15:05	**Bivalve body-size and geographical range variability: a long-term view on temperature effects (virtual) Montariol Coraline et al.	83
15:10	Cephalopods as ecosystem engineers Klug Christian et al.	72
15:15	**Functional Ecology of the Dorsal Sail in <i>Spinosaurus</i>: From Ornament to Utility (Adaptive Significance) Saraf Mihika	96

15:20	**Functional trade-offs and innovation shape the adaptive landscape of aquatic mammal feeding Park Travis <i>et al.</i>	88
15:25	Coffee Break <i>Lichthof Nord</i>	
16:00	*Biome Conservatism in Northern Hemisphere Tree Clades Yang Gengchen <i>et al.</i>	110
16:15	*Mammalian habitat specialization in a phylogenetic context Galli Emilia <i>et al.</i>	60
16:30	*The importance of savannas in the colonization of open environments during the ruminant evolution Quesada Álvaro <i>et al.</i>	92
16:45	**Climate Availability as an Attractor for Miocene Mammal Diversity Accumulation Pacheco Coelho Marco Túlio <i>et al.</i>	46
16:50	The biogeography of the Great American Biotic Interchange Carrillo Juan D. <i>et al.</i>	44
16:55	The local-scale spatial structure of immigrants during the Great American Biotic Interchange Luan Moldan Motta & Quental Tiago B. (presenter Quental Tiago B.)	84
17:30-19:30	Guided walking tour of Zurich	

Wednesday, July 30, 2025

08:00-09:00	Tea and coffee <i>Lichthof Nord</i> Presentation upload <i>KO2-F-180</i>	
Session 5	Conservation Paleobiology and Historical Ecology I Session Chairs: O'Dea Aaron and Saupe Erin <i>KO2-F-180</i>	Page number ↓
09:00	Keynote: Revealing past transformations in marine social-ecological systems from historical sources Thurstan Ruth	34
09:45	*Exploring the historical ecology of the Southern Central American Pacific Coast and its conservation implications (virtual) Cybulski Jonathan D. <i>et al.</i>	47

10:00	Using the (sub)fossil record of the Australian Anthropocene to inform biodiversity conservation Louys Julien & Boivin Nicole	77
10:15	**Palaeoecological perspectives on Mountainous vegetation succession and land-use in the Peloponnese (southern Greece) over the last millennium (virtual) Vasileiadi Grammatiki et al.	107
10:20	**History's Wild Ride: Zoological Baselines Through Time in the Bear River Range (virtual) Dunn Auriana et al.	58
10:25	Crossing the Gap to Help Restore Indigenous Socio-Environmental Systems in the Bear River Basin, USA Codding Brian F. et al.	45
10:30	Coffee Break <i>Lichthof Nord</i>	
11:00	*Using paleoecology to explore resilient lifeways in the face of abrupt climate change Landrum Madeleine M. et al.	74
11:15	Conservation-led palaeoecology: lessons from practitioners to improve accessibility and value to conservation practice (virtual) Siggery Benjamin et al.	100
11:30	Leveraging the past to strengthen conservation stories Jaleigh Q. Goben et al. (presenter Dietl Gregory P.)	54
11:45	Securing the Future Through the Past: Analysing Conservation Paleobiology in South America (virtual) Arboitte de Assumpção Anna Clara & Ritter Matias	36
12:00	Addressing the Gap between a place and its Paleontological-Ecological record: Case Study Bahamas (virtual) Davis Ancilleno O.	50
12:15	**A ~1,200 year record of common eider population trends in the Eastern Canadian Arctic (virtual) Lau Katie Hong Kiu et al.	68
12:20	**Disentangling the seabird nesting history of Green Island in Witless Bay Ecological Reserve, NL using paleolimnology (virtual) Mack Elizabeth et al.	79
12:25	**Do oryx fit in? An unintentional test case of ungulate rewilding in New Mexico (virtual) Hedberg Carson P. et al.	66

12:30- 13:30	Lunch Break <i>Lichthof Nord</i>	
Session 6	Conservation Paleobiology and Historical Ecology II Session Chairs: Albano Paolo G. and Pimiento Catalina <i>KO2-F-180</i>	Page number ↓
13:30	Keynote: Using mechanistic biodiversity models to navigate the paleoenvironmental–ecological–evolutionary gap Hagen Oskar	32
14:15	*Using species distribution models to assess faunal extinction risk in the past Lazagabaster Ignacio A. et al.	75
14:30	*Understanding the causes and chronology of local extinctions of the Cuban crocodile (<i>Crocodylus rhombifer</i>) across the Holocene Caribbean to inform its future conservation Bhardwaj Lock Sachin et al.	76
14:45	*Climate-proofing’ lion conservation by integrating modern and palaeontological data in forecasts of habitat suitability. Pavey Thomas et al.	90
15:00	The Llamara Salt Flat Tamarugo (<i>Strombocarpa tamarugo</i>) Population: A Refuge Under Millennial and Contemporary Global Change Díaz Francisca P. et al.	53
15:15	**Dispersal Syndrome and Climatic Niches of Holocene and Late Pleistocene Birds Villar Daniel A. et al.	107
15:20	**Back to the Future: The historical distribution of the Eurasian lynx (<i>Lynx lynx</i>) in the Iberian Peninsula (virtual) Barrocal Afonso et al.	38
15:25	Coffee Break <i>Lichthof Nord</i>	
16:00	*Effects of long-term environmental changes and human impacts on the functional diversity of molluscan nearshore communities of the Po-Adriatic System (Italy) Schweigl Lukas et al.	97
16:15	*Emergence of a megacity and its impact on shallow marine benthic ecosystem: A case study from Mumbai, India Dahakey Avinash & Chattopadhyay Devapriya	48

16:30	Combining Environmental Monitoring and the Fossil Record to Support Coral Reef Management in the East Portland Special Fishery Conservation Area, Jamaica (virtual) Williams Claire M. et al.	108
16:45	Tracking refugee species in forests with carbon stable isotopes: implications for conservation Bocherens Hervé	40
16:50	Hermann's tortoise (<i>Chersine hermanni</i>) from Cueva de la Buena Pinta (Middle to Late Pleistocene; Pinilla del Valle, Spain): Palaeoecological Insights and Conservation Implications (virtual) Marquina-Blasco Rafael et al.	81
16:55	**A dhole's tale: using the Pleistocene fossil record of the dhole (<i>Cuon alpinus</i> , Pallas 1811) to understand modern threats and future conservation challenges Mills Mollie et al.	82
17:30-19:30	Informal gathering and networking <i>Polyterrasse, ETH Zurich Building, Leonhardstrasse 34, 8001 Zürich</i>	

Thursday, July 31, 2025

08:00-09:00	Tea and coffee <i>Lichthof Nord</i> Presentation upload <i>KO2-F-180</i>	
Session 7	Biotic Responses to Environmental Change Session Chairs: Cantalapiedra Juan L. and Dillon Erin <i>KO2-F-180</i>	Page number ↓
09:00	Keynote: To see the forest for its leaves: Evolution, extinction and ecology of Neotropical forests in deep (and recent) time (virtual) Carvalho Mónica	31
09:45	Spatiotemporal Dynamics of Mollusk Communities in Response to Emergence of the Isthmus of Panama Godbold Amanda et al.	62
10:00	*Patterns of intrinsic vulnerability to range shift and extinction Pliocene to present in northeastern Atlantic bivalves. Gale Sarah C. et al.	60
10:15	Slimehead size through time: testing the temperature-size relationship in Late Cretaceous Trachichthyidae (virtual) Griffiths Chloe V. et al.	64

10:20	**Establishing a Late Cretaceous baseline for present rates of biodiversity change with the fossil record of Dinosaur Provincial Park, Alberta, Canada Demers-Potvin Alexandre V. et al.	52
10:25	Environmentally-suppressed speciation, not higher extinction, emptied the megaherbivore niche in Africa Cantalapiedra Juan L. et al.	42
10:30	Coffee Break <i>Lichthof Nord</i>	
11:00	*Tracking sharks' responses to climate disturbances on coral reefs over millennia in the Panamanian Pacific Dillon Erin M. et al.	55
11:15	*Coral reef refugia through time: Insights from the fossil record Dimitrijević Danijela et al.	55
11:30	*Tracing coral morphological traits during the Early Paleogene hothouse Mariani Luca et al.	80
11:45	*Functional overlap between Last Interglacial (MIS5e, Pleistocene) 'warm guests' and resident temperate species in the Mediterranean Sea Ye Facheng et al.	111
12:00	Lessons from coral reefs that accrete to the beat of their own drum (virtual) Toth Lauren T. et al.	104
12:15	**Millennial scale reef community shifts in the Spermonde Archipelago, South Sulawesi Hynes Michael G. et al.	68
12:20	The Last Interglacial (MIS5e, Pleistocene) as an analog of future climatic and biotic scenarios in the Mediterranean Sea Albano Paolo G. et al.	35
12:25	**Before and After Glaciation: Isotopic Insights from Antarctic Peninsula Molluscan Communities Dutta Saurav et al.	59
12:30-13:30	Lunch Break <i>Lichthof Nord</i>	
Session 8	Fossil Record Bias and Methodological Advances Session Chairs: Allen Bethany and Cooper Rebecca <i>KO2-F-180</i>	Page number ↓

13:30	*Plotting on possible Earths: deep time and future geography Dowding Elizabeth M. et al.	58
13:45	*Characterizing interaction and coexistence in clades and assemblages in deep time Nakamura Gabriel & Quental Tiago	85
14:00	*A Recommender Systems Approach to Estimating Population Densities in Fossil Faunas Parker Abigail K. et al.	89
14:15	*Space-for-time substitution depends on ecological and spatial scales Rillo Marina C. et al.	93
14:30	*Information loss in the fossil record (virtual) Matamala-Pagès Marta et al.	82
14:45	*Environmental Controls on the Depositional Resolution of the Stratigraphic Record Hohmann Niklas & Jarochowska Emilia	67
15:00	Testing hypotheses on the fossil record in silico: stratigraphic forward models of carbonate environments (virtual) Jarochowska Emilia et al.	70
15:05	How well does the fossil record represent key biodiversity metrics? A test of palynological data as an archive of vegetation phylogenetic diversity Jardine Phillip E.	69
15:10	**Weak support for ergodic processes in fossil mammal community structure in Western Europe Rowe Joshua M. & Louys Julien	93
15:15	**Morphometric and spatial analyses of <i>Charniodiscus</i> from the Ediacaran of Newfoundland, Canada Buma-at Princess et al.	41
15:20	Using archaeological data to map parasite diversity throughout Holocene De Baets Kenneth & Vanadzina Karina	51
15:25	**Decoding the secrets of cave bear behaviour using ancient DNA Caldwell Alice et al.	42
15:30	Coffee Break <i>Lichthof Nord</i>	
16:00	Correcting marine community composition estimates from biological sedimentary archives using paleontological and ecological-derived sampling methods (virtual) Sibert Elizabeth C.	100

16:15	Live-dead comparisons of the marine benthos suggest that fossil assemblages archive trophic information with high fidelity Tyler Carrie L. & Kowalewski Michal	105
16:30	Same variables, different results: the importance of sensitivity analyses in deep-time evolutionary studies Godoy Pedro L.	63
16:45	The impact of fossil biases on phylogenetic inferences: a simulation approach using mammals (virtual) Sotelo Graciela et al.	102
17:00	Closing remarks and prizes announcement Pimiento Catalina	

Friday, August 1, 2025

08:00-19:00	Field trip to Holderbank and Lenzburg	9
-------------	--	---

Poster presentations

Monday, July 28, 2025

**Posters eligible for the Student/Postdoc Best Poster Award*

Poster Number ↓		Page number ↓
1	Systematics and Paleoecology of New Mammalian Remains from the Middle Siwalik Deposits of Northern, Pakistan Amanullah Hamza et al.	113
2	Systematics and Paleoclimate of Terrestrial Mammalian Fauna from the Late Miocene (11.2 – 3.58 Ma) Siwalik Deposits of Pakistan Ameen Muhammad et al.	114
3*	Deep-time extinction and diversity patterns of <i>Crocodylia</i> indicate high susceptibility of the clade to environmental changes Annes Ana Clara M. G. et al.	114
4*	Small Carnivores and Human Impact: Tracing Adaptations from Deep Past to Future Baumann Chris	115
5	Small bodied mammals show more constraint in their jaw ecomorphologies than large bodied mammals Benevento Gemma L. et al.	116

6*	Plant-insect response to disturbance in two modern forests provide insight into deep-time forest responses in elevated global temperatures Bugos Beatrice V. et al.	116
7	Piecing Together the Past: Harnessing AI for Dinosaur Fossil Reconstruction Busso Juan Pablo	117
8*	Age-Dependent extinction in Carnivora: exploring the role of species pools as adaptive zones and ecological assemblages. Calderón del Cid Carlos & Quental Tiago	118
9	How many characters are needed to reconstruct a phylogeny? Capobianco Alessio	118
10	Sloths (<i>Phyllophaga</i>) from the Urumaco Neogene sequence of Venezuela - the challenge of diversity estimates in view of biased preservation of skeletal parts Carlini Alfredo Armando et al. (presenter Sánchez-Villagra Marcelo R.)	119
11*	Ediacaran phylogenetic community analyses Chang Shujie et al.	120
12*	Where the shuck did the oysters go? A gap in the Neogene oyster record Chilcoat Gwyneth & Hill Tessa	120
13*	Open Palaeontology – a community-driven diamond open access journal with preregistration Drage Harriet B. et al.	121
14*	Experimental Fluid Dynamics: validating Computational Fluid Dynamics palaeoecological simulations Drage Harriet B. et al.	122
15*	Can ecological features predict the quality of the Carnivoran fossil record? Faria Thaís & Quental Tiago	123
16*	The phylogenetic signal of extinction through the rise and fall of early vertebrates – field of bullets or clustered strike? Flannery-Sutherland Joseph et al.	123
17	Refined taxonomy and chronology to understand faunal changes and extinction: New investigations on megamammals from the Argentinean Pampas and the historical Roth collection Forasiepi Analía M. et al.	124

18*	New insights on Cruziana ecology during the Early Ordovician Fuertes Murciego Inés et al.	125
19	The South American rat-kangaroo <i>Argyrolagus</i> (<i>Marsupialia</i> , <i>Argyrolagidae</i>): Paleoecological reconstructions based on CT and new fossils from the Pliocene of Argentina Gaillard Charlène et al. (presenter Forasiepi Analía M.)	125
20	Reconstructing Late Miocene freshwater ecosystems at Toros-Menalla (Chad), through aquatic vertebrate paleocommunities study Gardin Axelle et al.	126
21*	rredlist 1.0: an updated R client for the IUCN Red List API Gearty William	127
22*	Interspecific competition in deep-time: a new species-level approach Gonçalves-Neto Salatiel et al.	127
23	Ecomorphological diversity in Cambrian rhynchonelliformean brachiopods from the middle Cambrian of north Spain. González-Cloquells Alejandro & Esteve Jorge	128
24	A tale of cities: cylindrical enrolment in the Cambrian and Ordovician trilobites González-Cloquells Alejandro et al.	129
25*	Australian Veneridae (<i>Mollusca: Bivalvia</i>): Palaeoclimate change, future climate impacts; exploring morphological shifts linked with environmental change in deep time. Gray Michelle et al.	129
26	A new fossil insect fauna of the northern neotropics (Pliocene, San Gregorio Formation, Venezuela) Guerrero Edmundo (presenter Sánchez-Villagra Marcelo R.)	130
27*	Refining the use of oxygen isotopes of southern hard clam (<i>Mercenaria campechiensis</i>) shells as archives for paleoclimatic reconstructions. Hardin Alizé M.	131
28*	Elucidating diversity dynamics in Cenozoic marine tropical hotspots Jones Lewis A.	131
29	Palaeoverse: a community-driven R package to support palaeobiological analysis Jones Lewis A.	132
30	The Mio – Pliocene Tragulids (<i>Mammalia</i>) from the Siwaliks of Pakistan Khan Muhammad Akbar	133
31*	Past and present climate change effects on mesophotic benthic communities in the Central Mediterranean Kiani Harchegani Farkhondeh & Micallef Aaron	134

32*	Does spatial range determine the longevity of shark species? Kocáková Kristína et al.	134
33	Impacts of Environmental Change on Pleistocene and Holocene Animal-Sediment Interactions, Willapa Bay, Washington, USA LaGrange Rao Maya T. et al.	135
34*	Reinterpreting the affinity of <i>Retidiporites magdalenensis</i> : evidence of extinction in the fossil record. León-Carreño Mauricio	136
35*	Morphometric analysis with quantitative measurements of fairy shrimps reveals size differences between fossil and extant species and indicates different feeding strategies. Mahdipour Elham et al.	136
36*	Gone in the blink of an eye: the effects of rock-weathering rates in the preservation of Cambrian acritarch and carbonaceous microfossils Martínez-Benítez Blanca et al.	137
37*	Unravelling the ecology of aquatic turtles from the Late Jurassic of Europe through stable isotope analysis Mazier Chloé et al.	138
38*	The past, present, and future of the Indigenous maize farming niche in the American Southwest Medina Ishmael D. et al.	138
39*	Ecological drivers of cranial morphological evolution in equids Menéndez González Iris et al.	139
40*	Where the wild cats aren't Mills Mollie et al.	140
41*	Climate's impact on the biodiversity patterns of <i>Diplodocoidea</i> during the Jurassic-Cretaceous transition Órfão Joana et al.	140
42*	Oxygen controls lanternfish growth across the Isthmus of Panama: Insights from geohistorical otolith assemblages Pallacks Sven et al.	141
43	Identification of environmental parameters through stable isotopes in Quaternary and present continental mollusc assemblages from Uruguay. Pastrana Fiorella et al.	142
44*	Smear slide analysis of lake sediments to evaluate impacts of humans on eight lakes on the Lac du Flambeau Reservation in Northern Wisconsin, USA Patel Saheli et al.	142

45*	Utilising the archaeological record to create long-term biodiversity baselines for declining UK bird populations: Enhancing conservation and ecological understanding. Pittard Bethany E. et al.	143
46*	Spatiotemporal Phylogeography of the Endangered African Wild Dog Ramage Amelia et al.	144
47	Advancing Conservation Paleobiology in South America: Teamwork, Perspectives, and Hurdles Ritter Matias et al. (presenter Godoy Pedro)	145
48*	Diversity of temperate and tropical molluscs across the Mediterranean Sea during the Last Interglacial (Late Pleistocene, MIS5e) Saha Ranita et al.	146
49*	First Coleoptera fossil records from Lithuania: Late Glacial paleoenvironmental reconstructions from beetle remains Schafstall Nick et al.	146
50	Some Like it Hot: Examining Thermal Tolerance at Extreme Body Size Schroeder Katlin & Hull Pincelli	147
51*	Can polymorphism-aware phylogenetic models improve inference with discrete morphological data? Sexton Walker & Höhna Sebastian	147
52*	Extinction patterns of marine turtles throughout the Mesozoic and Cenozoic: insights for Conservation Biology Silva Jorge L. R. S. et al.	148
53*	Long tails and no eiderdown: paleontological research reveals different Quaternary distributions of North Sea ducks van der Meer Martijn et al.	149
54	Is there a pattern of convergence in the cochlea of river dolphins? Viglino Mariana & Park Travis	149
55	New stories from Ancient Tagua Tagua Lake (Central Chile): What does the vertebrate record tell us beyond the Late Pleistocene? Villavicencio Natalia A. et al.	150
56	The progressive disappearance of fossils and fossils imprints in south western Madagascar: challenges and conservation perspectives Voajanahary Ranaivosoa	108
57*	Past ranges and future habitats: Paleogenomic and ecological insights into <i>Gopherus</i> tortoise conservation Xu Tianyi et al.	110

ABSTRACTS

Invited Keynote Speakers

To see the forest for its leaves: Evolution, extinction and ecology of Neotropical forests in deep (and recent) time

Mónica R. Carvalho^{1,2}

¹University of Michigan, Museum of Paleontology, Ann Arbor, MI, USA

²University of Michigan, Department of Earth and Environmental Sciences, Ann Arbor, MI, USA

Neotropical rainforests are global centres of biodiversity and are major controls on regional climate, hydrology and productivity. These ecological services are highly dependent on numerous factors, including tree composition, canopy structure, and a high complexity of biotic and abiotic interactions that affect forest function. How have rainforest structure and function changed through geological time?

Fossil leaves are essential for understanding the evolution and ecology of rainforests in deep time. Leaves reflect their specific growth conditions, record biotic interactions and can be used to identify natural affinities of plants, proving direct evidence of past forest composition, structure and paleobiology. In this talk we will use fossil leaves to explore how Neotropical rainforests have responded to past and recent ecological perturbations. The Cretaceous-Paleocene leaf record of Northern South America shows how the ecological catastrophe that characterized the end-Cretaceous led to the evolution of Neotropical rainforests. Ecological recovery and diversification characterized the early history of Neotropical rainforests, prompting the establishment of modern terrestrial tropical ecosystems. Recent findings of subfossil leaf deposits in Northwestern Amazonia provide direct evidence of forest communities living in pre-Columbian time and nearly perfect setting to test for consequences of our current ecological crisis. Studying these recent deposits through a paleobiological lens will allow quantifying ongoing ecological responses to recent anthropogenic perturbations, including changes in water and nutrient uptake, community composition and plant-insect interactions.

Climate impacts on terrestrial tetrapods in deep time

Emma Dunne¹

¹Friedrich-Alexander-Universität Erlangen-Nürnberg, GeoZentrum Nordbayern, Erlangen, German

Climate variation is a fundamental control on biodiversity, both in the present day and in the geological past. In the face of the current climate crisis, understanding the long-term impacts of climate change on species diversity and distributions is critical. To achieve this, we must look to the fossil record, our only direct evidence of how species have responded to past environmental events of this magnitude. However, until recently, studies linking past climate to major

evolutionary and ecological patterns in the fossil record has been restricted, such as by using a single global mean variable as a proxy for global climate. Earth system models are simulation the interactions between Earth's spheres that can provide estimates of global climate conditions at much finer scales. By combining advances in computational methods in palaeobiology with outputs from Earth system models, palaeobiologists are now able to investigate climate impacts on deep-time biodiversity more rigorously than ever before. This presentation will focus on how integrating general circulation (palaeoclimate) and climate-biogeochemical models with fossil occurrence and phylogenetic data is providing critical insights into how climate has influenced the diversity and distributions of terrestrial vertebrates during the Mesozoic (approx. 251–66 Ma). In particular, this approach has illuminated the role of climate in the rise of dinosaurs to ecological dominance, the early diversification of pterosaurs, and the evolution of notable evolutionary innovations such as gigantism in sauropods and herbivory in theropod dinosaurs. This integrative approach has broad applications and enormous potential to generate insights into fossil species responses to major climate events similar in magnitude to the current climate crisis (e.g. hyperthermal events), and even bridge methodological gaps between palaeontological and ecological studies.

Using Mechanistic Biodiversity Models to Navigate the Paleoenvironmental–Ecological–Evolutionary Gap

Oskar Hagen¹

¹German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig

Mechanistic biodiversity simulation models provide a powerful framework for integrating paleontological and modern biodiversity data across disparate timescales. By uniting geological records with historical and contemporary observations, these models help us decipher how shifting environments, evolutionary processes, and ecological dynamics drive the generation, maintenance, and erosion of biodiversity over time. They also enable “virtual experiments” or counterfactual analyses that disentangle the relative contributions of climate change, biotic interactions, and trait evolution under specific environmental, ecological, and evolutionary assumptions. In this talk, I will discuss how incorporating paleontological datasets into simulation models can reveal long-term biodiversity trajectories and extinction mechanisms, offering insights that are directly relevant to modern conservation challenges. I will then address some of the ongoing hurdles in model development and show how these models can be scaled to tackle questions in population ecology, biogeography, and community assembly (traditionally explored by ecologists on much shorter timescales). By integrating these approaches, we can begin to unify the theoretical foundations of multiple life science disciplines, paving the way for broader, more collaborative research. Ultimately, we will see how diverse datasets and perspectives from paleontology, geology, climatology, ecology, and evolutionary biology can be harmonized through collaborative efforts supported by mechanistic biodiversity models. This allows researchers to connect empirical evidence with theoretical predictions more effectively, fostering a richer understanding of biodiversity dynamics from deep time to the present.

Using ecology to unlock the secrets of early animal evolution

Emily Mitchell¹

¹Department of Zoology, University of Cambridge

The sudden appearance of animals in the fossil record 580 million years ago, during the Ediacaran time period, after billions of years of microbial life, is one of the most important events in the history of life on Earth. Studying Ediacaran evolution is fraught with difficulties due to uniqueness of Ediacaran anatomies which lack clear Phanerozoic counterparts. However, the preservation of Ediacaran fossils is exceptional, with thousands of organisms preserved where they lived. This exceptional preservation means that we can use a suite of ecological methodologies, normally only used on extant communities to understand the ecology and evolution of the first animals. In order to map out these Ediacaran communities, we laser-scan hundreds of square meters of Ediacaran bedding planes to capture over 30,000 fossils in-situ across from Newfoundland, Canada and Charnwood Forest, UK. Using spatial, Bayesian network and metacommunity analyses, we have started to tease apart Ediacaran eco-evolutionary dynamics, revealing how Ediacaran dynamics shifted from a stochastic start, dominated by clonal reproduction, reduced competition, and limited environmental interactions to more complex dynamics, with niche specialization and strong biotic interactions just prior to the Cambrian.

Leveraging AI to understand past and present biodiversity dynamics

Daniele Silvestro^{1,2,3}

¹Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland

²Swiss Institute of Bioinformatics, Basel, Switzerland

³Department of Biological and Environmental Sciences and Gothenburg Global Biodiversity Centre, University of Gothenburg, Sweden

Throughout the long evolutionary history of life, species of all kingdoms have undergone staggering diversification and faced countless environmental changes and extinction events. Since the great majority of species that lived on Earth have since gone extinct, it is difficult to infer how biodiversity dynamics unfolded over millions of years and yet crucial to understand the fundamental evolutionary processes driving them. Today, with over a million species threatened with extinction, biodiversity is facing unprecedented challenges, urging the need for conservation policies that maximize its protection and sustain its manifold contributions to people. Here we present a suite of new supervised and unsupervised models with applications in evolutionary and conservation paleobiology. Specifically, we show how deep learning models can be used to infer biodiversity dynamics in deep time and predict current extinction risks. We then introduce a reinforcement learning framework to integrate our knowledge about species distribution and ecology and the threats they face to optimize nature restoration toward both biodiversity and climate targets. Coupling artificial intelligence with biological models holds great promise for advancing our understanding of biodiversity and its evolution across time scales, and for contributing to halt human-drive extinctions.

Deep-time ecology and evolution of dietary adaptations through chemical fingerprints

Julia Tejada¹

¹California Institute of Technology, Division of Geological and Planetary Sciences, Pasadena, California, USA

Diet alters genetic expression and regulation (e.g., lactate persistence in dairying populations, resistance/predisposition to chronic diseases) and shapes phenotypic evolution at deep-time scales (e.g., morphoanatomy, brain development, pigmentation). But to fully understand the interplay between resource availability and ecological functions, and the selective pressures influencing morphological and physiological adaptations to diets, we must assess feeding ecologies at paleontological time scales. Nitrogen isotope ratios ($\delta^{15}\text{N}$) of amino acids have proved reliable at tracking feeding behaviors of extant and extinct animals because they record the $\delta^{15}\text{N}$ at the base of the food web (i.e., that of the primary producers) and the trophic position in the same organism. However, the absence of extensive comparative datasets for many animal groups limits the precise identification of feeding categories and the predictive power of this technique. In this talk, I will show how integrating new isotopic measurements and methodologies, along with leveraging recent advancements in instrumentation, is bridging the paleontological-ecological gap, enabling access to geochemical information preserved in previously inaccessible tissues.

Revealing past transformations in marine social-ecological systems from historical sources

Ruth H Thurstan¹

¹Department of Ecology and Conservation, University of Exeter

Historical sources have great potential to enrich our understanding of marine social-ecological dynamics over the past decades and centuries, but these sources remain underutilised. Using examples from popular media, government records, and oral histories, I will showcase the variety and resolution of information that can be gained by analysing a diverse range of historical sources, including the use of (i) maritime charts, government sources and popular writings to reveal the European-wide loss of a once dominant biogenic shellfish reef ecosystem, (ii) newspaper articles and fisher testimonies to uncover the hidden histories of recreational fisheries, and (iii) previously untapped government records and newspaper articles to map the spread and early ecological impacts of bottom trawl fisheries. I will discuss the importance of critically examining such sources to understand and ameliorate potential biases, and the hurdles and opportunities for incorporating this information in marine conservation and management. Historical sources challenge our ingrained perceptions of the health and ‘permanence’ of marine ecosystem structure and functioning observed today, and illuminate our past uses of ocean resources, providing both cautionary lessons and exemplars of sustainable

human–ocean interactions. Historical sources not only place the longevity and scale of human activities into present day context, they reconnect us to our pasts in ways that can be communicated across stakeholder groups, cultures and generations. Historical sources thus present multiple opportunities to re-envision our future relationships with the oceans, moving towards interactions that support and foster healthy marine ecosystems while maximising their benefits to society.

Oral presentations

The Last Interglacial (MIS5e, Pleistocene) as an analog of future climatic and biotic scenarios in the Mediterranean Sea

Paolo G. Albano¹, Facheng Ye¹, Ranita Saha², Marco Taviani³, Silvia Danise²

¹Stazione Zoologica Anton Dohrn, Department of Marine Animal Conservation and Public Engagement, Naples, Italy

²University of Florence, Department of Earth Sciences, Florence, Italy

³National Research Council, Institute of Marine Sciences, Bologna, Italy.

Global warming is causing numerous direct impacts on biodiversity. First, it is causing major poleward shifts in the distribution of organisms. Second, it is facilitating the spread and success of non-indigenous species. Third, it is causing biotic attrition in areas where climate-driven eradications are not compensated by species from more thermally suitable species pools. Forecasting the whole array of consequences of global warming on marine biodiversity is extremely difficult due to the idiosyncratic response of species to warming that will also cause the assembly of novel biotic communities. The fossil record of past analogs – warm climate intervals in the Earth’s history – represent the only observational source of information for how the climate system operates in a state much warmer than the present. Similarly, past biotic assemblages represent windows into how communities responded to warming, enabling predictions under future climate scenarios. The warmest interval of the Last Interglacial (MIS5e, Pleistocene epoch), ca 135–116 ka, represents one of the most recent analogs in geologic time to what is expected to be the climate of the coming decades. This stage possessed a coastal geography and marine species diversity very similar to the present, enabling highly meaningful comparisons of taxonomic and functional composition and turnover. By building a multi-temporal envelope of a representative set of recent and fossil molluscs that used to occur in the Mediterranean during the Last Interglacial but then regressed into the tropical belt during the following cooling, we showed that tropical Atlantic species may soon reinvade the basin, highlighting the importance of the fossil record to predict future scenarios. The potential in the use of analogs may require more conceptualization, consideration of differences (e.g. causes of climate forcing, lack of human footprint), and quantification of uncertainties, a promising avenue for research bridging paleontology and ecology.

Evaluation of the third law of paleobiology in large herbivorous mammals

Samuel A. A. Anjos¹, Juan L. Cantalapiedra², Tiago B. Quental¹

¹University of São Paulo, Department of Ecology, São Paulo, Brazil

²Museum of Natural Sciences, Madrid, Spain

Globally, species richness results from the balance between speciation and extinction rates, and at smaller spatial scales, also from the immigration rate. Previous studies suggest a strong correlation between average speciation and extinction rates, where lineages with higher speciation rates tend to have higher extinction rates. This pattern has been termed the "Third Law of Paleobiology" or "Stanley's Rule." Despite the high reported correlation (e.g., $r = 0.973$, Pearson), the formulation of this "law" presents conceptual and methodological limitations, particularly due to supra-specific analysis and the temporal scale of analysis, where the association between rates is expected by definition. This project aims to reassess this law, considering the limitations of previous studies. We will use fossil data from large herbivorous mammals (at the species level), applying a hierarchical Bayesian approach and phylogenetic comparative methods. The hypothesis of correlation between rates will be tested across different time windows, reflecting different diversification dynamics (radiation, equilibrium, and decline), both at global and regional scales. Preliminary results analyzing 84 families at the global scale show a significant positive correlation between rates in all windows. As expected, this correlation is very high in equilibrium ($r = 0.87$, Spearman) but still present in the radiation ($r = 0.61$, Spearman) and decline phases ($r = 0.78$, Spearman). These findings suggest that, even after accounting for important methodological limitations, the Third Law of Paleobiology remains valid. Future analyses will explore further methodological limitations, the geographic influence and the impact of immigration.

Securing the Future Through the Past: Analysing Conservation Paleobiology in South America

Anna Clara Arboitte de Assumpção¹, Matias do Nascimento Ritter^{1, 2, 3}

¹Universidade Federal do Rio Grande do Sul, Programa de Pós-Graduação em Geociências, Porto Alegre, Brasil

²Universidade Federal do Rio Grande do Sul, Centro de Estudos Costeiros, Limnológicos e Marinhos, Imbé, Brasil

³Universidade Federal do Rio Grande do Sul, Centro de Estudos de Geologia Costeira e Oceânica, Instituto de Geociências, Porto Alegre, Brasil

In 2002, driven by the interdisciplinary perspective of taphonomy and the need for long-term data in conservation, the field of conservation paleobiology emerged. South America, with its rich yet vulnerable paleo-biodiversity and lack of long-term monitoring programs, holds the potential to become a leading center for this field, contributing meaningfully to global conservation efforts. While conservation paleobiology has grown globally, the contributions of Brazil and South America, especially in the early stages, are often overlooked in English-language publications. Analysis of research articles in the Web of Science (1987-2023, using a

broad search term beyond "conservation paleobiology") and Scopus (1996-2023, restricted to "conservation paleobiology") reveals the underrepresentation of South American research in this discipline. Out of 2,927 articles in the Web of Science, only 10% were from South American countries, while in Scopus, just 5.5% of 181 articles were regionally affiliated. Within South America, Brazil leads with the highest number of publications, contributing to 50% of the region's output in the Web of Science and 66.7% in Scopus. Additionally, according to Scopus, the National Council for Scientific and Technological Development (CNPq, Brazil) ranks third among the funding agencies for these studies. These findings highlight a significant disparity in research output between South America and more developed countries. Furthermore, most authors and co-authors in conservation paleobiology are geoscientists, both globally and locally. This concentration of research in developed countries and the dominance of geosciences pose challenges, such as underutilizing geohistorical data and a gap between theory and practice. Future research should integrate conservation perspectives and better align with societal and environmental needs. With continued growth, conservation paleobiology in South America can enhance global conservation efforts and contribute to sustainable solutions for future generations.

Small fossils, big insights: mites and ecological interactions preserved in amber

Sofía I. Arce¹, Yanzhe Fu¹, Patrick Müller³, Joachim T. Haug^{1,2}, Carolin Haug^{1,2}

¹ Ludwig-Maximilians-Universität München, Faculty of Biology, Zoomorphology, Großhaderner Str. 2, 82152 Planegg-Martinsried, Germany

² Geo-Bio Center, Ludwig-Maximilians-Universität München, Germany

³ Independent Researcher, 66482 Zweibrücken, Germany

Biosyninclusions, or multiple specimens preserved in a single amber piece, provide insights into microhabitat use, food webs, and ecological interactions in deep time. Clear cases of animal-to-animal interactions are rare and must be interpreted cautiously, as amber formation can distort the original positioning of fossilised specimens. Although often overlooked due to their small size, mites offer a unique glimpse into past ecosystems since they frequently appear associated with other organisms in amber pieces. One of the interactions often reported for fossilised mites is parasitism. When considering parasitism *sensu lato*, considering both phoresy (using the host only as a mean of transportation) and parasitism *sensu stricto* (where feeding is involved), this lifestyle seems to be quite widespread among mites. This type of association in mites can be traced back as far as the Carboniferous (ca. 320 million years ago). Here we report findings that involve possible parasitic interactions between representatives of Acariformes and other euarthropodans fossilised in amber. Some of these findings are examples of clear frozen behaviour of parasitism *sensu stricto*, in which larvae of parasitengonan mites are fossilised still attached to their hosts through their mouthparts. We also report a syninclusion in Eocene Baltic amber (ca. 40 mya) in which a possible example of parasitism *sensu lato* is displayed. In this case, three mite specimens, possibly nymphs of astigmatan mites, are in close proximity to a mirid bug, one of which is positioned just beside the leg of their possible host. Additionally, we present a more complex interaction in a piece of Cretaceous Kachin amber (ca. 100 mya), in which more

than 40 heterostigmatan mite specimens that carry sporothecae (organs for storing and transporting fungal spores) are surrounding a possible ground beetle larva. We discuss the potential parasitic and symbiotic interactions between them.

Herbivory through the ages: Applying paleoecological methods to herbaria to investigate modern global change

Lauren Azevedo-Schmidt¹, Emily K. Meineke¹

¹University of California Davis, Entomology and Nematology, Davis, USA

Plant-insect interactions are the focus of much research within paleo and modern ecology because of their importance. Together, plants and insects represent a large proportion of biodiversity and cycle massive amounts of biomass through the terrestrial ecosphere. Due to anthropogenic climate change, many insect taxa are facing unprecedented declines while others flourish. The extent of warming today, and its co-occurrence with other anthropogenic changes, are unprecedented. Even so, the paleo record can provide insights into how we should expect plant-insect herbivore interactions to shift with climate change. Connecting ecological data between modern observations and the fossil record is challenging due, in part, to divergent methodological approaches and temporal extent of research. Bridging the gap between modern and palaeoecological methods is important for understanding how modern and past plant-insect interactions are shaped by 1) the extent to which the temporal resolution was studied and 2) what drives patterns in insect damage and diversity. Here we provide an example wherein we apply palaeoecological methods to herbarium specimens to understand how modern patterns in insect herbivory and insect diversity are shifting today.

Back to the Future: The historical distribution of the Eurasian lynx (*Lynx lynx*) in the Iberian Peninsula

Afonso Barrocal¹, Luís Miguel Rosalino¹, Miguel Clavero²

¹CE3C – Center for Ecology, Evolution and Environmental Change & CHANGE – Global Change and Sustainability Institute, Faculdade de Ciências, Universidade de Lisboa, 1749-016 Lisboa, Portugal

²Estación Biológica de Doñana – CSIC, Departamento de Biología de la Conservación, Sevilla, Spain

The assessment of species distributions is an essential tool for the effective design and implementation of conservation actions. However, anthropogenic activity has drastically altered the range of most species. Therefore, their use in conservation is limited as many species currently present a fraction of their indigenous distribution. The historical and paleontological records are a window into a time when species distributions had not yet been tainted by human activity. In this work, a compilation of historical and fossil occurrences of lynxes in the Iberian Peninsula is presented. This database is used to model the distribution of the Eurasian lynx, one of two lynx species that historically occur in Iberia, to create a distribution baseline for the species. Furthermore, this work presents a multi-modelling framework (i.e., using GLM, GAM, and MaxEnt approaches) that aims to quantify the uncertainty of its predictions, thus increasing

their reliability. It is hypothesized that this lynx species will have a greater probability of occurrence in the Temperate Broadleaf & Mixed Forests biome. This hypothesis is explicitly tested by a binomial GLM that shows a significant positive association between lynx presence and this biome. The availability of prey is also hypothesized to increase the probability of occurrence of this species. Both hypotheses are supported by those variables' importance in the distribution models. All species distribution modelling approaches used predicted that the Eurasian lynx was found in the north and northwest of the Iberian Peninsula during the 19th century. When compared with previous European-wide studies, our best performing modelling approach (GAM) increased in 436 times the estimated suitable area for the Eurasian lynx in the Iberia. This work establishes the first distribution baseline of the species at the Iberian level, and once again highlights the importance of historical and paleontological data for designing quantitative targets for conservation strategies.

264 North American Trophic Networks through the Cenozoic and the Future of the World's Food Chains

Louis-Philippe Bateman¹, Hans C.E. Larsson¹

¹ McGill University, Department of Biology, Montreal, Canada

Trophic networks are an emerging approach to paleocology thanks to their potential to combine biodiversity, species interactions, and ecosystem function. However, few neontological or paleontological studies have studied their long-term evolution, leaving the future of modern networks in the face of climate change and anthropogenic disturbance unclear.

In this study, we reconstruct 264 Cenozoic mammal trophic networks in North America. Our model predicts interactions using matching species traits like body size, broad dietary category, and life habit, and refines these predictions using phylogenetic comparisons. Cross-validation using modern interaction databases shows it predicts most interactions accurately (true skill statistic between 0.75-0.95).

We then track how network properties change over the Cenozoic. We find that connectance, mean trophic level, proportion of omnivores, mean incoherence, and clustering decrease, while proportion of herbivores and mean interaction weight increase over time. Other metrics, such as modularity, mean trophic similarity, mean generality, and proportion of carnivores, are either variable or constant. This suggests that some network properties are constrained while others fluctuate with biotic and abiotic conditions.

Grouping species into guilds based on body size, life habit, and broad dietary category reveals patterns of guild longevity. While some guilds and interactions have persisted through the Cenozoic, median interaction persistence time is only about 4 million years, and 7.5 million years for guilds. Network clusters based on their network properties, guilds, and interactions, reveal the existence of at least three "states": a post-K-Pg extinction recovery state, a warm Paleogene state, and a post-Paleogene cool state. We discuss the factors that mediated these state shifts, including biotic change and climate change.

Finally, we outline the implications of this study for the future of the world's ecosystems. Specifically, we discuss what factors indicative of upcoming state shifts are observable—or not—in today's trophic networks, based on our results.

Breaking the code of diversification: deciphering 60 million years of large herbivore evolution through unsupervised neural networks

Fernando Blanco¹, Torsten Hauffe², Søren Faurby³, Juan L. Cantalapiedra⁴, Daniele Silvestro²

¹The Open University, Milton Keynes, UK

²Université de Lausanne, Lausanne, Switzerland

³University of Gothenburg, Gothenburg, Sweden

⁴Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain

How did the diversity and distribution of present-day species originate? Why have some lineages persisted and diversified while others vanished? What ecological traits and environmental factors shape these evolutionary trajectories? Answering these questions will shed light on the connections between ecological function, extinction, and the persistence of functional systems—key insights to understand current ecosystems and the threats they face. The fossil record offers a unique perspective, allowing us to trace the evolution of species and ecosystems over millions of years, revealing long-term patterns of speciation, extinction, and ecological adaptation. Here, we apply a new birth-death Neural Network (BDNN) model to analyze the diversification dynamics in relation to both biotic and abiotic drivers in a comprehensive dataset of more than 2,600 large herbivore species distributed worldwide and spanning the last 60 million years. Our analysis incorporates 14 functional traits (including 13 dental features and body size), along with temperature, human presence, phylogenetic relationships, carnivore pressure, and herbivore competition, to assess the impact of ecological and environmental change on diversification dynamics. Our results reveal a multifaceted influence of biotic and abiotic factors on large herbivore evolution. Body size and human presence had the strongest effects on extinction patterns, suggesting that larger species were particularly vulnerable, especially toward the end of the Cenozoic, when humans began impacting ecosystems. In contrast, temperature and phylogenetic relationships played a dominant role in speciation dynamics, indicating that climate fluctuations and evolutionary constraints shaped the emergence of new species. These findings highlight the intricate interplay between ecological traits, environmental change, and evolutionary processes that have governed large herbivore diversity throughout the Cenozoic. By integrating deep-time perspectives with novel analytical tools, our study provides crucial insights into the mechanisms that drive biodiversity change, offering valuable context for predicting and mitigating future biodiversity loss.

Tracking refugee species in forests with carbon stable isotopes: implications for conservation

Hervé Bocherens^{1,2}

¹University of Tübingen, Department of Geosciences, Tübingen, Germany

²Senckenberg Centre for Human Evolution and Palaeoenvironment at the University of Tübingen, Tübingen, Germany

Many endangered large mammals have their ranges restricted to forested habitats, and conservation efforts typically focus on preserving these habitats for their benefit. However, human activities are increasingly encroaching on these forests, and climate change is causing rapid ecological shifts that could affect the suitability of these protected areas for endangered species populations. In light of these challenges, it is crucial to assess whether these forested habitats represent the optimal niche for these species or if they function more as refuges where the species have managed to survive under suboptimal conditions. Species in the latter category may potentially thrive in other habitats from which they have been extirpated. Examining past individuals of such species, as well as fossil members of their evolutionary lineage, can help determine whether forested habitats are a recent development or have historically been the species' core habitat.

Carbon stable isotopic ratios could help identify whether these species are merely surviving in suboptimal habitats. These ratios vary between plants in closed-canopy forests and more open environments, both in tropical and temperate climates. These differences are reflected in the tissues of herbivores through their diet and are preserved in the organic and mineral components of skeletal fossil remains. This provides an opportunity to test hypotheses about the historical habitats of specific species, considering various levels of human interference and changing climatic conditions.

This presentation will explore exemplary studies of Eurasian large herbivores, highlighting the potential of this approach to inform conservation strategies. By understanding that some endangered species of forested habitats may have better chances of long-term survival outside these areas, decision-makers can design more effective conservation plans.

Morphometric and spatial analyses of *Charniodiscus* from the Ediacaran of Newfoundland, Canada

Princess Aira Buma-at^{1,2}, Nile Stephenson^{1,2}, Neil Mitchell³, Jason Head^{1,2}, Charlotte Kenchington⁴, Emily Mitchell^{1,2}

¹University of Cambridge, Department of Zoology, Cambridge, UK

²University of Cambridge, University Museum of Zoology, Cambridge, UK

³Independent

⁴University of Cambridge, Department of Earth Sciences, Cambridge, UK

Ediacaran macrofossils (580-539 Ma) represent the earliest-known complex animals, revealing critical insight into the evolution of life. This study focuses on *Charniodiscus*, an upright, sessile, frondose organism morphologically simpler than the iconic rangeomorphs, enabling the refinement of new quantitative techniques. One of the largest in situ *Charniodiscus* populations occurs within the Main E Surface community in the UNESCO Mistaken Point Ecological Reserve (Newfoundland, Canada). This population can be utilized to explore physical variation across specimens, as well as the spatial distributions of variations within a community. We generated a

photogrammetric map of E Surface and obtained morphological traits by marking up the branching architecture of 116 well-preserved *Charniodiscus* specimens. We used multivariate cluster techniques to identify different morphogroups and to constrain defining physical traits. We then used random labelling analyses to investigate how the spatial patterns of specific characteristics varied across the population, and to identify the spatial patterns of the different morphogroups identified. We find that traits showing distinctive spatial patterns and defined morphogroups are likely to be more ecologically significant than those which vary randomly. Therefore, this novel approach is the first step in elucidating which morphological traits, or combinations of traits, are key drivers of Ediacaran evolutionary dynamics.

Decoding the secrets of cave bear behaviour using ancient DNA

Alice Caldwell¹, Ioana Meleg², Gloria Gonzales-Fortes³, Aurora Grandal-D'Angelade⁴, Johanna L. A. Paijmans¹, Axel Barlow¹

¹Bangor University, School of Natural Sciences, Bangor, United Kingdom

²Babeş-Bolyai University Cluj-Napoca, Romania

³Universitat di Ferrara, Department of Biology and Evolution, Ferrara, Italy

⁴Universidade da Coruña, Instituto Universitario de Xeoloxía, A Coruña, Spain

Since the establishment of the field 40 years ago, ancient DNA has revolutionised our understanding of the evolution and ecology of extinct species. Despite this potential, insights into the behaviour of extinct species has been provided by only a handful of studies. For example, ancient mitochondrial DNA has suggested annual homing behaviour in cave bears (*Ursus spelaeus* complex) in northern Spain, which went extinct during the Pleistocene, around 25,000 years ago. This could show mating occurred between populations during the summer, and during winter individuals returned to their natal sites for hibernation and to give birth. However, the idiosyncrasies of mitochondrial evolution in populations makes it difficult to test for this behaviour across all populations. Here, we use whole genome analysis to compare genetic variation in autosomal and sex chromosomes across Europe. We find evidence of female philopatry compatible with homing behaviour, although direct evidence of this specific behaviour remains elusive. Understanding these sex-biased dispersal patterns will allow us to gain a more general and robust understanding of the discrepancies in cave bear movement between sexes within individuals' lifetimes. Our study also highlights the potential and the challenges of using palaeogenomics to uncover the behavioural ecology of extinct species.

Environmentally-suppressed speciation, not higher extinction, emptied the megaherbivore niche in Africa

Juan L. Cantalapiedra^{1,2,3}, Ignacio A. Lazagabaster^{4,5}, Fernando Blanco^{3,6,7}, Torsten Hauffe⁸, Faysal Bibi³, María Ríos⁹, Bastien Menecart^{10,11}, Juha Saarinen¹², Daniele Silvestro^{6,8}, Manuel Hernández Fernández^{13,14}, Oscar Sanisidro²

¹Departamento de Paleobiología, Museo Nacional de Ciencias Naturales, MNCN-CSIC, 28006, Madrid, Spain

- ² Universidad de Alcalá, Department of Life Sciences, 28805, Alcalá de Henares, Madrid, Spain
- ³ Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, 10115 Berlin, Germany
- ⁴ National Research Center On Human Evolution, 09002, Burgos, Spain
- ⁵ Department of Ecology, Evolution & Behaviour, University of Liverpool, CH64 7TE, Liverpool, UK
- ⁶ Gothenburg Global Biodiversity Centre, Department of Biological and Environmental Sciences, University of Gothenburg, 40530 Gothenburg, Sweden
- ⁷ The Open University, Turing Building 310, Walton Hall, Milton Keynes MK7 6AA
- ⁸ Department of Biology, University of Fribourg and Swiss Institute of Bioinformatics, 1700 Fribourg, Switzerland
- ⁹ Department of Earth Sciences, GeoBioTec, Nova School of Science and Technology, Universidade NOVA de Lisboa, Campus de Caparica, 2829-516, Caparica, Portugal
- ¹⁰ Naturhistorisches Museum Basel, 4001, Basel, Switzerland
- ¹¹ Natural History Museum of Lille, 23 Rue Gosselet, 59000 Lille, France
- ¹² Department of Geosciences and Geography, University of Helsinki, FI-00014, Helsinki, Finland
- ¹³ Departamento de Geodinámica, Estratigrafía y Paleontología, Facultad Ciencias Geológicas, Universidad Complutense de Madrid, 28040, Madrid, Spain
- ¹⁴ Departamento de Geología Sedimentaria y Cambio Medioambiental, Instituto de Geociencias (CSIC, UCM), 28040, Madrid, Spain

Diversity crises are complex events shaped by the interplay of abiotic and biotic factors, as reflected in the fossil record. Simplistic, uni-variable approaches to these events often bias our understanding of the mechanisms driving biodiversity collapses. The Plio-Pleistocene decline of megaherbivores, for example, has been primarily attributed to size-selective extinction, neglecting the broader ecological and evolutionary processes involved. To address this, we analyzed the fossil record of ~400 African ungulate species spanning 24 million years, using diversification models based on neural networks. These models disentangle the contributions of environmental change, body mass, and phylogeny to speciation and extinction rates. Our findings reveal that aridification and associated vegetation changes, such as the expansion of C4 plants driven by declining atmospheric CO₂, suppressed the already-low speciation potential of larger-bodied herbivores. Speciation rates exhibited a strong phylogenetic signal, with smaller-bodied lineages proliferating more readily in increasingly arid environments. In terms of extinction, aridification triggered a significant turnover event across ungulate lineages, with smaller species experiencing accelerated extinction rates. However, larger taxa and those with durable dentitions were relatively buffered from this phase of extirpation. These results emphasize that the decline of African megaherbivores was not solely due to size-selective extinction but instead emerged from a multifaceted interplay of environmental disruptions, lineage-specific speciation potentials, and phylogenetic constraints. Ultimately, our study underscores the importance of incorporating multiple correlates of diversity dynamics—such as environmental change, phylogeny, and functional traits—to unravel the complexity of diversity crises. This approach reveals that turnover events involve not only extinction risks but also the suppression or promotion of evolutionary potential, fundamentally reshaping ecosystems over time.

Are introduced species appropriate ecological substitutes for Pleistocene megafauna?

Thayara S. Carrasco¹, Pedro L. Godoy¹

¹Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil

Large herbivores play key ecological roles in terrestrial ecosystems. Consequently, the loss of South American megafauna during the Pleistocene-Holocene transition may have led to drastic changes in biotic interactions, connectivity and stability of food webs, energy flow, and community structure. In this context, some studies suggest that the livestock in Brazilian biomes can be considered a tool for maintaining biodiversity and ecological processes, particularly in the grasslands of southern Brazil. Under the lens of functional diversity, we assessed if anthropogenically introduced species are good ecological substitutes for the extinct megafauna in the Brazilian grasslands. For this, we constructed functional spaces based on traits related to the ecology and life history (diet, habitat, mass, foot posture, and digestive physiology) of each species from the Quaternary of southern Brazil for different temporal scenarios (Pleistocene fauna, native Holocene fauna, and modern fauna). Based on richness metrics, measured as the volume of the convex hull of the first two principal component axes, we observed a reduction of approximately 15% in functional richness of the mammal community after the Late Quaternary extinctions. This loss was partially compensated by surviving and introduced species. However, the functional space of the introduced species is about three times smaller than that of the extinct community. This suggests that introduced species have less diverse functional traits, as they mainly consist of grazing ungulates. On the other hand, it is important to highlight that part of the lost functional space is also compensated by the ecological role of surviving small and medium-sized mammals, most of which have ecological preferences for forests, instead of grasslands. These results have important implications in terms of conservation and ecological restoration, which should be considered in future discussions on the topic.

The biogeography of the Great American Biotic Interchange

Juan D. Carrillo¹, Nathan S. Upham², Carlos Jaramillo³, Dayenari Caballero³, Walter Jetz⁴

¹Muséum national d'Histoire naturelle, CR2P (CNRS, MNHN, Sorbonne Université, Paris, France

²Arizona State University, School of Life Sciences, Tempe, USA

³Smithsonian Tropical Research Institute, Panama, Panama; ⁴Yale University, Department of Ecology and Evolutionary Biology, New Haven, USA

The faunal exchange between North and South America (Great American Biotic Interchange – GABI) is one of the greatest biotic exchanges at a continental scale. Diversification and dispersal dynamics of the GABI have been studied at the continental level, but the regional biogeographic patterns remain unexplored. We analyze the spatio-temporal distribution of fossil and modern mammals to evaluate biome-wide differences in GABI diversity and dispersal dynamics. We find that the success of mammals with North American origin (NAO) in South America was unequal across biomes, contrary to the traditional view of its widespread continental success in terms of species richness and persistence of lineages. NAO clades dominate in temperate biomes of both

continents and the Andean highlands, but not in tropical biomes of South America. When examining the latitudinal gradients of speciation rates, NAO clades show higher rates than South American origin (SAO) clades, especially at higher latitudes of South America. For lowland forests and grasslands, the NAO clades have higher rates of speciation in temperate regions than SAO clades, and this difference decreases toward the tropics. Our results suggest that biome preference and size played a major role in GABI dispersal and diversification dynamics. Moreover, the latitudinal distribution of SAO and NAO clades shows that the modern latitudinal diversity gradient is mostly driven by the SAO clades, which show the strongest gradient. Pliocene extinction of several SAO fossil clades in temperate South America seems to be the primary reason for the strong latitudinal diversity gradient seen in SAO clades today.

Neotropical lungfish and bonytongues: the fossil record of geologically resilient and currently endangered clades

Jorge D Carrillo-Briceño¹; Gabriel Aguirre¹; Edwin-A Cadena², Marcelo R. Sánchez-Villagra¹

¹University of Zurich, Department of Paleontology, Zurich, Switzerland

²Universidad del Rosario, Facultad de Ciencias Naturales, Grupo de Paleontología Neotropical Tradicional y Molecular (PaleoNeo), Bogotá, Colombia

Besides diversification and morphological divergence, a key process of macroevolution is the persistence of branches through time (i.e. survival). Here we focus on two species-poor clades of large-bodied taxa with a very long survival time: the Neotropical lungfish (Dipnoi) and bonytongues (Osteoglossiformes), both having phylogenetic origins that go back to the split of Africa and South America in the Cretaceous period. In South America, the lungfishes are represented today only by *Lepidosiren paradoxa*, whereas the bonytongues by two species of arowanas (*Osteoglossum*) and four of pirarucu (*Arapaima*), often described as apex-predators. We assembled an extensive fossil dataset of lungfish and bonytongues (ca. 550 specimens from seven Neogene geological basins) as part of a larger effort to study neotropical freshwater fishes. Based on novel data, we present an overview of the distribution and paleodiversity of these clades. The fossil record provides evidence of local extinctions, given the presence of these clades in Northwestern areas of the continent before the rise of the Andes. Furthermore, we document a new form of lungfish from Paleogene deposits of Colombia, characterized by unique features of its dental elements. The uniqueness of these resilient phylogenetic clades is challenged by the current human-led biodiversity crisis.

Crossing the Gap to Help Restore Indigenous Socio-Environmental Systems in the Bear River Basin, USA

Brian F. Coddig,¹ Bradley Parry,² Rios Pacheco,² Kasey E. Cole,³ Ishmael D. Medina,¹ Weston C. McCool,¹ Daniel Dalmas,¹ Hailee McOmber,⁴ Caitlin Quirk,⁵ Callum Dingley,¹ Matthew Eisenberg,¹ Zachary Lundeen,⁴ Andrea Brunelle,⁴ Jennifer Watt,⁴ Danielle Endres,⁵ Jerry D. Spangler,⁶ Simon C. Brewer⁴

¹University of Utah, Department of Anthropology

²Northwestern Band of the Shoshone Nation

³University of Utah, Science Research Initiative

⁴University of Utah, School of Environment, Society, and Sustainability

⁵University of Utah, Environmental Humanities Program

⁶Colorado Plateau Archaeological Alliance

Indigenous land-use decisions influenced plants and animals across North America for thousands of years. These dynamics were disrupted by settler-colonial invasions, leading to declines in ecosystem function and health. Restoring Indigenous socioenvironmental systems and the cultural keystone species they support requires identifying long-term baselines that cross the gap between paleontological, archaeological, historical, and ecological records. This requires flexible trans-disciplinary collaboration, novel analytical frameworks, and evolutionary ecological theory. Here we leverage this approach to model the factors that maximize cultural keystone species occurrence, biodiversity, and ecosystem function across the Bear River Basin, USA, and to forecast how these can be restored in the future under anthropogenic climate regimes.

Climate Availability as an Attractor for Miocene Mammal Diversity Accumulation

Marco Túlio Pacheco Coelho¹, Gemma Louise Benevento², Susanne Fritz², Catherine Graham¹, Pincelli Hull³

¹Swiss Federal Institute for Forest, Snow and Landscape Research, Birmensdorf, Switzerland

²German Centre for integrative Biodiversity Research (iDiv), Leipzig, Germany

³Department of Earth and Planetary Sciences, Yale University, New Haven, Connecticut, USA

The latitudinal diversity gradient is a well-documented macroecological pattern, with species richness increasing toward the tropics. While this pattern is well established for extant mammals, fossil mammals exhibit no latitudinal diversity gradient. Previous analyses have reported either an inverse latitudinal diversity gradient or no discernible relationship between fossil mammal diversity and latitude. However, these studies often overlooked the role of climate in shaping diversity patterns. Here, we assess whether fossil mammal diversity accumulates preferentially within climate conditions similar to those occupied by modern mammals. We compiled a spatially explicit dataset of Miocene mammal fossils from Europe and North America, regions with the most comprehensive fossil records and where prior studies have reported a lack of a latitudinal diversity gradient. For each Neogene time bin within the Miocene, we reconstructed paleoclimatic conditions by estimating average minimum and maximum temperatures within 110 × 110 km grid cells. We then tested whether fossil mammal diversity accumulated within specific temperature ranges and whether it aligned with the most prevalent temperature conditions of the time. Our findings indicate that across all Neogene intervals, fossil mammal diversity was consistently concentrated in the most prevalent temperature conditions rather than in the warmest environments. In contrast, modern mammals in these same regions exhibit a similar pattern of diversity accumulation in common climates, but these climates are now systematically warmer than in the fossil record. This shift suggests that climate availability, rather than temperature per se, acts as a primary attractor for species richness. Our results

provide new insights into the role of the prevalence of climate conditions in shaping biodiversity patterns over deep time, emphasizing how the most common climate conditions in a given period influence diversity patterns across time.

Spatial restructuring of bivalve diversity through the last mass extinction at the Cretaceous-Palaeogene boundary

Rebecca B. Cooper¹, Stewart M. Edie², David Jablonksi^{3,4}, Shan Huang¹

¹School of Geography, Earth and Environmental Sciences, University of Birmingham, U.K

²Department of Paleobiology, National Museum of Natural History, Smithsonian Institution, Washington, DC, U.S.A

³Department of the Geophysical Sciences, University of Chicago, Chicago, U.S.A

⁴Committee on Evolutionary Biology, University of Chicago, Chicago, U.S.A

Understanding patterns of extinction and rebound during and following mass extinction events in the geological past plays an important role in contextualising modern biodiversity loss at both global and regional scales, providing insight into the mechanisms governing the dynamics of biodiversity during drastic changes to Earth systems. The Cretaceous Palaeogene (K-Pg) mass extinction event is the most recent, and most studied, example in the palaeontological record. However, the consequence of the extinction, particularly for the rebound after the K-Pg boundary remains unclear, partially obscured by variation in preservation and sampling of the fossil record through time, space and across taxa. Here, we analyse the consequences of the K-Pg mass extinction for the spatial configuration of marine bivalves on a global scale, using simulation-based modelling and deep learning diversity inference.

We ask whether the biogeography of the immediate, post-extinction biota mirrored the pre extinction configuration, or was restructured so that provincial boundaries and richness peaks within families shifted, and if so, whether these shifts showed common directions latitudinally or longitudinally. To test for these patterns, we model the provincial distribution of genera within the latest Cretaceous and then within the early Paleocene, estimating uncertainties and imputing occurrence information using sampling and preservation controls.

These controls account for the impacts of shell mineralogy, organic content, body size, and sampling of adjacent provinces to estimate probabilities of taxon occurrence. Analysing shifts in the spatial structure of biodiversity through a global upheaval provides much needed insights into how predictable such shifts might be under the intensifying global pressures in today's oceans.

Exploring the historical ecology of the Southern Central American Pacific Coast and its conservation implications

Jonathan D. Cybulski^{1,2}, Ashley E. Sharpe¹, Diana Rocío Carvajal-Contreras^{1,3,4}, Brígida De Gracia¹, Erin M. Dillon¹, Irene Garcia¹, Ilean I. Isaza-Aizpurúa^{1,3}, Yahaira Núñez-Cortés¹, Susan Monge-Blanco⁵, Nicole E. Smith-Guzmán^{1,6,7}, Aaron O'Dea^{1,6}

¹Smithsonian Tropical Research Institute, Panama, Republic of Panama

²Graduate School of Oceanography, University of Rhode Island, Narragansett, Rhode Island, USA

³Estación Científica Coiba-AIP, Panama, Republic of Panama

⁴Universidad Externado, Bogotá, Colombia

⁵Department of Anthropology, University of Illinois at Chicago, USA

⁶Sistema Nacional de Investigación, Secretaría Nacional de Ciencia, Tecnología e Innovación, Panama, Republic of Panama

⁷Centro de Investigaciones Históricas, Antropológicas y Culturales-AIP, Panama, Republic of Panama

The Pacific coast of the Southern Central American Isthmus is a region with exceptional biodiversity and productivity that is shaped by millennia of human-environment interactions. Studies of this region's historical ecology have often remained siloed within distinct disciplines, limiting our understanding of the dynamic interplay between oceans, climate, biodiversity, and human systems and their potential conservation implications. To bridge these gaps, we conducted a comprehensive synthesis of paleoclimatological, paleoecological, archaeological, and ecological data, tracing socio-ecological transitions from the Last Glacial Maximum to the onset of industrial fishing in the mid-20th century. Our analysis revealed three key transitions that reshaped human-environment interactions: the shift to agriculture, the stabilization of sea levels, and the arrival of Spanish colonists. Despite these shifts, marine resources consistently served as ecological and cultural anchors for Isthmian societies, buffering against environmental and social upheavals. We further explored these dynamics through three case studies: the use of shells as cultural materials, the collapse of pearl oyster fisheries due to overexploitation, and the effects of colonization on Indigenous marine resource access. These stories illustrate how past human activities and ocean-land connections shaped the region's biodiversity and cultural landscapes. This presentation underscores the value of interdisciplinary approaches in reconstructing socio-ecological histories and their relevance to coastal conservation. By integrating paleontological and archaeological perspectives with ecological and cultural insights, we discuss the need for conservation strategies that incorporate historical data and lessons from the past to ensure the future sustainability of biodiverse coastal systems worldwide.

Emergence of a megacity and its impact on shallow marine benthic ecosystem: A case study from Mumbai, India

Avinash Dahakey¹, Devapriya Chattopadhyay¹

¹Indian Institute of Science Education and Research, Pune, Department of Earth and Climate Science, Pune, India

The tropical region of the globe, especially the Indian coast, is underrepresented in studies relating to anthropogenic changes and their impact on the shallow marine benthic ecosystem. The coastal city of Mumbai in India has a unique history, making it an ideal location for investigating these issues. Originally consisting of four major islands with a few small fishing villages, Mumbai underwent significant transformation starting in 1704 when colonial British rulers initiated a land reclamation project. By 1728, all the islands were connected, leading to the emergence of a bustling port city. From colonial rule to post-independence growth, the city has

seen a population explosion and industrial development. The shallow marine communities around it have consequently experienced increasing anthropogenic pressure over the last three centuries, beginning from a near-zero baseline of human disturbance.

We attempted to evaluate the impact of anthropogenic changes on the marine bivalve community by assessing the live-dead fidelity of open-shelf regions between Mumbai and a nearby pristine coastal area in Raigad, approximately 70 km away. Pristine sites exhibit higher live-dead (LD) agreement in paired abundance-based similarity (Jaccard-Chao Index) and rank-order correlation (Spearman's rho) with the dominance of filter feeder *Timoclea imbricata* in live and dead assemblages. In contrast, the polluted sites of Mumbai city show varying responses in LD agreement; while one site shows poor LD agreement with deposit feeder *Abra* sp. in live and *T. imbricata* in dead, another site shows a relatively good agreement with dominance *T. imbricata* in both live and dead assemblage. These different responses to anthropogenic pressure may be influenced by additional environmental factors, including nutrient levels, substrate, and water current. Understanding these factors is essential for designing effective conservation strategies for sensitive tropical marine ecosystems.

Addressing cryptic diversity in crocodylian diversification dynamics analysis

Gustavo Darlim^{1,2}, Sebastian Höhna^{1,2}

¹Ludwig-Maximilians-Universität München, GeoBio-Center, Munich, Germany

²Ludwig-Maximilians-Universität München, Department of Earth and Environmental Sciences, Munich, Germany

Crocodylia is currently composed of 26 formally recognized species, whereas the rich fossil record illustrates a higher diversity with approximately 140 described species and earliest unambiguous fossil from ca. 85 million years ago. Advances in molecular studies, however, have been able to recognize multiple evolutionarily independent lineages amongst living crocodylians, thus indicating a considerably higher cryptic diversity that is generally untraceable by morphological observations. Diversification dynamics studies in Crocodylia commonly show overall low diversification and slowdowns in speciation rates towards the recent time, however molecular evidence of cryptic lineages have never been considered. Limiting the recognition of extant species under traditional taxonomic practices (e.g. disregarding cryptic diversity) illustrate incomplete sampling, thus hampering comprehensive understanding of different areas of biodiversity research, including, taxonomy, macroevolution, and conservation, for instance. Here, we explore the effects of incorporating detected cryptic lineages from published studies in a diversification dynamics analysis in Crocodylia under available protocols in RevBayes. We used cytochrome *b* sequences from the mitochondrial genome of 45 lineages, including formally recognized crocodylian species and recently delimited Evolutionarily Significant Units (ESUs) within cryptic species complexes. Our results show increasing speciation rates towards the present, which is contrasting to an observed slowdown or decrease of speciation rates when cryptic diversity is excluded from the analysis. Our results support discussions on incorporating a multi-faceted approach to address species compared to traditional taxonomic practices. As evidenced by considerable changes on the outcomes of our diversification analysis, cryptic

diversity should be considered in future macroevolutionary studies for a robust evaluation of crocodylian diversification over time coupled with data from the fossil record. Similarly, our results support and emphasize the importance of cryptic diversity for the understanding of crocodylian extant diversity, reinforcing conservation efforts towards smaller populations that are overlooked by a traditional taxonomic nomenclatural status.

Addressing the Gap between a place and its Paleontological-Ecological record: Case Study Bahamas

Ancilleno O. Davis¹

¹University of The Bahamas, Small Island Sustainability, Freeport, The Bahamas

The Bahamas has a rich history of archaeological, ecological, geological, paleontological and cultural discovery, exploitation, and colonization. The first natural history records of the region may indeed have saved Cristobal Colon's life and led to the colonization of the Americas. However, those events started a trend of collectors visiting the islands to collect various natural resources and records. Many of these records lack the equitable contribution of local voices. They are maintained beyond the reach of native scholars and investigators. In some cases, these records are used to influence practical and tangible aspects of local people's lives, knowledge development. This exploration traces the origins of records collected regarding the Bahamas, ownership of those records and access pathways and barriers.

The author uses a mixture of open access and proprietary databases to explore published records of paleontology and ecology from the Bahamas and describes the geographic distribution of the authors' academic and funding institutions. The costs and pathways to access the published full articles and databases from the Bahamas are described and compared. The goal of this oral presentation is to spark conversation and generate action to improve access for Bahamians and global south students to the records and publications related to the places they live in.

Occupancy modelling as a novel approach for conservation palaeobiology

Christopher D. Dean¹, Samuel T. Turvey², Philip D. Mannion¹

¹University College London, Department of Earth Sciences, London, UK

²Zoological Society of London, Institute of Zoology, London, UK

Palaeontological data provides a unique avenue to investigate climatic, habitat and ecosystem change over longer temporal scales than typically examined in ecology and conservation, contributing critical data in the face of our current biodiversity crisis. However, it is well known the fossil record is systematically and non-randomly biased by a variety of factors. In particular, the issue of data absence (i.e. does the lack of a fossil occurrence indicate genuine absence or imperfect detection?) causes a genuine concern when attempting to discern the historical distribution of species. Occupancy modelling, a technique commonly applied in the

fields of ecology and conservation, provides an avenue to simultaneously estimate the probability of occupancy and detection of fauna, allowing unique insight as to their historic distribution and the factors influencing perceived patterns. Here, we use Holocene palaeontological and zooarchaeological records for 15 mammal species in conjunction with Bayesian occupancy models and a variety of palaeoclimatic, geographic, and anthropogenic covariates to simultaneously estimate the probability of species occupying and being detected in geographic sites across Europe. This approach allows us to establish patterns in the occupancy and detection probability of fauna over the last 12,000 years, as well as uncover their potential drivers and examine shifts in latitudinal range. We find that patterns in raw and modelled occupancy through time do not always match, and that detection probability exerts an influence over our perception of past distributions of taxa. Our models also fail to resolve the distributions of species with fewer than 500 occurrences, providing clear limits to the utility of the recent fossil record. These results highlight the use of occupancy modelling as a novel approach for tackling issues of fossil record bias in conservation palaeobiology, and the necessity for understanding the 'structure' of the fossil record.

Using archaeological data to map parasite diversity throughout Holocene

Kenneth De Baets¹, Karina Vanadzina²

¹University of Warsaw, Faculty of Biology, Warsaw, Poland

²University of Helsinki, Faculty of Biological and Environmental Sciences, Helsinki, Finland

Parasites make up a significant portion of the global biomass and are integral to the healthy functioning of modern ecosystems. Despite their importance today, past changes in parasite distribution and diversity remain largely unexplored due to their limited preservation potential in the fossil record. Using information from more than 700 archaeological and paleoparasitological studies, we compiled a comprehensive database of parasite finds from the Holocene to address this knowledge gap. Our aim was to provide high-resolution spatial and temporal data on parasite occurrences to facilitate their use beyond archaeological literature, e.g., in macroevolutionary analyses and in ecological modelling of future trends in parasite distribution. The database includes more than 3,000 occurrences, which, along with information on their locality, age, taxonomic identity of the parasite and its potential hosts within relational database framework, allows users to build comprehensive profiles of parasite diversity on different geographical scales or spanning a particular time period. The majority of parasite finds consist of resistant eggs (~80%) or trace evidence (~16%) recovered from sediment samples and coprolites associated with human settlements or burials. The database is dominated by the remains of intestinal helminths, such as nematodes (particularly genera *Ascaris* and *Trichuris*) and flatworms (genera *Dibothriocephalus*, *Taenia* and *Fasciola*), with the proportion of commonly encountered genera within samples increasing towards the present day. Most parasite finds have been identified to at least the genus level and are mostly concentrated in the late Holocene period, with a significant increase in occurrences at the start of the Middle Ages. Using various modelling approaches, we demonstrate that the presence of the most common genera of intestinal parasites in archaeological record throughout the Holocene correlate with increases in human population density and climate seasonality.

Establishing a Late Cretaceous baseline for present rates of biodiversity change with the fossil record of Dinosaur Provincial Park, Alberta, Canada

Alexandre V. Demers-Potvin¹, Louis-Philippe Bateman², André Mueller², Hans C.E. Larsson²

¹Department of Bioengineering and Redpath Museum, McGill University, Montréal, Québec, Canada

²Department of Biology and Redpath Museum, McGill University, Montréal, Québec, Canada

There is growing interest among palaeontologists and ecologists in assessing the persistence of past communities at different periods in deep time, notably due to their assembly under higher atmospheric carbon and lower oxygen levels which are becoming more and more relevant today. In this regard, the Late Cretaceous Dinosaur Provincial Park (DPP) palaeobiota offers a relatively detailed glimpse into the response of a Mesozoic non marine community to sea level rise over ~2.5 million years. Considering the high biodiversity of DPP's fossil record and its relatively high spatiotemporal resolution, we can now ask whether its palaeoecological trends can become a baseline for modern biotic responses. In this respect, our main objective is to determine how close DPP's temporal resolution is to an ecological time scale in order to track its climate and diversity patterns as precisely as possible. Radiometric dates have calibrated the absolute age duration of sedimentary rock accumulation in DPP, but a successful stratigraphic correlation of individual skeleton quarries and bonebeds enabling robust species stratigraphic distributions remains elusive. Therefore, we are now mapping all sedimentary exposures in DPP with drones to make a 3D outcrop model for them through georeferenced photogrammetry. The images resulting from this method have a sufficiently high resolution to distinguish broad sedimentary facies types, and to trace individual layers continuously to theoretically enable quarry correlations. Refining the stratigraphic positions of individual fossil sites thus informs our next two major objectives, which are to track how palaeoclimate and palaeodiversity (including interspecific interactions) changed in DPP through time. For the former, we estimated palaeotemperature and precipitation parameters based on angiosperm leaves from a newly discovered fossil plant site. For the latter, we have created one of the first site-specific quantitative ecological networks for a dinosaur-dominated community, at different time intervals within its host sedimentary units.

Ecological dynamics and conservation paleobiology implications of *Thylacoleo carnifex* extinction in Australia

Larisa DeSantis¹, Michael Archer², Julien Louys³, Gilbert Price⁴

¹Vanderbilt University, Department of Biological Sciences, Nashville, USA

²University of New South Wales, School of Biological, Earth & Environmental Sciences, Sydney, Australia

³Griffith University, Australian Research Centre for Human Evolution, Brisbane, Australia

⁴University of Queensland, School for Earth & Environmental Sciences, Brisbane, Australia

The dietary ecology of marsupial carnivores has been debated for decades. Most notably, the marsupial lion *Thylacoleo carnifex* evolved from herbivorous ancestors to become one of the

most formidable predators on the landscape. Prior work has demonstrated that while *Thylacoleo* was only 30% of the body size of African lions, it had a nearly similar bit force (~70%). Further, its postcranial morphology has been described as more "bear-like" and well suited for ambush hunting. Stable isotopes in carnivores can help clarify the habitat of consumed prey, and hence where predators hunted. Here, we examined the stable isotopes of marsupial carnivore tooth enamel including *Thylacoleo*, *Thylacinus*, and *Sarcophilus* from throughout Australia to clarify the paleobiology of these mammalian carnivorous mammals and infer potential drivers of their extinction. Stable carbon isotopes demonstrate that *Thylacoleo* consumed primarily prey that occupied forested environments, with significantly lower $\delta^{13}\text{C}$ values than both *Thylacinus* and *Sarcophilus* in areas where they co-occur—suggesting that *Thylacoleo* specialized on forest dwelling prey that occupied the densest forests available in the Pleistocene. However, all marsupial carnivores here examined show a reliance on prey that consumed primarily C_3 resources. While *Thylacoleo* is found (and examined for stable isotopes) in regions spanning Western Australia to Queensland to Victoria, their stable isotope values are highly conserved in demonstrating the consumption of forested prey. While dental microwear texture analysis reveal that *Thylacoleo* could consume flesh and bone, with “bolt cutter” sheering facets for teeth, they were nevertheless highly susceptible to declines in forests and forest browsing prey. The aridification of the continent (with pronounced changes occurring since ~350,000 years ago) may have detrimentally impacted the hunting effectiveness or prey-base of *Thylacoleo* contributing to its extinction, in contrast to other mammalian carnivorous mammals that survived into the 20th Century.

The Llamara Salt Flat Tamarugo (*Strombocarpa tamarugo*) Population: A Refuge Under Millennial and Contemporary Global Change

Francisca P. Díaz^{1,2}, Virginia Mc Rostie^{1,3}, Matias Frugone-Álvarez^{1,4}, Paula C. Ugalde^{1,5}, Calogero Santoro^{1,4}, José F. Blanco^{1,5}, Claudio Latorre H.^{1,7}, Roberto O. Chávez^{1,2}, Javiera Palma M.^{1,2}, Matias Olea^{1,2}, Elena Balmaceda^{1,3}

¹Millennium Nucleus of Applied Historical Ecology for Arid Forests (AFOREST), Santiago, Chile

²Pontificia Universidad Católica de Valparaíso, Instituto de Geografía, Valparaíso, Chile

³Escuela de Antropología, Pontificia Universidad Católica de Chile, Centro del Desierto de Atacama UC, Chile

⁴Instituto de Alta Investigación, Universidad de Tarapacá, Chile

⁵Sociedad Chilena de Arqueología, Santiago, Chile

⁶Departamento de Antropología, Universidad Alberto Hurtado, Santiago, Chile

⁷Institute of Ecology and Biodiversity (IEB), Santiago, Chile; Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Chile

Tamarugo (*Strombocarpa tamarugo*) is an endemic Fabaceae tree that grows almost exclusively in the Pampa del Tamarugal, northern Chile, playing a crucial role in the sociocultural and economic adaptation of human populations in the Atacama Desert for millennia. This species is uniquely adapted to hyperarid conditions, relying on deep groundwater sources. However, past and present human activities have significantly shaped its distribution and survival.

Tamarugo forests have coexisted with human populations for approximately 12,000 years, providing essential resources and influencing settlement patterns. In the 18th century, its wood became the primary fuel source for small-scale mining operations, particularly for charcoal production. This exploitation intensified in the 19th century with the nitrate industry's expansion, leading to extensive deforestation. In response, state agencies implemented large-scale afforestation efforts, establishing the largest native tamarugo plantation in Chile in the 1960s and 1970s. This intervention reshaped the Pampa, creating a mosaic of planted and natural forests. However, today, these trees face new threats from excessive groundwater extraction by mining companies, putting their long-term survival at risk.

This study applies a historical ecology approach to reconstruct the millennial history of tamarugo populations in the Llamara Salt Flat, one of its last natural refuges, and assesses their recent decline using remote sensing and paleoenvironmental analyses. We combined radiocarbon dating (^{14}C), satellite imagery, and species distribution modeling to examine past and present tamarugo distributions. High-resolution satellite imagery identified 4,164 living tamarugo trees in Llamara and detected recent signs of water stress.

Our findings confirm that Llamara has long functioned as a climatic refuge, sustaining tamarugo populations through extreme aridification events. However, increasing groundwater extraction and expanding mining activities threaten their survival. This study highlights the need for conservation strategies integrating paleoecological history, resilient forest patches, and remote sensing monitoring as a baseline to identify relict populations and climate refuges.

Leveraging the past to strengthen conservation stories

Jaleigh Q. Goben¹, Mychajliw, A.M.^{2,3}, Olson, O.L.^{3,4}, Dietl, G.P.^{1,5}

¹Cornell University, Department of Earth and Atmospheric Sciences, Ithaca, NY, USA

²Middlebury College, Program in Environmental Studies, Middlebury, VT, USA

³Middlebury College, Department of Biology, Middlebury, VT, USA

⁴University of Maine, Climate Change Institute, Orono, ME, USA;

⁵Paleontological Research Institution, Ithaca, NY, USA

Conservationists are increasingly harnessing the power of storytelling to advance their objectives. Here, we introduce the Past Stories Hypothesis, which posits that conservation storytelling can be enhanced by integrating the long-term perspectives offered by geohistorical records—such as fossils, sediment cores, and other natural archives of the past. Expanding conservation stories beyond the scale of years or decades allows for the reframing of biodiversity and ecosystem change, equipping conservationists with tools to “unshift” previously unrecognized shifted baselines by redefining when the story begins. Geohistorical data restore lost environmental memory—collective knowledge of past ecosystems—while reducing unintended biases. Layering geohistorical data and insights onto what a conservationist already knows about the present may not only enhance the effectiveness of conservation messaging but also invite a wider audience into the conversation, broadening participation and creating new perspectives and ways of perceiving a conservation story.

Tracking sharks' responses to climate disturbances on coral reefs over millennia in the Panamanian Pacific

Erin M. Dillon¹, Irene García¹, María Mercedes Gómez Benalcázar^{1,2}, Brígida de Gracia¹, Jonathan D. Cybulski^{1,3}, L. Felipe Opazo^{4,5}, Kimberly García-Méndez¹, Aaron O'Dea^{1,6}

¹Smithsonian Tropical Research Institute, Balboa, Republic of Panamá

²Faculty of Life Sciences, Escuela Superior Politécnica del Litoral, Guayaquil, Ecuador

³Graduate School of Oceanography, University of Rhode Island, Narragansett, Rhode Island, USA

⁴Departamento de Ecología, Facultad de Ciencias, Universidad Católica de la Santísima Concepción, Concepción, Chile

⁵School of Geology, Faculty of Science, Engineering and Technology, Universidad Mayor, Santiago, Chile

⁶Sistema Nacional de Investigación (SENACYT), Panamá, Republic of Panamá

Climate change threatens the persistence of coral reefs, which in turn has affected reef-associated predators such as sharks. However, the relationship between reef health and shark abundance remains uncertain, and we know little about how it might shift under future environmental change. This is particularly true in the Tropical Eastern Pacific, where reefs experience large climatic variability. Here, we leverage a past climatic episode in the Panamanian Pacific—a climate-driven slowdown of reef accretion and loss of coral habitat—to assess how shark communities respond to reef degradation following climate stress. The reef collapse, which lasted over 2,500 years (~4.2–1.5 ka), has been well-documented through estimates of reef accretion and analyses of coral community composition in reef matrix cores collected throughout the region. We quantified the accumulation of shark scales (dermal denticles) in cores spanning the last ~6,000 years to reconstruct shark communities before, during, and after the reef collapse at two locations within the Gulf of Panama (Las Perlas Archipelago and Isla Iguana). Dermal denticles were also measured and classified by morphotype to track changes in the functional structure of shark communities through time. Finally, ratios of shark dermal denticles to fish otoliths (ear stones) accumulating in the same samples were used as a proxy of relative trophic structure. Our preliminary data suggest that 1) shark abundances might have decreased during the reef collapse but were able to recover and 2) both the functional composition of shark communities and relative trophic structure remained fairly stable across the event. These results evidence the historical resilience of shark communities during past environmental disturbances along Panama's Pacific coast, enabling predictions of how different ecological groups of sharks might fare under intensifying fishing and climate impacts in the region.

Coral reef refugia through time: Insights from the fossil record

Danijela Dimitrijević¹, Lewis A. Jones², Markus Aretz³, Francesca Bosellini⁴, Juan Carlos Braga⁵, Clara Diaz⁶, Elizabeth M. Dowding¹, Kenneth Johnson⁷, Wolfgang Kiessling¹, Bernard Lathuilière⁸, Kyle Morgan⁹, Michele Morsilli¹⁰, John Pandolfi¹¹, Mikołaj K. Zapalski¹², Nadia Santodomingo⁷

¹Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

²University College London, London, UK

³Université Toulouse III Paul Sabatier, Toulouse, France

⁴Università degli Studi di Modena e Reggio Emilia, Modena, Italy

⁵University of Granada, Granada, Spain

⁶University of Plymouth, Plymouth, UK

⁷Natural History Museum, London, UK

⁸Université de Lorraine, Nancy, France

⁹Nanyang Technological University, Singapore

¹⁰University of Ferrara, Ferrara, Italy

¹¹University of Queensland, Brisbane, Australia

¹²University of Warsaw, Warsaw, Poland

Modern coral reefs are the most vulnerable ecosystems on our planet today. They face unprecedented threats from rising global temperatures, resulting in widespread bleaching and mass mortality. Reef refugia—less vulnerable and resilient habitats—could reduce the risk of extinction and serve as a source of healthy organisms to repopulate shallow waters, thereby contributing to the long-term maintenance of coral diversity. In ecology, climate refugia for coral reefs are suggested for regions where the effects of marine heatwaves are less severe – along the depth gradient, in areas influenced by internal waves, in turbid waters, and at higher latitudes. However, evaluating the potential of these environments to act as refugia is challenging without a long-term perspective on changes in community composition and resilience. The fossil record provides empirical evidence of how ecosystems have historically responded to climate crises. In this study, we investigated the potential of reef environments, such as deeper (blue mesophotic), turbid (brown mesophotic), and subtropical regions, to serve as refugia for corals across warming-induced reef crises. We also explore the evidence needed to identify mesophotic reef ecosystems in the fossil record and develop a common data framework that facilitates meaningful quantitative comparisons between fossil and modern reefs. By analysing a comprehensive database of fossil reefs covering the last 485 million years (Ordovician - Pleistocene), we demonstrate that following rapid warming events, reef distributions shifted toward higher latitudes and deeper (blue mesophotic) environments, indicating their role as refugia. While our findings offer hope for the resilience of coral reefs in the face of current climate change, the fossil record shows that full ecosystem recovery, in most cases, took millions of years. Therefore, understanding the long-term dynamics of these potential refugia is essential amid the current climate crisis.

A Tale of Two Paleocommunities: Functional variation after the Permo-Triassic mass extinction

Ashley A. Dineen¹, Peter D. Roopnarine²

¹University of California Museum of Paleontology, Berkeley, USA

²California Academy of Sciences, Department of Invertebrate Zoology and Geology, San Francisco, USA

The Permo-Triassic mass extinction (PTME), the largest extinction in Earth's history, is believed to have played a key role in shifting faunal dominance in the ocean from the Paleozoic Evolutionary Fauna (PEF) to that of the Modern Evolutionary Fauna (MEF). This transition indicates that the new Triassic ecosystems were distinct from Permian ones, possibly being better described as restructured rather than simply recovered. And while previous studies have primarily focused on the taxonomic diversity shift following the PTME, less consideration has been given to the

functional differences between the surviving PEF and the new MEF members during this period. Here we quantify the functional diversity and trait space of two Early Triassic (Spathian) paleocommunities, that of the recently discovered offshore Paris Biota from southeastern Idaho and the shallow onshore Virgin Limestone Member of southwestern Nevada. Despite being established at roughly the same time after the PTME, the two communities represent different depositional environments and what appears to be differing degrees of restructuring. Results indicate that while both communities were roughly equivalent in terms of functional richness, the distribution of that richness in functional ecospace varied. For example, whereas newly originated Triassic taxa shared ecospace with Permian survivors in the Virgin Limestone, they differed significantly in distribution in the Paris Biota. This indicates that the Paris Biota may represent a more complex ecosystem than has been previously documented in the early Triassic, and a community at the start of an ecological and macroevolutionary transformation. Overall, these results emphasize the need to examine both the spatial and temporal patterns of ecospace occupation after mass extinctions, as well as highlight the intricate connection between taxonomic and functional diversity through time.

Compound-specific stable isotopes of amino acids reveal ecology of planktic foraminifera species

Shannon C. Doherty¹, Matthew D. McCarthy², Stephanie Christensen², Catherine V. Davis³

¹University of Alaska Fairbanks, College of Fisheries and Ocean Sciences, Fairbanks, Alaska, USA

²University of California Santa Cruz, Ocean Sciences, Santa Cruz, California, USA

³North Carolina State University, Department of Marine, Earth, and Atmospheric Sciences, Raleigh, North Carolina, USA

Although planktic foraminifera are essential proxies for paleoceanographic reconstructions, their behavior and ecology are poorly constrained. In this study, we adapted isotope ecology tools using compound-specific stable isotopes of amino acids (CSI-AA) from foraminifera shell-bound organic matter. Our results suggest that both nitrogen and carbon CSI-AA tools are promising for elucidating the trophic ecology of planktic foraminifera in modern and past oceans.

Furthermore, nitrogen CSI-AA of the three most abundant species of planktic foraminifera from Santa Barbara Basin revealed that all three species occupied the same trophic level, while carbon CSI-AA revealed that each species had a highly specific diet. Despite its omnivorous behavior in culture, *Globigerina bulloides* fed exclusively on phytoplankton, adjusting diet to seasonal changes in phytoplankton community assemblage. *Turborotalita quinqueloba* subsisted on a diet of almost exclusively diatoms, suggesting that this species may be a good proxy for diatom abundance and therefore upwelling in the Santa Barbara Basin. Finally, *Neogloboquadrina incompta* fed on primarily heterotrophic bacteria, supporting hypotheses about its niche as a particle-dwelling species, where bacteria would be concentrated. Additional preliminary data from planktic foraminifera collected along the U.S. Atlantic and Pacific margins suggest shared ecology within genera and varied symbiotic relationships. We propose that our findings may inform the use of these species as ecosystem proxies in the geologic record. We also discuss future work, which includes adapting this methodology to fossils with the goal of uncovering the ecology of extinct planktic foraminifera species.

Plotting on possible Earths: deep time and future geography

Elizabeth M. Dowding¹, Trond H. Torsvik², and Ádám T. Kocsis¹

¹ Friedrich-Alexander-Universität Erlangen-Nürnberg, GeoZentrum NordBayern, Erlangen, Germany

² University of Oslo, the Centre for Planetary Habitability, Oslo, Norway

Plate tectonics is the unifying theory that explains Earth's geological processes, from its core to its crust, shaping both past and future landscapes. It governs the interactions between the mantle, lithosphere, hydrosphere, atmosphere, and biosphere, forming the foundation for Earth system modelling. In reconstructing past environments, *Global Plate Models* – digital representations of the mantle and lithosphere – provide a critical framework for deep-time and long-timescale biogeographic analyses, where climate and geography drive species distributions at regional and global scales.

This study explores different approaches to integrating global plate models in biogeographic research using fossil data. I examine the effects of model selection, pre-analysis area assignment, and range characterisation within a phylobiogeographic framework. By assessing the joint dispersal and evolutionary histories of fossil arthropods across multiple reconstructions, I identify patterns that persist across models. The findings reveal that while fine-scale results vary significantly, broader patterns remain consistent. Positively, this reinforces the robustness of large-scale biogeographic interpretations despite uncertainties and variations between Earth reconstructions.

Working within the R-environment I also present ‘*rgplates*’, an R-language package to assist palaeontologist, ecologists, and biogeographers (amongst others) interact with *Global Plate models* and their associated products, such as digital elevation and climate models. ‘*rgplates*’ increases access whilst building in key features designed for model users. This work aims to establish an interdisciplinary discussion between *Global Plate Model* developers and model users.

History's Wild Ride: Zoological Baselines Through Time in the Bear River Range

Auriana Dunn^{1,2}, Dr. Kasey Cole^{1,2,3}, Dr. Austin Green^{2,3}, Dr. Tyler Faith^{1,4}, Dr. Randal Irmis^{4,5}

¹ Department of Anthropology, University of Utah, Salt Lake City, Utah

² College of Science, University of Utah, Salt Lake City, Utah

³ Science Research Initiative, University of Utah, Salt Lake City, Utah

⁴ Natural History Museum of Utah, Salt Lake City, Utah

⁵ Department of Geology and Geophysics, University of Utah, Salt Lake City, Utah

The effects of anthropogenic climate change on contemporary animal communities are a key concern for climate and environmental experts going forward. Importantly, however, to fully understand the potential impacts of climate change on zoological life today requires an understanding of how animal populations responded to past climatic changes that occurred

over timescales exceeding those of direct human observations. Paleozoological data provides such a record and documents baselines of animal communities that can be used to evaluate historic anthropogenic change and attest to the responses of species to ecosystem changes over geological timescales. This project builds paleo and modern zoological baselines for Western North America's Bear River Basin, straddling modern-day Utah, Idaho, and Wyoming, using three data types: 1) Paleontological survey of two high-elevation cave assemblages (Boomerang and Thundershower Caves), 2) modern camera trap data, and 3) modern museum live trapping surveys. Using these baselines, we compare and evaluate changes in species diversity and richness over time. Additionally, using Random Forest statistical analysis, we highlight the analytical power of machine learning for understanding variation in species that exists among the datasets. Finally, we discuss the implications of our findings for Tribal-led ecological restoration efforts taking place in the region.

Before and After Glaciation: Isotopic Insights from Antarctic Peninsula Molluscan Communities

Saurav Dutta¹, Rowan Whittle¹, James Witts², Katie Collins², Samuel Hunt¹, Andy Moles¹

¹British Antarctic Survey, Cambridge, United Kingdom

²Natural History Museum, London, United Kingdom

The Eocene-Oligocene transition (~34 Ma) represents a critical climate shift from greenhouse conditions to the initiation of Antarctic glaciation. While deep-ocean records provide valuable insights into this cooling trend, shelf environments - where most macrofaunal marine fossils are found - remain underrepresented in palaeoclimate reconstructions, particularly at high latitudes. Our research addresses this gap through isotopic analysis of exceptionally preserved molluscan fossils from two complementary Antarctic Peninsula locations: Seymour Island (La Meseta and Submeseta Formations) and King George Island (Polonez Cove Formation).

These sites provide a unique opportunity to examine the greenhouse-icehouse transition from different temporal perspectives. Seymour Island preserves a mostly Eocene record spanning pre-glacial conditions, and possibly captures the initial glaciation events, while King George Island deposits represent Oligocene benthic communities that developed after major ice sheet formation. This temporal sequence allows us to track ecological responses across the climate threshold.

We have collected and prepared bivalve from each locality for analysis, using *Cucullaea* sp. and *Retrotapes* sp. from Seymour Island, and *Leoclunipecten gazdzickii* from King George Island. These specimens will undergo high-resolution oxygen and carbon isotope analysis to reconstruct shelf palaeotemperatures and identify carbon cycle perturbations. Preliminary observations of growth banding patterns suggest seasonal variations in growth, with implications for interpreting bulk isotopic values.

Our research aims to identify precise timing and magnitude of cooling events on the Antarctic shelf and characterize the environmental conditions experienced by benthic communities before, during, and after glaciation. By integrating isotopic data with faunal composition

changes, we can evaluate how benthic ecosystems responded to this major environmental transition. These insights will enhance our understanding of how marine ecosystems may respond to current climate change, particularly in polar regions that remain highly vulnerable to warming temperatures.

Patterns of intrinsic vulnerability to range shift and extinction Pliocene to present in northeastern Atlantic bivalves

Sarah C Gale¹, Katie S. Collins², Shan Huang¹

¹University of Birmingham, School of Geography, Earth and Environmental Sciences, Birmingham, United Kingdom

²Natural History Museum, Department of Earth Sciences, London, United Kingdom

As global climate changes, many marine species are expected to move to higher latitudes, likely shifting their ranges to track preferred temperatures and habitats, or in some cases becoming extinct entirely. Which species are expected to expand or contract their geographic ranges, or which may suffer global extinction, is a result of a complex mixture of factors, and a close examination of deep-time dynamics can highlight groups that may have a higher degree of intrinsic vulnerability.

The Pliocene fossil record of the northeast Atlantic presents an opportunity to identify risk across a significant climatic change. The Pliocene is in many ways comparable to the modern oceans; it was the most recent time during which atmospheric CO² levels were comparable to the modern day, and it featured a near-contemporary ocean geography. The Plio-Pleistocene transition around 2.3 million years ago coincided with colder global temperatures, the onset of glaciations, lower sea level, and a pulse of extinction which can be observed across many different taxonomic groups, including the marine bivalves (Class: Bivalvia) which have an excellent fossil record of this period in the northeast Atlantic.

The range of many bivalve species contracted or shifted southwards during this time, presumably driven by their thermal tolerance. Besides global extinction, some regional diversities were further reduced by extirpation, especially at higher latitudes. These patterns urged us to investigate the predictability of the sensitivity of bivalves to climate change due to intrinsic properties.

In this study, we examine fossil occurrences along the northeast Atlantic coast to estimate the intrinsic vulnerability to climate change of shallow marine bivalves. We compare the geographic range of species and analyse taxonomic identities or functional traits as correlates of range shift or extinction and build a model for predicting which taxa today have high intrinsic vulnerability to regional or global extinction.

Mammalian habitat specialization in a phylogenetic context

Emilia Galli¹, Sara Gamboa^{2,3}, S. Kathleen Lyons⁴, Manuel Hernández Fernández¹, Iris Menéndez⁵

¹Universidad Complutense de Madrid, Departamento de Geodinámica, Estratigrafía y Paleontología, Madrid, Spain

²Universidade de Vigo, MAPAS Lab, Departamento de Ecoloxía e Bioloxía Animal, Vigo, Spain

³Universidad Complutense de Madrid, Madrid, Spain

⁴University of Nebraska-Lincoln, School of Biological Sciences, Lincoln, USA

⁵Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany

The degree of biome specialization (defined as the number of biomes in which a species is present) varies among terrestrial mammal species, reflecting their climatic tolerance and potentially influencing their response to climate change. For instance, species that are specialized in a single biome (biome specialists) may exhibit lower tolerance to climate fluctuations. In this study, we aim to identify the ecological and geographical factors that influence the percentage of biome specialists found within each mammal family. We built a dataset including evolutionary (e.g. mean body size, clade age), specialization (e.g., percentage of specialists in a specific biome) and geographical (e.g. mean range area, altitudinal range) traits, gathering up to 110 variables from multiple sources (e.g. the IUCN, PBDB and COMBINE databases). Using the percentage of total biome specialists in each family as the dependent variable, we ran a correlation test and performed a Classification and Regression Tree (CART) analysis to order the variables according to their importance for biome specialization. This allowed us to select the most relevant variables for the subsequent Phylogenetic Generalized Least Squares (PGLS) analyses. All the work was performed in R. Our results show that tropical specialization has largely contributed to the general patterns of specialization, which is consistent with the greater availability of niches in tropical regions. Regarding geographical and evolutionary traits, we found that mean distribution area, altitudinal range, and body size of the species in the family were the most significant variables, all showing a positive correlation. This suggests that habitat specialization is not necessarily linked to narrow distribution ranges, and that the degree of specialization might be influenced by the body size of species.

Future paleontologists will detect current mammal Latitudinal Biodiversity Gradient

Sophia Galván¹, S. Gamboa^{1,2}, A. A. Chiarenza³, F. M. Rotatori⁴, A. Oliver¹, S. Varela^{1,5}

¹University of Vigo, Department of Ecology and Animal Biology, Vigo, Spain

²Universidad Complutense de Madrid, Madrid, Spain

³University College London, Department of Earth Sciences, London, UK

⁴Universidade NOVA de Lisboa, Department of Earth Sciences, Caparica, Portugal

⁵Axencia Galega de Innovación, Santiago de Compostela, Spain

Fossil data provides a unique tool for answering questions about how life emerged and diversified through time. However, the fossil record is characterized by a series of biases related to the preservation and the sampling of the specimens. For example, fossil preservation and recovery depend on the surrounding environment, the biology of the individuals and scientific preferences. Current paleontologists only retrieve a fraction of past biotic information, so future paleontologists will get a biased sample of current biodiversity. Here, we aim to quantify how these biases compromise the detection of a conspicuous current biogeographic pattern; the

latitudinal biodiversity pattern (LBG). In order to do that, we applied a bias-filtering process on current mammal species distribution maps, focusing on a) geological, b) biological and, c) anthropogenic bias-sources. These filters were applied subsequently to mimic a realistic fossilization process, considering different preservation rates. Results showed that the LBG is generally maintained through the implemented filters, although consecutively losing its intensity. Thus, there is an optimistic scenario in where, although the LBG may be sensitive to a skewed extirpation of species, a detectable signal can be retrieved for all scenarios. Considering this, our study supports the potential of the fossil record in detecting latitudinal gradients under a biased mammal fossil record.

The Impact of Tip Age Distribution on Reconstructing Trait Evolution Using Phylogenetic Comparative Methods

William Gearty¹, Bethany J. Allen^{2,3}, Pedro L. Godoy⁴, Alfio Alessandro Chiarenza⁵

¹Syracuse University, Open Source Program Office, New York, USA

²ETH Zürich, Department of Biosystems Science and Engineering, Basel, Switzerland

³Swiss Institute of Bioinformatics, Computational Evolution Group, Lausanne, Switzerland

⁴University of São Paulo, Department of Zoology and Institute of Bioscience, São Paulo, Brazil

⁵University College London, Department of Earth Sciences, London, UK

Collecting data for use in constructing phylogenies is a valuable but time- and resource-consuming pursuit. As a result, indicators of the potential value of including certain species in a phylogeny a priori could prove useful when planning this stage of research. Here, we used a simulation approach to investigate whether there are trends in the ability for phylogenetic comparative methods to recover the correct model of trait evolution based on certain characteristics of the phylogeny. First, we used multiple diversification rates to simulate phylogenies containing varying proportions of fossil and extant tips. We then simulated the evolution of a single trait across each phylogeny using multiple continuous trait evolution models. We then compared the fit of the correct and incorrect models to the simulated traits. This quantitative evaluation allows us to discern whether there are certain tip characteristics associated with identifying the correct trait evolution models. Our results indicate that the inclusion of fossils can be highly beneficial to reconstructing certain trait histories (e.g., Ornstein-Uhlenbeck and ACDC) but not to others (e.g., Brownian motion). In fact, in many cases, increasing the proportion of fossils in a phylogenetic dataset is far more beneficial, and perhaps more time- and resource-efficient, than increasing the number of extant taxa in the dataset. Our results corroborate previous findings that the inclusion of fossil tips can vastly improve the reconstruction of trait histories but also show that this effect is often stronger with the inclusion of older fossils.

Spatiotemporal Dynamics of Mollusk Communities in Response to Emergence of the Isthmus of Panama

Amanda Godbold¹, Aaron O'Dea^{1,2}, Jonathan Todd³, Kenneth Johnson³, Sean R. Connolly¹

¹Smithsonian Tropical Research Institute, Panamá

²Sistema Nacional de Investigación, SENACYT, Panamá

³Natural History Museum of London, England

Understanding how environmental changes influence the structure and diversity of ecological communities is a critical objective for both ecologists and paleontologists. A key step in linking paleoecological insights to modern ecological concerns lies in the application of analytical approaches that reconcile differences in scale, biases, and temporal resolution.

This study utilizes the Panama Paleontology Project (PPP), a 35-year initiative documenting biological responses to the emergence of the Isthmus of Panama. Spanning the last 12 million years, the PPP dataset uniquely combines fossil records and modern ecological samples, collected using standardized methodologies to enable direct comparisons. The progressive closure of oceanic pathways during this period serves as a natural experiment to investigate patterns of biological turnover in response to major environmental shifts, including ocean circulation changes and productivity declines in the Western Atlantic.

Our analysis focuses on bivalve and gastropod abundance data from 245 bulk samples organized into 64 faunules, lithological units of defined spatial and stratigraphic extent. Faunule ages were updated to the GTS 2020 timescale, ensuring more precise correlations with geological events. We employed the bivariate Poisson-lognormal model of species abundances to quantify spatial and temporal faunal turnover. This model accounts for incomplete sampling and biases in abundance estimates, providing explicit uncertainty measures. By independently estimating taxonomic richness and evenness, the model offers a bivariate partitioning of alpha diversity, surpassing the limitations of traditional methods that assume perfect representation of community abundances.

Our preliminary findings help reveal how ecological communities in the southwestern Caribbean responded to the progressive oceanographic reorganization caused by the emergence of the Isthmus. These results highlight the utility of integrating ecological sampling theory to provide a more nuanced understanding of biodiversity dynamics across geological timescales. This approach not only enhances our ability to interpret past environmental changes but also offers useful insights for predicting future ecosystem responses under analogous conditions of environmental stress.

Same variables, different results: the importance of sensitivity analyses in deep-time evolutionary studies

Pedro L. Godoy¹

¹Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil

Characterising long-term patterns of evolution, such as changes in biodiversity or in morphological traits, is a crucial step for understanding the evolutionary processes and the drivers underlying these changes. From a palaeontological perspective, using data from extinct species seems imperative for documenting such deep-time patterns. Nevertheless, the uneven

nature of the fossil record makes it challenging to recover true signals, particularly when using statistical methods to test for correlations. Here, I use Crocodylomorpha (Archosauria, Reptilia) as a study system to demonstrate the importance of employing sensitivity analyses when testing possible drivers of deep-time evolutionary patterns. Regression models were used to test for correlation between two variables, crocodylomorph body size and palaeotemperature, with the premise that the two are indeed associated. Overall, results vary according to how the data is structured and analysed. First, regressions with an autocorrelation model show no through-time correlation between palaeotemperature and crocodylomorph mean, maximum or minimum body size. Nevertheless, after exploring the relationship among other crocodylomorph subgroups, a significant correlation between the variables was found for the crown group Crocodylia, in which mean body size increases as temperatures decrease. Furthermore, when a differently-structured palaeotemperature dataset is used (i.e., geographically-specific climate data), the association between body size and temperature changes. In particular, for the crocodylian clade Caimaninae, phylogenetic regressions show that increased temperatures are associated with larger body sizes. Combined, these results show the impact on the results of inspecting the data, using varied methodology and exploring different temporal and taxonomic scopes when assessing deep-time associations of biotic variables and possible drivers, highlighting the importance of sensitivity analyses.

Slimehead size through time: testing the temperature-size relationship in Late Cretaceous Trachichthyidae

Chloe V. Griffiths^{1,2}, James D. Witts¹, Julie Brown², Emma L. Bernard¹, Richard J. Twitchett¹

¹Natural History Museum, Cromwell Road, London, SW7 5BD, UK

²University College London, Gower Street, London, WC1E 6BT, UK

As global temperature rises, fish are predicted to become smaller. Body size is a fundamental trait impacting many aspects of an animal's life history and ecology, and understanding how it may respond to climate change in particular fish groups, especially commercial or keystone species, is critical. The slimeheads (Family Trachichthyidae) include several commercially important species, but because they are deep-dwelling, long-lived fish, which reproduce slowly, directly testing the temperature-size relationship in this family is challenging. Fortunately, the Trachichthyidae have a long evolutionary history beginning in the Cretaceous and their fossil record provides empirical data on the response of this family to past climate change events. In this study, we leveraged the extensive fossil record of the Late Cretaceous trachichthyid genus *Hoplopteryx* from the British Chalk Group of southern England to test whether its size declined at higher temperatures. Standard Lengths were measured from complete individuals and estimated from partial remains. Palaeotemperature estimates were derived from stable isotope analysis ($\delta^{18}\text{O}$) of the bulk chalk rock surrounding the fossils using standard techniques and assumptions. Individual fish ranged from 56.3 to 253.5 mm in length, and measured seawater palaeotemperature estimates ranged from 19.5 to 27.1 °C. We recorded a significant negative correlation between estimated seawater temperature and Standard Length in the most common species *Hoplopteryx lewesiensis*, supporting the prediction that higher temperatures lead to

smaller body size. In addition, we found a significant negative correlation between the lengths of *H. lewesiensis* and stable carbon isotope ($\delta^{13}\text{C}$) values of the chalk matrix, suggesting that other environmental factors such as productivity, the burial of organic matter, and/or water depth may also have affected body size.

Occupancy and extinction dynamics in Phanerozoic bivalves

Torsten Hauffe¹, Juan Lopez Cantalapiedra², Diana Delicado Iglesias³, Daniele Silvestro⁴

¹University of Fribourg, Department of Biology, Fribourg, Switzerland

²Museo Nacional de Ciencias Naturales, Departamento de Paleobiología, Madrid, Spain

³Museo Nacional de Ciencias Naturales, Departamento de Biodiversidad y Biología Evolutiva, Madrid, Spain

⁴ETH Zurich, Department of Biosystems Science and Engineering, Basel, Switzerland

Ecological studies on extant species have demonstrated that genetic diversity, population size, abundance, or geographic range – collectively termed occupancy – are influenced by traits and environmental conditions. Moreover, occupancy is one of the strongest predictors of contemporary (and past) extinction risk, making it central to understand the evolution of biodiversity and the threats it faces today. Neutral theory predicts that a taxon's occupancy follows a hump-shaped trajectory over its evolutionary lifespan: it is low at origination, peaks somewhere in the middle, and then declines before its extinction. An alternative hypothesis, postulates that stasis – a prolonged constant occupancy – is the result of changes in biotic interaction strength over the taxon's lifespan. In contrast, a gradual rise followed by an abrupt population collapse could be linked to a rapid change in climate or a catastrophic event. Occupancy dynamics can help us to validate ecological hypotheses leading to extinction and are pivotal for understanding macroevolutionary diversification processes. Yet, the inevitable incompleteness of the fossil archive, affected by spatial, temporal, and taxonomic biases, means that fossil occurrences cannot be reliably used at face value to infer occupancy. Here we present a novel Bayesian model powered by an unsupervised neural network to infer occupancy dynamics over a lineage's lifespan. Our approach accounts for sampling biases unrelated to paleoenvironmental conditions while leveraging explainable artificial intelligence to assess the influence of ecological factors, such as life history traits and paleoenvironmental conditions. For 1700 marine bivalve genera spanning 450 million years, we show that stasis in occupancy or sustained increases are rare, with most orders exhibiting a decline prior to their disappearance, and paleoenvironmental change playing an important role in shaping these dynamics. Our approach advances our ability to infer occupancy in deep time and its determinants, and our understanding of the population dynamics preceding extinction.

Regional and Global Drivers of Mesozoic Dinosaur Diversification

Joel A. Heath^{1,2}, Natalie Cooper², Paul Upchurch¹, Alfio Alessandro Chiarenza¹, and Philip D. Mannion¹

¹University College London, Department of Earth Sciences, London, UK

Dinosaurs first appeared in the Late Triassic as minor components of terrestrial ecosystems but rapidly diversified in the Early Jurassic, dominating until the extinction of non-avian groups at the Cretaceous/Paleogene boundary. The drivers of this radiation remain debated, with evidence for both abiotic factors (e.g. climate shifts, tectonics—Court Jester model) and biotic interactions (e.g. pseudosuchian decline, angiosperm radiation—Red Queen hypothesis). Most studies have evaluated diversity and diversification patterns at global scales, but this is problematic given the spatiotemporally heterogeneous sampling of the dinosaurian fossil record. Here, we estimate regional diversification rates in Mesozoic dinosaurs using both PyRate and Shareholder Quorum Subsampling (SQS) and test for correlations with biotic and environmental factors. By incorporating regional data, we account for the uneven distribution of fossil occurrences and the variability of environmental conditions across different landmasses, which strongly influence diversification estimates. This approach allows us to assess how key drivers of evolution varied spatially and whether regional ecosystems responded differently to global events. We also compare results from PyRate and SQS to evaluate how differences in methodology impact diversification estimates. Our findings suggest that dinosaur diversification was shaped by a complex interplay of ecological and environmental factors, with significant variation between regions. PyRate and SQS provide complementary perspectives on diversification dynamics, enabling us to disentangle the effects of preservation biases and sampling heterogeneity. By refining regional estimates, we show how global and local processes influenced Mesozoic dinosaur evolution and highlight the importance of spatially explicit analyses in palaeobiology.

Do oryx fit in? An unintentional test case of ungulate rewilding in New Mexico

Carson P. Hedberg^{1,2,3}, Tyler R. Kartzinel^{1,2}, Felisa A. Smith³

¹Brown University, Department of Ecology, Evolution, and Organismal Biology, Providence, RI, USA

²Brown University, Institute at Brown for Environment and Society, Providence, RI, USA

³University of New Mexico, Department of Biology, Albuquerque, NM, USA

Human impacts over millennia have reduced the diversity of megafauna in modern ecosystems. Yet, because of their ecological importance, there is growing interest in “rewilding” large mammals, either through repopulating native fauna or introducing non-native fauna as functional replacements for extinct or extirpated species. Underlying this approach is the assumption that species ecology is primarily mediated by functional and physiological traits, with a limited influence of nativeness or evolutionary coexistence. Empirical testing of rewilding initiatives is still somewhat limited, but communities that contain naturalized exotic ungulates offer opportunities to investigate novel assemblages of coexisting native and introduced fauna. Here, we examined the dietary ecology of introduced oryx (*Oryx gazella*) in New Mexico within the context of the native ungulate community. Importantly, this region has experienced prolonged defaunation of large herbivores starting in the Terminal Pleistocene and continuing historically with the extirpation of bison (*Bison bison*) and bighorn sheep (*Ovis canadensis*). We used DNA metabarcoding to test whether oryx dietary diversity, composition, and partitioning follows expected trends based on body size, digestive morphology and other functional traits, or

whether they fundamentally differ in these respects from native species. We found that introduced oryx do indeed “fit” within the native community as expected in terms of diet diversity and composition, however oryx exhibit lower dietary partitioning compared to native species. This may reflect competitive release due to limited coexistence time, although the role of interspecific competition in structuring native ungulate diets is uncertain. Importantly, oryx diet is highly similar to bison, suggesting they may restore some lost ecological function associated with large grazers in their introduced range. Our results underscore the importance of empirical data in informing both rewilding initiatives and introduced species management. Furthermore, we highlight how a broader temporal lens can provide valuable context for managing modern systems.

Environmental Controls on the Depositional Resolution of the Stratigraphic Record

Niklas Hohmann¹, Emilia Jarochowska¹

¹Department of Earth Sciences, Faculty of Geosciences, Utrecht University, The Netherlands

Reconciling observations made of different timescales is one of the major challenges for bridging the gap between paleoecology and neontological ecology. Due to mixing of sediments by burrowing organisms, paleorecords are time-averaged: fossils of different ages can be found at the same position. This limits the temporal resolution achievable in paleoecological studies. Considerable effort has been put into understanding depositional resolution of modern environments. However, estimates of time-averaging are based on dating individual fossils, a work-intensive approach that cannot be expanded beyond the time span of radiocarbon dating. As a result, researchers lack simple methods to constrain time-averaging (specifically in pre-Quaternary records), hindering comparisons made across timescales and depositional environments.

Mixing of surface sediments is controlled by ecological and sedimentological parameters such as sedimentation rate and bioturbation intensity, opening the opportunity to estimate the depositional resolution based on empirically traceable extrinsic factors. To explore the role of external controls of time-averaging, we inform the PartiMoDe model of particle movement with surface mixed layer parameters of modern marine environments taken from a global literature compilation published as the SMLBase. Surprisingly, we find that sedimentation rate, not bioturbation intensity, has the strongest effect on time-averaging, with values above 10000 years in deep sea environments. In addition, we find that below decimeter scale, the law of superposition begins to break down due to stratigraphic disorder.

Our results suggest that high sedimentation rate settings are most suitable to reconstruct rapid environmental and ecological transitions, and that recovery of age reversals will be increasingly common when sampling below decimeter scale in typical marine sediments. Applied to deep time, our model provides first insights into secular changes in depositional resolution throughout the Phanerozoic.

A ~1,200 year record of common eider population trends in the Eastern Canadian Arctic

Lau Katie Hong Kiu¹, Maliya Cassels¹, H. Grant Gilchrist², Greg J. Robertson³, John P. Smol⁴, Kathryn E. Hargan¹

¹Department of Biology, Memorial University of Newfoundland, 45 Arctic Avenue, St. John's, NL, Canada

²National Wildlife Research Centre, Environment and Climate Change Canada, Ottawa, Ontario, Canada

³Wildlife Research Division, Environment and Climate Change Canada, Mount Pearl, NL, Canada

⁴Paleoecological Environmental Assessment and Research Laboratory, Department of Biology, Queen's University, Kingston, Ontario, Canada

Often the lack of long-term monitoring data for seabird populations is a limiting factor in establishing meaningful and achievable conservation goals. To fill in this critical information gap, the sedimentary archives of lakes and peat receiving bird inputs (e.g., feces, feathers) can be used to track past changes in population size and dynamics. Common eider, a key species in the Arctic ecosystem, experienced significant population decline in the mid-20th century due to overhunting and climate change. The objectives of this study were to reconstruct population trends in a common eider nesting colony in the Eastern Canadian Arctic using peat deposits and to understand the impacts of changing climate, sea ice dynamics, and human influence on seaducks in the past ~1200 years. The beginning of peat accumulation at ~900 CE, along with high $\delta^{15}\text{N}$ values, likely indicates establishment of the eider colony around this time or shortly earlier. Seaduck nesting history was tracked using stable nitrogen isotopes ($\delta^{15}\text{N}$) and metal(loid)s and this was compared to climate reconstructions for the North Atlantic Oscillation, spring air temperature and sea surface temperature (SST). We found local eider population on the study island was greatest (i.e., above the long-term mean) during the Little Ice Age/ from 1600-1800 CE, when spring temperature and SSTs were low. We attribute this population increase to local topography—the study island is located at substantially higher elevation than other regional nesting islands, and thus greater nesting substrate and potentially less predator access would have been possible during colder climatic periods. Our record demonstrates that the eider nesting population on the study island during the post-industrial era dipped to its lowest over the 1200-year record. This confirms that the 20th century population decline was unprecedented within the eider nesting history.

Millennial scale reef community shifts in the Spermonde Archipelago, South Sulawesi

Michael G. Hynes^{1,2}, Dedi Parenden³, Sai Ke⁴, Kiri Spanowicz⁵, Halwi Masdar⁶, Singgih Afifa Putra⁷, Rohani Ambo-Rappe⁶, Jody M. Webster⁸, Bert Hoeksema^{1,9}, Nicole J. de Voogd^{1,5}, Willem Renema^{1,2}

¹Naturalis Biodiversity Center, PO Box 9517, 2300RA Leiden, The Netherlands

²Institute for Biodiversity and Ecosystem Dynamics (IBED), Universiteit van Amsterdam, P.O. Box 94240, 1090 GE Amsterdam, The Netherlands

³Department of Fisheries, Faculty of Fisheries and Marine Science, Universitas Papua, Manokwari 98314, West Papua Province, Indonesia

⁴Sorbonne Université, CNRS, EPHE, PSL, UMR METIS, Paris, France

⁵Institute of Biology, Leiden University, 2333 CC, Leiden, The Netherlands

⁶Marine Science Department, Faculty of Marine Science and Fisheries, Universitas Hasanuddin, Makassar, Indonesia

⁷Center for Quality Assurance Development of Vocational Education in Maritime, Fisheries, Information and Communication Technology (BPPMPV KPTK), 91271, Makassar, Indonesia

⁸Geocoastal Research Group, School of Geosciences, The University of Sydney, Sydney, NSW 2006, Australia

⁹Groningen Institute for Evolutionary Life Sciences, University of Groningen, P.O. Box 11103, 9700 CC, Groningen, The Netherlands

The Coral Triangle (CT) is the region in the Indo-Pacific with the highest diversity of reef organisms. Coral reefs in this area have experienced increased anthropogenic stressors since well before the 1980's due to factors such as increased destructive fishing practices, population growth, land reclamation/clearing, industrialization, and agriculture. Most biological observations began only after large-scale disturbances had already occurred in the region, resulting in limited insights into long-term community dynamics. To address this knowledge gap and mitigate shifting baseline bias, we documented community shifts over centennial and millennial timescales using 16 reef cores from two islands in the Spermonde Archipelago. These cores were previously dated using radiocarbon methods, and were analysed for the geomorphic history of these islands. Here we expand upon this by examining coral, sponge and foram community shifts over the past 7200 years. Our findings reveal a transition from more mixed morphologies (foliose, massive, and free living) to predominantly branching forms over the last 6000 years, likely driven by changing sea level regime and increased accommodation space. Furthermore, the species *Palauastrea ramosa* was identified in several core samples but has never been observed in modern surveys, suggesting historical shifts in coral communities. Foraminiferal assemblages on the reef flat transition from a more coral/rubble substrate assemblage to one increasingly associated with algal substrates in recent times. Finally, sponge spicule assemblages indicate an increase in cryptic/excavating sponges from the past to the present. Since these sponges are often found within coral rubble, their increase suggests that declining coral cover has created more habitat for these sponges. These findings demonstrate that community shifts were already occurring hundred to thousands of years before modern anthropogenic stressors began to accelerate these changes.

How well does the fossil record represent key biodiversity metrics? A test of palynological data as an archive of vegetation phylogenetic diversity

Phillip E. Jardine¹

¹University of Münster, Institute of Geology and Palaeontology, Münster, Germany

Reconstructing past biodiversity changes, and integrating these with modern biodiversity assessments, requires that fossil assemblages accurately capture key aspects of diversity (as represented by biodiversity metrics, for example). This is particularly challenging for the plant fossil record, where separate organs such as sporomorphs (pollen and spores) and leaves must be used as proxies for understanding vegetation composition and diversity change through time. Although much attention has been focused on how well fossil plant assemblages capture

variations in species richness, other aspects of diversity have until recently been relatively overlooked.

Here, I focus on phylogenetic diversity (PD), which represents the amount of evolutionary history contained in an assemblage of taxa. It can therefore provide a more detailed assessment of biodiversity gains and losses through time and space, and their underlying causes and consequences, relative to simple counts of the number of species present in a sample, and as such is used both as a conservation metric and as a tool to understand community assembly. To date, however, PD has been underexplored by palaeoecologists, and it is not currently known how well variations in vegetation PD across broad spatial scales are captured by sporomorph assemblage data. I compare estimates of seed plant PD from vegetation data and surface pollen samples from across North and South America. The results indicate a relatively low concordance between vegetation and pollen PD, and differing relationships with climate data, suggesting that sporomorph data cannot be used as a straightforward PD record. Other data sources (e.g. aDNA data for late Quaternary datasets, macrofossil data in deeper time settings) need to be considered for reconstructing vegetation PD through time. More generally, how well sporomorph data captures other aspects of plant biodiversity, and how successfully the plant fossil record can be used for conservation-relevant questions, ought to be critically (re-)assessed.

Testing hypotheses on the fossil record *in silico*: stratigraphic forward models of carbonate environments

Emilia Jarochowska¹, Johan Hidding², Xianyi Liu¹, Peter Burgess³, Hanno Spreeuw², Niklas Hohmann¹

¹Utrecht University, Department of Earth Sciences, Utrecht, the Netherlands

²The Netherlands eScience Center, Amsterdam, the Netherlands

³University of Liverpool, Department of Geology, Liverpool, United Kingdom

We do not have the tools to date precisely all events forming the geological record nor the gaps between them. As a result, empirical data on the timing of fossil dynamics comes with large uncertainties. It can be shown that under different hypotheses on how time is preserved in the geological record, opposing conclusions can be drawn on the dynamics of biodiversity and evolution.

We present an Open Source stratigraphic forward model of carbonate platforms, CarboKitten.jl. Forward models allow simulating stratigraphic architectures *in silico*, e.g. in order to understand how individual parameters affect these architectures and thus the preservation and recovery of fossils. Carbonates differ from other depositional models in being mostly produced by biomineralizing organisms. As a result, modelling them requires accounting for biological interactions in addition to physical environmental controls. CarboKitten.jl emulates spatial heterogeneity using cellular automata.

In this presentation, we propose examples of applications to paleoecological and evolutionary questions and give a short introduction to CarboKitten.jl. The software is developed in Julia, a performant language which allows rapid runs of large-scale models and attractive graphics.

Snake diversification rates estimated from occurrence data reveal a significant impact of the K-Pg extinction event on the group

Gabriela Karam¹, Tiago R. Simões², Daniele Silvestro³, Pedro L. Godoy¹

¹Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil

²Princeton University, Department of Ecology and Evolutionary Biology, Princeton, United States of America

³ETH Zurich, Department of Biosystems Science and Engineering, Basel, Switzerland

Snakes (Squamata: Serpentes) are one of the most diverse vertebrate groups, with more than 4,000 living species (35% of all extant squamates), and pronounced morphological and ecological diversity. Research on the group's diversification dynamics have been mostly focused on data from extant species, thus neglecting fossil evidence of extinct lineages. Debates surrounding the relationship between snakes and other squamates and the origin of the group further highlight the central role of their fossil record to better comprehend squamate evolutionary dynamics. Here we compile data from more than 1,400 fossil occurrences and estimate rates of speciation, extinction, and diversification for total group Pan-Serpentes using birth-death models within a Bayesian framework. Our analyses revealed time varying dynamics of diversification in the group. In addition, in contrast to the findings of previous studies on squamates, we identified a significant effect of the end Cretaceous extinction event in snake evolution. The event resulted in a major drop in diversification at the K-Pg boundary caused by higher extinction rates, followed by an increase in net diversification, driven by lowering extinction rates and higher speciation rates. This finding shows that snakes, as well as other vertebrates, were highly affected by the changes in ecosystems at the time, but also responded to the opening of ecological opportunities in the subsequent millions of years. By integrating paleontological data with an innovative methodology, this study expands the knowledge on the evolution of a group of enormous scientific and popular interest, shedding light on periods of greater and lesser diversification in Pan-Serpentes.

The impact of Permian–Triassic mass extinction on marine trophic web structure

Baran Karapınar¹, Tanya Strydom², Andrew Beckerman², William Foster³, Alex Dunhill¹

¹University of Leeds, School of Earth and Environment, Leeds, United Kingdom

²School of Biosciences, Ecology and Evolutionary Biology, University of Sheffield, Sheffield, United Kingdom

³Universität Hamburg, Institut für Geologie, Hamburg, Germany

The fossil record has great potential to improve our understanding of community response to significant ecosystem perturbations. In most palaeobiological studies, extinctions are assumed as primary loss of taxa due to environmental perturbations, but the degree to which primary extinctions cause secondary extinction cascades is not well understood. Here, we modelled food webs of marine communities across the Permian–Triassic mass extinction, the largest extinction

event in Earth's history that is associated with extreme global warming. We use an ecological modelling approach in combination with the most comprehensive occurrence dataset from Meishan, China, at a very high stratigraphical resolution. Using the modelled food-webs, we evaluated which extinctions were likely a result of secondary cascades, tested for extinction selectivity against ecological traits using simulations, and tested for robustness of food-webs against secondary extinctions throughout the pre-extinction, extinction, and post-extinction intervals. Most of the extinctions can be attributed to secondary cascades either caused by perturbations in primary productivity or changes in trophic interactions. Despite significant diversity loss, especially amongst primary consumers, four trophic levels persisted throughout the extinction interval. However, these low diversity post-extinction communities had lower functional redundancy which appears to have driven higher levels of connectance by generalists. Extinction simulations suggest that these densely connected post-extinction communities displayed increased robustness against secondary extinction cascades compared to the highly diverse, less connected pre-extinction communities with high functional redundancy. These results raise a question as to whether diverse communities with high degrees of specialism and functional redundancy are more prone to high magnitude of extinctions rather than being more resilient.

Cephalopods as ecosystem engineers

Christian Klug¹, Dirk Fuchs², Alexander Pohle³, Dieter Korn⁴, Kenneth De Baets⁵, René Hoffmann³, Peter Ward⁶, Gregor Mathes⁷

¹University of Zurich, Dept. Of Palaeontology, Zürich, Switzerland

²Bayerische Staatssammlung Für Paläontologie Und Geologie, Munich, Germany

³Ruhr-Universität Bochum, Institut für Geologie, Mineralogie & Geophysik, Bochum, Germany

⁴Leibniz Institute for Research on Evolution and Biodiversity, Museum für Naturkunde, Berlin, Germany

⁵University of Warsaw, Institute of Evolutionary Biology, Warsaw, Poland

⁶University of Washington, Department of Biology, Seattle, USA

⁷Friedrich-Alexander-Universität, GeoZentrum Nordbayern, Erlangen, Germany

During their almost half a billion years of evolutionary history, cephalopods repeatedly diversified, overall increased in size and also in abundance. We sought the literature and collections for the largest representatives of the four major groups, (1) early cephalopods with straight conical shells (orthocones), (2) nautilids including their modern species, (3) ammonoids, and (4) neocoleoids including squids and octopuses (taxonomy after Hoffmann *et al.* 2022). We measured their size and determined their volumes for comparability. It turned out that all groups except the orthocones (1) showed an overall exponential size increase throughout their evolution, where the increase is the steepest among the neocoleoids (4) and the shallowest among nautilids (2). Conch length reached at least five metres among the orthocones, in the coiled forms the maximum diameter was about two meters, and the mantle length among neocoleoids reaches over three meters today. Although both their diversity and abundance fluctuated profoundly, they were often very important components of marine foodwebs.

Most of the included taxa evolved means to regulate their buoyancy. Swimming abilities in horizontal and vertical direction varied significantly between taxa. Importantly, many

cephalopod taxa from the Ordovician until today migrate vertically, often even diurnally. By doing so, they transport oxygen and nutrients into deeper regions of the marine realm and likely improved living conditions for many organism groups (Butterfield 2017). Our new data suggest that cephalopods contributed greatly to the expansion of the marine ecospace during their evolution.

Invasion and Interaction: Diversity shifts in the Nashville Basin during the Late Ordovician Richmondian Invasion

Shymah Beegam Kundladi¹, Alycia L. Stigall¹

¹Department of Earth, Environmental & Planetary Sciences, The University of Tennessee, Knoxville. 1621 Cumberland Avenue, Knoxville, TN 37996-1526, USA

Biotic immigration events significantly reshape ecosystems, altering biodiversity patterns and community structures. One of the most well-documented fossil invasions is the Late Ordovician (Katian) Richmondian Invasion, during which over 60 genera—including brachiopods, bryozoans, mollusks, and corals—expanded into the Eastern Laurentian basin. Spanning roughly three million years, this invasion dramatically transformed marine communities and is particularly well-documented in geological strata around Cincinnati, Ohio, and Nashville, Tennessee, USA. It serves as a prime example of a coordinated invasion, where multiple taxa invade simultaneously, leading to substantial and lasting ecological shifts. Such events affect species richness, evenness, dominance, and niche partitioning, ultimately influencing biomass distribution and biodiversity structure.

While the Richmondian Invasion's impact on the Cincinnati Basin has been extensively studied, its effects on the Nashville Basin remain less explored. This study investigates how faunal responses to the invasion in Nashville basins, focusing on ecological and taxonomic aspects. To analyze these dynamics, stratigraphically constrained species occurrence data for the Katian stage were compiled from literature, databases (PaleoDB and iDigBio), and fieldwork. The diversity trends and interactions between native and invasive species were examined using PyRate, a Bayesian framework that estimates speciation, extinction, and preservation rates from fossil records. Specifically, the Multivariate Birth-Death Model in PyRate was used to assess whether the diversity of one clade—such as specialists versus generalists or invasive versus native taxa—suppressed or promoted the origination and extinction of other clades.

The results reveal significant diversity shifts in the Nashville Basin following the Richmondian Invasion. Native taxa experienced declines, whereas invasive taxa exhibited increased diversification. Invasive generalists suppressed the origination of native generalists while promoting their extinction due to niche overlap and differing ecological tolerances. However, the rise in standing diversity contributed to ecosystem stability, with invaders potentially enhancing food web complexity.

Extinction patterns in sloths are explained by life history traits, not phylogeny

Fernanda D. P. Landim¹, Daniel M. Casali², Thayara S. Carrasco¹, Pedro L. Godoy¹

¹Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil

²Department of Biology, University of São Paulo, Ribeirão Preto, Brazil

Sloths (Folivora, Xenarthra) are a peculiar mammalian clade that maintained high diversity throughout most of its evolutionary history, but showing a significant decline towards the present. Multiple extinction events reduced the group's richness, ecomorphological diversity, and geographic range, with the Pleistocene-Holocene megafaunal extinction being a key example. Extinction selectivity can be influenced by phylogenetic factors—in which closely related taxa share traits that increase their susceptibility to extinction—or by non-phylogenetic factors, such as ecological or environmental pressures affecting taxa independently of their evolutionary relationships. To investigate the drivers of such decline in Folivora, the association between extinction and both phylogeny and paleobiology was analyzed using quantitative methods. Two time-calibrated phylogenies were employed to account for temporal and phylogenetic uncertainties. To assess whether extinctions were phylogenetically clustered, the *D*-statistics method was applied, considering extinction/survival as a binary trait across different time bins. Values close to 0 indicate clustered extinctions, whereas values near 1 suggest a random distribution. Significance was evaluated using *p*-values by comparing observed patterns to expectations under random and Brownian motion models, the latter representing phylogenetically-structured extinctions. The results revealed non-phylogenetic extinctions in Folivora throughout their entire evolutionary history. To test for ecological drivers, phylogenetic generalized linear models were applied, considering three variables: diet, substrate use, and body size. Results showed a significant association between substrate use and extinction risk during the Early Miocene in both phylogenies, as well as associations between extinctions and both substrate use and body size during the Pleistocene in one phylogeny. These findings indicate that extinctions in Folivora are non-phylogenetic and driven by ecological factors, such as body size and substrate use in certain periods, whereas other potential drivers remain to be evaluated.

Using paleoecology to explore resilient lifeways in the face of abrupt climate change

Madeleine M. Landrum^{1,2}, Kit M. Hamley^{1,2}, Bonnie D. Newsom^{2,3}, Reuben Hudson⁴, Chris Guiterman^{5,6}, Chris Sockalexis⁷, Donald Soctomah⁸, Jacquelyn L. Gill^{1,2}

¹University of Maine, School of Biology and Ecology, Orono, USA

²University of Maine, Climate Change Institute, Orono, USA

³University of Maine, Department of Anthropology, Orono, USA

⁴College of the Atlantic, Department of Chemistry, Bar Harbor, USA

⁵University of Colorado at Boulder, Cooperative Institute for Research in Environmental Sciences (CIRES), Boulder, USA

⁶NOAA's National Centers for Environmental Information (NCEI), USA

⁷Penobscot Nation Tribal Historic Preservation Office, Indian Island, USA

⁸Passamaquoddy Tribal Historic Preservation Office, Princeton, USA

The transition between the Atlantic and Subatlantic chronozones (6,000 – 4,000 BP) was a period of widespread global changes, resulting in increased aridity in the subtropics of the Northern Hemisphere, cooling at mid- and high-latitudes, and the establishment of a regular El Niño cycle. Northeastern North America experienced significant climatic and ecological changes, including persistent drought, declining temperatures along the coasts, and shifts in forest composition. We reconstructed fire regimes, vegetation dynamics, and human presence to investigate the relationships between people and their environment during this period of abrupt change using a multi-proxy sediment record from Witch Hole Pond in Acadia National Park, Maine, USA. Our results revealed that regional fire decreased during the transition period, while local fire persisted. Pollen data indicated increased abundance of fruit- and nut-bearing taxa alongside fire-reliant taxa, despite declining temperatures and high fuel loads from the regional hemlock decline. These patterns suggest anthropogenic burning played a key role in shaping landscape and fire dynamics during a period of declining precipitation that reduced access to traditional lifeways during the climatic transition. Despite these difficult conditions, people remained consistently present in the watershed, as evidenced by fecal sterols and the archaeological record. By diversifying their diets to include new forest resources, people promoted ecological resilience during a period of widespread and abrupt environmental change. Our findings provide critical insights into the interplay between cultural practices and ecological resilience via the adaptive strategies of the ancestors of the Wabanaki peoples. By exploring past human-environment interactions, we aim to support a growing understanding of how traditional ecological knowledges and anti-colonial approaches to paleoenvironmental science can inform modern approaches to climate adaptation and forest resilience while also supporting tribal goals today.

Using species distribution models to assess faunal extinction risk in the past

Ignacio A. Lazagabaster^{1,2}, Chris Thomas³, Juliet V. Spedding⁴, Salima Ikram⁵, Steven Snape⁴, Jakob Bro-Jorgensen²

¹National Research Center on Human Evolution (CENIEH), Burgos, Spain

²University of Liverpool, Department of Ecology and Behaviour, Liverpool, United Kingdom

³University of York, Department of Biology and Leverhulme Centre for Anthropocene Biodiversity, York, United Kingdom

⁴University of Liverpool, Department of Archaeology, Classics and Egyptology, Liverpool, United Kingdom

⁵The American University in Cairo, Department of Sociology, Egyptology and Anthropology, New Cairo, Egypt.

The analysis of faunal extinctions has traditionally relied on fossil records, which are often limited by temporal and spatial biases. To broaden this approach, species distribution models (SDMs) combined with paleoclimatic simulations offer a comprehensive method to predict the distribution of past suitable habitats and enhance our understanding of extinction risk patterns based on fossil data. This case study investigates the impacts of climate change, biodiversity shifts, and human activities on large mammal taxa in Holocene northeast Africa. Utilizing modern occurrence data from online repositories and documented range distributions, we modeled the historical habitat suitability for 56 large mammal taxa. The results are integrated

with societal changes observed in ancient Egypt and its zooarchaeological record, facilitating a comparative analysis of extinction risks derived from zooarchaeological records and paleoclimatic models. This approach helps hypothesize the distinct roles of climate change and human activities in shaping past biodiversity. While some species likely became extirpated from the region due to climatic changes, the persistence of suitable habitats for other taxa through time underscores the potentially significant role of human impacts on biodiversity, extending beyond the effects of climate change.

Understanding the causes and chronology of local extinctions of the Cuban crocodile (*Crocodylus rhombifer*) across the Holocene Caribbean to inform its future conservation

Sachin Bhardwaj Lock^{1,2,3}, James Hansford⁴, Samuel Turvey³, Advait Jukar⁵, Philip Mannion¹

¹University College London, Department of Earth Sciences, London, UK

²Natural History Museum London, Department of Earth Sciences, London, UK

³Institute of Zoology, Zoological Society of London, London, UK

⁴Queen Mary University of London, School of Biological and Behavioural Sciences, London, UK

⁵Florida Museum of Natural History, Vertebrate Paleontology, Gainesville, Florida, USA

The Cuban crocodile (*Crocodylus rhombifer*) is today one of the most critically endangered and range-restricted extant crocodylian species. Its present endemism belies a recent history that saw its populations span the Greater Antilles and the Lucayan Archipelago. Despite a rich fossil record, the chronology and causes of the species' decline over the course of the Holocene remain largely unknown. Using a holistic approach, incorporating data from the fossil record and historical archives into species distribution models, we disentangle the compounding factors that drove a formerly widespread species to the brink of extinction. Extinction chronology mapping strongly implicates anthropogenic drivers of extinction, suggesting extinction events correlating with the spread of Taíno peoples over the past millenium and accelerating following the arrival of Europeans in the late 15th century. With exceptions, the observed pattern of range collapse is generally consistent with the theory of island biogeography, with larger and less-isolated landmasses providing the most enduring refugia. Estimates of body sizes from zooarchaeological and historical specimens suggest patterns of evolution driven by insular biogeography, with smaller landmasses generally associated with smaller morphologies. New, reduced estimates for the upper limits of *C. rhombifer* body sizes suggest the necessity of a revision of our understanding of the species' palaeoecology. This longer term approach to assessing threats to species survival can track extinction events and anthropogenic forces across much longer timescales than are usually considered in conservation, contributing novel baselines for species status, an increased understanding of extinction dynamics, and a more robust assessment of species vulnerability and resilience to human pressures. This work aims to inform potential future rewilding efforts that may prove vital to this marginalised species' ongoing survival.

Using the (sub)fossil record of the Australian Anthropocene to inform biodiversity conservation

Julien Louys¹, Nicole Boivin^{2,3,4}

¹Griffith University, Australian Research Centre for Human Evolution, Brisbane, Australia

²Max Planck Institute for Geoanthropology, Jena, Germany

³Griffith University, School of Environment and Science, Brisbane, Australia

⁴University of Queensland, School of Social Sciences, Brisbane, Australia

Australia is unique amongst major landmasses in having an endemic fauna that was largely (but not wholly) isolated from all other biogeographic regions for millions of years. It is also home to the world's oldest continuous living culture, which emphasises 'caring for Country' - the management of landscapes and environments through practices such as using controlled fire application, hydrological manipulation and the shaping of plant and animal distributions. Both natural and anthropogenic systems were severely disrupted by the arrival of Europeans, who brought with them foreign invasives and pathogens, and displaced thousands of Indigenous communities and millions of native species to make way for European-derived systems of agriculture and urbanisation. This has resulted in Australia recording the largest number of modern mammal extinctions of any continent. While the Australian fossil record is beginning to shed light into Australian ecosystems in the last few thousand years, one aspect of the (sub)fossil record which has received very little attention is that of the last few hundred years. This is a critical period that in other countries is tolerably well documented in historical (written) records. Such records do not exist for Australia, or were created well after most changes had occurred. Here, we present a multidisciplinary effort to use the faunal, geological, and ecological record to shed light on this key transitional period of Australian history, including ancient and sedimentary DNA, palaeogenomics, morphological analyses, rock art research as well as traditional excavations and other palaeontological techniques, and outline how these findings might help inform modern conservation efforts.

The evolution of ecosystem and Earth system engineering

Kathleen S. Lyons¹, Shupinski, Alex B.^{1,2}, Bates, Amanda E.³, Casey, Michelle M.⁴, Clapham, Matthew E.⁵, Contreras, Dori L.⁶, Craffey, Matthew¹, Cribb, Alison T.⁷, Darroch, Simon A.F.⁸, Duijnste, Ivo A.P.^{9,10}, Gearty, William¹¹, Hamilton, Marcus J.^{12,13}, Hayes, Riley F.^{9,10}, Hull, Pincelli M.¹⁴, Ibarra, Daniel E.¹⁵, Lee, Jaemin^{9,10}, Looy, Cindy V.^{9,10}, Lyson, Tyler R.¹⁶, Muddiman, Benjamin¹⁷, Roopnarine, Peter D.¹⁸, Sjosten, Sara¹⁹, Smith, Felisa A.²⁰, Stigall, Alycia L.²¹, Tomé, Catalina P.²², Turk, Katherine A.²³, Villaseñor, Amelia²⁴, Wagner, Jenn^{9,10}, Wagner, Peter J.^{1,25}, and Wang, Steve C.²⁶

¹School of Biological Sciences, University of Nebraska Lincoln, Lincoln NE, USA

²Department of Natural Resource Management, South Dakota State University, Rapid City, SD, USA

³Biology Department, University of Victoria, Victoria, British Columbia, Canada

⁴Department of Physics, Astronomy and Geosciences, Towson University, Towson, MD, USA

⁵Department of Earth and Planetary Sciences, University of California, Santa Cruz, CA, USA

⁶Science Division, Perot Museum of Nature and Science, Dallas TX, USA

⁷School of Ocean and Earth Science, University of Southampton, Southampton, UK

⁸Senckenberg Museum of Natural History, Frankfurt am Main, Germany

- ⁹Department of Integrative Biology, University of California, Berkeley, CA, USA
- ¹⁰University of California Museum of Paleontology, Berkeley, CA, United States
- ¹¹Open Source Program Office, Syracuse University, Syracuse, NY USA
- ¹²Department of Anthropology & School of Data Science, University of Texas at San Antonio, San Antonio, TX, USA
- ¹³Santa Fe Institute, Santa Fe, NM, USA
- ¹⁴Department of Earth and Planetary Sciences, Yale University, New Haven, CT USA
- ¹⁵Department of Earth, Environmental and Planetary Science, Brown University, USA
- ¹⁶Department of Earth Sciences, Denver Museum of Nature & Science, Denver, CO, 80205, USA
- ¹⁷Department of Biological and Chemical Sciences, Thomas Jefferson University, Philadelphia, PA, USA
- ¹⁸Department of Invertebrate Zoology and Geology, California Academy of Sciences, San Francisco, CA, USA
- ¹⁹Faculty of Environment, Science and Economy, University of Exeter, Exeter, UK
- ²⁰Department of Biology, University of New Mexico, Albuquerque, NM, USA
- ²¹Department of Earth, Environmental & Planetary Sciences, University of Tennessee, Knoxville, TN, USA
- ²²Indiana State Museum and Historic Sites, Indianapolis, IN, USA
- ²³Department of Paleobiology, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA
- ²⁴Department of Anthropology, University of Arkansas, Fayetteville, AR, USA
- ²⁵Department of Earth & Atmospheric Sciences, University of Nebraska–Lincoln, Lincoln, NE, USA
- ²⁶Department of Mathematics and Statistics, Swarthmore College, Swarthmore, PA, USA

Over the last ~3.5 billion years, life has increasingly modified our planet with successive waves of evolutionary innovation leading to stronger controls over the distribution and flow of resources and influencing the character and distribution of ecological niches. The recognition that some taxa have oversized effects on other species and the environment led to the concept of ‘ecosystem engineers’ (EE). Extending this concept into a deep-time and evolutionary context poses conceptual challenges. To accommodate uncertainty and unknowns in the fossil record, we focus on the resultant processes rather than on specific taxa as ecosystem engineers. We also propose a new concept – ‘Earth system engineering’ (ESE) – to describe biologic processes whose influence is particularly extensive, altering the structure and function of planetary spheres and impacting the habitability of the planet as a whole. Using this framework, we quantify the richness and functional diversity of ecosystem and Earth system engineering processes over the last 4 billion years encompassing six broad organismal groups (microbes, fungi, vertebrates, invertebrates, plants, and humans). We find that ecosystem and Earth system engineering processes appear as soon as life evolves, and once they appear they rarely go extinct. Ecosystem engineering processes are much more common than Earth system engineering processes, but the diversity of both increases with the evolution of multicellular life. The functional diversity of ecosystem engineering processes reached its maximum by the Cambrian and has remained at that level to the present. In contrast, functional diversity of Earth system engineering processes increased in a stepwise manner with the acquisition of new areas of the planet or new morphologies. Humans, a single species, perform almost as many ecosystem or earth system engineering processes as entire divisions of the tree of life, but they do not increase the overall functional diversity of ecosystem or Earth system engineering processes.

Disentangling the seabird nesting history of Green Island in Witless Bay Ecological Reserve, NL using paleolimnology

Elizabeth Mack¹, A. Lang¹, K. Hargan¹

¹Memorial University of Newfoundland, Biology, St. John's, Canada

Seabird colonies transport marine-derived nutrients to their terrestrial nesting sites, influencing nutrient dynamics in nearby terrestrial, freshwater, and marine ecosystems. In remote northern regions, where census data are sparse, reconstructing historical seabird populations is key to understanding long-term ecological changes and informing conservation. This study aims to reconstruct seabird population dynamics on Green Island (47°14'17" N, 52°46'49" W) in the Witless Bay Ecological Reserve, a major nesting site for Atlantic puffin (*Fratercula arctica*) and common murre (*Uria aalge*). Limited access due to steep cliffs surrounding the colony has resulted in sparse census data. A multi-proxy paleolimnological approach was used to validate and extend seabird population records beyond existing data (circa 1940 CE), integrating $\delta^{15}\text{N}$ isotopes, diatom assemblages, chlorophyll a concentration, and metal(loid) concentrations from a dated sediment core. In addition, pollen analysis and aerial photographs were used to track ecosystem changes, particularly related to a shift from burrow to cliff-nesting species.

The sediment core provides a chronological record spanning approximately 170 years, from the surface to a depth of 20 cm. Preliminary results indicate a steady increase in seabird population on Green Island, with $\delta^{15}\text{N}$ values peaking in the early 1950s, suggesting a period of peak seabird influence. However, these elevated $\delta^{15}\text{N}$ values during this period may also reflect seabirds foraging at higher trophic levels, possibly due to ocean warming at that time. Furthermore, an increase in Z-scores across all parameters throughout the core suggests a consistent environmental or ecological shift over time. This trend of increasing seabird presence validates historical seabird surveys conducted on the island. By extending seabird population records beyond existing census data, this research provides new insights into past seabird dynamics and their relationship with environmental change. Understanding these long-term patterns is crucial for developing effective conservation strategies in a rapidly changing climate.

The impact of the quality of the fossil record on reconstructing niches

Katherine M. Magoulick^{1,2}, Mac Boroza^{1,2}, Charles R. Marshall^{1,2}

¹University of California Museum of Paleontology, University of California, Berkeley, CA, USA

²Department of Integrative Biology, University of California, Berkeley, CA, USA

Paleontological data has been used to improve the quality of Ecological Niche Models (ENMs) including by showing that human disturbance has driven some species to sub-optimal habitats. However, no studies have directly examined the degree to which “fossil” and modern ENMs are in agreement. To fossilize, organisms must be preserved in areas with sedimentation, so the overlap between a species’ current geographic range and the geographic distribution of sedimentary basins can serve as a first order approximation of what the observed geographic range of the species will look like in the future fossil record. Pineda-Munoz *et al.* (2021) found

that in the United States, terrestrial mammals altered their niches most in areas that overlap with human impacts. In this study we utilize these same data to compare the modeled niches based on all modern occurrences with the modeled niches based on the inferred future fossil record. Our results indicate differences in the modeled niches between the present and future fossil record for the terrestrial mammals analyzed by Pineda-Munoz *et al.* (2021). The results have important implications for the effectiveness of paleontological ENMs.

Tracing coral morphological traits during the Early Paleogene hothouse

Luca Mariani¹, Francesca Bosellini¹, Andrea Benedetti³

¹University of Modena and Reggio Emilia, Department of Chemical and Geological Sciences, Modena, Italy

²Department of Natural Sciences, Liceo “Isabella d’Este”, Tivoli, Italy

Coral morphological traits encompass the physical and structural characteristics that define the shape, size, and growth patterns of coral species. Studies on modern corals show that these traits are critical for understanding how corals interact with their environment, influencing their ability to capture light for photosynthesis, withstand water currents, resist sedimentation, and provide habitats for marine organisms. Additionally, morphological traits play a crucial role in determining coral resilience to environmental stressors including temperature fluctuations, ocean acidification, and physical damage from storms or anthropogenic activities. Recent studies have extended the analysis of these traits to the fossil record, in order to characterize corals ecological strategies and extinction risk.

To investigate how morphological traits evolved and/or responded to a climate significantly warmer than the present, we focused on the early Paleogene “hothouse”, the warmest interval of the Cenozoic. We utilized the record of reef corals (i.e., zooxanthellate colonial corals) from the Western-Central Tethys, which was a global center of reef coral diversity, preserving the most comprehensive record for this time interval. We compiled a dataset of morphological traits from literature sources and both personal and museum collections. Our dataset includes data about colony size, colony integration, budding type, colony form and degree of branching, corallite size, corallite spacing, number of septa, and columella type, on a total of more than 1300 occurrences. Data were grouped according to the age bins of the Paleocene-Eocene (Danian, Selandian, Thanetian, Ypresian, Lutetian, Bartonian and Priabonian) and were analyzed using descriptive, bivariate, and multivariate statistics.

Our study represents the first analysis of a broad suite of fossil coral morphological traits conducted at a regional scale with fine stratigraphic resolution. Results may pave the way for further research about the use of coral traits as paleoclimatic and paleoenvironmental proxies.

Hermann's tortoise (*Chersine hermanni*) from Cueva de la Buena Pinta (Middle to Late Pleistocene; Pinilla del Valle, Spain): Palaeoecological Insights and Conservation Implications

Rafael Marquina-Blasco^{1,2,3}, Clara Mielgo^{4,5}, David Martín-Perea^{4,6,7}, Hugues-Alexandre Blain^{4,5}, Rosa Huguet^{4,5,8}, César Laplana^{9,10}, Alfredo Pérez-González^{7,11}, Juan Luis Arsuaga^{6,12}, Enrique Baquedano^{7,10}

¹Universitat de València, Departament de Botànica i Geologia, Valencia, Spain

²Centro de Investigação em Ciências Geo-Espaciais, Universidade do Porto, Vila Nova de Gaia, Portugal

³Museu Valencià d'Història Natural, Alginet, Spain

⁴Institut Català de Paleoecologia Humana i Evolució Social, Tarragona, Spain

⁵Universitat Rovira i Virgili, Departament d'Història i Història de l'Art, Tarragona, Spain

⁶Universidad Complutense de Madrid, Departamento de Geodinámica, Estratigrafía y Paleontología, Madrid, Spain

⁷Universidad de Alcalá de Henares, Institute of Evolution in Africa, Alcalá de Henares, Spain

⁸Museo Nacional de Ciencias Naturales (CSIC), Departamento de Paleobiología

⁹Universidad de Alcalá de Henares, Department of Geology, Geography and Environmental Sciences, Alcalá de Henares, Spain

¹⁰Museo Arqueológico y Paleontológico de la Comunidad de Madrid, Alcalá de Henares, Spain

¹¹Asociación Nacional El Hombre y el Medio, Madrid, Spain

¹²Centro Mixto UCM-ISCIII de Evolución y Comportamiento Humanos, Madrid, Spain

The Calvero de la Higuera Archaeological Complex (Pinilla del Valle, central Spain) consists of five karstic sites which have yielded a large number of vertebrate fossils, mostly from the Late Pleistocene. Among them, Cueva de la Buena Pinta stands out for its complex stratigraphy, covering part of the Middle Pleistocene (> MIS 7) and the first half of the Late Pleistocene. Successive excavation campaigns at the site from 2011 to 2019 have yielded numerous tortoise remains (an almost complete carapace and 91 isolated elements) in Units 23 (Late Middle Pleistocene) and 2/3 (Middle Late Pleistocene), located in the western area of the site. The morphology of these elements is consistent with *Chersine hermanni*, the only native tortoise in the Iberian Peninsula.

Due to the high altitude at which the site is located, approximately 1,100 meters above sea level, the presence of *Chersine hermanni* has interesting implications from both a palaeoecological perspective and for the current conservation of the species. *C. hermanni* is an endangered species with a highly fragmented distribution. Two subspecies are recognized: one inhabiting Western Europe, *Chersine hermanni hermanni*, and another located in Eastern Europe, *Chersine hermanni boettgeri*. Both taxa exhibit significant differences in their conservation status and distribution, with the Eastern European subspecies having a more continuous range, composed of less fragmented populations, and reaching significantly higher altitudes.

Our results indicate that *C. h. hermanni* had a broader ecological tolerance in the past and inhabited conditions not currently found within the species' climatic range in Spain. Furthermore, our work highlights the need to consider the recent historical distribution when developing conservation policies for endangered species.

Information loss in the fossil record

Marta Matamala-Pagès¹; Adrián Castro-Insua¹; Adriana Oliver¹; Eduardo Méndez-Quintas¹, Graciela Sotelo¹, Iván Rey-Rodríguez¹; Sara Gamboa¹; Sofía Galván¹; Sara Varela^{1,2}

¹Centro de Investigación Mariña, Universidade de Vigo, MAPAS Lab. 36310 Vigo, Spain

²Oportunus. Axencia Galega de Innovación, 15702 Santiago de Compostela, Spain

Data from the fossil record have allowed (and continue to allow) the reconstruction of the palaeoenvironments and ecological niches occupied by different species over time. However, the large-scale fossil record is biased, which presents an important challenge for the interpretation of past evolutionary trajectories and climatic changes. In fact, these uncontrollable biases can lead to an incomplete view of diversity, affecting the ability to accurately reconstruct evolutionary trajectories and adaptive patterns. Thus, this work aims to identify the areas with the greatest potential for fossil preservation and to quantify the fossil information lost over time. To do so, we have combined: 1) climatic data of temperature and precipitation (from the HadCM3 model), 2) data from fossil observations (NOW database and PaleobioDB) and 3) layers of sedimentary areas (generalized global geological map compiled by Chorlton, 2007). The Köppen-Geiger climate classification has been then applied to assign climatic categories to the different regions of the planet to compare which biomes have a lower potential for fossilisation and thus a higher loss of the fossil record over time. How much information is available for each biome across time?

A dhole's tale: using the Pleistocene fossil record of the dhole (*Cuon alpinus*, Pallas 1811) to understand modern threats and future conservation challenges

Mollie Mills¹, Danielle Schreve², David Redding³, Simon Blockley¹

¹Royal Holloway University of London, Department of Geography, Surrey, United Kingdom

²University of Bristol, School of Geographical Sciences, Bristol, United Kingdom

³Natural History Museum, Biodiversity and Health, London, United Kingdom

The dhole (*Cuon alpinus*, Pallas 1811) is a medium-sized evolutionarily distinct canid, currently distributed only in Southeast Asia after experiencing drastic range contraction and eventual extirpation from North America and Europe after the Late Pleistocene. Despite being threatened by prey depletion, habitat destruction and competition, little is known about the dhole's distribution and ecology. Dhole-specific conservation strategies are minimal, if not entirely absent in most range countries. Populations reside mainly in areas designated as protected for other charismatic species, such as tigers and elephants, but their adequacy for dhole conservation is undetermined. Species distribution models (SDMs) that relate georeferenced occurrence records to environmental variables could be used to identify suitable dhole conservation strategies. However, modern dhole distribution data is sparse and heavily influenced by human interactions, which could introduce bias into model projections and misinform conservation actions. Incorporating the dhole's Pleistocene fossil record into models could potentially reduce the effects of limited contemporary ecological data, by including palaeoclimate, palaeoenvironmental and competitive forcing factors over a longer time period.

Fossil records can offer deep time insights into the responses to past environmental change of both individual species and ecological communities, as well as broadening understanding of species' full environment relationships prior to extensive human activity.

Bivalve body-size and geographical range variability: a long-term view on temperature effects

Coraline Montariol¹, Claude Monnet¹, Sébastien Clausen¹

¹Université de Lille, EEP, Lille, France

The relationship between body size and geographical range of marine organisms are two essential parameters to understanding the evolution of species, as well as their ecology and ecosystems. This study investigates the patterns of temperature-related body size evolution and the impact of temperature variations on the geographical distribution of bivalve genera over geological time. Using fossil records available on paleobiological databases, body size and geographical trends have been reconstructed from the Ordovician to Neogene at a genus level. A correlation has been made with paleotemperature proxies to explore how climatic fluctuations have driven size and range expansion, contraction, or shift. To do this, the median latitudinal range and the median volume of each species are calculated for all the Phanerozoic stages included in our analysis.

Our results confirm that periods of global warming were generally associated with reductions in body size, supporting Bergmann's rule, which suggests smaller body sizes in warmer climates. Conversely, cooler periods coincided with larger body sizes and expanded geographical ranges, indicating that temperature was critical in shaping bivalves' body size and biogeography. Furthermore, we noted that genera with larger body sizes tend to inhabit wider ranges, possibly due to their enhanced ecological adaptability and ability to withstand environmental changes.

This research corroborates the crucial role of temperature as a primary driver of macroecology patterns in marine invertebrates. It offers valuable insights into how forthcoming climate change might impact bivalve species' body size and distribution. Our findings enhance our understanding of the long-term dynamics of marine biodiversity and the evolutionary strategies organisms adopt to adapt to climatic changes.

Dietary partitioning and ecosystem structural shifts revealed by dental microwear in faunivorous megatheropod dinosaurs during the Cretaceous

Cassius Morrison^{1,2}, James Gregory^{3,4}, Christopher Jackson^{3,4}, Katlin Schroeder⁵, Jordan Bestwick⁶, Samuel Gascoigne⁷, Paul Bills^{3,4}, Laura Porro⁸, Philip Mannion¹, Paul Barrett²

¹Department of Earth Sciences, University College London, Gower Street, London WC1E 6BT, UK

²Fossil Reptiles, Amphibians and Birds Section, Natural History Museum, Cromwell Road, London SW7 5BD, UK

³EPSRC Future Metrology Hub, School of Computing & Engineering, University of Huddersfield, Queensgate, Huddersfield HD1 3DH

⁴Centre for Bio-Interface Engineering, School of Computing & Engineering, University of Huddersfield, Queensgate, Huddersfield HD1 3DH

⁵Yale Institute for Biospheric Studies, Yale University, New Haven, Connecticut, 06520, US

⁶Paläontologisches Institut und Museum, Universität Zürich, Karl-Schmid-Strasse 4, Zürich, 8006, Switzerland

⁷School of Biological Sciences, University of Aberdeen, King's College, Aberdeen, AB24 3FX

⁸Centre for Integrative Anatomy, Department of Cell and Developmental Biology, University College London, Gower Street, London WC1E 6BT, UK

The presence of numerous sympatric medium- to large-bodied theropod dinosaurs in Cretaceous formations raises questions regarding inter- and intraspecific competition, and its effects on community structure. Dietary niche partitioning may decrease such competition. However, establishing dinosaurian diets has often relied on tooth morphology or stomach contents, both of which have limitations. Recent work examining the dental microwear of extant and extinct archosaurs and lepidosaurs has shown that dietary guilds can be determined for fossil taxa more precisely. Here, we use 3D dental microwear texture analysis (DMTA) to constrain the diet of 20 species across all dentulous neotheropod clades. Dietary guilds are defined via DMTA of extant crocodylians with known diets. Our results show evidence for piscivory in *Torvosaurus* and *Ceratosaurus*, and possible invertivory in the tyrannosauroid *Eotyrannus*, suggesting that faunivorous theropod diets were more diverse than previously thought. Finally, preliminary results suggest theropod clades exhibit different magnitudes of ontogenetic dietary shifts. Spinosaurid ontogenetic dietary shifts appear to be less pronounced than the clear shifts previously inferred in tyrannosaurids. Consequently, interspecific competition was likely less pronounced with respect to variation in dietary specialization and prey acquisition in non-tyrannosaurid-dominated communities. The statistically significant inferred ontogenetic shifts in tyrannosaurid diets suggests that these genera occupied several distinctive roles during their life cycles, which might have prevented the sympatry of other large-bodied theropod taxa by competitive exclusion. This inferred mechanism of competitive exclusion is supported by the absence of more than one medium-to-large-bodied faunivorous theropod from most Late Cretaceous Laurasian formations. By contrast prior to the Turonian diversification of tyrannosaurids, sympatry was most likely permitted by the clear dietary differences between allosauroid, ceratosaurian, tyrannosauroid, and megalosauroid taxa. Our results suggest significant ontogenetic niche shifts in some tyrannosaurids and provide an explanation for the increased diversity of carnivorous dinosaur guilds prior to the Turonian.

The local-scale spatial structure of immigrants during the Great American Biotic Interchange

Luan Moldan Motta¹, Tiago Bosisio Quental¹

¹Universidade de São Paulo, Departamento de Ecologia, São Paulo, Brasil

The Great American Biotic Interchange (GABI) took place when the isthmus of Panama formed a land bridge between North and South America. This significant event resulted in a well-documented asymmetry in mammalian immigration, showing a higher percentage of northern species in South America compared to southern species in North America. To delve deeper into

the GABI, we examined whether the proportion of immigrants in local communities displayed a spatial pattern based on their distance from the entry point connecting the two continents. We also looked at potential temporal changes by analyzing the local immigrant structure during two distinct periods of the Pleistocene. Our analysis utilized mammal fossil data downloaded from the Paleobiology Database (PBDB) and employed Generalized Linear Mixed Models. The results indicated a negative correlation between the proportion of immigrants and their distance from the connection point during the Early-Mid Pleistocene across both continents. Although this negative relationship remained in North America through the late Pleistocene, it faded away in South America, signaling a new form of asymmetry between the continents. We accounted for various uncertainties related to fossil dating, local assemblage spatial definitions, potential spatial autocorrelation, and biases in fossil preservation. Overall, our findings are qualitatively robust despite these uncertainties. We interpret our results within the framework of classical hypotheses that aimed to explain regional asymmetries in immigrant proportions, suggesting that the duration of full immigrant expansion and other ecological and abiotic effects may have significantly influenced the local spatial patterns and their temporal asymmetry at the local scale.

Characterizing interaction and coexistence in clades and assemblages in deep time

Gabriel Nakamura¹, Tiago Quental¹

¹Universidade de São Paulo, Instituto de Biociências, São Paulo, Brazil

To understand the role of biotic factors in the origin and maintenance of biological diversity, approaches are needed that capture ecological signals from processes such as competition and coexistence. At recent temporal scales, detecting these processes is facilitated by comprehensive occurrence data and statistical tools. However, at deeper temporal scales, challenges arise, such as sampling biases and the lack of suitable computational tools to characterize ecological processes. Despite advancements in estimating diversity, speciation, extinction, and lineage longevity, capturing ecological signals at deep temporal scales remains a difficult task.

In this study, we developed an R package to process occurrence and species longevity data, aiming to calculate diversity, coexistence, and competition metrics across deep temporal scales and different levels of biological organization. The package includes three modules tailored to the biological organization level (clades, assemblages, or individual species). For assemblages, it offers a range of spatial sampling options, including points, buffers, and grids. All modules allow consideration of species' dispersal abilities to generate temporal and spatial coexistence matrices.

We demonstrate the package's application using data on both extant and extinct carnivore species. Currently, the package includes functions to calculate diversity time series and competition metrics based on species attributes and morphological similarities, with the potential for future expansions. Our goal is to facilitate the investigation of diversity patterns, in

particular the potential role of biotic interactions, across various levels of biological organization and to promote integration between macroevolution and community ecology.

Ecosystem Recovery Following the Permo-Triassic Mass Extinction

Annabel L. Nicholls¹, Paul B. Wignall¹, Andrew P. Beckerman², Haijun Song³, Jack O. Shaw⁴, Alexander M. Dunhill¹

¹University of Leeds, Earth & Environment, Leeds, UK

²University of Sheffield, School of Biosciences, Sheffield, UK

³China University of Geoscience, State Key Laboratory of Biological and Environmental Geology, Wuhan, China

⁴Santa Fe Institute, USA

The Permo-Triassic mass extinction (PTME ~252Ma) was the most catastrophic biotic event of the Phanerozoic and recovery was protracted due to environmental instability through the Early Triassic. Although the PTME itself is well studied, there is debate surrounding the nature and timing of marine ecosystem recovery in the aftermath of the extinction. It is argued whether ecological recovery occurred in a step-wise bottom-up manner, with full recovery occurring contemporaneously with recovery of taxonomic diversity by the Anisian stage of the Middle Triassic (some 5-8 million years after the PTME), or whether Early Triassic communities recovered rapidly albeit with markedly different structure to pre-extinction ecosystems. We used lagerstätten data to track ecological recovery via snapshots of marine communities through the Triassic by modelling community structure and function. We show that marine communities recovered quickly in the aftermath of the PTME, but Middle Triassic communities show a significant increase in diversity and vertical structure compared to Early Triassic communities. This suggests that alpha diversity as well as marine community structure and function recovered fully by the Middle Triassic, in line with global taxonomic diversity, but this recovery did not occur via a step-by-step rebuilding of marine ecosystems through the Early Triassic.

Prehistoric archives provide evidence for a cascading effect of predator loss in Caribbean reef fish communities

Aaron O'Dea^{1,2†}, Erin M. Dillon^{1†}, Simon J. Brandl³, Katie L. Cramer^{1,4}, Jonathan D. Cybulski^{1,5}, Brígida de Gracia¹, Kimberly García-Méndez¹, Katherine Griswold^{1,6}, Chien-Hsiang Lin⁷, Matthieu Leray¹, Jessica A. Lueders-Dumont^{1,8}, Andrew J. Sellers¹, Thomas A. Wake^{1,9}

¹Smithsonian Tropical Research Institute, Balboa, 0843, Republic of Panamá

²Sistema Nacional de Investigación (SENACYT), Panamá, Republic of Panamá

³Department of Marine Science, The University of Texas at Austin, Marine Science Institute, Port Aransas, TX 78373, USA

⁴Center for Biodiversity Outcomes, Arizona State University, Tempe, AZ USA

⁵Graduate School of Oceanography, University of Rhode Island, Narragansett, Rhode Island, USA

⁶The Nature Conservancy, Protect Oceans, Lands and Waters Global Team, Arlington, VA 22043, USA

⁷Biodiversity Research Center, Academia Sinica, 128 Academia Road, Sec. 2, Nankang, Taipei 11529, Taiwan

⁸Department of Earth & Environmental Sciences, Boston College, Chestnut Hill, MA 02467, USA

⁹The Cotsen Institute of Archaeology and Department of Anthropology, 308 Charles E. Young Dr., N., University of California, Los Angeles, 90095, USA

How humans have altered coral reef food webs is hard to document due to the absence of baseline information about trophic structure before human impact. We examined fish remains (807 shark dermal denticles and 3,724 bony fish otoliths) preserved in fossil and archeological deposits in Caribbean Panama and the Dominican Republic to reconstruct abundances and body sizes of key trophic groups on Caribbean coral reefs over the last 7,000 years. Estimates reveal similar patterns in both regions, including a 75% loss of sharks and a 23% decline in body sizes of higher-trophic level, human-targeted fishes, consistent with long-term exploitation. Common prey fishes showed an opposing trend; their abundance on modern reefs has doubled and body sizes increased by around 17% on average, indicating a release from predation. Notably, predator-sheltered, cryptobenthic fishes showed no change in either abundance or size over millennia, suggesting that bottom-up factors were not responsible for the observed changes in community structure. Multi-proxy paleoecological approaches can help contextualize long-term changes in trophic structure and reveal processes beyond timescales available to modern studies, while also establishing critical baselines for reef conservation.

Ontogeny and Population Structure of the Early Jawless Fish *Protaspis* (Heterostracan) from the Devonian Period

Nanako Okabe¹, Lauren Sallan¹

¹Okinawa Institute Science and Technology, Macroevolution Unit, Okinawa, Japan

Ontogeny is fundamental to understanding life history, ecology, and population structure. However, growth series of Paleozoic fishes remain poorly understood due to the fragility of larval and juvenile specimens. Hard tissue structures such as otoliths, scales, and bones are commonly used for age estimation in both fossil and extant fishes. However, these structures are rarely preserved in Paleozoic fishes, making it challenging to reconstruct early fish ontogeny. While visiting the Field Museum in Chicago, I examined an extensive collection of over 600 specimens of *Protaspis*, an early jawless fish (Heterostracan) from the early Devonian period. Analysis of its population structure revealed evidence of seasonal birth cycles and high mortality rates, leading to an annual decline in population size. Based on these findings, we estimated the lifespan of this species. *Protaspis* was covered by a rigid dermal skeleton, and its dorsal plate exhibited concentric ornamentation patterns. We hypothesize that these patterns function similarly to otolith growth rings and can serve as markers for growth stage estimation. By utilizing these structures, we aim to reconstruct the ecology and life history of *Protaspis*, providing new insights into the developmental and ecological strategies of early vertebrates. Furthermore, this study offers a unique opportunity to compare the population structure and ecology of Paleozoic fishes with those of modern species, shedding light on the evolutionary trajectory of vertebrate life histories.

Geographical patterns in the diversity of small mammal species in mainland Spain related to contemporary climate and its potential use for palaeoecological inferences.

Rachel V. Pacheco-Scarpitta¹, García-Morato, Sara.², Jarochowska, E.³

¹Utrecht Universiteit, Department of Earth Sciences, Utrecht, The Netherlands

²Université de Bordeaux, Environnements et Paléoenvironnements Océaniques et Continentaux (EPOC, UMR 5805), Pessac, France

³Utrecht Universiteit, Department of Earth Sciences, Utrecht, The Netherlands

A key goal in ecology is understanding the mechanism underlying species diversity. Many factors operating over a wide range of temporal and spatial scales have been linked to species richness. Climate variables related to temperature and precipitation have been correlated with small mammal species diversity at regional scales due to their high sensitivity to disturbances in climate and vegetation. This study examines the current geographical patterns of small mammal richness in 18.5 x 18.5 km UTM grid cells along mainland Spain in relation to five climate gradients obtained by applying Principal Component Analysis (PCA) to climate variables. We performed a regression analysis based on Generalized Additive Models (GAMs) to analyse the relationship between richness and climate, accounting for spatial terms. We conducted a variance partitioning analysis to assess the relative contribution of climate, spatial and spatially structured environmental fractions. Small mammal richness increases northward, concentrating mostly in the Atlantic and Alpine biogeographical regions. The lowest richness values are found in the southeastern part of peninsular Spain within the Mediterranean region. The species richness accounted for the predictors was high (~79%). The annual mean precipitation seems to be the variable most significant in explaining richness, followed by climatic seasonality. The variance partitioning analyses show that a spatially structured environmental component, usually related to historical factors, is greatly noteworthy (~60%) in explaining the current richness patterns of Spain. This suggests that the current climate has a limited influence on species richness. We highlight the importance of long-term biogeography and climate factors related to the Pleistocene Quaternary glaciation and the role of the Iberian Peninsula as a glacial refugium in explaining their contemporary small mammal biodiversity patterns. Therefore, paleontological data must be considered in biodiversity modelling. Finally, we suggest that paleoclimate inferences based only on small mammal richness should be considered with caution.

Functional trade-offs and innovation shape the adaptive landscape of aquatic mammal feeding

Travis Park^{1,2,3}, Robert. J. Brocklehurst^{4,5}, Stephanie E. Pierce⁴, William M.G. Parker^{1,6}, Ellen J. Coombs⁷, Tahlia I. Pollock^{1,8}, James P. Rule^{1,2}, Alistair R. Evans¹

¹School of Biological Sciences, Monash University, Melbourne, Victoria, Australia

²Science Group, Natural History Museum, London, United Kingdom

³Sciences, Museums Victoria Research Institute, Museums Victoria, Melbourne, Victoria, Australia

⁴Museum of Comparative Zoology and Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA

⁵Department of Biological Sciences, University of Massachusetts Lowell, Lowell, MA, USA

⁶Natural History, Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand

⁷Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington DC, USA

⁸Palaeobiology Research Group, University of Bristol, Bristol, United Kingdom

Functional trade-offs are inherent in phenotypes due to the need to balance multiple competing selection pressures. Traditionally regarded as constraints on evolution, trade-offs have recently been reframed as facilitators of adaptation via the changing relative importance of competing functions. Here, we examine these ideas through the lens of aquatic mammal feeding, testing a behavioural aquatic feeding framework where feeding strategies form an evolutionary continuum from terrestrial to increasingly more specialised water-based feeding styles. Specifically, we hypothesised that suction, suction-filter and ram-filter feeding would have adaptive peaks closer together than raptorial feeding, and that taxa follow the functionally optimal evolutionary path (Pareto front) between adaptive peaks. Constructing morphofunctional adaptive landscapes based on a broad sample of living and extinct cetacean mandibles ($n = 107$) revealed strong support for this framework, providing quantitative evidence that these feeding strategies are closely linked in evolutionary terms. Surprisingly, most cetaceans do not lie along the Pareto front between peaks, suggesting that novel functional innovations—most likely the specialised cetacean auditory pathway—are also influencing mandibular evolution.

A Recommender Systems Approach to Estimating Population Densities in Fossil Faunas

Abigail K. Parker¹, Liping Liu^{2,3,4}, Miikka Tallavaara², Indrė Žliobaitė^{1,2}

¹University of Helsinki, Department of Computer Science, Helsinki, Finland

²University of Helsinki, Department of Geosciences and Geography, Helsinki, Finland

³Swedish Museum of Natural History, Stockholm, Sweden

⁴Stockholm University, Bolin Center for Climate Research, Stockholm, Sweden

We here present a method to estimate population densities for fossil taxa based on binary (presence/absence) occurrence data. Many fossil assemblages preserve too few individual elements to confidently estimate relative abundance statistics such as the minimum number of individuals for taxa, but cross-site analyses aiming to understand patterns such as rise and decline in ecological dominance between groups over time would benefit from abundance data. We use Recommender Systems, a type of machine learning method based on identifying associations between items present in matrices, to estimate the propensities of taxa to occur at sites. These recommendations result from co-occurrence patterns mined from a large dataset of sites sharing some taxa, in this case 758 fossil sites from the Pleistocene of Eurasia preserving large mammals. We estimate population densities, first based on known scaling between body mass and density (individuals/km²), which we take to represent the maximum density for a taxon. Then, we use the recommender score, which is lower for sites whose observed taxa co-

occur less frequently with the taxon of interest, to scale down this maximum population density for sites less suitable for the taxon. This results in estimates, for every site in our fossil dataset, of population density and biomass for all large mammals in its fauna.

These abundance estimates have myriad possible applications, but we first apply them, in the Pleistocene Eurasian context, to analyze geographic patterns of mammalian biomass distribution and relationships between modelled densities of *Homo* and other mammals over time. Across seven time bins subdividing the Pleistocene and Holocene, we observe that *Homo* biomass is higher at sites with higher estimates of both total herbivore and total carnivore biomass. Estimated carnivore biomass is lower in earlier time bins than expected from modern herbivore: carnivore mass ratios.

Climate-proofing' lion conservation by integrating modern and palaeontological data in forecasts of habitat suitability

Thomas Pavey¹, Benjamin R. Shipley², Andrew J. Loveridge¹, Paul J. Johnson¹, Erin E. Saupe²

¹University of Oxford, WildCRU, Department of Biology, Oxford, UK

²University of Oxford, Department of Earth Sciences, Oxford, UK

Climate change poses one of the biggest threats to biodiversity, yet there is uncertainty surrounding how species will respond to future change. The lion, *Panthera leo*, is a vulnerable species currently living in highly fragmented landscapes, and alongside predicted population growth and land-use change, Africa is projected to experience rising temperatures, changing precipitation systems and increases in the frequency and intensity of weather extremes. The palaeontological record provides an excellent resource for exploring how species have responded to environmental change. Building upon my previous work modelling relationships between extant lions and climate and projecting them into the future under climate change, I have combined a detailed record of Quaternary lion occurrences with high resolution palaeoclimate data to constrain estimates of their niche and improve prediction accuracy. The results provide the first dispersal-limited, annual forecasts of climatic suitability across the African continent. I highlight which areas of current lion range are under threat from becoming climatically unsuitable, and whether there are areas which could become suitable for lions. This information will be used to predict the risk posed by climate change to areas with high conservation potential and delivered to appropriate stakeholders to 'future-proof' protected area planning.

Rise, demise, and replacement: The evolutionary history of Cenozoic South American mammals

Kateryn Pino¹, Juan D. Carrillo², Fernando Blanco³, Rebecca B. Cooper⁴, Enrique Rodríguez-Serrano¹, Daniele Silvestro⁵

¹Universidad de Concepción, Facultad de Ciencias Naturales y Oceanográficas, Concepción, Chile

²CR2P (CNRS, MNHN, Sorbonne Université), Département Origines et Évolution, Muséum national d'Histoire naturelle, Paris, France

³The Open University, School of Mathematics and Statistics, Milton Keynes, U.K.

⁴University of Birmingham, School of Geography, Earth and Environmental Sciences, Birmingham, U.K.

⁵ETH, Department of Biosystems Science and Engineering, Zurich, Switzerland

Biotic replacements are a persistent feature of biodiversity dynamics throughout time. Yet, the role of biotic interactions—such as competition and predation—in shaping diversity changes during biotic replacements is poorly understood. Functional diversity can be decoupled from taxonomic diversity during biotic replacements, with extinction processes having a stronger impact on taxonomic replacement and selective extinctions targeting functionally redundant species—allowing ecosystems to persist—or unique functional entities, leading to ecosystem collapse or reshaping. South American (SA) mammals are characterized by a long evolutionary history marked by phases of biogeographic isolation punctuated by dispersal events during the Cenozoic, followed by increased connectivity with North America via the Panama Isthmus. Here, we study the biotic replacement of SA mammals during the Cenozoic focusing on how the taxonomic and functional diversity of the native lineages of this continent respond to the dispersal and diversification of immigrant groups. To this aim, we compiled a detailed dataset of SA fossil occurrences and applied a new method that uses deep learning-based biodiversity simulations to reconstruct the diversity trajectories of native and immigrant lineages through time. Furthermore, we gather information for three functional traits (locomotion, diet, and body mass) to analyze their functional diversity dynamics and characterize their functional structure using a network analysis approach. The results indicated that migration events negatively affect the diversity of native herbivore lineages, as immigrant herbivores from Africa (caviomorphs) and North America (artiodactyls, perissodactyls, proboscidean) partially replace them. A negative impact on native carnivores (sparassodonts) was also observed due to placental carnivore diversity. Despite diversity declines in native lineages, these migration events led to overall increases in taxonomic diversity on the continent, consistently with a process of clade competition and partial replacement.

The Biogeography of Specialization: Spatial and Temporal Trends of Substrate-boring Mytilids

Alejandro L. Prieto¹

¹Vanderbilt University, Department of Earth and Environmental Sciences, Nashville, TN, USA

A fundamental unit of biogeography is the geographic range, or the spatial realization of a species' niche, which is the result of local biotic and abiotic factors as well as large-scale evolutionary and physical-environmental factors. These factors interplay on million-year timescales and ranges are a common proxy when interpreting the biodiversification of modern species. Mytilidae, a family of Bivalvia, are a clade of substantial economic and ecologic importance that are globally distributed today. This clade can be divided into four main lifestyles: substrate-boring, epifaunal, infaunal and semi-infaunal. Substrate-boring (endolithic) mytilids are a group of highly specialized mussels that have adapted to bore into various hard

substrates but are closely tied to the availability of carbonate platforms. Extant mytilid genera were among the oldest bivalve lineages to develop endolithy and have an excellent fossil record. Broadly, bivalves abide by the latitudinal diversity gradient, being most speciose in the tropics. However, for mytilids and their lifestyles, this is not always the case, raising the question of why some lifestyles follow the latitudinal diversity gradient while others do not. This can have implications for determining ancestral origins, diversity and geographic dispersal through time, topics that have not been fully contextualized in paleoecology. Here, I leverage both fossil and modern occurrence datasets of endolithic mytilids to reconstruct their ranges, quantify characteristics of their ranges (size, centroid, breadth) and compare these with the diversification of other mytilid lifestyles through deep time. In doing so, I show that certain mytilid biogeographical patterns, like the latitudinal diversity gradient, are dependent on spatial scale and lifestyle rather than being a general pattern. This study aims to disentangle the relationship between a clades' specialization and their biogeographic characteristics which contribute to our understanding of macroevolutionary and biological processes.

The importance of savannas in the colonization of open environments during the ruminant evolution

Álvaro Quesada¹, Manuel Hernández Fernández^{1,2}, Laura Domingo^{1,3}, Juan L. Cantalapiedra⁴, Iris Menéndez⁵

¹Complutense University of Madrid, Department of Geodynamics, Stratigraphy and Paleontology, Madrid, Spain

²Instituto de Geociencias (UCM, CSIC), Departamento de Cambio Medioambiental, Madrid, Spain

³University of California Santa Cruz, Department of Earth and Planetary Sciences, Santa Cruz, California, USA

⁴Museo Nacional de Ciencias Naturales-CSIC, Department of Paleobiology, Madrid, Spain

⁵Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany

Savannas appeared in the early Oligocene and have been expanding since then, reaching a widespread distribution during the middle-late Miocene that continues to the present day. Savannas are grassland ecosystems characterized by relatively high temperatures throughout the year and marked precipitation seasonality. The diversity of environments within these conditions, from open woodlands to treeless grasslands, and their vast extent during the Neogene and Quaternary in tropical and subtropical regions as well as in many areas that today are characterized by temperate climates, suggest that savannas might have acted as transitional environments in the colonization of more open and arid environments by many groups with origins as tropical forest inhabitants. To study this macroevolutionary process, ruminants (Ruminantia) are an ideal taxon as they occupy all terrestrial biomes and are particularly abundant in savannas and dry tropical forests. This allows us to explore how biome shifts occurred during their evolutionary history, with a particular focus on the role of savannas in these processes. Using the R package BioGeoBEARS, we inferred the biogeographic and ecological history of ruminants through a likelihood-based analysis. Once the ancestral biomes probabilities were inferred for each node in the phylogeny, we performed 200 stochastic mapping simulations and quantified the average number of new biome colonizations during the

evolution of ruminants. The results show frequent colonization between tropical biomes, with savanna being very important as both, destination of colonization events from tropical forest biomes and source for species colonizing other open biomes such as desert or steppe. We conclude that the great extension of the savannas during the Neogene and its connectivity with both forested and open biomes facilitated the colonization and adaptation to subtropical and temperate open biomes from tropical forest biomes.

Space-for-time substitution depends on ecological and spatial scales

Marina C. Rillo¹, Julian Merder², Ivan Hernandez-Almeida³, Lukas Jonkers⁴, Tonke Strack⁴, Michal Kucera⁴ & Helmut Hillebrand^{1,5,6}

¹Institute for Chemistry and Biology of Marine Environments [ICBM], Carl-von-Ossietzky University Oldenburg, Wilhelmshaven, Germany

²Department of Global Ecology, Carnegie Institution for Science, Stanford, CA, USA

³PAGES, University of Bern, Bern, Switzerland

⁴MARUM, University of Bremen, Bremen, Germany

⁵Helmholtz-Institute for Functional Marine Biodiversity at the University of Oldenburg [HIFMB], Oldenburg, Germany

⁶Alfred Wegener Institute, Helmholtz-Centre for Polar and Marine Research [AWI], Bremerhaven, Germany

Spatial relationships between biodiversity and climate are often used to predict biodiversity dynamics under future climatic scenarios. This space-for-time substitution underpins widely used species distribution models; however, its fundamental assumption - that spatial responses can be extrapolated to temporal responses - is rarely tested. Moreover, community-level pollen data and population-level tree-ring data have shown contrasting support for the space-for-time substitution, suggesting its use might be scale-dependent. Here, we compiled community- and population-level data of planktonic foraminifera with wide spatial (modern global ocean) and temporal (up to the past 250 thousand years) distributions, combined with corresponding sea-surface temperature (SST) data (based on satellite data and proxy-based reconstructions). We modelled compositional turnover (community-level) and species' distributions (population-level) responses to SST across space and through time and used the spatial model to predict the temporal ecological responses. We found that the predictions are scale-dependent: predictions are reliable at the community- and global-levels, but inaccurate at the population- and local-levels. Our results based on marine microfossil data show that the widely used method of forecasting the ecological impacts of climate change based on spatial climatic variation might be misleading at local and population scales.

Weak support for ergodic processes in fossil mammal community structure in Western Europe

Joshua M. Rowe¹, Julien Louys²

¹Griffith University, School of Environment and Science, Brisbane, Australia

²Griffith University, Australian Research Centre for Human Evolution (ARCHE), Brisbane, Australia

The idea that space and time act equivalently in structuring ecological communities has historically been the product of qualitative observation. The space-time equivalence hypothesis can be stated in terms of ergodicity: that averages over space and time are equivalent. We explicitly examine ergodicity in the fossil mammal community structures of Western Europe's Middle and Late Pleistocene, focusing on warm periods (corresponding to odd marine isotope stages). Evidence for ergodicity is weakly present in highly diverse guilds but absent in the most sparsely occupied guilds. Absence of ergodicity can be attributed to chaotic responses to climate cycles over the study region, which have previously shown to violate traditional community convergence models. We suggest that these responses disproportionately disrupted sparsely occupied guilds, leading to the dominance of non-ergodic processes in their community assembly. Ergodicity may be better established across glacial refuges, at finer temporal scales, or across more climatically stable geographic regions.

Neotropical freshwater fish faunal extinction and diversification in the Neogene

Marcelo R. Sánchez-Villagra¹, Gabriel Aguirre-Fernández¹, Alexandra Wegmann¹, Aldo Benites Palomino¹, Rodolfo Salas-Gismondi², Andrés Link³, Masanaru Takai⁴, Jorge D. Carrillo-Briceño¹

¹University of Zurich, Department of Paleontology, Zurich, Switzerland

²Museo de Historia Natural-Universidad Nacional Mayor de San Marcos, Departamento de Paleontología de Vertebrados, Lima, Peru

³Universidad de Los Andes, Departamento de Ciencias Biológicas, Bogotá, Colombia

⁴The Kyoto University Museum, Kyoto University, Kyoto, Japan

The evolution of freshwater fish diversity from the Orinoco and Amazon basins (> 3000 species) has been influenced by the uplift of the Andes mountains and the restructuring of hydrographic systems. Fishes are used as excellent indicators for past environmental and ecological inferences, and their still scarce fossil record has provided a better understanding of their origin and extinctions. Our recent efforts in surface collecting and screenwashing, and the examination of microvertebrate concentrations in unstudied collections, is yielding thousands of new samples from different Neogene stratigraphic intervals across Colombia, Peru and Venezuela. The data allow us to better assess the systematic affinities, phylogeny and chronological context of diverse fish groups. Using non-invasive imaging (μ CT scans) of bone/scale remains has provided new markers of taxonomic allocations to poorly understood extinct groups (e.g. Neotropical Neogene polypterids). Identification of the numerous otoliths and isolated remains of cichlids from Miocene sites fostered a reference collection of previously unavailable materials from extant species. The sheer number of species and the fragmentary nature of most fossils make robust assignments beyond 'genus level' previously inaccessible for many groups. Further studies will inform us if the almost complete absence of extinct species in the Neogene fossil record respond to sampling bias or an unusual resilience of these faunas. Evidence of extinction of apex predators and megafauna fish – for which different alternative definitions exist in the literature – have been assessed in association to Andean uplift, as connections are now lost with the Paraná Basin and Greater Amazonia. The fossil record in some of the peripheral basins of the Greater Amazonia provide evidence on how local extirpation of some fishes, especially those of

large body-size (> 30 kg) was likely associated with environmental changes and habitat reductions that occurred in the region following the isolation of major hydrographic river systems.

Hominin isotopic niche in arid palaeoecosystems of the Southern Iberian sub-plateau during the Middle Pleistocene

Paula Sanz-Henche¹, Darío Fidalgo², Miriam Pérez de los Ríos¹, Carlos Palancar², Sara Díaz Pérez³, Josu Aranbarri⁴, Lucía Bermejo⁵, Isidoro Campaña Lozano⁶, Oscar Cambra-Moo⁷, Gabriel Cifuentes-Alcobendas^{8,9}, Almudena Estalrrich², Anna Rufà^{11,12}, Daniel García-Martínez^{1,12,13}

¹Physical Anthropology Unit, Biodiversity, Ecology and Evolution Department, Universidad Complutense de Madrid, Madrid, Spain

²Department of Palaeobiology, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain

³Institute of Archaeology, University of Wrocław, Wrocław, Poland

⁴Department of Geography, Prehistory and Archeology, Universidad del País Vasco/Euskal Herriko Unibertsitatea, UPV/EHU

⁵Primeros Pobladores de Extremadura (EPPEX), Extremadura, Spain

⁶Department of Ecology and Geology, Faculty of Sciences, Universidad de Málaga, Spain

⁷Laboratorio de Poblaciones del Pasado (LAPP), Department of Biology, Faculty of Sciences, Universidad Autónoma de Madrid

⁸Instituto de Evolución en África, Universidad de Alcalá, Madrid, Spain

⁹Universidad de Alcalá, Department of History and Philosophy, Madrid, Spain

¹⁰Interdisciplinary Center for Archaeology and the Evolution of Human Behaviour (ICArEHB), Universidade do Algarve, Faro, Portugal

¹¹UMR 5199 – De la Préhistoire à l'Actuel: Culture, Environnement et Anthropologie (PACEA), Universidad Bordeaux, CNRS, MCC, Pessac, France

¹²Laboratory of Forensic Anthropology, Centre for Functional Ecology, Department of Life Sciences, Universidade de Coimbra, Coimbra, Portugal

¹³CENIEH (National Research Center on Human Evolution), Paseo de la Sierra de Atapuerca 3, Burgos, Spain

The recently discovered Middle Pleistocene palaeoanthropological site of Ruidera opens a new window to the study of human and ecosystemic evolutions in the Iberian Peninsula during the Quaternary. In particular, the great abundance, good preservation and peculiar diversity of macro-mammals together with the presence of human fossils at this site is remarkable. Along with the human remains we found numerous individuals of European tahr, deer, horses, lions, leopards, lynxes, wolves, lagomorphs and birds. In this work we present a palaeoecological approach using stable isotopic enamel analysis of human and macro-mammals of six different taxa.

The aim of this study is to determine the type of ecosystem encountered in this site during the Middle Pleistocene, focusing on the hypothesis that it represents the most arid record in Europe during this period given its latitude. Of particular interest is the comparison of the hominine isotopic niche at Ruidera with other European Middle Pleistocene sites.

Preliminary results of the analysis indicate a Mediterranean interglacial ecosystem, with an arid environment inferred. However, it is not so unexpected given that this is the southernmost site

analysed with enamel stable isotopes in Europe with this chronology. The taphonomy and faunal list indicate an environment that favoured the characteristic biases of mountainous areas with a strong influence of accumulation by carnivores. Moreover, our results of the analysed hominin suggest a similar isotopic niche to that of the leopards of the same site. The proposed high proteic diet in humans in Ruidera would align with the results from some other European Middle Pleistocene sites.

Although these results are in line with palynological, taphonomic and palaeontological approaches, the peculiar arid environment inferred stands out, unique among the European Middle Pleistocene sites and far removed from the environment we observe today.

Functional Ecology of the Dorsal Sail in Spinosaurus: From Ornament to Utility (Adaptive Significance)

Mihika Saraf¹

¹Dnyanganga Education Trust, Junior College of Science, Thane, Maharashtra, India

The function of the dorsal sail of *Spinosaurus aegyptiacus* has been widely debated, with several hypotheses proposed over time. This presentation reviews these theories, compares *Spinosaurus* with extant species having similar adaptations, and introduces new ideas to further explore the sail's adaptive significance. It assesses the pre-existing thermoregulation hypothesis, aquatic maneuverability, and social signaling, while also proposing three original concepts, namely:

Canopy feeding theory: The large sail may have created shade during sunny conditions, attracting fish, much like the Black Heron that uses its wings to create shade and lure aquatic prey. This method could have provided the *Spinosaurus* with a hunting advantage.

Wind direction indication theory: The sail might have functioned like a boat's sail, helping *Spinosaurus* catch wind-borne scent trails and air currents, aiding its hunting abilities, similar to modern crocodiles.

Mock-spine theory: The sail may have acted as a 'mock-spine,' making *Spinosaurus* appear larger and deterring predators like *Carcharodontosaurus*, protecting its vulnerable back (a common target area, as evidenced by bite marks on hadrosaurs), similar to the frilled lizard.

This framework highlights the multifunctionality of the sail, supporting *Spinosaurus*' semi-aquatic lifestyle and potentially aiding in combat, mating, and hunting. By drawing comparisons with modern animals such as herons, sailfish, thresher sharks, and crocodiles, the presentation suggests the sail may have been a multipurpose appendage that enhanced the predator's efficiency, helping it thrive as an apex predator in the Cretaceous period.

Pathologies, Inbreeding, and Extinction: On the dwindling populations of *Smilodon fatalis* of the La Brea Tar Pits

Hugo Schmökel¹, Aisling Farrell², Francesca Del Chicca³, Regine Hagen Argudin Pina³, Alessandro Urciuoli⁴, Marcelo R. Sánchez-Villagra⁴

¹Evidensia Academy, Division of Veterinary Orthopaedics and Spine Surgery, Stockholm, Sweden

²La Brea Tar Pits and Museum, Los Angeles County, California, United States of America

³Clinic for Diagnostic Imaging, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland

⁴Department of Paleontology, University of Zurich, Zurich, Switzerland

Towards the end of the Pleistocene, mammal populations became more and more geographically isolated, accelerating inbreeding prior to extinction and leading to more frequent inherited diseases. An example is the transitional vertebrae reported from dwindling populations of woolly mammoth, rhinoceros, gray wolf, and Neandertals. At the junctions of the major segments of the vertebral column, a single vertebra may possess characteristics typical of either segment. The thousands of specimens of the saber-toothed cat *Smilodon fatalis* from Late Pleistocene sites of the La Brea Tar Pits in Los Angeles offer a unique possibility to study morphological changes across time, close to the species extinction.

We examined the vertebrae, sacra, and pelves belonging to at least 849 *S. fatalis* individuals. In total, 226 transitional vertebrae were identified. The most common malformations were at the lumbosacral (15%) and the thoracolumbar (11%) junctions, whereas cervical vertebrae showed intrasegmental transitions (2%). Asymmetry, particularly in L1, and severe lumbosacral transitions (3%) that also affected pelvic position were also recorded. All cervical transitions and severe lumbosacral transitions were found in the youngest pits (< 21 ka), close to the disappearance of the La Brea *S. fatalis* population. Relative to extant large felids and domestic cats, *S. fatalis* showed a higher incidence of severely asymmetrical lumbosacral transitions and cervical malformations, the latter being involved in negative pleiotropic effects in humans. We interpret the high rates of malformations in *S. fatalis* as clear evidence of inbreeding, possibly related to population isolation preceding extinction.

Effects of long-term environmental changes and human impacts on the functional diversity of molluscan nearshore communities of the Po-Adriatic System (Italy)

Lukas Schweigl¹, Vaishnavi Pittala¹, Rafał Nawrot², Daniele Scarponi¹, Michał Kowalewski³

¹University of Bologna, Department of Biological, Geological and Environmental Sciences, Bologna, Italy

²University of Vienna, Department of Paleontology, Vienna, Austria

³University of Florida, Florida Museum of Natural History, Gainesville (FL), USA

Most studies evaluating shifts in community composition in response to natural environmental changes or anthropogenic impacts focus on taxonomic diversity, while functional diversity remains underexplored, particularly in marine ecosystems. This study evaluates shifts in the functional diversity of molluscan nearshore communities in the Po-Adriatic System (Italy) in

response to late Pleistocene and Holocene environmental fluctuations and anthropogenic pressures of the past centuries. We apply Biological Traits Analysis (BTA) based on a broad range of behavioral and morphological characteristics to assess these changes.

Previous research has shown that nearshore molluscan communities in the Po Basin exhibited a resilient response to large-scale climatic fluctuations of the late Pleistocene and Holocene. Taxonomic composition remained stable during the last two interglacial highstands but shifted to a different state during the last glacial lowstand. This study investigates whether these glacial assemblages also exhibited distinct functional compositions compared to their interglacial counterparts, providing insights into the natural range of variability in functional diversity during major shifts in climate and sea level.

Despite the taxonomic similarity of late Pleistocene and Holocene interglacial assemblages, modern communities - impacted by bottom trawling, eutrophication, hypoxia, and mucilage events - show significant deviations from the pre-industrial baseline. Previous research in offshore transition environments has associated recent shifts in taxonomy in the Adriatic with alterations in functional traits, especially regarding feeding strategies and substrate preferences. This study will broaden the exploration to shallower settings and, through the use of BTA, provide a more detailed understanding of how human-induced community turnover has impacted functional diversity. Additionally, it establishes a valuable baseline for nearshore settings of the Po-Adriatic System, which could inform future restoration efforts.

Causes and consequences of a marine megafaunal extinction

Amy E. Shipley¹, Andrew P. Beckerman², Catalina Pimiento^{3,4}, Jennifer A. Dunne⁵, Tracy Aze⁶, Alexander M. Dunhill¹

¹University of Leeds, School of Earth and Environment, Leeds, UK

²University of Sheffield, School of Biosciences, Sheffield, UK

³Swansea University, School of Biosciences, Swansea, UK

⁴University of Zurich, Department of Paleontology, Zurich, Switzerland

⁵Santa Fe Institute, Santa Fe, USA

⁶University of Plymouth, School of Biological and Marine Sciences, Plymouth, UK

The end Pliocene extinction event saw significant losses in large-bodied marine taxa, with ~36% of marine megafaunal genera going extinct across this boundary. This extinction is currently under-studied but could provide useful insight into the drivers and impacts of marine megafauna extinctions on a global scale. Extant marine megafauna are facing increasing threats of extinction from anthropogenic activities yet little is understood about the long-term impacts of their absence, meaning a good understanding of past extinctions is of great relevance.

Here we address gaps of knowledge in the causes and consequences of marine megafauna extinctions through investigation of this Pliocene extinction event. We assess:

1) The primary extinction drivers of this event through modelling various environmental factors against extinction rates. This is assessed on a global scale and within different ocean basins.

2) The impact on trophic dynamics and food web structure through food web modelling. In particular, the impact of losing the giant apex predator, *Otodus megalodon*.

We find extinction rates vary on a geographic scale with North Atlantic ecosystems more robust to marine megafaunal losses. Further, loss of neritic zone (highly productive, shallow habitat) is found to be a primary driver of these extinctions. Increases in generalism and a drop in vertical trophic complexity following the extinction event is found, suggesting a reduction in energy flow to higher trophic levels across the extinction event. This supports a primary extinction driver of decreased productive neritic habitat area which limited resources. However, overall food web structure was robust to these marine megafauna extinctions with few changes to structural and functional metrics. Trophic positions of taxa were also consistent across this boundary with the loss of *O. megalodon* from the highest trophic level having no cascading structural impacts.

Climate velocity and extinction in ancient and modern communities

Benjamin R. Shipley¹, Malanoski, C.M.¹, and Saupe, E.E.¹

¹Department of Earth Sciences, University of Oxford, Oxford, GB

Climate velocity, or the speed needed to maintain constant climate across a dynamic landscape, has been used to measure species' vulnerability to climate change, identify refugia in the past and present, and to predict movement and reorganization across communities. Because climate velocity is influenced by both site-level changes in climate through time and topographic patterns across space, it provides a holistic view of the abiotic pressures that combine to make a region suitable or unsuitable for a species. The shape of landmasses may also influence climate velocity. For example, velocities may be lower in the marine realm along north-south coastlines compared to east-west coastlines because of the strong latitudinal temperature gradient. However, the effect of landmass shape on climate velocity and therefore species vulnerability has yet to be explored.

Here, we explore patterns of extinction probability in the context of landmass shape across space and time, combining paleontological and neontological records of shallow-sea marine invertebrates. For both modern and fossil communities, we hypothesised higher climate velocities and subsequently higher extinction probabilities for taxa on east-west oriented coastlines, as species will be unable to track climate effectively. Our hypothesis was supported in the paleontological record, in which taxa on north-south coastlines were less likely to go extinct than those on east-west coastlines throughout the Phanerozoic. On local scales, we also found modern climate velocity to be weakly associated with coastline orientation in oceans. However, changes to global circulation patterns affect climate velocity much more broadly than landmass shape, suggesting that landmass shape may only influence extinction risk for the smallest-ranged, most specialist coastal species. Combined, our results suggest landmass orientation is an important component of extinction on geological timescales, but that this extinction-orientation link may not exist on decadal scales.

Correcting marine community composition estimates from biological sedimentary archives using paleontological and ecological-derived sampling methods

Elizabeth C. Sibert¹

¹Woods Hole Oceanographic Institution, Geology & Geophysics, Woods Hole, MA, United States

Marine sediments contain records of ancient ocean life, often at high temporal resolution, ranging from microfossil plankton tests to fish teeth and scales, to fragments of ancient DNA. These records, coupled with concurrently preserved environmental proxies, provides an excellent testbed for exploring interactions between biodiversity, ecology, and environmental conditions across space and time. However, the contribution of individuals within a population to the deep-sea sedimentary record can be highly variable: while an individual foraminifera will produce only a single test, a fish might produce dozens of teeth, and a shark, hundreds of thousands or millions of scales. This variability is also found in ancient DNA fragments sampled in sediments. For example, while diatoms and dinoflagellates have 10s or 100 copies of ribosomal subunit genes such as 18S, radiolarians may have thousands or even millions of copies of those same genes. Thus, any analysis of community composition that is based on observable count-data from a sedimentary archive is biased towards the organisms which produce the most of whatever is being sampled, and may therefore mask underlying but significant community composition shifts. Here I develop a statistical framework for correcting for this production variability bias and estimating error in community composition reconstruction in the sedimentary record. I then apply this to a record of sedimentary ancient DNA from the Southern Ocean to explore changes in the Southern Ocean plankton community over the past million years, and discuss applications of this framework for reconstructing ecological change in other systems which have this highly variable production bias, such as fossil pollen and ichthyoliths.

Conservation-led palaeoecology: lessons from practitioners to improve accessibility and value to conservation practice

Benjamin Siggery^{1,2}, **Helen Bennion**³, **Richard Murphy**¹, **Stephen Morse**¹, **Mike Waite**²

¹Centre for Environment and Sustainability, University of Surrey, Guildford, United Kingdom

²Surrey Wildlife Trust, School Lane, Woking, United Kingdom

³Department of Geography, University College London, London, United Kingdom

The integration of palaeoecology into conservation practice is crucial for effective ecosystem management and restoration. Palaeoecological data provide a unique long-term perspective on key ecological challenges and enable decision makers to better understand pre-disturbance conditions, natural system dynamism and responses to change. Despite this there exist well-recognised accessibility issues and a clear research-implementation gap, in particular, poor communication and lack of understanding of conservation practitioners' constraints.

We interrogated 60 examples of applied research papers and assessed them on the use of best practice accessibility criteria, and gathered conservation-practitioner feedback on the value of conservation recommendations made within the papers.

Despite widespread recognition of the importance of accessible research, our review revealed that essential accessibility criteria are inconsistently applied. Although there has been an increase in accessibility practices over time, co-production practices showed no significant increase, despite being advocated for by the research community. Practitioner reviews highlighted the need for research to provide clear, actionable recommendations, and papers that detailed specific management or restoration guidance were particularly well-received, as were those that considered financial implications that gave simple, clear summaries of their findings. Equally, many papers were criticised for overly technical language and poor expression, generic suggestions, and a lack of practical consideration in their recommendations.

The study highlights the importance of improving accessibility and co-production of knowledge to ensure that research outputs are accessible, relevant, and feasible to guide conservation efforts. To enhance the relevance and impact of applied palaeoecology, we propose five key recommendations for progressing towards a 'gold standard' of applied research, where it can be employed to greater effect to support conservation practice.

The differing response of carnivores to the terminal Pleistocene extinction

Felisa A. Smith¹, Emma A. Elliott Smith¹, Catalina P. Tomé², S. Kathleen Lyons³

¹Department of Biology, University of New Mexico, Albuquerque, NM 87131

²Indiana State Museum and Historic Sites, Indianapolis, IN, USA

³School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE 68588

Modern trophic downgrading is leading to changes in the ecological interactions within communities. For carnivores in particular, the loss of apex species may lead to a cascade of effects. Here, we use the fossil record of the terminal Pleistocene megafauna extinction to explore the consequences of such past trophic downgrading. We characterize both the isotopic and body-size niche of a mammal community in Texas before and after the biodiversity loss to assess the influence on the ecology and ecological interactions of surviving species (>1kg). This was a rich and diverse mammal community before the extinction, with a variety of C₄-grazers, C₃-browsers, and mixed-feeders, quite similar to African savannas today. There was a strikingly regular partitioning of dietary isotopic niche with body size within each carnivore family with the various carnivore guilds (Ursidae, Felidae, and Canidae) largely non-overlapping. Post-extinction, considerable body size and isotopic niche space were lost, especially among the hard hit Felidae. We find significant changes in the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of surviving felids and a movement towards C₄ food resources. Indeed, the Felidae display mesocarnivore release: the jaguar, now an apex carnivore, shifting into the specialized isotopic niche previously occupied by extinct sabretooth cats. Puma, previously rare, became common and lynx shifted towards consuming more C₄-based resources. These changes persisted in the modern. Patterns for the Canidae are more complex and may reflect a reduction in scavenging. In contrast, we observed little change in diet or body size among the surviving Ursidae. Overall, considerable ecological

complexity was lost in the Holocene community. Our results suggest that the impact of trophic downgrading on communities may be taxonomically specific.

From extirpation to reintroduction: investigating the trophic ecology of the Dalmatian pelican (*Pelecanus crispus*) in England using stable isotopes

Lucia S. Snyderman^{1,2}, Samuel T. Turvey², Stuart Black¹, Andrew Kitchener³, Juliette Waterman¹, William F. Mills¹

¹Department of Geography and Environmental Science, University of Reading, Reading, UK

²Institute of Zoology, Zoological Society of London, London, UK

³National Museums Scotland, Edinburgh, UK

Palaeontological, zooarchaeological, and historical archives contain information about lost species and ecosystems that is valuable for establishing biodiversity baselines and informing modern conservation. The Dalmatian pelican (*Pelecanus crispus*) is the world's largest freshwater bird and is classified as Near Threatened by the IUCN, with its current Eurasian distribution representing a contraction of its former Holocene range. Zooarchaeological remains confirm the past occurrence of northern European populations and bear marks of butchery. The species is now a reintroduction candidate to England, where it became extirpated possibly due to human hunting thousands of years ago. However, it remains unclear what ecological role pelicans played in historical wetland ecosystems. We conducted stable isotope analyses of carbon ($\delta^{13}\text{C}$), nitrogen ($\delta^{15}\text{N}$) and sulphur ($\delta^{34}\text{S}$) of bone collagen to investigate the former feeding ecology of the extirpated Dalmatian pelican population in England. We sampled pelican specimens recovered from archaeological contexts in the Cambridgeshire Fens and Somerset Levels spanning the Iron Age and Roman periods (~3000–2000 BP). We also conducted isotope analysis on co-occurring wetland bird species to reconstruct historical food webs and determine whether pelicans were foraging primarily in freshwater, marine, or brackish systems. This information illuminates the ecological and landscape needs of the English Dalmatian pelican population, and highlights the specific resources and habitat types they needed to perform their functional ecological role. Our research provides essential ground truthing for informing a potential reintroduction and emphasizes the relevance of past data for the fields of ecology and conservation in the present.

The impact of fossil biases on phylogenetic inferences: a simulation approach using mammals

Graciela Sotelo¹, Sofía Galván¹, Sara Gamboa¹, Adrián Castro-Insua¹, Alfio Alessandro Chiarenza², Emma M. Dunne³, Lewis A. Jones², Marta Matamala-Pagès¹, Eduardo Méndez-Quintas¹, Adriana Oliver¹, Iván Rey-Rodríguez¹, Sara Varela¹

¹University of Vigo, Department of Ecology and Animal Biology, Vigo, Spain

²University College London, Department of Earth Sciences, London, UK

³Friedrich-Alexander Universität Erlangen-Nürnberg, Erlangen, Germany

Our understanding of past biodiversity and evolution relies on the incomplete and non-uniform fossil record, shaped by factors like sedimentation rates, species' range and body size, and biases in fossil sampling effort. This study quantifies the potential difference between evolutionary scenarios based on the fossil record and on complete phylogenies. Using current mammal distribution and phylogeny as baselines, we simulated fossil sampling by filtering species according to sediment availability, species traits (range/body size), and taxonomic biases under three filter levels (25%, 50%, 75%). Dropped species were pruned from the phylogeny, and the effects on diversification rates and trait evolution (body size and diet) were assessed. Results show that body size and taxonomy significantly influence phylogenetic inferences, particularly under stringent filtering. The impact varies depending on the traits, analysis methods, and mammal clades. This simplified approach highlights the potential distortion that biases in the fossil record may pose to understanding biodiversity and evolutionary trends, providing a lower bound of these effects.

The Lost World: Building Food Webs for Paleo Communities

Tanya Strydom¹, Baran Karapınar ², Andrew P. Beckerman¹, Alexander M. Dunhill²

¹School of Biosciences, Ecology and Evolutionary Biology, University of Sheffield, Sheffield, United Kingdom

²School of Earth and Environment, University of Leeds, Leeds, United Kingdom

Food webs represent the feeding relationships between species and can help infer ecosystem-level processes. Alongside the development of food web theory, methods for constructing food webs have been developed to infer species interactions when empirical data is lacking. Food web construction methods are diverse, each utilising different approaches to infer species interactions —such as the use of traits to infer mechanistic relationships vs using gut content as a proxy for species diets. These methods have distinct theories, mechanisms, and data requirements. In paleoecology, where direct evidence of feeding interactions is rare, food web construction methods are especially valuable and affords us the opportunity to make inferences about paleo communities beyond simply a record of species composition. However, the limitations of paleontological data (e.g., information of species traits is limited to that which can be preserved) restrict which methods can reliably be used. By considering both ecological theory and the constraints of what can be derived from the fossil record, we identify the methods best suited for the construction of paleo food webs. Specifically, we focus on how these methods differ in the networks they produce and what these networks can reveal about species interactions. In doing so we hope to clarify the ecological nuances of network prediction and help prevent the accidental misuse or misinterpretation of paleo food webs.

Taxonomic Distinctness of Triassic Bivalves: How a Taxonomic Tree Rebuilds After a Global Biodiversity Crash

M. Gabriela Suarez¹, Michael Hautmann¹

¹Department of Paleontology, University of Zurich, Karl- Schmid- Strasse 4, 8006 Zürich, Switzerland

Conventional approaches to studying biodiversity in deep time have focused on taxonomic richness, quantifying the number of taxa at specific Linnaean levels. However, this method overlooks deeper phylogenetic diversity within the evolutionary tree, failing to capture the taxonomic structure. To address this, we apply two Taxonomic Distinctness metrics, Average Taxonomic Distinctness (AvTD) and Variation in Taxonomic Distinctness (VarTD). Jointly, AvTD and VarTD offer a robust framework for analyzing changes in the taxonomic structure, which is crucial for understanding macroevolutionary processes. Originally developed in conservation biology, these metrics provide a novel approach to macroevolutionary studies, allowing us to explore how the taxonomic structure of marine bivalves evolved after the end-Permian mass extinction. Using a dataset of 60 Triassic fossil assemblages, we analyze changes in AvTD and VarTD across different stages of the Triassic. Our results indicate a delayed increase in AvTD, suggesting that despite available ecological opportunities, taxonomic disparity did not immediately increase post-extinction. Instead, AvTD gradually increased, peaking in the Late Triassic, supporting the hypothesis that diversification primarily occurred through a stepwise process, initially within surviving genera before expanding to higher taxonomic levels. In contrast, VarTD exhibits an overall decreasing trend, suggesting to the establishment of a more balanced distribution of species among higher taxa over time. Furthermore, paleolatitudinal trends reveal higher AvTD and lower VarTD in subtropical regions compared to the tropics, reinforcing structured rediversification patterns linked to ecological niche availability. By integrating TD metrics into paleontology, this study offers deeper insight into bivalve recovery after the end-Permian mass extinction, extending the perspective beyond species richness alone. These findings provide new insights into post-extinction recovery dynamics, emphasizing the role of taxonomic structure in macroevolution.

Lessons from coral reefs that accrete to the beat of their own drum

Lauren T. Toth¹, Anastasios Stathakopoulos¹, Alex Modys², William F. Precht², Víctor Rodríguez-Ruano^{4,5}, Richard B. Aronson⁴

¹U.S. Geological Survey, St. Petersburg Coastal and Marine Science Center, St. Petersburg, FL, USA

²Department of Geosciences, Florida Atlantic University, Boca Raton, FL

³Bio-Tech Consulting, Miami, Florida

⁴University of Miami, Cooperative Institute for Marine and Atmospheric Studies, Miami, FL, USA

⁵Florida Institute of Technology, Department of Ocean Engineering and Marine Sciences, Melbourne, FL, USA

Climate change and other stressors are driving a global-scale transformation of coral-reef ecosystems. Recent coral-reef degradation is largely unprecedented in most tropical locations; however, in more marginal environments, like subtropical south Florida or the oceanographically variable eastern Pacific, environmental perturbations during the Quaternary drove millennial-scale interruptions of reef growth and local extirpations of reef-building taxa. In a time when ecological and climatic novelty is becoming the norm for coral reefs globally, we argue that these exceptions to more typical coral-reef histories could, paradoxically, provide the best geologic analogues for the future. In this presentation, we provide examples of how the

impacts of past climate change in marginal coral reefs could serve as a bellwether for predicting the future of reefs globally. We also demonstrate that it is possible for coral-reef scientists to effectively cross the paleontological-ecological gap, by providing quantitative comparisons of reef accretion and paleoecology across geological and ecological datasets. We show that not only can the geological record provide a valuable baseline for contextualizing modern change, but that information can also be applied to improve ecological forecasts for populations and processes under different scenarios of environmental perturbations and management interventions. Although there are fundamental challenges associated with merging ecological- and geological-scale inferences, rising to that challenge is essential to providing paleoecological information that can be directly applied to improve the efficacy of management and restoration.

Live-dead comparisons of the marine benthos suggest that fossil assemblages archive trophic information with high fidelity

Carrie L. Tyler¹, Michal Kowalewski²

¹University of Nevada, Geoscience, Las Vegas, USA

²Florida Museum of Natural History, University of Florida, Gainesville, USA

As humans continue to alter environments, researchers strive to reconstruct pristine ecosystems to inform future conservation efforts. Fossils are the most obvious and widely accessible archive of past ecosystems, and the youngest fossil record (Late Quaternary) can provide a historical framework for conservation and restoration. Although functional composition can be used to understand organic-matter processing and ecosystem functioning, quantitative assessments of the preservation of relative proportions of organisms from various trophic groups in paleontological data, or trophic fidelity, are rare.

To assess how well fossils preserve functional diversity using multiple types of marine invertebrates with varying preservation potential, we compared live assemblages (135 species from 6 phyla) with sympatric dead skeletal accumulations (150 species) and the predicted fossil record (112 species) for 51 sites in coastal North Carolina (U.S.A.). High functional fidelity between the live, dead, and fossil assemblages was supported by congruence among functional diversity indices (functional richness, redundancy, over-redundancy, and vulnerability), overlap in multidimensional functional space, and species distributions within functional groups ($\rho > 0.85$, $p < 0.001$). Calculating vulnerability using a threshold of ≤ 2 species also better approximated the vulnerability in the live assemblages. We found that trophic fidelity was high, and nearly all trophic groups were represented in similar proportions in death assemblages and the fossil record.

These results suggest that functional estimates based on fossils may allow for historical assessments of ecological and evolutionary processes, including short-term community responses to human impacts as well as long-term macroevolutionary dynamics of marine ecosystems. In addition, preservable taxa may be an excellent proxy for all taxa when tracking shifts in community composition, diversity, or trophic structure. This is a promising outcome considering that conservation and paleoecology focus largely on relative changes.

Low diversity in semicircular canal shape mirrors the reduced genetic variation of Late Pleistocene Neandertals

Alessandro Urciuoli^{1,2,3,4}, Ignacio Martínez³, Rolf Quam^{5,6,7,3}, Juan Luís Arsuaga^{6,8}, Brian A. Keeling^{5,3}, Julia Diez-Valero³ Mercedes Conde-Valverde³

¹Department of Paleontology, University of Zurich, Karl-Schmid-Strasse 4, 8006, Zurich, Switzerland

²Institut Català de Paleontologia Miquel Crusafont (ICP-CERCA), Universitat Autònoma de Barcelona, 08193 Cerdanyola del Vallès, Barcelona, Spain

³Universidad de Alcalá, Cátedra de Otoacústica Evolutiva y Paleoantropología (HM Hospitales-UAH), Departamento de Ciencias de la Vida, 28871 Alcalá de Henares, Madrid, Spain

⁴Division of Palaeoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt, Senckenberganlage 25, 60325, Frankfurt am Main, Germany

⁵Department of Anthropology, Binghamton University (SUNY), Binghamton, NY 13902-6000, USA

⁶Centro Mixto (UCM-ISCIII) de Evolución y Comportamiento Humanos, Madrid, Spain

⁷Division of Anthropology, American Museum of Natural History, New York, New York, USA

⁸Departamento de Geodinámica, Estratigrafía y Paleontología, Facultad de Ciencias Geológicas, Universidad Complutense de Madrid, Madrid, Spain

Neandertals have been the subject of intense research aiming to understand their evolutionary history and relationship with modern humans. Genetic analyses have consistently shown that Neandertal populations exhibited low genetic diversity during the Late Pleistocene, likely due to small population sizes and limited gene flow before the extinction of the clade. This study investigates whether this trend of progressive reduction in genetic variation is also reflected in their morphological diversity (i.e., disparity). We focus on semicircular canals and vestibule, crucial structures of the inner ear responsible for balance and often used in phylogenetic studies.

Using a sample of pre-Neandertals from Sima de los Huesos (n=13), early Neandertals from Krapina (n=11), and late Eurasian Neandertals (n=9), we analyze within-group semicircular canal and vestibule shape variation and compare it to that of a group comprised of two Upper Paleolithic modern humans (Cro-Magnon and Laugerie-Basse) and extant Europeans (n=18). We employ diffeomorphic deformation analysis (DDA), a landmark-free geometric morphometric method that allows direct comparison of continuous surfaces and is readily sensitive to changes in volume proportions.

Our results reveal distinct shape differences among the groups and demonstrate that Sima de los Huesos and, particularly, Krapina, exhibit the highest disparity, despite representing geographically and chronologically constrained assemblages. Conversely, late Neandertals show significantly lower disparity than earlier groups, with levels similar to modern humans. This decrease in phenotypic variation aligns with the genetic bottleneck and population turnover identified by ancient DNA analyses at the onset of the Last Glacial Cycle. Conversely, the continuity in disparity among Middle Pleistocene groups challenges the hypothesis that the origin of Neandertals was associated with a bottleneck, prompting the need for alternative explanations.

Palaeoecological perspectives on Mountainous vegetation succession and land-use in the Peloponnese (southern Greece) over the last millennium

Grammatiki Vasileiadi¹, Georgios C. Liakopoulos², Katerina Kouli^{1,2}, Dimitrios Lamprakis³, Alexis Malliaris⁴, Lucrezia Masci⁵, Alessia Masi⁵, Matthias Moros⁶, Maria Papadaki⁷, Cristiano Vignola⁵, Pavlos Avramidis⁸, Adam Izdebski^{2,9}

¹Department of Geology and Geoenvironment, National and Kapodistrian University of Athens, Athens, Greece

²Palaeo-Science and History (PS&H) Independent Research Group, Max Planck Institute of Geoanthropology, Kahlaische Str. 10, 07745 Jena, Germany

³Department of Archives, Library Science, and Museology, Ionian University, 72 Ioannou Theotoki, 491-32, Corfu, Greece

⁴Gennadius Library, American School of Classical Studies at Athens, Soudias 54, 106-76, Athens, Greece

⁵Department of Environmental Biology, Sapienza University of Rome, P.le Aldo Moro 5, 00185 Rome, Italy

⁶Leibniz Institute for Baltic Sea Research, Rostock, Germany

⁷Open University of Cyprus

⁸Department of Geology, University of Patras, 265-04 Rio, Patra, Greece

⁹Institute of History, Jagiellonian University in Krakow, Gołębia 24, 31-007 Kraków, Poland

During the late Holocene, the expansion of human settlements, accompanied by climatic variability in the Mediterranean region, significantly influenced vegetation dynamics and landscape evolution. The Peloponnese peninsula (southern Greece) exhibits diverse topography and a rich history of anthropogenic activity within a well-defined area, constituting an ideal setting for studying the long-term interaction between humans and their natural environment. To decipher human impact and evidence plant response, a pollen-based vegetation reconstruction was conducted, combined with detailed historical and archaeological data. While numerous palynological studies have been performed in the lowlands of the peninsula, the mountainous regions remain unexplored in this regard. Hence, we focus on a sediment core obtained from an isolated upland wetland located in Achaia, northwestern Peloponnese. The high-resolution pollen profile covers the last 1,100 years, corresponding to the Middle Ages, providing insights into vegetation and landscape alterations, in response to the socio-economic changes and climatic instability observed in the Rakita upland area. Over the centuries a shift from a forested landscape with restricted human influence to a semi-open vegetation pattern shaped by extensive anthropogenic activity —though with notable fluctuations— is documented. By contextualizing the paleoecological data with detailed taxation registers, cadastres, and censuses produced by the Ottoman and Venetian authorities, valuable insights emerge regarding land use preferences, trade systems, and population density in the mountainous area.

Dispersal Syndrome and Climatic Niches of Holocene and Late Pleistocene Birds

Daniel A. Villar¹, Runbei Cheng², Andrew G. Gosler¹

¹University of Oxford, Department of Biology, Oxford, UK

²University of Oxford, Department of Biomedical Engineering, Oxford, UK

Studying past responses of species to climate change, and specifically drivers of what makes species vulnerable to it, can provide an important window on future responses to climatic change. This will be especially important in coming decades, as climate change is expected to become an ever-growing threat to global biodiversity. One aspect of species biology which is thought to be important in modulating species responses to changing climates is their dispersal syndrome – the ability to move from their present location to a new location. Two related hypotheses arise from consideration of this issue. First, that species with a greater ability to disperse would have wider climatic niches than species with a lesser ability to disperse, and secondly, that species with poor ability to disperse would have experienced selection for greater flexibility in their fundamental, as opposed to realised, climatic niche. We tested these hypotheses using fossil birds from the Holocene and Late Pleistocene, using a morphological (Hand-Wing-Index) and behavioural (locomotory style) proxy for dispersal syndrome. We found no support for the latter hypothesis, and mixed support for the first hypothesis, suggesting that while dispersal syndrome may be important to shaping short-term changes in climatic niche, it might be less important for shaping longer term patterns in climatic niche evolution.

The progressive disappearance of fossils and fossils imprints in south-western Madagascar: challenges and conservation perspectives

Ranaivosoa Voajanahary¹

¹University of Antananarivo, Department of Sedimentary Basin, Faculty of Sciences, Madagascar

The progressive disappearance of fossils and fossil imprints in the south-western region of Madagascar raises significant concerns about the preservation of the island's paleontological heritage. This region, known for its rich fossil deposits, holds key insights into the geological and biological history of the island and the Gondwana supercontinent. However, various anthropogenic and environmental factors, including deforestation, illegal fossil trade, and erosion exacerbated by climate change, threaten these invaluable resources. The loss of fossils and fossil imprints not only undermines scientific research but also deprives Madagascar of its natural and cultural heritage, which could serve as a foundation for educational, ecological, and economic opportunities. Urgent conservation measures, awareness-raising initiatives, and policy development are essential to ensure the sustainable protection and valorization of Madagascar's paleontological treasures.

Combining Environmental Monitoring and the Fossil Record to Support Coral Reef Management in the East Portland Special Fishery Conservation Area, Jamaica

Claire M. Williams¹, Debbie-Ann Gordon-Smith², Pearl Bergan², Matthew Rahamut², Rowan Martindale¹, and Denise Henry³

¹University of Texas, Austin, TX, USA

²The University of the West Indies Mona, Kingston, Jamaica

³Alligator Head Foundation, Portland, Jamaica

Within the Caribbean, Jamaican reefs have some of the poorest ratings of reef health. Although reefs in some parts of Jamaica, such as Discovery Bay, are well studied, few ecological studies have been extended to other regions. One such locality is the East Portland Special Fishery Conservation Area (EPSFCA) in northeast Jamaica. The unique reefs lack critical data necessary for conservation efforts. Reef management and protection require information about reef responses to changes on short and geological time frames.

To obtain an ecological baseline, this project synthesizes environmental and water quality data (nutrient concentrations, alkalinity, pH, temperature, and light) with community assemblage data (fish counts, benthic community assessments, and invertebrate counts) from EPSFCA reefs. Sites in the EPSFCA are compared using ordinations, regressions, and analyses of variance. To address a longer timeframe, similar techniques are used on 130,000-year-old fossil reefs on the shores of the sanctuary.

Assessments of EPSFCA reefs monitored from 2017-2024 found that many sites are distinct, and all show signs of degradation (e.g., coral disease and high algal cover). Much of the variation between sites can be attributed to the abundance of algae. Although all sites are temperature stressed, some sites in the sanctuary are cooler than others due to varying depths and inflowing groundwater. In addition, some sites in the sanctuary experience periodic nutrient spikes linked to freshwater inputs. Preliminary results from the fossil reefs illustrate that 130,000 years ago, their composition was different from the reefs growing today. The fossil reefs had high coral cover with dominant compositions of *Acropora palmata* and *Acropora cervicornis*; however, the modern reefs of the EPSFCA have less than 10% coral cover and the most abundant coral species is *Porites astreoides*. The results of this study are being used by the EPSFCA to guide conservation efforts.

Are ecological and dental traits conserved along the shark tree of life?

Lewis Williams¹, William Allen¹, Daniele Silvestro², Catalina Pimiento^{1,3}

¹Swansea University, Department of Biosciences, Swansea, United Kingdom

²University of Fribourg, Department of Biology, Fribourg, Switzerland

³University of Zurich, Palaeontology Institute and Museum, Zurich, Switzerland

Understanding the link between phylogenetic signal and functional traits is crucial as it informs us about the extent to which evolutionary history influences the ecological roles of species. Currently, functional traits and phylogenetic relationships in sharks are thought to be decoupled, suggesting that closely related species do not share more similar functional traits, and by extension ecological functions, than randomly selected species.

To investigate whether functional traits, including tooth shape as a proxy, exhibit a phylogenetic signal, we construct a comprehensive phylogenetic tree of extant sharks. Our methods utilize new deep learning tools to extract shape data from images of shark teeth and apply Elliptical

Fourier Analysis to quantify morphological variation. Phylogenetic signal tests are then conducted to assess the extent of evolutionary influence on tooth shape and functional traits.

Our findings contradict the current consensus by revealing a significant phylogenetic signal conserved in several key functional traits and tooth shapes, linking sharks' evolutionary history to their ecological and biological roles. This insight into trait inheritance and the evolutionary processes shaping them could have important implications for conservation strategies and our understanding of ecological dynamics.

Past ranges and future habitats: Paleogenomic and ecological insights into *Gopherus* tortoise conservation

Tianyi Xu¹, Lauren C. Springs¹, Melissa E. Kemp¹

¹The University of Texas at Austin, Department of Integrative Biology, Austin, Texas, USA

Human activities have profoundly shaped global biodiversity, driving population declines, range shifts, and extinctions, particularly among megafauna. *Gopherus*, one of the largest terrestrial ectotherms and the only surviving genus of tortoises in North America, has undergone significant range contractions since the late Pleistocene. For example, the critically endangered Bolson tortoise (*Gopherus flavomarginatus*) currently occupies only 20% of its presumed Pleistocene range, highlighting its vulnerability to anthropogenic pressures and environmental change. Understanding the evolutionary history and historical distributions of *Gopherus* tortoises is essential for informing conservation strategies, yet taxonomic delineation and lineage continuity between fossils and extant species remain poorly resolved. To address these gaps, this study applies paleogenomic and ecological modeling approaches to investigate *Gopherus* evolutionary history, past distributions, and habitat suitability. Ancient DNA (aDNA) techniques are applied to four late-Pleistocene *Gopherus* fossil specimens excavated from Texas to assess DNA preservation and explore the feasibility of species-level identification. Preliminary analyses confirm low DNA concentrations (0.7-1.9 ng/μl), consistent with fossil specimen preservation, and efforts to maximize DNA recovery through double-stranded libraries preparations and targeted capture using probes designed from existing *Gopherus* mitochondrial genome are underway. Concurrently, species distribution models will be used to identify potential habitats for the Bolson tortoise within the United States, offering insights into conservation and reintroduction efforts. By integrating paleogenomics with ecological modeling, this research not only enhances our understanding of *Gopherus* natural history and the past ecosystems but also demonstrates the value of historical perspectives in biodiversity conservation. These findings will enhance conservation strategies for this ecologically significant taxon and underscore the importance of combining fossil, ecological, and molecular data to inform protection and management for threatened species.

Biome Conservatism in Northern Hemisphere Tree Clades

Gengchen Yang¹, Wenna Ding¹, Niklaus E. Zimmermann¹

¹Swiss Federal Research Institute WSL, Dynamic macroecology, Birmensdorf, Switzerland

Phylogenetic biome conservatism, the tendency of species to retain ancestral biome distributions, has been increasingly recognized as a key factor in shaping global biodiversity patterns and influencing species' potential responses to climate change. This pattern suggests an inherent limitation for lineages to adapt to new environments through niche shifts, resulting in a higher risk of maladaptation or even extinction for species with lower dispersal capacities. Although several clade-specific studies have tested the biome conservatism hypothesis, comprehensive synthesizing studies across biomes and clades are scarce, particularly in the Northern Hemisphere.

The Northern Hemisphere, with its distinct environmental conditions, harbours a wide variety of tree species that have evolved by adapting to different habitats. In this study, we applied the Cladogenetic State change Speciation and Extinction (ClasSE) model to jointly reconstruct the evolution of biome occupancy and geographic ranges in 15 tree clades representing various biomes in the Northern Hemisphere, from tropical to boreal forests. Our results provide strong evidence of biome conservatism within these clades, showing that over 80% of transitions from ancestors to descendants occurred within, rather than across, biomes. Furthermore, our analysis revealed that sympatric speciation rates within biomes were significantly higher than those of biome shifts in most of these clades. Clades exhibiting weaker biome conservatism tended to be less structurally dominant and represented early successional stages, suggesting that canopy-structured clades, which experience stronger selective pressures, display more pronounced biome fidelity.

These findings emphasize the limited ability of the Northern Hemisphere tree clades, especially canopy-structured ones, to adapt to new biomes. This could hinder their capacity to cope with rapid climate change unless their migration capacity is high. Species with high biome fidelity are particularly vulnerable, underscoring the need for conservation strategies that account for the limited adaptability in the context of global change.

Functional overlap between Last Interglacial (MIS5e, Pleistocene) ‘warm guests’ and resident temperate species in the Mediterranean Sea

Facheng Ye¹, Silvia Danise², Ranita Saha², Marco Taviani³, Alice Giannetti⁴, Salih Gucel⁵, Pierluigi Santagati⁶, Paolo G. Albano¹

¹Stazione Zoologica Anton Dohrn, Department of Marine Animal Conservation and Public Engagement, Naples, Italy

²University of Florence, Department of Earth Sciences, Florence, Italy

³National Research Council, Institute of Marine Sciences, Bologna, Italy

⁴Departamento de Ciencias de la Tierra y del Medio Ambiente, Universidad de Alicante, Alicante, Spain

⁵Environmental Research Center, Near East University, Nicosia, Cyprus

⁶Dipartimento di Ingegneria dell'Ambiente, Università della Calabria, Arcavacata di Rende, Cosenza, Italy

Climate-driven species range expansions are critical processes that alter biodiversity patterns and reshape ecosystems. Numerous range expansions have already been detected and more are expected as they respond to a warming climate. How do range-extending species interact with

resident species? Is there potential for direct competition, or successful range-extending species differ in resource use? During the Last Interglacial (Marine Isotope Stage 5e, Pleistocene), a time characterized by temperatures slightly warmer than today, numerous tropical Atlantic species extended their ranges poleward, entering the Mediterranean Sea (so-called ‘warm guests’). Therefore, this is an ideal analog to test ecological hypotheses developed in invasion biology (e.g. limiting similarity hypothesis, environmental filtering hypothesis) on a realized large-scale range expansion. We here quantified functional overlap between ‘warm guests’ and the resident temperate fauna of the Mediterranean Sea during the Last Interglacial. We targeted molluscs because their shells are durable and thus offer a very good fossil record, and explored a longitudinal transect in the Mediterranean Sea from Spain in the west, to southern Italy, to Cyprus in the east. We applied fuzzy correspondence analysis to detect differences in trait composition of the resident and ‘warm guest’ component of assemblages, and hyperdimensional functional space to quantify functional diversity and explore patterns at the species level. We focused on multiple spatial scales (sample, region, basin). Our expectation is that Last Interglacial ‘warm guests’ poorly overlapped with the resident fauna, similarly to what is currently observed in the eastern Mediterranean between tropical Indo-Pacific non-indigenous species and the native fauna.

Modelling punctuated evolutionary change in Bayesian phylogenetics

Robert Haobo Yuan^{1,2}, Bethany J. Allen³, Timothy G. Vaughan^{1,2}, Ewan Ciuffi^{1,2}, Ugnė Stolz^{1,2}, Jordan Douglas^{4,5}, Tanja Stadler^{1,2}

¹ETH Zürich, Department of Biosystems Sciences and Engineering, Basel, Switzerland

²Swiss Institute of Bioinformatics (SIB), Lausanne, Switzerland

³GFZ Helmholtz Centre for Geosciences, Potsdam, Germany

⁴University of Auckland, Department of Physics, Auckland, New Zealand

⁵University of Auckland, Centre for Computational Evolution, Auckland, New Zealand

Divergence time estimates derived from molecular clock analyses often conflict with those suggested by the fossil record, especially for highly diverse extant clades such as placental mammals, crown birds, and angiosperms. Despite advancements in phylogenetic methods integrating both neontological and palaeontological data, such inconsistencies are yet completely resolved. One hypothesis suggests that current clock models assume gradual accumulation of character change over time and may overestimate node ages when this assumption is violated. With increasing evidence from ecological studies supporting sudden evolutionary change taking place at speciation, it is necessary to account for punctuated evolution in phylogenetic research.

A new clock model, known as the Gamma Spike model, was recently implemented in BEAST2. The model allows rapid bursts of molecular or morphological change to occur at speciation events, in addition to the continual evolution permitted by standard clock models. Here, we assess the impact of incorporating punctuated evolution in Bayesian timetree inference, using a well-studied Eutherian total-evidence dataset that encompasses major living clades as well as key fossils of placental mammals.

We compare topologies and node ages estimated by the Gamma Spike model with derived from gradual relaxed clock models and previous clock dating studies. We interpret our results in light of the Cretaceous-Palaeogene (K-Pg) boundary, and therefore potential drivers of mammalian diversification. Our findings suggest that ignoring punctuated evolution may bias divergence time estimates, potentially obscuring the timing and origins of major clades.

Posters

Systematics and Paleoecology of New Mammalian Remains from the Middle Siwalik Deposits of Northern, Pakistan

Hamza Aman Ullah¹, Muhammad Ameen², Sidra Batool², Muneeb Rauf²

¹University of Sialkot, Department of Biological Sciences, Sialkot, Pakistan

²University of Sialkot, Department of Zoology, Sialkot, Pakistan

Among all the vertebrate taxa, mammalian fauna is well known and have been studied extensively. However, taxonomic status of some mammalian taxa is yet controversial and a lot of work is being done to remove the ambiguity found in their taxonomy. So, every new specimen may offer a valuable contribution in this daunting task. The present work is based on newly collected mammalian remains from the Nagri and Dhok Pathan formations of the Middle Siwaliks that dates to Late Miocene (10.1-6.0 Ma). The material includes two mandibular fragments, serially arranged upper deciduous third and fourth premolars, isolated upper deciduous third premolar, two upper third premolars, one isolated upper molar, one upper third molar, isolated lower canine, and two partially broken lower fourth premolars. The taxonomic study of the material revealed that it can be categorized into four families, viz. Suidae, Tragulidae, and Bovidae. The family Suidae is represented by an upper third deciduous premolar and an upper first molar of large sized species, *Hippopotamodon sivalense* and a mandibular fragment with p-m3 of *Propotamochoerus hysudricus*. The DP3 of *H. sivalense* so far represents only third specimen in the entire suid collection from the Siwaliks. A mandibular fragment with roots of p4 and m2 and well preserved m1 can be allocated to the genus *Siamotragulus* due to the presence of long premetacristid, and flat lingual cusps. *Siamotragulus* is currently known by postcranial elements. A partially broken isolated upper third molar can be associated with small sized bovid species, *Eotragus noyei*, while serially arranged DP3-DP4 and upper third premolar shows morphometric characters of *Miotragocerus*, hence allocated to *Miotragocerus gluten* while both lower fourth premolars are tentatively allocated to *Miotragocerus*. The dental structures indicate that the animals relied on mixed type of vegetation. The occurrences of such a wide variety of taxa provide evidences that Late Miocene possess semi-dry paleoenvironmental conditions similar to the present time savannas.

Systematics and Paleoclimate of Terrestrial Mammalian Fauna from the Late Miocene (11.2 – 3.58 Ma) Siwalik Deposits of Pakistan

Muhammad Ameen¹, Sayyed Ghyour Abbas¹, Ayesha Sania², Muneeb Rauf¹

¹University of Sialkot, Department of Zoology, Sialkot, Pakistan

²University of the Punjab, School of Biological Sciences, Lahore, Pakistan

The Siwaliks represent one of the best exposed and richest fluvial fossil deposits available in the world. Numerous mammalian lineages have been reported and presented to the world from the 18th century. Majority of these lineages have been retrieved from the Late Miocene Siwalik deposits including perissodactyls, artiodactyls (most abundant), carnivores, proboscideans, rodents (rarest). The current study describes 14 mammalian fossil remnants collected from Hasnot and Khokhar Zer localities of Dhok Pathan and Nagri Formations of the Late Miocene, Punjab, Pakistan, respectively following surface collection method and the measurements were taken for the identification of specimens. These fossil remnants belong to four orders viz. Perissodactyla, Artiodactyla, Proboscidea and Carnivora. The order Proboscidea is represented by a tusk fragment that lack enamel and has its oval cross section and allocated to *Choerolophodon corrugatus*. An isolated lower canine and an upper third premolar are designated to the genus *Machairodus*. The canine is small with crenulated anterior and posterior edges while upper premolar has typical machairodont morphology with broad crown and having anterior and posterior accessory conules. The order Perissodactyla is represented by a single species, *Brachypotherium perimense*, with two isolated upper premolars. Both premolars are brachyodont, large sized, and tend to have flattened buccal walls. The order Artiodactyls is represented by *Tragoportax*, *Selenoportax*, and *Miotragocerus* (family Bovidae) having six fossil specimens; *Propotamochoerus hysudricus* and *Hippopotamodon sivalense* (family Suidae), and *Merycopotamus dissimilis* (family Anthracotheriidae). The presence of machairodont specimens is a great find because this family is extremely rare in the Siwaliks and these specimens will add more morphological data to our existing knowledge. Dental morphologies and the existence of different taxa during the Late Miocene of the Siwaliks indicate grassland ecosystem with semi-arid paleoclimate.

Deep-time extinction and diversity patterns of Crocodylia indicate high susceptibility of the clade to environmental changes

Ana Clara M. G. Annes¹; Thayara S. Carrasco¹; Daniel M. dos Santos¹; Juan V. Ruiz²; Giovanna M. Cidade³; Erin M. Dillon⁴; Pedro L. Godoy¹

¹Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil

²Department of Biology, University of São Paulo, Ribeirão Preto, Brazil

³Department of Biology and Zootechnics, São Paulo State University, Ilha Solteira, Brazil

⁴Smithsonian Tropical Research Institute, Balboa, 0843, Republic of Panamá

Crocodylia is a currently depauperate group, with just around 30 modern species, relative to its much richer evolutionary history since the Late Cretaceous. Because of this apparent pattern of diversity decline, Crocodylia has been considered a model system for macroevolutionary

studies. On the other hand, conservation priorities and assessments of extinction risk of extant species often neglect this rich fossil record. This study uses a Conservation Paleobiology approach to provide potentially valuable data for crocodylian conservation. Comparative phylogenetic methods were used to characterize deep-time patterns of extinction and diversity, taking into account major phylogenetic uncertainties and spatial variation across continents. Our results indicate a predominance of phylogenetically-clustered extinctions during crocodylian evolutionary history, suggesting that factors associated with extinction risk can collectively affect closely-related taxa. Also, the pattern of through-time phylogenetic diversity for each continent is consistent with the Cenozoic global cooling, given the diversity decline on continents with more landmasses closer to the poles (e.g., Europe and North America) in comparison to regions at lower latitudes (e.g., South America, Africa and southern Asia). Today, the primary threat to modern crocodylians is related habitat loss. Although the origin of the current habitat loss (e.g. anthropogenic pressures) differ substantially from the drivers of the decrease in diversity seen in the Cenozoic, the effects on crocodylian diversity can be similar. Combined, our results shed light on the importance of using the fossil record to inform conservation priorities, revealing possible hidden risks. Indeed, closely-related species could be at risk even in regions with currently stable populations. Similarly, regions that are potentially more affected by environmental changes and extreme weather, such as those prone to desertification or at higher latitudes, should also be prioritized, given the susceptibility of the whole clade (or particular subclades) to habitat loss.

Small Carnivores and Human Impact: Tracing Adaptations from Deep Past to Future

Chris Baumann^{1,2}

¹Senckenberg Centre for Human Evolution and Palaeoenvironment (HEP), Tübingen, Germany

²University of Tübingen, Dept. of Geoscience, Tübingen, Germany

Globally, 22% of small carnivore species (average body mass <15 kg) are classified as threatened on the IUCN Red List, reflecting the disproportionate impact of biodiversity loss on this group. In Europe, major threats include ongoing urbanization, increased road connectivity, and the introduction of competitive invasive species. Paradoxically, many small carnivores demonstrate remarkable adaptability to anthropogenic landscapes, exemplified by synanthropic behaviours. The red fox (*Vulpes vulpes*), for instance, has successfully expanded its range into urban areas, altering its diet and behaviour to thrive alongside humans.

This talk explores the evolving interactions between humans and small carnivores, tracing their history from paleo-synanthropism in the Upper Palaeolithic to modern shifts in trophic ecology. A key focus will be on reconstructing trophic niches using stable isotope analysis ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$), a powerful tool for cross-temporal comparisons of ecological strategies. By examining these adaptations, I will highlight how some small carnivores navigate the challenges and opportunities presented by human-induced environmental changes.

Small bodied mammals show more constraint in their jaw ecomorphologies than large bodied mammals

Gemma Louise Benevento^{1,2}, John T. Clarke^{1,2}, Matt Friedman⁴, Susanne A. Fritz^{1,2}, Roger B.J. Benson⁵

¹German Centre for Integrative Biodiversity Research (iDiv) Halle–Jena–Leipzig, Germany

²Institute of Biodiversity, Friedrich Schiller University Jena, Germany

³Museum of Paleontology and Department of Earth and Environmental Sciences, University of Michigan, United States; ⁴American Museum of Natural History, USA

Mammals underwent a taxonomic and morphological adaptive radiation across the Cretaceous/Paleogene (K/Pg) boundary. Morphological adaptations to the jaw, relating to disparate feeding ecologies, have been shown to increase in disparity during the Cenozoic. Mammal body mass also increases across the K/Pg boundary and is intrinsically linked to many aspects of a mammal's ecological niche, including their feeding ecology and therefore jaw morphology. Here we test whether increases in jaw phenotypic disparity among early Cenozoic mammals is linked to their evolutionary expansion into larger body sizes that may have permitted the exploration of new feeding roles. Using jaw continuous character traits for Jurassic-Eocene and for Recent (including Pleistocene megafauna) mammals, we analysed jaw ecomorphological disparity across small and large bodied mammals using a principal component analysis. Additionally, using a recently published metatree of synapsids pruned to include the mammaliaform and mammal species from this study, we analysed rates of jaw morphological diversification and compared these rates to body mass evolution. We found that large mammals have higher jaw ecomorphological disparity than small mammal throughout the early Cenozoic and in the Recent. Moreover, extant and Pleistocene large mammals show higher disparity than Eocene large mammals, and there are some jaw morphologies that are unique to large mammals relative to small mammals.

Plant-insect response to disturbance in two modern forests provide insight into deep-time forest responses in elevated global temperatures

Beatrice V. Bugos¹, Alexander J. Lowe^{2,3}, Ellen D. Currano¹

¹University of Wyoming, Dept of Geology & Geophysics, Laramie, Wyoming, USA

²University of Washington, Dept of Biology, Seattle, Washington, USA

³National Museum of Natural History, Dept of Paleobiology, Smithsonian Institution, Washington DC, USA

The fossil record provides information about climatic and ecological responses to anthropogenic increases in carbon dioxide. As global warming drives more extreme weather events that greatly disturb forests, understanding how past forests responded to similar climatic events is important. The Miocene Climatic Optimum (MCO, ~16.9-14.7 Ma) and the Early Eocene Climatic Optimum (EECO, 53-51 Ma), in particular, provide analogies to Earth's future climate. If carbon emissions go unchanged, Earth will reach a climate more similar to the MCO in the next century and the EECO by 2140. To make predictions about how forests will respond to disturbance in the future, we must start by establishing how plants and insect herbivores respond to disturbance in

modern analog forests. The temperate forest of North Carolina, USA is a modern proxy for the Pacific Northwest, USA, in the MCO, while the tropical dry forest of Costa Rica is comparable to Wyoming, USA, in the EECO. Leaf litter was collected as a modern proxy to plant fossil assemblages in both forest; early, middle, and late successional stages were sampled in each forest. We expect that plant diversity and insect damage diversity will increase with time since disturbance. The results of these studies, together with information from previous work about how leaf traits vary along disturbance gradients, will allow us to better infer successional stage in the fossil record. The fine-scale trends captured on leaf litter and plant fossils can distinguish between the effects of warming and local disturbance on plant-insect interactions. Furthermore, the cost-effective and relatively simple methods to establish trends in modern analog forests for paleobotanical applications intend to push a deep-time perspective for modern ecological studies.

Piecing Together the Past: Harnessing AI for Dinosaur Fossil Reconstruction

Juan Pablo Busso¹

¹Independent

Reconstructing dinosaur skeletons from limited fossil remains is one of paleontology's greatest challenges. Traditional methods rely on comparative anatomy and expert interpretation, and AI can assist with a new, scalable approach. This study presents a machine learning model trained to predict missing bones from partial fossil data with striking accuracy.

To test the feasibility of this approach, the model was first trained using 2D skeletal diagrams of 26 Ceratopsian species. Although these diagrams are a simplified representation, they provided a controlled dataset to assess the model's ability to learn anatomical relationships. During training, different combinations of bones were systematically hidden in each round, forcing the model to reconstruct them based on the remaining elements. By continuously learning these interdependencies, the AI developed a robust latent-space representation of dinosaur morphology.

When tested on seven previously unseen Ceratopsian skeletal diagrams, the model achieved a remarkably low mean squared error (0.0006), closely matching the original skeletal structures. To further validate the model, its latent-space relationships were compared with known phylogenies. The results were striking—closely related species clustered together naturally in the model's latent space, demonstrating that the AI was not only reconstructing missing elements but also capturing meaningful evolutionary patterns without manually coded traits.

While this proof-of-concept relied on simplified 2D diagrams, the next step is to train the model on real fossil data, incorporating 2D photographs, CT scans, and 3D photogrammetry. This would provide richer morphological detail, allowing the AI to refine its predictions and adapt to the complexities of real-world fossilization.

This method is envisioned as a "first draft" tool—rapidly generating an initial reconstruction that paleontologists can validate and refine. By accelerating fossil restoration, standardizing

reconstructions, and offering new insights into skeletal evolution, this AI-powered approach can shine new light on how we study and interpret prehistoric life.

Age-Dependent extinction in Carnivora: exploring the role of species pools as adaptive zones and ecological assemblages

Carlos Calderón del Cid¹, Tiago Bosisio Quental¹

¹Universidade de São Paulo, Departamento de Ecologia, Instituto de Biociências, São Paulo, Brasil

This study explores how different species pool definitions and taxonomic units in Carnivora affect Age-Dependent Extinction (ADE) signals. We emphasize two aspects: (1) the impact of defining species pools at distinct phylogenetic levels (e.g., order, suborders, and families), which may capture different eco-evolutionary dynamics, and (2) the influence of analyzing lineages at different taxonomic scales within these species pools (i.e., genera and species). By considering species pools at different phylogenetic levels as plausible distinct ecological assemblages and adaptive zones where biotic forces operate, particularly competition, this approach allows us to address at least three important macroevolutionary issues. First, it enables a systematic evaluation of how species pool definitions and taxonomic resolutions affect our comprehension of extinction dynamics. Second, it provides an assessment of whether ADE signals follow a consistent direction within Carnivora, contributing to ongoing debates about the prevalence and eco-evolutionary drivers of ADE patterns in this group. Third, it will enable us to clarify whether Van Valen's Law of Constant Extinction— age independent extinction (AIE)— evaluated at higher phylogenetic and taxonomic levels (i.e., genera within orders), is a by-product of mixed ADE signals at lower phylogenetic/taxonomic levels. Because different phylogenetic pools might, at least broadly map to, slightly distinct ecological pools, this might also represent an opportunity to investigate how ecology might influence age-dependent extinction. By integrating empirical analyses and theoretical perspectives, this study will provide insights into the eco-evolutionary dynamics mediating the potential relationship between taxa longevity and extinction probability. We expect that the empirical evidence, and the discussions spurred from it, will contribute to the understanding of macroevolutionary processes within Carnivora and potentially across other taxonomic groups.

How many characters are needed to reconstruct a phylogeny?

Alessio Capobianco¹

¹LMU Munich, Department of Earth and Environmental Sciences, Munich, Germany

Morphological phylogenetics plays a fundamental role in the understanding of macroevolutionary processes, as morphology is the only source of information to place most extinct species in a phylogenetic context, and excluding extinct species from downstream analyses (e.g., biogeography, character evolution, diversification) might result in biased evolutionary inferences. Despite increased recent attention towards Bayesian morphological

phylogenetics and its applications, it remains unclear how many discrete characters are needed to accurately estimate tree topologies in a Bayesian framework. This is a key aspect of morphological phylogenetic analyses, as most empirical morphological datasets consist of a few dozens to a few hundreds of characters—several orders of magnitude smaller than molecular datasets.

I designed a simulation study in the software RevBayes to explore how the number of sampled discrete characters affects accuracy and precision of Bayesian phylogenetic estimates, under various setups differing in number of taxa, average number of state changes per character (i.e., tree length), and number of states per character. Results suggest that hundreds of characters might be necessary to reach a satisfactory level of accuracy in topological estimates for as low as 20 tips, and thousands of characters for more than 100 tips. All other parameters being equal, multistate characters produce more accurate estimates than binary characters, and longer trees produce less accurate estimates than shorter ones.

The results of this study provide to empirical researchers a baseline expectation for the accuracy of a phylogenetic estimate, given the size and other characteristics of the dataset used to generate it. Moreover, they outline the continuous need for global research efforts geared towards the characterization and digitalization of interspecific morphological diversity in both extant and extinct taxa, with the specific aim of building larger data matrices for phylogenetic studies.

Sloths (Phyllophaga) from the Urumaco Neogene sequence of Venezuela - the challenge of diversity estimates in view of biased preservation of skeletal parts

Alfredo Armando Carlini¹, Sánchez R², Carrillo-Briceño JD³, and Sánchez-Villagra MR³

¹CONICET and UNLP, Facultad de Ciencias Naturales y Museo, Laboratorio de Morfología Evolutiva y Desarrollo (Morphos), La Plata, Argentina

²Museo Paleontológico de Urumaco, Urumaco, Estado Falcón, Venezuela

³Universität Zürich, Paläontologisches Institut, Zürich, Switzerland

The Urumaco sequence from Northwestern Venezuela consists of thousands of meters of sediments comprising four geological Formations that document biodiversity changes over some 20 million years of the northern neotropics. After the first systematic expeditions in the 70's and more than 20 years of regular fieldwork in the area by us, we report a remarkable diversity of Phyllophaga of different clades, and of different body sizes. The most common records are centered on postcranial remains in different degrees of preservation, and very secondarily by craniomandibular remains that frequently show a deep plastic deformation that makes a precise comparative analysis difficult.

The clades represented in the Urumaco sequence are Megatheriinae, Notrotheriinae, Mylodontinae, Lestodontinae, a new Subfamily, and Megalonychidae. Several species have been reported or described from the sequence and others are recognized as potentially new but remain unnamed. Considering those that we can identify as different species (and respecting the

previous order), in the Socorro Fm. there would be 0-0-1-0-1-0-2; in the Urumaco Fm. 1-0-1-0-3-1-3; in the Codore Fm. 1-1-0-1-0-0-0 and in the San Gregorio Fm. 1-0-0-0-0-0-0. Clearly, in the Urumaco Fm. there is the greatest diversity of sloths, not only taxonomically but also in terms of sizes and adaptive types. Remarkably, this conservative estimate of diversity does not include any Scelidotheriinae, a diverse clade in other rich units of the northern neotropics (e.g. La Venta sequence, Colombia), hypothesized as indicative of environmental or even chronological differences.

Ediacaran phylogenetic community analyses

Shujie Chang^{1,2}, Nile Stephenson^{1,2}, Frances Dunn³, Emily Mitchell^{1,2}

¹University of Cambridge, Department of Zoology, Cambridge, UK

²University Museum of Zoology, University of Cambridge, Cambridge, UK

³Oxford University Museum of Natural History, UK

The fossil record of early animals from the Avalon (Ediacaran, ~570–560 Ma) represents the earliest known metazoan marine communities. Their in-situ, near-census, non-time-averaged preservation enables the use of spatial ecological methods commonly applied to modern plant communities, facilitating detailed exploration of Ediacaran community dynamics. Here, we applied spatial point pattern analysis to 18 populations across 7 communities to investigate the drivers of pairwise interactions, specifically competition. Most communities appear governed by non-competitive neutral processes, yet some show spatial segregation, potentially indicating the emergence of competitive interactions. We further examined the drivers of such competition by comparing tiering (extent of vertical niche partitioning) with phylogenetic relatedness. As in modern sessile communities, height is a key functional trait linked to competition and is frequently compared to phylogenetic relatedness, with contentious conclusions on their relative strength. We quantified the degree of tiering through vertical overlap in both height and feeding zones between populations and leveraged a newly established phylogenetic tree of all rangeomorphs to calculate the phylogenetic affinities. Finally, we test these two factors separately to explore whether the strength of competition changes with each, then combined them into a single model to determine which factor exerts a stronger influence on competition at the metacommunity level. By investigating the relative importance of height and phylogenetic relatedness within the earliest metazoan communities, this work provides new insight into the assembly and ecological processes operating at the dawn of complex animal life.

Where the shuck did the oysters go? A gap in the Neogene oyster record

Gwyneth Chilcoat¹, Tessa Hill¹

¹University of California - Davis, Department of Earth and Planetary Sciences and Bodega Marine Laboratory, Davis, USA

Oysters (Ostreidae) are foundation species that were overharvested near the point of extinction, making them a focus of coastal conservation efforts on the North American west coast. The

oyster is a resilient animal that was historically distributed near-globally on rocky shorelines, extending back to at least the early Mesozoic.

We seek to inform restoration projects and contextualize the range and thermal tolerance of oysters based on their evolutionary biogeographic history, with a focus on the North American west coast. In this study, we collated and visualized oyster occurrence data using museum repositories digitized in the EPICC (Eastern Pacific Invertebrate Communities of the Cenozoic) project. We compared occurrence data with paleogeography and paleotemperature records. Oysters are diverse and widespread in the Paleogene. In the Miocene, the dominant taxon is the giant *Ostrea titan*, but oysters are nearly absent north of the San Francisco Bay throughout the Neogene. In the Pleistocene, the native Olympia oyster (*Ostrea lurida*) becomes dominant, and communities start resembling modern species makeup and faunal distribution.

By improving our understanding of the history of oysters, we contribute to a fundamental understanding of the organism's resilience to environmental change and historical distribution that can guide coastal managers in restoration decision making.

***Open Palaeontology* – a community-driven diamond open access journal with preregistration**

Harriet B. Drage¹, Joseph N. Keating², Morten Lunde Nielsen³, Farid Saleh¹ and Thomas W. Wong Hearing⁴

¹ University of Lausanne, Switzerland

² University of Bristol, UK

³ Independent researcher outside academia

⁴ University of Leicester, UK

We present *Open Palaeontology*, a new diamond open access journal. *Open Palaeontology*'s scope covers all aspects of palaeontology, including, but not limited to, taxonomic descriptions, field studies, method developments, experimental taphonomy, and computational work. *Open Palaeontology* operates a flexible publishing model focused on transparency and accountability. Uniquely, *Open Palaeontology* offers a range of publication media, considering rigorously researched submissions in written, audio, and audiovisual formats, as well as recognising the step-wise nature of much research and providing opportunities to publish at different stages of development.

The founding principles of *Open Palaeontology* arise from our concerns with the current academic publishing landscape and our desire to provide an accessible, transparent, accountable, and innovative publishing space for palaeontological research. *Open Palaeontology* draws on the wealth of established and emerging good practice that can be found across the academic publishing landscape. This includes our diamond open access status, supported by SOAP2 (Switzerland), which mitigates financial accessibility issues, a transparent peer review procedure, with optional double-blinded reviewing followed by publication of reviews to mitigate lack of accountability in the editorial and review process, and research preregistration to mitigate the bias against publishing null results. We require all authors and reviewers to follow

our code of conduct, which includes following and declaring ethical good practice in all aspects of the research process. *Open Palaeontology* began as an exercise in innovation and will continue to evolve its approach as new ideas and best-practices develop.

We hope that *Open Palaeontology* will help transform our understanding of how palaeontological research can be rigorously assessed and published. We encourage interested researchers, particularly those working outside Europe and North America, to get in touch as we continue to diversify our Handling Editor and journal management pool. We are open for submissions and look forward to receiving your contributions!

Experimental Fluid Dynamics: validating Computational Fluid Dynamics palaeoecological simulations

Harriet B. Drage¹, Stephen Pates², Nicholas J. Minter³

¹ University of Lausanne, Switzerland

² University of Exeter, UK

³ University of Portsmouth, UK

Computational Fluid Dynamics (CFD) simulations are increasingly used to test palaeoecological hypotheses. These analyses output simulated velocity and pressure profiles and drag and lift forces values acting on a model. These outputs are internally consistent, assuming consistent parameters. However, many simulations lack validation at the flow speeds and animal sizes modelled, and so the margins of error remain unquantified. Without having certainty in simulated outputs, we risk the resulting palaeoecological hypotheses lacking robustness. To test the differences between simulated and real-world forces, Experimental Fluid Dynamics (EFD) analyses using flume tanks can be performed, though these have rarely been done for palaeobiological research. We present preliminary work producing a broadly applicable protocol for performing EFD analyses to validate CFD results. We tested idealised sphere models against theoretical drag calculations, recorded lift forces, and carried out experiments with animal models used in comparable CFD simulations. We discuss the considerations involved in 3D-printing EFD models, present the low-cost, open-source circuitry equipment used to measure forces, and display the jig built to support the circuitry above the flume tank during experiments. Our sphere experimental results tracked the theoretical drag force patterns reasonably well, though were too high in magnitude. Experimental drag for an ammonite model almost exactly replicated data reported from CFD simulations, though other animal models differed due to the experimental conditions. This protocol is subject to future refinement, including the attachment method of the model to the jig, using median logged force values, and testing benthic regimes. Following refinement, a series of validation values will be produced for major early Palaeozoic arthropod body plans under different flow regimes in varied water column positions. These values can be used to validate CFD results of varied future studies, and the protocol replicated to support and inspire others in performing EFD validation of palaeoecological hypothesis-testing.

Can ecological features predict the quality of the Carnivoran fossil record?

Thaís Faria¹, Tiago Bosisio Quental¹

¹University of São Paulo, São Paulo City, Brazil

The quality of the fossil record of organisms can be impacted by several biotic, abiotic, and human factors, known as "fossil record biases", which can affect macroecological and macroevolutionary inferences. Mathematical models have been proposed to explicitly consider the incompleteness of the fossil record or even directly estimate fossil preservation rates, with previous attempts to estimate preservation rates having considered temporal and spatial variation, as well as preservation heterogeneity among species. Including ecological or morphological information would be a step further into developing more sophisticated models. The first aim of this project was to investigate the phylogenetic signal of the extant Carnivoran fossil record quality, measured as the presence or absence of known fossils for each species, while the second goal was to check whether the average body size, a trait regularly used as a general proxy for several ecological aspects, could impact the quality of the fossil record, measured as the number of fossil occurrences of each species. To achieve our goals, we used fossil occurrence data downloaded from the Paleobiology and NOW Databases, body mass data from the COMBINE Database, and 200 molecular phylogenies. The phylogeny tips are taken as a reference point for extant Carnivoran diversity, for only extant species can be known with or without a fossil record. The presence or absence of a fossil record showed a moderate phylogenetic signal (D-Value index). The number of fossil occurrences was recorded for each extant species, and preliminary analyses, not taking phylogeny into account but analyzing each family separately, suggest that larger species also have more fossil occurrences for 7 families with more than 10 species. As our next step, we will use phylogenetic comparative methods to properly investigate the relationship between occurrence count and body mass, which should be done by the conference.

The phylogenetic signal of extinction through the rise and fall of early vertebrates – field of bullets or clustered strike?

Joseph Flannery-Sutherland¹, Amy Tims², Laura Soul³, John Clarke⁴, Matt Friedman⁵, Sam Giles¹

¹University of Birmingham, School of Geography, Earth and Environmental Sciences, Birmingham, UK

²Monash University, School of Biological Sciences, Monash, Australia

³University of Oxford, Department of Earth Sciences, Oxford, UK

⁴Ludwig-Maximilians-Universität, Department of Earth and Environmental Sciences, Munich, Germany

⁵University of Michigan, Department of Earth and Environmental Sciences, Ann Arbor, USA

Early vertebrates provide a remarkable study system for investigating the drivers of extinction and turnover in Palaeozoic ecosystems. Phylogenetic conservation of ecological traits that promoted or alleviated extinction risk has the potential to explain differential patterns of extinction across early vertebrate groups. Elucidating the factors that shaped their rise and fall, however, is challenged by a lack of phylogenetic trees which include an adequate proportion of their taxonomic diversity, coupled with the unavailability of the well-revolved fossil occurrence

data required to characterise the spatiotemporal distribution of early vertebrate taxonomic diversity. To address these issues, we construct a formal supertree of over 1000 early vertebrate species, time calibrated using an expanded fossil occurrence dataset compiled through an intensive databasing campaign. We use this supertree to assess the phylogenetic signal of extinction clustering across early vertebrate phylogeny, and through geological time. Preliminary results indicate substantial variability across both temporal and phylogenetic axes but indicate that clustering was most severe amongst jawless vertebrates as gnathostomes became increasingly prominent within Palaeozoic ecosystems. Conversely, clustering within gnathostomes was strongest during the Hangenberg mass extinction at the end of the Devonian. This work forms the basis for linking their phylogenetic and taxonomic diversity patterns to explanatory ecological and geographic factors in future work.

Refined taxonomy and chronology to understand faunal changes and extinction: New investigations on megamammals from the Argentinean Pampas and the historical Roth collection

Analia Marta Forasiepi¹, Voglino D.², Prevosti F.J.³, Le Verger K.⁴, Sánchez-Villagra M.R.⁴

¹CCT-CONICET Mendoza, Instituto Argentino de Nivología, Glaciología y Ciencias Ambientales, Mendoza, Argentina

²Museo de Ciencias Naturales “A. Scasso”, San Nicolás de los Arroyos, Argentina

³Museo de Ciencias Antropológicas y Naturales, Universidad Nacional de La Rioja, La Rioja, Argentina

⁴University of Zurich, Department of Paleontology, Zurich, Switzerland

The Argentinean Pampas offer a reference sequence of mammalian faunas to reveal community changes and extinction during Pleistocene times. The tempo and mode of such changes – including the effect of Quaternary climatic fluctuations and human action – are measurable only in the light of a robust taxonomy and accurate chronology. Our work concerns the study of the historical collection and new fieldwork in sites investigated by the pioneering work of Santiago Roth (1850–1924), a naturalist of Swiss origin that greatly influenced the paleontology in Argentina. Roth made remarkable discoveries, including complete skeletons of megamammals and human remains. Some of his fossils were sold to museums in Europe (Copenhagen, Geneva, Lausanne, Zurich) while others are in Argentina (Museo de La Plata). In 1888, Roth published a stratigraphic model, which was later re-adapted to define the biostratigraphic units still in use (Ensenadan 1.78–0.4 Ma, Bonaerian 400–126 ka, and Lujanian 126–7 ka Ages/Stages). However, the definition and precise boundaries of this scheme is still unprecise and has been challenged by different working teams. Recent fieldwork studies and fossil prospecting were focused on the northern part of the Buenos Aires province, including sites at the riverbanks of the Parana River, where Roth established his stratigraphic scheme. Our results include: (i) a new integrated regional stratigraphic model that provides a general framework to interpret Roth’s Pampean sites and fossils; (ii) samples for electron spin resonance and radiometric dating to calibrate the sequences; (iii) the study of new fossils with precise stratigraphic origin. Our collaborative work on museum collections led to many taxonomic reassessments and new digital repositories gathering the new fossils and the historical material from Roth inside and

outside Argentina to fostering wider access, exploring the diversity dynamics at the end of the Pleistocene and reassessing hypothesis of extinction.

New insights on *Cruziana* ecology during the Early Ordovician

Inés Fuertes¹, Jorge Esteve¹, Zain Belaústegui²

¹Universidad Complutense de Madrid, Department of Geodynamics, Stratigraphy and Palaeontology, Madrid, Spain

²Universitat de Barcelona, Department of Earth and Ocean Dynamics, Barcelona, Spain

The relationship between animals and the substrate initiated biogeochemical cycles among other mechanisms, driving evolution during the Cambrian and Ordovician periods. This emphasizes the importance of trace fossils, which are crucial for understanding the early stages of metazoan evolution. Among the most iconic trace fossils is the ichnogenus *Cruziana*, generally attributed to trilobites in Palaeozoic strata. Typically preserved as convex hyporeliefs, occurrences as concave epireliefs are rare in the fossil record. Here, we report a new locality with unusual preservations, ranging from convex to concave epireliefs (and even the transition to full reliefs), providing fresh insights into trilobite ecology during the Early Ordovician.

The newly discovered trace fossils attributed to *Cruziana* were found in the Armorican Quartzite facies north of Puertollano, Southern Spain. Many are preserved as concave epireliefs, occasionally displaying bioglyphs, and often transitioning into convex epireliefs and eventually also into full reliefs. These convex forms exhibit active meniscate fills, suggesting that at least some of them were infaunally produced through the excavation of burrows and not from surface trails. Outcrops reveal size biases, with stratigraphic levels tending toward either larger or smaller traces. This indicates gregarious behaviour in these arthropods, likely segregated by age, consistent with other arthropod behaviours related to mating or moulting. Some traces are associated with ripple marks, indicating a shallow marine environment. This supports the idea that the gregarious behaviour in these trilobites may have had the purpose of moulting or mating, as shallower environments likely provided better protection from predators during the Lower Ordovician.

The South American rat-kangaroo *Argyrolagus* (Marsupialia, Argyrolagidae): Paleoeological reconstructions based on CT and new fossils from the Pliocene of Argentina

Charlène Gaillard¹, Forasiepi A.M.¹, MacPhee R.D.²

¹CCT-CONICET Mendoza, Instituto Argentino de Nivología, Glaciología y Ciencias Ambientales, Mendoza, Argentina

²American Museum of Natural History, Department of Mammalogy, New York, United States

Argyrolagus and closest relatives were outlier marsupials with peculiar cranio-dental and postcranial features, including a form of bipedal locomotion unique among Cenozoic South

American mammals. A new skull of *Argyrolagus scagliai* collected from a paleoburrow from the Buenos Aires Atlantic coast, Argentina, together with μ CT scanning of the holotype and the new fossil permitted re-study of its cranial anatomy and exploration of aspects of its paleoecology. *Argyrolagus* was a small marsupial (about 150gr body mass) with an elongated, projecting rostrum somewhat like *Dipodomys*, *Sommeromys*, or *Elephantulus* among elephant shrews. Reconstruction of the orbit of *Argyrolagus* suggests an eyeball diameter of ~6.0 mm, not particularly large considering the total area of the orbit, and placed in the caudal part of the orbital fossa. Orbital convergence was low (25°) while the angle of orbital verticality was high (84°), indicating panoramic vision. Virtual reconstruction and interpretation of the auditory region (including the tympanic membrane, middle ear ossicles, middle ear volume, inner ear) indicates that hearing in *Argyrolagus* was shifted towards low frequencies. This correlates with hearing capabilities of extant small mammals (mostly rodents) that live in desert environments and/or inhabit underground tunnels. Both interpretations seem plausible for *Argyrolagus* considering the geological context and reconstructed paleoenvironments where its fossils have been recovered.

Reconstructing Late Miocene freshwater ecosystems at Toros-Menalla (Chad), through aquatic vertebrate paleocommunities study

Axelle Gardin^{1,2}, Olga Otero², Géraldine Garcia², Clarisse Nekoulngang³, Mahamat Adoum³, Jean-Renaud Boisserie^{4,2}, Soizic Lefur², Fabrice Lihoreau⁵, Andossa Likius⁶, Hassane Taïssou Mackaye⁶, Abderamane Moussa⁶, Mathieu Schuster⁷ & Franck Guy²

¹Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, USA

²Laboratoire PALEVOPRIM (UMR 7262 CNRS – Université de Poitiers), Poitiers, France

³Centre National de Recherche pour le Développement, N'Djamena, Chad

⁴Centre Français des Etudes Ethiopiennes, Addis Ababa, Ethiopia

⁵Institut des Sciences de l'Evolution de Montpellier, ISEM (UMR 5554 CNRS – Université Montpellier), Montpellier, France

⁶Département de Paléontologie, Université de N'Djaména, N'Djaména, Chad

⁷Institut Terre & Environnement de Strasbourg (UMR 7063 CNRS – Université de Strasbourg), Strasbourg, France

Freshwater environments play an essential role in shaping ecosystems, yet their reconstruction often remains secondary to terrestrial ones in paleoenvironmental studies in intertropical African sites. However, understanding freshwater ecosystems is crucial, as they intersect hydrography, climate, and biodiversity, by influencing species distribution and survival. The Toros-Menalla fossil area in northern Chad (ca. 7 Ma) provides a unique window into Late Miocene ecosystems, preserving an exceptional vertebrate assemblage, including *Sahelanthropus tchadensis*, the earliest known hominin. Although aquatic environments are supposed to have been abundant in Late Miocene landscapes of Toros-Menalla, detailed characterizations of its freshwater species habitats are still lacking.

We investigate the diversity of freshwater environments in Toros-Menalla through the study of aquatic and semi-aquatic vertebrate assemblages (actinopterygians, crocodilians, chelonians, and hippopotamoids), from five sites selected based on consistent sampling strategies,

extensively focusing on aquatic vertebrates. By examining community composition, skeletal element representation, and fossil preservation, we assess how sampling and taphonomic processes influence paleoecological interpretations. Community composition and structure were further analysed in relation to habitat preferences and ecological tolerances, providing insight into waterbodies diversity.

Our results, contextualized with previously published and unpublished isotopic data, shows that each site correspond to a specific freshwater environment. They thus reveal various perilacustrine environments displayed along the margin of a Late Miocene mega lake stage, including floodplain, drying pond, and vegetated marginal environments.

rredlist 1.0: an updated R client for the IUCN Red List API

William Gearty¹

¹Open Source Program Office, Syracuse University, Syracuse, NY, USA

Earth is currently undergoing a human-induced extinction crisis, with over one thousand species documented as having gone extinct in the wild since 1500 and thousands, if not millions, more currently endangered due to habitat loss, climate change, and other anthropogenic causes. With little to no respite in sight for many of these species, it is critical that we assess and document the extinction risk of the world's species and make this information as accessible as possible to various stakeholders. The IUCN Red List is the world's most comprehensive information source on the global extinction risk status of animal, fungus, and plant species. Each assessment of a species contains information on extinction risk, geographic range, population size, habitat, ecology, use/trade, threats, and current conservation actions, making it a valuable resource for ecologists, conservationists, and conservation paleobiologists. Here I present a software package, *rredlist*, which provides direct access to this database from within the R statistical coding environment. Specifically, I introduce the first new major version of *rredlist* since its inception in 2016, tracking the recent developments of the IUCN Red List Application Programming Interface (API). The functions within the package cover all endpoints of the API, making all public data available within R. Furthermore, *rredlist* is designed to easily integrate into existing research workflows to enable users to explore and analyze assessment data across time, space, taxonomy, and many other dimensions of variation. My hope is that *rredlist* helps facilitate accessible, standardized, and reproducible research far into the future.

Interspecific competition in deep-time: a new species-level approach

Salatiel Gonçalves-Neto¹, **Torsten Hauffe**^{2,3}, **Daniele Silvestro**^{4,5}, **Tiago Bosisio Quental**¹

¹Universidade de São Paulo, Departamento de Ecologia, São Paulo, Brasil

²University of Fribourg, Department of Biology, Fribourg, Switzerland

³Swiss Institute of Bioinformatics, Fribourg, Switzerland

⁴Department of Biosystems Science and Engineering, ETH Zurich, Switzerland

⁵University of Gothenburg, Gothenburg Global Biodiversity Centre, Department of Biological and Environmental Sciences, Gothenburg, Sweden

Emerging evidence suggests that biotic interactions, such as interspecific competition within and among clades, may play a more critical role as a driver of diversification dynamics than previously recognized. While existing research often infers competition indirectly from diversity-dependent diversification patterns or rate correlations, crucial aspects of interspecific competition, such as ecological similarity and spatial overlap, are frequently oversimplified or overlooked. We build upon a recently developed framework that quantifies competition intensity using fossil occurrences, spatial distribution and ecomorphological traits. More specifically, we develop a new approach that model competition as a dynamic, species-specific process rather than a clade-level effect. This metric captures how individual species experience competition as a function of their ecological similarity and spatial overlap with coexisting taxa, varying dynamically over their evolutionary history. We apply this framework to assess the role of interspecific competition within the evolution of the Canidae family, where dietary and spatial competition are likely pivotal. We hypothesize that as ecological similarity and spatial overlap between coexisting species increase, we should observe a decline in speciation rates and a rise in extinction rates. By treating our competition metric as a time-varying, species-specific feature, our framework avoids clade-level averaging and instead captures how competition affects the diversification dynamic of each species individually while controlling for unrelated rate changes over time. We hope our new approach enhances our understanding of macroevolutionary processes by integrating ecological aspects and spatial information at the species-level.

Ecomorphological diversity in Cambrian rhynchonelliformean brachiopods from the middle Cambrian of north Spain

Alejandro González-Cloquells¹, Jorge Esteve¹

¹Universidad Complutense de Madrid, Departamento de Geodinámica, Estratigrafía y Paleontología, Madrid, España

The replacement of stabilized substrates by microbial mats with softer, unconsolidated substrates is one of the most significant events associated with the Cambrian Explosion. However, while this phenomenon has been studied from the perspective of trace fossils, few studies to date have explored the interaction between sessile organisms and a changing substrate. On the other hand, research on morphological diversity reveals that many organisms such as trilobites or brachiopods exhibit remarkable variability. Among the most important and abundant metazoans during the early stages of the Cambrian Explosion are brachiopods, which also display significant morphological diversity. Nevertheless, there appears to be no direct relationship between their shape and the type of substrate to which they attach. Could there, however, be some connection between the degree of substrate consolidation or grain size and the morphology of these organisms? Brachiopods are filter feeders, relying on inhalant currents carrying food particles into their bodies, which they then filter before expelling water via exhalant currents. In this study, we analysed the morphological diversity of a rhynchonelliform brachiopod species that exhibits three distinct morphotypes, putatively related with different sedimentological settings although ontogenetically controlled.

Through 3D modelling and printing, we have studied the ecomorphological behaviour of these

animals in a recirculating flume. The analyses were conducted under two conditions: with the brachiopod's valves open and closed, and in two scenarios: (i) epifaunal and (ii) with dorsal valves partially buried. The results reveal that the stabilization of morphotypes is directly related to grain size, and that greater fold height favours deeper burial, allowing for more efficient filtration in stable substrates. This finding explains how the ecomorphological variation of this brachiopod reflects a direct adaptation of its shape (morphotype) to its life habit, optimizing its interaction with the sedimentary environment.

A tale of cities: cylindrical enrolment in the Cambrian and Ordovician trilobites

Alejandro González-Cloquells¹, Alejandro Corrales-García², Jorge Esteve¹

¹Universidad Complutense de Madrid, Departamento de Geodinámica, Estratigrafía y Paleontología, Madrid, España

²University of Saskatchewan, Department of Geological Sciences, Saskatoon, Canada

Spinosity in the pleural tips was one of the key morphological traits that contributed to the evolutionary success of early Cambrian trilobites. These segmented arthropods developed pleural spines as an effective defence mechanism against predation. However, very early in their evolutionary history, these animals innovated a new method of defence: enrolment. Cambrian trilobites, particularly redlichiids, exhibited long pleural spines that served as a deterrent to predators. Yet, many representatives of this diverse order lacked the ability to perform encapsulated enrolment, often displaying only a cylindrical style of rolling up. One likely reason for this limitation is that the spines themselves posed an obstacle to fully closing the body. Fossil evidence reveals that trilobites capable of encapsulated enrolment typically lacked long spines, suggesting that enrolment alone provided sufficient protection against predators.

Our 3D kinematic studies on *Bathynotus* and *Ecceoparadoxides* from the Cambrian and *Cybele* from the Ordovician show that long spines are challenging to overlap during the enrolment process, which explains why evolution often favoured either effective enrolment or prominent spines, but rarely both traits simultaneously. Interestingly, the fossil record from the Ordovician radiation presents an exceptional case: trilobites developed relatively fragile, elongated spines while exhibiting encapsulated enrolment. This anomaly highlights the distinctive nature of the Ordovician radiation. While the Cambrian saw the emergence of most major trilobite groups, the Ordovician stands out as a period of ecological innovation. This makes the Ordovician an extraordinary window into the evolutionary dynamics of the early Phanerozoic.

Australian Veneridae (Mollusca:Bivalvia): Palaeoclimate change, future climate impacts; exploring morphological shifts linked with environmental change in deep time

Michelle Gray^{1,2}, Mark T Warne^{1,2}, Elizabeth A Weldon^{1,2}

¹Deakin University, School of Life and Environmental Science, Burwood, Vic, Australia

The ocean's amelioration of anthropogenic forcing on climate by absorbing excess anthropogenic heat carbon dioxide (CO₂) emissions is predominantly tied to the marine benthic environment. Here, bivalves are vital benthic bioturbators, contributing to the storage and cycling of nutrients and pollution and sequestering tons of CO₂ per year through shell building.

Deep-time evolutionary impacts of ocean warming and acidification can persist far into the future. Morphological shifts impact functional diversity and susceptibility to a rapidly changing benthic environment. Although neo-ecological studies provide an understanding of short to mid-term faunal response to climate change, they provide limited insight into extended temporal consequences of changes in functional diversity. Palaeontological data can identify hotspots of diversification, broadscale drivers of faunal range shifts, ecosystem tolerances, and tipping point precursors in the Earth's systems.

Southern Australia's benthic system is under great threat from rapid ocean warming. With a view to understanding the potential response of modern bivalves to future climate change, we examine fossil bivalves from the family Veneridae in Australia and use palaeontological data to investigate morphological responses to environmental shifts in deep time.

A new fossil insect fauna of the northern neotropics (Pliocene, San Gregorio Formation, Venezuela)

Guerrero, E.¹, García-León, V.¹, Morales, A.¹, Cisneros, L.¹, Seguela, J.¹, Tampoa, J.², Haug, C.^{3,4}, Haug, J.^{3,4}, Rölz, R.³, Carrillo-Briceño, J.D.², Sánchez-Villagrà, M.R.²

¹Universidad Central de Venezuela, Facultad de Ciencias, Instituto de Zoología y Ecología Tropical, Laboratorio de Biología de Vectores y Parásitos, Caracas, Venezuela

²University of Zurich, Department of Paleontology, Zürich, Switzerland

³Ludwig Maximilians University Munich, Biocenter, Planegg-Martinsried, Germany

⁴LMU, GeoBio-Center, München, Germany

Arthropods is a group greatly affected by the biodiversity crisis. They perform environmental functions that are fundamental to the ecological stability of ecosystems. In paleoecological environments, terrestrial arthropods are usually poorly represented due to their fragility and small size, hindering any paleontological insights into extinction patterns and clade antiquity in this huge clade. Here we report on a new insect fossil assemblage from a neotropical fossiliferous site rich from the Pliocene of San Gregorio Formation (Urumaco Sequence), northwestern Venezuela. During the Pliocene, the region was characterized by a varied environments, dry forests, savannas and rivers that flowed towards the coastal area. The fossils described here come from sediment of fluvial origin, associated with a large diversity of aquatic fauna such as fish, turtles and crocodiles. Fossil arthropods are preserved as three-dimensional replicas in silts and very fine sandstones. The specimens, now in the collections of the Paleontological Museum of Urumaco, were obtained by sieving with a 0.5 mm mesh from sediments of a single outcrop. In total, 81 specimens were evaluated, of which 73 could be identified (53 Hymenoptera, including the genera *Atta*, *Odontomachus* and tentatively

Solenopsis, Pheidole and Pseudomyrmex; 7 Coleoptera [Curculionidae] and 13 Scorpiones [Tarsoporosus]). Scanning electron microscopy, reflected light microscopy, fluorescence microscopy and microcomputed tomography techniques were used. This insect fossil assemblage may indicate a surface layer of soil with abundant plant material, inhabited by predators such as scorpions and ants of the genus Odontomachus, and foraging ants of the genus Atta that inhabit tropical forests, both humid and dry. The presence of bushes or trees could also be inferred by the presence of the ants Pseudomyrmex, Pheidole and Solenopsis (also predators of other arthropods). The inferred paleoenvironment, based on the fossil insect assemblage, differs strongly from the semi-arid zone badlands.

Refining the use of oxygen isotopes of southern hard clam (*Mercenaria campechiensis*) shells as archives for paleoclimatic reconstructions

Alizé M. Hardin^{1,2}, Madelyn J. Mette², Gregory S. Herbert¹, Stephen Hesterberg³

¹University of South Florida, School of Geosciences, Tampa, FL, USA

²U.S. Geological Survey, St. Petersburg Coastal and Marine Science Center, St. Petersburg, FL, USA

³Gulf Shellfish Institute, Palmetto, FL, USA

One of the major challenges to the success of ecological restoration is the mismatch in suitability between past and present environments. Isotope sclerochronology can help ecologists understand the types and magnitudes of these mismatches. The growth rate and geochemistry of accretionary growth layers within mollusk shells is known to preserve a record of environmental conditions (temperature, salinity, etc.) at the time the layers formed. During periods of temperature extremes, however, some species slow or halt shell growth, limiting the utility of shell isotopes for reconstructing past temperature ranges. *Mercenaria campechiensis*, the southern hard clam, is a large, long-lived clam native to the Gulf of Mexico, thus making the species potentially useful for reconstructing temperature variability in the past. For instance, in Tampa Bay, water temperatures have increased by 1.3 to 1.7°C over the past 50 years, yet conservation and wildlife managers are uncertain whether this warming is unusual since reliable temperature records for the bay only began in the 1970s. In this study, we analyze growth increment and geochemical data (oxygen isotope ratio, $\delta^{18}\text{O}$) from shells of *M. campechiensis* to determine (1) the range of seasonal temperature extremes recorded by this species and, (2) whether physiological tolerance to temperature extremes changes with age. These results will guide future paleoclimate studies involving *M. campechiensis* and determine the fidelity of temperature reconstructions derived from the full ontogenetic range of individual shell records.

Elucidating diversity dynamics in Cenozoic marine tropical hotspots

Lewis A. Jones¹, Nadia Santodomingo², Daniele Silvestro³, Francesca R. Bosellini⁴, Martin Zuschin⁵, Sabin Zahirovic⁶, Alexander Farnsworth⁷, Ann Budd⁸

¹University College London, Department of Earth Sciences, London, UK

²Natural History Museum, London, UK

³ETH Zurich, Department of Biosystems Science and Engineering, Zurich, Switzerland

⁴University of Modena and Reggio Emilia, Department of Chemical and Geological Sciences, Modena, Italy

⁵University of Vienna, Department of Palaeontology, Vienna, Austria

⁶University of Sydney, School of Geosciences, Sydney, Australia

⁷University of Bristol, School of Geographical Sciences, Bristol, UK

⁸University of Iowa, Earth and Environmental Sciences, Iowa City, USA

Life on Earth is extraordinarily diverse. More than eight million species are recognised today, and yet they represent a tiny fragment of the total number of species that have ever existed. Today, this richness is unevenly distributed across the Earth's surface with biodiversity hotspots—areas of particularly high species richness—a macroecological phenomenon of the biosphere. Global marine biodiversity is concentrated in the Indo-Australian Archipelago today, where corals and other marine organisms achieve their greatest species richness. However, the fossil record suggests at least four marine biodiversity hotspots existed throughout the Cenozoic, waxing and waning in response to global environmental changes: (1) Western Tethys (Eocene–Oligocene); (2) Arabian (Eocene–Miocene); (3) Caribbean (Oligocene–Pliocene); and (4) Indo-Australian Archipelago (Miocene–Recent). While broadly recognised, fundamental gaps in our understanding of these biodiversity hotspots exist including the timing and drivers of their origin, persistence, and ultimate decline. We aim to elucidate the diversity dynamics within marine tropical hotspots throughout the Cenozoic, reconstruct their macroevolutionary history, and test their long-term drivers. Through comparison across multiple marine biodiversity hotspots, we will identify—if any—general drivers of such concentrations of biodiversity. Here, we present initial work focused on reconstructing the evolutionary history of the Caribbean marine biodiversity hotspot. Using a comprehensive dataset of fossil scleractinian coral occurrences and sampling-standardisation approaches, we first estimate alpha, beta, and gamma diversity for the region. Extending upon these analyses, we apply state-of-the-art Bayesian modelling to estimate diversification rates throughout the Cenozoic and assess how changes in shallow marine substrate area, coastline length, and habitat fragmentation may have driven origination and extinction in the region. Our results provide an evolutionary baseline for the Caribbean marine biodiversity hotspot, enabling comparison with other Cenozoic marine biodiversity hotspots.

palaeoverse: a community-driven R package to support palaeobiological analysis

Lewis A. Jones¹, William Gearty², Bethany J. Allen³, Kilian Eichenseer⁴, Christopher D. Dean¹, Sofía Galván⁵, Miranta Kouvari¹, Pedro L. Godoy⁶, Cecily S. C. Nicholl¹, Lucas Buffan⁷, Erin M. Dillon⁸, Joseph T. Flannery-Sutherland⁹, Alfio Alessandro Chiarenza¹, Harriet B. Drage¹⁰, and Bruna M. Farina¹¹

¹University College London, Department of Earth Sciences, London, UK

²Syracuse University, Open Source Program Office, Syracuse, USA

³GFZ Helmholtz Centre for Geosciences, Potsdam, Germany

⁴Durham University, Department of Earth Sciences, Durham, UK

⁵University of Vigo, Department of Animal Ecology and Biology, Vigo, Spain

⁶University of São Paulo, Department of Zoology, São Paulo, Brazil

⁷University of Montpellier, Institute of Evolutionary Science of Montpellier, Montpellier, France

⁸Smithsonian Tropical Research Institute, Balboa, Republic of Panama

⁹University of Birmingham, School of Geography, Earth and Environmental Sciences, Birmingham, UK

¹⁰University of Lausanne, Institute of Earth Sciences, Lausanne, Switzerland

¹¹University of Fribourg, Department of Biology, Fribourg, Switzerland

The open-source programming language ‘R’ has become a standard tool in the palaeobiologist’s toolkit. Its popularity within the palaeobiology community continues to grow, with published articles increasingly citing the usage of R and R packages. However, there are currently a lack of agreed standards for data preparation and available frameworks to support implementation of such standards. Consequently, data preparation workflows are often unclear and not reproducible, even when code is provided. Moreover, due to a lack of code accessibility and documentation, palaeobiologists are often forced to ‘reinvent the wheel’ to find solutions to issues already solved by other members of the community. Here, we present palaeoverse, a community-driven R package to aid data preparation and exploration for quantitative palaeobiological research. The package is freely available and has three core principles: (1) streamline data preparation and analyses; (2) enhance code readability; and (3) improve reproducibility of results. The palaeoverse toolkit provides a user-friendly platform for preparing data for analysis with well-documented open-source code to enhance transparency. The functionality available in palaeoverse also improves code reproducibility and accessibility, which is beneficial for both the review process and future research. Through palaeoverse, we hope to help bring palaeobiologists together to establish agreed standards for high-quality quantitative research.

The Mio – Pliocene Tragulids (Mammalia) from the Siwaliks of Pakistan

Muhammad Akbar Khan¹, Muhammad Adeeb Babar², Khalid Mahmood¹

¹Dr. Abu Bakr Fossil Display and Research Centre, Institute of Zoology, University of the Punjab, Lahore, Pakistan

²Zoology Department, University of Okara, Punjab, Pakistan

The family Tragulidae is an extant non-pecoran ruminant family comprising the smallest members of the sub-order Ruminantia. Currently, it is mainly restricted to Asia and Africa but in past it had a widespread distribution, and fossils of this family are found from Africa and Europe besides Asia. In Asia, it is known from Pakistan, India, China, Thailand and Myanmar. The family got diversified during the Middle Miocene and still present today. In Indian subcontinent (Pakistan and India), its fossils are numerous in the Siwalik Group. In the Siwaliks, these first appeared in the Kamli Formation with rare occurrence and became abundant during the Chinji to Dhok Pathan formations and became extinct during the Tatrot Formation of the Siwaliks. The present article deals with the description of some tragulid material collected from various sites of late Miocene to early Pliocene deposits of Hasnot, Padhri, Nagri, and Dhok Pathan areas of northern Punjab. The material includes the maxillary and mandibular fragments, and isolated, upper and lower dentition that include incisor, canine, premolars and molars. The morphometric study of the described material revealed that it belongs to *Dorcatherium minus*, “*Dorcatherium*” *majus*, *Siamotragulus* sp., and cf. *Siamotragulus* sp. the present work includes

the first description of *D. minus* incisor, and “*D.*” *majus* canine from Indian subcontinent Siwaliks. The article also deals with the taxonomic issues of the Siwalik tragulids.

Past and present climate change effects on mesophotic benthic communities in the Central Mediterranean

Farkhondeh Kiani Harchegani¹, Aaron Micallef^{1,2}

¹University of Malta, Marine Geology and Seafloor Surveying, 37, Triq ta' Xmiexi, Msida, Malta

²Monterey Bay Aquarium Research Institute, Moss Landing, CA, USA

Benthic marine habitats in semi-enclosed seas like the Mediterranean are highly sensitive to climate change stressors, such as marine heatwaves (MHWs). This threatens not only shallow benthic communities but also those thriving at greater depths. While much attention has been given to shallow-water communities, deeper mesophotic habitats (30–150 m) remain underestimated in conservation strategies. In this study, we investigated mesophotic benthic communities across warmer-than-present deep-time (Late Oligocene, ~27.30–23.04 Ma) and modern periods to evaluate their resilience and adaptability to environmental changes from past to recent climates. We specifically studied mesophotic benthic communities preserved in the Late Oligocene stratigraphic sequences of the Malta archipelago and compared them with recent mesophotic sediments collected from offshore Malta. Macro- and microscopic analyses revealed that coralline algae were the dominant framework builders in both time periods. In the Late Oligocene, rhodolith-forming coralline algae were associated with larger benthic foraminifers, warm-water corals, bryozoans, and echinoids, whereas modern mesophotic assemblages are characterized by coralline algae associated with bryozoans, serpulids, and cold-water corals. During the Late Oligocene, temperatures were approximately 8°C warmer than today. This warming was associated with changes in water circulation due to the gradual closure of the Tethyan gateways and fluctuations in sea level, leading to mesophotic ecosystems distinct from those of the present. Despite these differences, mesophotic coralline algae have demonstrated resilience over time, highlighting their critical role in carbonate production and ecosystem stability. Considering their ecological importance in the central Mediterranean ecosystem, stricter protection of mesophotic habitats through the expansion of Marine Protected Areas (MPAs) to deeper mesophotic depths is essential to ensuring the protection of these ecosystems in a rapidly changing climate.

Does spatial range determine the longevity of shark species?

Kristína Kocáková¹, Daniele Silverstro^{2,3,4}, Catalina Pimiento^{1,5}

¹University of Zurich, Department of Palaeontology, Zurich, Switzerland

²ETH Zurich, Department of Biosystems Science and Engineering, Basel, Switzerland

³University of Gothenburg, Gothenburg Global Biodiversity Centre, Department of Biological and Environmental Sciences, Gothenburg, Sweden

⁴Captain Technologies Ltd, London, UK

⁵Swansea University, Department of Biosciences, Swansea, UK

Understanding of mechanisms underlying extinctions is crucial to interpret the patterns of past and modern diversity, particularly in the face of the current biodiversity crisis. Neoselachii, comprising of modern sharks, rays and skates, are a clade with an abundant and well-sampled fossil record stretching deeply in time, making them an ideal model group to examine such mechanisms. It was recently uncovered that extinctions in neoselachians are age-dependant, whereby most species go extinct within the first 4 Myr of their existence. However, the mechanism driving the selection against younger taxa has not yet been examined. Here, we aim to assess whether the spatial range through the lifetime of a species can explain age-dependent extinction. We hypothesise that there are great differences in spatial range patterns through time between short- and long-lived species, with old species spreading more rapidly and through larger areas than young species. We also predict that long-lived species will start with broader spatial ranges in the early stages of their existence, compared to shorter-lived species. The results of this study could help us understand the forces affecting the survival of one of the most threatened groups in modern oceans, as well as provide important insights into the mechanisms shaping the past and present diversity of this group.

Impacts of Environmental Change on Pleistocene and Holocene Animal-Sediment Interactions, Willapa Bay, Washington, USA

Maya T. LaGrange Rao^{1,2}, Murray K. Gingras³, Kate H. Pippenger¹, Brette S. Harris³, and Lidya G. Tarhan^{1,2}

¹Department of Earth and Planetary Sciences, Yale University, USA

²Yale Institute for Biospheric Studies, Yale University, USA

³Department of Earth and Atmospheric Sciences, University of Alberta, Canada

Bioturbating animals that rework and mix marine sediments act as essential “ecosystem engineers” by substantially modifying the physical, chemical, and biological properties of the seafloor sediments they inhabit. Although coastal ecosystems are among those most heavily impacted by anthropogenic climate change, the impacts of warming on the physiologies and activities of the benthic animals that inhabit these settings are poorly understood. Experimental studies have investigated the short-term effect of heat stress (i.e., marine heat waves) on coastal bioturbators, but the impacts of long-term warming or shifts in climate state on animal-sediment interactions remain largely unknown. Willapa Bay, in Washington State, presents a unique opportunity to examine coastal bioturbation in the modern-day compared to warmer- and cooler-than-present times in Earth’s recent past. This “natural laboratory” along the U.S. Pacific coast preserves sedimentary successions deposited in this region during three previous interglacials of the Pleistocene, in addition to modern bay sediments. Our study compares the intensity, style, and scale of bioturbation in modern Willapa Bay sediments to bioturbation recorded in sedimentary strata that formed in this same region of coastline (and in a similar bay setting) during previous interglacials. Preliminary findings suggest that intertidal flat deposits formed during the (warmer-than-present) Last Interglacial are commonly characterized by larger animal burrows and a higher abundance of traces produced by decapod crustaceans relative to similar deposits from previous, cooler interglacials. This work enhances our understanding of

how changing global temperatures have influenced bioturbation by coastal animals in the recent past and will allow us to more robustly predict how climate change will influence coastal ecosystems in the future.

Reinterpreting the affinity of *Retidiporites magdalenensis*: evidence of extinction in the fossil record

Mauricio León-Carreño¹

¹Center for Tropical Paleoecology and Archaeology, Smithsonian Tropical Research Institute, Panama, Panama

Current biodiversity is the result of an extensive evolutionary history, where extinction plays a role as significant as speciation. The fossil record provides an essential perspective for understanding the emergence and disappearance of lineages that have shaped modern ecosystems. *Retidiporites magdalenensis*, a fossil pollen morphotype recorded in South America and Africa approximately 72 to 50 million years ago, has traditionally been associated with modern families such as Proteaceae and Bromeliaceae. However, preliminary observations suggest that it may represent an extinct taxon. This study aims to determine the biological affinity of *R. magdalenensis* and assess its relevance for understanding extinction processes and past diversity. To this purpose, confocal microscopy and morphometric analyses were employed to compare fossil pollen grains assigned to *R. magdalenensis* with modern pollen from Bromeliaceae, Proteaceae and other angiosperms with similar pollen morphology. The morphometric data revealed that *R. magdalenensis* occupies a distinct morphological space, with no significant overlap with Bromeliaceae or Proteaceae. Moreover, confocal microscopy allowed for the identification of diverse morphotypes within the *R. magdalenensis* assignment itself, unlike what was previously recognized through light microscopy. This clear morphological distinction raises the possibility that *R. magdalenensis* represents an extinct lineage. These results underscore the importance of paleontological data in understanding biodiversity loss and highlight the need to integrate paleontological and ecological perspectives to place current diversity in the context of past extinction.

Morphometric analysis with quantitative measurements of fairy shrimps reveals size differences between fossil and extant species and indicates different feeding strategies

Elham Mahdipour¹, Joachim T. Haug¹, Carolin Haug¹

¹LMU, Biocenter, Faculty of Biology, Munich, Planegg-Martinsried, Germany

Branchiopoda is a morphologically diverse group, including fairy shrimps, tadpole shrimps, clam shrimps, and water fleas, often crucial inhabitants of ephemeral freshwater bodies. They can be important in nutrient cycling by protecting small bodies of water against eutrophication. Fairy shrimps of the group Anostraca are characterized by an elongated body without a pronounced

shield. They typically feed on particles filtered from the water while swimming, albeit obligate or facultative predators are common among some species. As a component of trophic networks of the aquatic and terrestrial ecosystems, Branchiopoda can be crucial in nutrient cycling by protecting against the eutrophication of small bodies of water. Although the fossil record of some groups of Branchiopoda is comparably good, the fossil record of fairy shrimps is poor due to the delicate nature of their exoskeleton. The earliest known representative of Branchiopoda, *Rehbachella kinnekullensis*, from the Upper Cambrian of Sweden, has previously been discussed as a possible representative of the early lineage towards Anostraca. *Lepidocaris rhyniensis*, a Devonian representative of Branchiopoda from the Scottish Rhynie chert, has also been discussed as an early representative of Anostraca. Until now, the oldest modern-looking fossil anostracan that has been widely accepted as such is *Haltinnaias serrata* from the 365-million-year-old (Late Devonian) Strud locality of Belgium; it was part of the temporary-pool branchiopodan community closely resembling extant species.

We analyzed extant and fossil specimens of fairy shrimps selected from the literature and some new fossils documented with digital microscopy. Different length and width measurements were evaluated using ImageJ. The data analysis indicates that females, which are generally considered to be larger than males in extant species, are, in fact, similar in size. However, there are very few male fairy shrimps in the fossil record. Furthermore, two extant species stand out in their size of several centimetres. Large-sized predatory fairy shrimps might be a relatively young evolutionary development.

Gone in the blink of an eye: the effects of rock-weathering rates in the preservation of Cambrian acritarch and carbonaceous microfossils

Blanca Martínez-Benítez^{1,2}, Palacios, Teodoro³, Álvaro, J. Javier¹

¹Instituto de Geociencias (CSIC-UCM), Madrid, Spain

²Universidad Complutense, Department of Geodynamics, Stratigraphy and Palaeontology, Madrid, Spain

³ Universidad de Badajoz (UNEX), Department of Palaeontology, Badajoz, Spain

It is a well-known fact in palynology that “fresh stratigraphic sections”, like those unearthed by drill-holes and recent highways and tunnels, usually contain the richest and better preserved microfossil record. But, for how long do these sections remain “fresh”? Can microfossils that have endured millions of years of burial and diagenesis be severely damaged in the span of less than two decades? In this work, the results of three sampling fieldtrips in the vicinity of the Porma’s dam (Cantabrian Mountains, northern Spain), undertaken in 2006, 2014 and 2024, are compared to evaluate the effects of weathering on the palynological content using several different techniques, such as 3D confocal photography, light microscopy and Raman spectrometry.

The Porma’s dam section exposes strata from the lower member of the Láncara Formation, which has been dated as Cambrian Epoch 2. The first sampling campaigns, in 2006 and 2014, reported the presence of abundant and well-preserved acritarchs, alongside small carbonaceous fossils (SCF) identified as *Wiwaxia* sclerites. However, the section was not revisited until ten years later, in 2024. The results of the most recent campaign are clear: only 50% of the analysed

samples are positive, they display a dismissed acritarch association with lower patterns of biodiversity, and the weathered sclerites of *Wiwaxia* are much more fragmented and the majority are smaller in size. Therefore, it is vital to ask the question: what can we do to preserve the paleontological knowledge contained within these sections for future studies?

Unravelling the ecology of aquatic turtles from the Late Jurassic of Europe through stable isotope analysis

Chloe Mazier^{1,2}, Romain Amiot³, Jeremy E. Martin³, Arnaud Vinçon-Laugier³, Jérémy Anquetin^{1,2}

¹JURASSICA Museum, Porrentruy, Switzerland

²University of Fribourg, Department of Geosciences, Fribourg, Switzerland

³CNRS, Laboratoire de Géologie de Lyon, Terre, Planètes, Environnement, Villeurbanne, France

Are thalassochelydians the first marine turtles? With almost 30 species known to date from the Late Jurassic of Western Europe only, thalassochelydians could represent the first known radiation of turtles into marine environments. This group is traditionally separated into three informal families: Plesiochelyidae, Thalassemydidae, and Eurysternidae, with the addition of the Sandownidae, a group known from the Cretaceous until the Paleogene, still debated. The vast majority of thalassochelydians is found in the Late Jurassic of Western Europe, but representatives of the group are also known in Eastern Europe and even in Argentina from the same time period. While thalassochelydians are traditionally considered as coastal marine turtles, this interpretation is mostly based on the sedimentological context in which they are found. The morphology of these turtles does not show clear adaptation to marine life, and while numerous articulated specimens have been found in shallow marine settings, the possibility that at least some of them were washed from nearby islands into the sea cannot be excluded. To test the hypothesis of this group being the first radiation of marine turtles, we analysed the oxygen ($\delta^{18}\text{O}$) isotope composition from a first batch of specimens, all of which with a clear identification down to the species level. The $\delta^{18}\text{O}$ measured in bone apatite can be used to estimate the origin of the water as well as to reconstruct environmental paleotemperatures. By using the paleoenvironmental descriptions present in the literature and adding the data obtained with the isotopic analyses, the specimens recorded a wide range of environmental waters ranging from brackish for most of them, indicating coastal living environments, to clearly marine. Moreover, some specimens seem to have lived in aquatic environments submitted to high evaporation such as lagoons. No clear freshwater signal has been observed from this preliminary selection of fossil species.

The past, present, and future of the Indigenous maize farming niche in the American Southwest

Ishmael D. Medina¹, Jerry D. Spangler², Kenneth B. Vernon³, Brian F. Coddling¹

¹University of Utah, Department of Anthropology

²Colorado Plateau Archaeological Alliance

³University of Utah, Scientific Computing and Imaging Institute

Maize (*Zea mays ssp. mays*) was one of the most widespread domesticated plants in the Americas before European colonization and is currently the most produced grain around the world. Despite its widespread distribution and abundance, many Indigenous (heirloom) varieties are now extinct or at risk of extinction due to the industrialization of maize agriculture and climate change. Here we look at the northern margins of the American Southwest (Utah, USA) to determine where Indigenous maize farming would have been suitable, where it is suitable today, and where it will be suitable in the future. By coupling archaeological and historical accounts of Indigenous maize farming, we use a novel machine learning approach to predict where maize farming is suitable by incorporating multiple ecological variables. While highly modified, industrialized maize continues to dominate the world's grain production, many heirloom traits are being lost. Many of these heirloom varieties are not only culturally significant to thousands of Indigenous peoples, but they contain diverse traits that may be critical for expanding the adaptive capacity of maize under future climate change.

Ecological drivers of cranial morphological evolution in equids

Iris Menéndez¹, O. Sanisidro², G. Navalón³, I.A. Lazagabaster⁴, J.L. Cantalapiedra^{1,5}

¹Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany

²Departamento Ciencias de la Vida, GloCEE Global Change Ecology and Evolution Research Group, Universidad de Alcalá, Madrid, Spain

³Department of Earth Sciences, University of Cambridge, Cambridge, UK

⁴National Research Center for Human Evolution, CENIEH, 09002, Burgos, Spain

⁵Departamento de Paleobiología, Museo Nacional de Ciencias Naturales, CSIC, Madrid, Spain

The evolutionary history of horses represents a paradigm of adaptive evolution. Equids originated in North America shortly after the Paleocene-Eocene boundary, around 55.5 million years ago, providing a rich fossil record that serves as an ideal framework for studying adaptive evolutionary hypotheses. This record allows us to investigate how ecological factors have shaped the evolution of morphological traits in a lineage over time. Although body size and dental morphology have been extensively studied, cranial shape evolution remains less explored. This study analyzes cranial morphology in the Equidae family throughout their evolutionary history, focusing on how it relates to other traits, such as hypsodonty, dental morphology, and body size. We apply geometric morphometrics to quantify cranial morphology using landmarks and semilandmarks, followed by phylogenetic regressions to assess the influence of various factors on cranial shape. Our findings reveal that dental morphology has a stronger impact on cranial shape than body size, underscoring the role of ecological adaptations in shaping the skull. Basal equids were small, with low-crowned teeth and a cranial morphology markedly distinct from the rest of the family. The morphological differentiation between Anchiteriinae and Equinae is primarily driven by dental type rather than body size, suggesting that ecological shifts in feeding strategies (e.g., from low-crowned to high-crowned teeth) played a key role in cranial evolution. These results highlight how functional adaptations, such as dietary shifts, have influenced the evolutionary trajectory of equids' cranial morphology, with

important implications for understanding ecological and evolutionary dynamics in fossil lineages.

Where the wild cats aren't

Mollie Mills¹, Laura Hemmingham², Danielle Schreve²

¹Royal Holloway University of London, Department of Geography, Surrey, United Kingdom

²University of Bristol, School of Geographical Sciences, Bristol, United Kingdom

In Britain, the European wildcat (*Felis silvestris*, Schreber 1777) is located exclusively in Scotland. Considered to be Critically Endangered, the Scottish population is on the brink of extinction due to anthropogenic activities, contact with domestic cats and habitat loss. Urgent and effective conservation strategies are required to support existing populations and aide the species recovery. Understanding the species environmental requirements and identifying suitable areas for wildcat reintroductions is therefore essential. However, using the species' modern range characteristics for habitat suitability projections is problematic due to extensive range contraction and the wildcat now occupying a reduced set of environmental conditions. Incorporating the wildcat's historic and recent fossil distribution data into suitability projections can improve understanding of the species-environment relationship, prior to extensive range contraction. Here, we use the wildcat's historic and Holocene fossil record in Britain to construct multi-temporal habitat suitability models (HSMs) under current climate conditions. Our results show that modern wildcat populations have suffered species-environment truncation and now occupy only a portion of their potential environmental range across Britain, with a reduced realised niche breadth. The addition of Holocene fossil data into the models increased the amount of excellent and good habitat predicted by 37% and 197% respectively, extending into other parts of Scotland, as well as England and Wales, and decreased predicted unsuitable conditions by 97.7%, thereby offering new avenues for reintroduction programmes. Overall, our study underlines the benefits of using multitemporal HSMs to better represent species-environment relationships and improve habitat suitability projections under current and future climate change scenarios.

Climate's impact on the biodiversity patterns of Diplodocoidea during the Jurassic-Cretaceous transition

Joana Órfão^{1,2}; Emma Dunne³; Alexander Farnsworth⁴, Carolina S. Marques⁵; Francisco Ortega²; Pedro Mocho^{1,2,6}

¹IDL - Instituto Dom Luiz, Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal

²Grupo de Biología Evolutiva, Facultad de Ciencias, Universidad Nacional de Educación a Distancia (UNED), Madrid, Spain

³Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

⁴University of Bristol, Bristol, UK

⁵Centro de Estatística e Aplicações, Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal

⁶Dinosaur Institute, Natural History Museum of Los Angeles County, CA, Los Angeles, USA

Reconstructing the diversity of life through deep time is crucial for understanding the evolution of life, as well as the mechanisms behind extinction and recovery. The fossil record, in particular, provides insights into the factors influencing biodiversity, such as past climate and landmass distributions. Sauropoda, a major clade of non-avian dinosaurs, offers a unique opportunity to study long-term biodiversity patterns. These large herbivores, with diverse lineages and significant ecological roles, have an abundant fossil record and a global distribution. Research suggests a latitudinal constraint on their distribution, a peak in diversity during the Kimmeridgian-Tithonian linked to the radiation of Neosauropoda, and a shift in faunal composition during the Jurassic-Cretaceous transition. Diplodocoidea is a neosauropod group with three main subclades—Dicraosauridae, Diplodocidae, and Rebbachisauridae—showing recognizable cranial anatomy despite varied morphology. This group underwent a faunal shift during the Jurassic-Cretaceous transition, with Rebbachisauridae seemingly replacing Flagellicaudata (Dicraosauridae + Diplodocidae) and extending into the Early-Mid Cretaceous. In this study, we examine Diplodocoidea biodiversity patterns at the genus level using both raw taxonomic diversity and SQS (Shareholder Quorum Subsampling) metrics. Our results replicate previous findings, revealing distinct geochronological diversity patterns for Rebbachisauridae and Flagellicaudata, suggesting these patterns are biological rather than sampling artifacts. Dicraosauridae and Diplodocidae show a diversity peak during the Kimmeridgian-Tithonian, followed by a trough across the Jurassic-Cretaceous boundary. Rebbachisauridae presents consistently high diversity from the Barremian through the Cenomanian, peaking in the Aptian (or Cenomanian if uncorrected). We also assessed the influence of climate variables as drivers of Diplodocoidea biogeographic distribution, using PCA, UMAP and t-SNE methods. Our findings suggest that each clade occupied distinct climatic niches, indicating different ecological constraints and highlighting the role of climate in the Jurassic-Cretaceous sauropod faunal transition.

Oxygen controls lanternfish growth across the Isthmus of Panama: Insights from geohistorical otolith assemblages

Sven Pallacks¹, Brigida De Gracia¹, Jessica Lueders-Dumont^{1,2}, Aaron O'Dea^{1,3}

¹Smithsonian Tropical Research Institute, Panama, Republic of Panamá

²Department of Earth and Environmental Sciences, Boston College, Chestnut Hill, MA 02467 USA

³Sistema Nacional de Investigación, SENACYT, Clayton Panama, Republic of Panamá

Lanternfish are integral to ocean food webs and play an important role for the transfer of energy, nutrients and carbon between different ocean layers, which makes them crucial for the functioning of marine ecosystems. Ongoing ocean deoxygenation is particularly severe at midwater depth in Oxygen Minimum Zones (OMZs) with unknown consequences for lanternfish. By making use of the strong environmental gradients between the Eastern Tropical Pacific (ETP) and the Caribbean, we assess the role of food availability and oxygen for growth and production of lanternfish. Comparing lanternfish size and growth-increment biochronologies with ocean conditions across the Isthmus will help to understand if lanternfish energetics are negatively affected in oxygen deprived Pacific waters. The developed morphometric techniques will be applied to explore lanternfish energetics through geological time, preferentially using the

Miocene as a critical reference point for understanding potential future climate scenarios. More than 700 lanternfish otoliths of the genus *Diaphus* are picked from surface sediment samples at 13 locations at the Caribbean and Pacific shelf edge of the coast of Panama and Honduras. To build a relationship between otolith size and growth we measure otoliths via ImageJ, before estimating lanternfish body size from otolith length through transfer functions. Additionally, we study growth bands in a subset from the ETP and the Caribbean, to detect differences in lanternfish growth rates. Preliminary results show smaller lanternfish in the ETP, a region otherwise famous for having larger fish compared to the Caribbean, highlighting first evidence for oxygen forcing on mesopelagic fish. With oxygen being the limiting factor for midwater fish growth and production, an intensification and expansion of the OMZ could have major consequences for the structure and functioning of the ETP ecosystem, with implications for the management of marine fisheries, marine conservation and ecosystem services.

Identification of environmental parameters through stable isotopes in Quaternary and present continental mollusc assemblages from Uruguay

Fiorella Pastrana¹, Cabrera, F¹, Martínez, S¹

¹Departamento de Paleontología, Facultad de Ciencias, UdelaR. Iguá 4225, 11400. Montevideo, Uruguay

While the isotopic composition of the shells and their environmental implications have been widely studied for marine molluscs, there is a lack of research for freshwater ones in general. The aim of this work is to create a calibration curve to compare the fractionation of ¹⁸O and ¹³C in shells of extant mollusc species and the water they inhabit, with the environmental parameters in which they live. Once this curve is obtained, we will compare it with the values of ¹⁸O and ¹³C acquired for freshwater fossil shells from the Quaternary of Uruguay, to estimate past environmental conditions. To achieve this, shells of extant and fossil species were collected in the same locations, along with water samples in which the extant species live. The sampling was made in summer and winter, for comparison of extreme temperature seasons. Additionally, water parameters were measured (temperature, oxygen, pH, depth and turbidity, among others). The fossil shells were collected as bulk samples, and for the isotope analyses, the best-preserved specimens were selected to ensure minimal contamination. The preliminary results show a link between the isotopic fractionation of ¹⁸O and ¹³C and the water in which they inhabit. Currently, a follow-up is being carried out by gathering the annual climatic parameters, such as seasonal temperature and rainfall rates, to ensure that the inferred parameters are valid. It is estimated that in the future the curve will serve as an asset to infer past environmental parameters using fossil mollusc shells.

Smear slide analysis of lake sediments to evaluate impacts of humans on eight lakes on the Lac du Flambeau Reservation in Northern Wisconsin, USA

Saheli Patel¹, Kristen Hanson², Joe Graveen², Hima Hassenruck-Gudipati³, Gene-Hua Crystal Ng⁴, Kat Cantner⁵, Mark Shapley⁵, Kristina Brady Shannon⁵, Brady Bettin⁴

¹Carleton College, Geology, Northfield, MN, USA

²Lac du Flambeau Band of Lake Superior Chippewa, Department of Natural Resources, Lac du Flambeau, WI, USA

³Southern Oregon University, Environmental Sciences, Ashland, OR, USA

⁴University of Minnesota, Earth and Environmental Sciences, Minneapolis, MN, USA

⁵University of Minnesota, Continental Scientific Drilling Facility, Minneapolis, MN, USA

Manoomin (Ojibwe)/Psiṅ (Dakota), or wild rice, grows in the Upper Great Lakes region and is a sacred food, medicine, gift, and relative to many Indigenous peoples. Unfortunately, Manoomin/Psiṅ has been declining in this area since the mid-1800s and is impacted by a number of environmental factors. This study involves sediment cores collected in 2013 from eight lakes that bear or have borne Manoomin/Psiṅ on the Lac du Flambeau Band of Superior Chippewa Indians Reservation, which is located in the area now known as northern Wisconsin. The smear slide method is one way to determine lake sediment composition based on the relative proportion of detrital mineral grains, algal and vascular plant material, carbonate minerals, and siliceous microfossils (diatoms). In this study, I used smear slide analysis of six to ten one-centimeter intervals of diatomaceous organic-rich sediment from eight lake cores, spanning approximately the last 200 years. For these specific lakes, only the top two most abundant components within the sediment can be reproducibly estimated using smear slides. Changes in the dominant sediment components over time in each lake relate to historic sedimentation rates and human impacts in the area. The studied lakes are unique in how they respond to human events and results demonstrate that federal land allotment, logging, recent climate change-related droughts, and shoreline development impact these lakes and watersheds. Ditching of wetlands in the mid-1900s may have also impacted these lakes. Detailed understanding of how, within each lake, sedimentation records information about the lake's response to human influenced environmental perturbation is necessary in order to understand how Manoomin/Psiṅ may be impacted in the future from similar events, as well as impending changes in climate.

Utilising the archaeological record to create long-term biodiversity baselines for declining UK bird populations: Enhancing conservation and ecological understanding

Bethany E. Pittard¹, Joanne H. Cooper², Ryan N. Felice³, James Hansford⁴, Philip D. Mannion¹

¹Department of Earth Science, University College London, London, UK

²Birds Curation Group, Department of Life Sciences, The Natural History Museum, Tring, Hertfordshire, UK

³Department of Genetics, Evolution, and Environment, University College London, London, UK

⁴Queen Mary, School of Biological and Behavioural Sciences, London, UK

Contemporary change in natural systems is occurring at an unprecedented rate and magnitude. Currently, 40% of birds are in population decline, with 20% of species at risk of extinction. Little availability of long-term avian monitoring data means timescales are relatively short compared to those needed to establish both biodiversity baselines prior to anthropogenic interference, and useful conservation goals. To overcome the limiting factor of a narrow temporal lens, the zooarchaeological and fossil record provides the only empirical data on long-term interactions between biodiversity, climate, and human impacts from the Pleistocene to present.

Here, we present five case studies based on the rich historical and archaeological archives of birds in the UK. (1) the Grey Partridge (*Perdix perdix*), (2) the Black Grouse (*Lyrurus tetrix*) and (3) the Curlew (*Numenius arquata*) are all relatively rare and demonstrate contracted habitats in the UK compared to their archaeological records, and are fast declining particularly on agricultural land. (4) the White-tailed Eagle (*Haliaeetus albicilla*) and (5) the Common Crane (*Grus grus*) both have previously experienced extinction UK and populations now reflect an artificial reintroduced distribution and abundance.

By creating species distribution models of the present and past distributions of these species, we show both the directional change and decline of their natural suitable habitats, but also pinpoint where there are possible suitable regions in the UK to reintroduce these once native species. With this, we are meaningfully contributing to UK conservation efforts against expected ongoing climatic and environmental changes that is expected to result in substantial loss in avian biodiversity, poleward dispersal and body size selective extinction.

Spatiotemporal Phylogeography of the Endangered African Wild Dog

Amelia Ramage^{1,2}, Day, JJ², Brace, S³, Woodroffe, R¹

¹Institute of Zoology, Zoological Society of London

²Department of Genetics, Evolution and Environment, University College London

³Department of Earth Sciences, Natural History Museum

Anthropogenic land-use change has significantly impacted global biodiversity for centuries. Resultant habitat fragmentation limits dispersal and impedes gene flow, isolating populations, making them vulnerable to processes such as genetic drift. The consequential loss of genetic diversity can potentially diminish adaptability to further environmental change. Whilst gene flow can be restored artificially between populations through translocations, their success can be curtailed if the intraspecific genetic variation of the species is not considered, as existing patterns of differential adaptation may be disrupted.

The African wild dog (*Lycaon pictus*) is an endangered species that plays a crucial ecological role in structuring savannah ecosystems and has been extirpated from over 93% of its former range. As a cooperatively breeding species that ranges widely and lives at low population densities, it is highly sensitive to habitat fragmentation. Previous studies of wild dog genomics have had limited geographical scope, whereas broader geographical coverage has been constrained to genetic analyses on relatively short (≥ 28 years) timescales. Given the recent interest to reintroduce wild dogs into western and central Africa, it is critical to elucidate spatial patterns of genetic diversity. This study harnesses low coverage whole genome sequencing of archival specimens and published contemporary sequences to reconstruct the phylogeographic and demographic patterns of wild dogs, across Africa. The dataset forms the most widespread representation of their spatiotemporal range to date, including areas in which they have gone extinct, or population data are otherwise unknown due to lack of study sites. Using a multi-model approach, Bayesian and maximum likelihood phylogenies have been constructed using both complete mitogenomes (24.8x) and a 327-bp segment alignment to the mitochondrial control region (18.24x). This has highlighted the classification of long-isolated populations, that

might have distinct gene pools and local adaptations, helping to inform management strategies and identify source populations for translocations and reintroductions.

Advancing Conservation Paleobiology in South America: Teamwork, Perspectives, and Hurdles

Matias do Nascimento Ritter¹; Fernando Archuby²; Fernanda Cabrera³; Claudio G. De Francesco⁴; Fernando Erthal⁵; Renato P. Ghilardi⁶; Pedro Lorena Godoy⁷; Gabriela S. Hassan⁴; Rodrigo S. Horodyski⁸; Sergio Martínez³; Marcelo Rivadeneira⁹; Sabrina C. Rodrigues¹⁰; Alejandra Rojas³; Leonardo Santos de Souza¹¹; Marcello G. Simões¹²

¹Centro de Estudos Costeiros, Limológicos e Marinhos, UFRGS Litoral, Imbé, RS, Brazil

²Centro de Estudios Integrales de la Dinámica Exógena (UNLP), La Plata, Buenos Aires, Argentina

³Facultad de Ciencias, UdelAR, Montevideo, Uruguay

⁴Instituto de Investigaciones Marinas y Costeras (IIMyC), Universidad Nacional de Mar del Plata – CONICET, Mar del Plata, Buenos Aires, Argentina

⁵Instituto de Geociências, UFRGS, Avenida Bento Gonçalves, 9500, Porto Alegre, RS, Brazil;

⁶Faculdade de Ciências, Unesp, Bauru, SP, Brazil

⁷Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil

⁸Programa de Pós-Graduação em Geologia, Museu de História Geológica do Rio Grande do Sul, Universidade do Vale do Rio dos Sinos, São Leopoldo - RS, Brazil

⁹Centro de Estudios Avanzados en Zonas Áridas (CEAZA), Coquimbo, Chile

¹⁰Instituto de Ciências Exatas e Naturais do Pontal, UFU, Ituiutaba, MG, Brazil

¹¹Instituto de Biociências, UFRGS, Avenida Bento Gonçalves, 9500, Porto Alegre, RS, Brazil

¹²Instituto de Biociências, Depto. de Biodiversidade e Bioestatística, UNESP, Botucatu, SP, Brazil

Since Charles Darwin's first observations, the southern South American coast has been recognized as a natural laboratory for addressing major scientific questions. Since the 1990s, we have conducted taphonomic research, including pioneering time-averaging estimates and establishing marine baselines for Conservation Paleobiology (CP). However, we continue to face significant challenges in this journey into the unknown. The most pressing issue is the lack of continuous funding as we strive to consolidate a research team. In addition to ongoing studies in embayment and inner-shelf areas (Ubatuba Bay, Brazil), many lagoons and estuaries along the coast remain unexplored. The Patos Lagoon (Brazil) and Río de La Plata (Uruguay and Argentina) are among the world's largest lagoons and estuaries. Southern Brazil, Uruguay, and Northeastern Argentina are rich in river basins containing Quaternary fossils that provide crucial baseline data. Numerous permanent and temporary shallow lakes also exist on the gently sloping Argentine plain (Pampas) in front of the Andes Cordillera, a region of paleoclimatic significance due to its sensitivity to interannual precipitation variations. Given the current scenario of anthropogenic global change, we hypothesize that past environmental impacts can be assessed by analyzing modern ecosystems through paleoenvironmental information derived from geological and paleontological records in these coastal and continental aquatic environments. The application of paleontological and geological data to understand environmental change over timescales longer than a few decades should be expanded in South America. Our research group aims to generate valuable insights for developing policies to mitigate regional threats from anthropogenic pressures, particularly in areas where long-term

ecological studies are scarce or absent, using a paleontological perspective and specialized expertise to address ongoing climate change.

Diversity of temperate and tropical molluscs across the Mediterranean Sea during the Last Interglacial (Late Pleistocene, MIS5e)

Ranita Saha¹, Paolo G. Albano², Marco Taviani³, Alice Giannetti⁴, Salih Gucel⁵, Pierluigi Santagati⁶, Facheng Ye², Silvia Danise¹

¹University of Florence, Department of Earth Sciences, Florence, Italy

²Stazione Zoologica Anton Dohrn, Department of Marine Animal Conservation and Public Engagement, Naples, Italy

³National Research Council, Institute of Marine Sciences, Bologna, Italy

⁴Departamento de Ciencias de la Tierra y del Medio Ambiente, Universidad de Alicante, Alicante, Spain

⁵Environmental Research Center, Near East University, Nicosia, Cyprus

⁶Dipartimento di Ingegneria dell'Ambiente, Università della Calabria, Arcavacata di Rende, Cosenza, Italy

The Mediterranean Sea, with only one narrow connection to the Atlantic Ocean, is a relatively small, semi-enclosed basin characterized by strong environmental gradients. During the warmest interval of the Last Interglacial (MIS5e, Late Pleistocene epoch, ca 135–116 ka), global temperatures were up to 2 °C higher than pre-industrial times, making this stage the most recent analog in geologic time for near-future Earth climate. During MIS5e, numerous tropical West African species entered the basin (so-called “warm” or “Senegalese” guests) but then regressed to lower latitudes with the last glacial cooling. Such tropical Atlantic enrichment mirrors what can be expected from the future Mediterranean under the forcing of global warming. In this context, assessing the response of MIS5e benthic assemblages to the Last Interglacial warm climate helps forecasting future changes. Therefore, we here analyse the diversity of MIS5e mollusc assemblages in shallow subtidal marine depositional environments across the entire Mediterranean Sea, including sites in Spain, Italy and Cyprus. We consider in our analysis both the resident component (i.e. species occurring in the Mediterranean even before the temperature peak of MIS5e) and the tropical component that responded to the warm peak and disappeared with the glaciation. In particular, we test whether the diversity of the tropical component decreased from the Gibraltar Strait eastward in the Mediterranean Sea, similarly to the current pattern of tropical Indo-Pacific species entering from the Suez Canal, whose diversity declines away from the point of entrance.

First Coleoptera fossil records from Lithuania: Late Glacial paleoenvironmental reconstructions from beetle remain

Nick Schafstall¹, Miglė Stančikaitė¹, Vaida Šeirienė¹

¹Nature Research Centre, Vilnius, Lithuania

Quaternary paleoenvironmental reconstructions from the Eastern Baltic region are rare or absent, since most of the area was repeatedly covered by the Scandinavian Ice Sheet. During the

Last Glacial Maximum (ca. 25,000 – 12,000 cal yr BP), however, parts of Southern Lithuania were left uncovered. In this project, bulk sediment from Late Glacial and Early Holocene aquatic organic deposits and peat layers were retrieved from three localities in Lithuania: Ventės Ragas in the west, and the Merkys River and Ūla River in the south-east. Sufficient insect (Coleoptera) remains were collected to not only reconstruct the local depositional environment but also the surrounding landscape. Coleoptera records have been used to discover past ecological baselines for conservation biology, but so far only in the western parts of Europe. These unique records provide valuable additional information about the local insect fauna, and associated environmental niches, in Lithuania during the Late Glacial and Early Holocene periods. This presentation will highlight the identified species and their current distributions, landscape dynamics during the Late Glacial and Early Holocene, and discuss the suitability of these records for paleo-temperature reconstructions.

Some Like it Hot: Examining Thermal Tolerance at Extreme Body Size

Katlin Schroeder¹, Pincelli Hull¹

¹Department of Earth & Planetary Sciences, Yale University, New Haven, Connecticut 06511 USA

As the planet continues to heat, the resulting biodiversity crisis has the potential to drastically reshape communities. As body mass is highly correlated with numerous diversity trends, examination of the extremes of terrestrial size has the potential to more clearly define the ecologically destabilizing effects of climate change. Dinosaurs represent the extreme-end of body masses in terrestrial vertebrates, the largest of which thrived during one of the hottest periods of earth's history, the Cretaceous Thermal Maximum (CTM). It remains unclear whether these extremely warm climates were approaching dinosaurs' physiological thermal maximum, and how these hot climate states may have affected primary productivity and food web structure. Here we explore the trophic implications of extreme heat through examination of trophic transfer efficiency and diversity metrics in two dinosaur communities. We analyzed the ratio of biomasses contained within each trophic level, the ratio of endotherms to ectotherms and median body size in the Maastrichtian Hell Creek and Turonian Bisseky Formations. Initial results indicate a decrease in trophic transfer efficiency and median body mass of terrestrial vertebrates during the hottest interval. Intriguingly, the number of endotherms increased at the same time. These results provide insight into the adaptations and adaptability of terrestrial communities to extreme heat.

Can polymorphism-aware phylogenetic models improve inference with discrete morphological data?

Walker Sexton^{1,2}, Sebastian Höhna^{1,2}

¹Ludwig-Maximilians-Universität München, GeoBio-Center, Munich, Germany

²Ludwig-Maximilians-Universität München, Department of Earth and Environmental Sciences, Munich, Germany

Morphological data is an important source of phylogenetic information since fossils generally cannot provide DNA and are critical for generating time-calibrated phylogenies and learning about evolutionary history; however, very few methods have been developed to address the rampant issues in morphological phylogenetic inference. Some such issues include the prevalence of polymorphic characters, which occur when a taxon exhibits multiple character states for a single given character, and the lack of differentiation between polymorphic and ambiguous characters. Coding polymorphic characters as ambiguous leads to underestimation of the actual number of character changes, while replacing polymorphic characters by a single character state can both over and underestimate the number of character changes. Polymorphism-aware phylogenetic models (PoMos) have been applied to genetic data, integrating populational evolutionary forces with deep-time phylogenetic models and estimating allele frequency change over time. Thus, PoMos can incorporate and appropriately model polymorphic characters at tips of the phylogeny. We utilize PoMos in RevBayes to infer phylogeny from simulated data and evaluate the efficacy of these models with polymorphic morphological datasets in comparison to other models of discrete character evolution and coding schemes. Our results suggest that PoMos are at least as good as Mk substitution models for reconstructing topology, though they may struggle with reconstructing tree length, in particular, by overestimating terminal branch lengths.

Extinction patterns of marine turtles throughout the Mesozoic and Cenozoic: insights for Conservation Biology

Jorge L. R. S. Silva¹, Gabriel S. Ferreira^{2,3}, Bruna M. Farina^{4,5}, Pedro L. Godoy¹

¹Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil

²Senckenberg Centre for Human Evolution and Palaeoenvironment at the University of Tübingen, Germany

³Geosciences Department, Eberhard Karls University of Tübingen, Germany

⁴Department of Biology, University of Fribourg, Fribourg, Switzerland

⁵Swiss Institute of Bioinformatics, Switzerland

Marine turtles are not only iconic characters of oceanic ecosystems, but also flagship species whose survival is crucial for maintaining marine biodiversity. Across the globe, numerous conservation policies have been implemented to protect the seven extant species. Metrics, such as the ones quantified by the IUCN Red List and the EDGE Program, are used to establish conservation priorities for the group, but these criteria are based on data limited to the living species. In the case of marine turtles, this is particularly relevant considering that its fossil record indicates a much higher past diversity. The oldest unambiguous occurrence of marine turtles dates to the Late Jurassic of Europe and South America, with the *Thalassochelydia*. Also, from the Eocene to the Miocene a lineage of pleurodiran turtles invaded marine environments. Therefore, the study of the extinction patterns of past marine turtles can help us understand the processes involved, such as the relationship between environmental changes and extinction in marine ecosystems. Here we use a phylogenetic approach to characterize extinction patterns of marine turtles and investigate possible drivers. We incorporated the uncertainties regarding the position of some marine lineages by using different tree topologies. Regardless of the tree used,

our results indicate the predominance of phylogenetically-clustered extinctions during all time intervals analyzed. This indicates that closely-related species are more prone to get extinct due to common causes, suggesting that factors such as climate change can collectively affect the group. Factors such as anthropogenic-driven climate change, habitat destruction and overexploitation of turtles as a food source have contributed to 52% of the modern turtle species being classified as threatened in the IUCN Red List. Our results provide further evidence from the fossil record that these threats can potentially affect all marine turtles species, following a similar pattern observed in the deep past.

Long tails and no eiderdown: paleontological research reveals different Quaternary distributions of North Sea ducks

Martijn van der Meer¹, Bram W. Langeveld², Isaak Eijkelboom^{3,4}, Anne S. Schulp^{3,4}

¹Utrecht University, Biology, Utrecht, Netherlands

²Natural History Museum Rotterdam, Netherlands

³Naturalis Biodiversity Center, Netherlands

⁴Utrecht University, Earth Sciences, Utrecht, Netherlands

Over the past decade, citizen scientists have collected rich fossil bird material from Pleistocene and Holocene dredged sediments that were used to nourish Dutch beaches. We examined 177 fossil duck (Anatidae) bones and identified at least 15 different species, 12 of which had not previously been identified (or confirmed) from these deposits. All species found are extant. Our three main results are: 1) The common eider *Somateria mollissima* is absent from all examined Late Pleistocene and Early Holocene North Sea fossil material. This is surprising, as the eider is currently the second-most common duck species in the area. The eider possibly stayed north of the ice sheet that lay between England and Norway and migrated around Ireland, to reach further south (as far as northern Spain). Thus, they avoided a significant part of their current wintering range. 2) The long-tailed duck *Clangula hyemalis*, currently quite rare in the study area, is the most common species found, indicative of a different past distribution. Today, it is abundant in the Baltic Sea. The poor fossil record of the area hinders interpretations of its past occurrence. It is possible that the current Baltic Sea populations are descendants of the common fossil North Sea long-tailed ducks. 3) One coracoid of the harlequin duck *Histrionicus histrionicus* was discovered. It is only the second fossil record of this species in Europe. Harlequin ducks occur around Iceland, but are seldom seen further east. Therefore, it is almost certainly a fossil of a vagrant, which are rarely recognised in the fossil record; particularly in osteologically homogeneous taxa, such as ducks. In conclusion, late Quaternary bird fossils from the North Sea area demonstrate concrete examples of birds' responses to climate change and new-found geographical limitations, and are therefore an excellent way of bridging the gap between paleontology and ecology.

Is there a pattern of convergence in the cochlea of river dolphins?

Mariana Viglino¹, Travis Park^{2,3,4}

¹Instituto Patagónico de Geología y Paleontología (IPGP-CONICET), Puerto Madryn, Argentina

²School of Biological Sciences, Monash University, Melbourne, Australia

³Science Group, Natural History Museum, London, United Kingdom

⁴Sciences, Museums Victoria Research Institute, Museums Victoria, Melbourne, Australia

Toothed whales (Cetacea, Odontoceti) comprise 78 living species that inhabit both riverine and marine environments. There are seven genera (*Inia geoffrensis*, *Pontoporia blainvillei*, *Lipotes vexillifer*, *Platanista* spp., *Neophocaena phocaenoides*, *N. asiaeorientalis*, *Sotalia fluviatilis*, and *Orcaella brevirostris*) that inhabit freshwater environments; the first four were traditionally considered as “river dolphins”. Given the endangered status of most of these taxa, understanding the evolutionary history and specific adaptations to such a challenging environment becomes a key question.

Hearing is a key sense for odontocetes communication and feeding, particularly in the muddy waters of the riverine environment. Cochlear morphology correlates with hearing frequencies and is an important proxy for inferring hearing abilities in extinct species. Previous studies have suggested some convergent anatomical adaptations among traditional river dolphins. However, no study has tested for cochlear convergence across all river dolphins and their fossil relatives. Therefore, our goal is to test for convergent patterns in cochlear morphology among river dolphins within a broader evolutionary framework.

The sample comprises 58 extant and 23 extinct toothed whale species. We calculated 13 measurements and applied 3D geometric morphometrics. We tested for significant morphological disparities between riverine and marine cochlear morphologies by calculating disparity metrics for both datasets. We also conducted C-metrics and SURFACE statistical convergence analyses. We expected a strong convergence signal among riverine toothed whale cochlea.

Disparity analyses did not differentiate riverine vs marine cochlea in either dataset. River dolphins are randomly scattered across the morphospace. Furthermore, statistical convergence analyses also did not reveal a convergent pattern for riverine cochlear morphology. Thus, environmental adaptations are not the strongest variable. We hypothesize a “many-to-one-mapping” phenomenon for river dolphins’ cochlear morphology. We also hypothesize that other structures of the underwater echolocation apparatus may have a convergence signal, but this remains to be tested.

New stories from Ancient Tagua Tagua Lake (Central Chile): What does the vertebrate record tell us beyond the Late Pleistocene?

Natalia A. Villavicencio¹, Elgueta, Sebastián², Lizama-Catalán, Álvaro³, Oyarzo, Cristóbal³, Labarca, Rafael⁴, González-Guarda, Erwin¹

¹Instituto de Ciencias de la Ingeniería, Universidad de O’Higgins, Rancagua - Chile

²Facultad de Ciencias de la Vida, Universidad Andrés Bello, Chile

³Investigador independiente Santiago, Chile

⁴Escuela de Antropología, Pontificia Universidad Católica, Chile

The archaeo-paleontological record of the Ancient Tagua Tagua Lake (34°S 71°W) represents a unique opportunity for a more complete reconstruction of the past ecosystems of central Chile. The findings previously published for the sites Taguatagua 1 and 2, together with paleoenvironmental reconstructions, have provided valuable information on the Pleistocene-Holocene ecosystems, covering moments of important environmental changes such as the glacial-interglacial transition, megafaunal extinctions, and the arrival of the first humans in the area. At the same time, the diverse faunal record of smaller vertebrates recovered from the aforementioned sites, represents the opportunity to reconstruct more complex ecological aspects during the Late Pleistocene in the area. Since 2019, new excavations have been carried out at a new site, Taguatagua 3. These efforts have provided the opportunity to perform environmental reconstructions with new and broader set of techniques, and with a detailed stratigraphic context of the archaeological and paleontological findings, covering a temporal range from the late Pleistocene (12,600 years before present BP) to the middle Holocene (6,000 years BP). In this work we present the progress of the taxonomic, taphonomic and paleoenvironmental study of the fossil vertebrate record from Taguatagua 3. The results consider the analysis of three excavation units (G5, E5 and C5), covering the approximate temporal range of 12,600-6,000 years BP. So far, bird, rodent, amphibian, fish and reptile taxa have been identified. Among the mammals, the finding of a specimen of the order Chiroptera stands out. In general terms, the faunal assemblages are representative of present-day environments of Central Chile with a marked lacustrine character. Subtle differences between the assemblages within the temporal range need further review considering the new environmental reconstructions that are being generated for the sector.