



# RESEARCH DATA MANAGEMENT - INTRODUCTION TO FAIR AND OPEN DATA

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Open for you! An introduction series to open science | 7 March 2022



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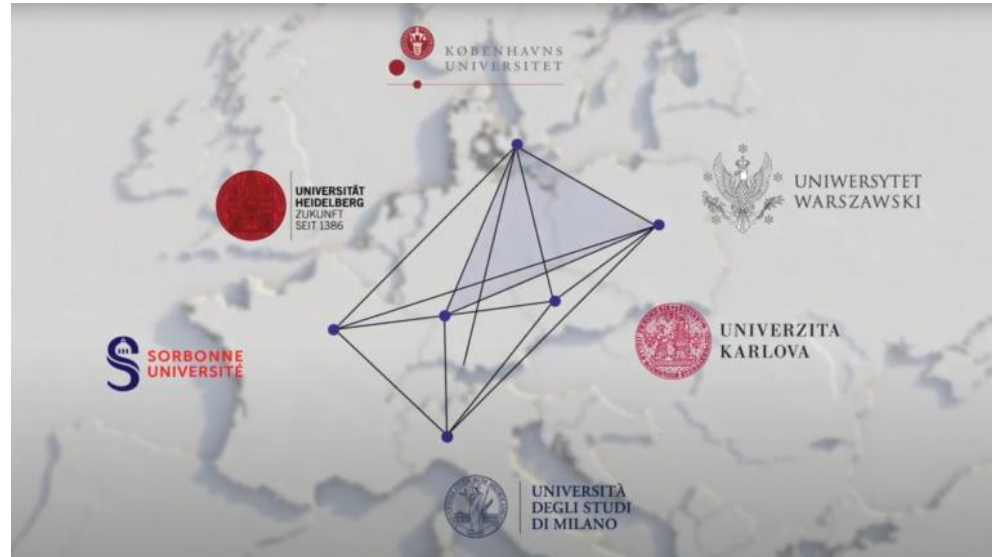
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## 4EU+ Alliance and Open Science

- 4EU+ is a transnational strategic university association.
- Aim: Strengthen the European vision of deepened cooperation and mutual enrichment in research and teaching
- Open Science is an integral part of this.
- Two 4EU+ projects currently work on Open Science.
- Open for you – an Introduction Series to Open Science“ – 14 session on OS topics!



## Agenda

- Introduction
- Why bother with FAIR Data?
- Why bother with Open Data?
- Good practices: a closer look on various data repositories
  - Subject-specific repositories
  - Generic Repositories
  - Institutional Repositories

## What we will talk about?

“An article [...] in a scientific publication is not the scholarship itself, it is merely advertising of the scholarship.”

Buckheit, Jonathan B., and David L. Donoho. “WaveLab and Reproducible Research.” In *Wavelets and Statistics*, edited by Anestis Antoniadis and Georges Oppenheim, 55–81. Lecture Notes in Statistics. New York, NY: Springer, 1995. <https://doi.org/10.1007/978-1-4612-2544-75>.



**The tip of the iceberg**

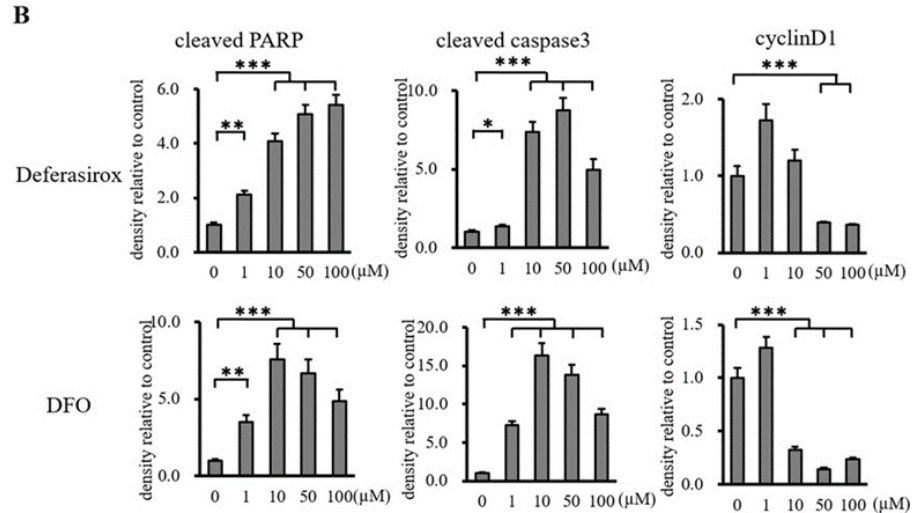
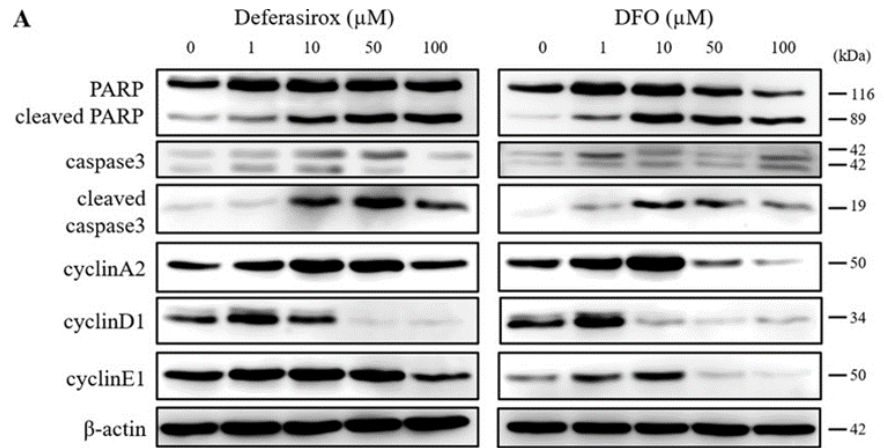
## What is research data?

## Is this data?

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29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Mod. 5611
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2	43	Dat.:																								78	2		
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7	45	Bibl.:																								76	0		
46	47																									75	SO		



# Is this data?





# Is this data?

+ Create

Home

Competitions

Datasets

<> Code

Discussions

Courses

More

Data Code (4) Discussion (2) Activity Metadata

Download (103 kB)

New Notebook

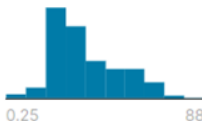
Vietnam\_COVID-19\_Hospital...

Vietnam\_COVID-19\_patient\_...

Vietnam\_province\_info.csv

Detail Compact Column

10 of 30 columns

ID	Gender	Age	Nationality	Detection Location
	F 55%		Vietnam 82%	Hanoi 39%
	M 45%		United Kingdom 7%	Ho Chi Minh City 19%
			Other (30) 10%	Other (120) 42%
BN1	M	66	China	Ho Chi Minh City
BN2	M	28	China	Ho Chi Minh City
BN3	F	25	Vietnam	Thanh Hoa
BN4	M	29	Vietnam	Vinh Phuc
BN5	F	23	Vietnam	Vinh Phuc
BN6	F	25	Vietnam	Khanh Hoa

288  
unique values

0.25 88

## What is research data?

Any information that has been

**collected,**

**observed,**

**generated,**

**created**

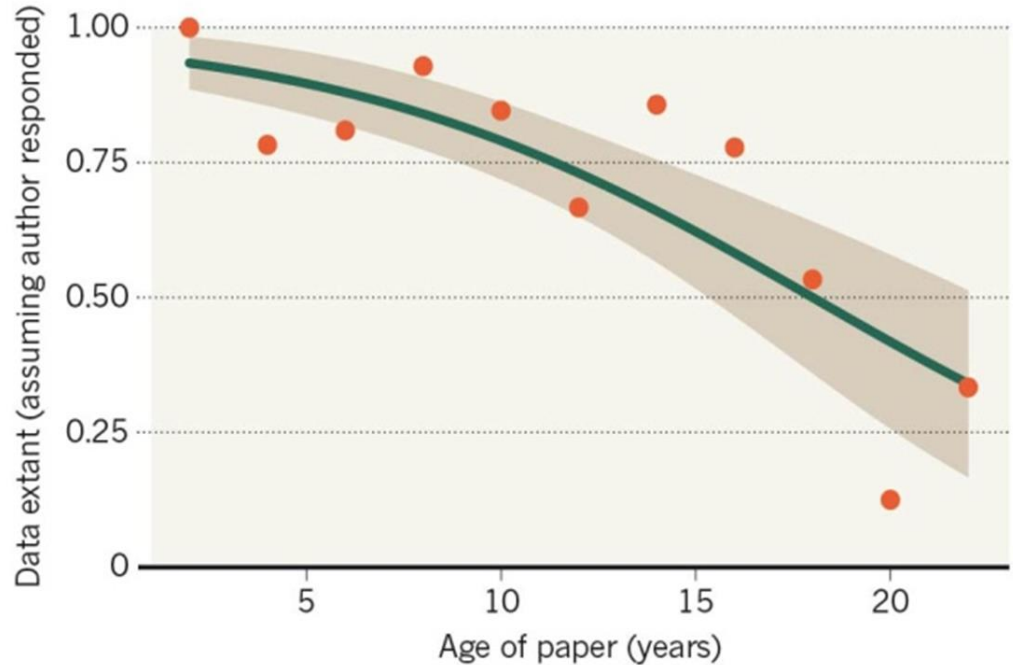
to validate original research findings

Research data is a very important resource, so we must ensure that it can be reused, first and foremost by ourselves.

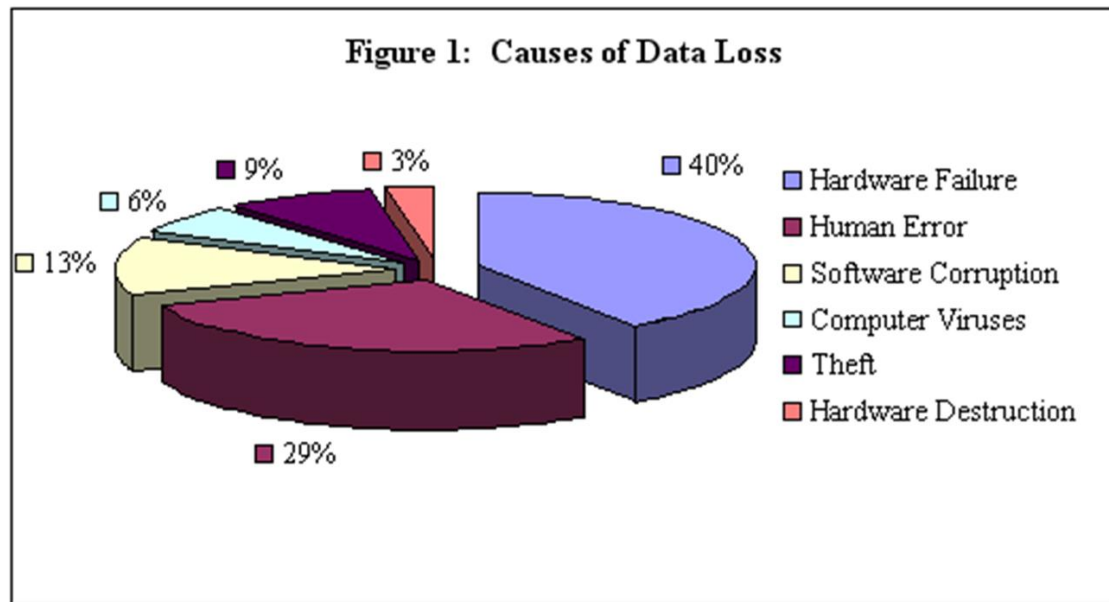
## Data can be missed

### MISSING DATA

As research articles age, the odds of their raw data being extant drop dramatically.



## Data can get lost



**Source:** Author's estimates based on data from Safeware, The Insurance Agency, Inc., "2000 Safeware Loss Study," 2001; and ONTRACK Data International, Inc., "Understanding Data Loss," 2003.

## Data can be manipulated or altered

Paul Jump, A Star's Collapse. Dutch begin documenting and trying to explain top psychologist's massive fraud.  
Times Higher Education, November 28, 2011

58 articles published by Diederik Stapel were withdrawn because they were based on **invented data**. His papers had been published in scientific journals considered prestigious (very high IFs!). Following reports from three doctoral students, the Dutch university for which he worked had started an investigation. Stapel then admitted that he had fabricated the data on numerous occasions. **If he had shared his data before, he probably wouldn't have been able to fabricate fakes for so long.**

This case led the Netherlands become one of the pioneer countries in Open Science policy and practices

**These problems can be partially solved through responsible research data management**

## Research Data Management to the resc

"Research data management concerns the organisation of data, from its entry to the research cycle through to the dissemination and archiving of valuable results. It aims to ensure reliable verification of results, and permits new and innovative research built on existing information."

(Whyte, A., Tedds, J. (2011). ['Making the Case for Research Data Management'](#). DCC Briefing Papers. Edinburgh: Digital Curation Centre.)





# The research infrastructure for language as social and cultural data

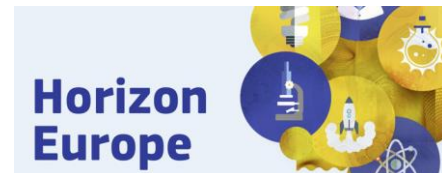
CLARIN is a digital infrastructure offering data, tools and services to support research based on language resources.

RDM applies to all disciplines including HSS





## Funders are pushing RDM & Open Data - European level



### Horizon 2020 & Horizon Europe: FAIR Data Management

- Participating projects will be required to develop a **Data Management Plan (DMP)**
- Participating projects are **required to deposit research data**, preferably into a research data repository
- “[...]as far as possible, projects must then **take measures to enable for third parties to access, mine, exploit, reproduce and disseminate (free of charge for any user) this research data.**“

[Guidelines on Open Access to Scientific Publications and Research Data in Horizon 2020](#) | [Guidelines on Data Management in Horizon 2020](#)

## Funders are pushing RDM & Open Data - example for a national funder

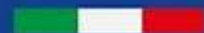


### [DFG Guidelines on the Handling of Research Data](#)

“[...] Assuming that the publication of research data from a DFG-funded project does not conflict with the rights of third parties (in particular data protection or copyright), **research data should be made available as soon as possible.**

[...]

**Applicants may request funding** for project-specific costs that arise in connection with a scientific project, for the preparation of research data for subsequent reuse and/or the transfer of research data to existing infrastructures as part of a proposal to the DFG. [...]”



## The National Recovery and Resilience Plan

Coerentemente con le finalità del presente Avviso, ai risultati del Programma di ricerca e ai relativi dati (ad esempio, le pubblicazioni di risultati originali della ricerca scientifica, i dati grezzi e i metadati, le fonti, le rappresentazioni digitali grafiche e di immagini e i materiali multimediali scientifici) deve essere garantito un accesso aperto al pubblico nel minor tempo e con il minor numero di limitazioni possibile, **secondo i principi “Open science” e “FAIR Data”**.

## Journals: Nature

An inherent principle of publication is that others should be able to replicate and build upon the authors' published claims. Therefore, a condition of publication in a Nature journal is that authors are required to make materials, data and associated protocols promptly available to readers without undue qualifications.

[...]The preferred way to share large data sets is via public repositories.

<http://www.nature.com/authors/policies/availability.html>



## Journals: PLOS

### Data Availability

PLOS journals require authors to make all data underlying the findings described in their manuscript fully available without restriction, with rare exception.

[...]

Refusal to share data and related metadata and methods in accordance with this policy will be grounds for rejection. [...]

<http://www.plosone.org/static/policies.action#sharing>



## FAIR Data Principles

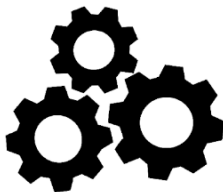
F  
Findable



A  
Accessible



I  
Interoperable



R  
Reusable



- [FAIR Data Principles](#)
- Wilkinson et al. (2016), The FAIR Guiding Principles for scientific data management and stewardship, Scientific Data 3, [doi:10.1038/sdata.2016.18](https://doi.org/10.1038/sdata.2016.18)
- SNF: [Explanation of the FAIR Data Principles](#)

## F - Findable

others can discover your data

- described using rich metadata
- using persistent identifiers
- indexed in catalogues or databases

## F - Findable

imagine looking for a book in a library

- you can use the catalogue
  - you need the book to be described (**metadata**)
    - e.g. Nordic crime series; encyclopedia of modern airplanes
- you will find the location
- you will need some kind of very specific (unified) identification
  - “6th floor, shelf 6A/276, HF5718 .22 .F85 2014”



## F - Findable – how to?

in libraries librarians create the description (metadata) for you

in online world, the author has to describe uploaded content himself (!)

repository can help you with identification – assign persistent identifiers (eg. DOI)

### DOI:

DOI [10.5281/zenodo.3978090](https://doi.org/10.5281/zenodo.3978090)

### Keyword(s):

pine wood nematode

*Bursaphelechus xylophilus*

quarantine pest

survey

Finland

### Subject(s):

*Bursaphelechus* [↗](#)

surveillance [↗](#)

data [↗](#)

### Related identifiers:

Supplement to

[10.3897/neobiota.58.38313](https://doi.org/10.3897/neobiota.58.38313) (Journal article)

[10.5281/zenodo.3842358](https://doi.org/10.5281/zenodo.3842358) (Software)

## Metadata

- metadata describe data
  - e.g. title, author, keywords, subject headings, identifiers...
- metadata help other people find your data!
- author of datasets usually chooses metadata when uploading to repository – do not underestimate this!
  - your data can be lost or found... it depends on you!
- libraries can help
  - librarians love metadata ;-)

## Persistent identifiers (PID)

- sequence of letters/numbers in specified format, managed by some service provider
- **unique** – different things have different identifiers
  - note: name is not unique identifier (e.g. Carl Johansson)
- **persistent** – should work ‘forever’
- **resolvable** – there is a way how to get representation of identified object (e.g. links - see below)

## Persistent identifiers (PID)

- provided by some service
  - DOI – digital object identifier **10.5281/zenodo.5665754**
    - articles
    - data
  - ORCID – Open Researcher and Contributor ID -- **0000-0002-8271-3674**
  - ROR.org – Research Organization Registry - **024d6js02**
- note: URL is NOT identifier - <https://zenodo.org/record/5665755#.Yh6O1-iZOUk>
- ..but most PIDs are resolvable (you can use them in URL):
- <https://doi.org/10.5281/zenodo.5665754>, <https://orcid.org/0000-0002-8271-3674>,  
<https://ror.org/024d6js02>

## A - Accessible

your data can be made available to others

- using some „simple protocol“ – e.g. web browser
- or using some more sophisticated way (asking for permission etc.)
  
- knowing persistent identifier should always help you
  - you should always get at least metadata
  
- not everything has to be shared without limitations
  - “As open as possible, as closed as necessary.”

## A - Accessible – how to?

- publish/share in a **repository**
- publish at least **metadata**

Cite
Download (7.59 MB)
Share
Embed
+ Collect

Dataset posted on 29.07.2020, 11:18 by [Petr Čermák](#), Rudolf Schönmann, Christian Franz, Astrid Schneidewind, Christian Pfeleiderer, Oleg Sobolev

**Abstract:**  
 Recently, time-of-flight neutron spectroscopy in polycrystalline samples of CeCuAl<sub>3</sub> has provided putative evidence for a so-called vibronic mode – a combined crystal field - phonon excitation. These types of modes may be responsible for certain forms of magnetically mediated superconductivity or non-Fermi liquid behavior. Our measurement on single-crystal CeAuAl<sub>3</sub> performed on the PUMA (p10684, see references) revealed a weakly dispersive excitation at energy 7.9 meV, which is clearly magnetically driven and connected to phonons. However to better understand the nature of this hybridized excitation, more phonon measurements are necessary. Therefore we propose to determine the detailed dispersion of the low lying optical phonons in the energy range between 12-50 meV.

**Place:**  
 Heinz Meier-Leibnitz Zentrum, Garching, Germany (MLZ)

**Instruments:**  
 PUMA (<https://mlz-garching.de/puma>)

**Date:**  
 Tue, 29. Nov 2016 to Sun, 04. Dec 2016

**Disclaimer:**  
 Abstract is not modified version of the abstract from original scientific proposal submitted to MLZ. Data are published exactly as they were send to us after the end of experiments (automatic email by NICOS). Authenticity of the data can be verified by the data scientists at MLZ, feel free to contact them.

**USAGE METRICS** [↗](#)

145 views	15 downloads	0 citations
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**CATEGORIES**

- Condensed Matter Physics
- Electronic and Magnetic Properties of Condensed Matter; Superconductivity

**KEYWORDS**

mlz garching

puma

inelastic neutron scattering

three axis spectrometer

**LICENCE**

CC BY 4.0

**EXPORTS**

Select an option
▼

## I - Interoperable

other people should be able to use your data (with their own data)

- it should be possible to understand the data
  - format should be readable
  - there should be helpful documentation
  - well known terminology should be used (domain standards)

# I - Interoperable – how to?

- use open formats  
(plaintext rules!)
- use the right language!



## 2019-nCoV Vaccine mRNA-1273 MeSH Descriptor Data 2022

Details   Qualifiers   **MeSH Tree Structures**   Concepts

Amino Acids, Peptides, and Proteins [D12]  
  Proteins [D12.776]  
    Recombinant Proteins [D12.776.828]  
      Vaccines, Synthetic [D12.776.828.868]  
        Nucleic Acid-Based Vaccines [D12.776.828.868.228]  
          mRNA Vaccines [D12.776.828.868.228.500]  
            **2019-nCoV Vaccine mRNA-1273 [D12.776.828.868.228.500.500]**  
              BNT162 Vaccine [D12.776.828.868.228.500.750]



## Interoperable

- open format is not enough by itself -
  - people should be able to understand your data
- example: temperature
  - 36,6
  - 36,1
  - 37,8
  - 41,5
- what is the context?
  - patient data or hot summer?
- **describe** your data to make it interoperable (and reusable)!

## R - Reusable

others should be allowed to (confidently) reuse your data

- it should be possible to trust the data
  - provenance
- it should be clear what are is allowed to do with the data
  - licensing conditions

## R - Reusable – how to?

- describe the origin of the data sufficiently
  - how did you get them?
  - how were the data modified/processed?
- use license describing what is possible/legal to do with your data
  - share it freely?

**Publication date:**  
April 4, 2021

**DOI:**  
DOI [10.5281/zenodo.4661737](https://doi.org/10.5281/zenodo.4661737)

**Keyword(s):**  
COVID-19 Air Traffic flight tracks fuel consumption  
Black Carbon emission contrail CoCiP

**License (for files):**  
[Creative Commons Attribution 4.0 International](https://creativecommons.org/licenses/by/4.0/)



# Why Open Data?

## “Currencies“ of science

- Peer-reviewed articles in “high-impact“ journals
- Publishing books with well-respected publishers
- Citations of your own work through other authors
- Conference contributions (talks, posters)
  
- At the end of the day, that’s what you get grants, funding, professorships,... for.

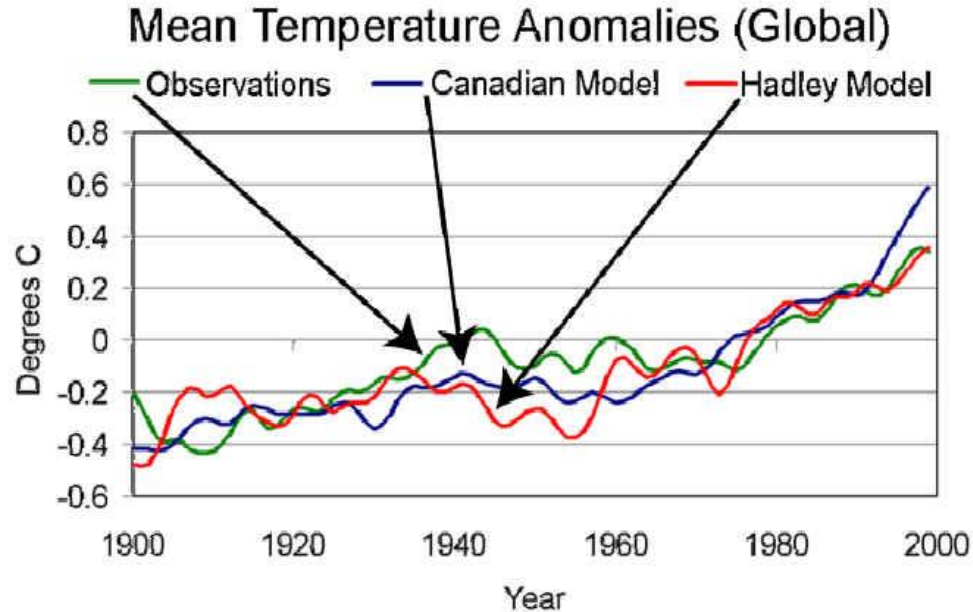
The scientific incentive system and the distribution of scientific results



Illustration from <http://blog.peerj.com/post/65345738206/changing-the-currency-of-science-to-solve-our-greatest>

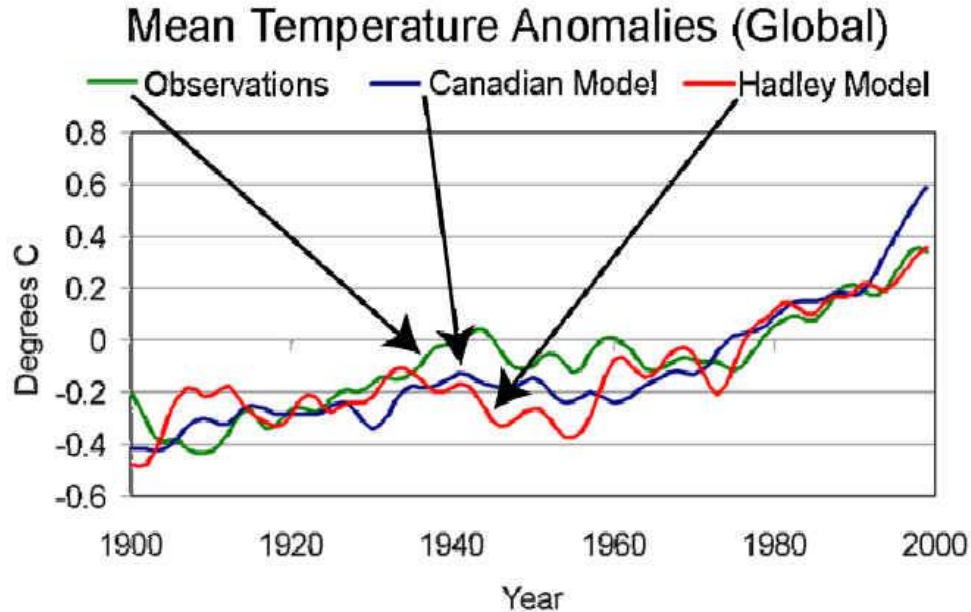
**But open data improve science!**

## **Example Climate Science**



# But open data improve science!

## Example Climate Science



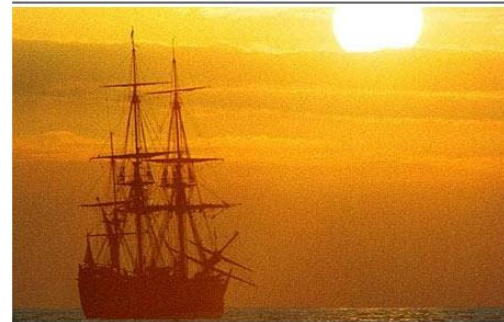
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### Captain Cook's log books help scientists chart climate change

Weather logs kept by Captain James Cook and other 18th and 19th century explorers are being used by scientists to predict the change in climate.



Log books from Captain Cook's Endeavour are being used to chart climate change. Photo: AP

7:57AM BST 06 Oct 2009

Captain Cook's weather reports from Discovery and Resolution, made at noon each day on his voyages to unknown lands, William Bligh's Bounty

#### Climate Change

News » UK News »  
 Earth News »  
 Environment »

#### In Climate Change



Bolivia's second largest lake dries up



China's dirty old town





# But open data improve science!

## Example DNA Sequencing Data

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide Search Advanced Help

Display Settings: GenBank Send Change region shown Customize view Analyze this sequence Run BLAST Pick Primers Highlight Sequence Features Find in this Sequence

### Homo sapiens hemoglobin, beta (HBB), mRNA

NCBI Reference Sequence: NM\_000518.4

[FASTA](#) [Graphics](#)

Go to

LOCUS NM\_000518 626 bp mRNA linear PRI 09-JUN-2015

DEFINITION Homo sapiens hemoglobin, beta (HBB), mRNA.

ACCESSION NM\_000518

VERSION NM\_000518.4 GI:28302128

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 626)

AUTHORS Pereverzev,A.P., Markina,N.M., Ianushevich,Iu.G., Gorodnicheva,T.V., Minasian,B.E., Luk'ianov,K.A. and Gurskaja,N.G.

TITLE [Intron 2 of human beta-globin in 3'-untranslated region enhances expression of chimeric genes]

JOURNAL *Bioorg. Khim.* 40 (3), 293-296 (2014)

PUBMED [25892735](#)

REMARK GeneRIF: We believe that introduction of beta-globin intron in the 3'-UTR of the chimeric gene can be used to enhance its expression and may be advantageous in some cases when usage of 5'-UTR intron is inappropriate

REFERENCE 2 (bases 1 to 626)

AUTHORS Vovor A. Feteke L. Kueviakoe IM. Khatarou L. Mavussi K. Maonand H

Articles about the HBB gene

[IDENTIFICATION OF MUTATION IVS1-5(G &G; C) OF THE  $\beta$ -HEMOGLOBIN [Tissot Genet. 2015]

The BioPlex Network: A Systematic Exploration of the Human Interactome. [Cell. 2015]

Xmnl POLYMORPHISM AND DISEASE SEVERITY I [J Ayub Med Coll Abbottabad. 2015] See all...

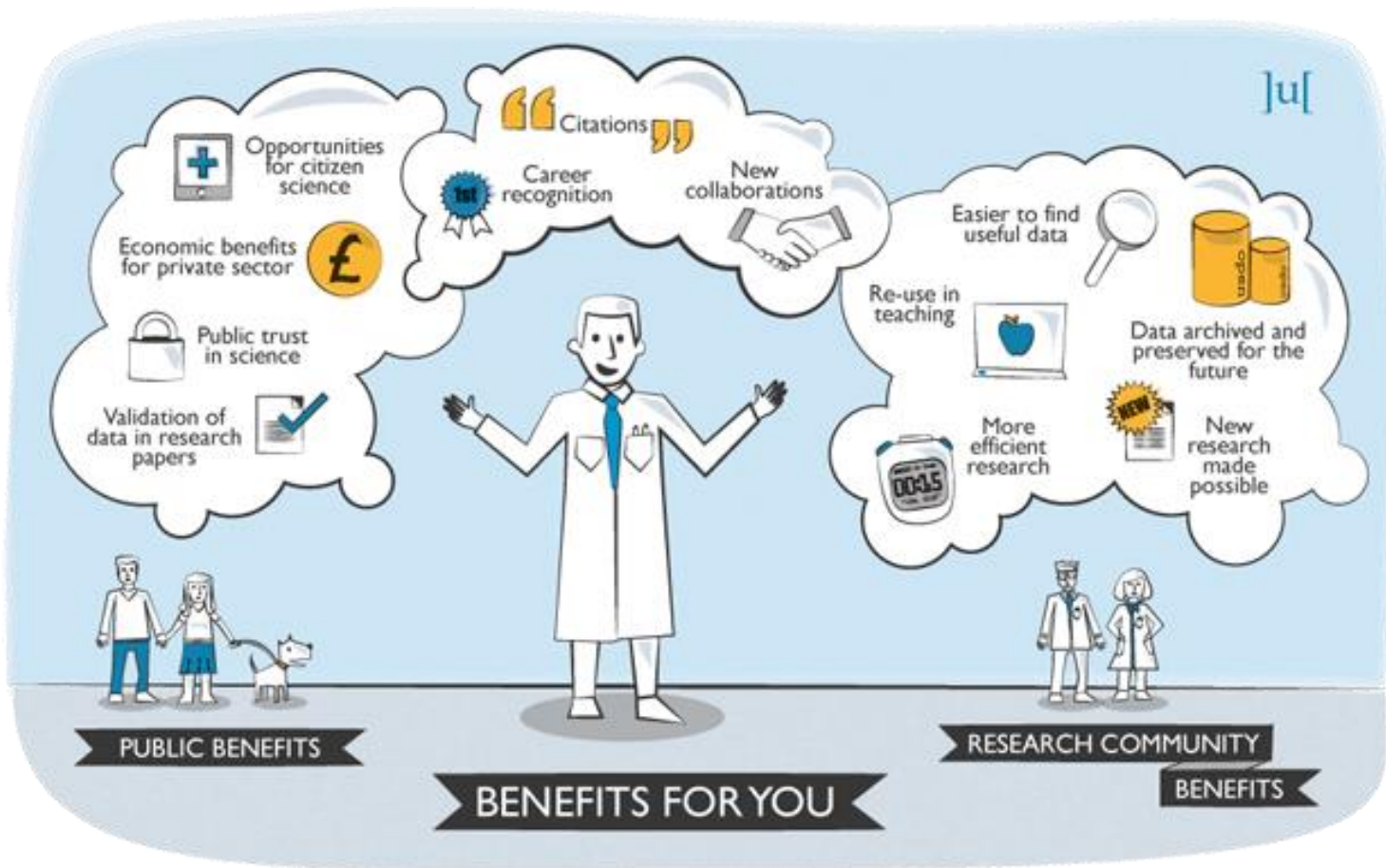
Pathways for the HBB gene

Erythrocytes take up oxygen and release carbon dioxide

Erythrocytes take up carbon dioxide and release

Human Genome Project: Sequencing and mapping of the human genome, completed 2003

"The success of the genome project is in no small part due to the fact that the world's entire library of published DNA sequences has been an open access public source for the past 20 years. If sequences could be obtained only in the way that traditionally published work can be obtained - there would be no genome project"  
(Prof. Patrick Brown, Biochemist at Stanford University, 2004)



Picture:  
 Hole, B. (2015). Open  
 Science: [A New publisher  
 Perspective](#). Ubiquity press.  
 (CC BY 4.0 International)

What kind of repositories are around for my field of research?



## Filter

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- Data access ⊞
- Data access restrictions ⊞
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- Data licenses ⊞
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- Data upload restrictions ⊞
- Enhanced publication ⊞
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- Institution type ⊞
- Keywords ⊞
- Metadata standards ⊞
- PID systems ⊞
- Provider types ⊞
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machine learning

Search

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UC Irvine Machine Learning Repository



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Content type(s)

[Standard office documents](#) [Archived data](#) [Plain text](#) [Databases](#)

Country

[United States](#)

The UCI Machine Learning Repository is a collection of databases, domain theories, and data generators that are used by the machine learning community for the empirical analysis of machine learning algorithms. It is used by students, educators, and researchers all over the world as a primary source of machine learning data sets. As an indication of the impact of the archive, it has been cited over 1000 times.

**OpenML**

Open Machine Learning



Subject(s)

[Education Sciences](#) [Computer Science](#) [Social and Behavioural Sciences](#) [Humanities and Social Sciences](#)
[Computer Science, Electrical and System Engineering](#) [Engineering Sciences](#)

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[Belgium](#) [European Union](#) [Netherlands](#)

OpenML is an open ecosystem for machine learning. By organizing all resources and results online, research becomes more efficient, useful and fun. OpenML is a platform to share detailed experimental results with the community at large and organize them for future reuse. Moreover, it will be directly integrated in today's most popular data mining tools (for now: R, KNIME, RapidMiner and WEKA). Such an easy and free exchange of experiments has tremendous potential to speed up machine learning research, to engender larger, more detailed studies and to offer accurate advice to practitioners. Finally, it will also be a valuable resource for education in machine learning and data mining.



# OpenML

General

Institutions

Terms

Standards

Name of repository	<b>OpenML</b>
Additional name(s)	Open Machine Learning
Repository URL	<a href="http://www.openml.org/">http://www.openml.org/</a>
Subject(s)	<span>Education Sciences</span> <span>Computer Science</span> <span>Social and Behavioural Sciences</span> <span>Humanities and Social Sciences</span> <span>Computer Science, Electrical and System Engineering</span> <span>Engineering Sciences</span>
Description	<p>OpenML is an open ecosystem for machine learning. By organizing all resources and results online, research becomes more efficient, useful and fun. OpenML is a platform to share detailed experimental results with the community at large and organize them for future reuse. Moreover, it will be directly integrated in today's most popular data mining tools (for now: R, KNIME, RapidMiner and WEKA). Such an easy and free exchange of experiments has tremendous potential to speed up machine learning research, to engender larger, more detailed studies and to offer accurate advice to practitioners. Finally, it will also be a valuable resource for education in machine learning and data mining.</p>
Contact	<a href="mailto:openmachinelearning@gmail.com">openmachinelearning@gmail.com</a>
Content type(s)	<span>Standard office documents</span> <span>Structured graphics</span> <span>Plain text</span> <span>Software applications</span> <span>Source code</span> <span>Configuration data</span> <span>other</span> <span>Databases</span>
Keyword(s)	<span>machine learning</span> <span>meta-learning</span> <span>experimental methodology</span> <span>datasets</span> <span>algorithms</span> <span>experiments</span>
Repository size	1700000 machine learning experiments on 19630 datasets and 3370 implementations
Repository type(s)	disciplinary
Mission statement for designated community	<a href="http://www.openml.org">http://www.openml.org</a>

# Databases

A registry of knowledgebases and repositories of data and other digital assets.

<a href="#">MATCH ALL TERMS</a>		<a href="#">MATCH ANY TERM</a>	
<a href="#">↻</a>	<a href="#">MAINTAINED</a>	<a href="#">NOT MAINTAINED</a>	
<a href="#">↻</a>	<a href="#">RECOMMENDED</a>	<a href="#">NOT RECOMMENDED</a>	
<a href="#">↻</a>	<a href="#">READY</a>	<a href="#">DEPRECATED</a>	<a href="#">UNCERTAIN</a>
		<a href="#">IN DEV.</a>	

Registry

 [APPLY](#)

Record Type

 [APPLY](#)

Subjects

 [APPLY](#)

Domains

 [APPLY](#)

[Clear All](#) Registry: Database

Show results as a grid.

< 1 2 3 ... 60 61 62 >

Displaying 1 to 30 of 1855.

WoRMS



World Register of Marine Species

The aim of a World Register of Marine Species (WoRMS) is to provide an authoritative and comprehensive list of names of marine organisms, including information on synonymy. While high...

[Environme...](#) [Taxonomic...](#) [All](#) +4 more tags

Standards Implemented: 3  
 Related Databases: 9  
 Endorsing Policies: 0

GlycoNAVI



GenBank



GenBank

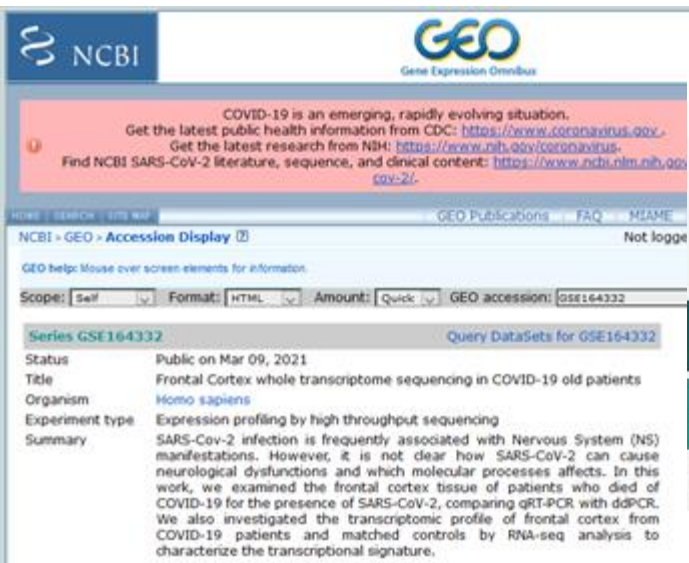
GenBank is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences. The complete release notes for the current version of GenBank are available ...

[Functional ...](#) [Nucleic Ac...](#) [All](#) +20 more tags

Standards Implemented: 11  
 Related Databases: 32  
 Endorsing Policies: 51

ADHDgene





NCBI GEO - Accession Display Not logged in

COVID-19 is an emerging, rapidly evolving situation. Get the latest public health information from CDC: <https://www.cdc.gov/coronavirus/>. Get the latest research from NIH: <https://www.nih.gov/coronavirus>. Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/cov-2/>.

NCBI - GEO - Accession Display Not logged in

GEO help: Mouse over screen elements for information.

Scope: Self Format: HTML Amount: Quick GEO accession: GSE164332

**Series GSE164332** [Query DataSets for GSE164332](#)

Status Public on Mar 09, 2021

Title Frontal Cortex whole transcriptome sequencing in COVID-19 old patients

Organism *Homo sapiens*

Experiment type Expression profiling by high throughput sequencing

Summary SARS-Cov-2 infection is frequently associated with Nervous System (NS) manifestations. However, it is not clear how SARS-Cov-2 can cause neurological dysfunctions and which molecular processes affects. In this work, we examined the frontal cortex tissue of patients who died of COVID-19 for the presence of SARS-CoV-2, comparing qRT-PCR with ddPCR. We also investigated the transcriptomic profile of frontal cortex from COVID-19 patients and matched controls by RNA-seq analysis to characterize the transcriptional signature.

Overall design Frontal cortex of healthy controls and COVID-19 patients. RNA-seq and ddPCR experiments.

Contributor(s) Gagliardi I, Visonà S,

Citation missing Has this series been cited?

Submission date Jan 06, 2021

Last update date Mar 10, 2021



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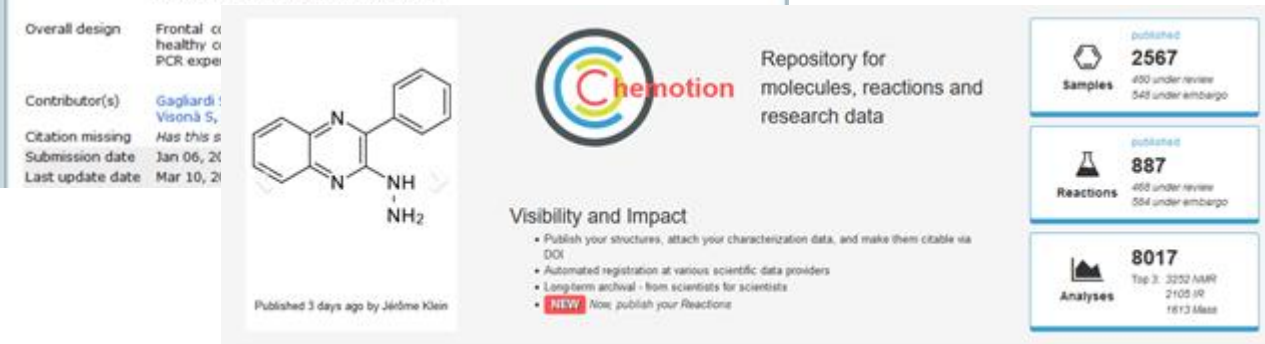
ALL TOPICS

Search for measurement type, author name, project, taxa...

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LITHOSPHERE  
BIOLOGICAL CLASSIFICATION  
ATMOSPHERE  
PALEONTOLOGY  
OCEANS  
ECOSYSTEMS  
LAND SURFACE  
BIOSPHERE  
GEOPHYSICS

A rough typology of data repositories:

- Controlled access repositories
- Subject- or domain-specific repositories
- Institutional repositories
- Generic repositories



Chemotion

Repository for molecules, reactions and research data

published 2567 Samples  
400 under review  
548 under embargo

published 887 Reactions  
408 under review  
504 under embargo

published 8017 Analyses  
Top 3: 3232 AMR  
2105 IR  
1813 MS

Visibility and Impact

- Publish your structures, attach your characterization data, and make them citable via DOI
- Automated registration at various scientific data providers
- Long-term archival - from scientists for scientists
- **NEW!** Now, publish your Reactions

Published 3 days ago by Jérôme Klein

# Domain repositories

**LINDAT** Linguistic Data and NLP Tools  
 CLARIN-CZ

Find Linguistic Data and NLP Tools  
 Custom Support (with Persistent IDs)

Advanced Search

Author	Subject	Language (ISO)
Veselý, Bohumil (787)	Galerie osobnosti (787)	Nolinguistic content (709)
Hajlé, Jan (86)	People (784)	Czech (439)
Straka, Milan (65)	Places (828)	English (302)
Krátký film (63)	machine translation (60)	German (210)
Žabokrtský, Zdeněk (60)	Germanistik (50)	French (110)
... View More	... View More	... View More

What's New

ToolService

**Image Annotation Tool**

**Author(s):**  
 Roček, Martin

**Description:**  
 Image annotation tool is a web application that allows users to mark zones of interest in an image. These zones are then converted to TEI P3 code snippet that can be used in your document to connect the image and the text. ...

Publicly Available

<https://lindat.mff.cuni.cz/repository/>

**NCBI** Resources How To Sign In to NCBI

GenBank Nucleotide Search

GenBank Submit Genomes WGS Metagenomes TPA TSA INSDC Other

**COVID-19 Information**  
 Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español

**GenBank Overview**

**What is GenBank?**

GenBank<sup>®</sup> is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (*Nucleic Acids Research* 2013 Jan 41(1):D36-42). GenBank is part of the *International Nucleotide Sequence Database Collaboration*, which comprises the DNA DataBank of Japan (DDBJ), the European Nucleotide Archive (ENA), and GenBank at NCBI. These three organizations exchange data on a daily basis.

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An [annotated sample GenBank record](#) for a *Saccharomyces cerevisiae* gene demonstrates many of the features of the GenBank flat file format.

**Access to GenBank**

There are several ways to search and retrieve data from GenBank.

- Search GenBank for sequence identifiers and annotations with [Entrez Nucleotide](#).
- Search and align GenBank sequences to a query sequence using [BLAST](#) (Basic Local Alignment Search Tool). See [BLAST info](#) for more information about the numerous BLAST databases.
- Search, link, and download sequences programmatically using [NCBI e-utils](#).
- The ASN.1 and flatfile formats are available at NCBI's anonymous FTP server: <ftp://ftp.ncbi.nlm.nih.gov/ncbi-ftp1> and <ftp://ftp.ncbi.nlm.nih.gov/genbank>.

**GenBank Data Usage**

The GenBank database is designed to provide and encourage access within the scientific community to the most up-to-date and comprehensive DNA sequence information. Therefore, NCBI places no restrictions on the use or distribution of the GenBank data. However, some submitters may claim patent, copyright, or other intellectual property rights in all or a portion of the data they have submitted. NCBI is not in a position to assess the validity of such claims, and therefore cannot provide comment or unrestricted permission concerning the use, copying, or distribution of the information contained in GenBank.

**GenBank Resources**

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- [Search GenBank](#)
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<https://www.ncbi.nlm.nih.gov/genbank/>



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[Advanced Search](#)

**Author**

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- machine translation (60)
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- ... View More

**Language (ISO)**

- Nolinguistic content (709)
- Czech (439)
- English (302)
- German (210)
- French (110)
- ... View More

What's New

ToolService

LINDAT / CLARIAH-CZ

Image Annotation Tool

**Author(s):**  
Roček, Martin

**Description:**

Image annotation tool is a web application that allows users to mark zones of interest in an image. These zones are then converted to TEI P5 code snippet that can be used in your document to connect the image and the text. ...

This item contains 1 file (8.35 MB).

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## LINDAT/CLARIAH-CZ

- linguistics / digital humanities repository
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## Universal Dependencies 2.9

Please use the following text to cite this item or export to a predefined format: [BIBTEX](#) [CMLH](#)

Zeman, Daniel; et al., 2021, *Universal Dependencies 2.9*, LINDAT/CLARIAH-CZ digital library at the Institute of Formal and Applied Linguistics (UFAL), Faculty of Mathematics and Physics, Charles University, <http://hdl.handle.net/11234/1-4611>

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LINDAT / CLARIAH-CZ

Authors	Zeman, Daniel ; et al. ▶ show everyone
Item identifier	<a href="http://hdl.handle.net/11234/1-4611">http://hdl.handle.net/11234/1-4611</a>
Project URL	<a href="http://universalddependencies.org/">http://universalddependencies.org/</a>
Referenced by	<a href="https://doi.org/10.1162/coli_a_00402">https://doi.org/10.1162/coli_a_00402</a>
Date issued	2021-11-15
Type	corpus, text
Size	29074543 tokens, 29592250 words, 1697879 sentences
Language(s)	Afrikaans , Akkadian , Akuntsu , Albanian , Amharic , AncientGreek (to 1453) , Apurinã , Arabic , Armenian , AssyrianNeo-Aramaic , Bambara , Basque , Beja , Belarusian , Bengali , Bhojpuri , Breton , Bulgarian , Catalan , Central Siberian Yupik , Chinese , Chukot , ChurchSlavic , Coptic , Croatian , Czech , Danish , Dutch , English , Erzya , Estonian , Faroese , Finnish , French , Galician , German , Gothic , Guajajára , Hebrew , Hindi , Hungarian , Icelandic , Indonesian , Irish , Italian , Japanese , Javanese , K'iche' , Kangri , Karelian , Karo(Brazil) , Kazakh , Khunsari , Komi-Permyak , Komi-Zyrian , Korean , Latin , Latvian , Ligurian , LiteraryChinese , Lithuanian , Livvi , LowGerman , Makuráp , Maltese , Manx , Marathi , MbyáGuarani , Modern Greek (1453-) , Moksha , Mundurukú , Nayini , Neapolitan , Nigerian Pidgin , NorthernKurdish , Northern Sami , Norwegian , OldFrench (842-ca. 1400) , OldRussian , Old Turkish , Persian , Polish , Portuguese , Romanian , Russia Buriat , Russian , Sanskrit , ScottishGaelic , Serbian , SkoltSami , Slovak , Slovenian , Sol , South Levantine Arabic , Spanish , Swedish , SwedishSign Language , SwissGerman , Tagalog , Tamil , Tatar , Telugu , Thai , Tupinambá , Turkish , Uighur , Ukrainian , UoerSorbian . Urdu . Urubú-Kaabor . Vietnamese . Warlpiri . Welsh . Western Armenian . WesternFrisian .

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- reference to the article
- languages are important
- PID is handle (not DOI)

, SwissGerman , Tagalog , Tamil , Tatar , Telugu , Thai , Tupinambá , Turkish , Uighur , Ukrainian , UpperSorbian , Urdu , Urubú-Kaapor , Vietnamese , Warlpiri , Welsh , Western Armenian , WesternFrisian , Wolof , Xibe , Yakut , Yoruba , YueChinese

#### Description

Universal Dependencies is a project that seeks to develop cross-linguistically consistent treebank annotation for many languages, with the goal of facilitating multilingual parser development, cross-lingual learning, and parsing research from a language typology perspective. The annotation scheme is based on (universal) Stanford dependencies (de Marneffe et al., 2006, 2008, 2014), Google universal part-of-speech tags (Petrov et al., 2012), and the Intersect Interlingua for morphosyntactic tagsets (Zeman, 2008).

Version 2.8.1 fixes a bug in 2.8 where a portion of the Dutch Alpino treebank was accidentally omitted.

#### Publisher

Universal Dependencies Consortium

#### Acknowledgement

Ministerstvo školství, mládeže a tělovýchovy České republiky

Project code: LM2018101

Project name: LINDAT/CLARIAH-CZ: Digitální výzkumná infrastruktura pro jazykové technologie, umění a humanitní vědy

#### Subject(s)

treebank dependency syntax morphology harmonized annotation intersect universal tagset  
stanford dependencies

#### Collection(s)

LINDAT / CLARIAH-CZ Data & Tools

#### Other versions

List all versions ▾

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#### Files in this item



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<b>Name</b>	ud-treebanks-v2.9.tgz
<b>Size</b>	441.62 MB
<b>Format</b>	application/x-gzip




- description
- subjects (keywords)
- different versions of the dataset
- license

Download instructions for command line

Download all files in item (534.14 MB)

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**Name** ud-treebanks-v2.9.tgz  
**Size** 441.62 MB  
**Format** application/x-gzip  
**Description** Treebank data  
**MD5** 2d5d04a1868093977cef42c92c870153

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**File Preview**

stats.xml	1 kB
README.md	1 kB
LICENSE.txt	202 B
nap_rb-ud-test.conllu	431 B
nap_rb-ud-test.txt	56 B
<b>UD_Sol-AHA</b>	
stats.xml	3 kB
so_aha-ud-test.txt	386 B
README.md	1 kB
LICENSE.txt	202 B

**Name** ud-documentation-v2.9.tgz  
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**MD5** 8f2ae73f46c35f19cdacb13a2442ea8b

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**Name** ud-tools-v2.9.tgz  
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**Description** Tools  
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- file preview
- this dataset = data + documentation + tools

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## Machine translation

Please use the following text to cite this item or export to a predefined format:

BIBTEX CMOI

Košarko, Ondřej; Variš, Dušan and Popel, Martin, 2019, *LINDAT Translation service*, LINDAT/CLARIAH-CZ digital library at the Institute of Formal and Applied Linguistics (UFAL), Faculty of Mathematics and Physics, Charles University, <http://hdl.handle.net/11234/1.2922>.

Share:



### Authors:

Martin Popel, Dušan Variš, Ondřej Košarko

### Description:

A neural networks based translation service provides a simple UI and API that lets you use Transformer models trained by our experts. Five models are currently provided with more to come.

[Project home](#) [Run](#)



## UDPipe

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Straka, Milan and Straková, Jana, 2016, *UDPipe*, LINDAT/CLARIAH-CZ digital library at the Institute of Formal and Applied Linguistics (UFAL), Faculty of Mathematics and Physics, Charles University, <http://hdl.handle.net/11234/1-1702>.

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### Authors:

Milan Straka, Jana Straková

### Terms of Use

Most popular

Machine translation

UDPipe

KonText

UWebASR

Text processing

Search services

Lexical resources

Automatic speech recognition

## LINDAT Translation

Translate Docs

The translation service is available for **personal and non-commercial use** (see [terms of use](#) for more details).

### Source

English

### Target

Czech

advanced

### Input sentences

Let's talk about **some specific repositories**.

### Translation

Pojdme se bavit o některých konkrétních úložiscích.

Translate Choose file

Credits: The service runs systems trained by:

Martin Popel  
CUBBITT models, en-<=>cs, en-<=>fr, en-<=>pl as described in  
Popel, M., Tomkova, M., Tomek, J. et al. Transforming machine translation: a deep learning system reaches news translation quality comparable to human professionals. Nat Commun 11, 4381 (2020). <https://doi.org/10.1038/s41467-020-18073-9>

As of Jan 19 2022, the en-<=>cs translation uses the upgraded CUBBITT document-level models. The advanced mode (and the API) still offers the old sentence-level models.

Shantipriya Parida  
en->hi model

Dušan Variš  
en-<=>ru, en-<=>de models

- repositories can be connected to infrastructures and provide services



NCBI Resources How To Sign in to NCBI

GenBank Nucleotide Search

GenBank Submit Genomes WGS Metagenomes TPA TSA INSDC Other

**COVID-19 Information**  
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### GenBank Overview

#### What is GenBank?

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An [annotated sample GenBank record](#) for a *Saccharomyces cerevisiae* gene demonstrates many of the features of the GenBank flat file format.

#### Access to GenBank

There are several ways to search and retrieve data from GenBank.

- Search GenBank for sequence identifiers and annotations with [Entrez Nucleotide](#).
- Search and align GenBank sequences to a query sequence using [BLAST](#) (Basic Local Alignment Search Tool). See [BLAST info](#) for more information about the numerous BLAST databases.
- Search, link, and download sequences programmatically using [NCBI e-utils](#).
- The ASN.1 and flatfile formats are available at NCBI's anonymous FTP server: <ftp://ftp.ncbi.nlm.nih.gov/ncbi-asn1> and <ftp://ftp.ncbi.nlm.nih.gov/genbank>.

#### GenBank Data Usage

The GenBank database is designed to provide and encourage access within the scientific community to the most up-to-date and comprehensive DNA sequence information. Therefore, NCBI places no restrictions on the use or distribution of the GenBank data. However, some submitters may claim patent, copyright, or other intellectual property rights in all or a portion of the data they have submitted. NCBI is not in a position to assess the validity of such claims, and therefore cannot provide comment or unrestricted permission concerning the use, copying, or distribution of the information contained in GenBank.

#### GenBank Resources

- [GenBank Home](#)
- [Submission Types](#)
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- [Search GenBank](#)
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## GenBank

“GenBank is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences”



NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide Search Help

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GenBank Send to Change region shown Customize view

**Saccharomyces cerevisiae TCP1-beta gene, partial cds; and Axl2p (AXL2) and Rev7p (REV7) genes, complete cds**

GenBank: U49845.1  
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LOCUS SCU49845 5028 bp DNA linear PLN 29-OCT-2018  
 DEFINITION Saccharomyces cerevisiae TCP1-beta gene, partial cds; and Axl2p (AXL2) and Rev7p (REV7) genes, complete cds.  
 ACCESSION U49845  
 VERSION U49845.1  
 KEYWORDS .  
 SOURCE Saccharomyces cerevisiae (baker's yeast)  
 ORGANISM [Saccharomyces cerevisiae](#)  
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina;  
 Saccharomycetes; Saccharomycetales; Saccharomycetaceae;  
 Saccharomyces.  
 REFERENCE 1 (bases 1 to 5028)  
 AUTHORS Roemer,T., Madden,K., Chang,J. and Snyder,M.  
 TITLE Selection of axial growth sites in yeast requires Axl2p, a novel plasma membrane glycoprotein  
 JOURNAL Genes Dev. 10 (7), 777-793 (1996)  
 PUBMED [8846915](#)  
 REFERENCE 2 (bases 1 to 5028)  
 AUTHORS Roemer,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-FEB-1996) Biology, Yale University, New Haven, CT 06520, USA  
 FEATURES  
 source  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4932"  
 /chromosome="IX"  
 mRNA  
 <1..>206  
 /product="TCP1-beta"  
 CDS  
 <1..206  
 /codon\_start=3  
 /product="TCP1-beta"  
 /translation="M...AAAGGQGGK..."

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 PubMed  
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 Full text in PMC  
 PubMed (Weighted)

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 Dryad Digital Repository [Dryad Digital Repository]

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- GenBank identifier (U49845)
  - reference to article is important
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- [Saccharomyces cerevisiae 228 CU-2](#)
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- [Saccharomyces cerevisiae CBS 7833](#)
- [Saccharomyces cerevisiae CBS 7834](#)
- [Saccharomyces cerevisiae CBS 7835](#)
- [Saccharomyces cerevisiae CBS 7836](#)
- [Saccharomyces cerevisiae CBS 7837](#)
- [Saccharomyces cerevisiae CBS 7838](#)
- [Saccharomyces cerevisiae CBS 7839](#)
- [Saccharomyces cerevisiae CBS 7840](#)
- [Saccharomyces cerevisiae CBS 7960](#)
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- [Saccharomyces cerevisiae CBS 9564](#)
- [Saccharomyces cerevisiae CBS 9565](#)
- [Saccharomyces cerevisiae CEN.PK113-7D](#)
- [Saccharomyces cerevisiae CLIB215](#)
- [Saccharomyces cerevisiae CLIB324](#)
- [Saccharomyces cerevisiae CLIB382](#)
- [Saccharomyces cerevisiae EC1118](#)
- [Saccharomyces cerevisiae EC9-8](#)
- [Saccharomyces cerevisiae FL100](#)
- [Saccharomyces cerevisiae Fleischmanns baking yeast](#)
- [Saccharomyces cerevisiae FostersB](#)
- [Saccharomyces cerevisiae FostersO](#)

- ORGANISM from taxonomy  
→  
Saccharomyces  
cerevisiae

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LISGDDKILNGVYSQYEEGESIFGSLF"

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ORIGIN

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```

- data have specified, well known format

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3361 attttgcgt caccctgat taattttca ctaactgat gaatacaaa aggccccacg

```

- data have specified, well known format  
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Bhatt, Rohit Prasad; Kilinc, Jan; Höcker, Lilo; Jendrzejewski, Fred, 2021, "Stochastic dynamics of a few sodium atoms in presence of a cold potassium cloud [data]", <https://doi.org/10.11588/data/HRCXIP>, heiDATA, V2, UNIF:6.JJwDhUuVkoOTFoMlyqAw== [file:UNF]

We provide the data and our jupyter notebooks used to generate the figures of our publication. Abstract: Single particle resolution is a requirement for numerous experimental protocols that emulate the dynamics of small systems in a bath. Here, we accurately resolve through

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Conference Meet Me Tonight 2021  
Feb 25, 2022 - ITACA

Sacco, Daniela, 2022, "Conference Meet Me Tonight 2021", [https://doi.org/10.13130/RD\\_UNIMI/SMSEBK](https://doi.org/10.13130/RD_UNIMI/SMSEBK), UNIMI Dataverse, V1

Presentation of the project ITACA by Daniela Sacco at the Meet Me Tonight 2021. Faccia a faccia con la ricerca

Interview with Jocelyn Sioui  
Feb 25, 2022 - Interviews

Sacco, Daniela, 2022, "Interview with Jocelyn Sioui", [https://doi.org/10.13130/RD\\_UNIMI/EYLM1](https://doi.org/10.13130/RD_UNIMI/EYLM1), UNIMI Dataverse, V2

Interview with Jocelyn Sioui, Quebecois director, actor, puppeteer of native descent

Interview with Dave Jenniss  
Feb 25, 2022 - Interviews

Sacco, Daniela, 2022, "Interview with Dave Jenniss", [https://doi.org/10.13130/RD\\_UNIMI/98XAER](https://doi.org/10.13130/RD_UNIMI/98XAER), UNIMI Dataverse, V2

Interview with Dave Jenniss, director of Ondinnok theatre company

Interview with Isabelle Payant and Robine Kaseka  
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## Experimental Biophysics Dataverse (Heidelberg University - Kirchhoff-Institute for Physics)

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## SPDM data capturing radiation induced chromatin conformation changes

Hausmann, Michael; Müller, Patrick; Hillebrandt, Sabina; Bach, Margund; Kaufmann, Rainer; Zhang, Yang, 2015.  
"SPDM data capturing radiation induced chromatin conformation changes." doi:10.11588/data/10031. heiDATA  
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## Description

Using stably transfected HeLa cells expressing either green fluorescent protein (GFP) labelled histone H2B or yellow fluorescent protein (YFP) labelled histone H2A, we investigated the positioning of individual histone proteins in cell nuclei by means of high resolution localization microscopy (Spectral Position Determination Microscopy = SPDM). The cells were exposed to ionizing radiation of different doses and aliquots were fixed after different repair times for SPDM imaging. In addition to the repair dependent histone protein pattern, the positioning of antibodies specific for heterochromatin and euchromatin was recorded by SPDM.

Experimental data was acquired in the Experimental Biophysics group by Michael Hausmann, Patrick Müller, Sabina Hillebrandt, Margund Bach and Rainer Kaufmann.

Kernel Density Estimations of the experimental data and the maskings of the regions of interest based on the KDEs were calculated by Yang Zhang, a member of the Statistical Physics and Theoretical Biophysics Group.

## Related Publication

Zhang Y, Máté G, Müller P, Hillebrandt S, Krutczik M, et al. (2015) Radiation Induced Chromatin Conformation Changes Analysed by Fluorescent Localization Microscopy, Statistical Physics, and Graph Theory. PLoS ONE 10(6): e0128555. doi: 10.1371/journal.pone.0128555

## Dataset Version: 3.0

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### SPDM data capturing radiation induced chromatin conformation changes

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#### Description

Using stably transfected HeLa cells expressing either green fluorescent protein (GFP) labelled histone H2B or yellow fluorescent

**Radiation Induced Chromatin Conformation Changes Analysed by Fluorescent Localization Microscopy, Stati...**  
 Yang Zhang, Gabriell Máté, Patrick Müller, Sabina Hillebrandt, Matthias Krufczik, Margund Bach, Rainer Kaufmann,



#### Abstract

Introduction

Materials and Methods

Results

Discussion

Acknowledgments

Author Contributions

References

**Citation:** Zhang Y, Máté G, Müller P, Hillebrandt S, Krufczik M, Bach M, et al. (2015) Radiation Induced Chromatin Conformation Changes Analysed by Fluorescent Localization Microscopy, Statistical Physics, and Graph Theory. PLoS ONE 10(6): e0128555. doi:10.1371/journal.pone.0128555

**Academic Editor:** Martin Fernandez-Zapico, Schulze Center for Novel Therapeutics, Mayo Clinic, UNITED STATES

**Received:** October 18, 2014; **Accepted:** April 28, 2015; **Published:** June 4, 2015

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Reader Media Figures

**Data Availability:** The experimental data and the in-house developed software used for the analysis can be reached through the HeiDATA Dataverse Network, DOI:10.11588/data/10031.

Findability  
- DOI's

<b>Title</b> ⓘ	GECCA mapped
<b>Subtitle</b> ⓘ	Mapping Western Group Exhibitions of Contemporary Chinese Art after 1979
<b>Author</b> ⓘ	Franziska Koch (Heidelberg Centre for Transcultural Studies, Global Art History, Heidelberg University, Germany)
<b>Contact</b> ⓘ	Use email button above to contact.  Franziska Koch (Heidelberg Centre for Transcultural Studies, Global Art History, Heidelberg University, Germany)
<b>Description</b> ⓘ	<p>GECCA mapped is a pilot project that visualizes and provides geo-referential metadata of sixty exhibition entries collected in the larger GECCA data base (more than 700 entries). The exhibition sample is limited to Western, i.e. Western European and Northern American group exhibitions, and excludes bi-/ triennials. With the support of the HRA (Heidelberg Research Architecture), GECCA mapped allows the user to trace the exhibition sample implemented in Google Earth. The GECCA mapped logo indicates the place where a particular exhibition was staged and is scaled according to the number of participating artists. A click on the logo opens a pop-up window presenting more information on the exhibition. The Google Earth timeline enables the user to follow the exhibition development in any chosen geographical area in the period from 1982 (earliest exhibition entry) to 2009 (latest exhibition entry).</p> <p>Group Exhibitions of Contemporary Chinese Art (GECCA): The medium of (group and panoramic) exhibitions has played a fundamental role in creating a global context for Chinese art within and outside of the People's Republic after the end of the "Great Proletarian Cultural Revolution" (1966-1976) and since the political reforms initiated by Deng Xiaoping in 1978/79. In economic, discursive, aesthetic and institutional terms, the Western reception of these shows was very influential for the establishment of a certain international canon of artworks, artists and curators. This particular canon in fact came to be considered representative of the whole of Chinese artistic production, although it actually tends to exclude large parts of the overall artistic activity such as "national ink painting" (guohua), conventional or conservative academic oil painting, as well as those works involving political or consumption oriented subject matter, including mass-produced decorative and popular artworks.</p> <p>With 60 exhibitions entries, the data that GECCA mapped visualizes is a comparatively small sample of the database GECCA - which contains more than 700 exhibition entries. The data was individually researched and includes information on the location, institution, dates, exhibition topic, participating artists and curators. The sources for the data stem from exhibition catalogues, museum websites, archival documentation of public art libraries and other archives.</p> <p>A typical use of the kmz-file that visualizes GECCA mapped is Google Earth.</p>
<b>Subject</b> ⓘ	Arts and Humanities
<b>Keyword</b> ⓘ	<p>contemporary Chinese art group exhibitions North America (general region) (TGN) <a href="http://vocab.getty.edu/tn/7029440">http://vocab.getty.edu/tn/7029440</a> Europe (continent) (TGN) <a href="http://vocab.getty.edu/tn/1000003">http://vocab.getty.edu/tn/1000003</a> Australia (nation) (TGN) <a href="http://vocab.getty.edu/tn/7000490">http://vocab.getty.edu/tn/7000490</a> Art, Chinese--20th century--Exhibitions (LCSH) <a href="http://id.loc.gov/authorities/subjects/sh2007101410">http://id.loc.gov/authorities/subjects/sh2007101410</a> GECCA mapped Geographic information systems (LCSH) <a href="http://id.loc.gov/authorities/subjects/sh90001880">http://id.loc.gov/authorities/subjects/sh90001880</a> Digital mapping (LCSH) <a href="http://id.loc.gov/authorities/subjects/sh85037980">http://id.loc.gov/authorities/subjects/sh85037980</a></p>
<b>Related Publication</b> ⓘ	Koch, Franziska. 2016. „Die »chinesische Avantgarde« und das Dispositiv der Ausstellung: Konstruktionen chinesischer Gegenwartskunst im Spannungsfeld der Globalisierung". Bielefeld: transcript. isbn: 978-3-8376-2617-9 <a href="http://www.transcript-verlag.de/978-3-8376-2617-9/die-chinesische-avantgarde-und-das-dispositiv-der-ausstellung">http://www.transcript-verlag.de/978-3-8376-2617-9/die-chinesische-avantgarde-und-das-dispositiv-der-ausstellung</a>
<b>Language</b> ⓘ	Chinese; English

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<b>Title</b> ⓘ	GECCA mapped
<b>Subtitle</b> ⓘ	Mapping Western Group Exhibitions of Contemporary Chinese Art after 1979
<b>Author</b> ⓘ	Franziska Koch (Heidelberg Centre for Transcultural Studies, Global Art History, Heidelberg University, Germany)
<b>Contact</b> ⓘ	Use email button above to contact. Franziska Koch (Heidelberg Centre for Transcultural Studies, Global Art History, Heidelberg University, Germany)
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<b>Subject</b> ⓘ	Arts and Humanities
<b>Keyword</b> ⓘ	<p>contemporary Chinese art group exhibitions North America (general region) (TGN) <a href="http://vocab.getty.edu/tgn/7029">http://vocab.getty.edu/tgn/7029</a> Europe (continent) (TGN) <a href="http://vocab.getty.edu/tgn/1000003">http://vocab.getty.edu/tgn/1000003</a> Australia (nation) (TGN) <a href="http://vocab.getty.edu/tgn/7000490">http://vocab.getty.edu/tgn/7000490</a> Art, Chinese--20th century--Exhibitions (LCSH) <a href="http://id.loc.gov/author/GECCA%20mapped">http://id.loc.gov/author/GECCA mapped</a> Geographic information systems (LCSH) <a href="http://id.loc.gov/authorities/subjects/sh90001880">http://id.loc.gov/authorities/subjects/sh90001880</a> Digital mapping (LCSH) <a href="http://id.loc.gov/authorities/subjects/sh85037980">http://id.loc.gov/authorities/subjects/sh85037980</a></p>
<b>Related Publication</b> ⓘ	Koch, Franziska. 2016. „Die »chinesische Avantgarde« und das Dispositiv der Ausstellung: Konstruktionen chinesischer Gegenwartskunst im Spannungsfeld der Globalisierung". Bielefeld: transcript. isbn: 978-3-8376-2617-9 <a href="http://www.transcript-verlag.de/978-3-8376-2617-9/die-chinesische-avantgarde-und-das-dispositiv-der-ausstellung">http://www.transcript-verlag.de/978-3-8376-2617-9/die-chinesische-avantgarde-und-das-dispositiv-der-ausstellung</a>
<b>Language</b> ⓘ	Chinese; English

## Findability

- DOI's
- Metadata

### Life Sciences Metadata

<b>Design Type</b> ⓘ	Not Specified
<b>Factor Type</b> ⓘ	Cell Type/Cell Line; Developmental Stage; Organism
<b>Organism</b> ⓘ	Homo sapiens; Mus musculus
<b>Other Organism</b> ⓘ	Monodelphis domestica
<b>Measurement Type</b> ⓘ	transcription profiling
<b>Technology Type</b> ⓘ	nucleotide sequencing
<b>Other Technology Type</b> ⓘ	single nucleus RNA-seq
<b>Technology Platform</b> ⓘ	Illumina
<b>Other Technology Platform</b> ⓘ	10x Chromium 3' protocol

Beliebige Zeit  
Seit 2022  
Seit 2021  
Seit 2018  
Zeitraum wählen...

Nach Relevanz sortieren  
Nach Datum sortieren

Beliebige Sprache  
Seiten auf Deutsch

Alle Typen  
Übersichtsarbeiten

Patente

[Peer Reviewed: Current Knowledge on Correlations Between Highly Prevalent Dental Conditions and Chronic Diseases. An Umbrella Review](#) [HTML] nih.gov  
 MW Seitz, S Listl, A Bartols, L Schubert... - ... chronic disease, 2019 - ncbi.nlm.nih.gov  
 ... We provide an overview of systematic reviews reporting on correlations between dental conditions and chronic diseases with an assessment of the evidence and extent of correlation ...  
 ☆ Speichern 90 Zitieren Zitiert von: 52 Ähnliche Artikel Alle 14 Versionen Web of Science: 27 88

[Current knowledge on correlations between highly prevalent dental conditions and chronic diseases: an umbrella review](#) [HTML] uni-heidelberg.de  
 MW Seitz, S Listl, A Bartols, L Schubert, K Blaschke... - 2019 heidata.uni-heidelberg.de  
 ... correlations with a dental condition was diabetes mellitus type 2, most common chronic disease correlations were ... type 2 and periodontitis and cardiovascular disease. Freque  
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Dataset Communities

### Understanding Bank-Run Contagion [Dataset]



We study experimental coordination games to examine through which transmission channels, and under which information conditions, a panic-based depositor-run at one bank may trigger a panic-based depositor-run at another bank. We find that withdrawals at one bank trigger withdrawals at another bank by increasing players' beliefs that other depositors in their own bank will withdraw, making them more likely to withdraw as well. Observed withdrawals only affect depositors' beliefs, and are thus contagious, when they form an informative signal about bank fundamentals.

Bank runs Contagion Social Sciences Systemic risk

#### Identifier

DOI

Related Identifier

Metadata Access

<https://doi.org/10.11588/data/10074>

<https://doi.org/10.1287/mnsc.2015.2416>

[https://heidata.uni-heidelberg.de/oa/?verb=GetRecord&metadataPrefix=oai\\_datacite&identifier=doi:10.11588/data/10074](https://heidata.uni-heidelberg.de/oa/?verb=GetRecord&metadataPrefix=oai_datacite&identifier=doi:10.11588/data/10074)

## Findability

- DOI's
- Metadata
- Indexing in catalogs and databases (enabling automatic harvesting of metadata)

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#### Understanding Bank-Run Contagion [Dataset]

Trautmann, Stefan; Brown, Martin; Vlahu, Razvan

Date:  
2016-05-03

#### Description:

We study experimental coordination games to examine through which transmission channels, and under which information conditions, a panic-based depositor-run at one bank may trigger a panic-based depositor-run at another bank. We find that withdrawals at one bank trigger withdrawals at another bank by increasing players' beliefs that other depositors in their own bank will withdraw, making them more likely to withdraw as well. Observed withdrawals only affect depositors' beliefs, and are thus contagious, when they form an informative signal about bank fundamentals.

Subject:

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	<b>00_xml_files_overview.tab</b> 0000_README/ Tabular Data - 12.1 KB Published Oct 26, 2020 4 Downloads 4 Variables, 112 Observations UNF:6:X76d...vpg== Overview of the XML-Documents Documentation CSV	
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<https://heidata.uni-heidelberg.de/privateurl.xhtml?token=ffb013cb-25ae-46f0-904d-381190a8ca13>

## Test Dataset

Draft

Unpublished



Apel, Jochen, 2022, "Test Dataset", <https://doi.org/10.11588/data/CKSXU7>, heiDATA, DRAFT VERSION 

Cite Dataset ▾

[Learn about Data Citation Standards.](#)

### Accessibility

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- “As open as possible, but as closed as necessary”
- **Private URLs for pre-publication access (e.g. for reviewers)**

## Interoperability

- **Metadata standards**

### Metadata References

The Dataverse Project is committed to using standard-compliant metadata to ensure that a Dataverse installation's metadata can be mapped easily to standard metadata schemas and be exported into JSON format (XML for tabular file metadata) for preservation and interoperability.

Detailed below are what metadata schemas we support for Citation and Domain Specific Metadata in the Dataverse Project:

- **Citation Metadata:** compliant with [DDI Lite](#), [DDI 2.5 Codebook](#), [DataCite 3.1](#), and Dublin Core's [DCMI Metadata Terms](#) (see [.tsv version](#)). Language field uses [ISO 639-1](#) controlled vocabulary.
- **Geospatial Metadata:** compliant with [DDI Lite](#), [DDI 2.5 Codebook](#), [DataCite](#), and Dublin Core (see [.tsv version](#)). Country / Nation field uses [ISO 3166-1](#) controlled vocabulary.
- **Social Science & Humanities Metadata:** compliant with [DDI Lite](#), [DDI 2.5 Codebook](#), and Dublin Core (see [.tsv version](#)).
- **Astronomy and Astrophysics Metadata :** These metadata elements can be mapped/exported to the International Virtual Observatory Alliance's (IVOA) [VOResource Schema format](#) and is based on [Virtual Observatory \(VO\) Discovery and Provenance Metadata](#) (see [.tsv version](#)).
- **Life Sciences Metadata:** based on [ISA-Tab Specification](#), along with controlled vocabulary from subsets of the [OBI Ontology](#) and the [NCBI Taxonomy for Organisms](#) (see [.tsv version](#)).
- **Journal Metadata:** based on the [Journal Archiving and Interchange Tag Set, version 1.2](#) (see [.tsv version](#)).

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## Interoperability

- Metadata standards
- **Advice on suitable file formats, support with format conversion**
- **Technical validity checks**

## Re-Usability


- Open content licenses

Files Metadata Terms Versions

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No waiver has been selected for this dataset.

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<input type="checkbox"/>	2.0	<b>Citation Metadata:</b> Description (1 Changed); Author (1 Changed); Related Publication (2 Added, 2 Changed); <b>Additional Citation Metadata:</b> (2 Added, 2 Changed); <b>Files (Added: 2; Removed: 2);</b> <a href="#">View Details</a>	Leonhard Maylein, Jochen Apel	Mar 26, 2021
<input type="checkbox"/>	1.2	<b>Citation Metadata:</b> Description (1 Changed); <a href="#">View Details</a>	Jochen Apel	Jun 7, 2019
<input type="checkbox"/>	1.1	<b>Additional Citation Metadata:</b> (1 Added); <a href="#">View Details</a>	Jochen Apel	Jun 6, 2019
<input type="checkbox"/>	1.0	This is the first published version.	Leonhard Maylein, Hubert Mara, Jochen Apel	Jun 6, 2019

## Re-Usability

- Open content licenses
- **Transparent versioning**

<b>Producer</b> ?	Hubert Mara (IWR, Heidelberg University) (HMara) <a href="https://orcid.org/0000-0002-2004-4153">https://orcid.org/0000-0002-2004-4153</a> Bartosz Bogacz (IWR, Heidelberg University) (BBogacz) <a href="https://orcid.org/0000-0002-2004-4153">https://orcid.org/0000-0002-2004-4153</a>
<b>Production Date</b> ?	2019-03-11
<b>Production Place</b> ?	Heidelberg, Germany
<b>Contributor</b> ?	Project Member : Bayer, Paul Victor
<b>Deposit Date</b> ?	2019-02-25
<b>Date of Collection</b> ?	Start: 2018-07-24 ; End: 2018-08-22 Start: 2019-03-01 ; End: 2019-03-11
<b>Kind of Data</b> ?	Cuneiform tablets; 3D Measurement data
<b>Software</b> ?	GigaMesh Software Framework, Version: 181100 to 190300
<b>Related Datasets</b> ?	Heidelberg Cuneiform 3D Database (HeiCu3Da) for the Hilprecht Collection: <a href="https://doi.org/10.11588/heidicon.hilprecht">https://doi.org/10.11588/heidicon.hilprecht</a>
<b>Origin of Sources</b> ?	Hilprecht Sammlung, Jena, Germany, <a href="https://hilprecht.mpiwg-berlin.mpg.de/">https://hilprecht.mpiwg-berlin.mpg.de/</a> Cuneiform Digital Library Initiative (CDLI) <a href="https://cdli.ucla.edu/">https://cdli.ucla.edu/</a>

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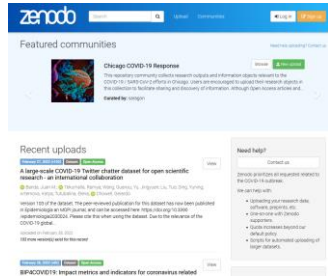
RData

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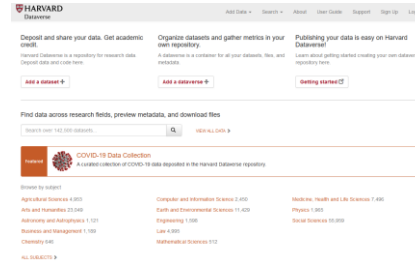
# Generic repositories



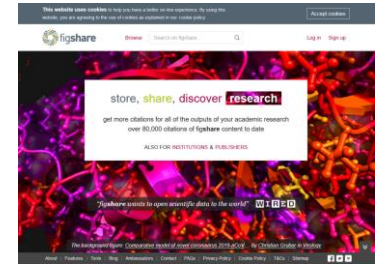
<https://zenodo.org/>



<https://osf.io/>



<https://dataverse.harvard.edu/>



<https://figshare.com/>

- Providing suitable technology for FAIR Data, partly even very elaborate functionality
- No or only basic domain-specific functionalities
- Only basic individual counselling
- Non-commercial and commercial providers

## **Wrap up**

Managing data properly allows for reuse - by you or your community!

Managing data costs less than not managing it!

Manage data from the beginning of your research!

Manage data according to FAIR principles!

Use trustworthy data repositories!

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# Thank you!

Jochen APEL  
Paola GALIMBERTI  
Milan JANÍČEK

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