



Scleractinian Connectivity, integrating modelling and genetics approaches

Alan Fox, Sophie Arnaud-Haond, Joana Boavida,
Ronan Becheler, José Manuel González-Irusta, Oscar Gaggiotti,
Stefan Gary, Arne Biastoch



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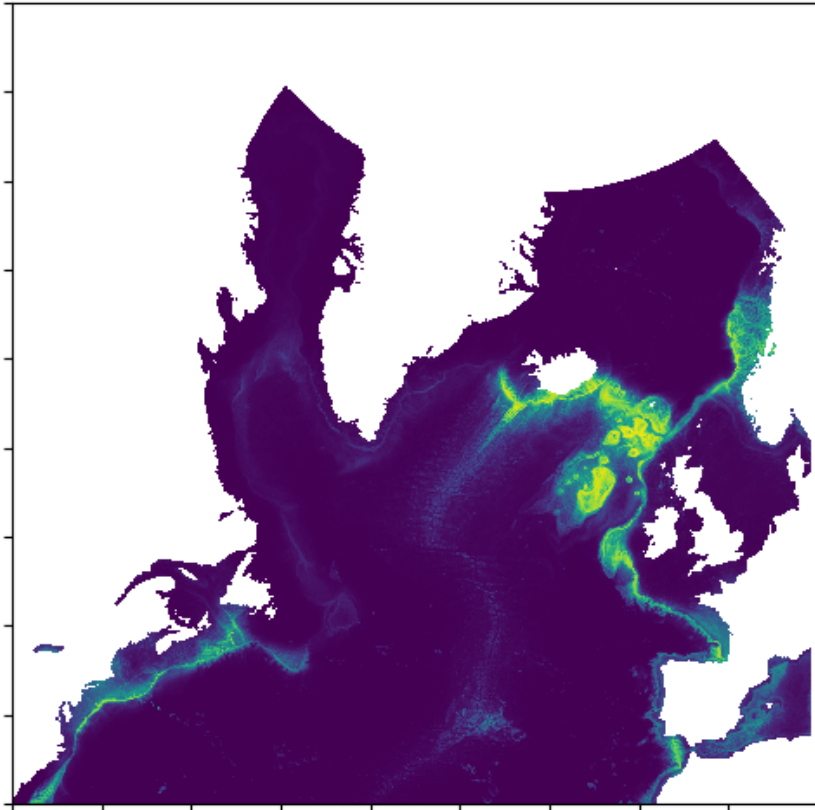
Modelling connectivity - requirements

- Where are the populations?
 - Observations and species distribution/habitat suitability modelling
- Life history traits – including larval behaviour
 - *Lophelia pertusa* (*Viminella flagellum*, *Cidaris cidaris* ??)
- Hydrodynamic model + larval tracking model
- Ground truth. Connectivity observations.
 - Genetics, biochemical tracers (otolith/vertebrae chemistry, ...)

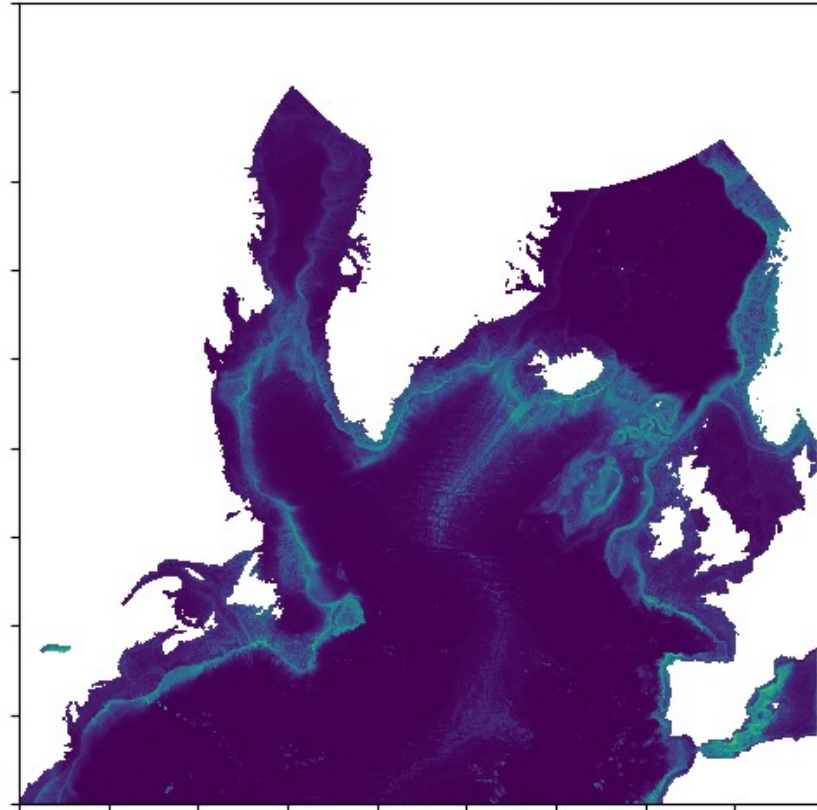
Lophelia pertusa – where are the populations

José Manuel González-Irusta

Habitat Suitability Index, present day



Habitat Suitability Index, future



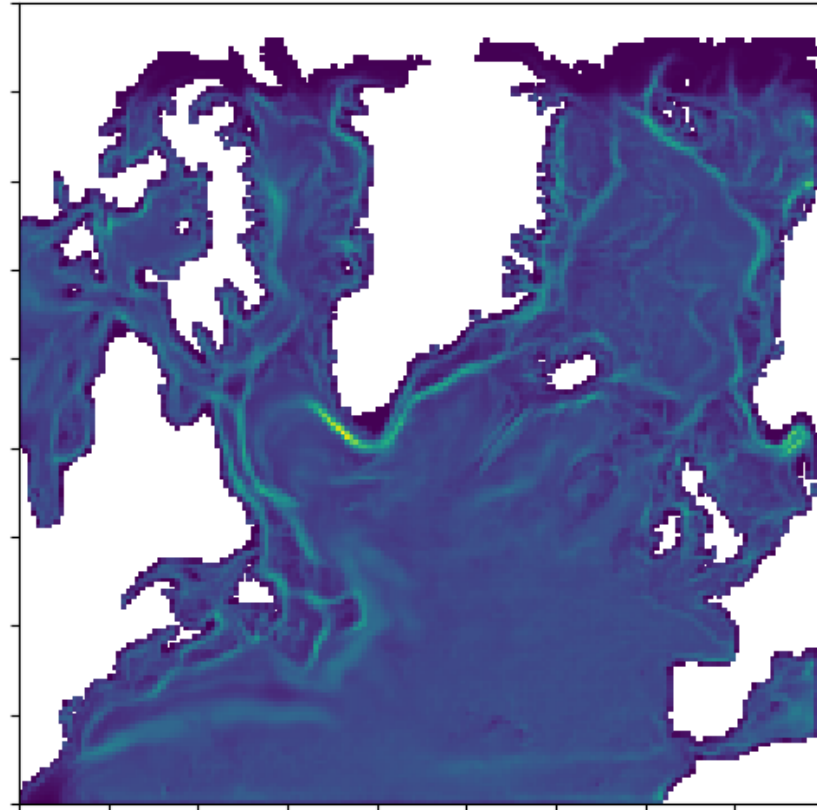
Lophelia pertusa – modelling, connectivity matrix

2 month maximum lifespan. Surface, near-bed, mid-column drifting

Connectivity. Sources.



Connectivity. Sinks.



Connectivity – source and sink weighting by habitat suitability index (HSI)

- Multiply each matrix row (all links from each source) by the HSI.

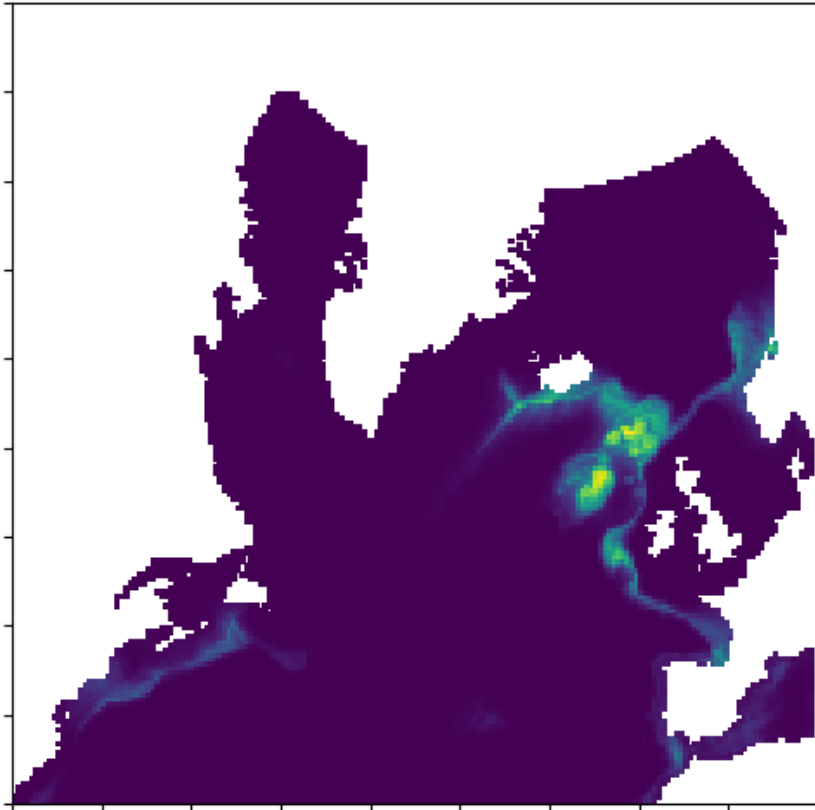
Better habitat → increased fecundity, more larvae produced

- Multiply each matrix column (all links into each target) by the HSI.

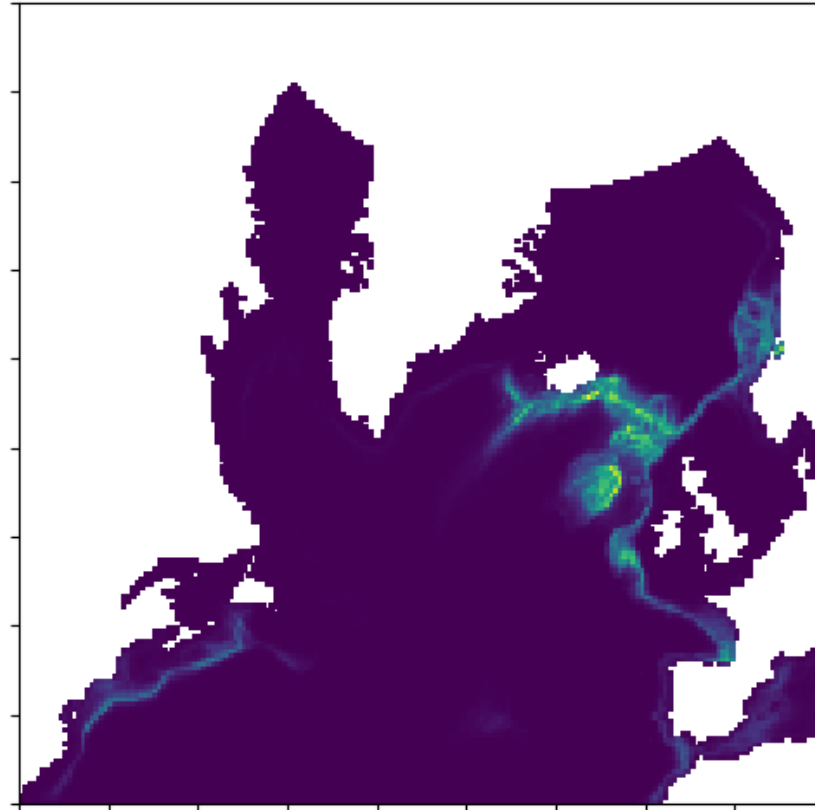
Better habitat → increased settlement success

Lophelia pertusa – Out-degree and in-degree, present
2 month maximum lifespan. Surface, near-bed, mid-column drifting

Connectivity. *Lophelia*. Source & sink weighted. Sources.

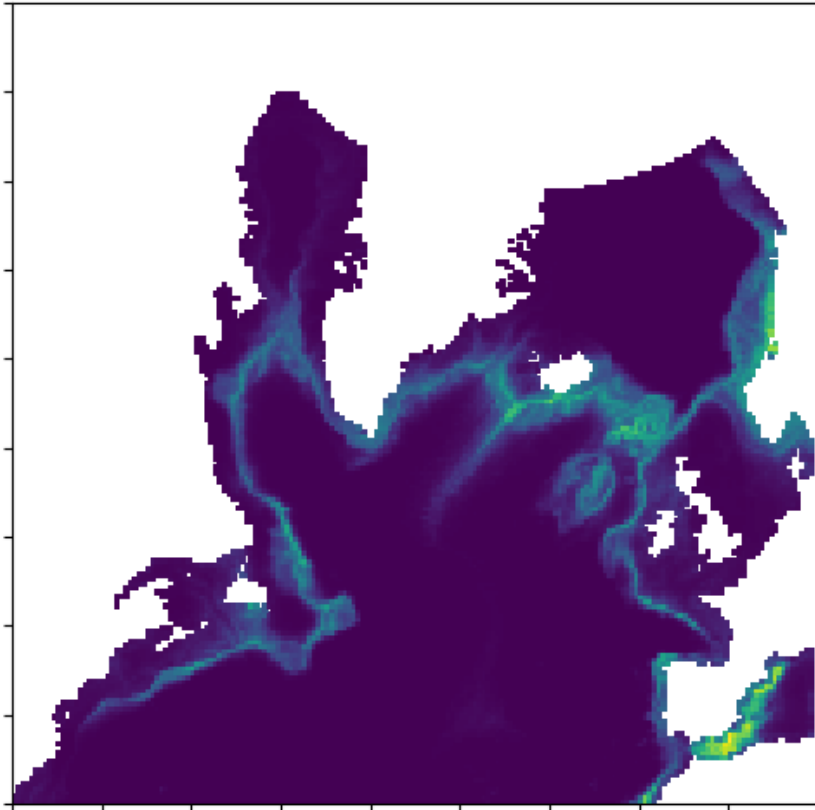


Connectivity. Source & sink weighted. Sinks.

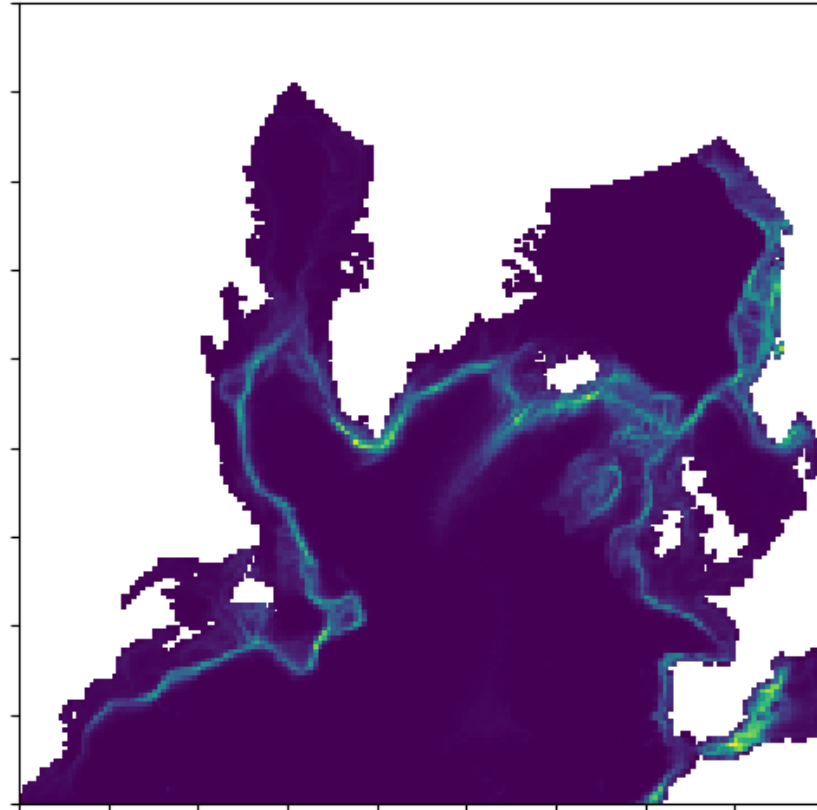


Lophelia pertusa – out-degree and in-degree, future
2 month maximum lifespan. Surface, near-bed, mid-column drifting

Connectivity. Lophelia. Source & sink weighted. Sources. Future.

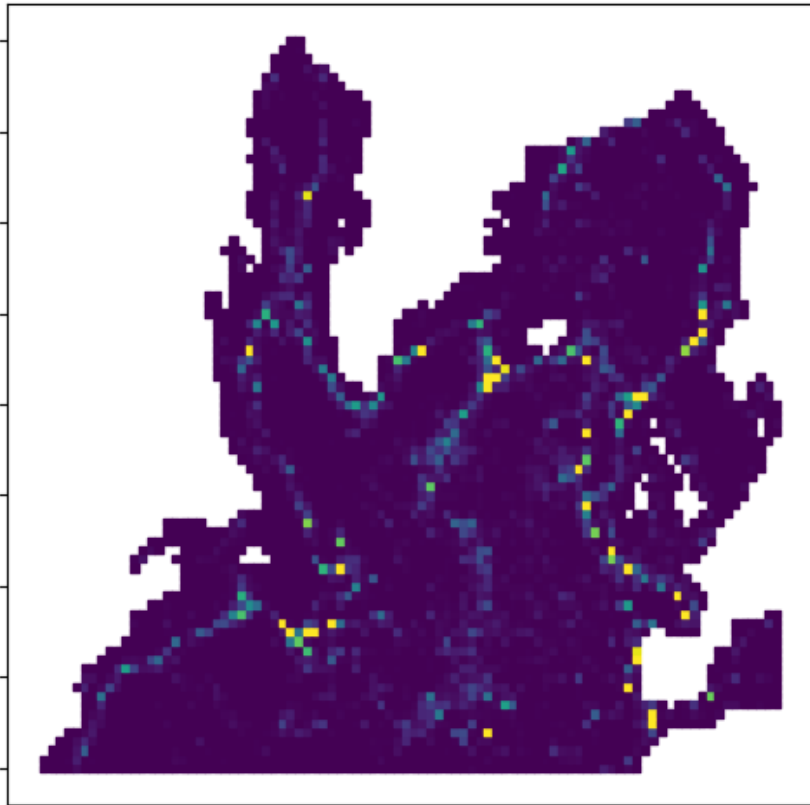


Connectivity. Source & sink weighted. Sinks. Future.



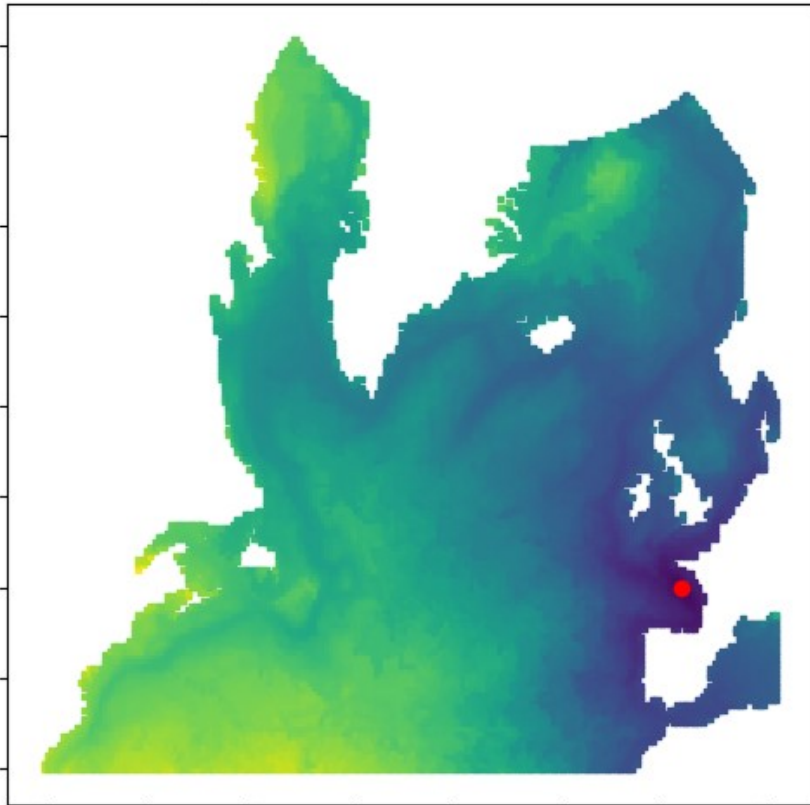
Lophelia pertusa – betweenness, present
2 month maximum lifespan. Surface, near-bed, mid-column drifting

Connectivity. Lophelia. Weighted betweenness.

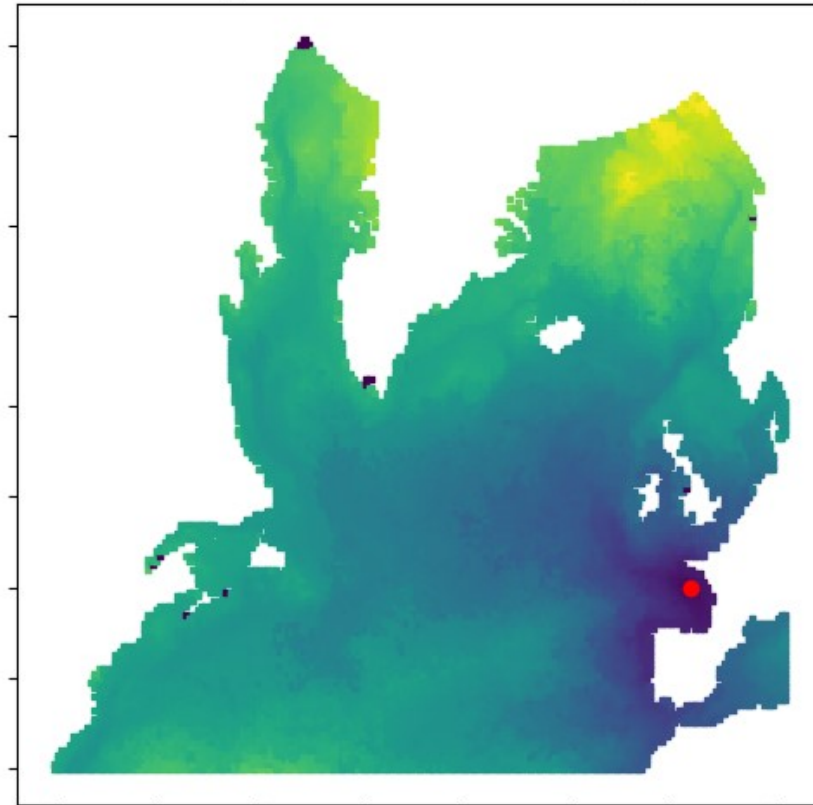


Lophelia pertusa – multigenerational spreading

Multigenerational distance from source.



Multigenerational distance to target.



Genetic Connectivity

Sampling
>200 samples
High latitudes
Mid Atl Ridge
Mediterranean
ITS, 7-8 msats
RAD-seq (being produced)

Iceland

Rockall bank

Bay of Biscay

Ionian Sea

W Med

Mid Atl Ridge

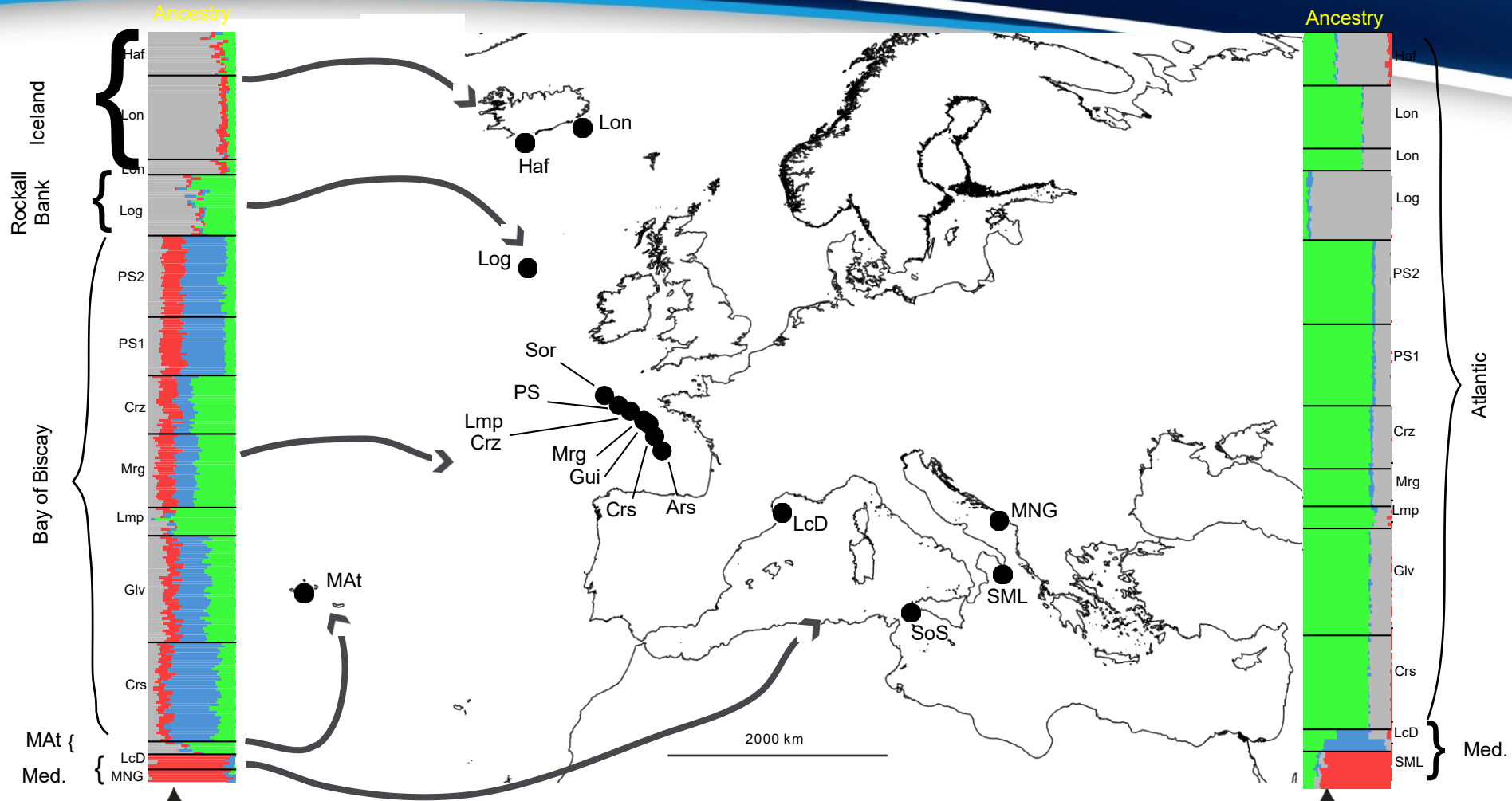
Bay of Cadiz



Madrepora oculata

Bayesian clustering, K=4, microsatellites

Lophelia pertusa



Restricted gene-flow Med-Atl
Higher gene-flow East-West Med
Azo-Lmp-Log similar ancestry, gene-flow?
Higher No. private alleles (west) Med.

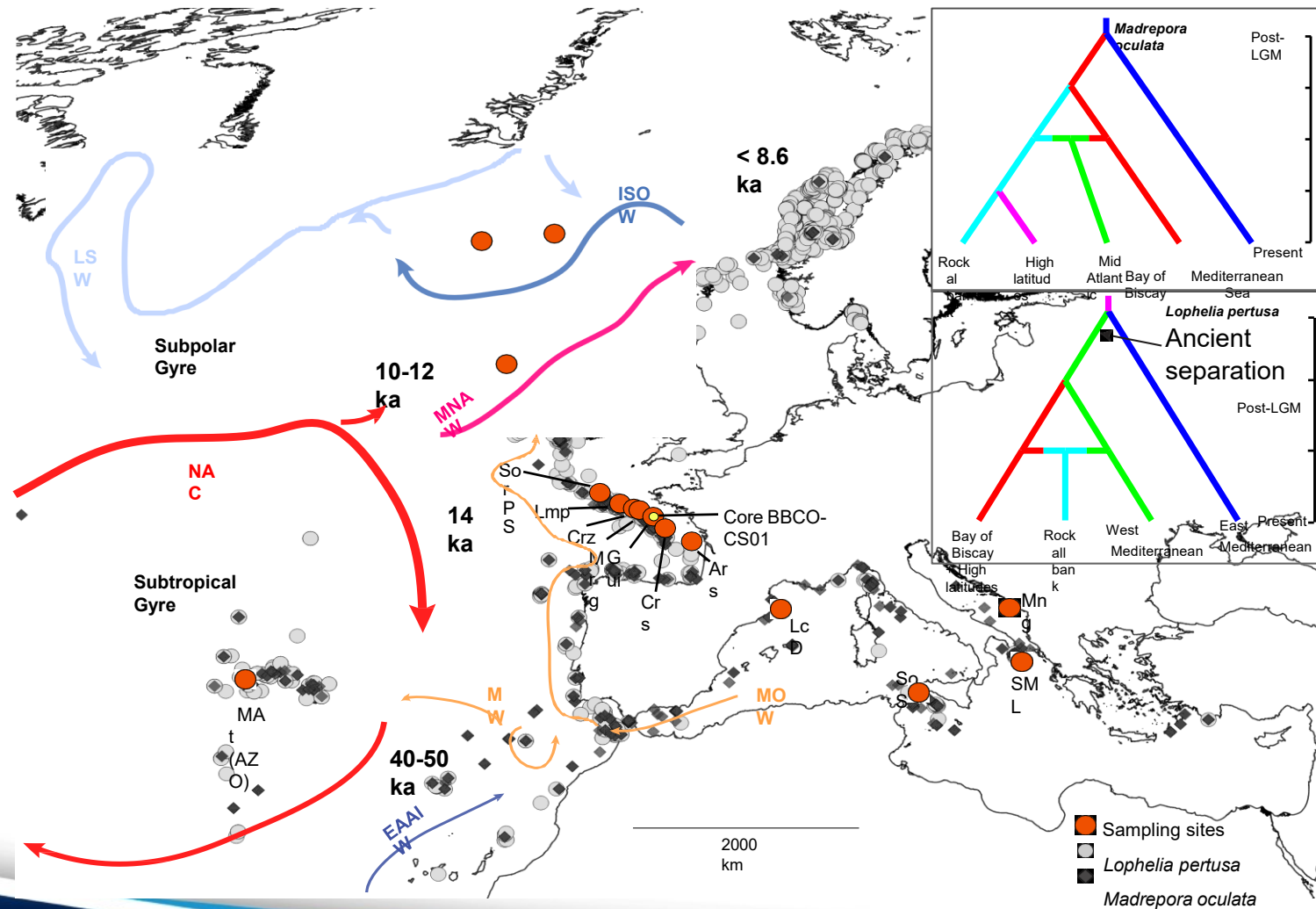
Restricted gene-flow East-West Med, Med-Atl, Log
Higher gene-flow in Atlantic
High No. private alleles everywhere



atlas

Reconstructing past scenarios

(Approximate Bayesian Computation ITS+msats)



Boavida et al., J. of Biogeography

Bayesian Approaches for Combining Genetic **Data** and **Output** of Biophysical models to Estimate Connectivity

Oscar E. Gaggiotti

Scottish Oceans Institute

School of Biology



University of
St Andrews | FOUNDED
1413 |



Stating the Obvious

- “Population” Connectivity is a fundamental ecological process but is very difficult to measure
- Lots of methods, the most popular are:
 - Molecular markers: the genotype of an individual is determined by the genetic composition of the population where it was born
 - Geochemical signatures: composition of calcified tissue depends on the seawater properties of habitat where individuals spawn and develop
 - Larval Transport models: ocean circulation & life history help us predict the movement of individuals across the “seascape”
- Let’s combine them!

But what do we mean by combining them??

- ❑ Should we calculate the **correlation** between estimates obtained by different methods?
- ❑ Should we incorporate a “genetic module” in Lagrangian particle tracking models?
- ❑ Should we use methods that allow us to **jointly** analyse genetic data and output of Lagrangian particle tracking models?

Look before you leap!

- ❑ Combining several methods to estimate connectivity is potentially useful but not straightforward
- ❑ Methods that quantify connectivity make specific assumptions about
 - dispersing life stage
 - time scale
- ❑ Different methods may measure **different** “types” of connectivity
- ❑ Combining them may backfire: increase in the uncertainty and bias of connectivity estimates

What do we want to measure?

- Broad definition of Connectivity: *the exchange of individuals among local populations (subpopulations)*
- It can cover many different aspects including physical transport, demographic exchanges, and gene flow – we need to be more precise

Type of Connectivity	Underlying process
Demographic	Between-subpopulation dispersal of individuals that survive until completion of the settlement process
Genetic or Reproductive	Between-subpopulation dispersal of individuals that survive to reproduce
Oceanographic	Between-subpopulation dispersal of individuals (or larvae) due to physical transport and life history attributes – neither settlement nor reproduction is assumed

More Caveats

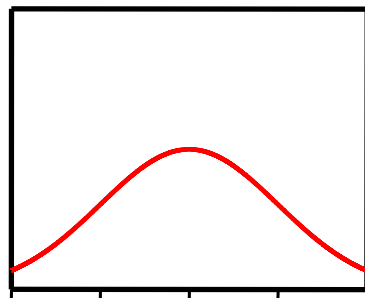
- ❑ In principle, differences in underlying processes can be incorporated in **model-based statistical methods**
- ❑ But what about time scale?
- ❑ The time scale of connectivity estimates obtained from genetic data depends on the type of data we use and the particular statistical method we apply

Combining different types of methods

Bayesian approaches allow us to combine different types of data (genetic, demographic, environmental, etc.)

They allow us to choose between alternative models to identify the factors responsible for observed patterns

Prior Distribution

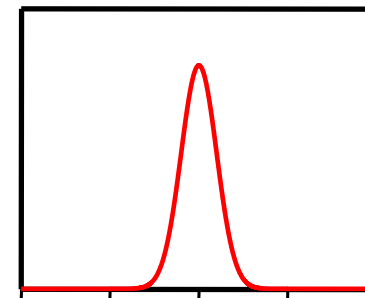


Non-genetic data

Likelihood

\times **G** \rightarrow

Posterior Distribution



Genetic data

Combining different approaches

Three existing alternatives:

- ❑ GESTE (Foll & Gaggiotti 2006) – Genetic Differentiation:
 - Prior based on closeness/centrality measures
 - Evolutionary time
- ❑ BIMr (Faubet & Gaggiotti 2008) – Population Assignment:
 - Prior based on oceanographic connectivity predictions
 - Ecological time – last two generations
- ❑ AllDAssign (Gaggiotti & Anjou in prep) – Microchemistry + Genetic Population Assignment:
 - Prior based on oceanographic connectivity
 - Ecological time – last reproductive period