

Marine population connectivity: bridging genetics and oceanography

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Key words:	Connectivity, dispersal, oceanography, genetics, coral, model
Research theme(s):	• Oceanography, Climate and Palaeoenvironment • Palaeobiology and Evolution
Eligible courses for this project:	• DPhil in Earth Sciences (3-4 years) • Interdisciplinary Life and Environmental Science Landscape Award (ILES�A) • Intelligent Earth (UKRI CDT)

Overview

Larval dispersal through ocean currents plays a key role in setting the *connectivity* of marine populations, particularly for non-migratory species. By determining the flow of individuals and genes between populations, larval dispersal is central to the ecology and evolution of marine life, driving population dynamics, setting population structure and biogeography, influencing ecological resilience, and implementing effective marine management (Cowen and Sponaugle, 2009).

While there are therefore many reasons to want to quantify marine population connectivity, in practice it is very difficult to measure as most larvae are too small to track directly. Two common alternatives are *population genetics* and *larval dispersal (oceanographic) modelling*. Genetic data allow us to infer historical population connectivity based on genetic differentiation between populations (e.g. Lowe and Allendorf, 2010) whereas larval dispersal models are used to simulate the movement of virtual larvae, predicting their movement based on ocean currents and/or larval behaviour (e.g. Cowen et al., 2000).

These approaches are in principle complementary, yet larval dispersal models are often weak at predicting genetic connectivity. Many explanations have been suggested (e.g. Jahnke and Jonsson, 2022) including inaccurate larval dispersal models, historical patterns of connectivity (changing over climate/geological timescales) that differ from the present, and inadequate methods of comparing modelled and genetic connectivity estimates. Another possibility is the effect of turbulent ocean currents that introduce short-term randomness to larval dispersal (fig. 1). It has been hypothesised that this short-term randomising effect of ocean currents may be large enough to fundamentally limit the

predictability of larval dispersal, even over longer timescales (Vogt-Vincent et al., 2023). This could explain the consistently poor performance of larval dispersal models in reproducing historical connectivity from population genetics but would also imply that population genetics provides only limited information about future connectivity. At present, this hypothesis is largely untested.

The goals of this DPhil project are to investigate (1) whether randomness in ocean currents at sub-climate timescales limits our ability to predict population genetic structure, and (2) what population genetics can tell us about future connectivity.

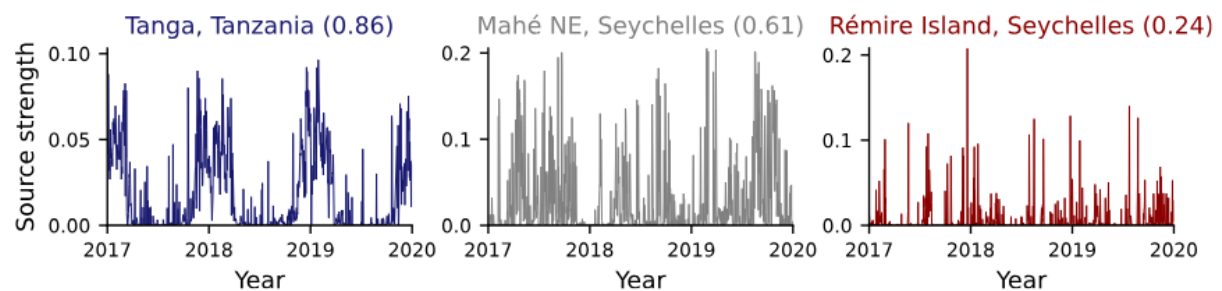


Figure 1: Simulated connectivity time-series from a larval dispersal model. At some locations (e.g. Tanga) connectivity is relatively predictable, whereas at other locations (e.g. Remiré) it is almost entirely random. Figure from Vogt-Vincent et al., 2023.

Methodology

For this project, you will first develop a population genetic model to directly compare simulated connectivity (from a larval dispersal model) to genetic data (fig. 2). This population genetic model will be designed to be flexible and user-friendly, to be useful for connectivity scientists beyond the scope of the project. You will then use your population genetic model in combination with oceanographic and genetic data to rigorously quantify uncertainty in both (larval dispersal model and genetic) estimates of connectivity, and will test whether this uncertainty can explain model-genetic mismatch in past research. For larval dispersal model uncertainty, we will focus on the uncertainty introduced by turbulence in ocean currents, but a broader consideration of larval dispersal model uncertainty may also be possible depending on student interests. Finally, you will use your population genetic model to investigate to what extent historical connectivity (from population genetics) can predict future connectivity, and any dependence on spatio-temporal scale and/or oceanographic and ecological context.



Figure 2: Comparing larval dispersal models to genetic data.

Timeline

Year 1: Training and rotation projects (ILES/Intelligent Earth).

Years 2 and 3: Developing and publishing the population genetic model, comparing connectivity inferred from genetics and larval dispersal models, and investigating to what extent population genetics can constrain future connectivity patterns.

Year 4: Completing investigation into connectivity predictability, thesis write-up and papers.

Training & Skills

The student will be provided training as required in population genetics, oceanography, and computational methods (e.g. SLiM, dispersal modelling). You will develop interdisciplinary quantitative skills spanning ecology, evolution, and oceanography. The project would best suit a student with a background in population genetics, otherwise a strong quantitative background would be useful.

References & Further Reading

Cowen, R.K. (2000). Connectivity of Marine Populations: Open or Closed? *Science*, 287(5454), pp.857–859. doi:10.1126/science.287.5454.857.

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Further Information

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