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## **Focusing regional marine conservation: merging seascape genetics and biophysical modeling within a graph-theoretic framework *and* Coral reef connectivity & conservation: an empirical and theoretical synthesis**

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**Project Description:** Marine population connectivity, via larval dispersal, is critical for population persistence and is a key factor influencing how a species might cope with global climate change. However, identifying the patterns in marine population connectivity poses one of the greatest challenges in marine ecology. Although several studies in population genetics have discovered a general scale of population connectivity, little progress has been made in identifying the spatial structure of this connectivity. The objectives of this research are to:



- 1) Identify the probable dispersal routes and spatial population structure for several marine species throughout the biodiversity hotspots of the Coral Triangle.
- 2) Develop new graph-theoretic and metapopulation approaches for quantifying marine connectivity and network resilience.
- 3) Integrate these connectivity estimates into marine conservation planning.

Exploiting new techniques in population genetics, biophysical modeling, and graph theory, this work tests the hypothesis that the spatial structure of marine populations is determined by the location and strength of connectivity. Dispersal probabilities will be derived for multiple species throughout the Coral Triangle using a spatially-explicit biophysical modeling approach. These probabilities will incorporate high-resolution hydrodynamics, pelagic larval duration, larval behavior, mortality, and settlement probability.

The resultant spatial structure, including persistent dispersal corridors and barriers, will be uncovered using clustering and connectivity algorithms from graph theory. Independent estimates of population connectivity will be made using mitochondrial DNA sequences from 8 - 10 coral reef species collected at 10 - 15 locations throughout the study area. Population subdivision and gene flow will be estimated using both classic and coalescent population genetic methods. The correlation between the biophysical connectivity predictions and the observed population genetic structure will be tested. Finally, the spatial structure of the marine population connectivity will be integrated into siting algorithms for the design of marine reserve networks.

### **Recent publications:**

- Bode, M., K. Burrage, and H. P. Possingham. 2008. Using complex network metrics to predict the persistence of metapopulations with asymmetric connectivity patterns. *Ecological Modelling* 214:201-209.
- Tremi, E., P. Halpin, D. Urban, and L. Pratson. 2008. Modeling population connectivity by ocean currents, a graph-theoretic approach for marine conservation. *Landscape Ecology* 23:19-36.
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