Hawaiian reef names for larval dispersal model

Website: https://www.bco-dmo.org/dataset/665742
Data Type: model results
Version:
Version Date: 2016-11-21

Project
» Multispecies connectivity: Comparative analysis of marine connectivity and its drivers for the coral reefs of Hawaii (Multispecies Connectivity)

Contributors	Affiliation	Role
Toonen, Robert J.	University of Hawaiʻi at Mānoa (HIMB)	Principal Investigator
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Dataset Description

You may access the data via the 'Map It' button at the top of this page or download the zipped files: HawaiiConnectivityFiles.zip (10 MB).

Related Datasets:
Larval Dispersal Model: raw output
Larval Dispersal Model: reef locations

Related References:

Polovina JJ, Kleiber P, Kobayashi DR (1999) Application of TOPEX-POSEIDON satellite altimetry to simulate transport dynamics of larvae of spiny lobster, Panulirus marginatus, in the Northwestern Hawaiian Islands, 1993-1996. Fish Bull 97:132–143

Wren JLK, Kobayashi DR (2016) Exploration of the "larval pool": development and ground-truthing of a larval transport model off leeward Hawaiʻi. PeerJ 4:e1636

Detailed description of the methods: Wren, J.L.K., Kobayashi, D.R., Jia, Y. and Toonen R.J. (in revision) Modeled population connectivity in the Hawaiian Islands. PLoS ONE.

Methods & Sampling

These data are output from a Lagrangian bio-physical particle tracking model coupled with the flow fields from the MITgcm simulation for the Hawaiian Archipelago (175°E to 150°W and from 15°N to 35°N at a 0.04° resolution). In the model, larvae are moved at each timestep by advective displacement caused by water flow combined with a random displacement caused by diffusion. Current velocities used by the model consist of daily snapshots of u (east) and v (north) velocities obtained from a regional implementation the MITgcm model.

Eddy diffusivity was set to 250 m2/sec, consistent with drifters in Hawaiian waters. We released 50 particles daily from May 2, 2009, until April 10, 2014, from 687 coral reef habitat pixels representing of all emergent land in the model domain, totaling just over 62 million released particles for each model run. We used a pelagic larval duration (PLD) of 45 days and for a particle to be considered "settled", it had to be within a 5 km radius of the center of a habitat pixel on the last day of its PLD. See Polovina et al. 1999 for a description of the model, and Wren and Kobayashi 2016 for modifications done to the model.

Data Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions

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Data Files

File
reef_names.csv(Comma Separated Values (.csv), 577 bytes) MD5:f098815f11d65b3897edde4476013544 Primary data file for dataset ID 665742

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Parameters

Parameter	Description	Units
reef_location_name	name of habitat site	unitless
name_code	code number for habitat site	unitless

[ ]

Deployments

Toonen_model

Website	https://www.bco-dmo.org/deployment/665735
Platform	Hawaii_reef
Start Date	2013-03-01
End Date	2016-11-15
Description	Modelling studies on Hawaiian reefs

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Project Information

Multispecies connectivity: Comparative analysis of marine connectivity and its drivers for the

coral reefs of Hawaii (Multispecies Connectivity)

Coverage: Hawaiian Archipelago (approx. 154 deg 40' to 178 deg 25' W longitude and 18 deg 54' to 28 deg 15' N latitude)

Description from NSF award abstract:
The exchange of individuals among populations, termed connectivity, is a central element of population persistence and maintenance of genetic diversity, and influences most ecological and evolutionary processes. To date, field studies of marine connectivity have necessarily focused on one or a few species at a time, providing little understanding of both the extent of variability in connectivity across a whole community and what factors drive that variability. This project will address these questions with population genetic datasets of a diverse marine fauna sampled across the Hawaiian Archipelago. By combining these genetic data with extensive oceanographic, ecological and historical data, this project can potentially transform our understanding of the basis of the genetic structure of populations and the processes influencing genetic patterns. This project will provide unique, and new, knowledge to basic marine ecology and the science of Ecosystem Based Management while incorporating the latest analytical and simulation approaches.

The results will be novel on several fronts: 1) advancing our understanding of community genetics and associated statistical techniques; 2) achieving true integration of genetic, ecological and oceanographic data over large spatial scales for many species simultaneously using a World Heritage Site; the Hawaiian Papahânaumokuâkea Marine National Monument; 3) factoring historical effects into connectivity studies; and 4) providing information on the location of barriers to connectivity, the sources and sinks of individuals and the physical processes influencing ecological patterns at a community level. This project will result in a quantum leap for both the conceptual and empirical understanding of marine connectivity and the utility of population genetic data in basic and applied marine science.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1260169

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