Simulations and Scripts to perform Hierarchical Approximate Bayesian Computation analysis (HABC) (Multispecies Connectivity project)

Website: https://www.bco-dmo.org/dataset/699774
Data Type: model results
Version: 1
Version Date: 2017-05-08

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

Contributors	Affiliation	Role
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Abstract

Simulations and Scripts to perform Hierarchical Approximate Bayesian Computation analysis (HABC) (Multispecies Connectivity project).

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Coverage

Spatial Extent: **Lat**:21.428 **Lon**:-157.792

Dataset Description

This dataset includes raw data for model simulations and scripts for analyzing the data and products of a Hierarchical Approximate Bayesian Computation analysis.

* **Download the associated files (12.4 GB)**: http://dmoserv3.bco-dmo.org/data/toonen/Multispecies_Connectivity/Toonen_et_al_OCE-1260169_Data_Submission_2017-05-04.zip

Methods & Sampling

hBayeSSC download available here: https://github.com/UH-Bioinformatics/hBayeSSC

hBayeSSC is a Python script that wraps around Serial SimCoal in order to simulate a multi-taxa community undergoing a coordinated demographic expansion.

Requirements:

The applications required to produce a set of simulations with multitaxa summary statistics for the hABC analysis described in Chan et al. 2014:

- BayeSSC - Serial Simcoal
- Python 2.x >= 2.4
- hBayeSSC.py
- msReject

Input files

The input files needed to produce a set of simulations with multitaxa summary statistics for the hABC analysis described in Chan et al. 2014:

- A table of observed summary statistics for each taxon in the community. (details)
- An input par file for serial simcoal. (details)

Observation summary statistics:

Sample observation file:

The table of observed summary statistics consists of columns with the following header names. hBayeSSC replaces the appropriate line in the par file with these values:
Column name = Description
species = Name of taxa
nsam = number of samples to be simulated
nsites = Number of base pairs
tstv = % transitions
gamma = Gamma shape parameter
gen = Numbers of years per generation
locuslow = Low estimate of the locus mutation rate per generation
locushigh = High estimate of the locus mutation rate per generation
Nelow = Low estimate for effective population size
Nehigh = High estimate for effective population size
SegSites = Segregating sites
nucdiv = Nucleotide diversity
Haptypes = Number of haplotypes
HapDiver = Haplotypic diversity
TajimasD = Tajima's D
F* = Fu's F
A more complete description of these values can be found on the BayeSSC website.

par file

Sample .par file

The par file contains one prior which is not individually replaced, such as expansion magnitude (under historical events) and will apply to all populations.

Then we use the following R-script and abc.R to do the final 1,000 acceptance and parameter estimation using local linear regression.

BayeSSC (Bayesian Serial SimCoal)http://web.stanford.edu/group/hadlylab/ssc/

Data Processing Description

Data was processed using R-3.2.1.

BCO-DMO Processing Notes:
Compressed submitted files into a .zip file.

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Data Files

File
Toonen_et_al_OCE-1260169_Data_Submission_2017-05-04.zip (ZIP Archive (ZIP), 11.80 GB) MD5:fc44e17636e6734f7926d9b9dc0c8a89

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Related Publications

Burbrink, F. T., Chan, Y. L., Myers, E. A., Ruane, S., Smith, B. T., & Hickerson, M. J. (2016). Asynchronous demographic responses to Pleistocene climate change in Eastern Nearctic vertebrates. Ecology Letters, 19(12), 1457–1467. doi:10.1111/ele.12695
General

Chan, Y. L., Schanzenbach, D., & Hickerson, M. J. (2014). Detecting Concerted Demographic Response across Community Assemblages Using Hierarchical Approximate Bayesian Computation. Molecular Biology and Evolution, 31(9), 2501–2515. doi:10.1093/molbev/msu187
Methods

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Parameters

Parameters for this dataset have not yet been identified

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Deployments

Chan_model

Website	https://www.bco-dmo.org/deployment/699787
Platform	UHawaii_HIMB
Start Date	2013-03-01
Description	Modeling of Hawaiian coral reef taxa

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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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