Simulations of probabilistic larval transport of blue crab (Callinectes sapidus) across Coastal Western Atlantic habitats for time range 2008 to 2017

Website: https://www.bco-dmo.org/dataset/990889
Data Type: model results
Version: 1
Version Date: 2023-05-22

Project
» Collaborative research: Variation in life history and connectivity as drivers of pathogen-host dynamics and genetic structure in a trans-hemispheric pathosystem (Blue Crab Connectivity)

Contributors	Affiliation	Role
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Abstract
Simulations of probabilistic larval transport of the blue crab (Callinectes sapidus) were conducted between coastal habitats in the western Atlantic and outputs are provided here. The individual-based Lagrangian stochastic biophysical model, Connectivity Modeling System (CMS; Paris et al 2012; https://doi.org/10.1016/j.envsoft.2012.12.006), was used offline with HYCOM+NCODA global 1/12 degree analysis (GLBu0.08) oceanographic models for release simulations starting every three days from January 1, 2008 thru December 28, 2017. Horizontal and vertical turbulence followed convention for the gridscale and was 15 m2/s2 and 0.15 m2/s2, respectively with an integration timestep of 1600 s. Habitat sites, inclusive of settlement boundaries and an approximately central release location, included all land bounding grids from 41N to -35S for a total of 6864 total sites. Each release was of 100 particles that became competent at 25 days and were tracked for a maximum of 55 days. Particles were released in the surface layer and a total of 823680000 were released over the decadal simulation. Two output types are provided: connectivity files and particle trajectories. Connectivity files are generated when particles successfully reach valid settlement habitat during the competency period. They include where and when a particle was released as well as where and when the particle settled. Trajectory files document the entire simulation, including parameterization metadata, and can reconstruct pathways for each released particle. Positions were recorded in the trajectory files every 10 days and also include data on particle fate (competent, settled, terminated).

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Coverage

Location: Coastal Western Atlantic from 41N to -35S
Temporal Extent: 2008-01-01 - 2017-12-28

Dataset Description

CMS = Connectivity Modeling System (Paris et al., 2023)
HyCOM = The Hybrid Coordinate Ocean Model (GLBu0.08, https://www.hycom.org/data/glbu0pt08)

NCODA = Navy Coupled Ocean Data Assimilation (Cummings, 2005)

Methods & Sampling

Simulations of probabilistic larval transport of the blue crab (Callinectes sapidus, LSID urn:lsid:marinespecies.org:taxname:107379) were conducted between coastal habitats in the western Atlantic and outputs are provided here. The individual-based Lagrangian stochastic biophysical model, Connectivity Modeling System (CMS; Paris et al 2012; https://doi.org/10.1016/j.envsoft.2012.12.006), was used offline with HYCOM+NCODA global 1/12 degree analysis (GLBu0.08) oceanographic models for release simulations starting every three days from January 1, 2008 thru December 28, 2017. Horizontal and vertical turbulence followed convention (Kough and Paris 2015) for the gridscale and was 15 m2/s2 and 0.15 m2/s2, respectively, with an integration timestep of 1600 s. Habitat sites, inclusive of settlement boundaries and an approximately central release location, included all land bounding grids from 41N to -35S for a total of 6864 total sites. Each release was of 100 particles that became competent at 25 days and were tracked for a maximum of 55 days. Particles were released in the surface layer and a total of 823,680,000 were released over the decadal simulation. Two output types are provided: connectivity files and particle trajectories. Connectivity files are generated when particles successfully reach valid settlement habitat during the competency period. They include where and when a particle was released as well as where and when the particle settled. Trajectory files document the entire simulation, including parameterization metadata, and can reconstruct pathways for each released particle. Positions were recorded in the trajectory files every 10 days and also include data on particle fate (competent, settled, terminated).

The Hipergator supercomputer cluster at the University of Florida was used to conduct the simulations (CMS 20170518). Simulations used the openmpi framework (intel 2018.1.163 and openmpi 3.1.2) and a SLURM batch scheduler. Simulations were run on 128 cores split between 8 nodes. Output is grouped by month and includes separate files from each process.

Data Processing Description

Connectivity and particle trajectory files from 2012 to 2017 are provided within the zip packages:
connectivity_and_trajectory_2008_2011.zip
connectivity_and_trajectory_2012_2017.zip

The combined fileset is inventoried in the supplemental file "connectivity_and_trajectory_file_inventory.tsv"

Simulation output is provided for each month of release in folders named for the year_month. Two output types are provided: connectivity files and particle trajectories.

Connectivity files (asci) are generated when particles successfully reach valid settlement habitat during the competency period. They include where and when a particle was released as well as where and when the particle settled. The column headers are:

origin site,The number of the site where the larva was released,unitless
settlement site,The number of the site where the larva settled,unitless
settlement year,Settlement year (strftime format %Y),unitless
settlement month,Settlement month (strftime format %m),unitless
settlement day,Settlement day (strftime format %d),unitless
settlement seconds,The age of the larva in seconds at the moment the larva settled,seconds
depth,The depth in meters at the moment the larva settled,meters
release year,Release year (strftime format %Y),unitless
release month,Release month (strftime format %m), unitless
release day,Release day (strftime format %d),unitless

Trajectory files (netcdf) document the entire simulation, including parameterization metadata, and can reconstruct pathways for each released particle. Positions were recorded in the trajectory files every 10 days and also include data on particle fate (competent, settled, terminated).

Example netcdf header:

```
> ncdump -h 2008_1/traj_file_081.nc
```

```
netcdf traj_file_081 {
dimensions:
particle = UNLIMITED ; // (53700 currently)
time = 7 ;
variables:
int time(time) ;
time:units = "seconds" ;
time:long_name = "Time after release" ;
time:_FillValue = -1 ;
int location(particle) ;
location:long_name = "Line number in the release file" ;
location:_FillValue = -1 ;
float lon(particle, time) ;
lon:units = "degrees_east" ;
lon:long_name = "Longitude" ;
lon:_FillValue = 1.267651e+30f ;
float lat(particle, time) ;
lat:units = "degrees_north" ;
lat:long_name = "Latitude" ;
lat:_FillValue = 1.267651e+30f ;
float depth(particle, time) ;
depth:units = "meter" ;
depth:long_name = "Depth" ;
depth:_FillValue = 1.267651e+30f ;
float distance(particle, time) ;
distance:units = "kilometer" ;
distance:long_name = "Cumulative distance" ;
distance:_FillValue = 1.267651e+30f ;
int exitcode(particle) ;
exitcode:long_name = "Status with which the particle exits" ;
double releasedate(particle) ;
releasedate:units = "Julian date" ;
releasedate:long_name = "Date the particle is released" ;
int releasepolygon(particle) ;
releasepolygon:long_name = "Number of release polygon" ;

// global attributes:
:nnests = 15 ;
:timeMax = 4752000 ;
:timeStep = 1600 ;
:releaseFilename = "CR_1_2008.txt" ;
:turb = ".true." ;
:horDiff = 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f, 15.f ;
:vertDiff = 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f, 0.15f ;
:turbTimestep = 1600 ;
:avoidcoast = ".true." ;
:polygon = ".true." ;
:polyFilename = "CrabPolys_2022.txt" ;
:settlementStart = 25.f ;
}
```

BCO-DMO Processing Description

Data version 1 (fileset assembled 2023-05-22):

Zip files provided to BCO-DMO included files organized in year/month subdirectories (e.g., 2008_1/, 2014_3/) corresponding to particle release dates.

BCO-DMO_1_May3.zip
BCO-DMO_2_May3.zip
BCO-DMO_3_May3.zip

* Tested archive integrity and identified incomplete, corrupted, or incompatible ZIP files.
* Files were unzipped and a file inventory was generated for the entire dataset with checksum checks to confirm completeness prior to publication and to clarify which file was published within which zip in the final dataset. See supplemental files section for file inventory. See "connectivity_and_trajectory_file_inventory.tsv"

Reorganized files into two publication-ready ZIP archives grouped by simulation year range and attached to BCO-DMO dataset page as:

Data File: connectivity_and_trajectory_2008_2011.zip
Data File: connectivity_and_trajectory_2012_2017.zip

* Preserved original file formats, filenames, directory structure, and file contents; no changes were made to the files within the zip packages.
* Tested archive integrity and identified incomplete, corrupted, or incompatible ZIP files.

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Related Publications

Cummings, J. A. (2005). Operational multivariate ocean data assimilation. Quarterly Journal of the Royal Meteorological Society, 131(613), 3583–3604. Portico. https://doi.org/10.1256/qj.05.105
Methods

Kough, A. S., & Paris, C. B. (2015). The influence of spawning periodicity on population connectivity. Coral Reefs, 34(3), 753–757. https://doi.org/10.1007/s00338-015-1311-1
Methods

Paris, C. B., Helgers, J., van Sebille, E., & Srinivasan, A. (2013). Connectivity Modeling System: A probabilistic modeling tool for the multi-scale tracking of biotic and abiotic variability in the ocean. Environmental Modelling & Software, 42, 47–54. https://doi.org/10.1016/j.envsoft.2012.12.006
Methods

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Related Datasets

IsRelatedTo

HYCOM Consortium. (n.d.). HYCOM + NCODA global 1/12° reanalysis (GLBu0.08/expt-19.1) [Data set]. HYbrid Coordinate Ocean Model. Available from https://www.hycom.org/data/glbu0pt08/expt-19pt1

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Parameters

Parameters for this dataset have not yet been identified

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Project Information

Collaborative research: Variation in life history and connectivity as drivers of pathogen-host dynamics and genetic structure in a trans-hemispheric pathosystem (Blue Crab Connectivity)

Coverage: Atlantic coast of north and south America from Massachusetts to Southern Brazil, Caribbean

NSF Award Abstract:

Marine invertebrates use an array of strategies to survive, move, and reproduce across diverse and dynamic environmental conditions. This project investigates the intersection of these strategies and how they facilitate the persistence of blue crabs and a pathogenic virus along the Atlantic coast of North and South America. The widespread distribution of this crab-virus system makes it useful for investigating host-pathogen interactions. Blue crabs can reduce their activity level and induce winter dormancy in colder climates, but it is unclear how this alters progression and transmission of the pathogen. Conversely, year-round growth and reproduction of tropical blue crabs may be offset by higher pathogen abundance and activity. This project will use a combination of field and laboratory studies to reveal how crab life history and pathogen dynamics interact and adapt at the extremes of their range. Genetic sequencing, crab movement tracking and oceanographic models will be used to understand how crab-disease dynamics vary across temperate and tropical latitudes. The blue crab is an ecologically and economically important species and knowledge generated in this project will help provide management guidance to support sustainable fisheries. Best practices to avoid and limit disease will be communicated to commercial and artisanal harvesters through partnerships and workshops. Local high school and undergraduate students from underrepresented groups will be engaged through a variety of formal and informal educational programs. Public outreach will be implemented through a museum partnership with the Shedd Aquarium and will include the training of a science communication intern.

This collaborative project will combine empirical field and laboratory experiments, population genomics, and biophysical modeling to explore the consequences of latitude-driven changes in life history and oceanic connectivity on a trans-hemispheric pathosystem comprised of the blue crab, Callinectes sapidus, and the pathogenic virus, CsRV1. The virulence of the CsRV1 virus from tropical and temperate latitudes and the impact of overwintering will be studied by experimental virus challenges of crabs transplanted between high and low latitudes. The impact of infection and virulence on crab movement will be investigated in laboratory raceway experiments of healthy and infected crabs and in the field with acoustically tagged crabs deployed in temperate and tropical locations. Population genetic studies using thousands of genome-wide RAD sequencing markers for crabs and whole-genome sequencing for the virus will define genetic connectivity of crab and virus populations across their range, and will investigate the possible latitudinal, seascape, and life history-driven changes in blue crab and virus genomes. The two population genomic data sets are expected to provide different inferences and scales of connectivity because CsRV1 virus genotypes are transmitted only among post-larval crabs while blue crab genotypes also move by a potentially long-range dispersive larval stage. Finally, integrated biophysical models will be used to investigate the relative contributions of adult and larval dispersal on the population structure of the crab and the pathogen across a broad swath of habitat between New England and Argentina with a decade of simulations. An open-source Lagrangian stochastic model will estimate pelagic larval transport, and spatially explicit biased-correlated random walk models will estimate adult movement. Models will be informed by experimentally-derived movement and behavior data, as well as information on crab larval and adult behavior and overwintering duration available in the published literature. Under a series of scenarios in which crab behavior is affected by latitude and virus infection, statistical comparisons will be made between biophysical model-based predictions of connectivity and genetic estimates of connectivity. These analyses will advance our understanding of the physical, environmental, and biological factors that shape the dynamics of the blue crab CsRV1 pathosystem.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658389

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