**SUPPORTING INFORMATION**

**Comparative Population Genomics and Biophysical Modeling of Shrimp Migration in the Gulf of Mexico Reveals Current-Mediated Connectivity**

L. E. Timm, L. M. Isma, M. W. Johnston, and H. D. Bracken-Grissom

**Supplemental Information 2.** Model Description using the Overview, Design concepts, and Details (ODD) Protocol

The model description herein follows the Overview, Design concepts, and Details (ODD) protocol for describing individual- and agent-based models (Grimm and Railsback, 2005; Grimm *et al.*, 2006) and consists of seven elements. The first three elements provide an overview of the model, the fourth element explains general concepts underlying the model’s design, and the remaining three elements provide details of the model processes.

**Purpose**

The herein described agent-based, biophysical model was used to analyse the effects of water flow on the diffusion and subsequent connectivity of migratory and non-migratory deep sea organisms (hereafter passively-dispersed ‘particles’) of the Gulf of Mexico (GOM). The purpose was to quantify and determine if animals that migrate into surface waters on a diel cycle show greater physical connectivity to locations outside of the GOM than those that do not migrate. This was done by quantifying the percentage of animals ‘flushed’ out of the GOM – i.e., transported by water flow east of -80° longitude – and also by measuring overall horizontal dispersal distance over a temporal span of 60 days. The outputs of the biophysical model were compared directly to genetic measures of population connectivity for three shrimp species (two that migrate and one that does not) to validate the results obtained separately between both methods.

**State variables and scales**

The starting quantity of particles was set at five from each of 46 sites (total n=230) in the northern GOM, the locations coinciding with stations sampled by the DEEPENED Consortium over the years 2015-2017. The quantity of individuals dispersed was fixed and did not change over the course of the simulation timeframe. Two sets of simulations were run: 1) a suite of 15 simulations representing non-migrating animals that occupy fixed depths of 1500-100 m depth in 100m intervals, and 2) a suite of 105 simulations whereas animals migrated upward and downward in the water column on a diel cycle over a range of depths in 100 m increments. The described migrations took place daily spanning five hours in each direction. Specific animal behaviour such as active retention, swimming orientation, ‘sensing’ behaviour, etc., was excluded from the model, with the exception of the diel vertical migrations. Though we were primarily interested in three shrimp species and their specific migratory behaviours, the comprehensive suite of simulations herein can be used in the future to study other deep pelagic organisms (e.g., fish, cephalopods, etc.) whose migratory behaviours differ from our study species.

Individual Variables:

Each particle was described by only one individual variable: spatial Location.

*Spatial Location:* Geographic location of the particle at the release site and the subsequent position of the particle within the three-dimensional water column over space and time. The horizontal transport distance of each particle was recorded and those particles that were ‘flushed’ from the GOM – i.e., transported east of -80° longitude were flagged as exported from the GOM.

Spatial Structure:

The primary ‘model domain’ for this study was a three dimensional grid defined as 98 –76.5° W longitude and 18 - 35° N latitude, comprising the entire GOM and the Atlantic Eastern Florida Shelf northward to 35° N. Water speed and direction from 1500m to the surface was provided by the 1/25° GOM HYCOM ocean condition model. Five individual particles were positioned at each of 46 sites (total n=230 per simulation) at stations sampled by the DEEPENED Consortium in the northern GOM over the years 2015-2017. As the swimming and orienting behaviour of deep sea organisms is largely unknown, dispersal was passive, with the exception of small stochastic movements as described below and the aforementioned diel vertical migrations for the migrating group.

Temporal Structure:

Diffusion was forecasted in hourly increments using daily snapshot (i.e., at 00:00 UTM) water flow conditions from HYCOM simulations for the year 2015. The duration of each simulation was 60 days, initiating January 1, 2015.

**Process overview and scheduling**

The model algorithm was used to forecast the diffusion of individual particles in hourly time-steps from model initiation to conclusion. At each hourly time-step, ocean condition variables (i.e., u, v, z, and velocity of water flow) and the depth-stratified geographic horizontal and vertical position of the particle being modelled were used to calculate the Lagrangian path that the particle followed, repeated for every particle over the simulation timeframe. The cumulative horizontal displacement distance of each particle was also recorded and reported as an overall average of all particles per simulation.

**Design concepts**

*Emergence*. – Each particle’s diffusion on water currents was calculated with a Lagrangian algorithm comprising three-dimensional oceanic water flow, which included stochasticity. Horizontal migration and local behaviour was not integrated into the model and individual particles did not interact.

*Fitness*. – Fitness of individuals in the model was not quantified.

*Sensing*. – Particles were not aware of their environment and made no active movements other than diel migrations.

*Interaction*. – Particles in the model did not interact and were modeled independent of population demographics.

*Stochasticity*. – One stochastic component as integrated into the model: hourly particle movements:

Hourly Particle Movement:

Stochastic particle movements were integrated at each hourly increment to reflect sub grid-scale processes, such as small animal movements, that were not otherwise considered by the algorithm. These movements were calculated by selecting a random number between 0.00 and 1.00 from a normal distribution. If the random number was greater than 0.95, the *u*, *v,* and *z* components of water flow speed and direction were individually and randomly halved or doubled. This process integrated small stochastic deviations from the expected particle trajectory. Eddy diffusivity as also integrated at each timestep, given the equations 5 and 6 described in the ‘Submodels’ section.

*Collectives*. – Schooling behaviour or other interactions between particles was not integrated into the algorithm.

*Observation*. – We assembled a three-dimensional animation (see Supplemental Information Animation 1) to help visualize the dispersal patterns of our study species: 1) animals that migrate from 1500m to 100m on a diel cycle (representing strong vertically migrating species *Acanthephyra purpurea* and *Systellaspis debilis*), and 2) animals that permanently reside at 1000m water depth and do not migrate into surface waters (representing the weak migrator, *Robustosergia robusta*). From this animation, it is possible to visualize the effects of water flow on the dispersal of the three shrimp species of interest in this study.

**Initialization**

To initiate a simulation, the entire population of particles was released at the release sites and then simulated ocean currents transported the particles throughout the model domain. A simulation counter was triggered that chronicled the total simulation time and a displacement counter was initiated that tracked the horizontal distance travelled by the particle. Throughout a simulation, the simulation counter was interrogated hourly to fetch the appropriate water flow data for that date, time, and location and the displacement counter was updated.

**Input**

HYCOM water flow data was used in the simulations, stratified into vertical layers for the top 1500m in the primary domain (1/25° resolution). Water flow was characterized by a three-dimensional vectorized flow-field comprised of u, v, and z components, measured in meters per second (m/s).

**Submodels**

*Lagrangian Particle Diffusion:*

Four key elements were tracked to calculate the hourly path of each particle: (1) the spatial location of the particle within the domain grid (i.e., comprised of x, y, and z components, represented by *Pi*), (2) the hourly transition time and distance covered (i.e., a step -), (3) the cumulative transition time, and (4) the particle’s relative position to the nearest eight water flow vectors (i.e., , , , , , , ,  ). The trilinear interpolation equation

 (2)

was used to estimate and correct the track (i.e., path) (i.e.,  ) of the larva at each .

*Spatial Positioning of a Particle Over the Simulation Timeframe:*

A timer was initiated at the start of the simulation for each particle which tracked the cumulative hourly duration of particle diffusion. The timer was queried hourly to retrieve time-stamped HYCOM ocean water flow data (i.e., velocity and direction of flow) which was then used to interpolate the path of the particle for any particular date and time. The spatial location of the particle within the model grid was computed with the equation

 (3)

whereas *P1* was the sequential spatial location, *P0* the release location, and  the computed particle path. The diffusion of each particle (*Pi*) spanning the 60-day simulation was calculated using

 (4)

To account for sub-grid scale turbulent processes that were not otherwise directly considered by the model, stochastic eddy diffusivity was included per hourly for the u (i.e., *Ku*) and v (i.e., *Kv*) components of water flow direction and speed individually over the simulation timeframe using the equations

 (5)

and

 (6)

whereas *Eh* is the horizontal turbulent diffusion coefficient, set to 1m2s-1 (Markay et. Al., 2016), is the time step (i.e., 3600 seconds), and *RNA* and *RNB*are random numbers between 0 and 1 selected from a normal distribution.

**References Cited**

Grimm V, Berger U, Bastiansen F, Eliassen S, Ginot V, Giske J, et al. (2006). A standard protocol for describing individual-based and agent-based models. Ecol Model **198**: 115–126.

Grimm V, Railsback SF (2005). Individual-based modeling and ecology. Princeton series in theoretical and computational biology. Princeton University Press, Princeton, p 428.

Markey KL, Abdo DA, Evans SN, Bosserelle C (2016) Keeping it Local: dispersal limitations of coral larvae to the high latitude coral reefs of the Houtman Abrolhos Islands. PloS one 11(1): e0147628.