

Modeling connectivity among fish populations: the snapper grouper species complex

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Contrasting reproductive strategies

Snapper (Lutjanidae)



Broadcast eggs at subsurface

Spawning Aggregations: at the shelf edge or on the inner shelf

PLD = 25-33 d

Peak spawning: Spring-Summer

Lane (*Lutjanus synagris*): May-June before full moon

Mutton snapper (*L. analis*): May-June, full moon

Dog, gray, cubera snappers (*L. jocu*, *griseus*, & *cyanoptera*): July-Aug, full moon

Grouper (Epinephaelinae)



Broadcast eggs at depth

Spawning Aggregations: at depth (30-40 m) over slope with high coral cover

PLD = 40-43 d

Peak spawning: Winter

Nassau grouper (*Epinephelus striatus*): Dec-Feb, full moon

Black & yellowfin (*Mycteroperca bonaci*, *M. venenosa*): Jan-March, full moon

What are spawning aggregations?

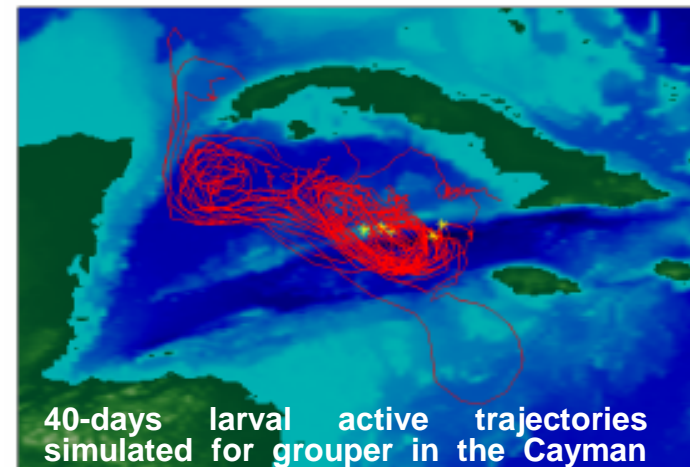


Snapper & Grouper

form predictable resident or transient large gathering (thousands of individuals) at specific time and places

are prime fishing targets & highly vulnerable to exploitation

are also important for the biodiversity of the region



Paris, Cowen, Chérubin, Srinivasan (TOS 2005)



Goal & Objectives

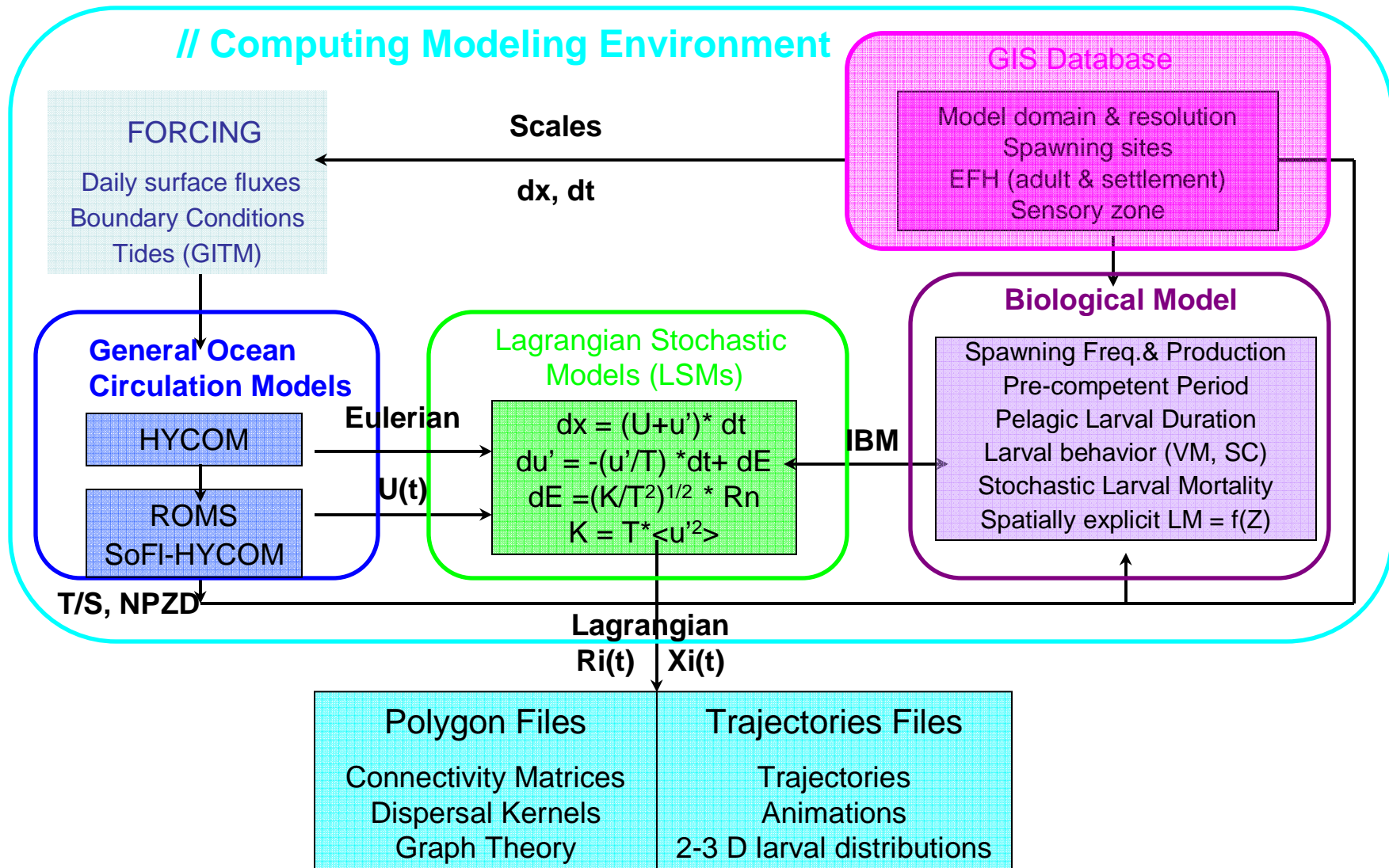
Main Goal: To understand the spatial structure of ecological interactions between breeding populations of snapper and grouper

Build a source/sink Lagrangian biophysical model of larval trajectories (including passive, active movement, and feeding) to assess the probability of successful dispersal **or larval dispersal kernels** and patterns of **population connectivity**

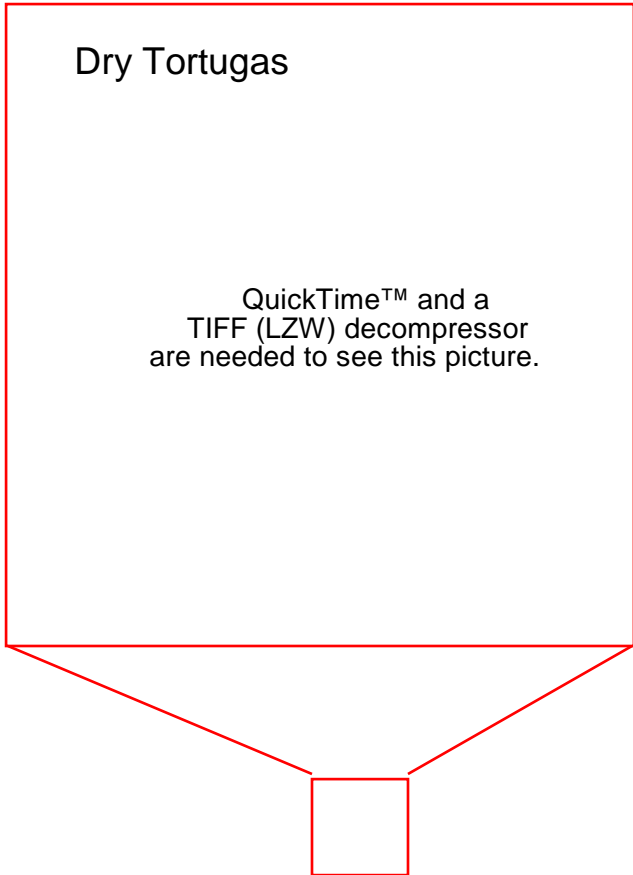
Interactions with oceanic environment: Characterize the hydrography at the spawning site (i.e. shelf break) via high resolution, near-real time coastal modeling with data assimilation (e.g. floats, ocean thermal fronts, fine scale topographic data)

Long-term goal: Utilize population connectivity simulation system for ecosystem management (population structure), effective spatial conservation measures (MPA network/size), and identification of EFH

Biophysical Modeling Environment: Coupling Framework

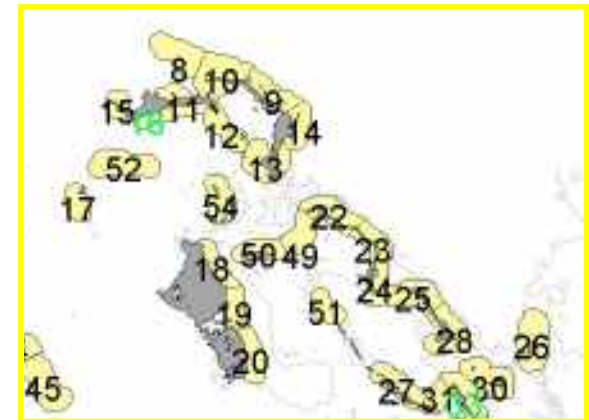


Biophysical Modeling Environment: GIS database

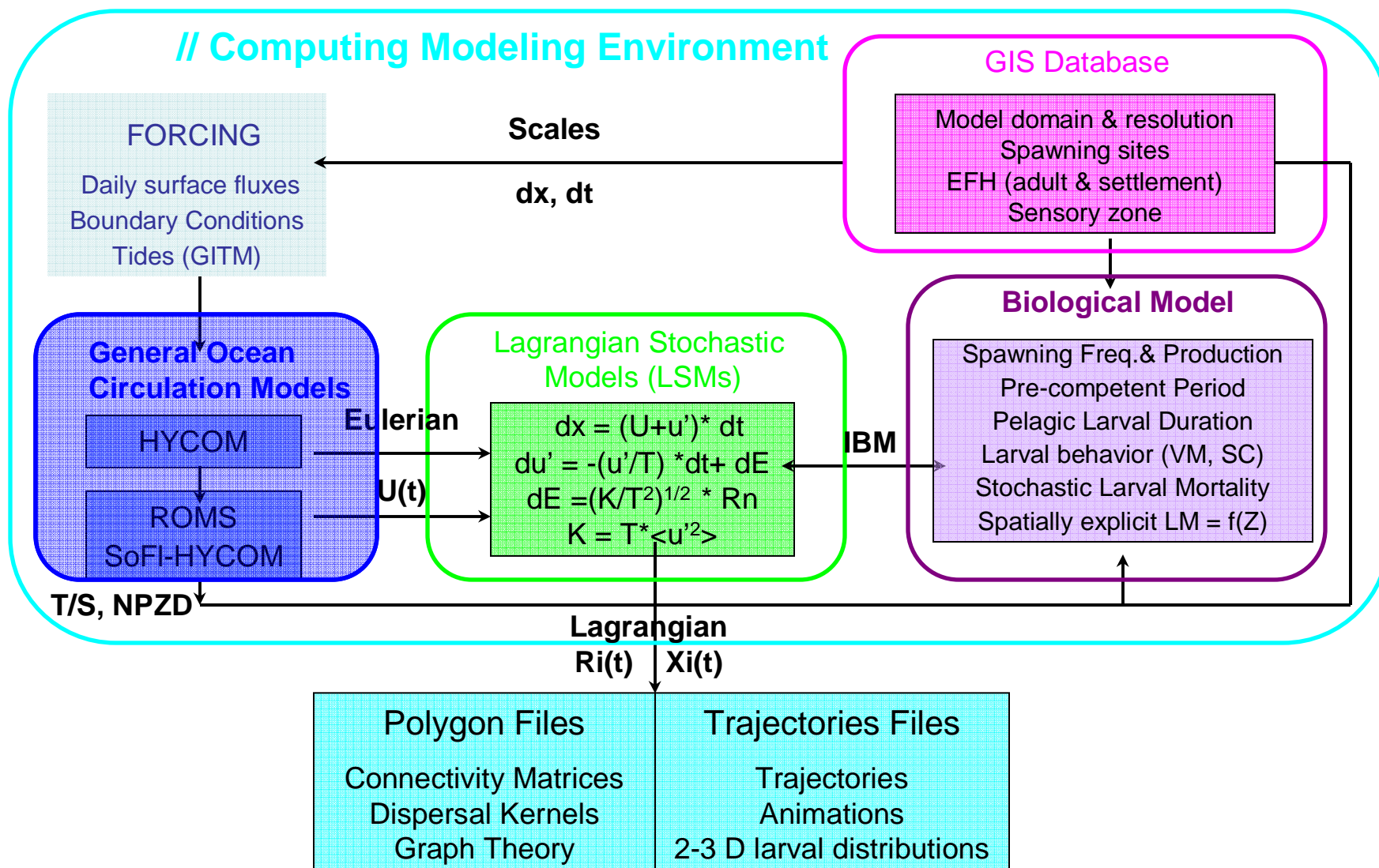


QuickTime™ and a TIFF (LZW) decompressor are needed to see this picture.

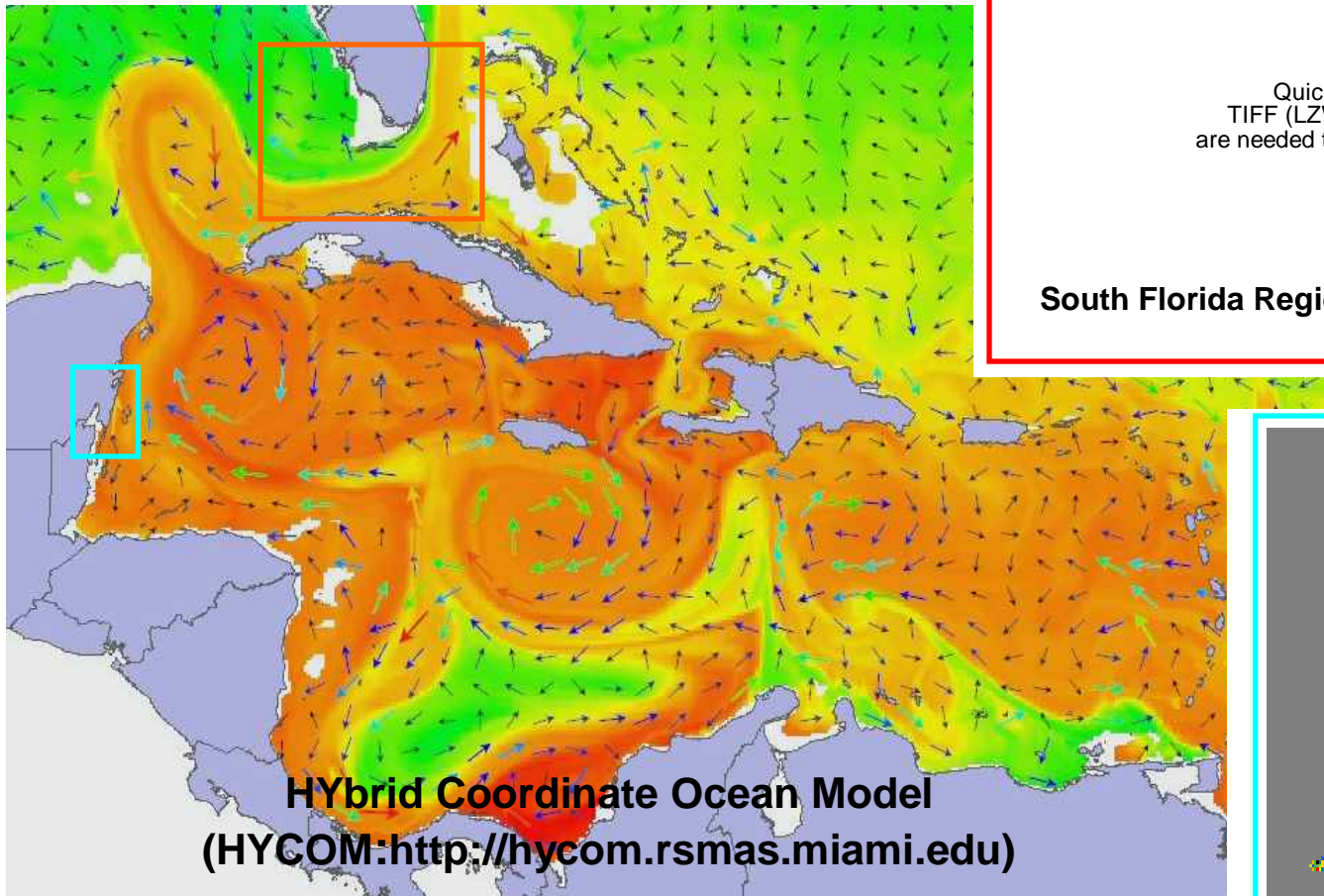
Kool and Andrefouet (Coral Reef Millennium data)



Biophysical Modeling Environment: Coupling Framework

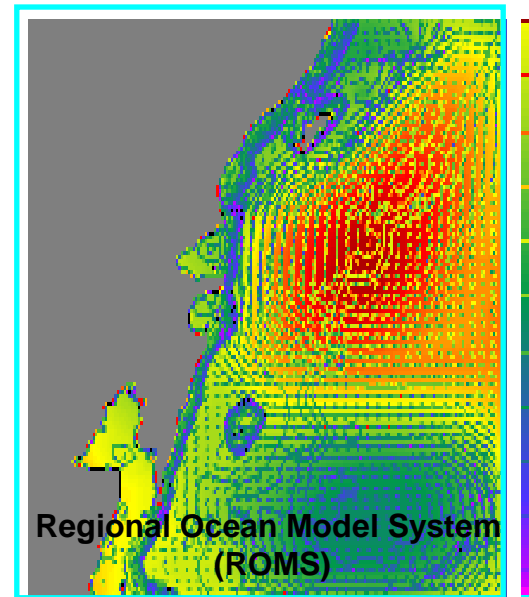


Biophysical Modeling Environment: GOCMs

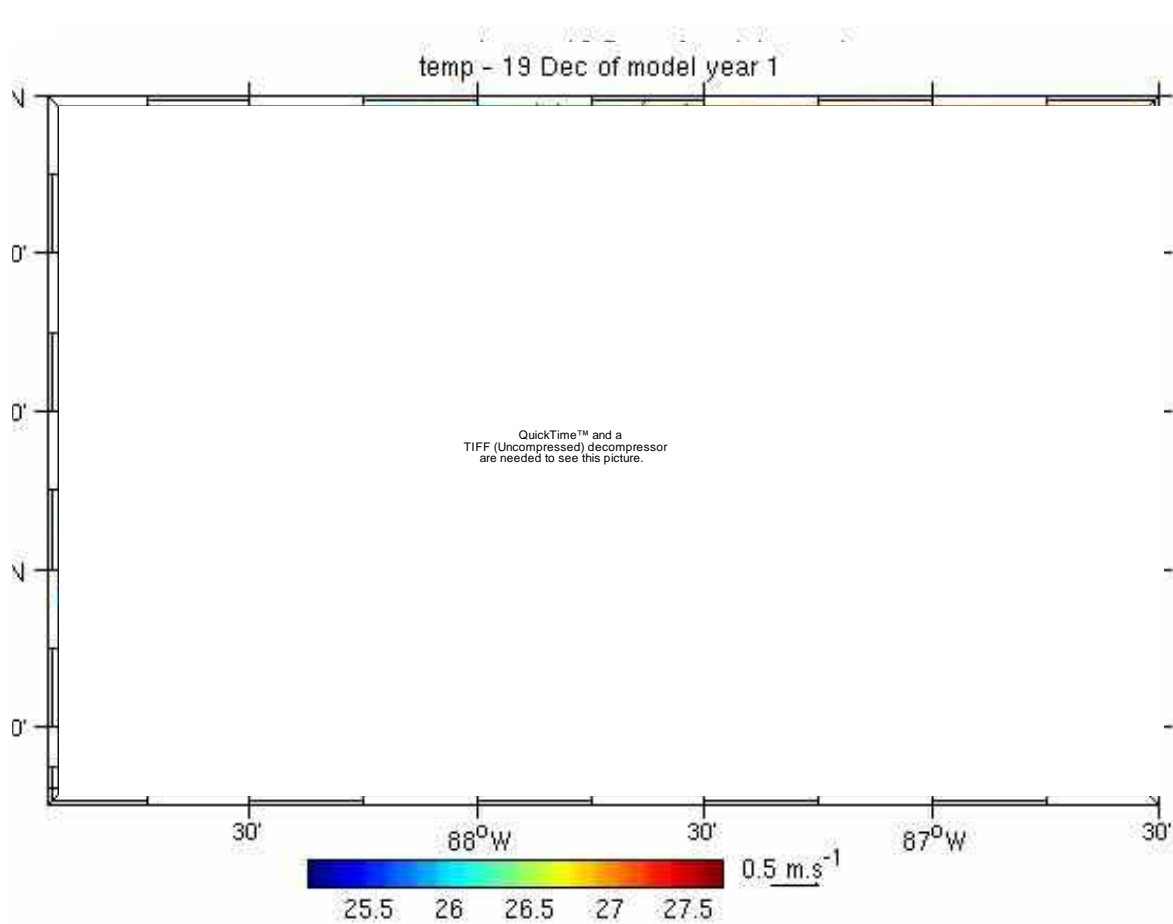


QuickTime™ and a TIFF (LZW) decompressor are needed to see this picture.

South Florida Regional Model (SoFI-HYCOM)



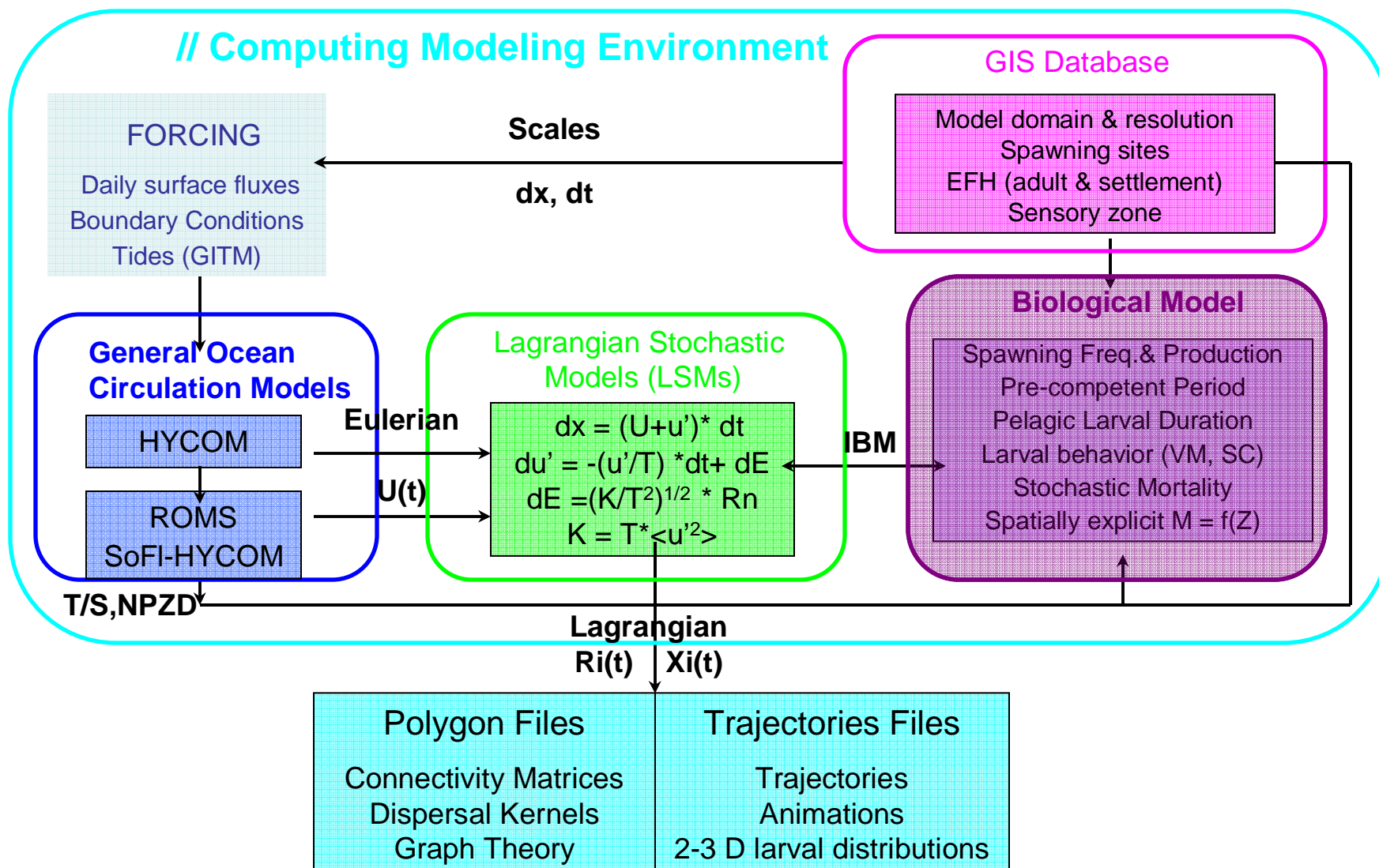
Biophysical Model Environment: ROMS superior nesting capabilities



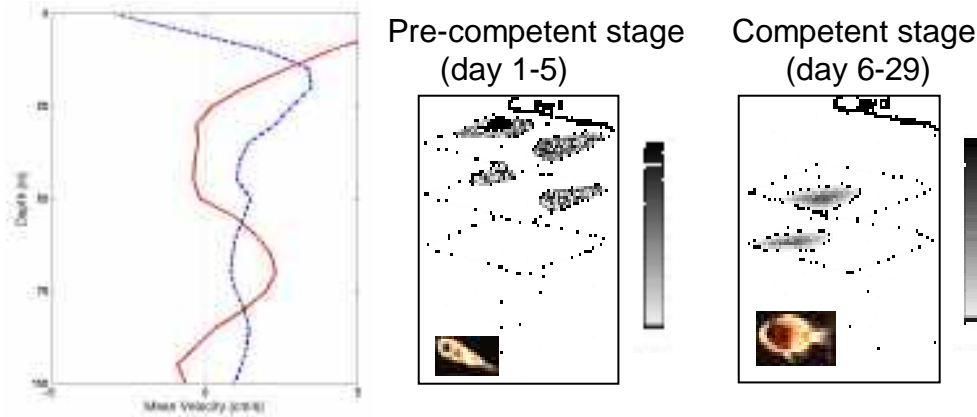
BC - climatology

- **Parent grid** = HYCOM 1/12°
Min Z = 10 m
- **Child grid 1** = 6km (1/18°)
Min Z = 8 m
- **Child grid 2** = 2 km (1/54°)
Min Z = 5 m
- **Child grid 3** = 660 m (1/162°)
Min Z = 3 m

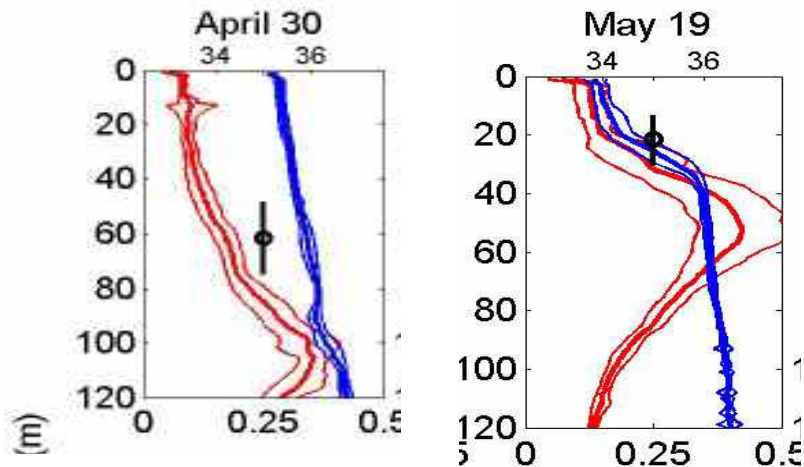
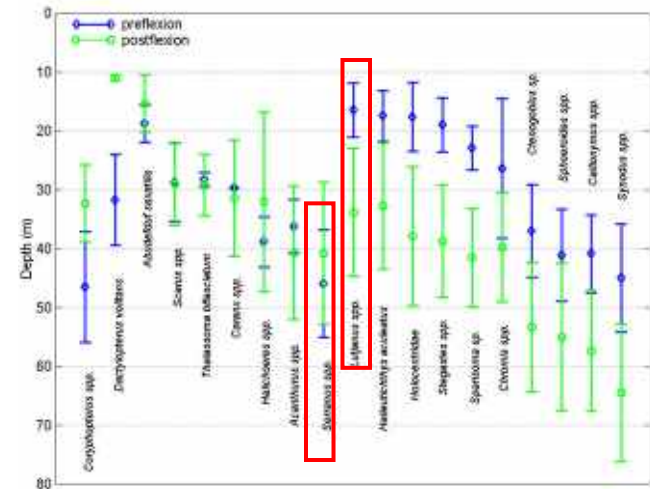
Biophysical Modeling Environment: Coupling Framework



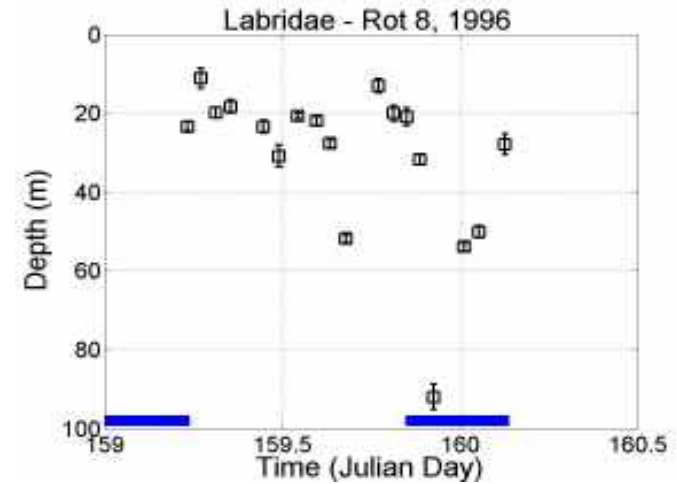
Field Studies: Species-specific stratification of larvae



Ontogenetic vertical migration (Paris and Cowen 2004)

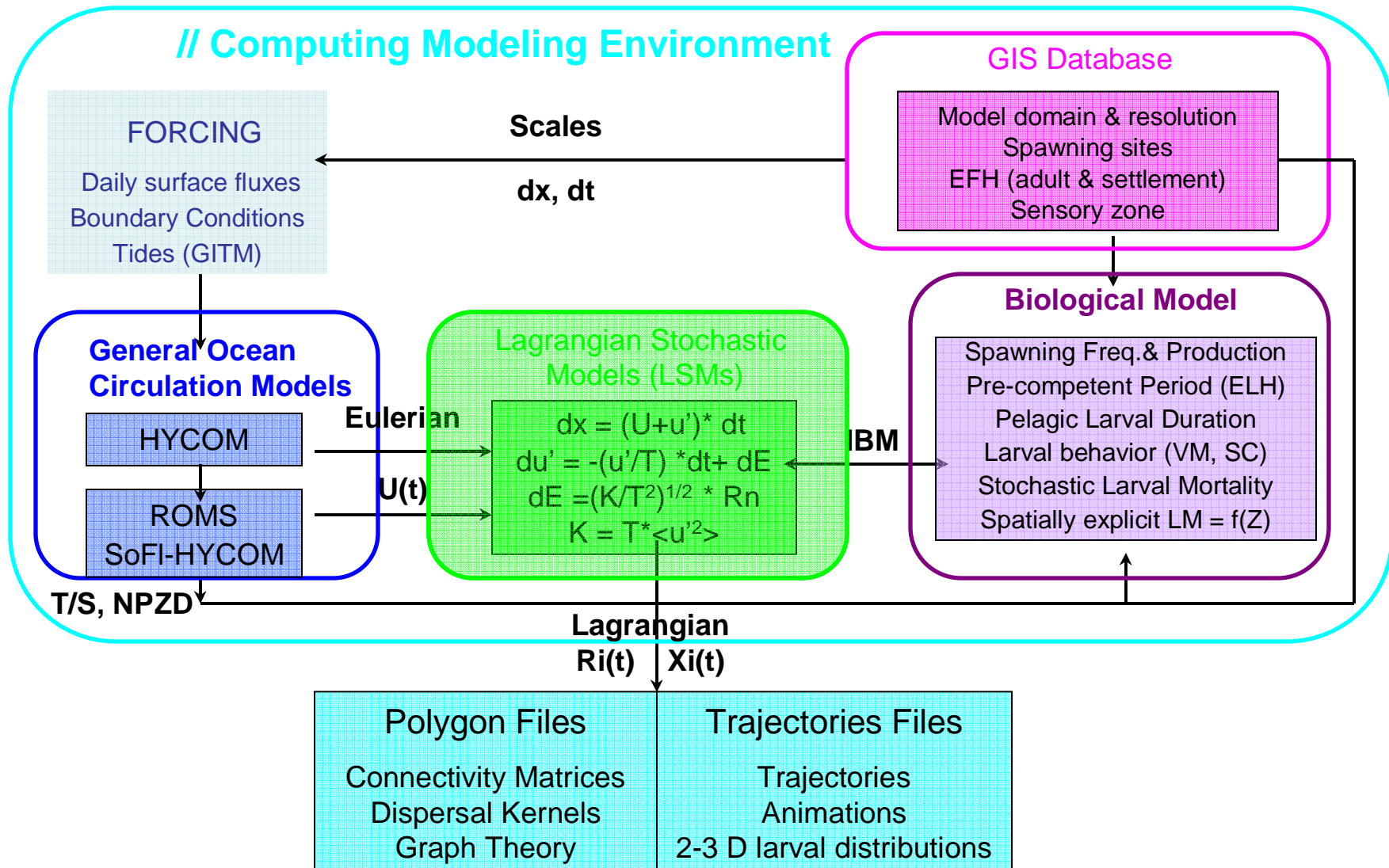


ZCM, Salinity, and Chl_a (Cowen et al., 2003)



Vertical migration (Paris and Cowen in prep.)

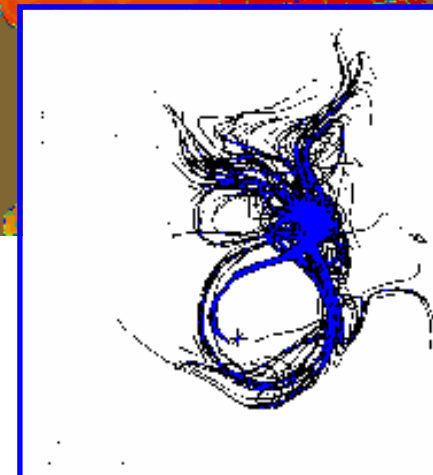
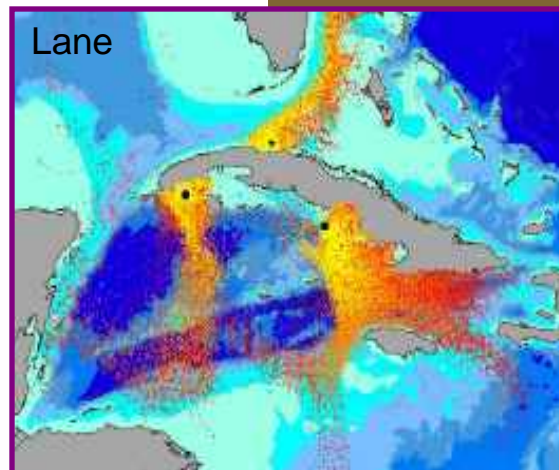
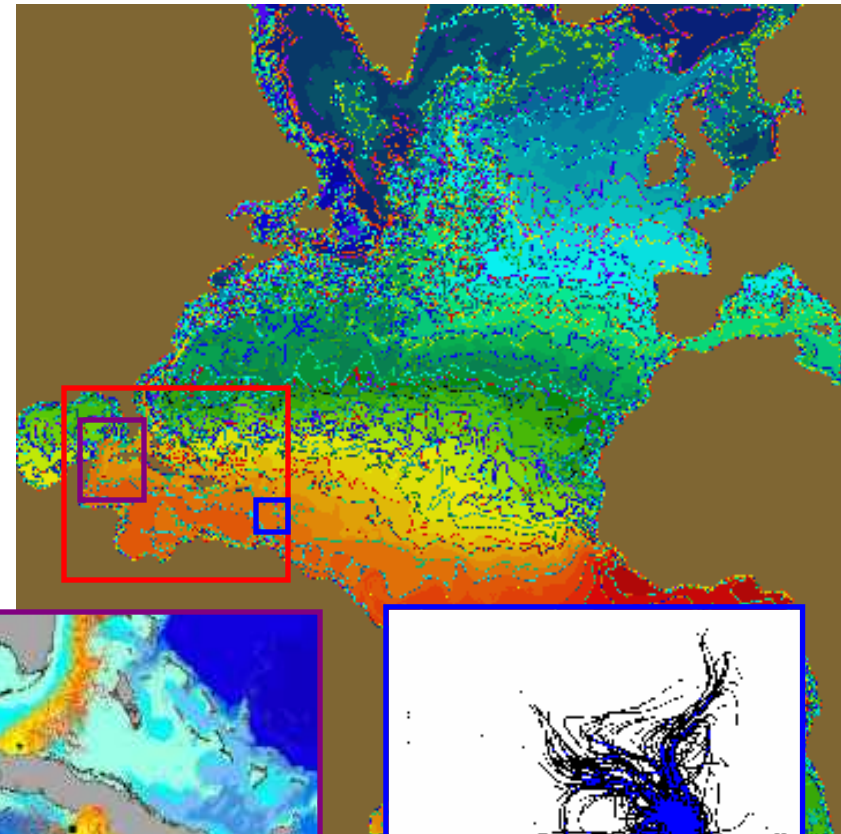
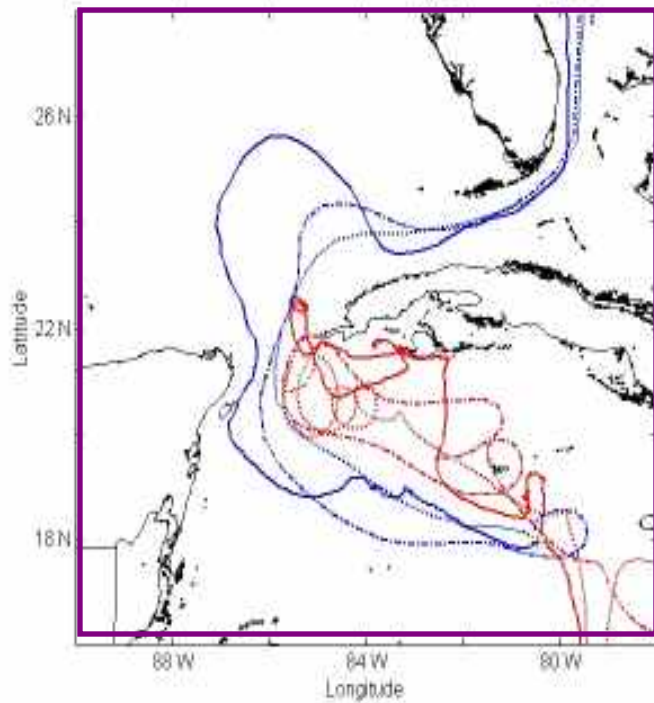
Biophysical Modeling Environment: Coupling Framework



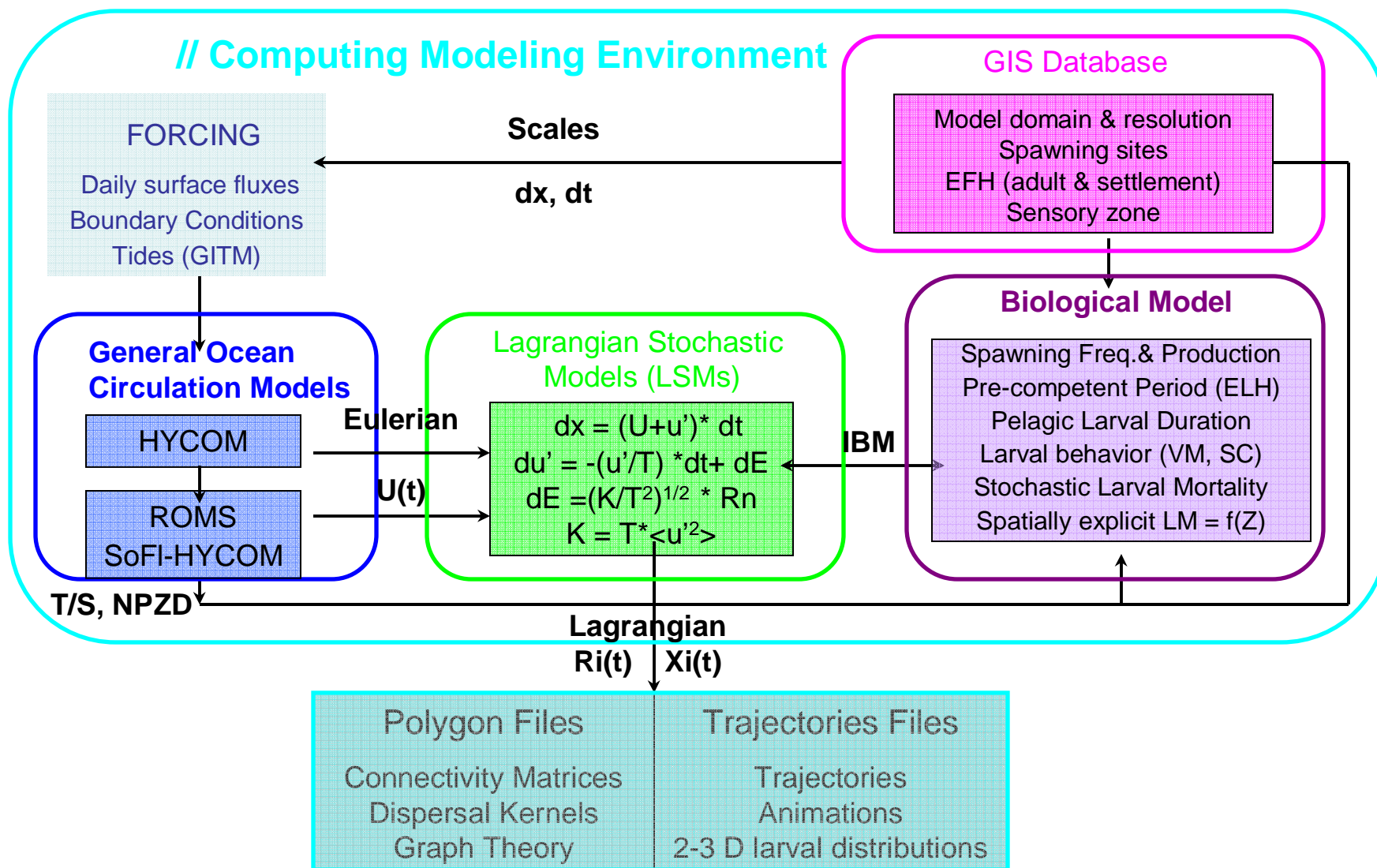
Biophysical Modeling Environment: LMS



$K_{ed} = T * \langle u'^2 \rangle$ (Griffa 1996)
MICOM resolution 1/12 (ca. 8km)
Scaling of $K_{ed} \sim 10^5 \text{ cm}^2 \cdot \text{s}^{-1}$ (Okubo 1987, Paris et al. 2002)



Biophysical Modeling Environment: Coupling Framework



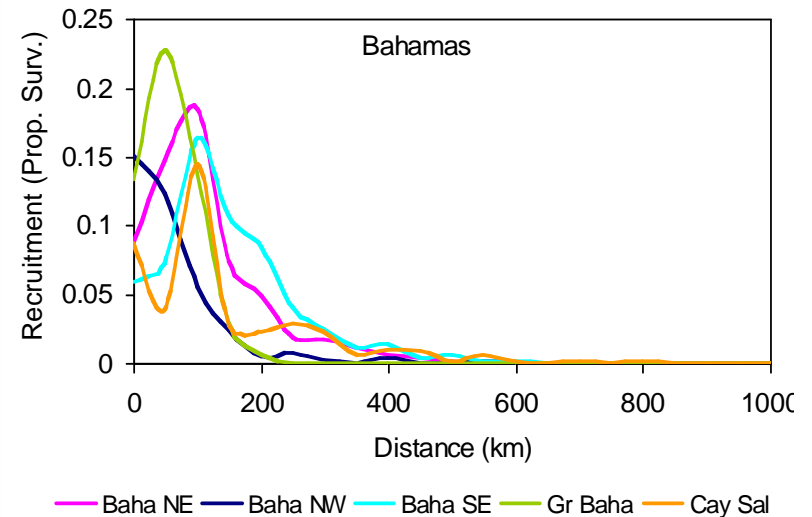
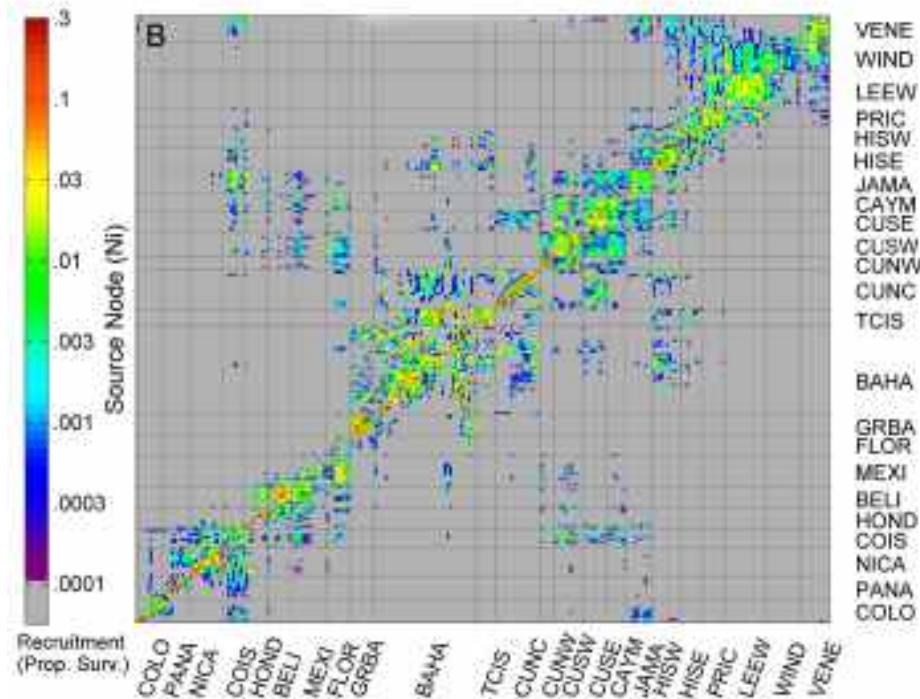
Demographically-relevant Recruitment Rates (from fishery-independent surveys)



Species	Adult Annual Mortality Rate	Longevity	Age of 50% maturity	Batch Fecundity	Spawns per year	PLD	larval mortality rate	Eggs Produced per yr	Prop. surv. larvae required to settle/yr
Snapper	0.2	~ 15 yr	4-5	75,000	90	45	0.3	1,552 M	0.11
Damsel-fish	0.9	~ 4-5yr	1-2	2500	56	30	0.3	42 M	0.28
Goby	2.0	~ 1-2 yr	1	500	100	30	0.3	47M	1.097

Cowen, Paris, Srinivasan (in press)

Model output: Dispersal Kernels - scaling connectivity



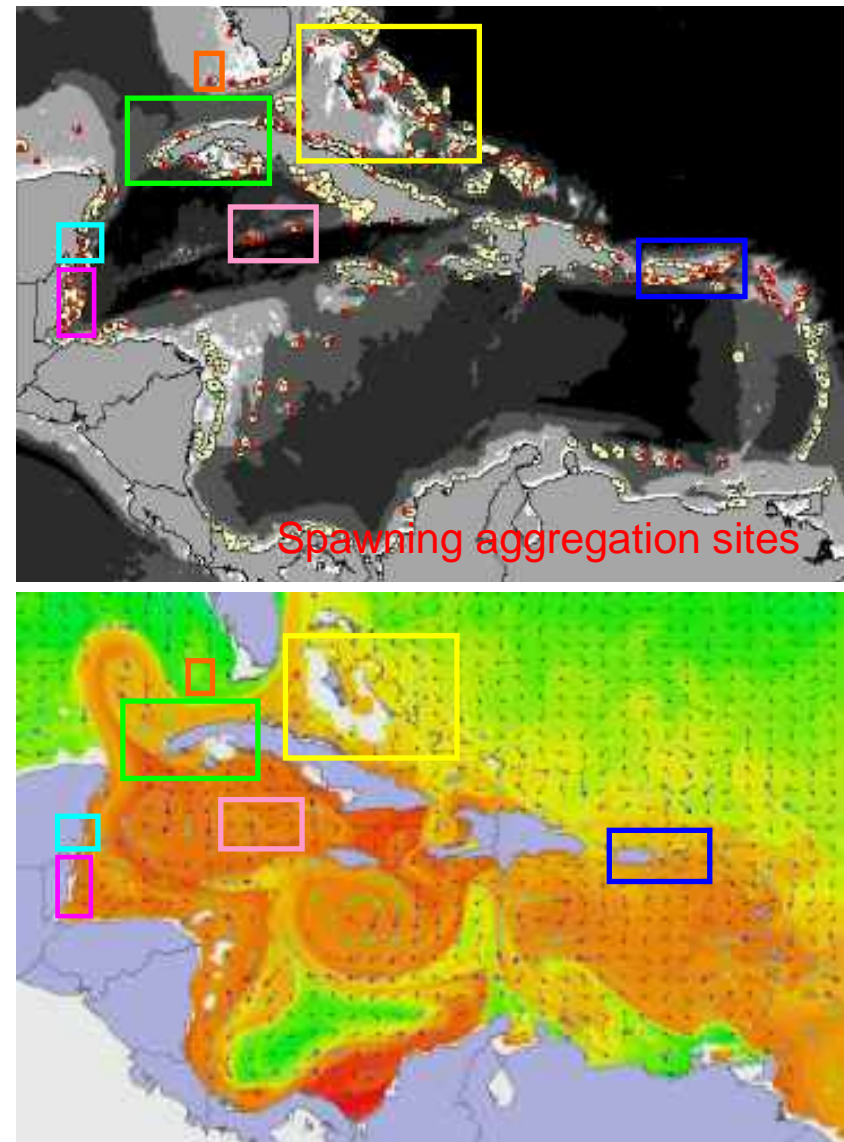
The **dispersal probability matrix** $P = p_{ij}$ represents the probability that an individual in node i at time t will disperse to node j at time $t + k$, where k = pelagic larval duration (PLD).

Dispersal curves = Probability density function standardized by settlement levels (i.e. proportion of surviving virtual larvae) given the probability of dispersal for coral reef fish larvae with a 30-d PLD

Large-scale experiment: HYCOM 2003-2005

Larval transport from grouper & snapper SAs in the Caribbean

- **Currents** - HYCOM Jun 2003- Feb 2005
- **Forcing**: daily winds ECMWF, heat fluxes
- **integration time step** - $dt = 6h$
- **Number days of integration** - PLD = 30-40 d
- **SLM Offline**
 - **Decorrelation time** $T_L = 60 h$
 - **Eddy Diffusivity** : $K_{ed} \sim 10^5 \text{ cm}^2 \text{ s}^{-1}$
- **Spawning Freq (SF)** - FM Dec-Feb & May-Jul
- **Number particles** - $n = 1000/\text{site-year} \times \text{SF} \sim 15M$
- **Reef polygons** = 50 km (self-recruitment scale)
- **Release sites**- historical (exact locations) and reported (GPS location unknown) SA sites (~138 locations) assumed to be shared by both families.
- **Behavior** - vertical migration at flexion (15 d)
- **Sensory capability**- recruitment within 9km reef

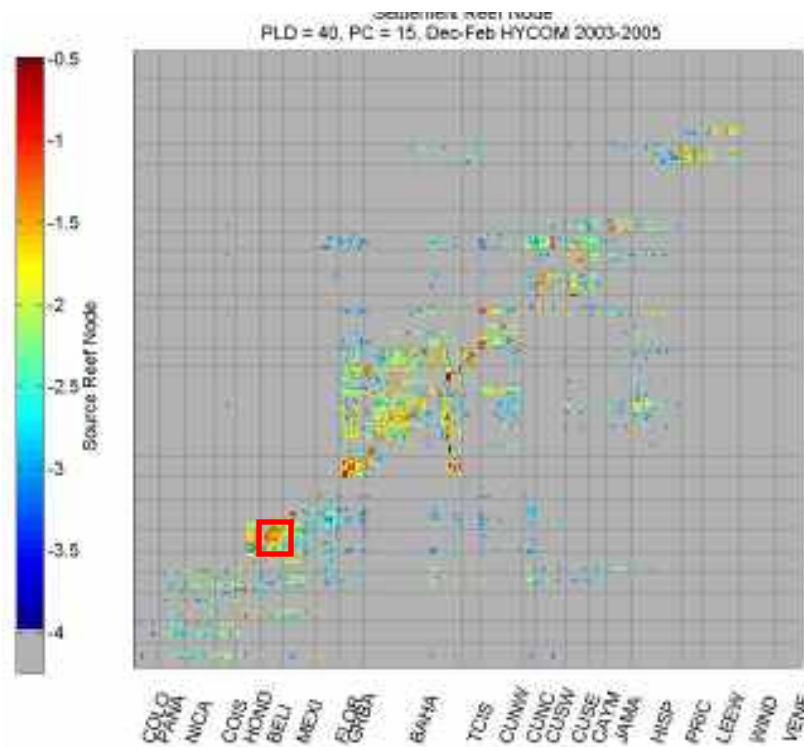


HYCOM 2003-2005: Connectivity matrix in the Caribbean



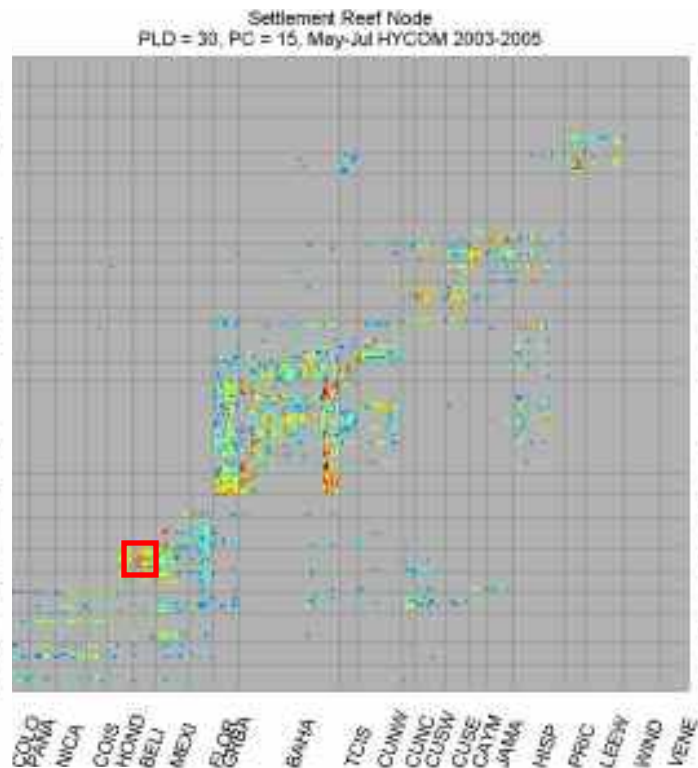
Grouper

Dec-Feb 2003-2005, PLD = 40 d



Snapper

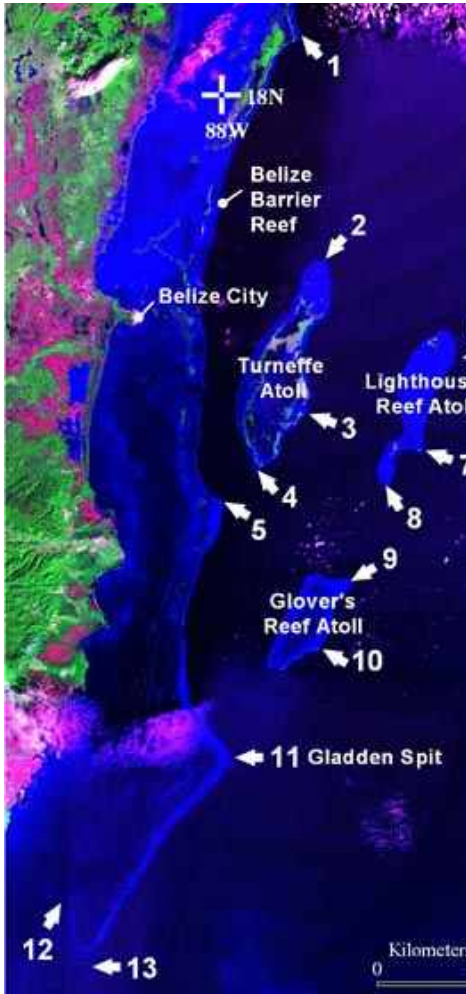
May-Jul 2003-2005, PLD = 30 d



Spawning Sites

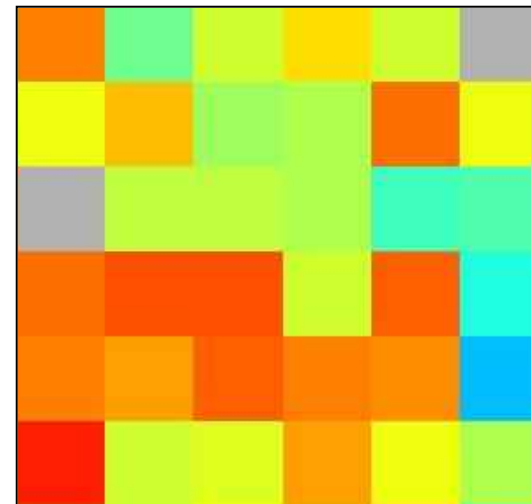
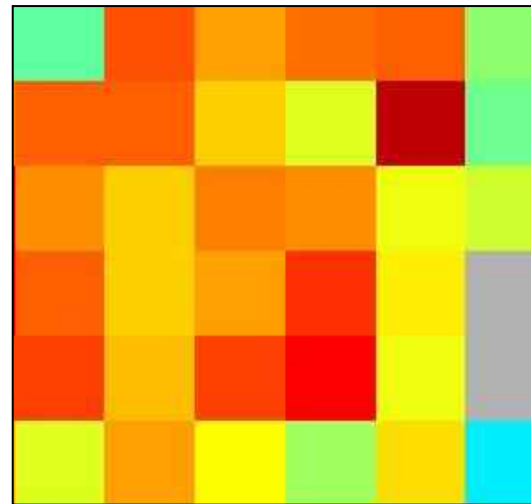
Receiving Sites

HYCOM 2003-2005: Belize Connectivity Matrix

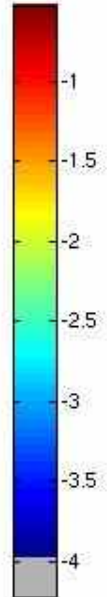


GROUPE

SNAPPER



RP(1)
LH(7)
GS(11)
CG(5)
TS(3)
GR(10)



GR TU CG GS LH RP GR TU CG GS LH RP

Receiving Sites

Graph Theory: Connectivity network



Connections between nodes are represented by several types of matrices:

• The **distance matrix** $D = d_{ij}$ represents the distances between patches ij

• The **dispersal probability matrix** $P = p_{ij}$ represents the probability that an individual in node i at time t will disperse to node j at time $t + k$, where k = pelagic larval duration (PLD).

• The **adjacency matrix (or edge)** $A = a_{ij}$ is a binary matrix in which each element is defined as $a_{ij} = 1$ if node i and j are connected, otherwise $a_{ij} = 0$. The diagonal of A is set to zero (i.e., no self loop) and A is generated from P by choosing a threshold probability to define adjacency.

The expected flux from node i to node j is:

$$F_{ij} = S_i / S_{tot} * p'_{ij}, \text{ where } S_i = \text{size of } i$$

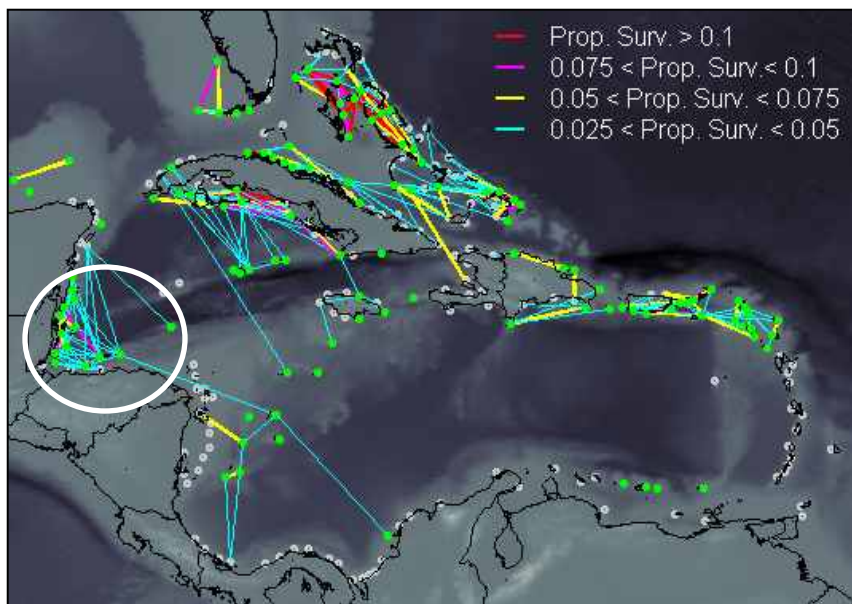
$$S_{tot} = \sum S_i$$

$$p'_{ij} = p_{ij} / \sum p_i \text{ standardized probability of dispersal}$$

Connectivity network - Graph Theory



Graph Theory: Demographically relevant settlement rates are estimated for the life histories of grouper and snappers to establish **ecological criteria for spatial management and conservation of the breeding populations**



A. GROUPEL - PLD = 40 d
HYCOM Dec 2003- Feb 2005



B. SNAPPER - PLD = 50 d
HYCOM Jun 2003-Jul 2004
Distance

Summary



Innovative features from the Biophysical Connectivity Modeling System

1. Coupled modeling system focusing on key target species
2. Individual-based variability (i.e. displacement and mortality)
3. Probabilistic simulations with ensemble and iterative approaches
4. Explicit treatment of spatial and temporal ELHs (advection at pre-flexion, active at post-)
5. Parallel computing system >> large-scale releases in space (multiple locations) and time (sequential runs)

Model Results:

1. **Distinct patterns of connectivity at the family level** due to lag in spawning schedules (i.e. temporal variability effect) and strong isolations due to **limited dispersal**
2. **despite shorter PLDs, snapper larvae are on average less retained near the source than grouper.** Yet, differential site utilization needs to be investigated further
3. **Inter-annual oceanographic variability plays also a significant role in larval linkages.** Full scale study of temporal variability is needed for effective spatial management.

Overall benefit of the model:

Effectively quantifies and maps demographically relevant dispersal distances (e.g. for population connectivity) as well as extreme spread scales (e.g. for invasive species)

What are data needs for the biophysical model?

GIS database:

- exact spawning aggregation locations
- Settlement habitat of snapper and grouper

Biological model:

- fecundity and spawning frequency
- spawning depth
- egg buoyancy
- larval vertical migration, orientation, swimming behaviors

LSM - IBM:

- horizontal & vertical diffusivity in steep slopes and other spawning areas (floats)
- Lagrangian time scales of velocity field at spawning locations (ADCP)

Checking consistency of biophysical model with observation:

- ocean observation systems (i.e. SEACOOS, CaroCOOPS) ✓
- recruitment levels (recruitment & settlement surveys)

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