

Dispersal of Larval Mussels and Population Connectivity in Eastern Maine



Photo credit – Wes Hedlund

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Biol. Oce.
Program

Methods of assessing population connectivity

Traditional genetics - limited number of selectively neutral loci

Genomics - vast number of loci, some under selection

Parentage analysis

Elemental fingerprinting (of shells, otoliths, etc.)

Coupled biophysical models

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Generate patterns (and can reveal biological processes, in the case of genomics)

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Coupled biophysical models

Generate patterns (and can reveal biological processes, in the case of genomics)

Can be used to address oceanographic processes

The weakest part of a coupled biophysical model is generally the biology!

Larvae of different taxa are more or less easy to model

Physical environment

Horizontal current speeds: $10^{-2} – 10^1 \text{ m s}^{-1}$

Vertical current speeds: $10^{-5} – 10^{-3} \text{ m s}^{-1}$

Weakly swimming larvae

(e.g., molluscs, echinoderms)

Swimming speed: 10^{-4} to 10^{-3} m s^{-1}

Relevant movement largely limited to vertical
migration

Herbivores

Limited behavioral repertoire

Strongly swimming larvae

(e.g., crustaceans, fish)

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Directed movement in all 3 dimensions

Carnivores

Behaviorally very sophisticated

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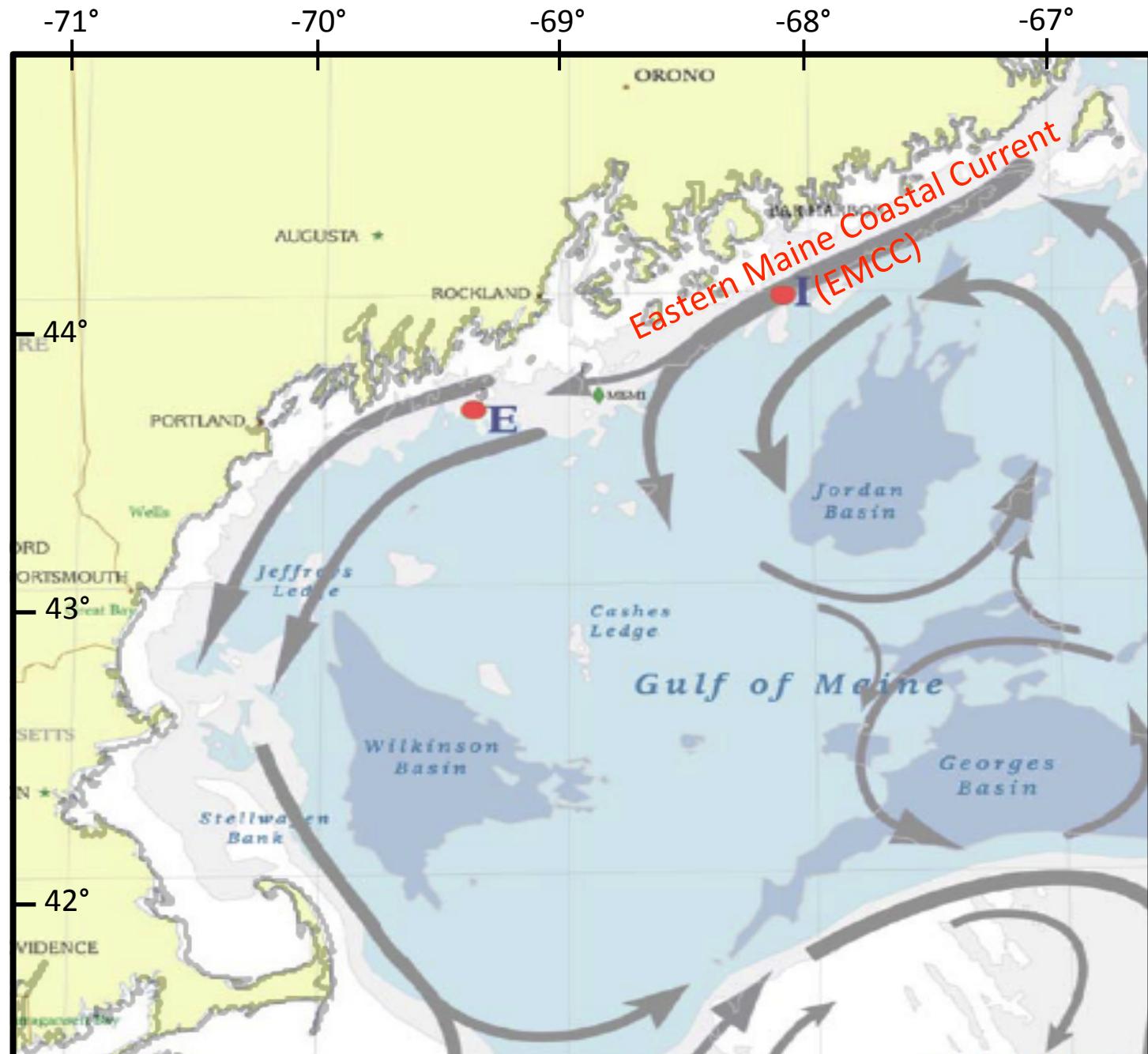
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Models at this end of the
spectrum can come closer to
capturing biological reality



Pettigrew et al., 2005, Deep Sea Research II 52:2369-2391

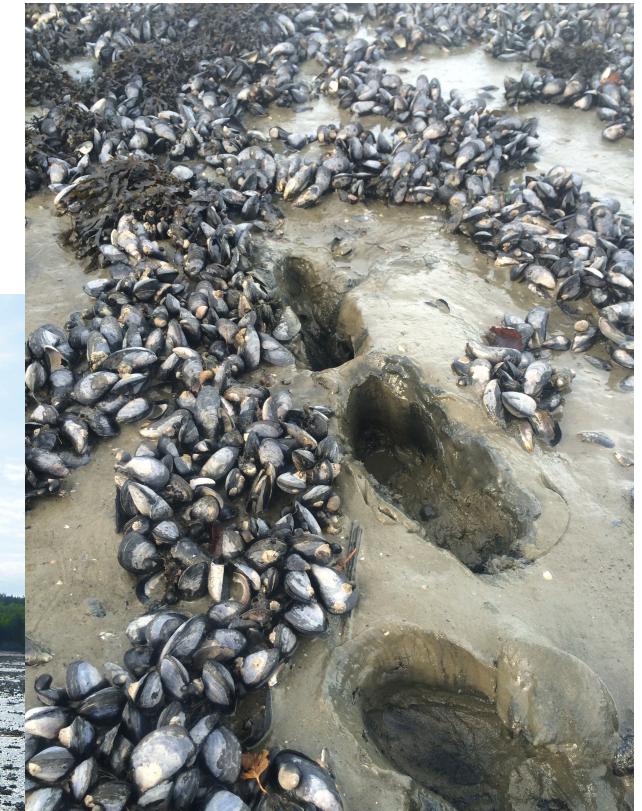
Blue mussels (*Mytilus edulis*) in eastern Maine

Do not live on the exposed coast or on rocks

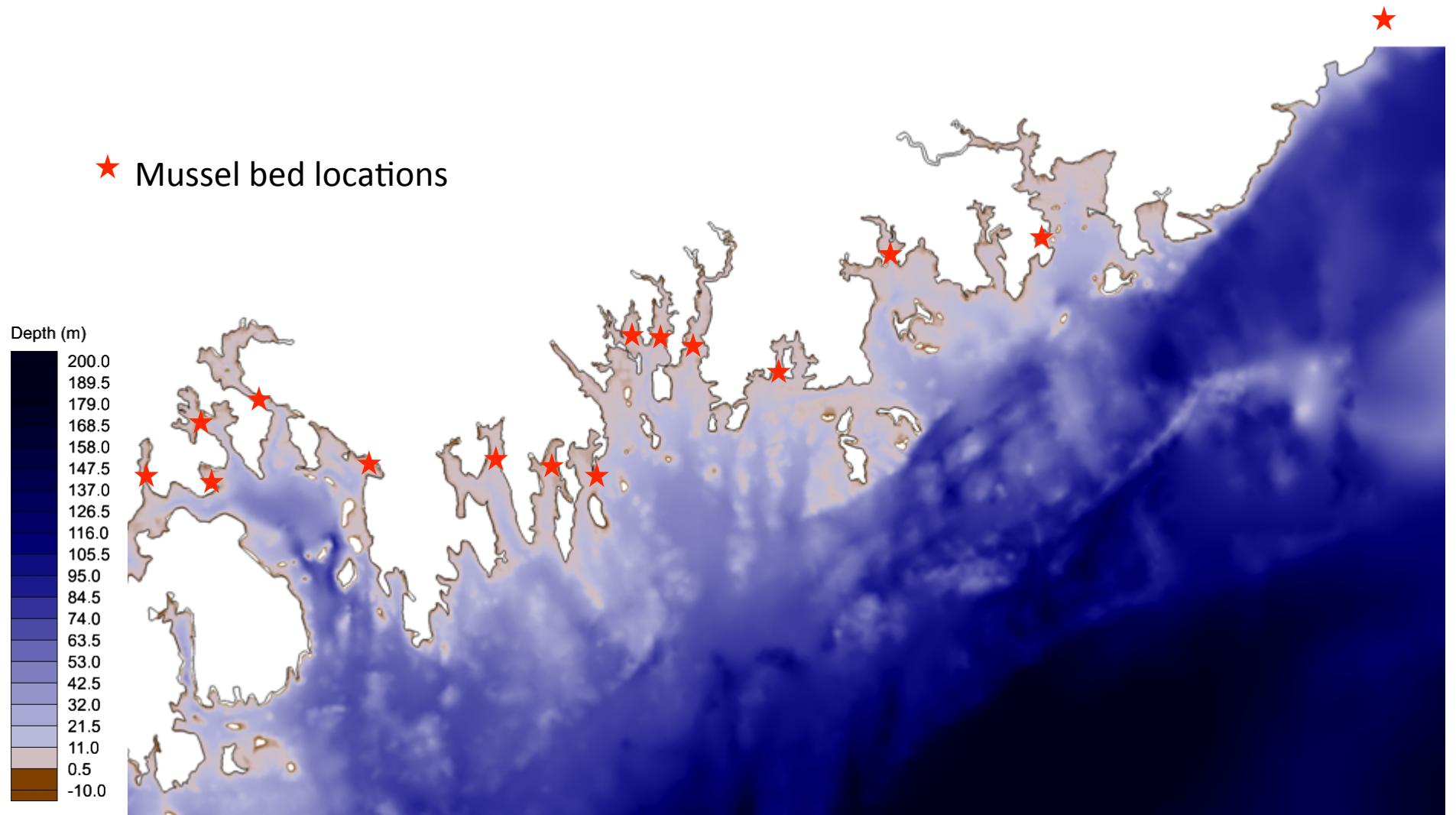
Form huge beds on soft sediment in estuaries

Distributed as discrete populations separated by mussel-free habitat

Historically, formed pseudo-populations (comprised of small, non reproductive individuals) on the exposed coast



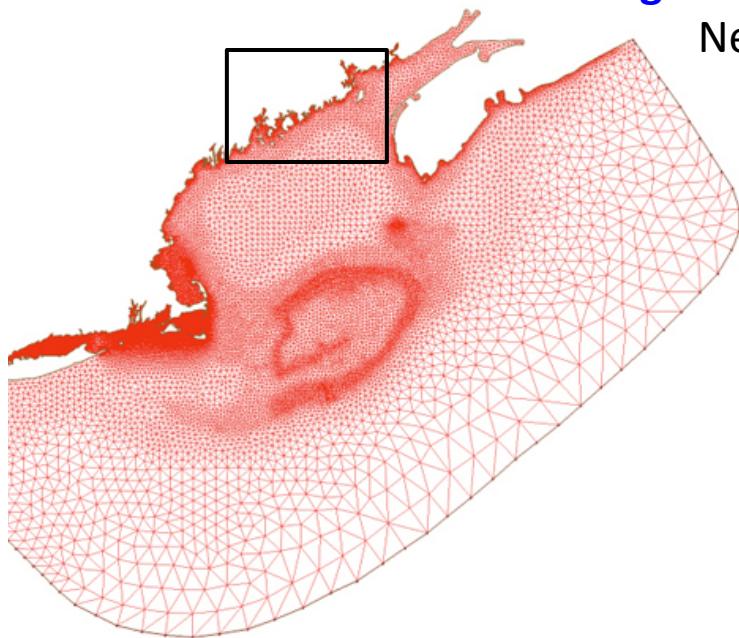
Eastern Maine mussel beds



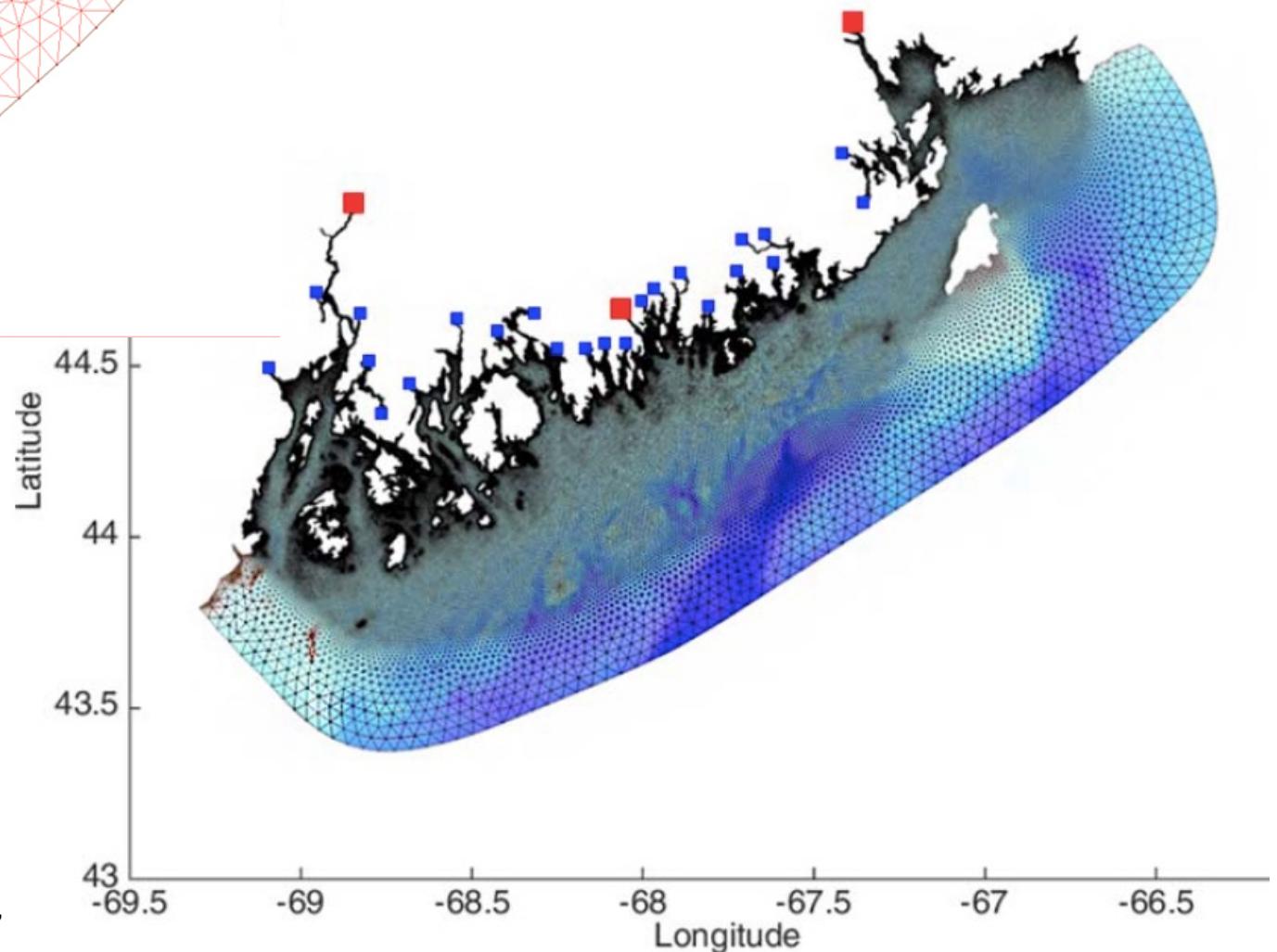
<http://fvcom.smast.umassd.edu/>

High resolution coastal circulation model implemented in FVCOM

Nested within larger scale NECOFS model (NERACOOS)

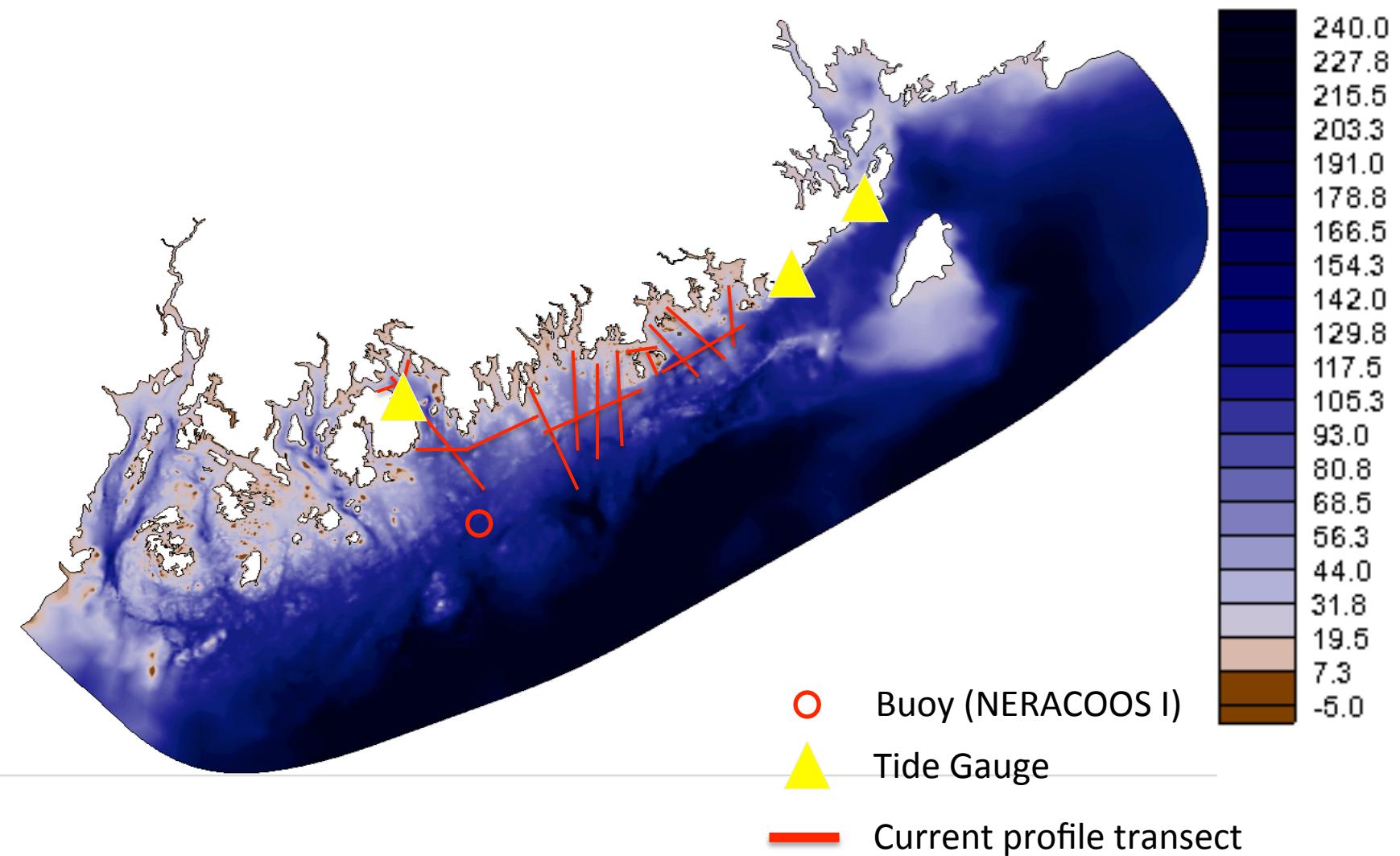


Flow speed and direction calculated for 20 depths at each point in grid.
Horizontal resolution 100 m. inshore.

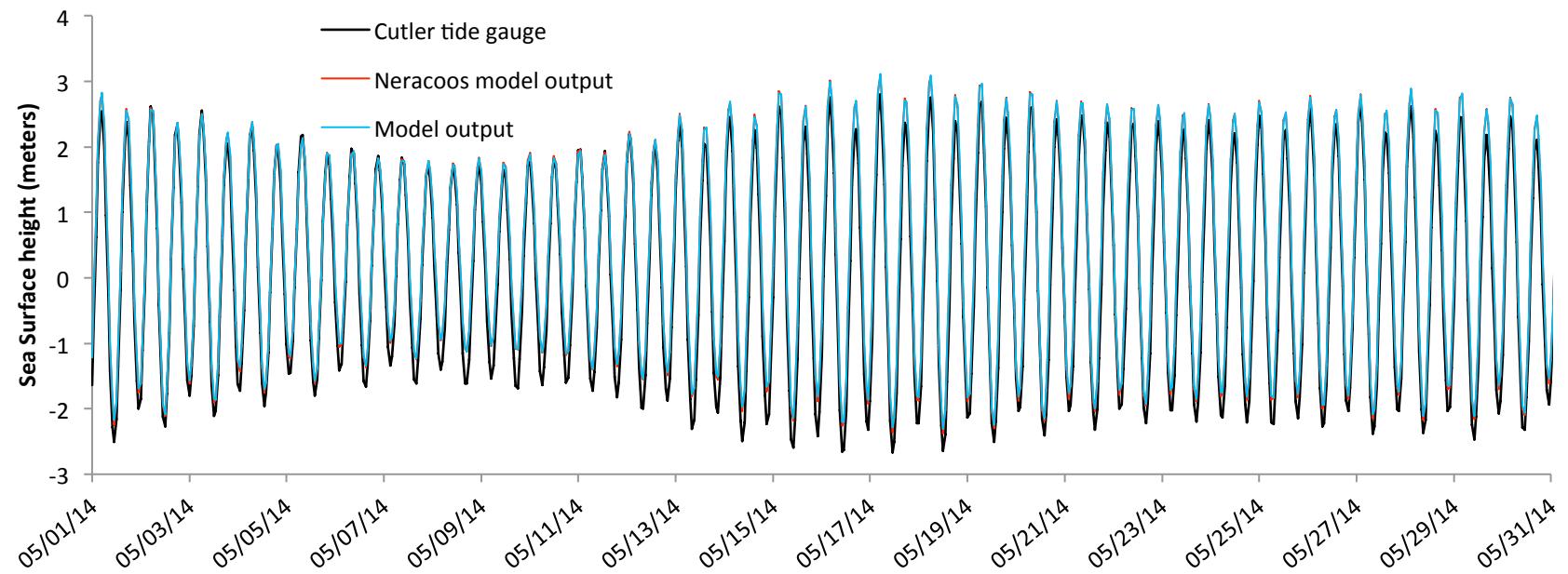


Conlon, Xue, Morello & Yund,
2018, JGR Oceans 123.

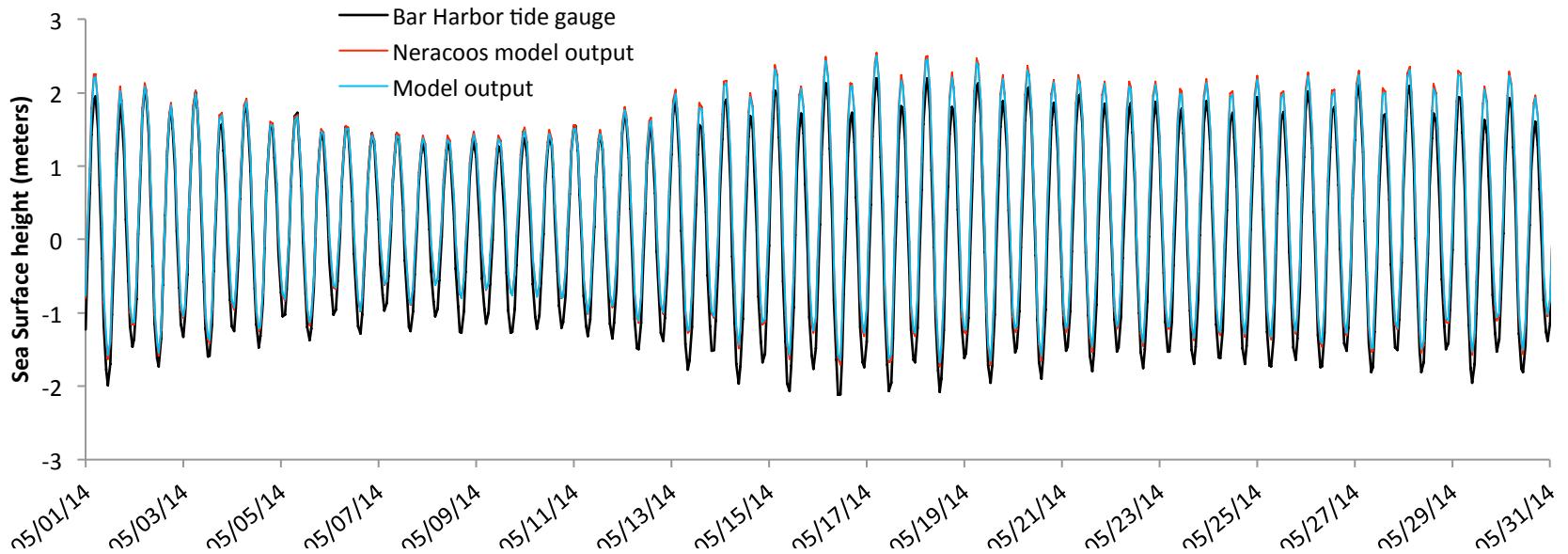
3 Methods of Model Validation



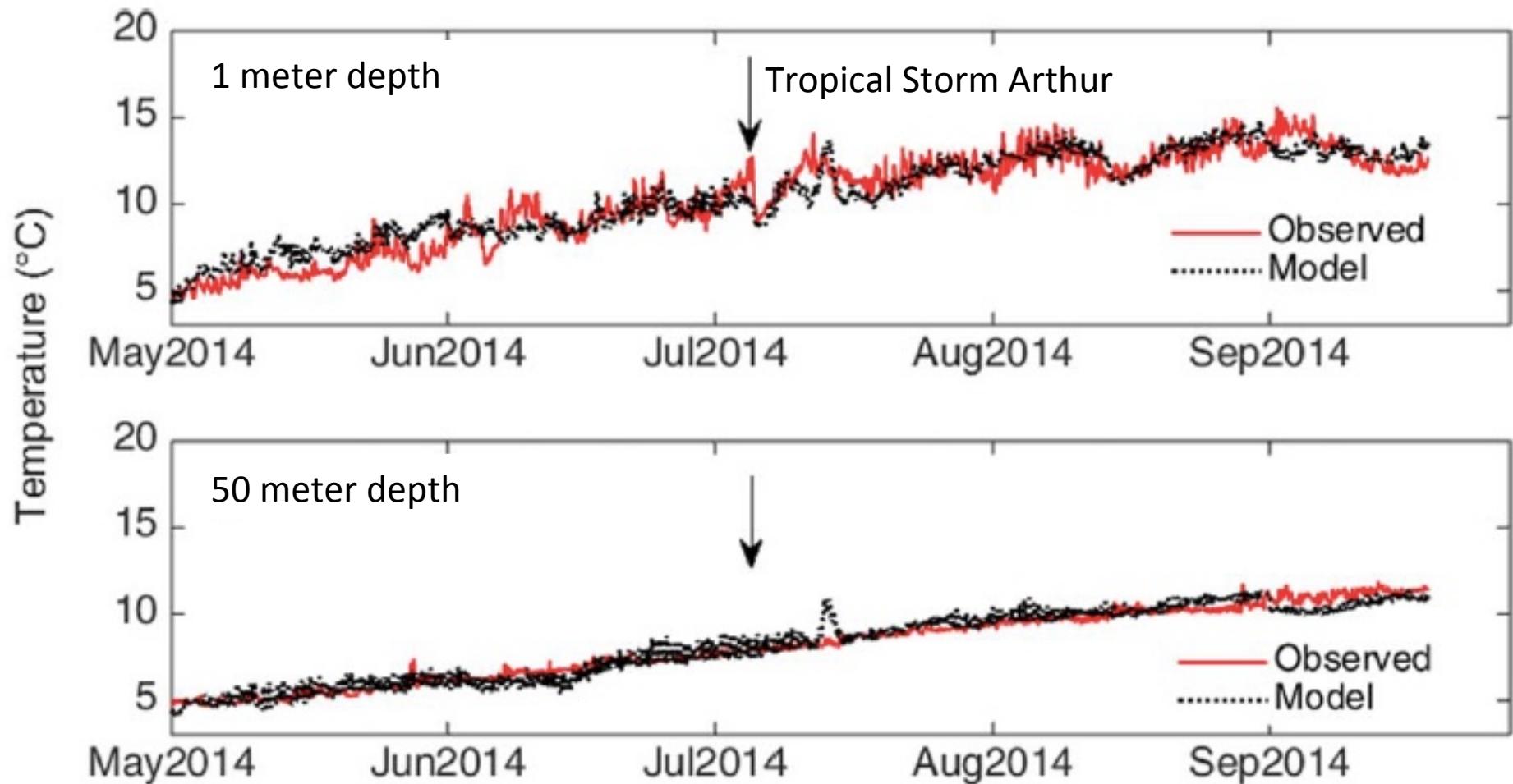
Tide height comparison - Cutler



Tide height comparison – Bar Harbor

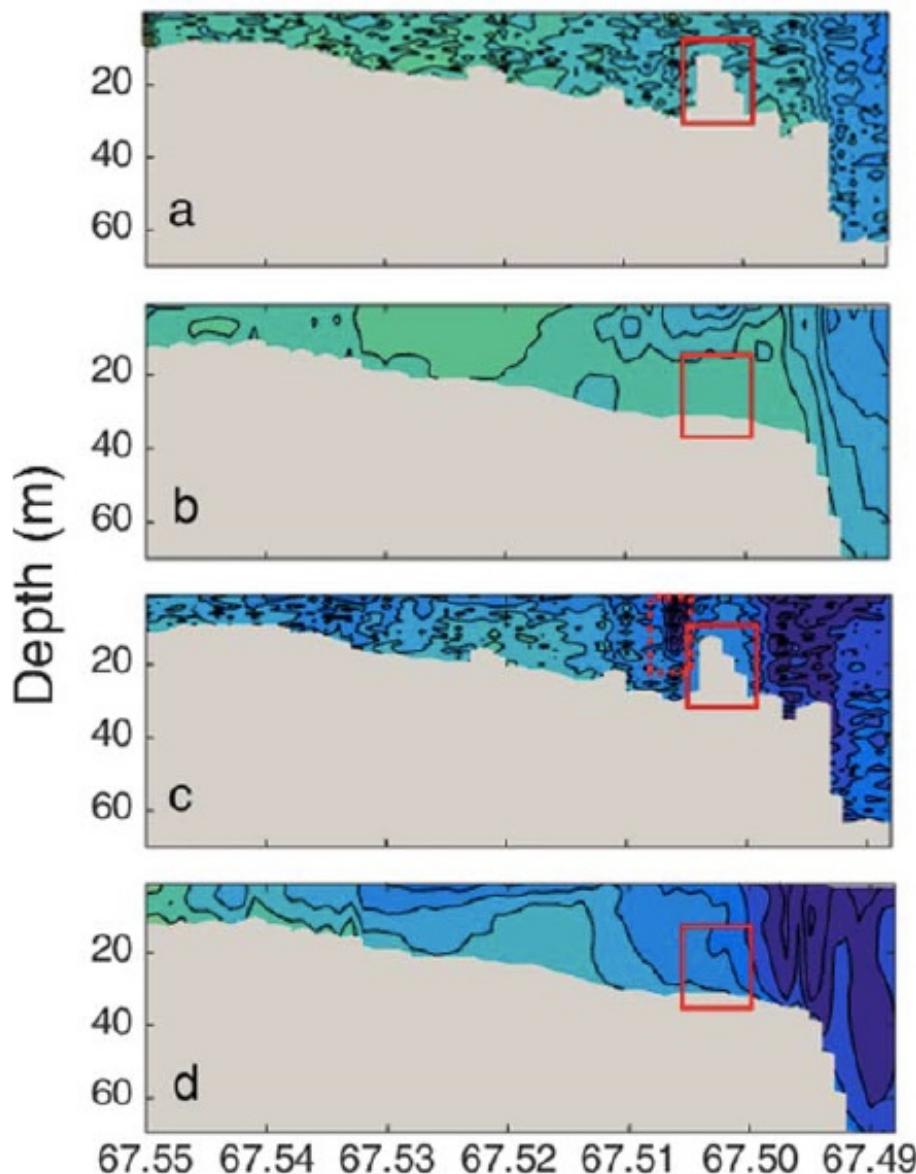


Comparison between model and buoy I - temperature

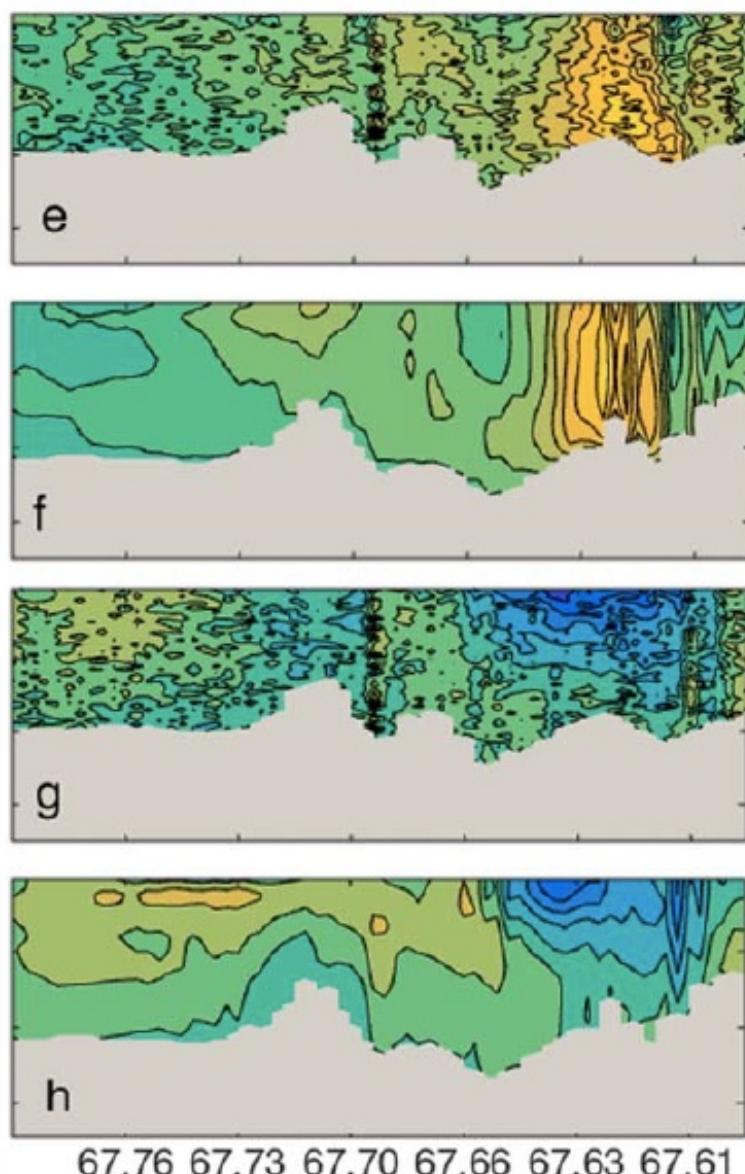


Current Profile Comparison

Transect 11

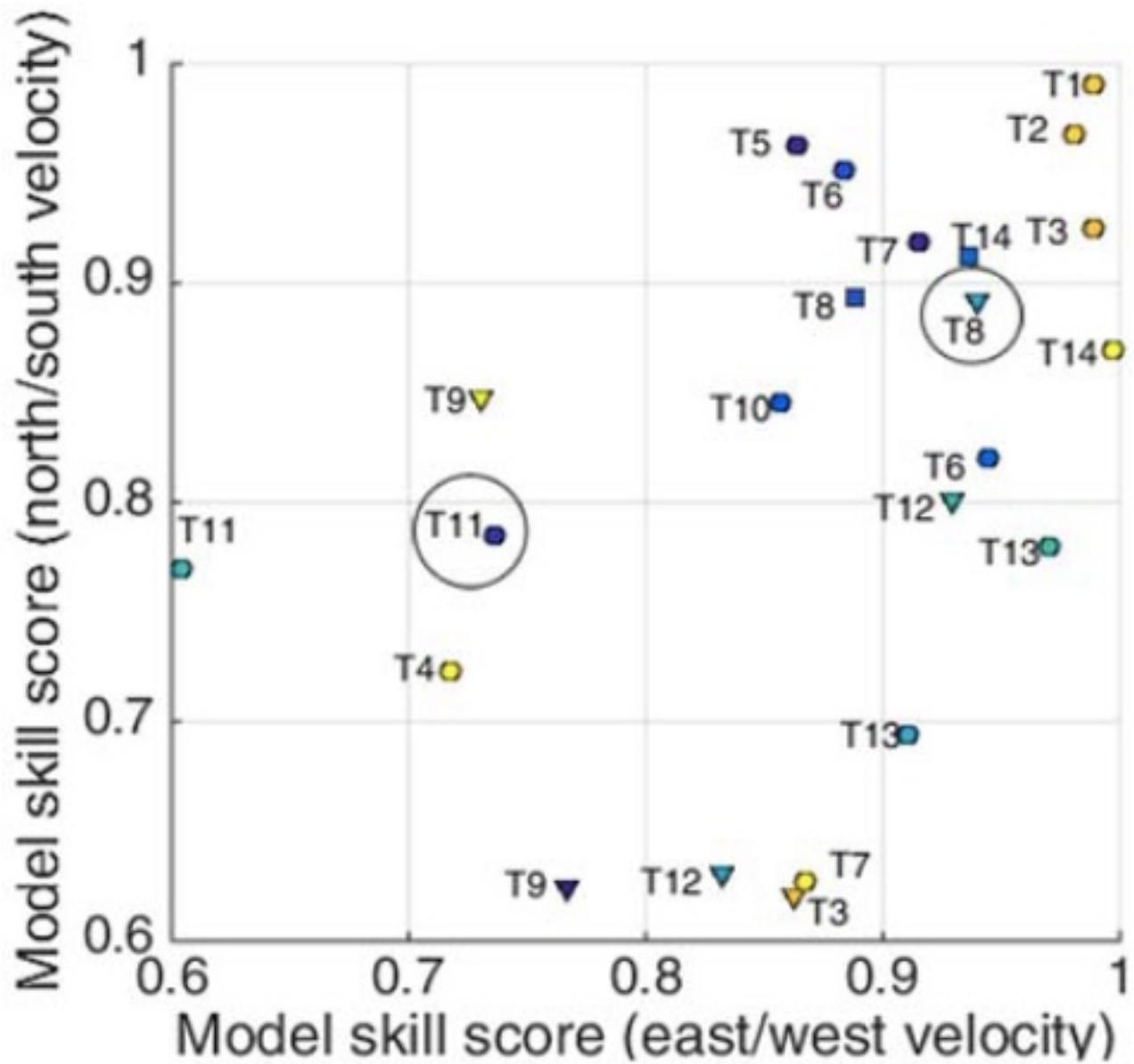


Transect 8



Conlon, Xue, Morello & Yund,
2018, JGR Oceans 123.

Longitude ($^{\circ}$ W)

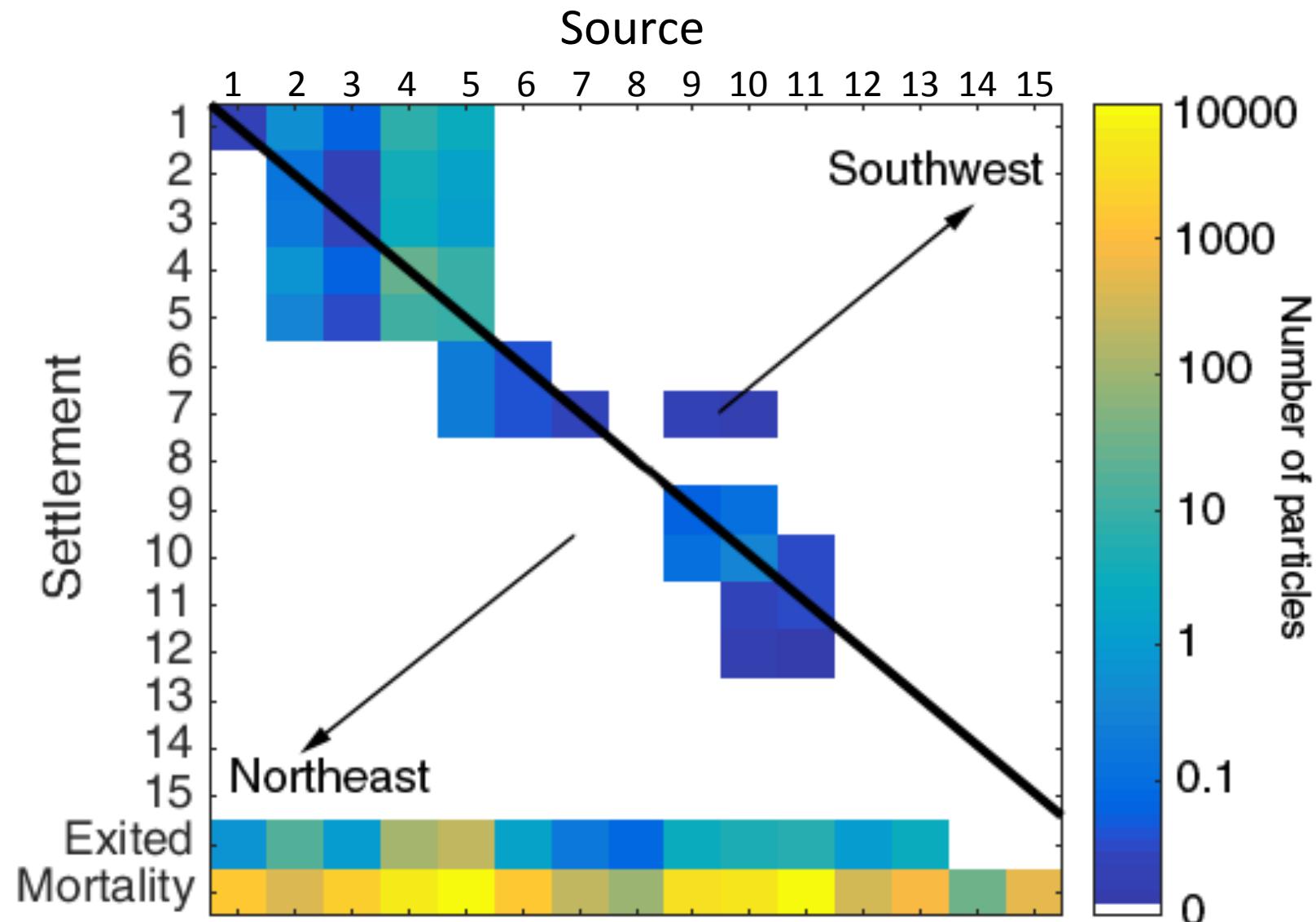


Biological Component of the Coupled Model

- 1) Temperature-dependent larval growth
- 2) Temperature-dependent larval mortality
- 3) Diel vertical migration
- 4) Population-specific spawning times
- 5) Number of virtual larvae released in each population proportional to reproductive output of each bed

Animation

Exchange among populations



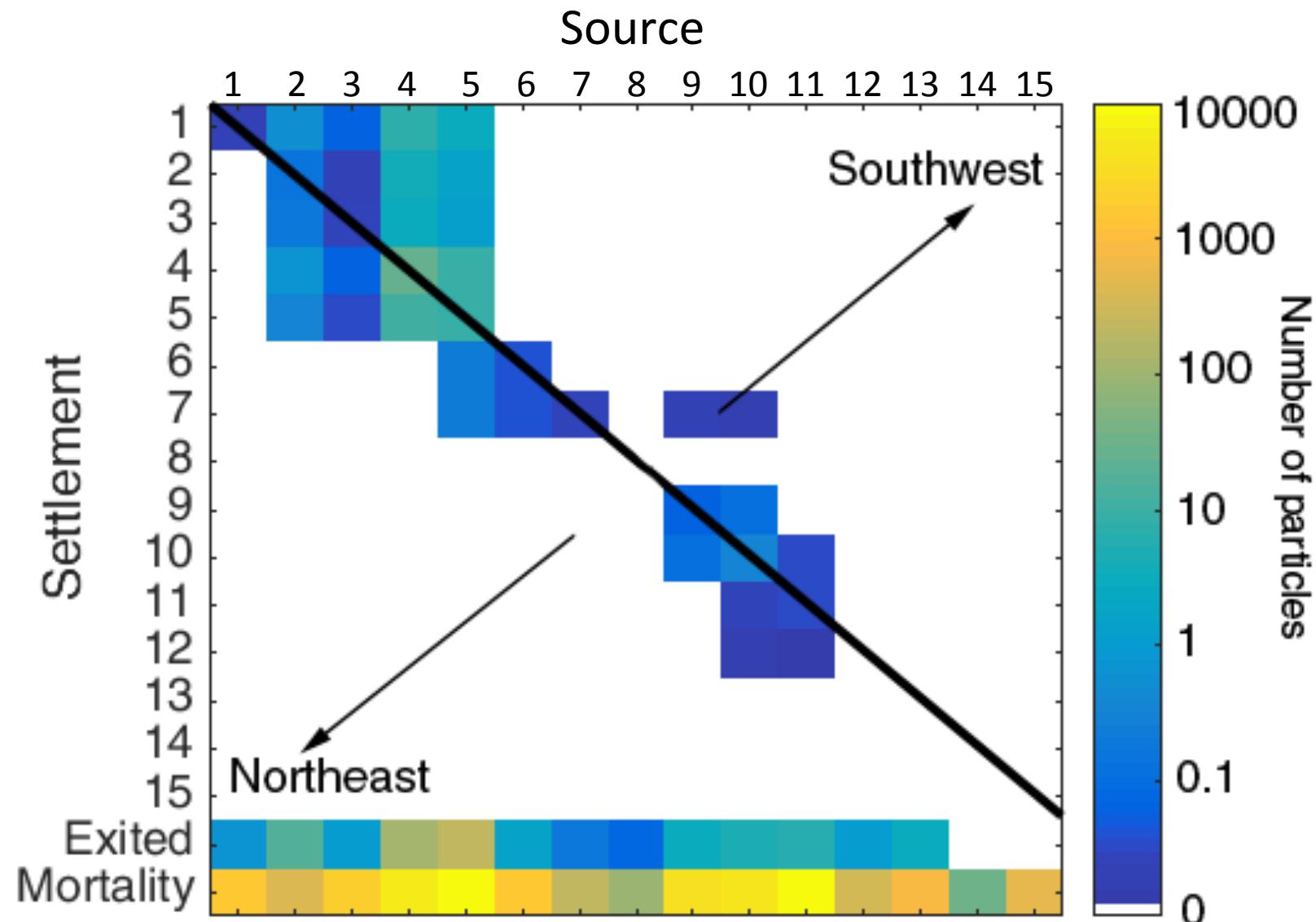
General Conclusions

- 1) Tidal exchange is the main source of across-shelf movement
- 2) Transport is mainly to the southwest, but limited northeasterly transport is possible
- 3) Most larvae that exit bays leave the eastern Maine system
- 4) Connectivity among bays is highest within 3-4 clusters
- 5) Larvae from sites down-bay of a basin tend to have greater retention and higher connectivity than sites at the top of a bay

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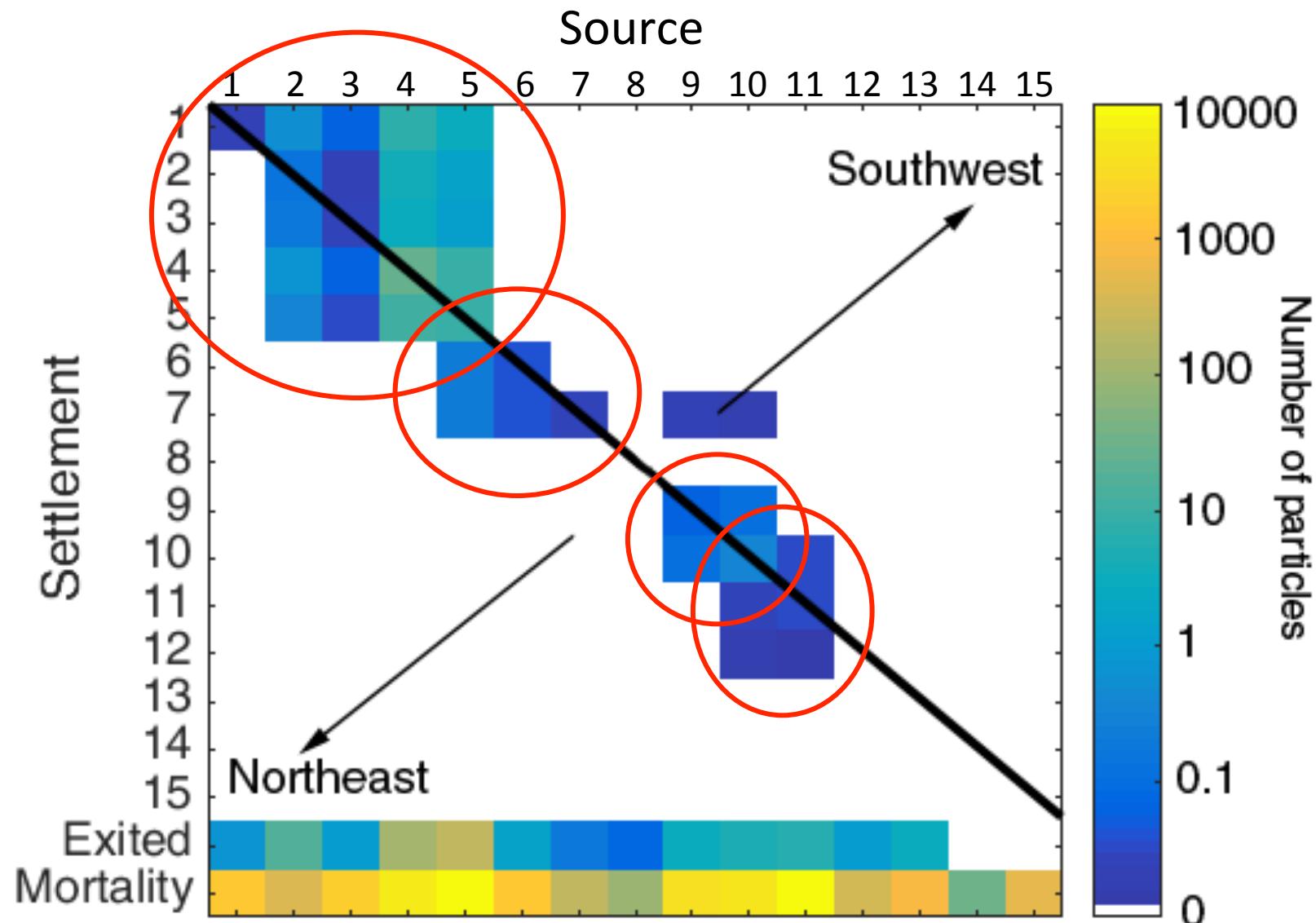
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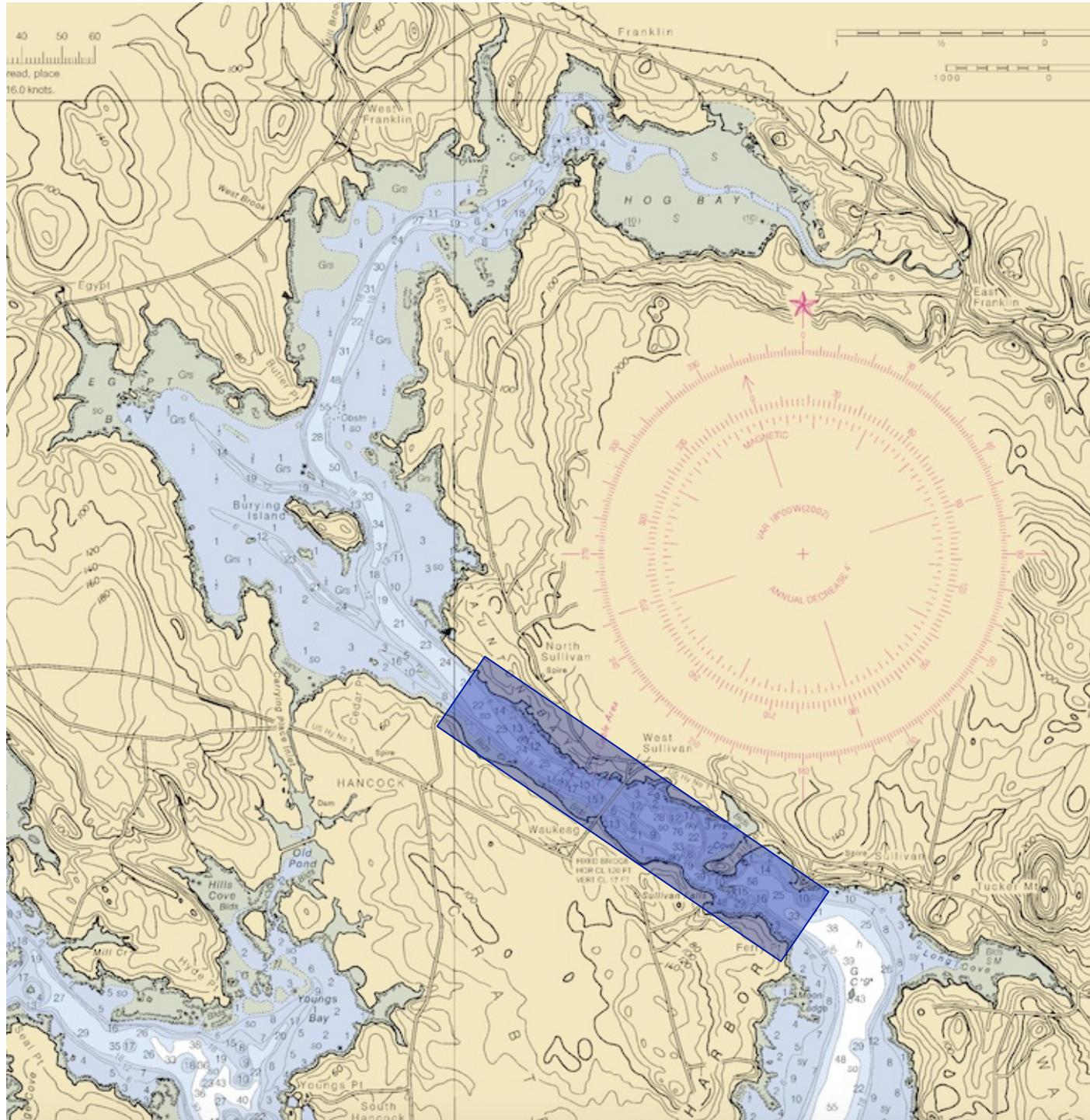
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Mussel bed in Taunton Bay

Because initial dispersal is in two directions, some larvae entrain within the bay and are further along in development when they exit the bay

Overall Conclusions

Coupled biophysical models have the potential to produce valuable information on oceanographic processes affecting larval transport, especially for weakly swimming larvae.

Models are most effective when implemented with high spatial and temporal resolution, supported by substantial larval and spawning data, and extensively validated with field data

Models are very useful in combination with other approaches:

- Assess physical environment experienced by larvae traveling different paths
- With a genomic approach, generate selection-free null hypotheses
- Allow sensitivity analyses for biological parameters