Update on Phase 7 Main Bay Model (MBM) Progress

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Outline

- **Development of living resource modules**
  - SAV, Tidal Marsh, Benthic Algae, Clam/Oyster
- **Clam/oyster model configuration, and preliminary results**
- **Sensitive studies on the MBM to assess effects of ocean boundary conditions**

Enhancement of the ICM model interfaces: output, initialization

- The ICM is one module in the SCHISM modeling systems. Its output and some model initialization used to be handled by SCHISM subroutines. This is not convenient
- **Added new interface for ICM output and initialization**
  - This new interface simplifies the process in outputting ICM variable values. It supports 2D and 3D global outputs, and both ICM state variables and intermediate variables (debug purpose).
  - It significantly simplifies the effort in adding new output variables, and all work can be done just on the ICM side.
  - Also, It facilitates addition of new outputs variables needed by the phase-7 assessment (requested by Richard).
  - Similarly for initialization of ICM variables

Work on the living resource modules in ICM

- **Background:** current ICM framework provides many new features and capabilities, and flexibility, which allows living resource modules to build on
- **Acknowledgement**: earlier works done by Carl Cerco, Nicole Cai, et al.

Available living resource modules

1. Submerged Aquatic Vegetation (SAV)
2. Tidal wetland/marshes (Marsh)
3. Oyster/Clam (Clam)
4. Benthic Algae (BA)

Documentation

- We first reviewed literatures and earlier model code about these modules, and then organized the model kinetics systematically.
- The documentation is not only an user manual, but also model developer's notes. The code structure and variable names/units generally follow the equations listed in the documentation.
- We have started documentation process for LR module.

Some new features on living resource modules

Note: we have documentation with consistent names to see how each parameter affects the model process.

- All module parameters support 2D spatially variable inputs.
- Each module can be activated in certain regions specified by users. Multiple modules can be run simultaneously.
- There is only one control file: ICM parameter input. To configure the modules, users only need to edit the parameter values.

CLAM parameters

cpatch0 determines the clam regions

```
&CLAM_ICM
!------------------------------------------------------------------------
!clam model:  (number of clam species is defined in the MARCO)
!calpha(clam=1:nclam, PC); cKTFR=(clam,2);  cTSS=(clam, 4)
!------------------------------------------------------------------------
cpatch0 =  -999           !region flag for clam. (1: ON all elem.; -999: spatial)
clam0   =  0.1    0.1    0.1    0.1    0.1     !initial clam conc. (g[C].m-2)
cfrmax  =  0.55   0.55   0.55   0.55   0.55    !maximum filtration rate (m3.g[C]-1.day-1)
cTFR    =  25.0   25.0   25.0   25.0   25.0    !optimal temperature of filtration (oC)
cKTFR   =  0.01   0.01   0.01   0.01   0.01    0.01 0.01 0.01 0.01 0.01   !T dependece of fil
csalt   =  7.0    7.0    7.0    7.0    7.0     !salinity when filtration is halved (psu)
cKDO    =  3.5    3.5    3.5    3.5    3.5     !DO dependece of filtration (mg-1.L)
cDOh    =  1.0    1.0    1.0    1.0    1.0     !DO conc. when filtration is halved (mg/L)
cfTSSm  =  0.1    0.1    0.1    0.1    0.1     !minimum value of TSS factor on filtration
cKTSS   =  1.0  1.0  1.0  1.0  1.0     1.0  1.0  1.0  1.0  1.0   !contribution coefficients
cTSS    =  4  4  4  4  4    5  5  5  5  5    20  20  20  20  20   25  25  25  25  25 !TSS values for its effect
cRF     =  0.1    0.1    0.1    0.1    0.1     !active respiration rate when filtering water
cIFmax  =  0.12   0.12   0.12   0.12   0.12    !maximum ingestion rate (g[C_food].g[C_clam]-1
calpha  =  0.75 0.75 0.75 0.75 0.75   0.75 0.75 0.75 0.75 0.75   0.75 0.75 0.75 0.75 0.75   1
cMTB    =  0.008  0.008  0.008  0.008  0.008   !basal metabolism rate (day-1)
cTMT    =  20.0   20.0   20.0   20.0   20.0    !reference temperature for metabolism (oC)
cKTMT   =  0.069  0.069  0.069  0.069  0.069   !temperature dependence for metabolism (oC-1)
cMRT    =  0.03    0.03    0.03    0.03    0.03     !mortality rate (day-1)
cPRR    =  0.00   0.00   -999   -999   0.005   !seasonal predation rate (day-1)
cHSR    =  -999   -999   -999   -999   -999    !seasonal harvest rate (day-1)
cDoyp   =  0   0   152 152  0      0  0  304  304  0 !date range for predation (day of year)
cDoyh   =  122  122  122  122  122    274  274  274  274  274 !date range for predation (day of year)
cn2c    =  0.167  0.167  0.167  0.167  0.167   !nitrogen to carbon ratio
cp2c    =  0.011  0.011  0.011  0.011  0.011   !phosphorus to carbon ratio
/
```

'-999' means 2D spatial values

explanation of the parameters, and units

Submerged Aquatic Vegetation (SAV)

❑ Major Variables

- SAV leaf, stem and root biomass (g[C].m^{-2})
- SAV canopy height (m)

❑ Major processes

- Effects on the hydrodynamics (new to P7)
- Light attenuation by SAV leaf and stem
- Photosynthesis at SAV leaves
- Effects of temperate, light, nutrients
- Respiration of SAV leaf/stem/root
- Interaction with water column variables
- Interaction with sediment layer

snapshot of developer's notes

The Development of SAV Model in SCHISM-ICM

1 Introduction

This manual is written to document the development of submerged aquatic vegetation (SAV) model in SCHISM-ICM (EPA Phase-7 model). It is largely based on (Cai, Xun, 2018; Cerco et al., 2010)

2 Kinetics

2.1 SAV biomass and canopy

The current SAV model only supports one species by simulating the total biomasses of SAV leaf, stem and root in dry weight (g[C]·m^{-2}) with the following denotation:

$$C_m = \begin{cases} leaf, & \text{m=1} \\ stem, & \text{m=2} \\ root, & \text{m=3} \end{cases}. \tag{1}$$

$$C_m^Z = \frac{C_m}{H_S}, \quad \text{m=1, 2} \tag{2}$$

$$H_S = \min\left(\sum_m c2h_m \cdot \frac{C_m}{c2dw} + H_S^{\min},\ H_S^{\max}\right) \tag{3}$$

where C_m represents the total biomass of leaf/stem/root (g[C]·m^{-2}), $C_m^w(z)$ is the leaf/stem/root concentration in the vertical (g[C]·m^{-3}), H_S is the canopy height (m), $c2h_m$ is the coefficient converting SAV biomass to canopy height (g^{-1}[C]·m^{3}), H_W is water depth (m), and $c2dw$ is coefficient converting wet weight to dry weight, $H_S^{\min}$ and $H_S^{\max}$ are the minimum and maximum SAV canopy heights allowed (m). At the beginning of each time step, the total biomass of SAV leaf and stem will be distributed to the water column using Eq. (2). Then, the biological processes will be computing at each layer based on C_m^Z. At the end of each time step, the total SAV biomass C_m will be updated:

$$C_m = \int_{-H_w}^{-H_w+H_S} C_m^Z \cdot dz, \quad \text{m=1, 2} \tag{4}$$

where H_w is the water depth (m).

Benthic Algae (BA)

Major Variables

- It currently supports one specie (can be extended).
- Benthic algae biomass (g[C].m^{-2})

Major processes

- Algal growth
- Effects of temperate, light, nutrients
- Respiration
- Predation
- Interaction with bottom water
- Interaction with sediment layer

snapshot of developer's notes

The Development Manual of Benthic Algae Model in SCHISM-ICM

1 Introduction

This manual document the development of benthic algae module in SCHISM-ICM (Phase-7 EPA model) framework, which is largely based on CH3D-ICM (Phase-6) and (Cerco & Seitzinger, 1997).

2 Kinetics

2.1 The growth, metabolism and predation of benthic algae

Currently, only one benthic algae species is supported. The key processes related to the benthic algae are growth, basal metabolism and predation by higher trophic organisms. The mass-balance equation is:

$$\frac{dBA}{dt} = GP - MT - PR \tag{1}$$

$$GP = GPM \cdot f(T) \cdot f(I) \cdot f(N) \cdot BA \tag{2}$$

$$MT = MTB \cdot \exp\left[KTR \cdot (T - TR)\right] \cdot BA \tag{3}$$

$$PR = PRR \cdot \exp\left[KTR \cdot (T - TR)\right] \cdot BA \tag{4}$$

where BA standards for the biomass of benthic algae (g[C]·m^{-2}), GP is the growth rate (g[C] ·m^{-2}·day^{-1}), MT is the metabolism rate (g[C] ·m^{-2}·day^{-1}), and PR is the predation rate (g[C] ·m^{-2}·day^{-1}), GPM is maximum growth rate (day^{-1}), $f(T)$, $f(I)$ and $f(N)$ are the limiting factors from temperature, light and nutrient ($0 \le f \le 1$), MTB is the metabolism rate (day^{-1}) at reference temperature TR (°C), PRR is the predation rate (day^{-1}) at reference temperature TR, and KTR is the temperature dependence for metabolism and predation (°C-1).

The temperature limiting factor is:

$$f(T) = \begin{cases} \exp\left[-KTGP_1 \cdot (T - TGP)^2\right], & \text{if } T < TGP \\ \exp\left[-KTGP_2 \cdot (T - TGP)^2\right], & \text{if } T < TGP \end{cases}, \tag{5}$$

Oyster/Clam

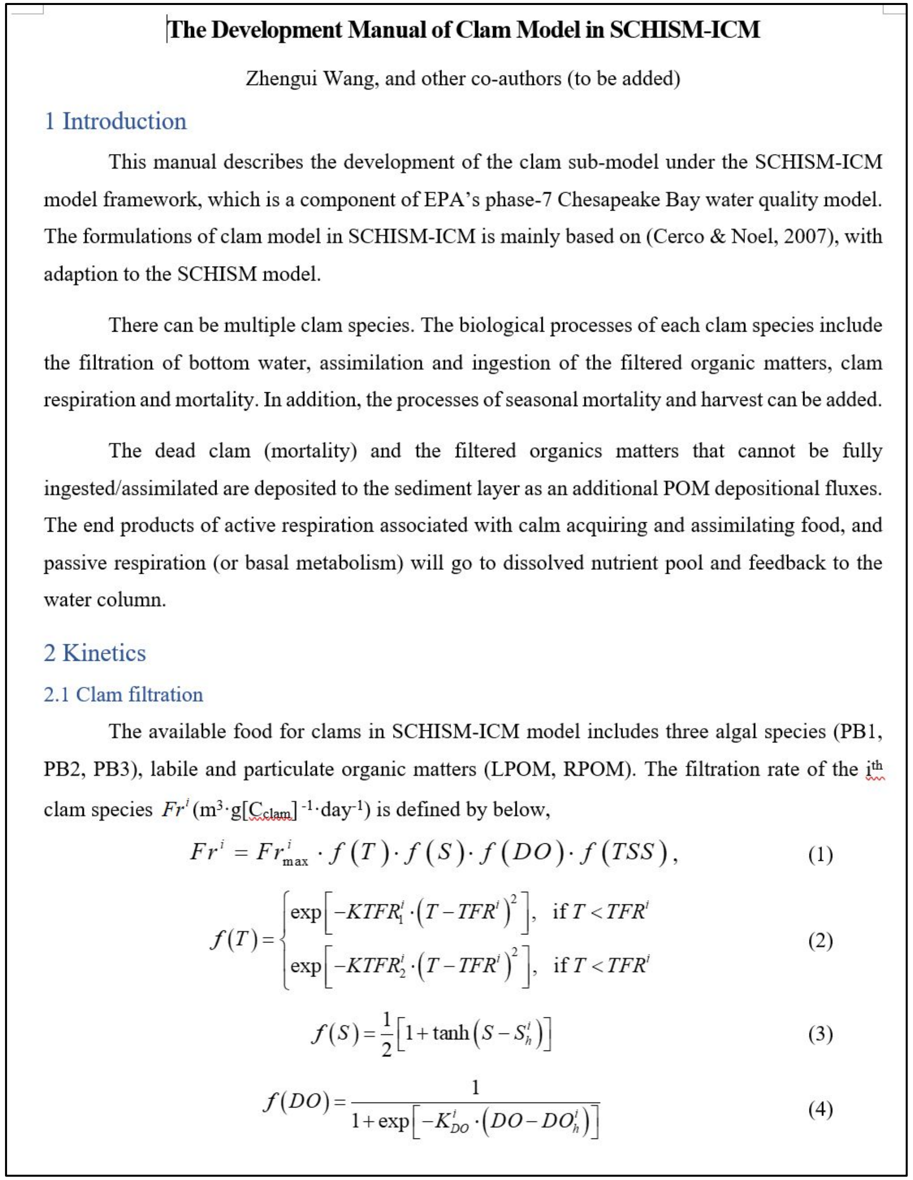
❑ Major Variables

- It supports any number of clam species.
- Clam biomass of each species (g[C].m^{-2})

❑ Major processes

- Clam/oyster filtration: phytoplankton, POMs
- Effects of temperate, salinity, DO, and TSS on filtration
- Growth
- Metabolism
- Mortality
- Predation
- Harvest
- Interaction with water column variables
- Interaction with sediment layer

snapshot of developer's notes



The Development Manual of Clam Model in SCHISM-ICM

Zhengui Wang, and other co-authors (to be added)

1 Introduction

This manual describes the development of the clam sub-model under the SCHISM-ICM model framework, which is a component of EPA's phase-7 Chesapeake Bay water quality model. The formulations of clam model in SCHISM-ICM is mainly based on (Cerco & Noel, 2007), with adaption to the SCHISM model.

There can be multiple clam species. The biological processes of each clam species include the filtration of bottom water, assimilation and ingestion of the filtered organic matters, clam respiration and mortality. In addition, the processes of seasonal mortality and harvest can be added.

The dead clam (mortality) and the filtered organics matters that cannot be fully ingested/assimilated are deposited to the sediment layer as an additional POM depositional fluxes. The end products of active respiration associated with calm acquiring and assimilating food, and passive respiration (or basal metabolism) will go to dissolved nutrient pool and feedback to the water column.

2 Kinetics

2.1 Clam filtration

The available food for clams in SCHISM-ICM model includes three algal species (PB1, PB2, PB3), labile and particulate organic matters (LPOM, RPOM). The filtration rate of the ith clam species Fr^i (m^3·g[C$_{clam}$]$^{-1}$·day^{-1}) is defined by below,

$$Fr^i = Fr^i_{max} \cdot f(T) \cdot f(S) \cdot f(DO) \cdot f(TSS), \qquad (1)$$

$$f(T) = \begin{cases} \exp\left[-KTFR_1^i \cdot \left(T - TFR^i\right)^2\right], & \text{if } T < TFR^i \\ \exp\left[-KTFR_2^i \cdot \left(T - TFR^i\right)^2\right], & \text{if } T < TFR^i \end{cases} \qquad (2)$$

$$f(S) = \frac{1}{2}\left[1 + \tanh\left(S - S_h^i\right)\right] \qquad (3)$$

$$f(DO) = \frac{1}{1 + \exp\left[-K_{DO}^i \cdot \left(DO - DO_h^i\right)\right]} \qquad (4)$$

Tidal Marsh

- **Use the simple P6 approach as a start**
- **Prepare for future development, with a WQ module for marsh**
- **Major Variables**
  - It supports any number of marsh species.
  - Marsh leaf, stem and root biomass (g[C].m^{-2})
  - Marsh canopy height (m)
- **Major processes**
  - Effect on the hydrodynamics
  - Light attenuation by marsh
  - Photosynthesis at marsh leaves
  - Effects of temperate, light, nutrients, salinity stress, inundation stress
  - Respiration of marsh leaf/stem/root
  - Interaction with water column variables
  - Interaction with sediment layer

snapshot of developer's notes/manual

The Development of Marsh Model in SCHISM-ICM

1 Introduction

This manual is written for the development of marsh model in SCHISM-ICM (Phase-7 EPA model) framework. It largely based on (Cai, Xun, 2022; Cerco & Noel, 2017).

2 Kinetics

There can be multiple marsh species. The model simulates the total biomass in dry weight of marsh leaf/stem/root with no vertical discretization. To simplify the representation, C_m^i will be used to represent the biomass of marsh leaf/stem/root (g[C].m^{-2}), where the superscript denotes the i^{th} marsh specie, and the subscript denotes the leaf/stem/root:

$$C_m^i = \begin{cases} leaf^i, & \text{m=1} \\ stem^i, & \text{m=2} \\ root^i, & \text{m=3} \end{cases} \qquad (1)$$

Canopy height is an important property of marsh with its formulation as:

$$h_c^i = \begin{cases} h_0^i + c2h_1^i \cdot C_{12}^i, & C_{12}^i \le C_{cr}^i \\ h_0^i + c2h_1^i \cdot C_{cr}^i + c2h_2^i \cdot \left(C_{12}^i - C_{cr}^i\right), & C_{12}^i > C_{cr}^i \end{cases}, \qquad (2)$$

$$C_{12}^i = \frac{\left(C_1^i + C_2^i\right)}{c2dw^i} \qquad (3)$$

where h_c^i is the canopy height (m), C_{12}^i is the sum of leaf and stem biomass in wet weight (g[C]·m^{-2}), $c2dw^i$ is the conversion coefficient from wet weight to dry weight, h_0^i is the base height (m), $c2h_1^i$ is the conversion coefficient from marsh biomass to canopy height (m^3·g^{-1}[C]) when C_{12}^i is less than the reference biomass C_{cr}^i (g[C]·m^{-2}) in wet weight.

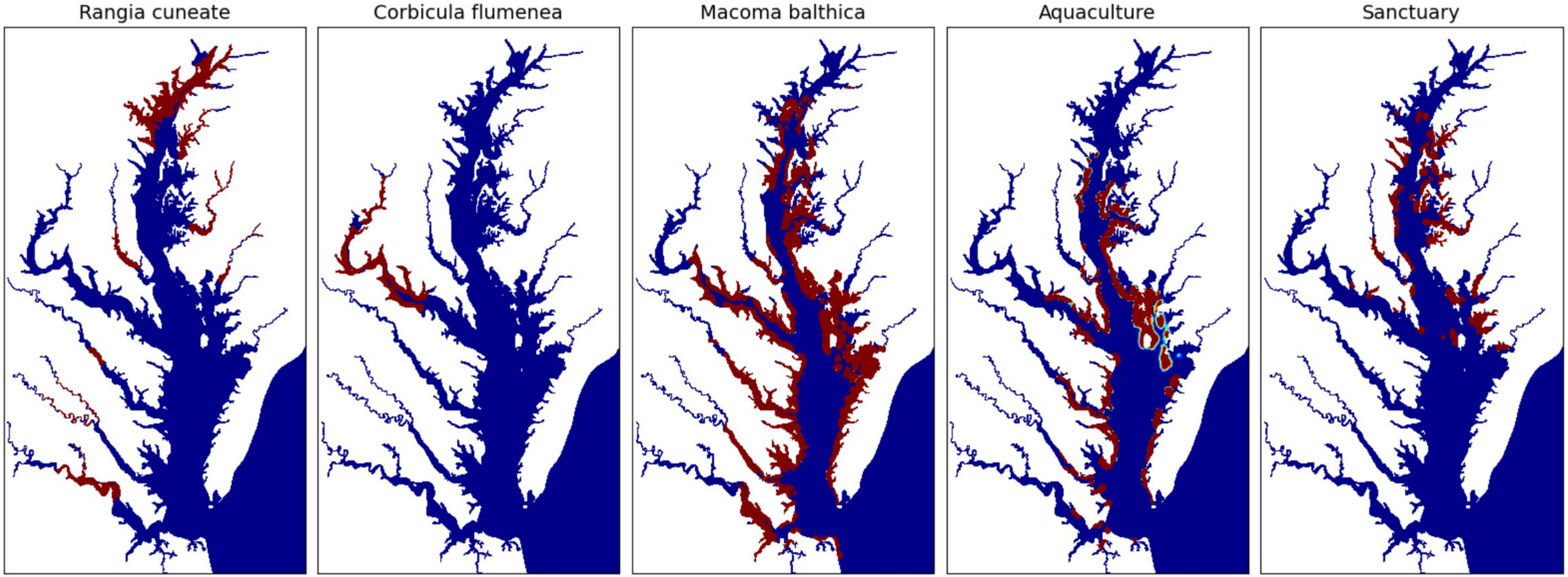
2.1 Marsh Growth Rate

The photosynthesis of marsh growth only happens in the leaf, and the total growth rate is:

$$GP^i = GPM^i \cdot f^i(I).f^i(T) \cdot f^i(N) \cdot f^i(ST) \cdot f^i(IS) \cdot C_1^i, \qquad (4)$$

First test of Clam Module

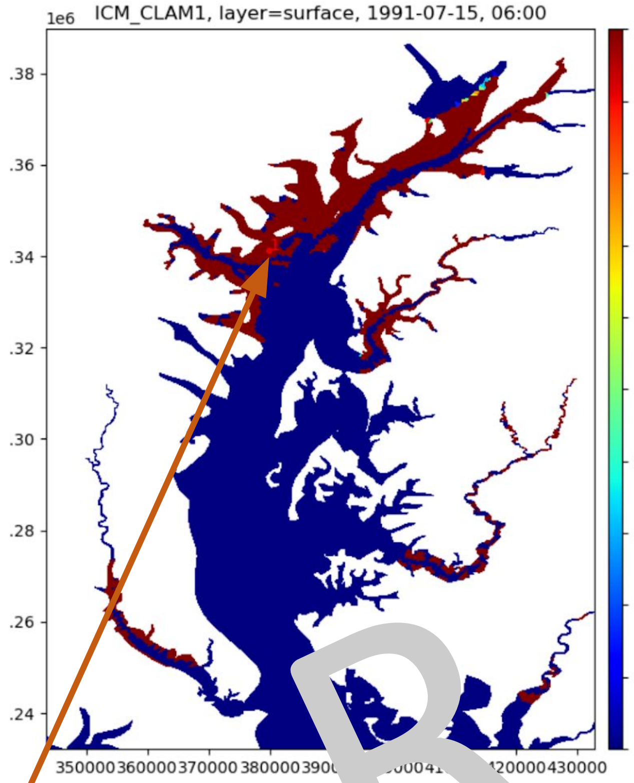
- ❖ The model configuration is largely based phase-6 model input (provided by Richard)
- ❖ Five oyster/clam species are simulated
  - **Natural species:** *Rangia cuneate (1st panel), Corbicula flumenea, Macoma balthica*
  - **Aquaculture species**
  - **Sanctuary species**
- ❖ **First test results: validation pending**

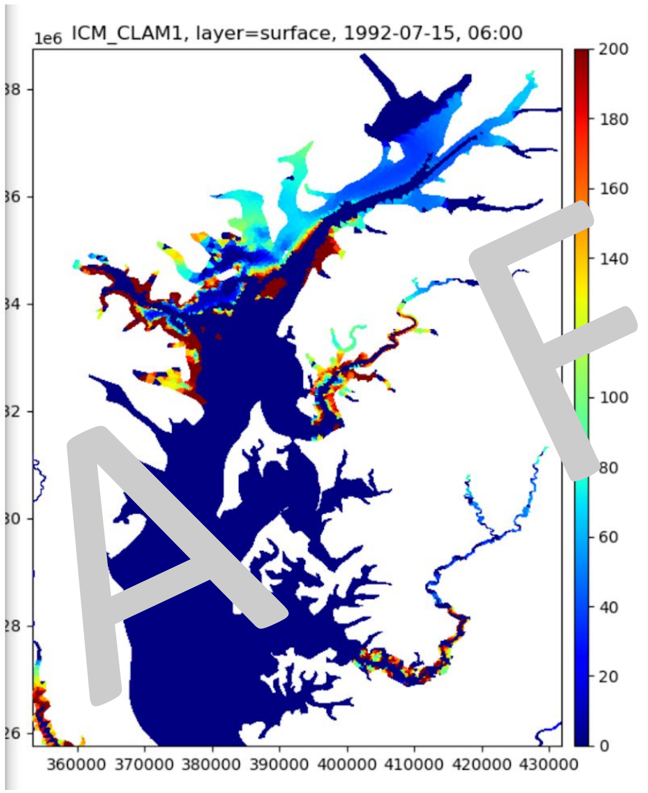


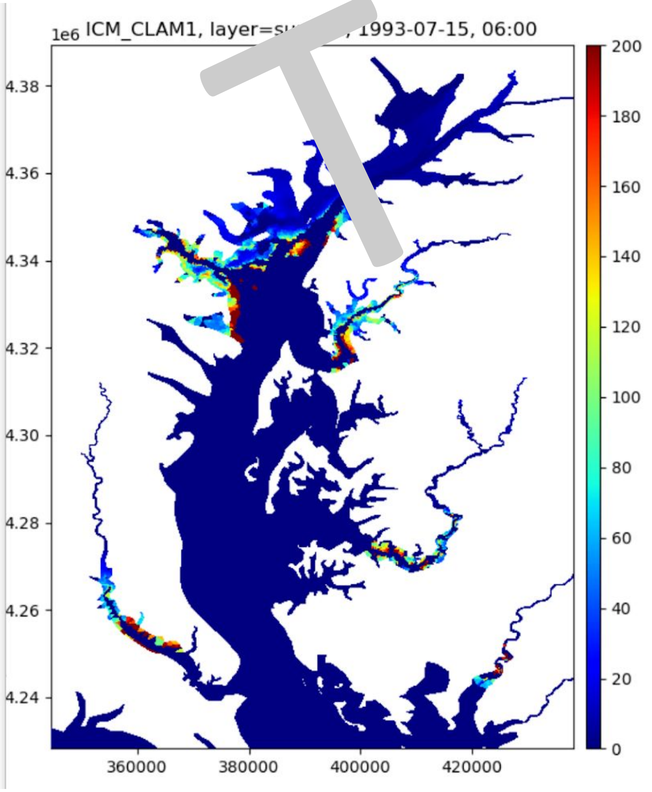
Test Results: *Rangia cuneate*

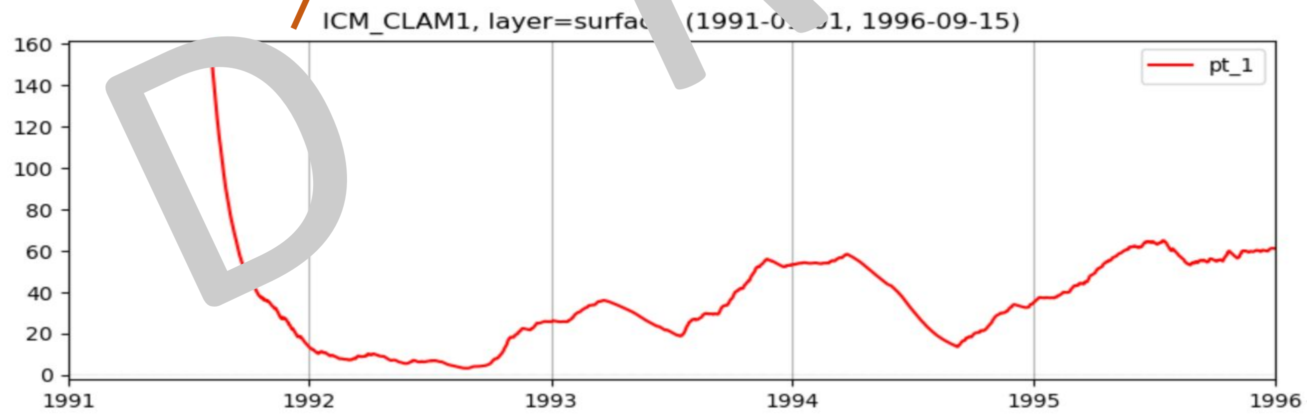
7/15, 1991 **7/15, 1992** **7/15, 1993**

Biomass Conc ($g[C].m^{-3}$)







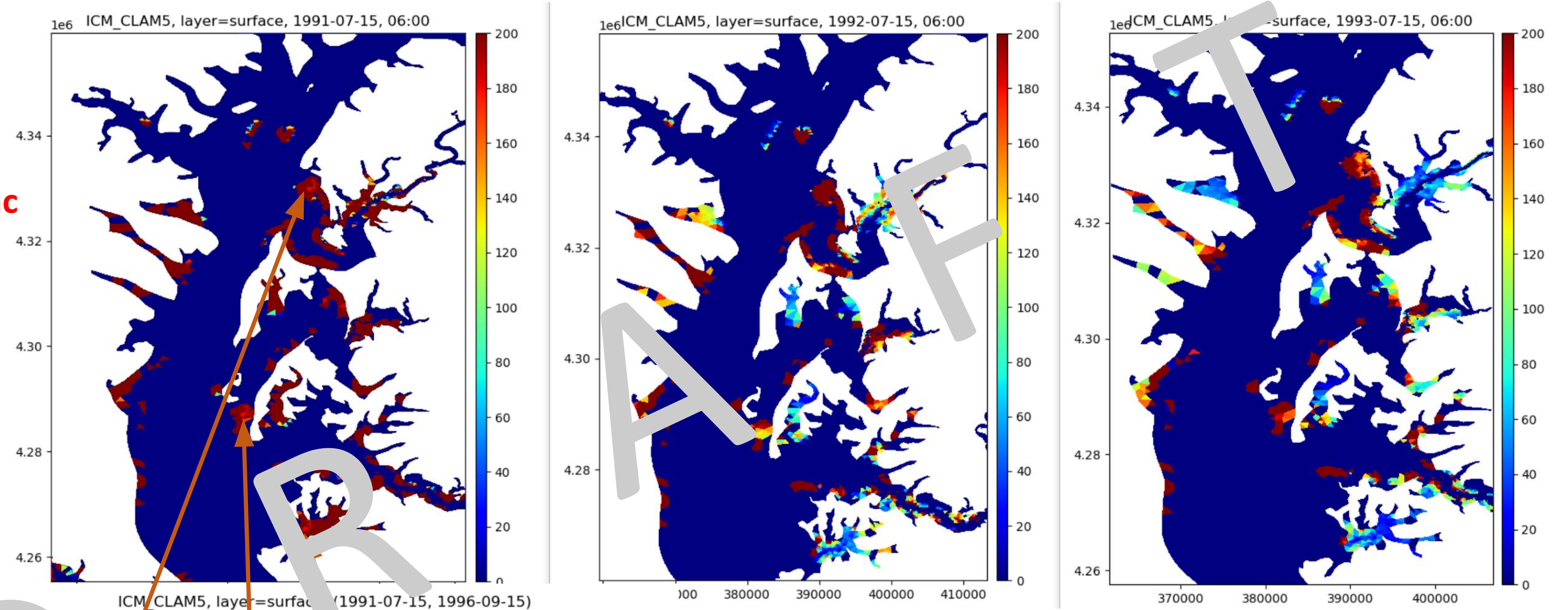


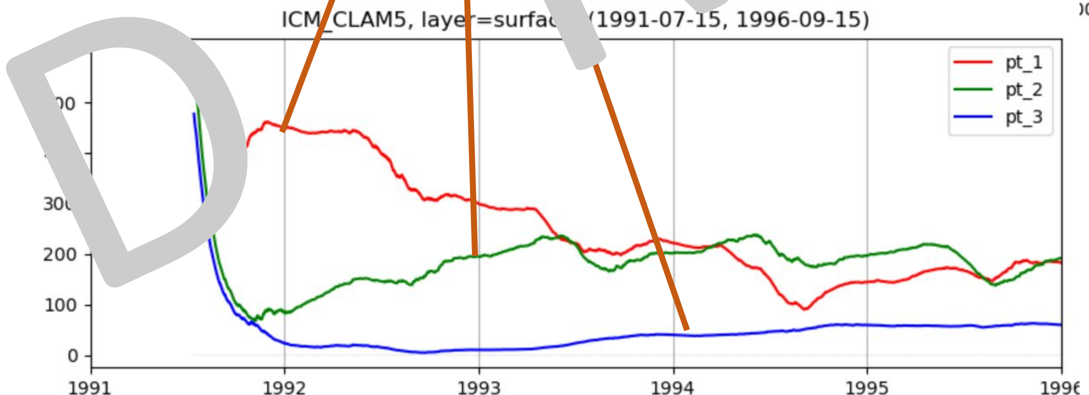
- After the spin-up in the first 2 years, seasonal cycle seems stable.
- Next step: model result needs to be further tuned, and compared with observations.

Test Results: Sanctuary species

7/15, 1991 | **7/15, 1992** | **7/15, 1993**

Biomass Conc ($g[C].m^{-3}$)

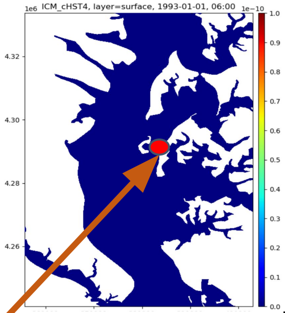




- After the spin-up in the first 2 years, seasonal cycle seems stable.
- Model result needs to be further tuned, and compared with observations.

Diagnostic variables: Sanctuary species

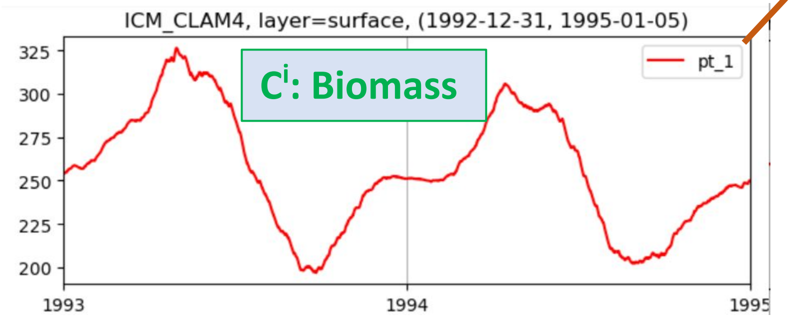
- The current clam model allows easy examination of each process in detail.
- The seasonal patterns of clam growth, metabolism and Harvest seem reasonable.

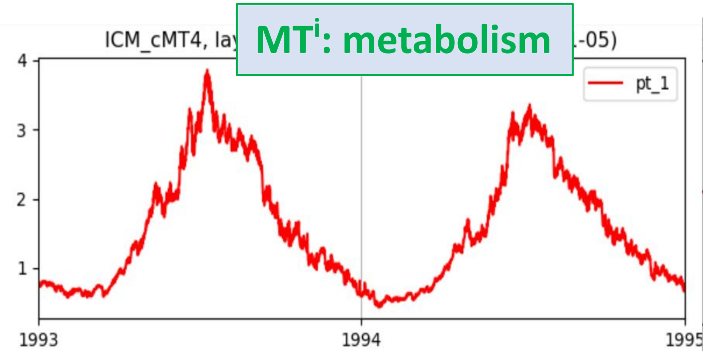


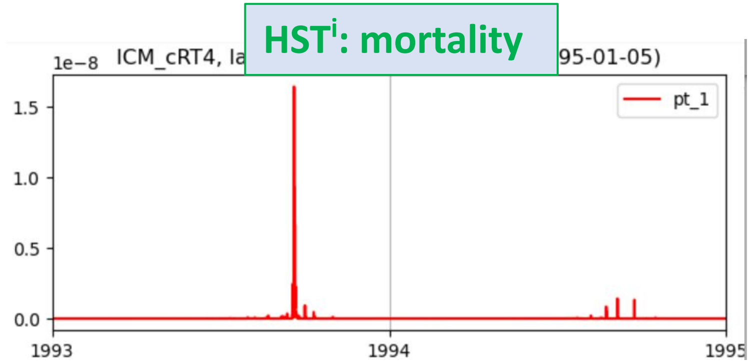
$$\frac{dC^i}{dt} = GP^i - MT^i - RT^i - PR^i - HST^i, \qquad (13)$$

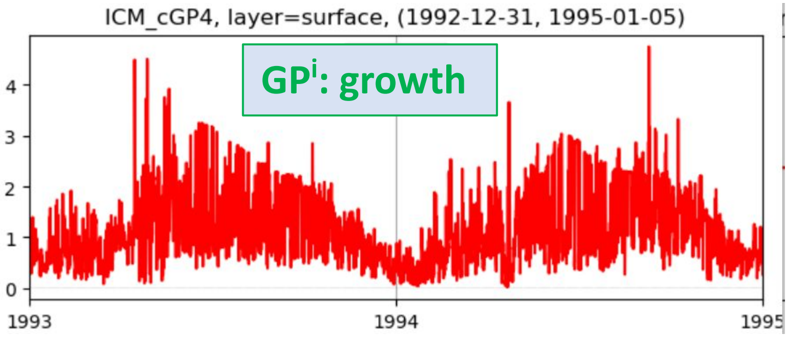
$$GP^i = \sum_m f(N)\cdot \alpha_m^i \cdot IF^i \cdot \left(1 - RF^i\right)\cdot PC_m \cdot Fr^i \cdot C^i \qquad (14)$$

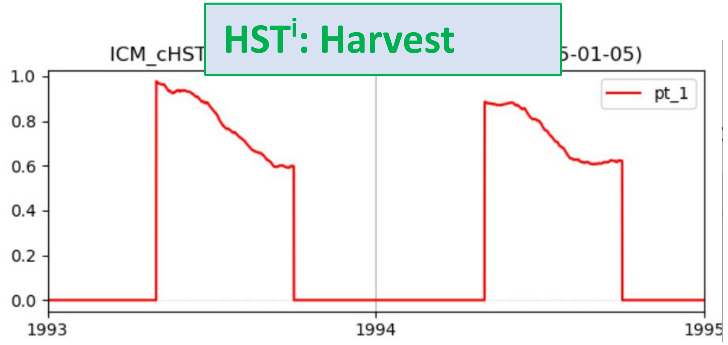
where GP^i, MT^i, RT^i are the clam growth, basal metabolism, and mortality (g[C].m^{-2}.day^{-1}), respectively, PR^i and HST^i are the seasonal clam predation, and harvest (g[C].m^{-2}.day^{-1}), $f(N)$

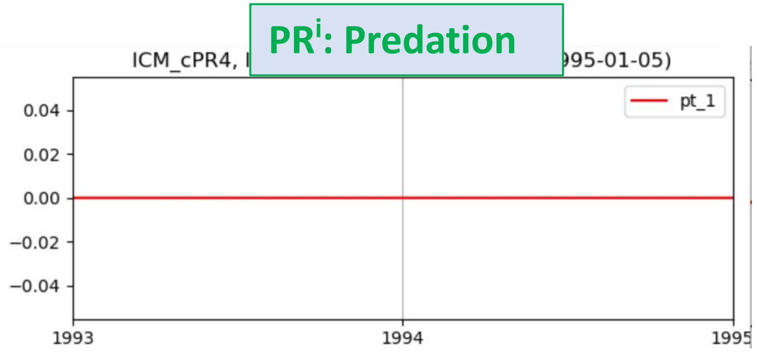








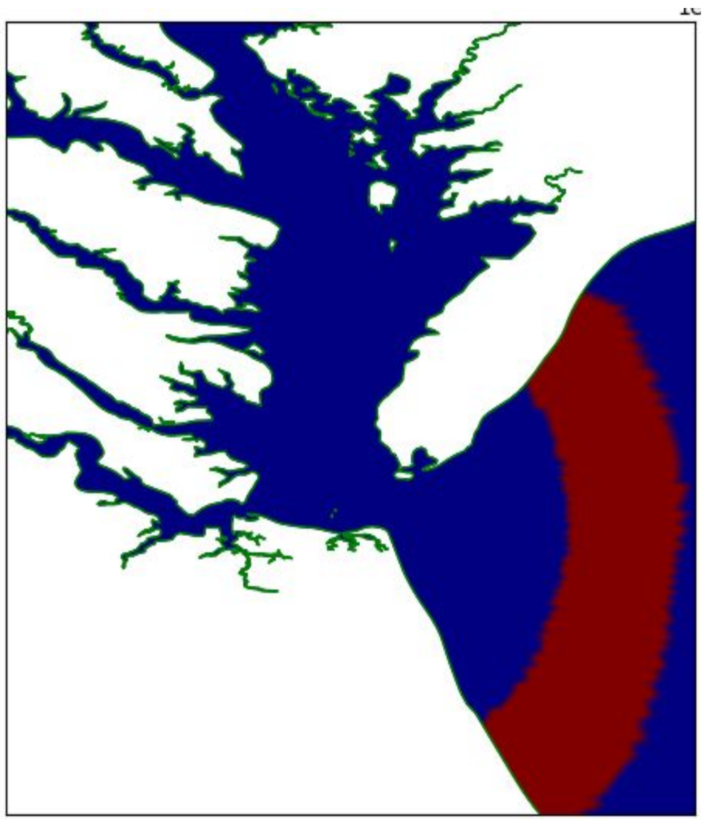


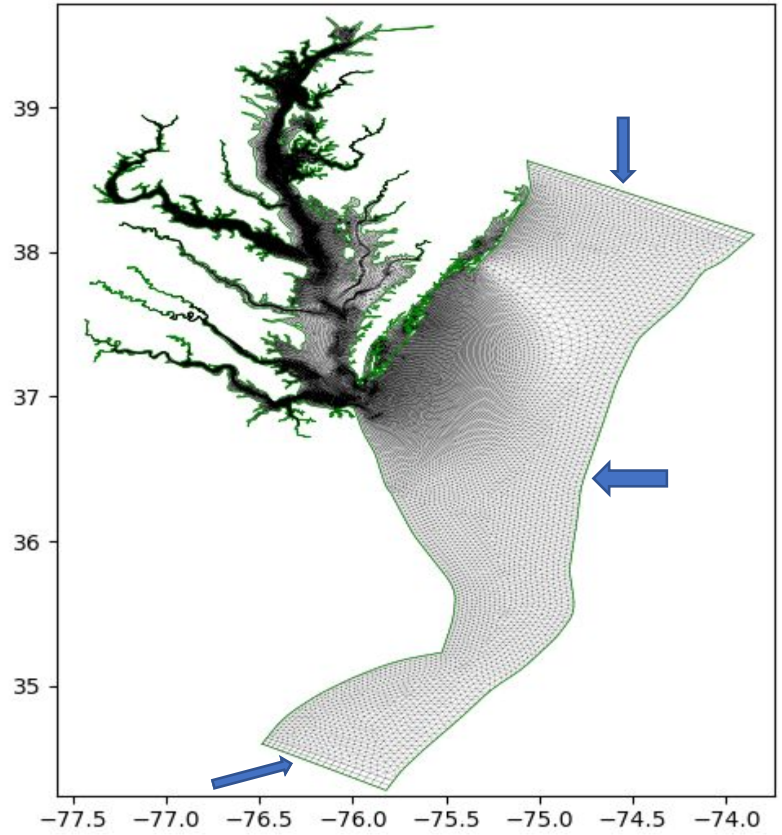


Exploratory study for ocean boundary condition

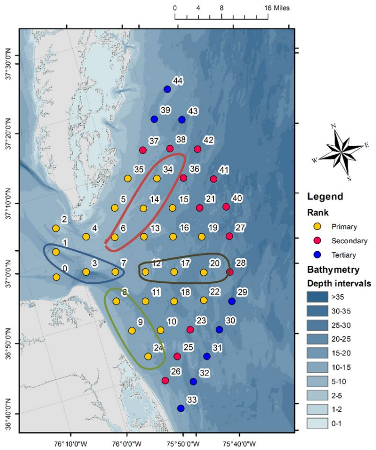
Motivation

- Previously, coastal relaxation was used to constrain WQ variables (e.g. DOC)
- It’d be more convenient to use the original ocean boundary for climate change studies.
- Sensitive tests were conducted to explore the feasibility of imposing b.c. at the original ocean boundary.



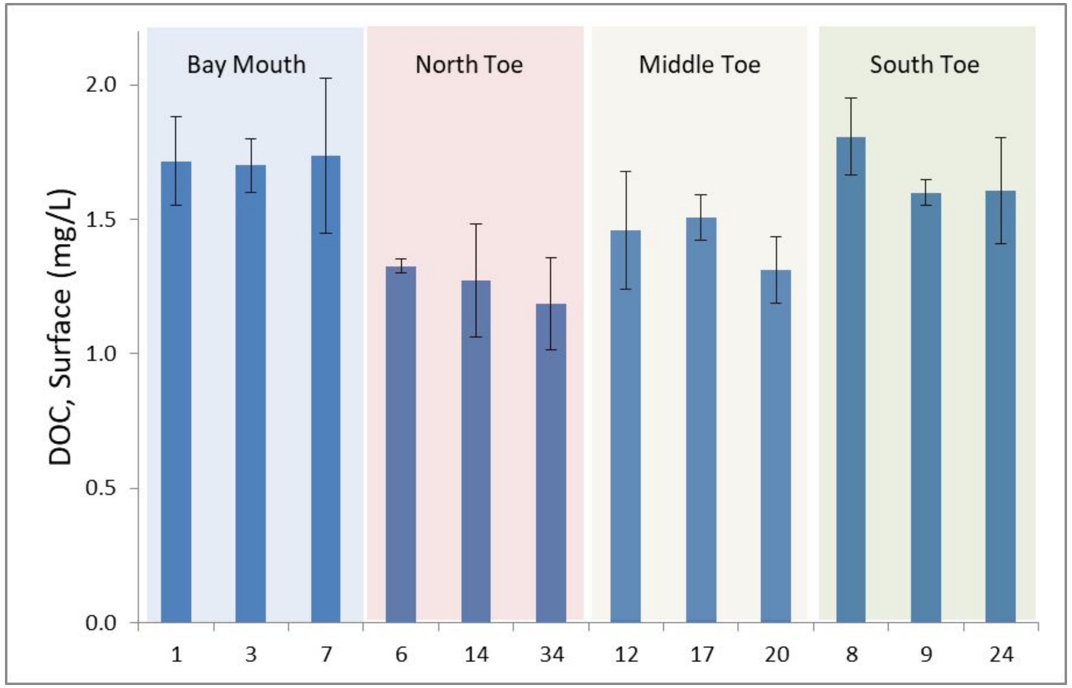


DOC Observation

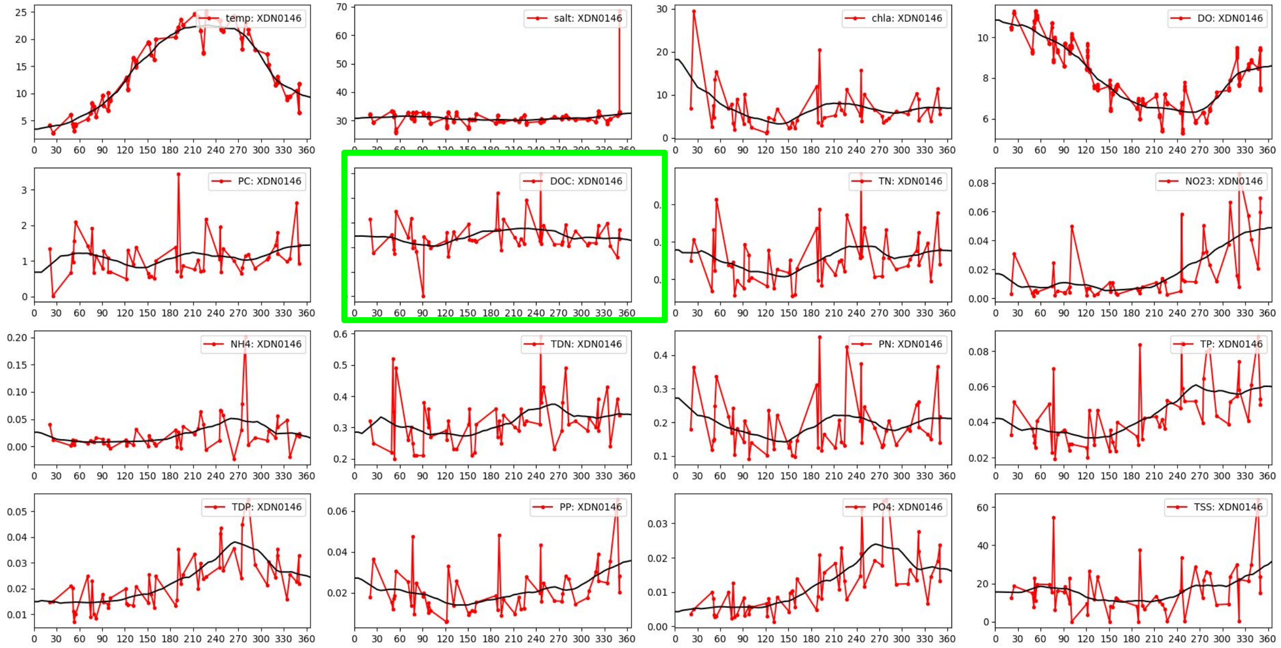


- In our current MBM setup, relaxation was used to reproduce the high DOC concentrations in the coastal region

DOC: Bay Mouth (from Testa)



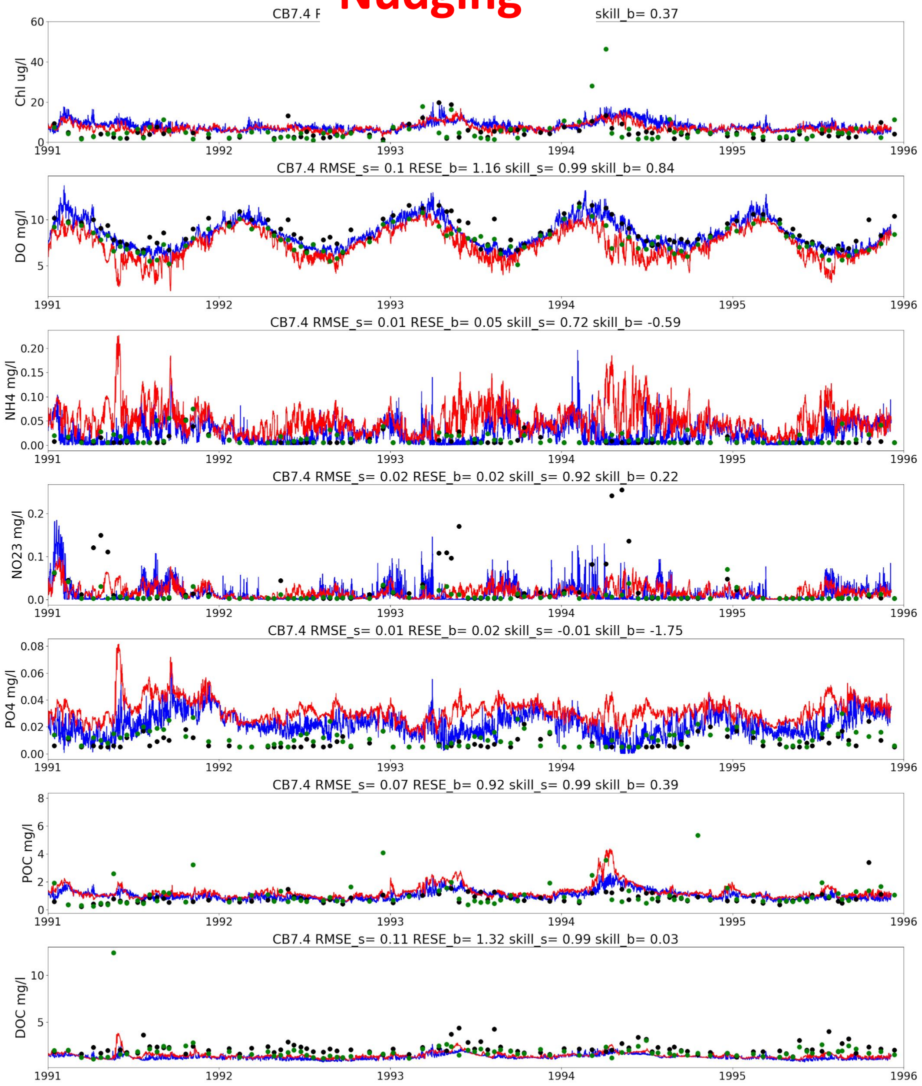
DOC: Maryland Coastal Bay Inlet



Comparison: nudging VS original boundary @CB7.4

- Using boundary condition at ocean, the model seems to get reasonable results at Bay mouth, except for lower nutrient concentrations (DOC, NH4, PO4) and higher bottom DO.

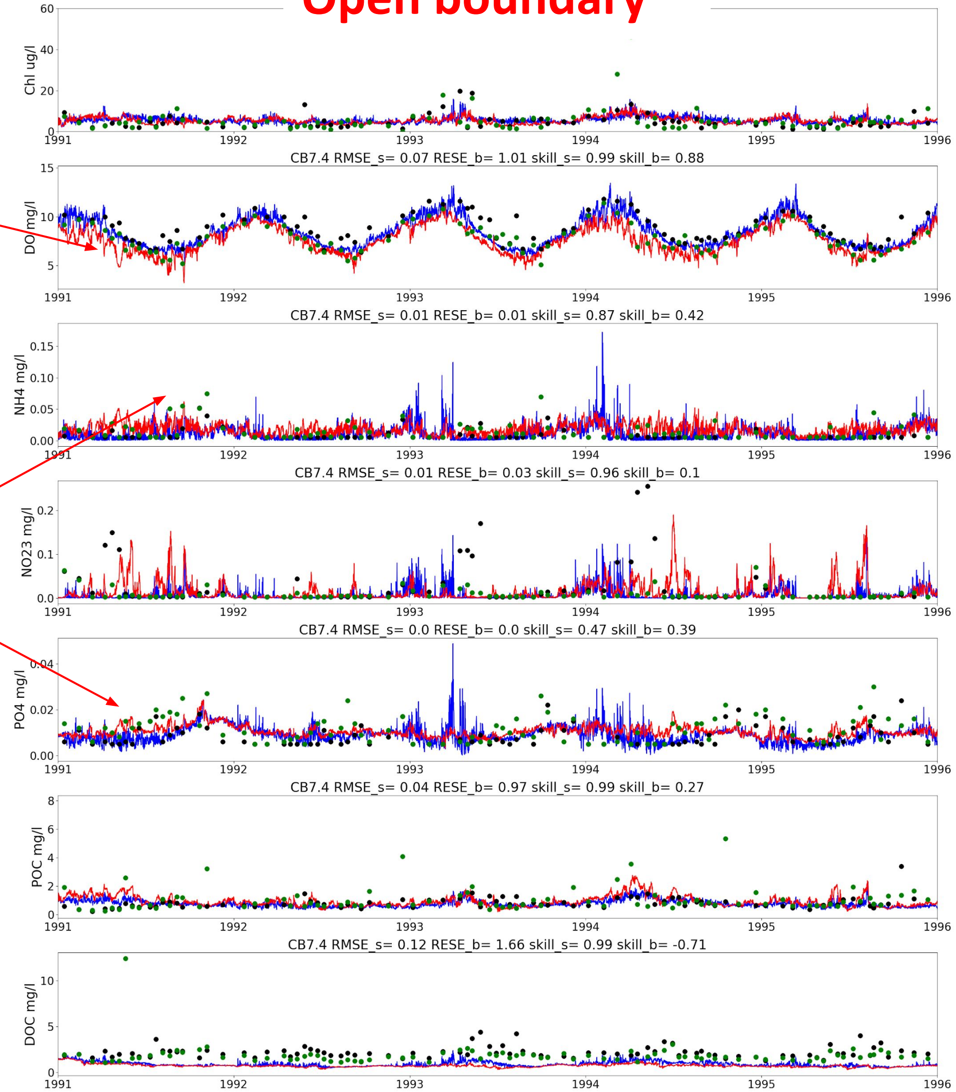
Nudging



Lower DOC
Higher DO

lower NH4
lower PO4

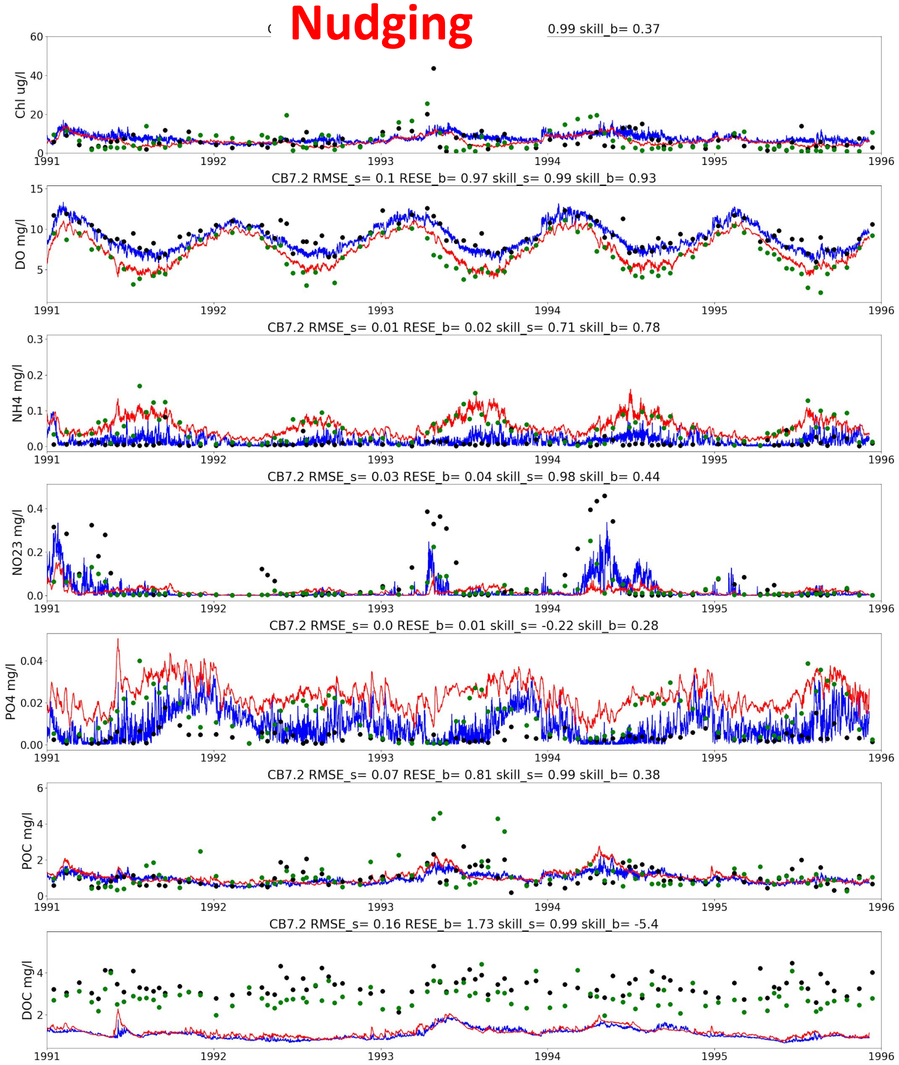
Open boundary



Comparison: nudging VS original boundary @CB7.2

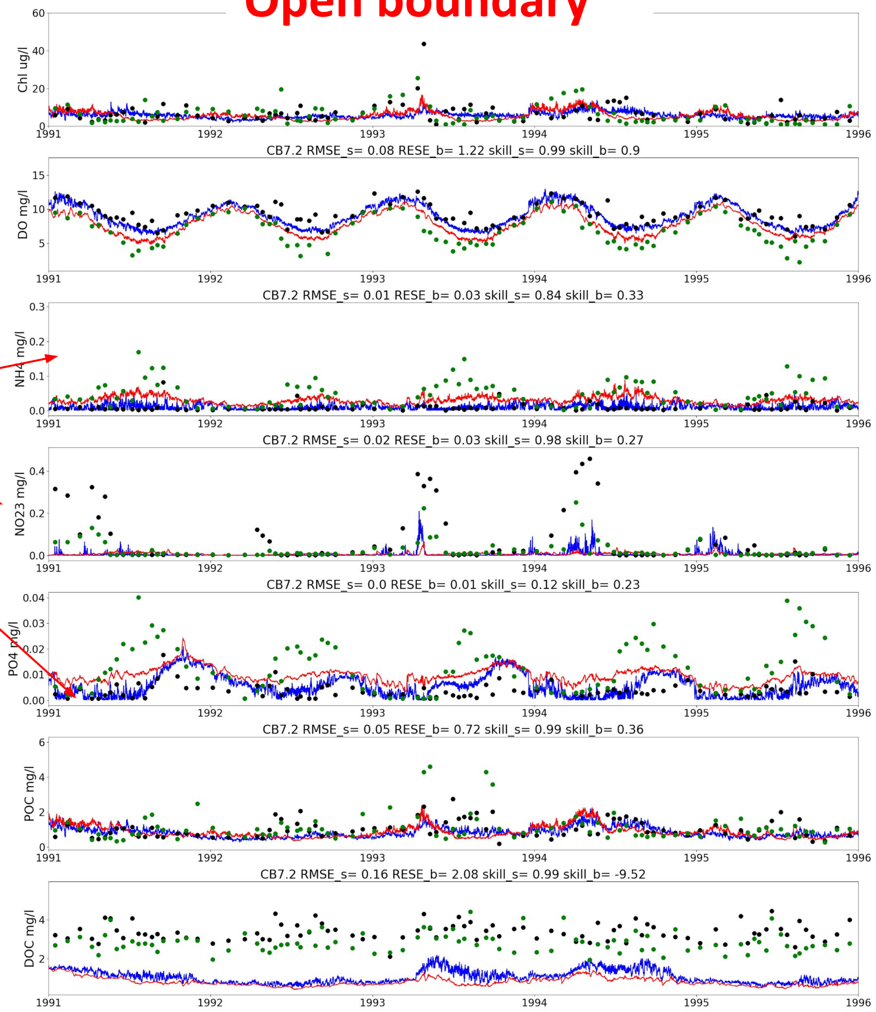
- ❖ Inside the bay, the model results with boundary condition needs more improvements.

Nudging



need to increase NH4, NO3 and PO4

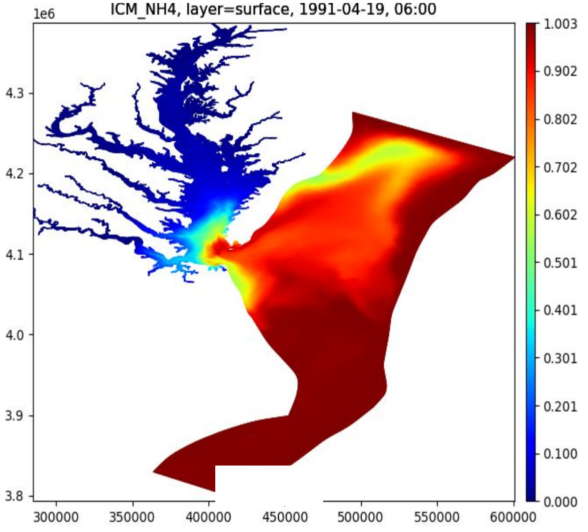
Open boundary



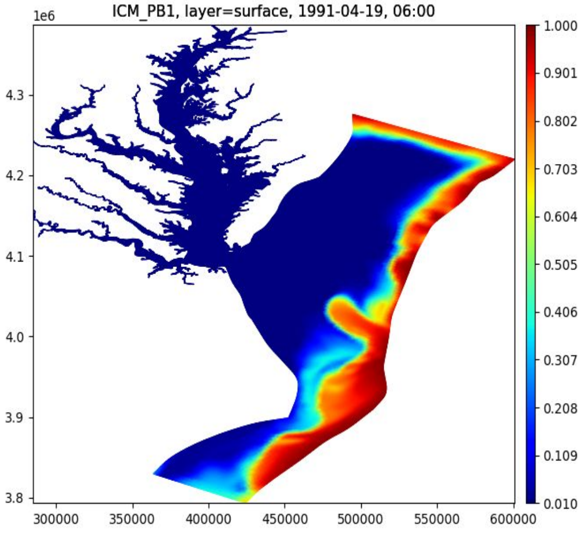
Dye experiment of DOM: boundary effect on the bay

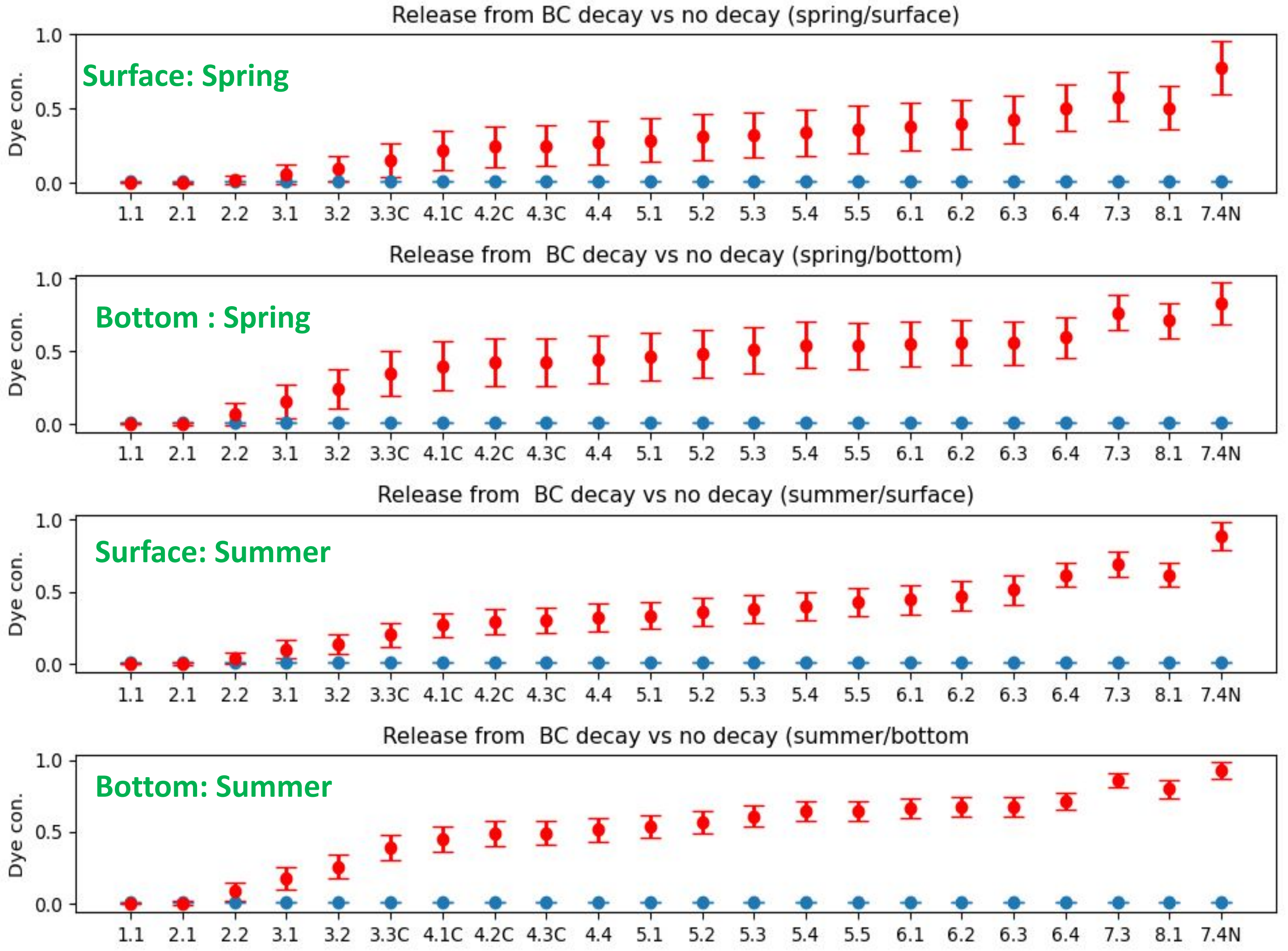
- Release dye from ocean boundary
- The boundary influence can reach entire bay (it is significant in mid-bay under 'no decay' case), but decay rate plays a very important role.

no decay



with decay 0.05 day^{-1}



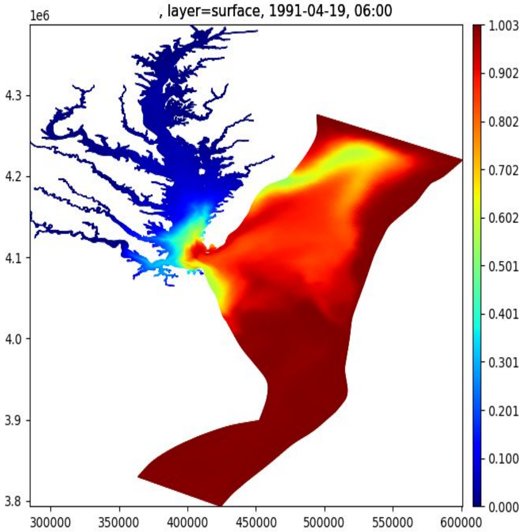


Red: no decay; **Blue**: decay rate 0.05 day^{-1}

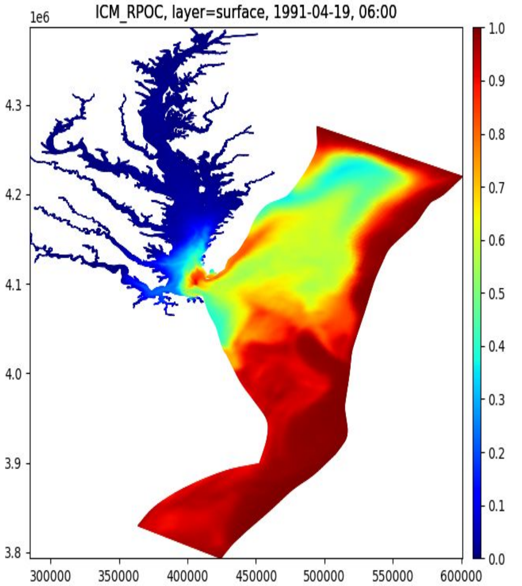
Dye experiment for POM: boundary effect on the bay

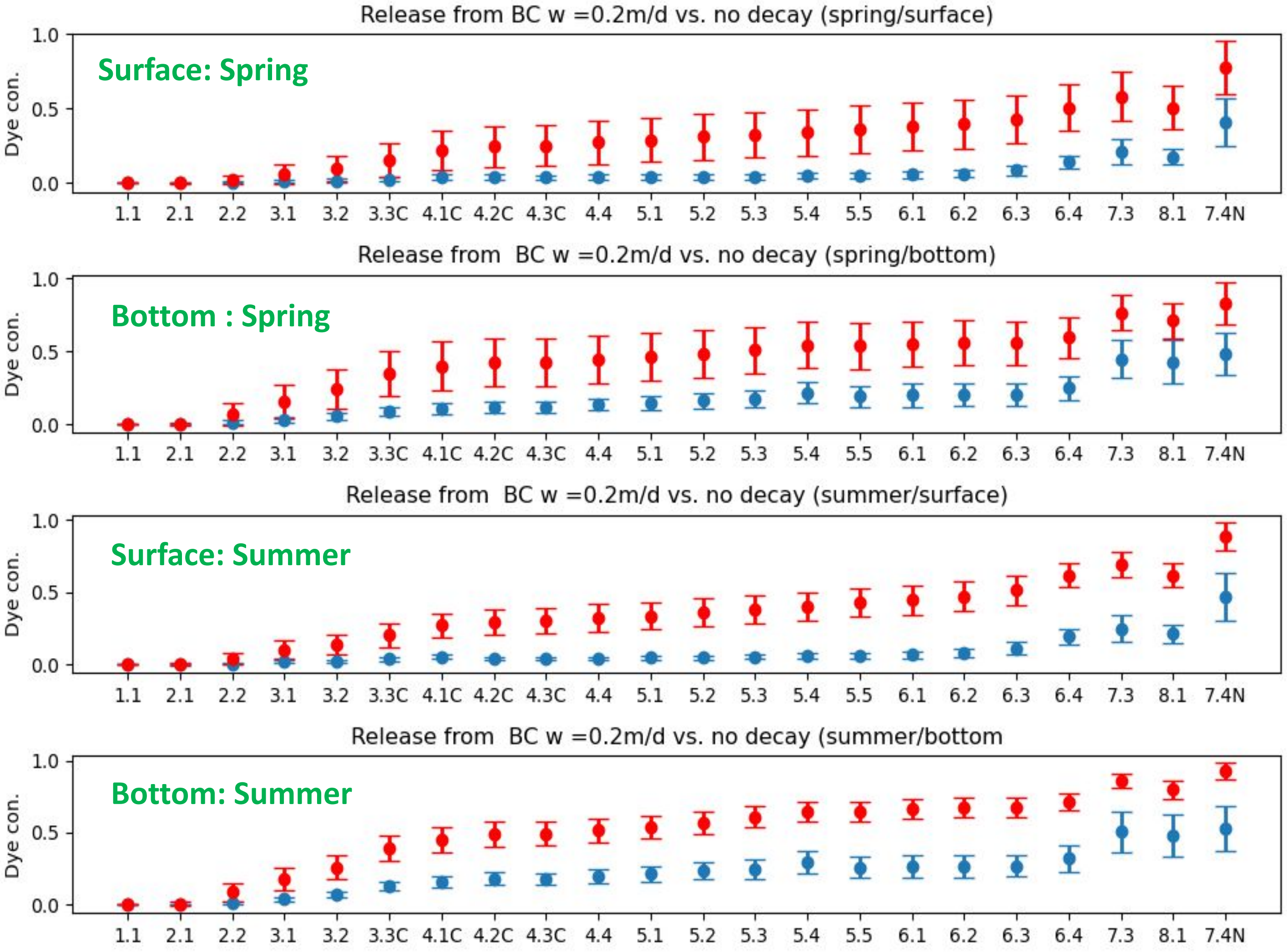
- ❖ The boundary influence of POM can reach entire bay, but settling plays a very important role.
- ❖ Potentially we can adjust the rates when using the ocean boundary condition?

no settling



settling rate 0.2 m/day





Red: no decay; **Blue**: decay rate 0.2 m/day

Summary

- In the last quarter, we have added new interfaces for ICM outputs and initialization, which greatly streamlined model simulation.
- We have developed new shallow water living resource modules in SCHISM-ICM along with documentation.
- Test results of clam model indicate reasonable representation of processes but need more validation
- Sensitivity tests on the MBM ocean boundary conditions were conducted to make the climate change simulation more straightforward, but more work is needed
- Future work
  - (Numerous) sensitivity simulations for L.R. and boundary
  - Documentation
  - Compilation of info for climate change simulations
  - ….