Update on the Phase 7 Main Bay Model (MBM): Living Resources

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VIMS | WILLIAM & MARY
VIRGINIA INSTITUTE OF MARINE SCIENCE

Outline

- ❑ **Development of living resource (LR) modules in ICM**
  - Finished first version of the LR; validation and documentation on-going
- ❑ **Preliminary validation of LR modules**
  - Worked with Bay Program Office and others on the model configurations.
  - Progress on the LR calibration
    - ▪ **Oyster**: simulated biomass magnitude is consistent with observations
    - **Wetland**: captured the effect of wetland on the ecosystem!
    - **SAV**: reproduced the seasonal pattern
- ❑ **Summary and future work**

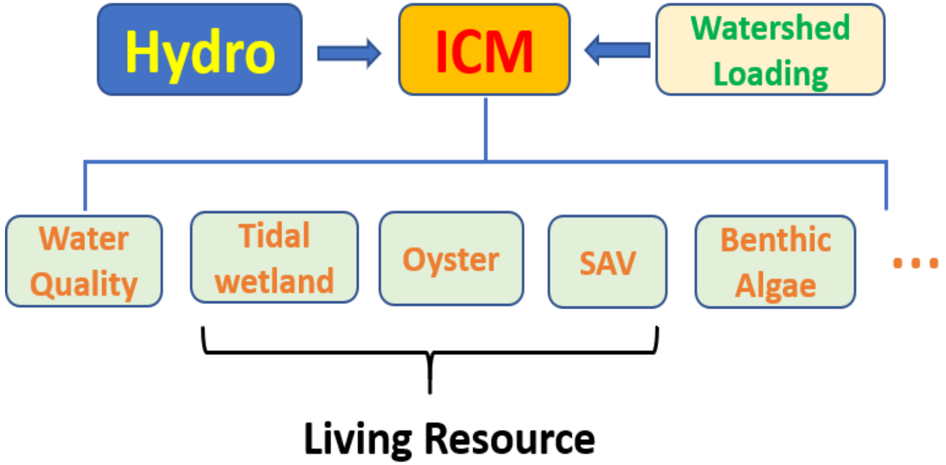
Development of living resource modules

- In phase-7 MBM, three LR modules (Oyster, Tidal Wetland, SAV) are included
- Development and validation of these modules are on-going

❑ We reviewed more reports, literatures, and phase-6 ICM code regarding LR modules, and documented model kinetics systematically

❑ We added more functionalities of LR modules such as:

- Both simple and process-based tidal wetland formulations
- SAV Tuber and Epiphytes
- Fraction of coverage in each SCHISM cell for all modules



❑ ICM code structure and interface for LR are streamlined regarding outputs, initialization, and parameters, by following SCHISM convention

- Added more model outputs, and diagnostic variables (e.g. growth rates, decay rate, limitations)

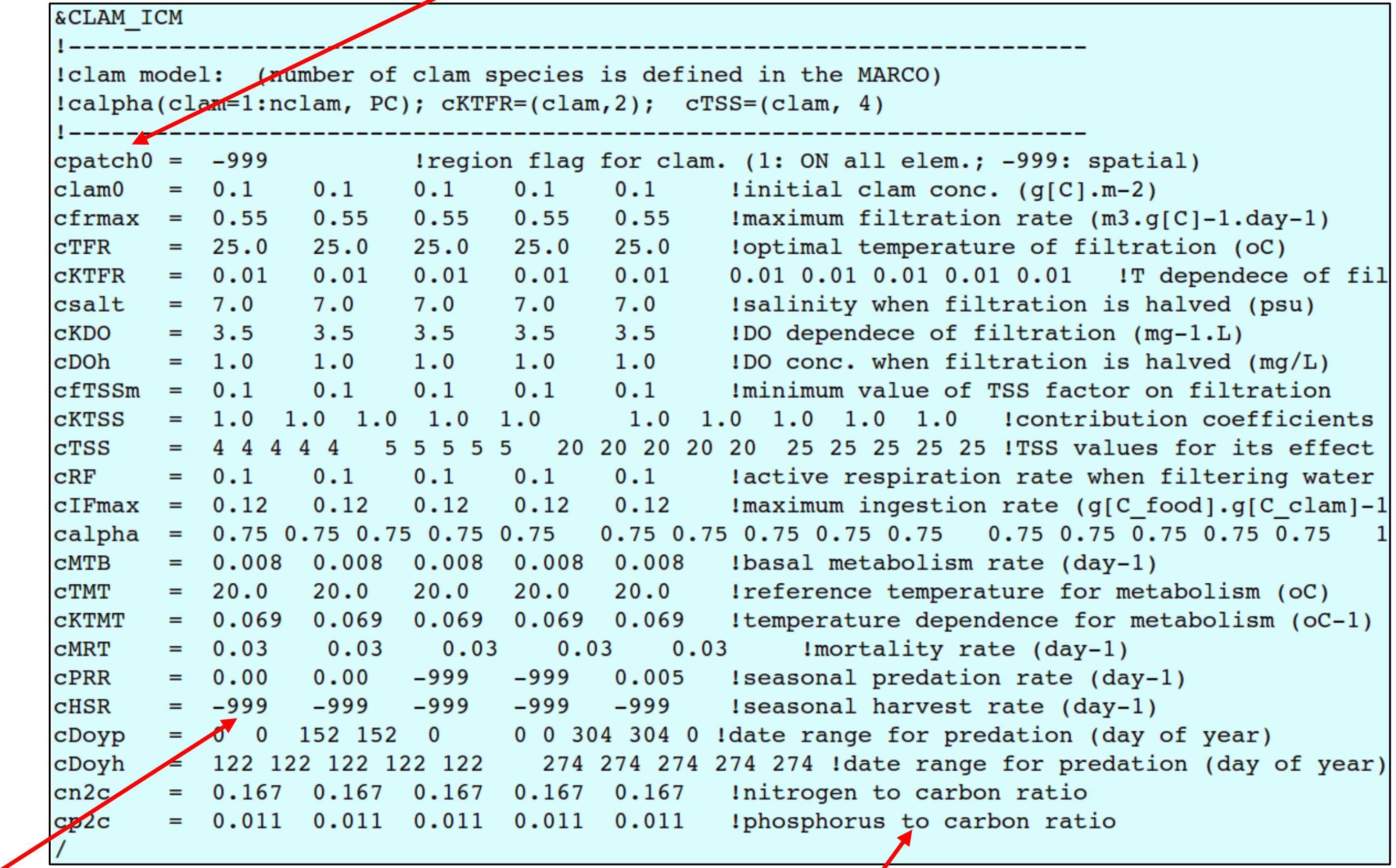
Some new features on living resource modules

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 relevant sections (1 for each module).

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

Acknowledgment

In the past months, We had worked closely with Bay Program Office on the model calibration. We held a post Ad Hoc meeting every week, reported the modeling progress, and got help/comments/suggestions from the team members to improve the models. Here, I want to greatly thank the CBP team:

- **Carl Cerco**
- **Lewis Linker**
- **Richard Tian**
- **Gopal Bhatt**

Oyster Model

- **In the oyster model, five species are simulated**

1. **Rangia** cuneate (freshwater)
2. **Corbicula** flumenea (freshwater)
3. Natural population (**Reef**)
4. **Aquaculture**
5. Natural population (**Sanctuary**)

Major Oyster Processes simulated

$$\frac{dC^i}{dt} = \underset{\text{growth}}{GP^i} - \underset{\text{metabolism}}{MT^i} - \underset{\text{mortality}}{RT^i} - \underset{\text{predation}}{PR^i} - \underset{\text{harvest}}{HST^i},$$

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

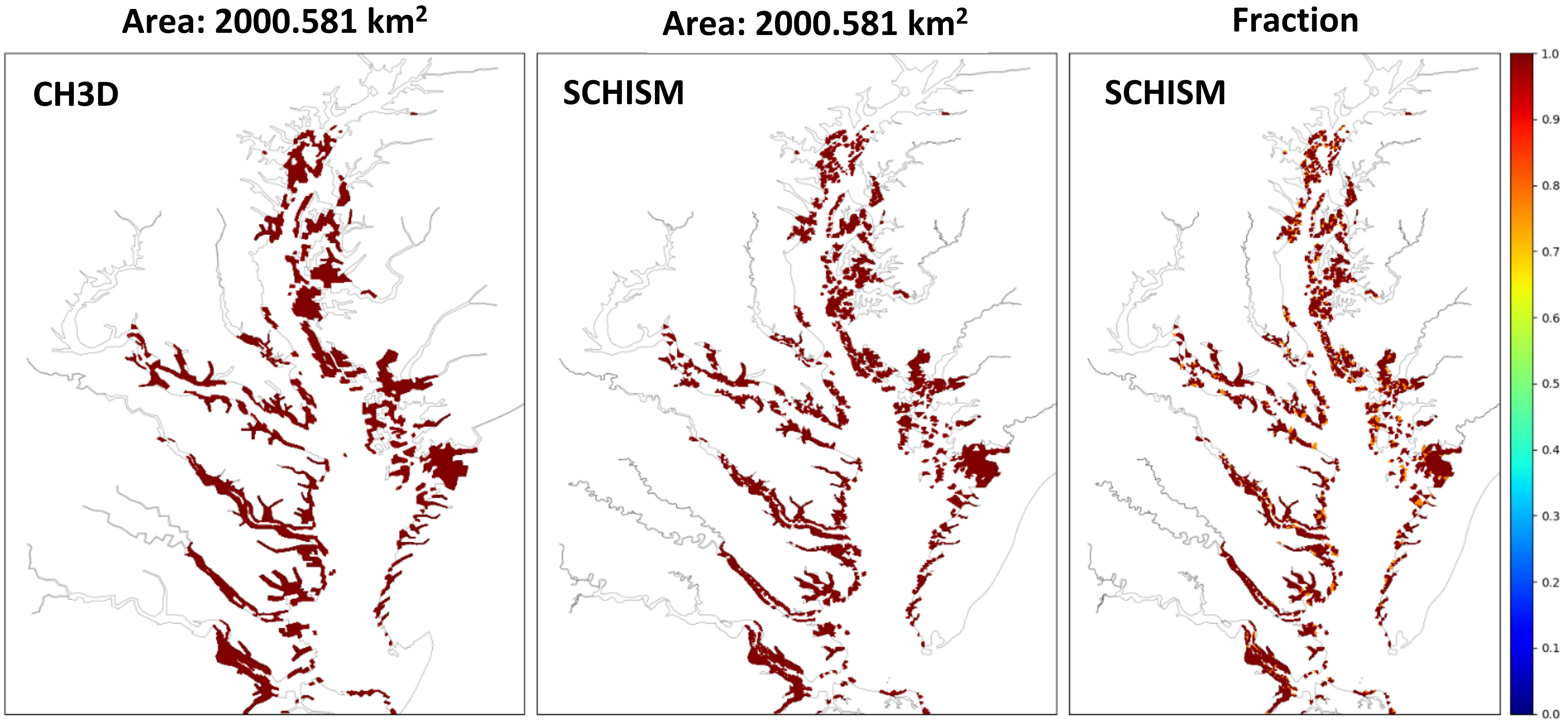
Filtration

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

Oyster Coverage

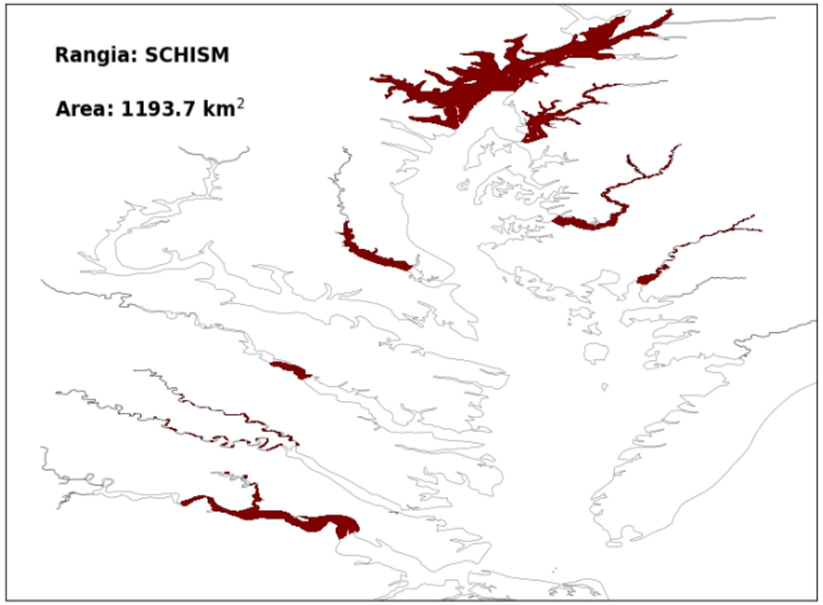
- Oyster coverage from phase-6 MBM model was interpolated onto MBM grid. Different methods were explored to more accurately capture areas of oyster beds.
- For each schism cell, a coverage fraction is assigned to account for sub-grid features
- The interpolation method [searching both the MBM grid nodes and element centers inside oyster beds] works well that ensures a consistent oyster distribution and total area between P6 and P7

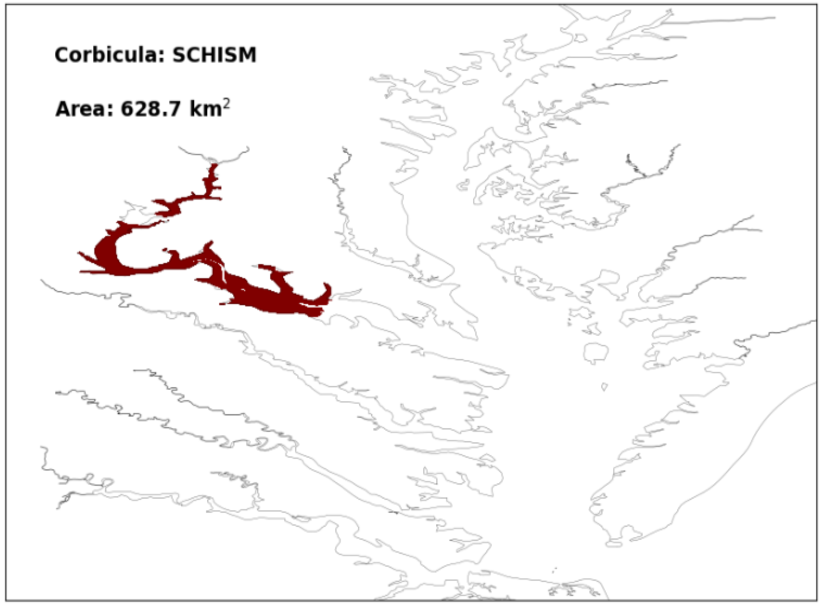
Reef Coverage

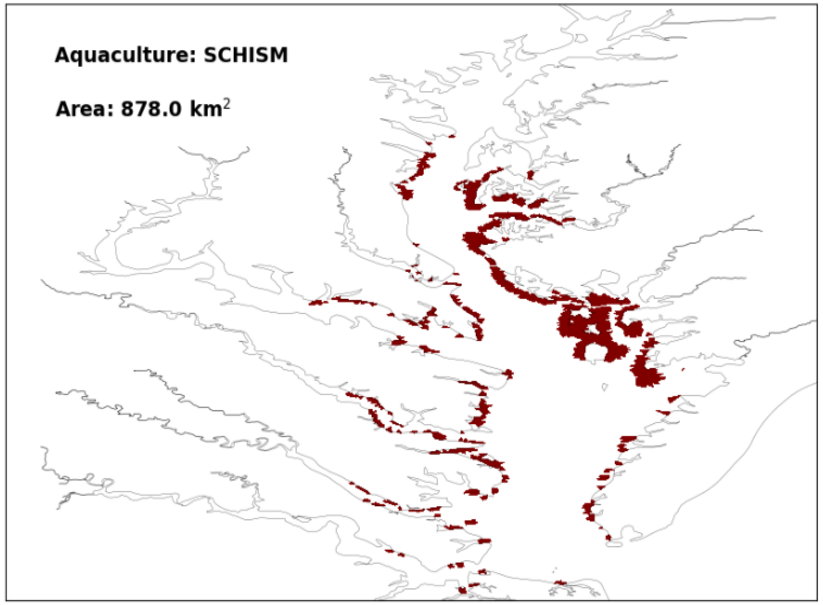


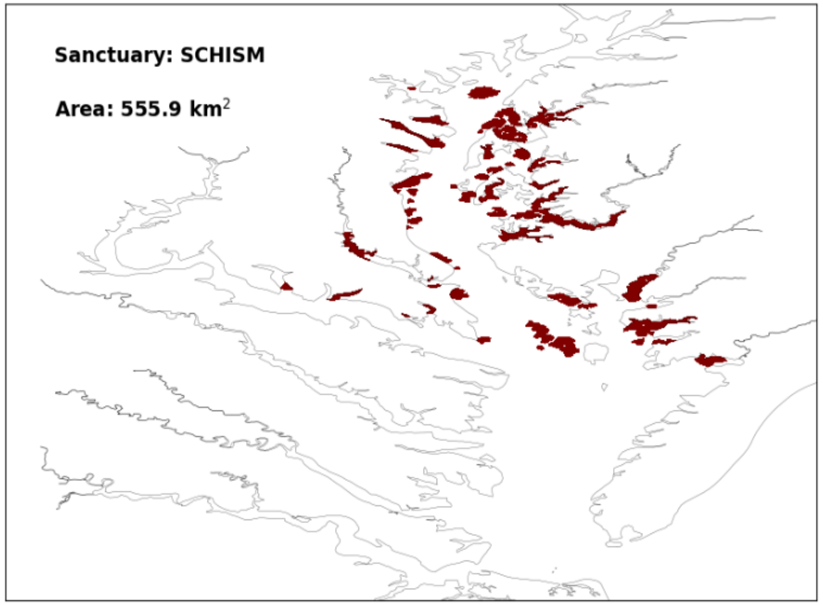
Oyster Coverage for Other Species

- MBM calibration period is 1991-2000
- Since aquaculture activity commenced in 2005, they will not be in the final calibration, but will be in the model scenarios.
- Harvest occurs for Reef oyster, but not for Sanctuary oyster.
- Currently, we only have limited data for Reef for model validation.



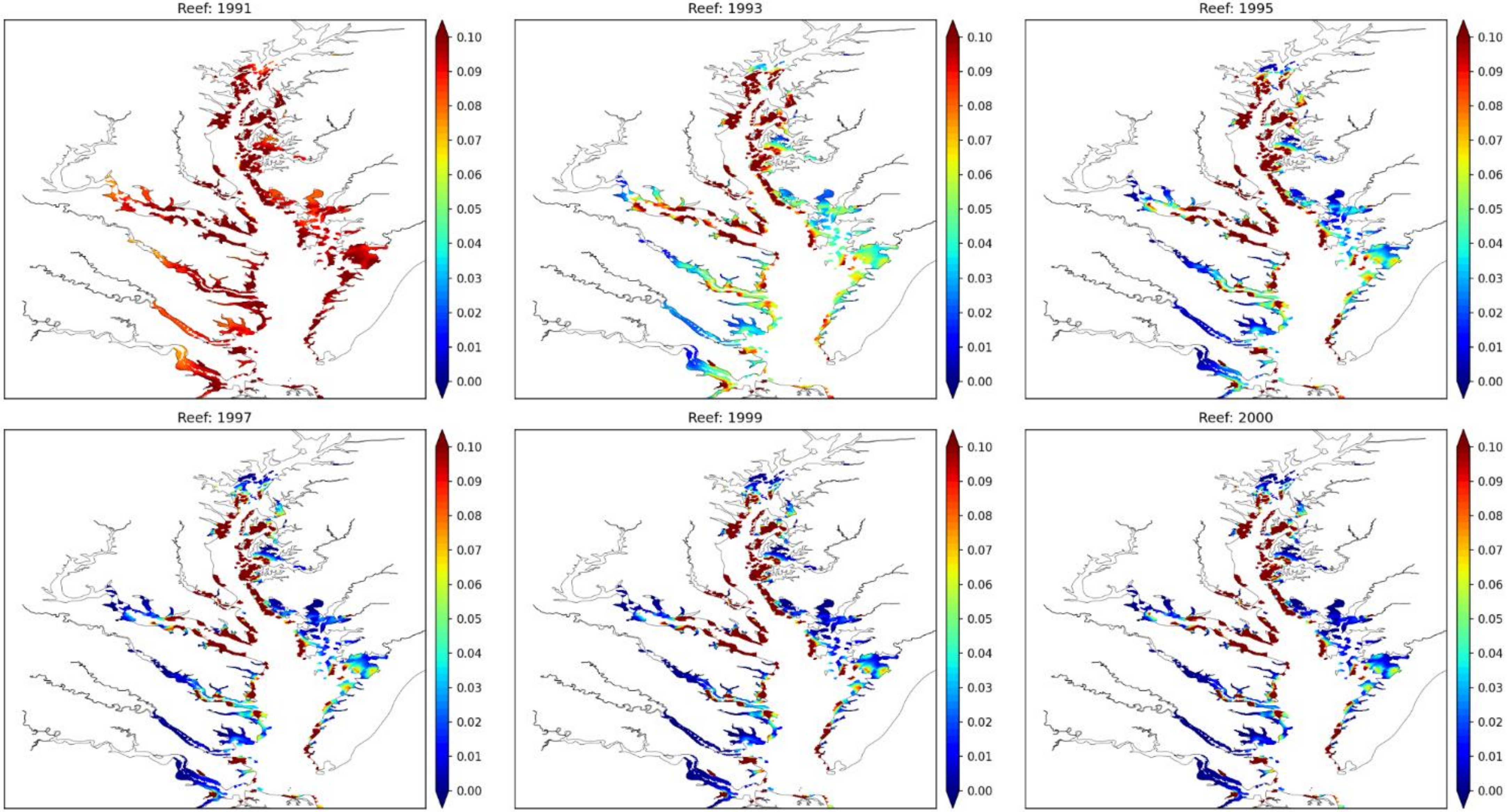






The spatial distribution of Reef biomass (g[C].m^{-2})

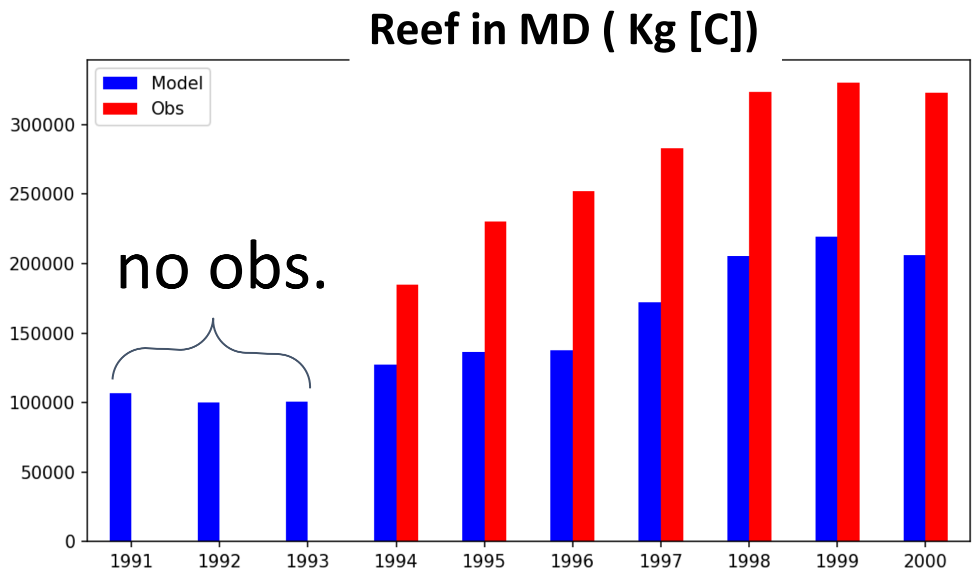
- Simulated oyster biomass reached a steady state after several years (e.g. 1995 onward), with reasonable biomass in magnitude (Note: initial condition of constant Reef biomass was used).

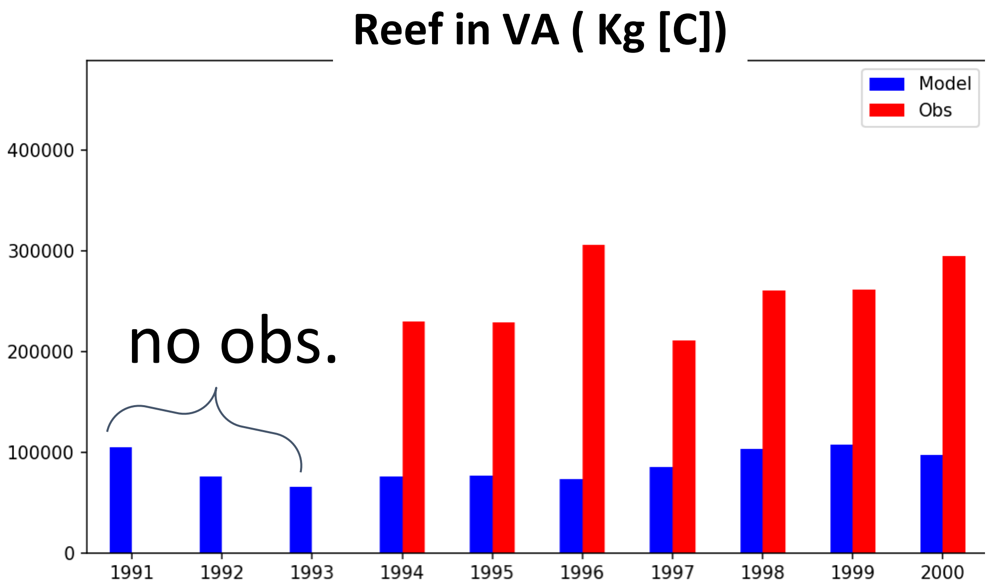


Comparison of Reef Biomass with data

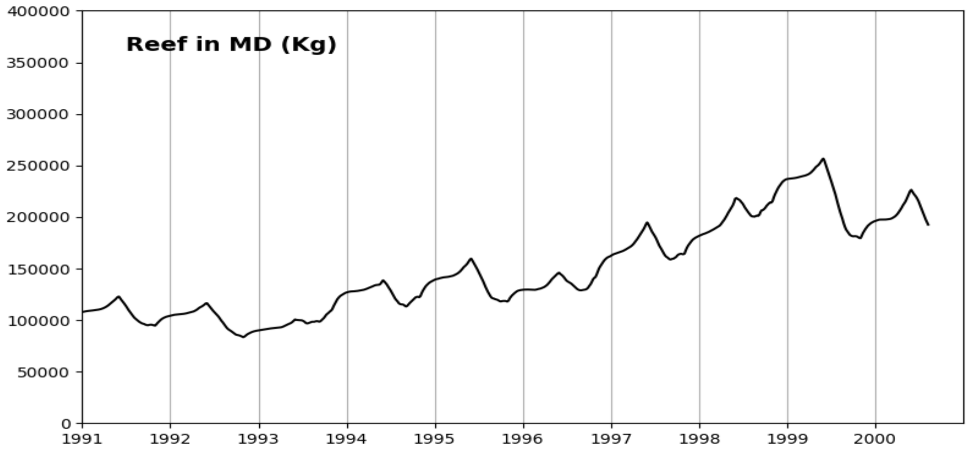
- Reef biomass was underestimated, but the magnitude was about correct
- Seasonal variation seems reasonable

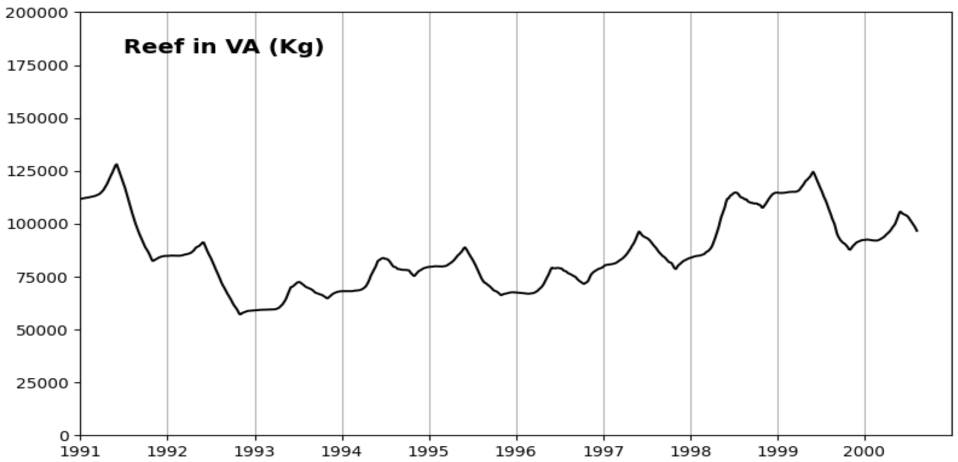
Annual Mean


Reef in MD (Kg [C])


Reef in VA (Kg [C])

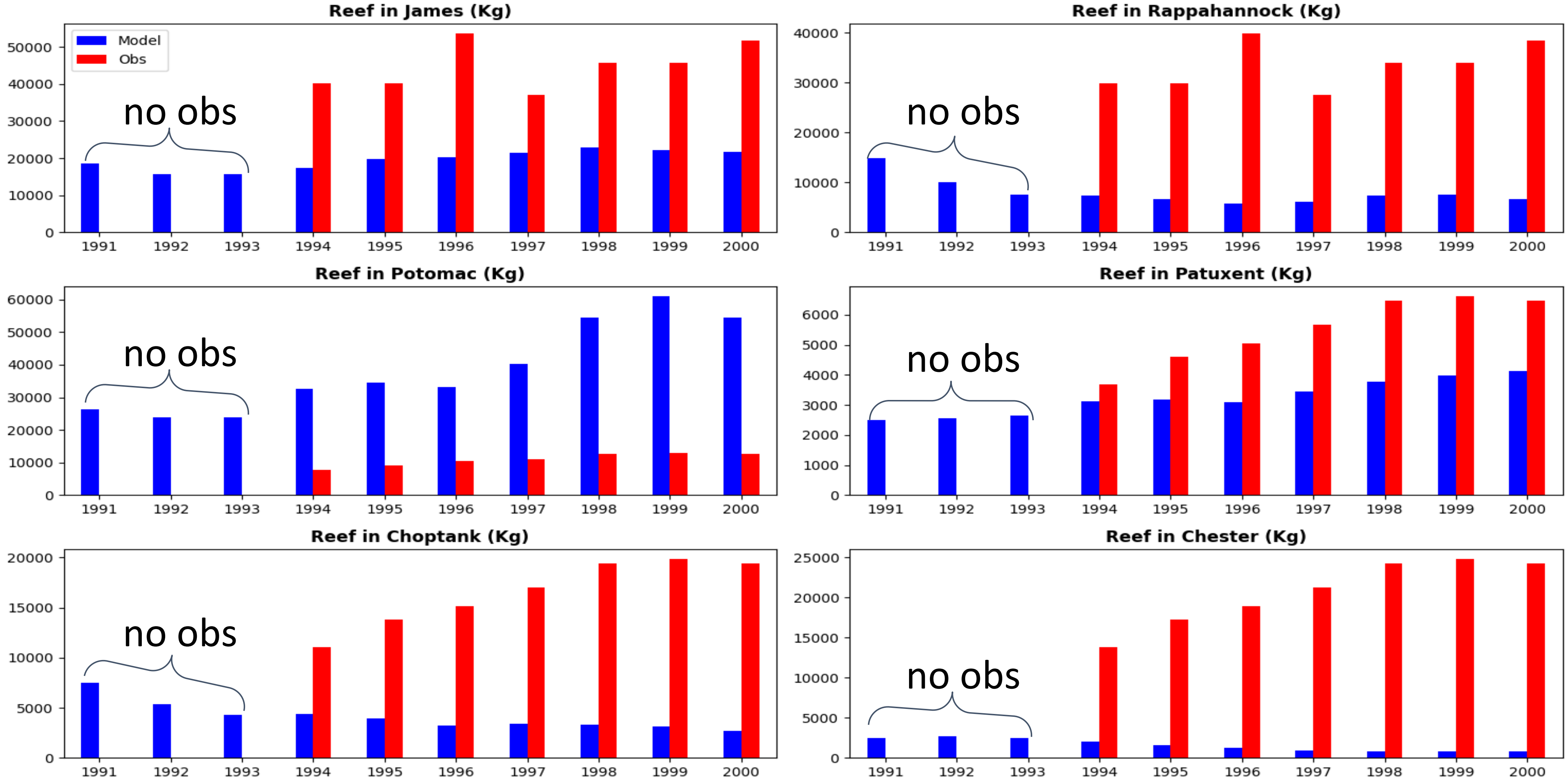
Time Series





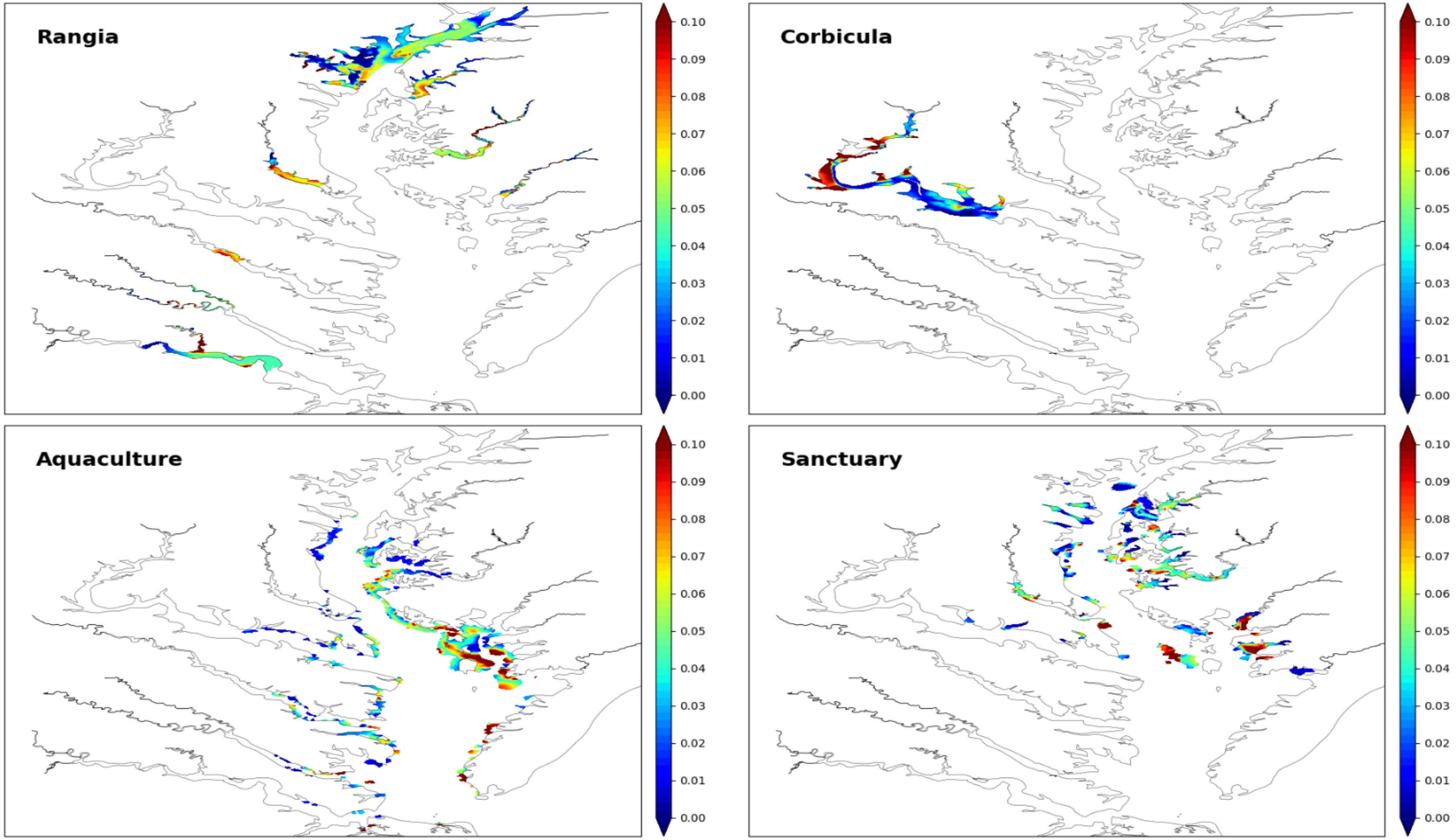
Reef Biomass in different regions

- In most regions, the biomass was underestimated except for Potomac River
- Further calibration is on-going



Spatial distribution of biomasses for other species in 1995 (g[C].m^{-2})

- Overall, different spatial patterns for different oyster species with reasonable magnitude
- Waiting for observational data before further calibration



Tidal Wetland

- We have developed both simple and process-based tidal wetland formulations
  - In phase-7 MBM, only simple formulation will be used.
- Tidal wetland can remove nutrient loading (NO3), increase the settling of particulate organic matter (POM), and consume oxygen (DO).
- A key parameter is the wetland area to MBM-cell volume ratio (*A^w*), used to determine the wetland impact on the adjacent water.

$$\frac{dNO3}{dt} = -K^W_{NO3} \cdot A^W \cdot f(T) \cdot NO3$$

$$\frac{dPOM}{dt} = -K^W_{POM} \cdot A^W \cdot POM$$

$$\frac{dDO}{dt} = -A^W \cdot f(DO) \cdot f(T) \cdot OC^W$$

A^w : wetland area to MBM-cell volume ratio (m^{-1})

K^W_{NO3} : mass-transfer coefficient for NO3 removal ($m \cdot day^{-1}$)

K^W_{POM} : settling velocity of POM caused by marsh ($m \cdot day^{-1}$)

OC^W : wetlands oxygen consumption rate ($g.m^{-2}.day^{-1}$)

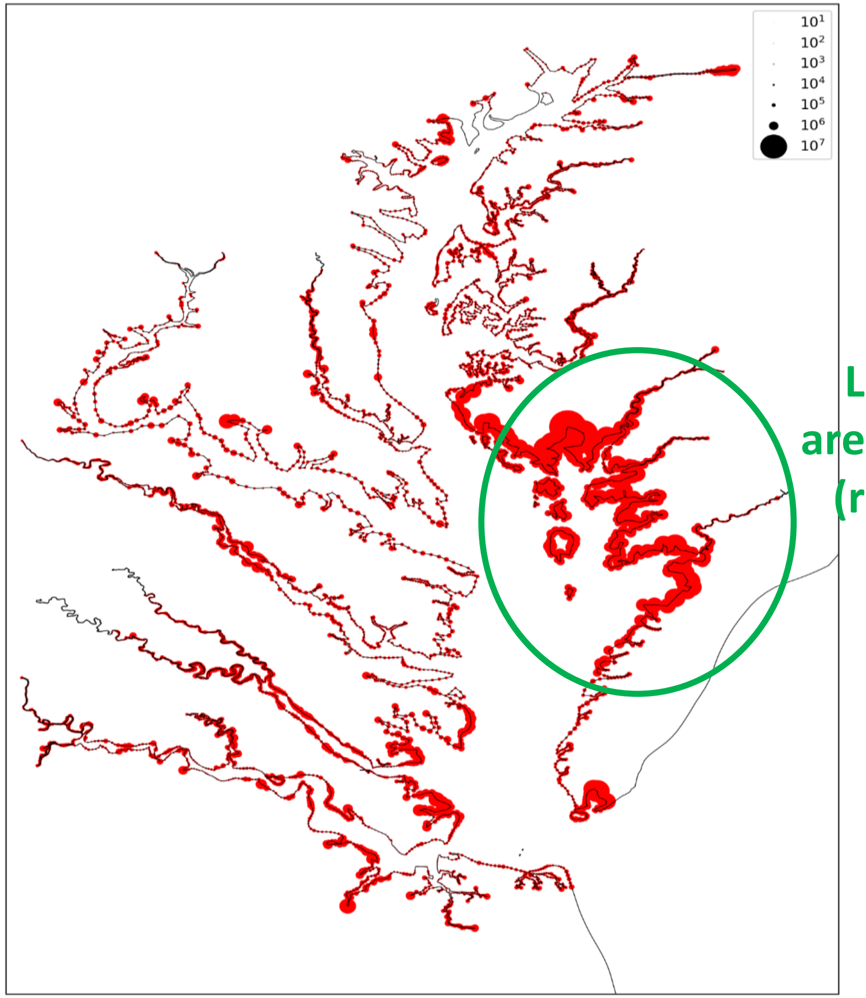
Linking Wetland area to MBM model

- Large wetland area may be distributed among multiple adjacent MBM grid cells
- Total wetland area is conserved (~1148 km^2 in Chesapeake Bay)

Observation: Wetland Coverage

Figure 1. The black line indicates MBM grid boundary. The red dots (10x10 m cells) represents the tidal wetland coverage.

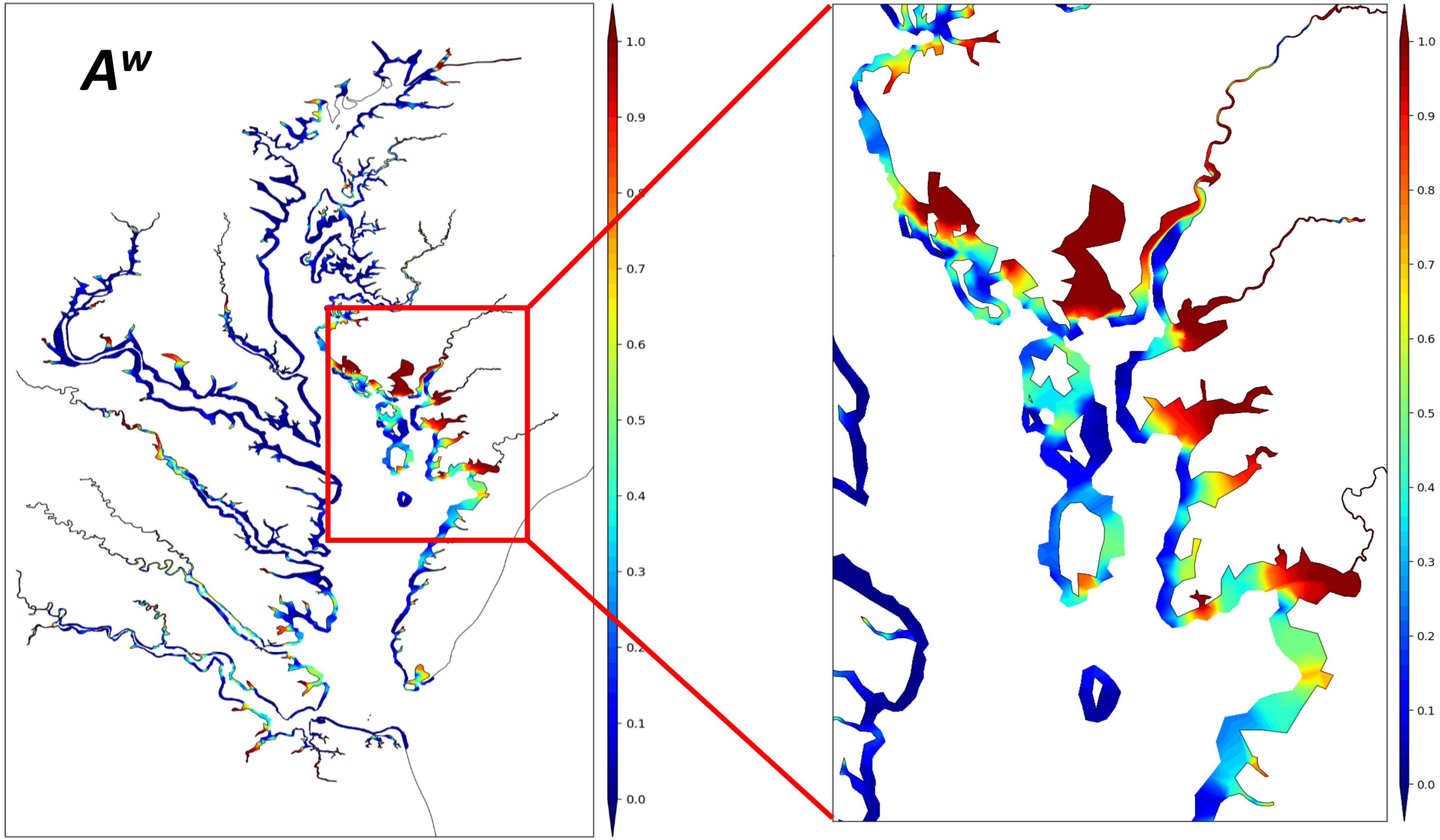
Allocation of Wetland Area to SCHISM Cells (m^2)



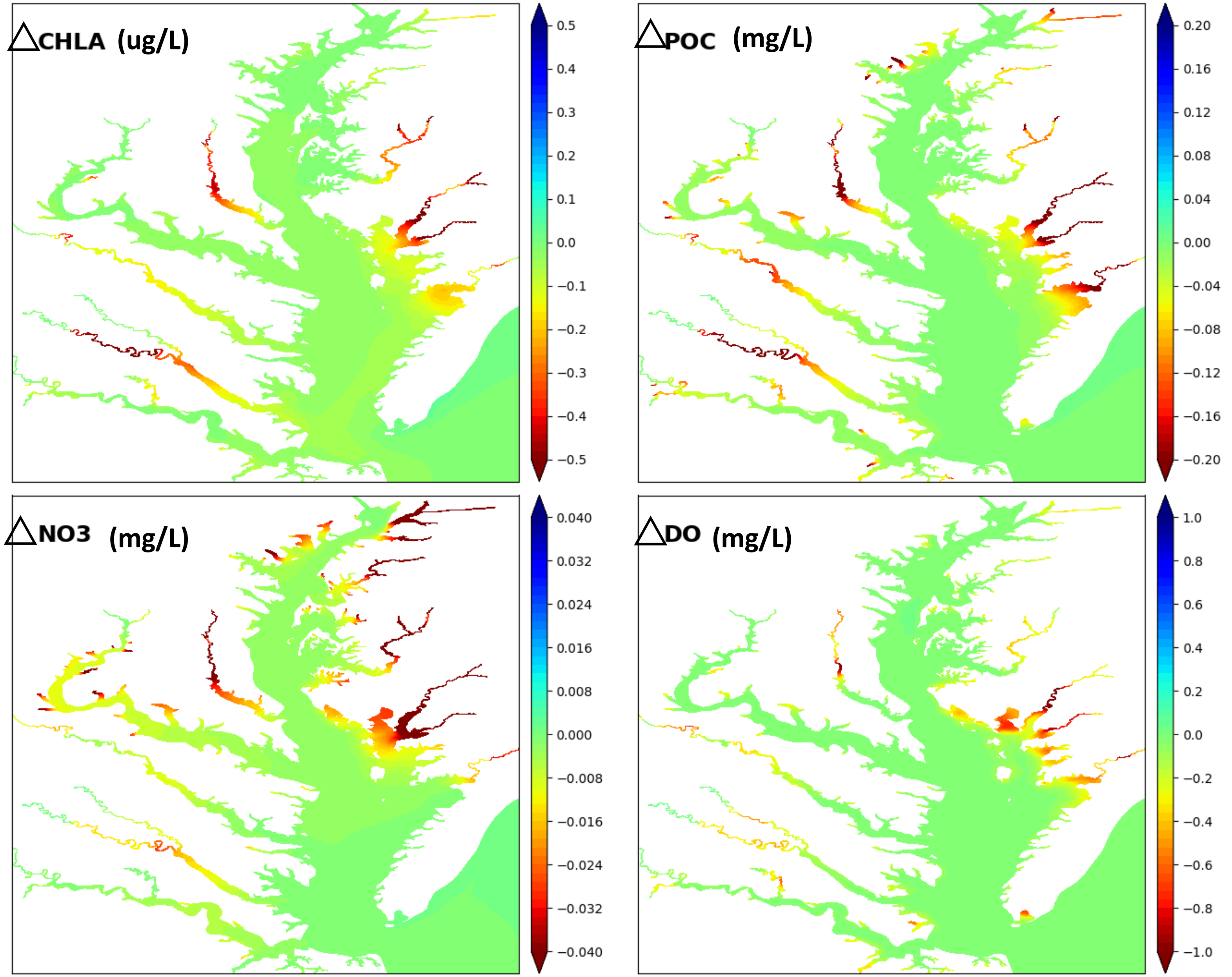
Large wetland area in Fishing Bay (re-distributed)

Computation of wetland area to volume ratio (A^w)

- A^w is an important model parameter used to estimate the wetland impact
- Since MBM cells can be very high in resolution, to prevent the wetland overwhelming the adjacent water body in high-resolution region, we smooth the A^w near the land boundaries (while conserving the total area)



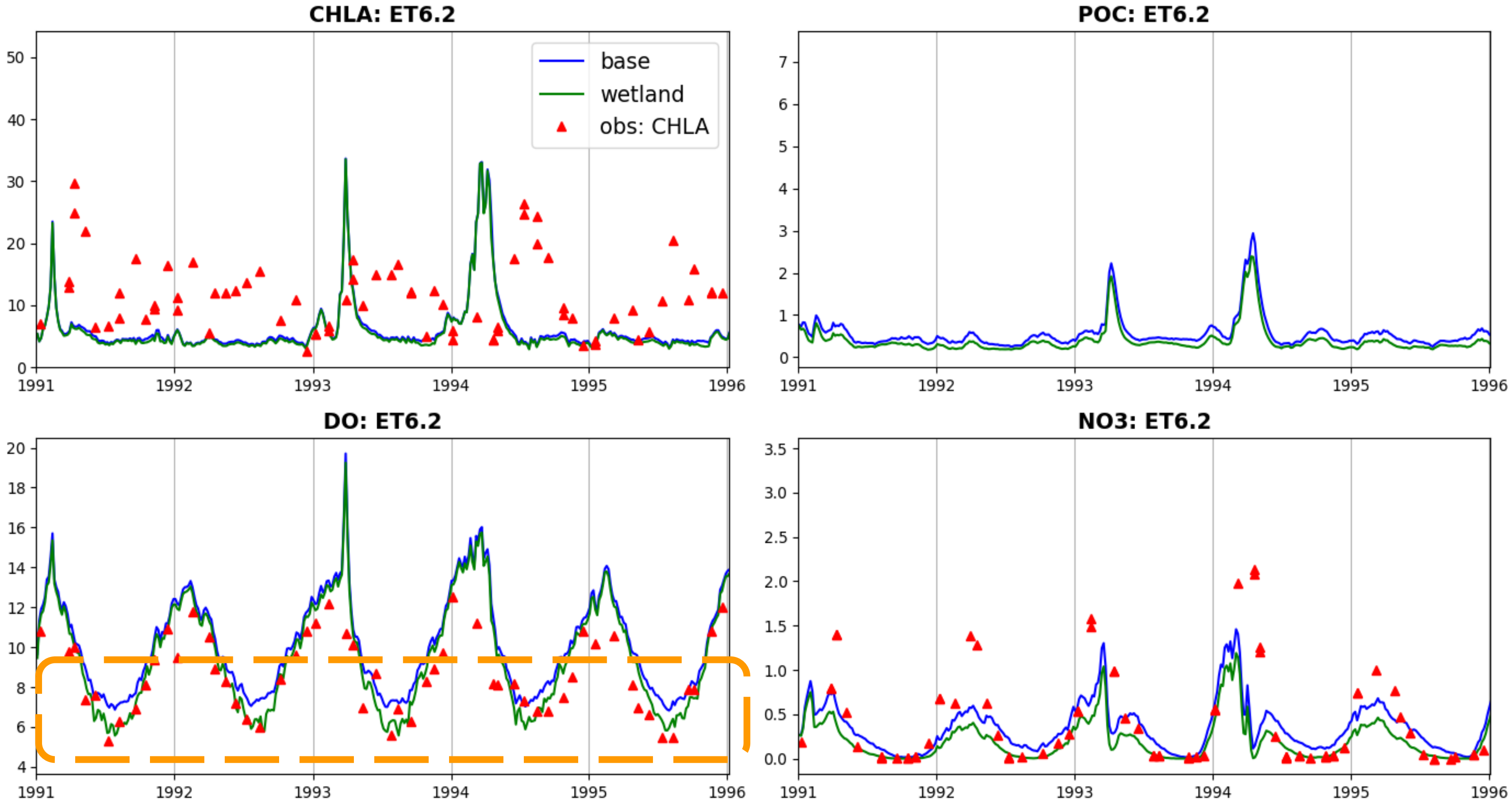
Impact of Wetland on Water Quality

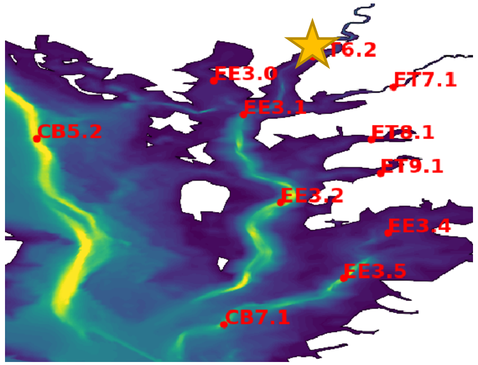


- Diagrams show the changes of water quality parameters when tidal wetland module was activated.
- Difference is calculated from multi-year mean
- Most impacted regions are the upstream tributaries and Fishing Bay area
  - nutrient reduction
  - DO consumption
  - lower Chl-a
- Other parameters (NH4, PON, POP) are also impacted (not shown).

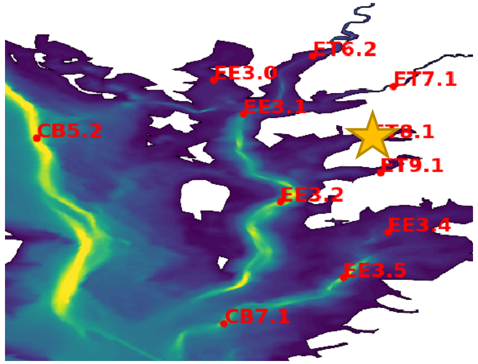
Wetland Impact: ET6.2

- At the upstream station ET6.2 (near Fishing Bay), the wetland module has limited impact on Chl-a and POC
- Major impact on DO
  - With wetland module, the summer minimum is better captured, due to DO consumption through respiration (Cerco, 2019)
- Impact on NO3 simulation is more nuanced

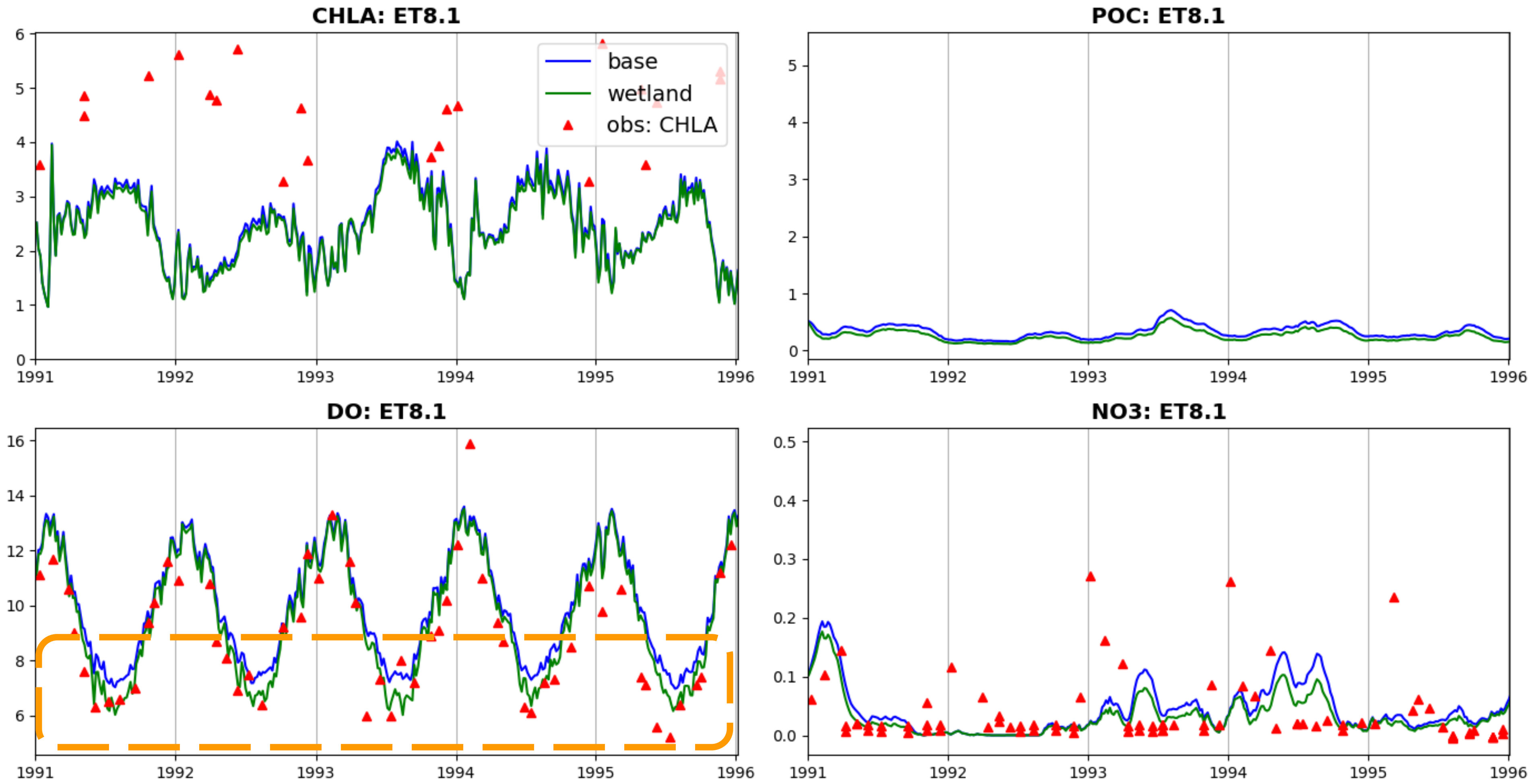




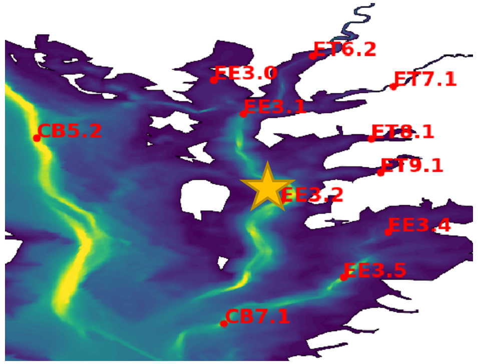
Wetland Impact: ET8.1



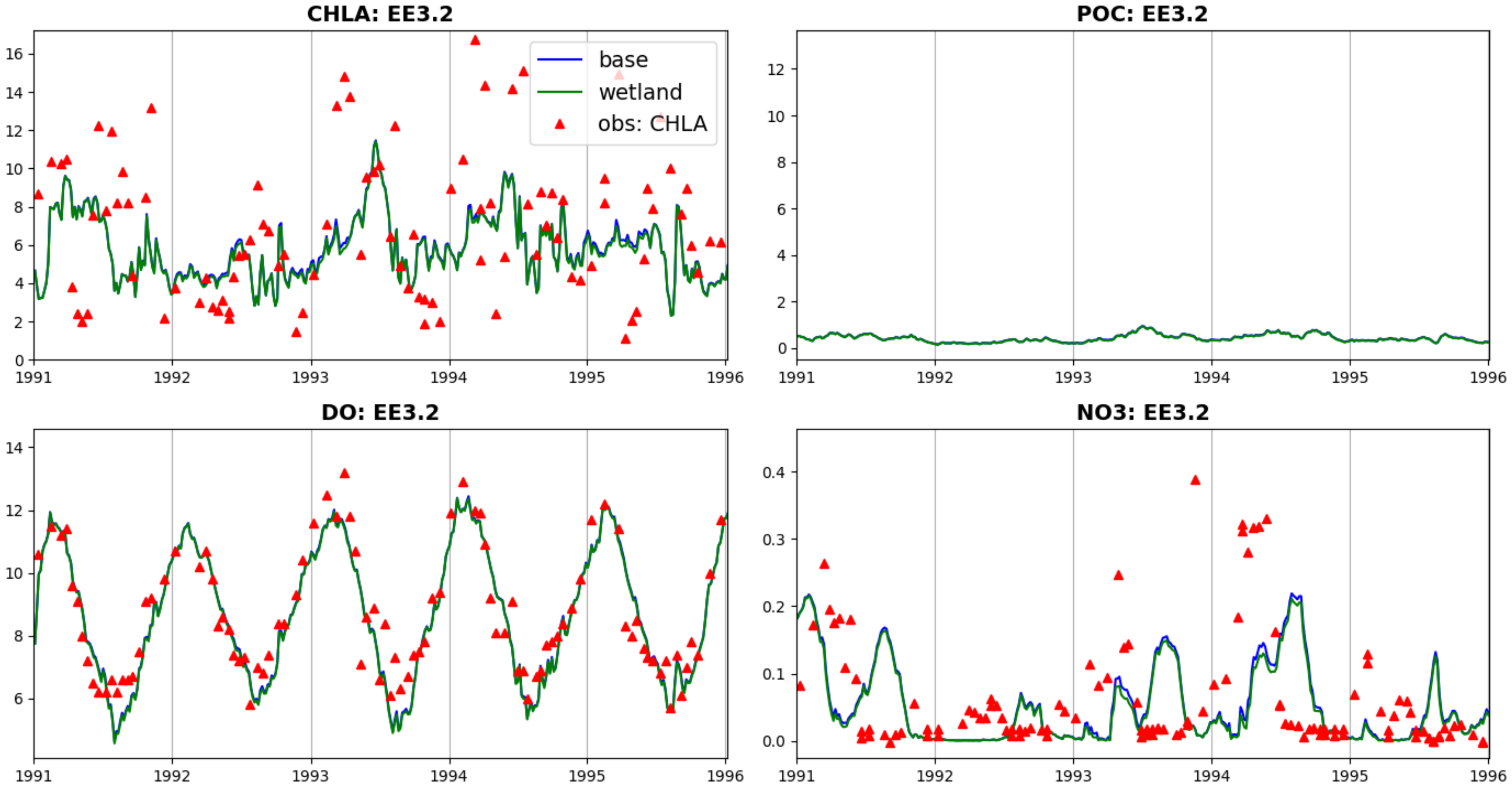
- At upstream station ET8.1, the wetland module has little impact on Chl-a , NO3 and POC
- Wetland module also helped reduce summer DO at this location



Wetland Impact: EE3.2



- Wetland impact diminishes away from the wetland area
- No appreciable differences at this downstream station, as expected


CHLA: EE3.2

POC: EE3.2

DO: EE3.2

NO3: EE3.2

Submerged Aquatic Vegetation (SAV)

❑ Major Variables

- SAV leaf, stem, root, tuber biomass (g[C].m^{-2})
- SAV canopy height (m)
- Epiphyte component was developed, but not activated yet

❑ Major processes

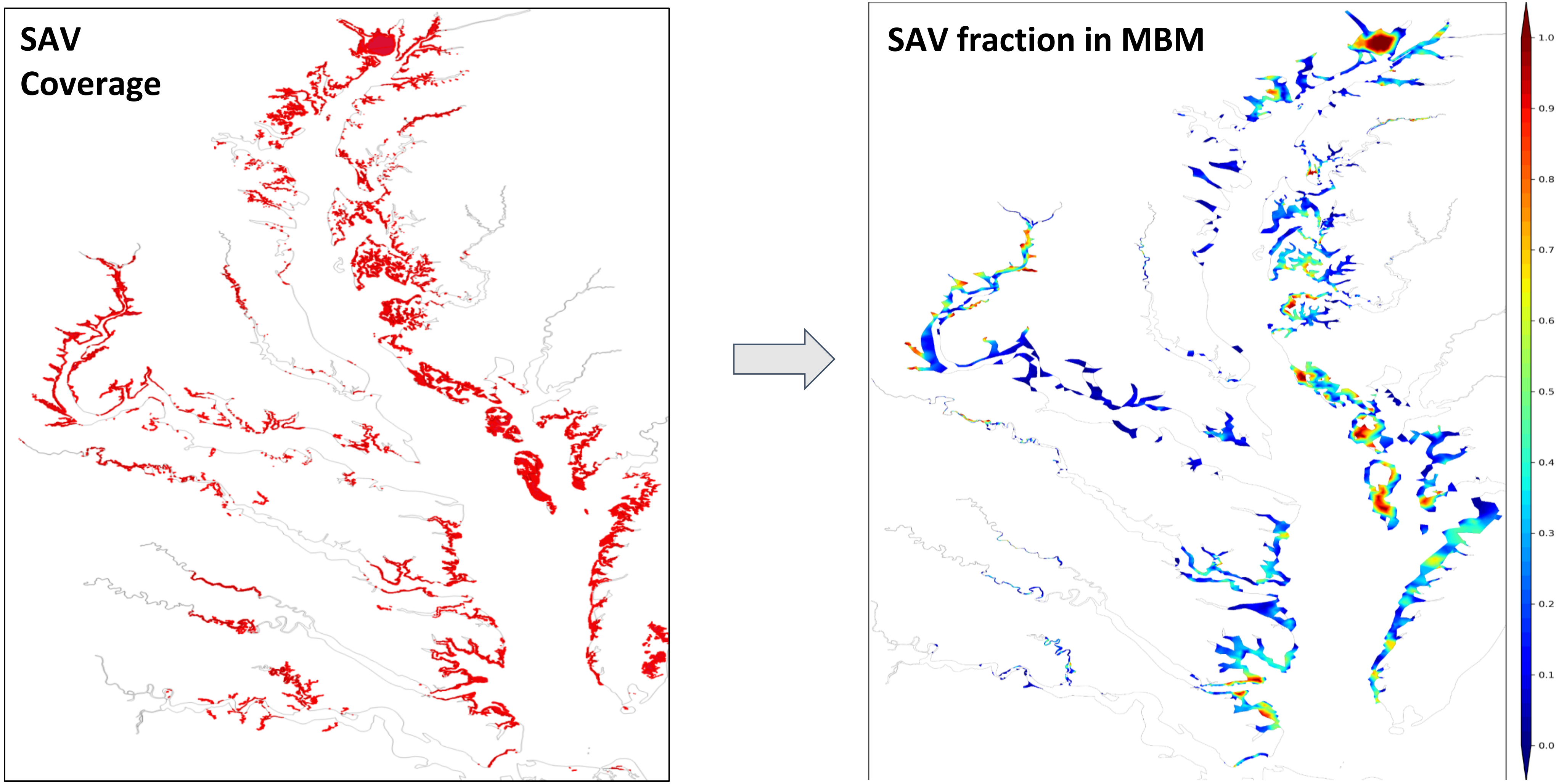
- Effects on the hydrodynamics (new to P7)
- Light attenuation by SAV leaf and stem
- Photosynthesis at SAV leaves
- Effects of temperate, light, nutrients
- Respiration of SAV leaf/stem/root
- Interaction with water column variables
- Interaction with sediment layer

❑ Major hypothesis to test

- Net source or sink for DO, nutrients? Region dependent?

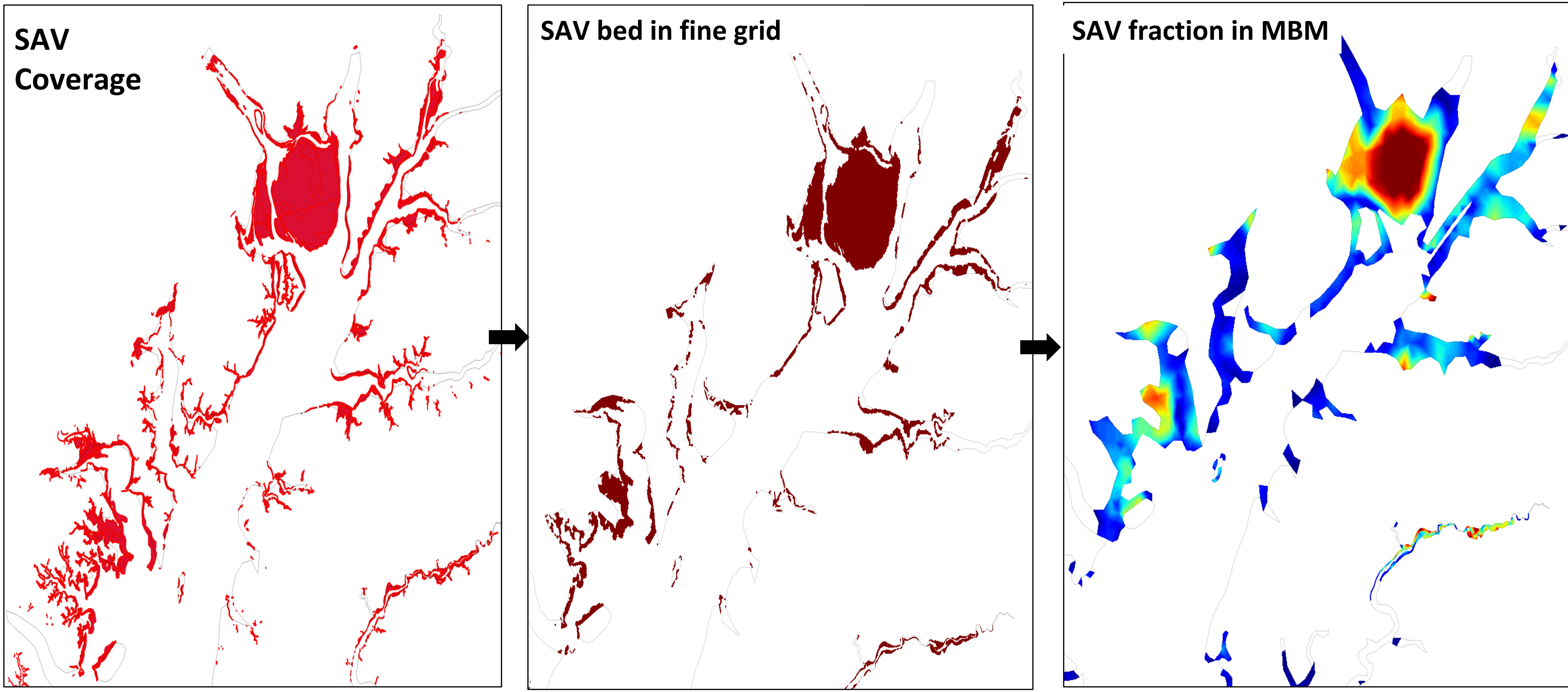
SAV representation in MBM grid

- SAV beds are usually small and patchy and most SAV beds barely overlap our MBM boundaries.
- Care must be taken to translate SAV beds onto MBM grid
- We used a fine grid as an intermediary and compute the bed **fraction in each MBM cell**



SAV representation in MBM grid: upper bay

- Using a very fine grid as intermediary, we get a good representation of SAV in our MBM grid



SAV Coverage

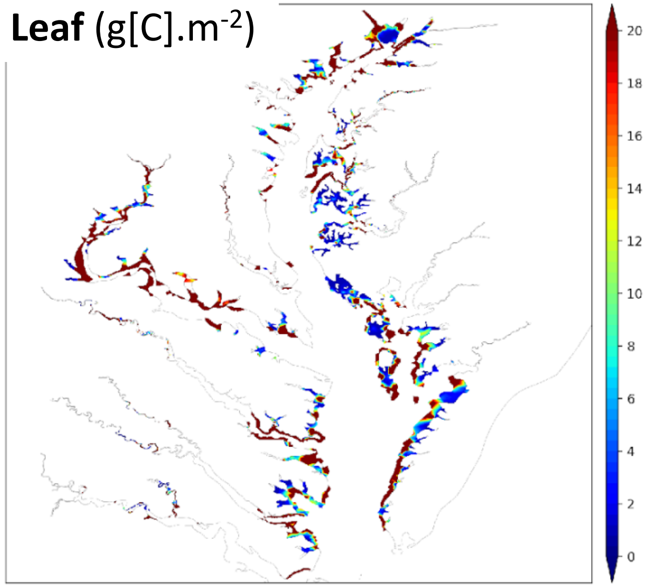
SAV bed in fine grid

SAV fraction in MBM

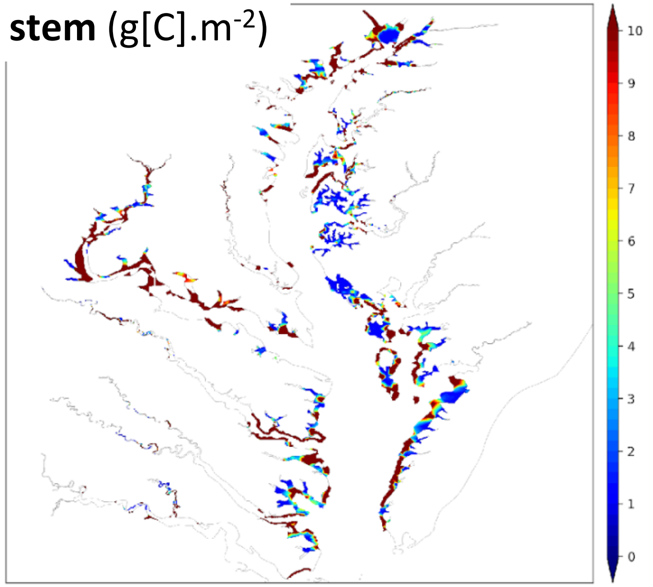
Spatial distribution of SAV biomass

- The spatial distribution of SAV canopy height, leaf, stem, root and tuber biomass are stimulated.

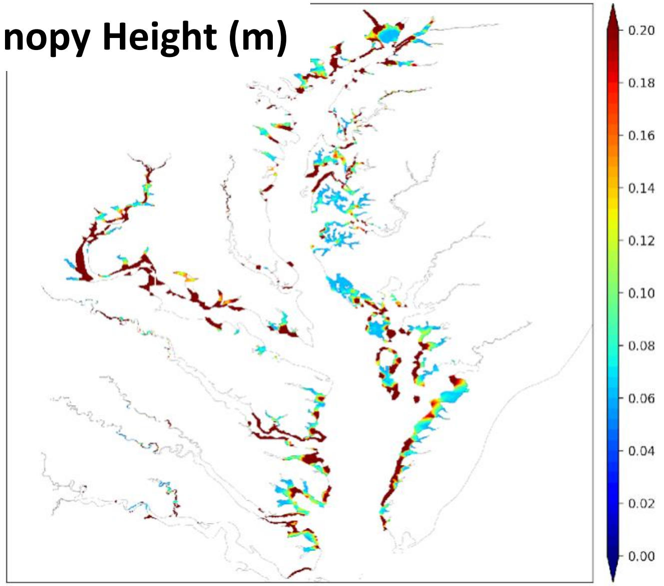
- The results are still preliminary, and model-observation comparison are needed to validate the model.



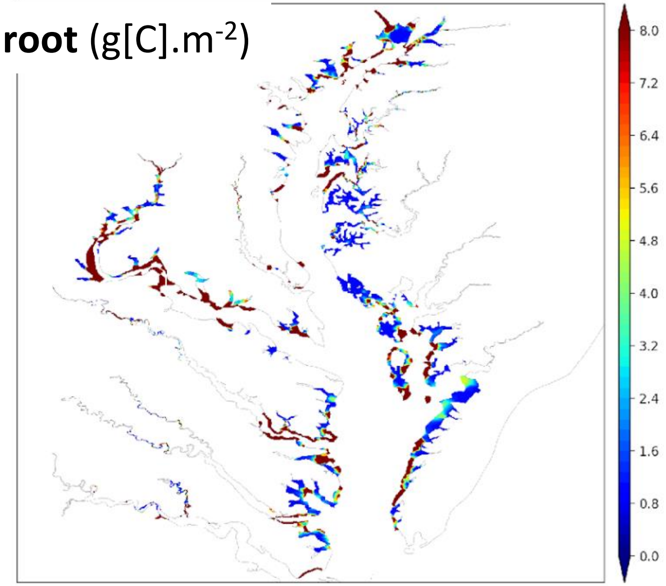
Leaf (g[C].m^{-2})



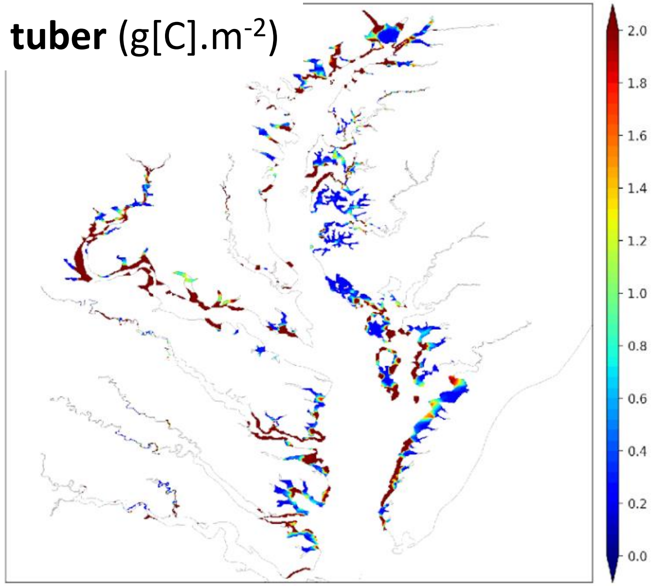
stem (g[C].m^{-2})



Canopy Height (m)



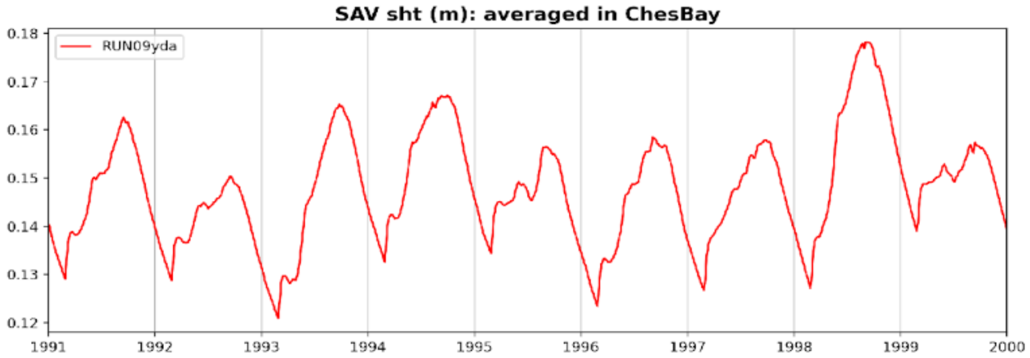
root (g[C].m^{-2})

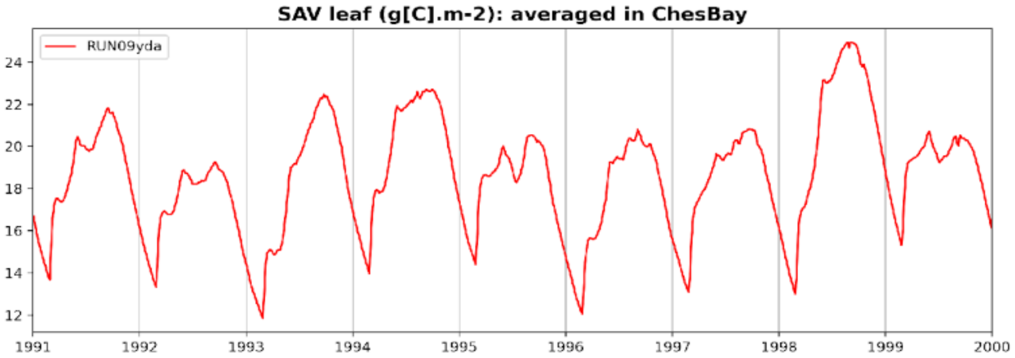


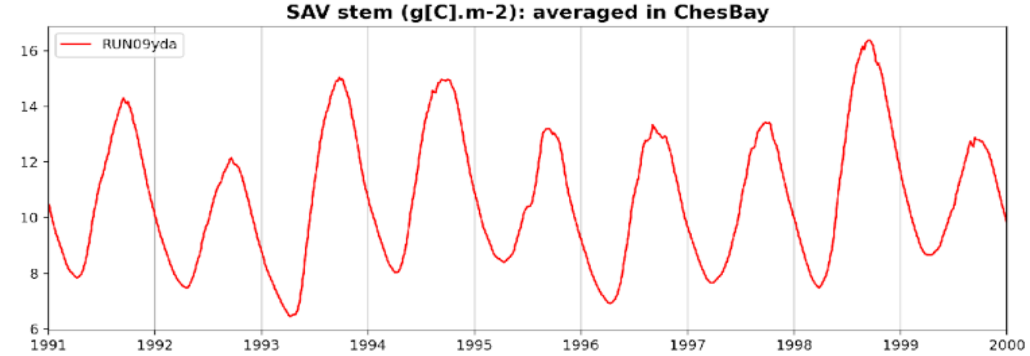
tuber (g[C].m^{-2})

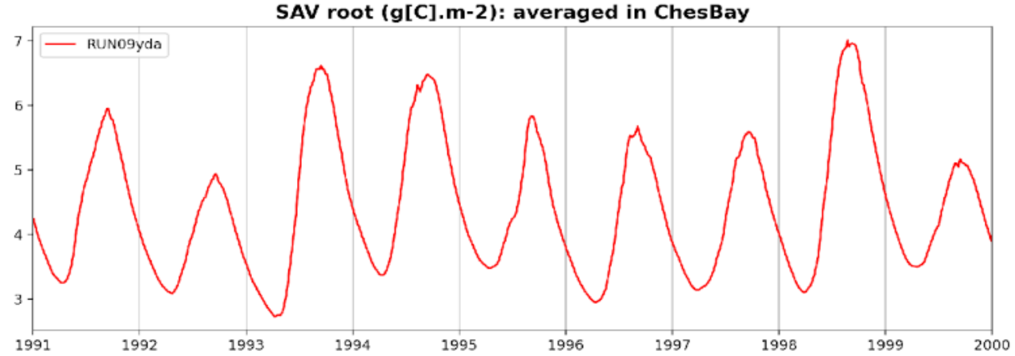
Bay-Averaged SAV Biomass and Canopy Height

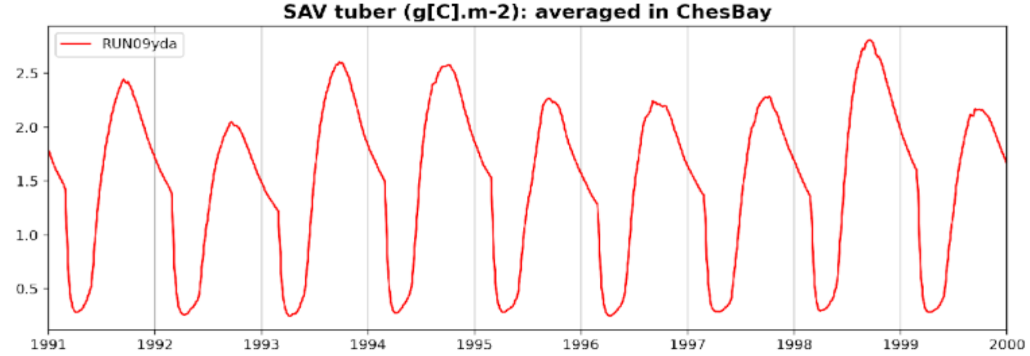
- Modeled seasonal variation of SAV seems correct
- Further validation is needed for comparison with observation


SAV sht (m): averaged in ChesBay


SAV leaf (g[C].m-2): averaged in ChesBay


SAV stem (g[C].m-2): averaged in ChesBay

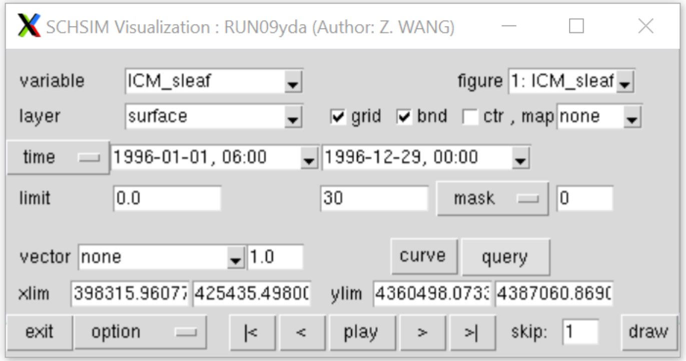

SAV root (g[C].m-2): averaged in ChesBay


SAV tuber (g[C].m-2): averaged in ChesBay

SAV diagnostic

- We have developed powerful diagnostic tool that enables use to analyze each processes, identify the model problem, and improve the model performance.

Visualization Tool



SCHSIM Visualization : RUN09yda (Author: Z. WANG)

variable ICM_sleaf

figure 1: ICM_sleaf

layer surface

☑ grid ☑ bnd ☐ ctr , map none

time 1996-01-01 , 06:00 1996-12-29, 00:00

limit 0.0 30

mask 0

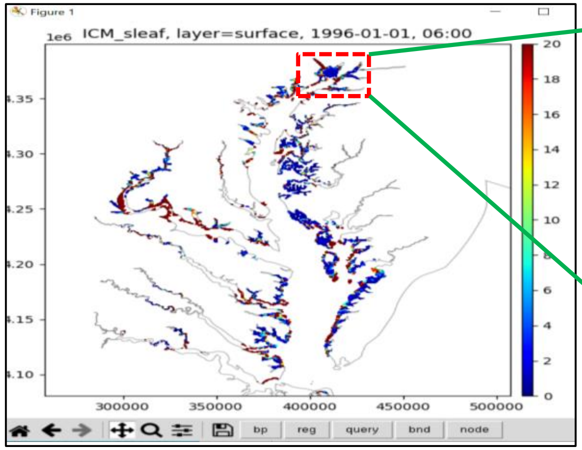
vector none 1.0

xlim 398315.96077 425435.49800

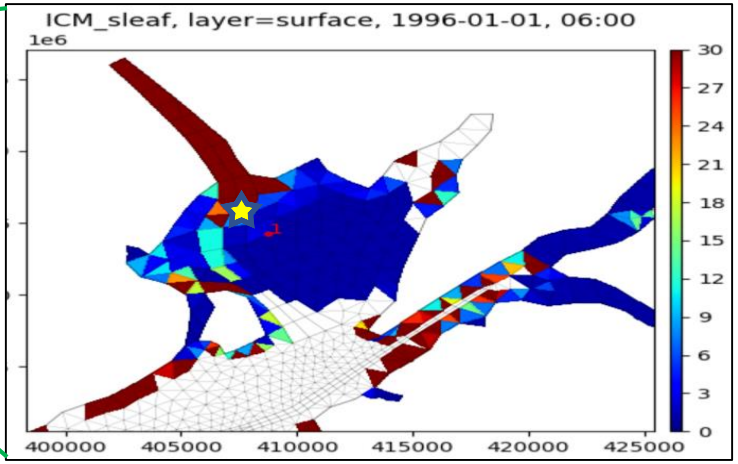
ylim 4360498.0733 4387060.8690

skip: 1

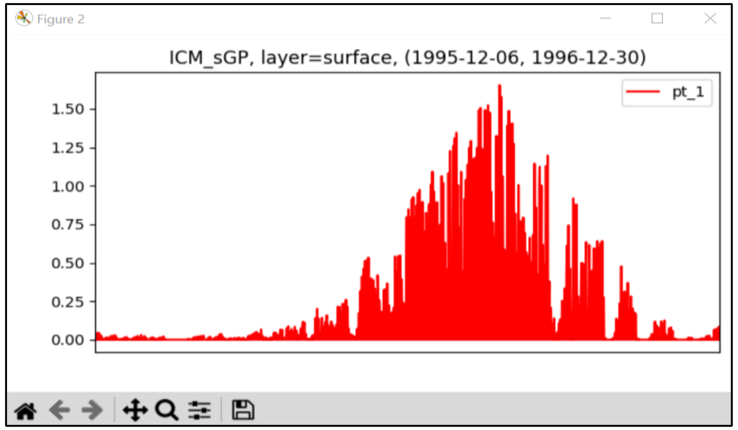
SAV leaf biomass



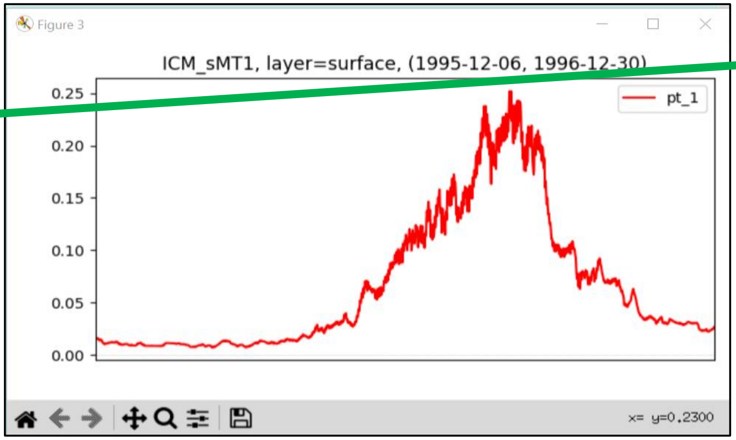
SAV leaf in Susquehanna Flat



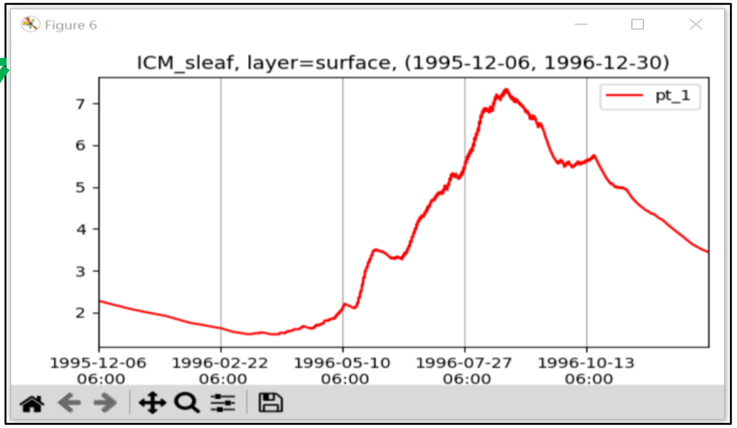
SAV Growth Rate



SAV metabolism Rate



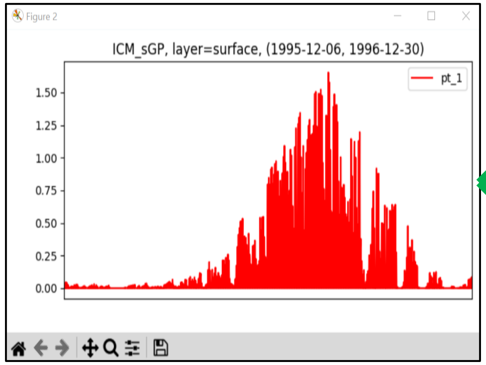
Time Series of SAV leaf



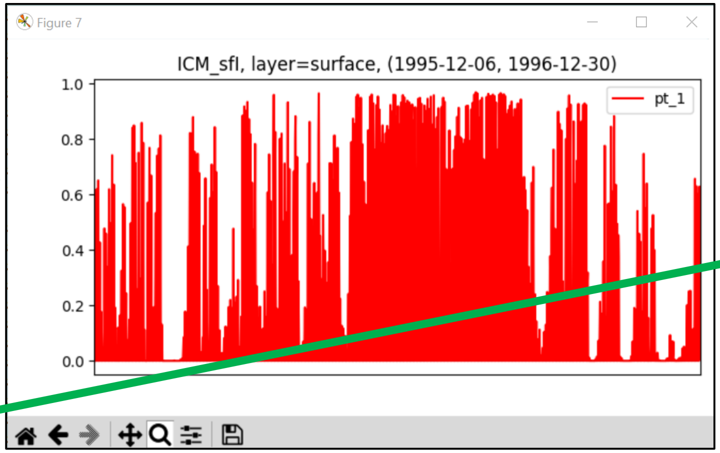
SAV diagnostic

- We have developed powerful diagnostic tool that enables use to analyze each processes, identify the model problem, and improve the model performance.

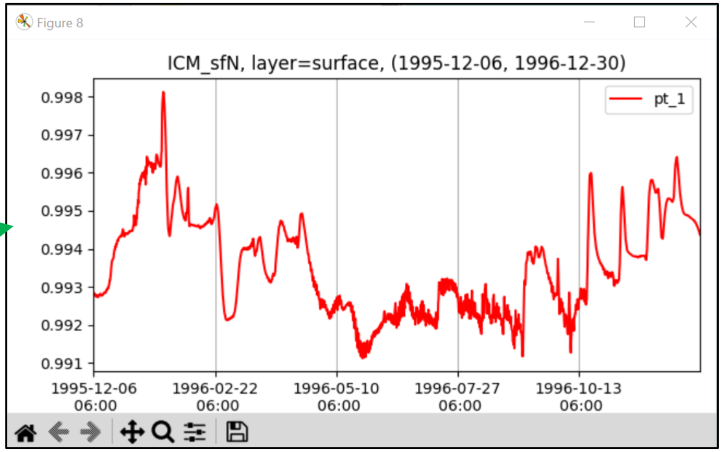
SAV Growth Rate



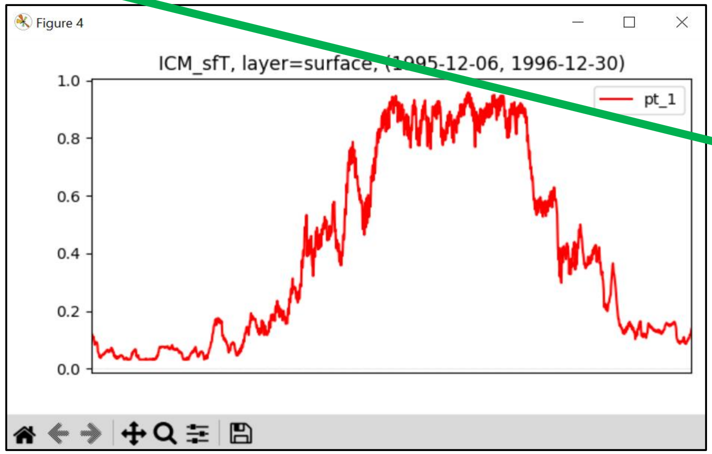
Light limitation



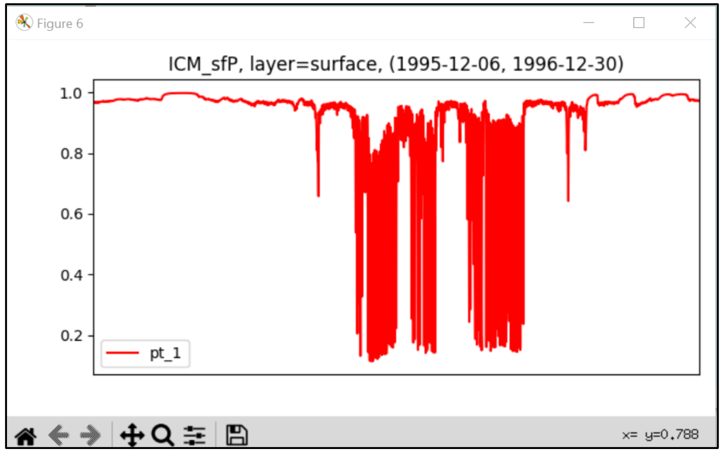
Nitrogen Limiation



Temperature Limitation



Phosphorus Limitation



Summary & future work

- We have completed the development of living resources modules (oyster, wetland, SAV) in the MBM.
- Initial calibration of LR modules has been conducted. Most results are still preliminary, and more model-data comparison is on-going.
- The magnitude of Reef oyster is captured, but the total biomass is underestimated at the moment
- DO simulation is improved with wetland module. The wetland impact decreases away from wetland area.
- For SAV simulation, the model reproduced reasonable seasonal variation.
- On-going work: finish documentation, more results analysis, conduct sensitivity runs.