Update on the Phase 7 Main Bay Model (MBM)

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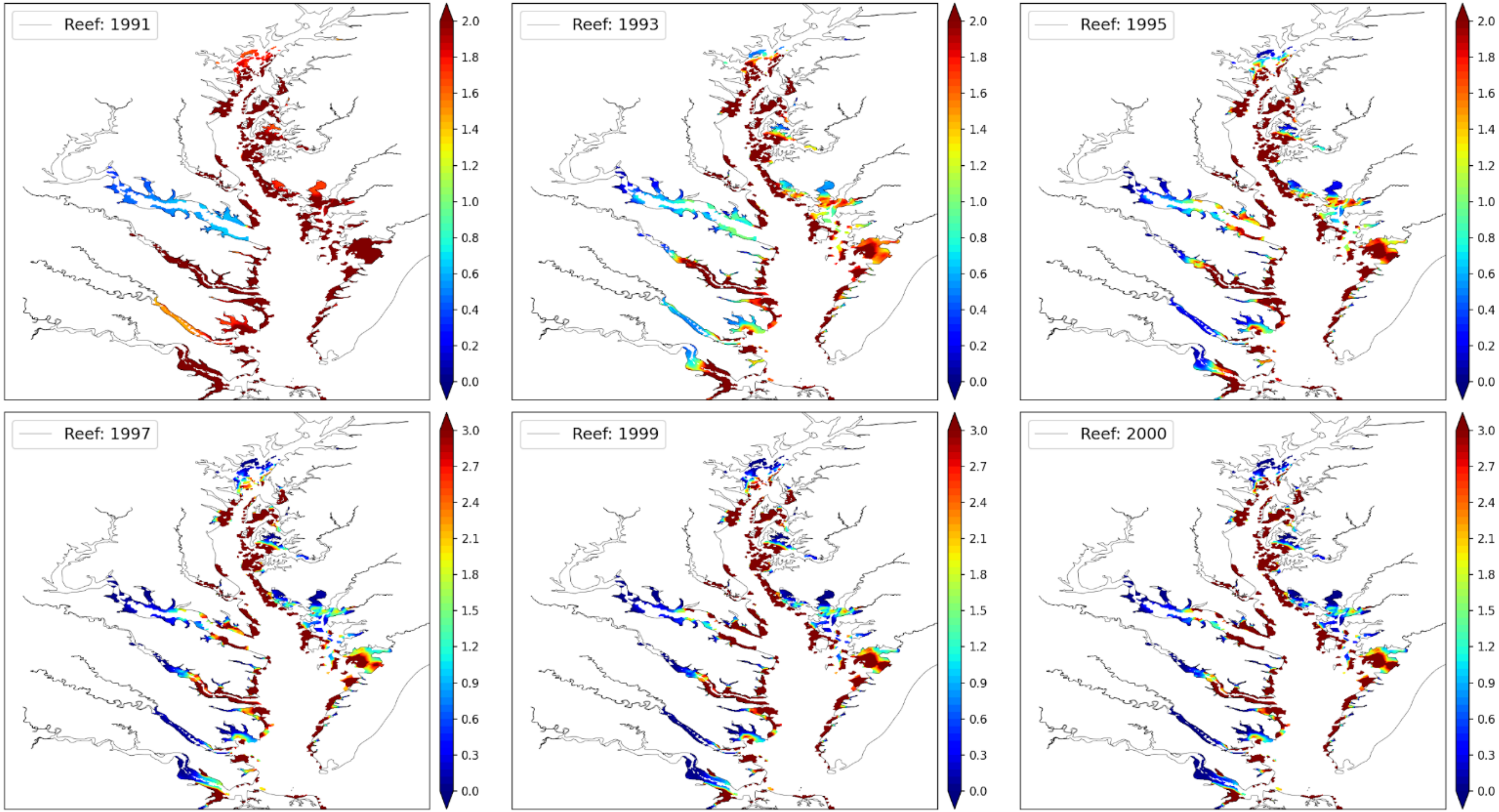
Outline

- **Updates on living resource (LR) modules in ICM**
  - Latest oyster model calibration and sensitivity tests
- **New workflow incorporating latest phase-7 (P7) watershed loading**
  - Processing P7 loading for MBM workflow
  - Allocating P7 loading to MBM grid
- **Hydrodynamic results with the P7 loading (preliminary)**
  - Assessment of elevation, temperature and salinity
- **Summary & next steps**

Oyster Model

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

- Latest model calibration of Reef oyster shows reasonable biomass (too large or small in earlier runs)
  - The major processes controlling the oyster growth (e.g. filtration rate etc) are carefully calibrated
- Simulated oyster biomass reached a quasi-steady state (after recycling the model with end state).

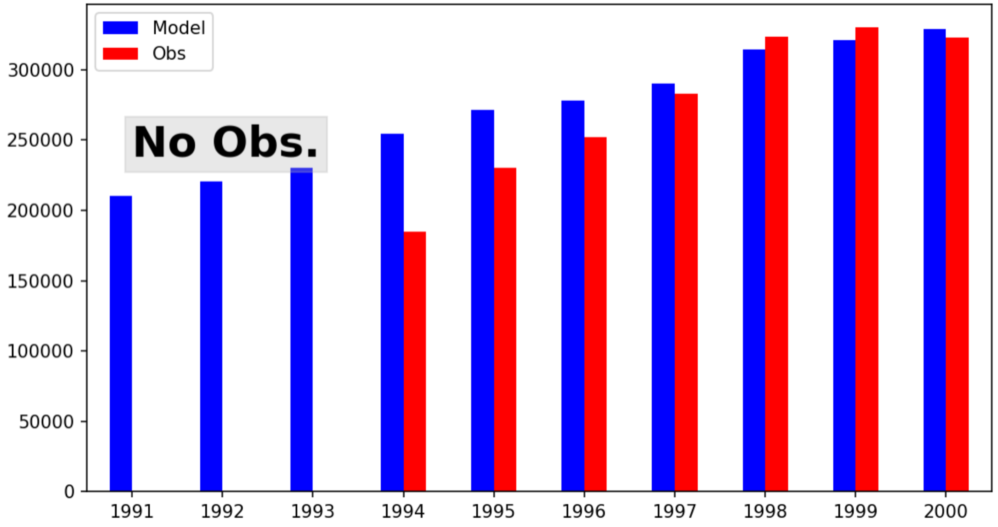


Comparison of Reef Biomass with data

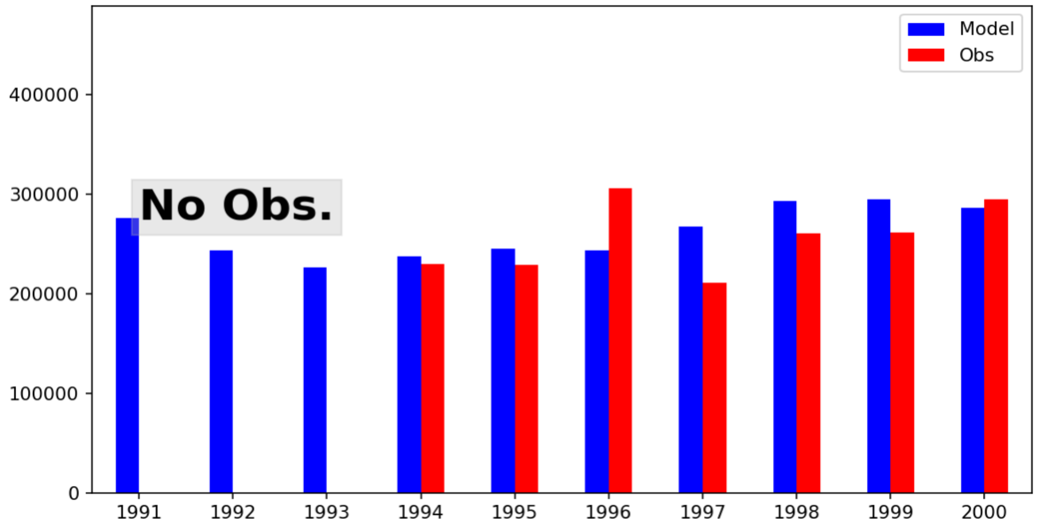
- Simulated Reef biomass matches observation well.
- The Reef biomass time series shows good seasonal cycles

Annual Mean

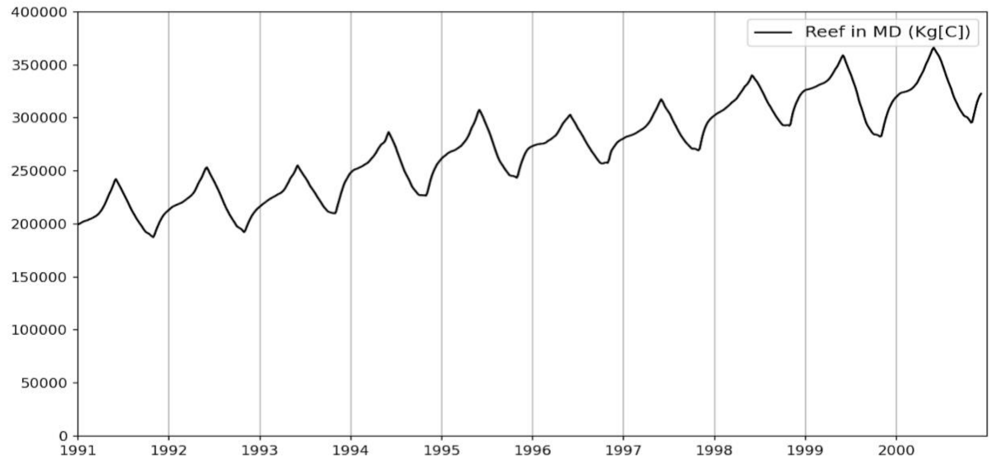
Reef in MD (Kg [C])

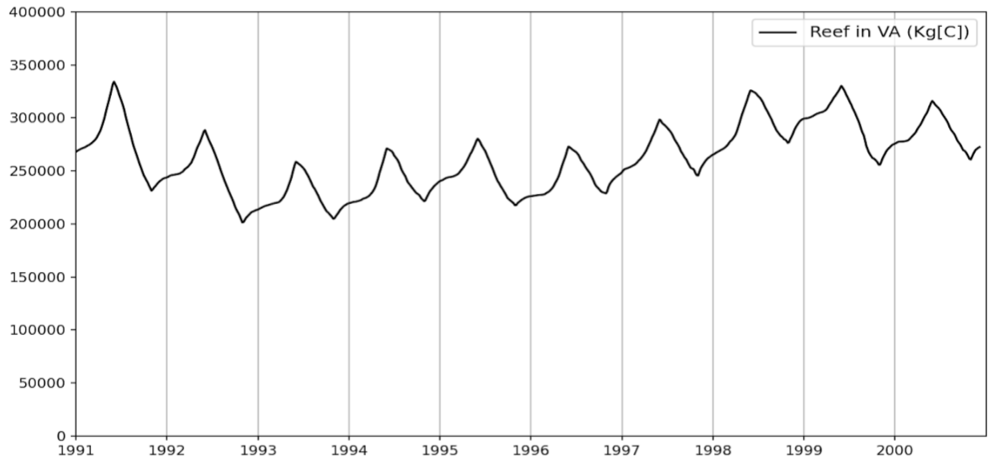


Reef in VA (Kg [C])



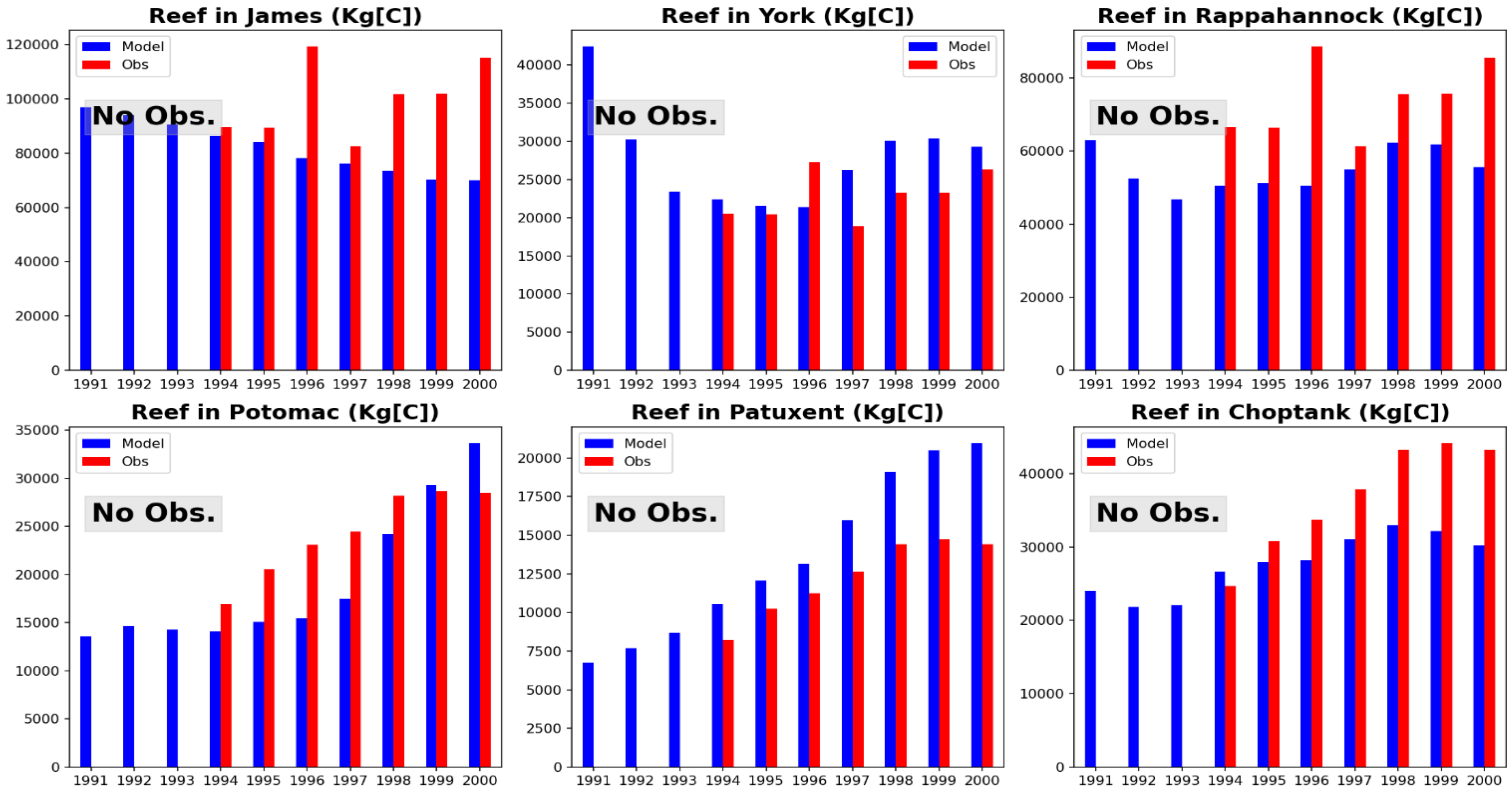
Time Series of biomass





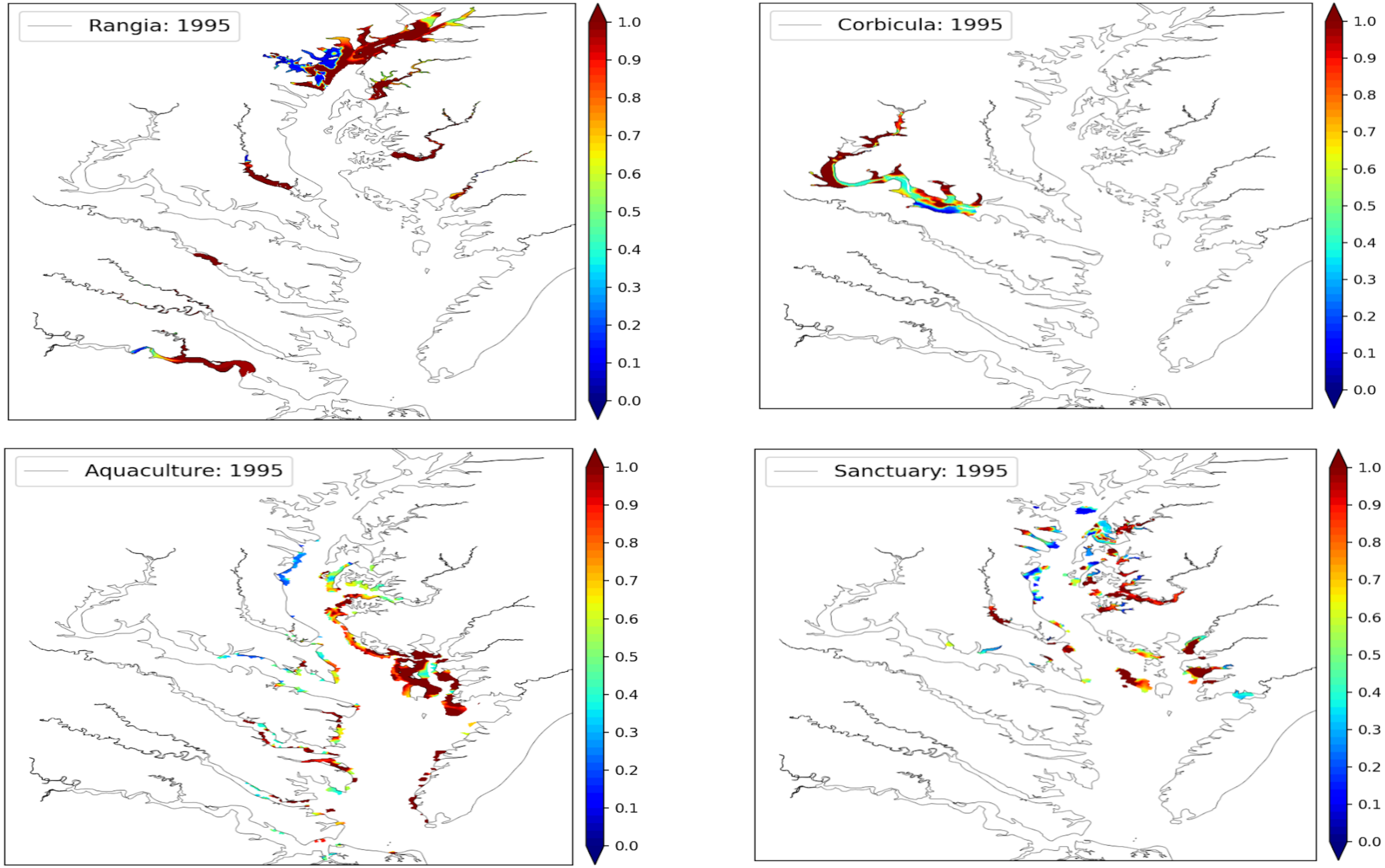
Reef Biomass in tributaries

- Overall, the Reef biomass matches with observation in different tributaries



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

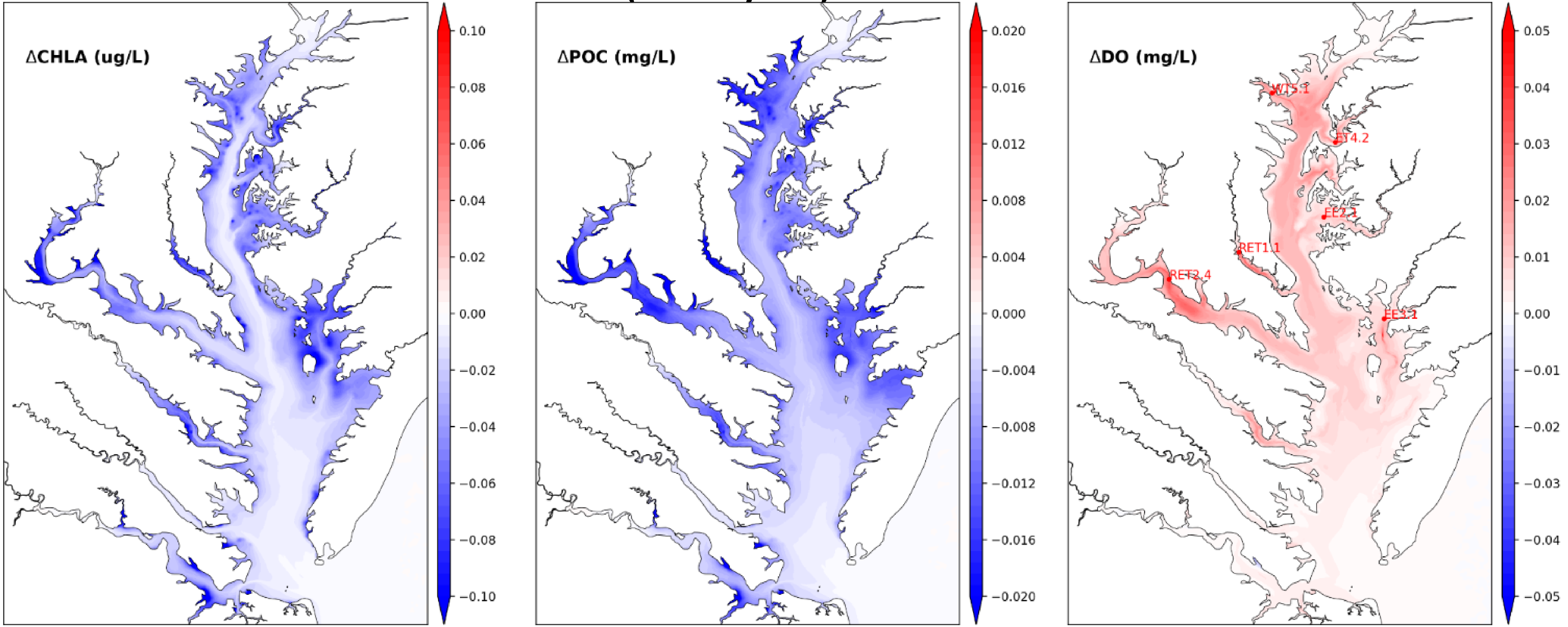
- Overall, reasonable spatial patterns and temporal variations for different oyster species
- Note: in the final calibration (not scenarios), constant Aquaculture biomass will be applied in the model



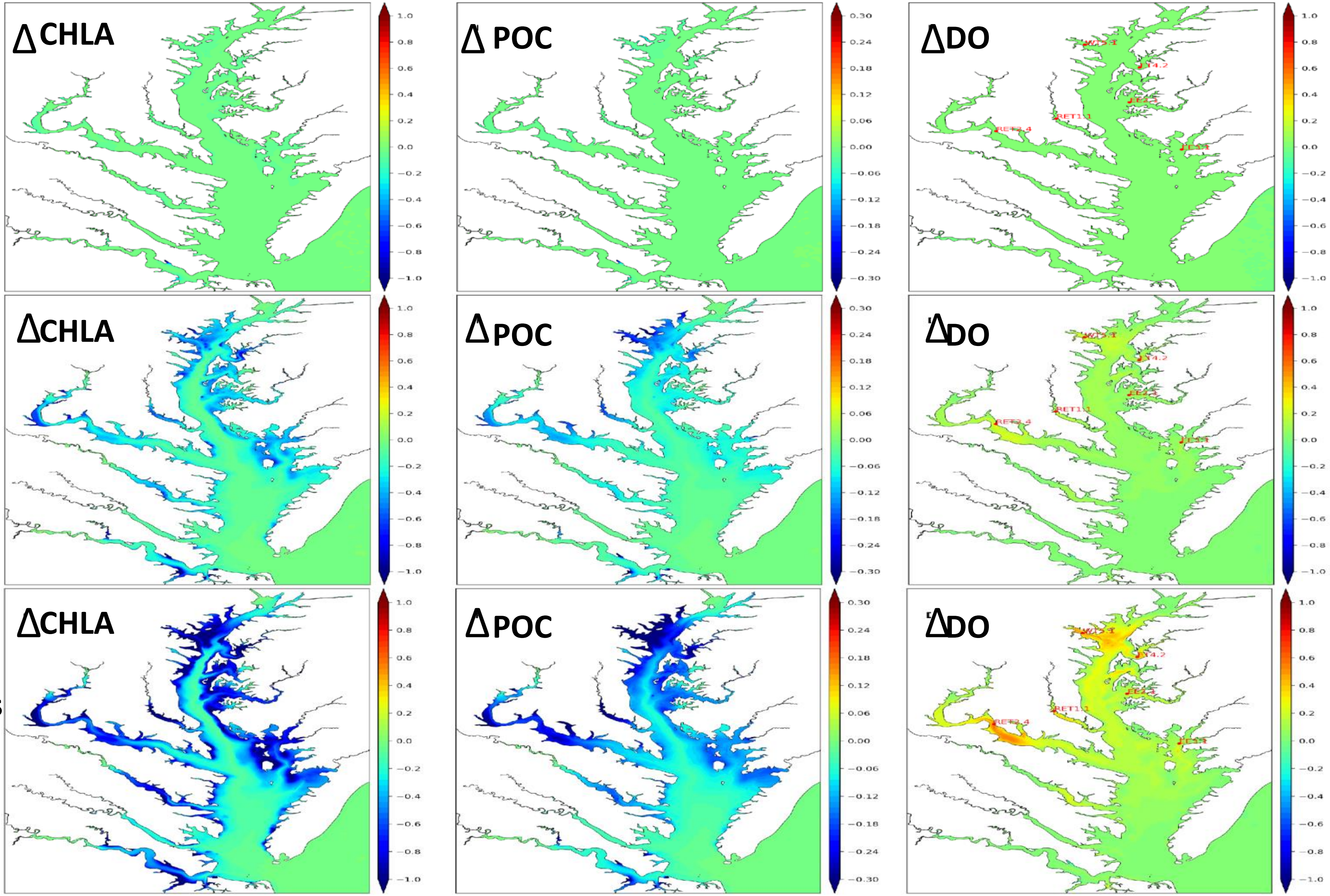
Oyster impact on water quality

- Overall, the oyster impact is relatively small.
- Oyster filtration removes the Chl-a and POC concentrations, making the water cleaner. As a result, DO increases in some regions

(With oyster) - without



Oyster impact: sensitivity test by increasing oyster biomass by 10 and 30 times



- Oyster impact becomes stronger with larger oyster biomass.

30 times experiment

Chl-a: -1 ug/L

POC : -0.3 mg/L

DO : ~0.5 mg/L

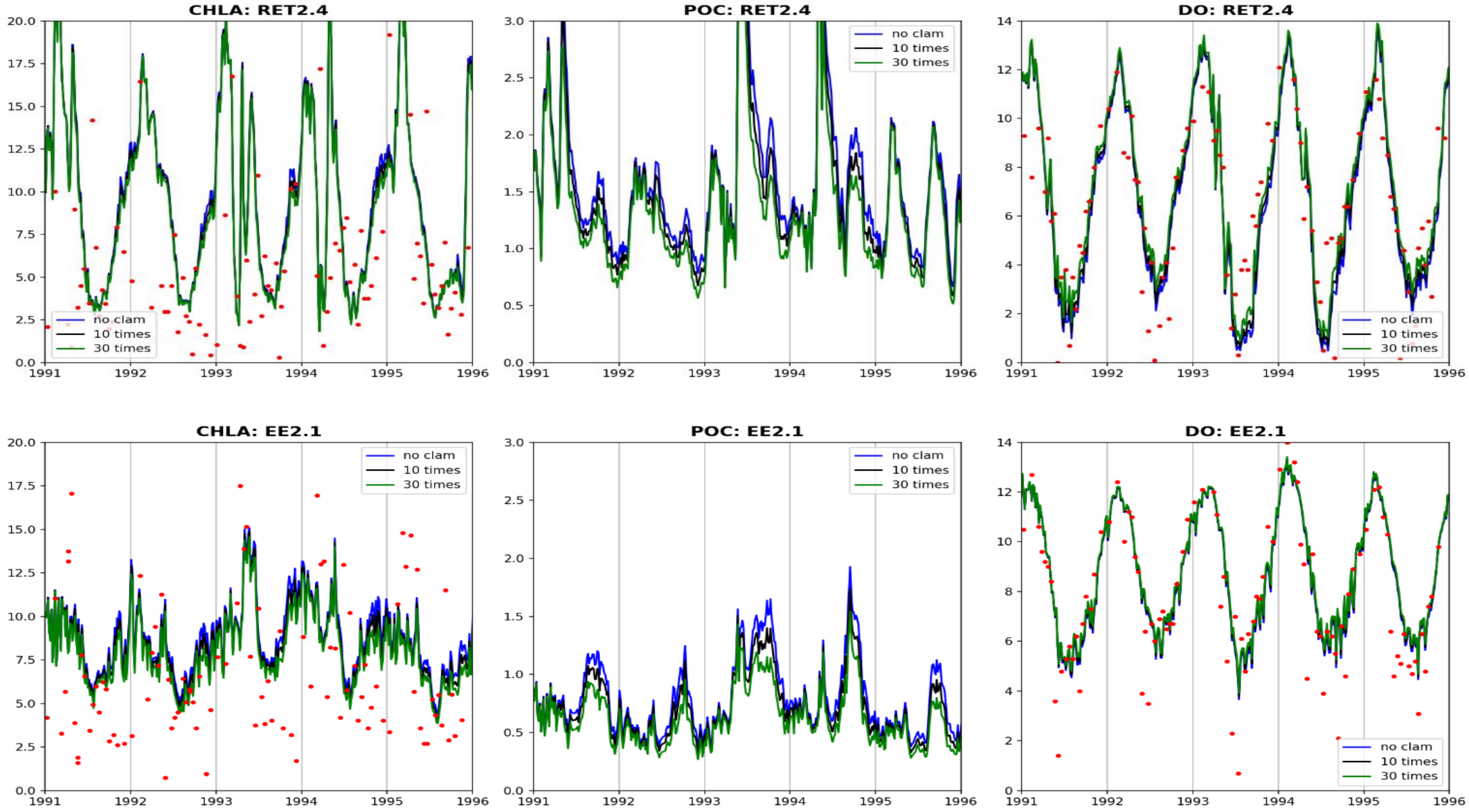
Oyster impact in sensitivity tests

without oyster
10 times
30 times

- Overall, the oyster impact is still relatively small even with 10/30 times increase
- The impact on POC is most evident.

Potomac

Choptank



P7 load

Incorporating P7 watershed loading into MBM modeling workflow

❖ Gopal provided us with the P7 loading. With his help, we finished processing the data with a revised workflow

- ❑ Reorganization of P7 files with more than 220 K files (removed invalid files)
- ❑ Pre-processing the watershed loading (parallel reading)
  - Changed the format to our database format
- ❑ Organized the watershed segments information
  - Collected the watersheds corresponding to the loading
  - Computed *cbseg* and *river basin* information
  - *Better to use new shapefile from Gopal*
- ❑ Computed the allocations of watershed loadings to MBM grid (including SHO)
- ❑ Preparing the input of watershed loading for P7 MBM
- ❑ Reorganized the workflow for the new coupling
- ❑ Validating new watershed inputs
  - Checked the watershed loading received by the MBM
  - Model runs fine with P7 loading (yay!)

Creating database for P7 watershed loading

- Originally, we have 50 k terminal inputs and 175 k tidal inputs (> 220 k files). It requires parallel computing (multiple CPUs) to process the data

- After we reformatted the data, the database is only one file (5.6 G). It contains all the information, which allows us to easily performance various operations on the datasets (filter, read, search, etc.)

snapshot of p7 loading database

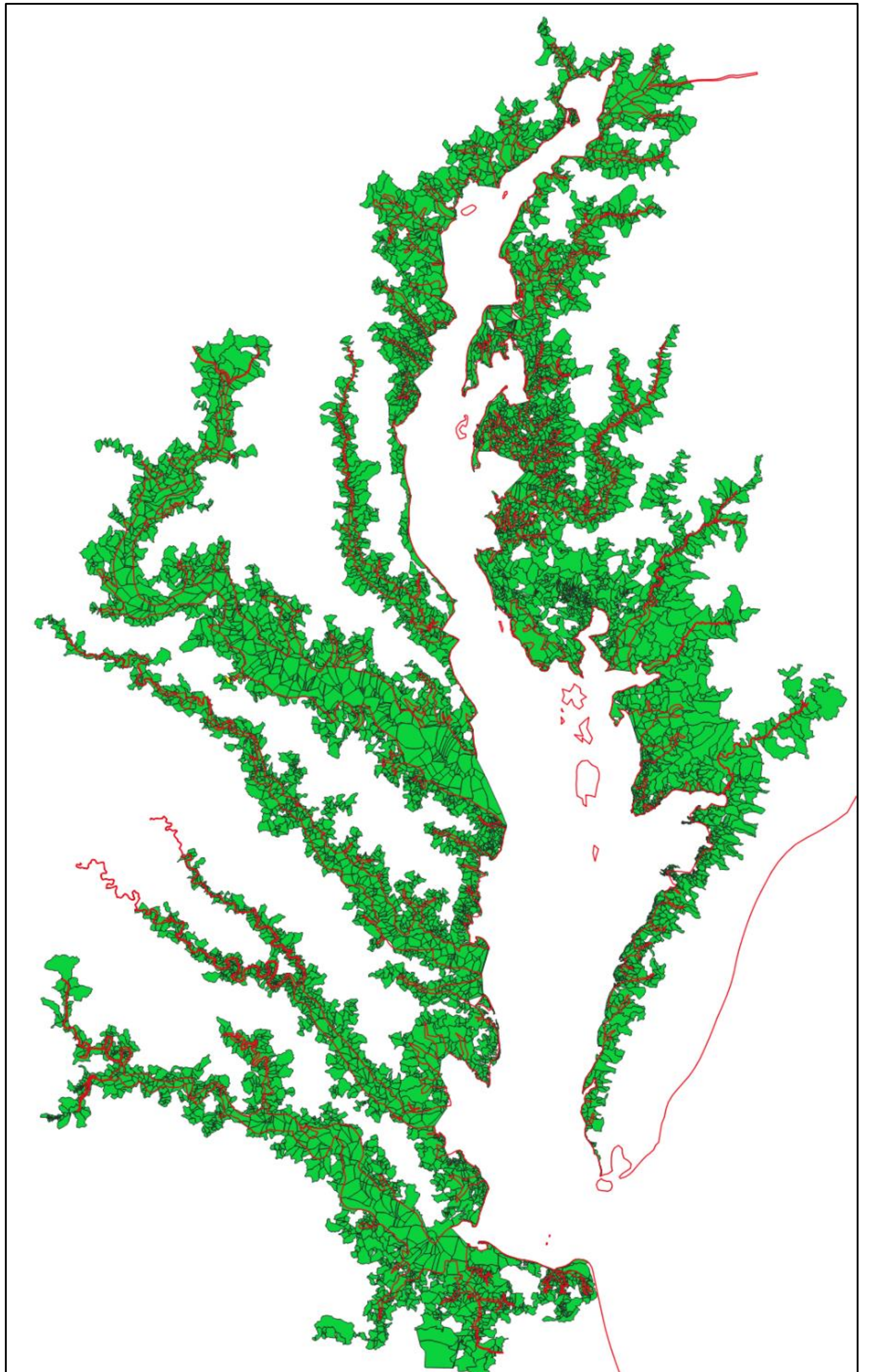
```
In [1]: C=read('wsm_v1.npz')

In [2]: C.VINFO
Out[2]:
['chla   : array(12479, 13149), float32',
 'clay   : array(12479, 13149), float32',
 'doxx   : array(12479, 13149), float32',
 'flow   : array(12479, 13149), float32',
 'nh4x   : array(12479, 13149), float32',
 'no3x   : array(12479, 13149), float32',
 'orgn   : array(12479, 13149), float32',
 'orgp   : array(12479, 13149), float32',
 'phyt   : array(12479, 13149), float32',
 'pipx   : array(12479, 13149), float32',
 'po4x   : array(12479, 13149), float32',
 'sand   : array(12479, 13149), float32',
 'silt   : array(12479, 13149), float32',
 'snames: array(12479,), <U13',
 'stypes: array(12479,), <U8',
 'time   : array(13149,), float64',
 'tocx   : array(12479, 13149), float32',
 'totn   : array(12479, 13149), float32',
 'totp   : array(12479, 13149), float32',
 'tssx   : array(12479, 13149), float32',
 'units  : dict(18,)',
 'vars   : array(18,), <U4',
 'wtmp   : array(12479, 13149), float32']
```

Shapefile of P7 watershed segments

- We received two shapefiles for watershed segments
  - CBW_NHDv21_catchment_20230630_P7Attributes_v3.shp (all information)
  - CBW_NHDv21_catchment_20230630_P7Attributes_v3_xNonTidal.shp (selected by Gopal)

- We created a new shapefile to include watershed information needed for MBM
  - We couldn't directly use the 2nd shapefile as 2 segments were missing
  - We extracted the information from the 1st one, and might combine it with the 2nd file to include all watershed segments.

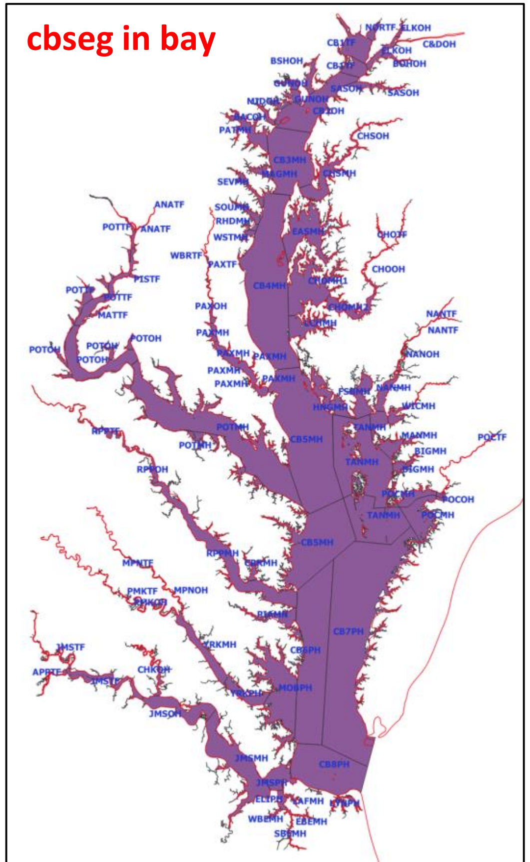
- In total, we have 12749 watershed segments in P7 (2745 terminal, 9734 tidal)
  - In comparison, P6 loading has 601 NPS, and 557 PS

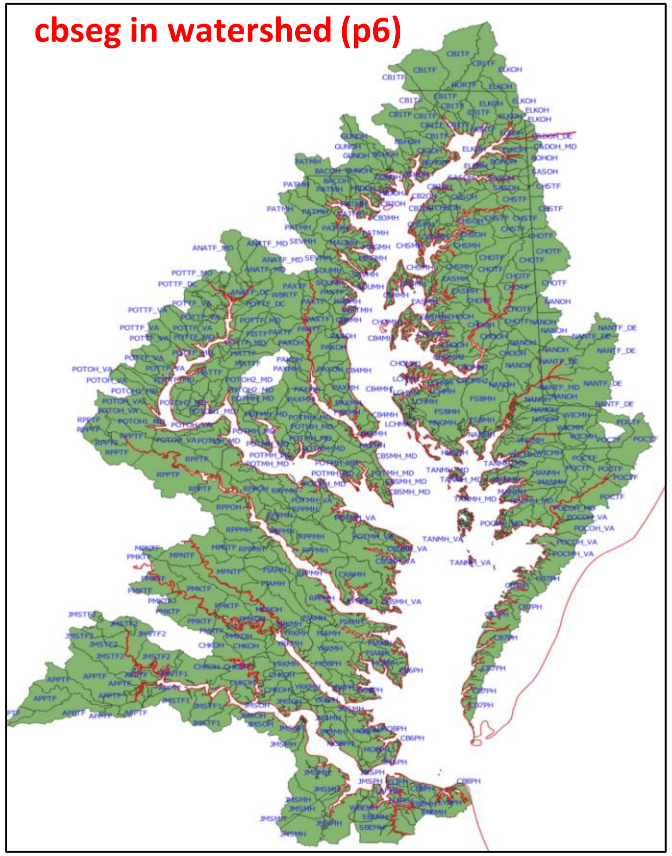


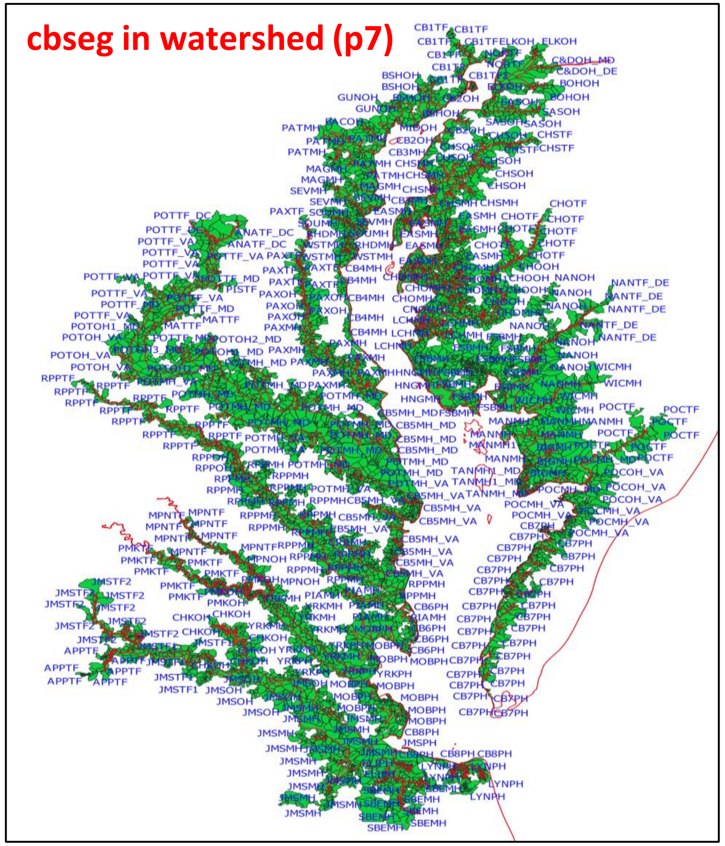
Adding attributes for watershed segments

- In order to accurately mapping the watershed loading onto MBM grid, more information about watershed segments is needed
  - Nearest interpolation method may have error locally

- Information on ***cbseg*** and ***river basin*** can help find the correct segment for a MBM boundary location
  - cbsegs_104_v2.shp (from Richard)
  - p6 watershed (from Gopal)



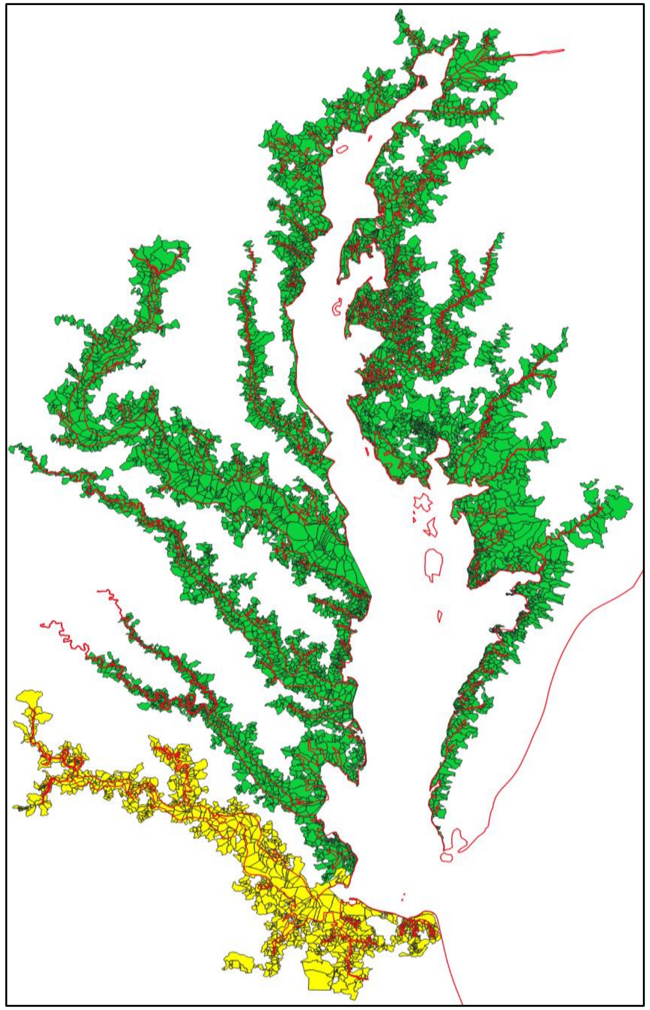




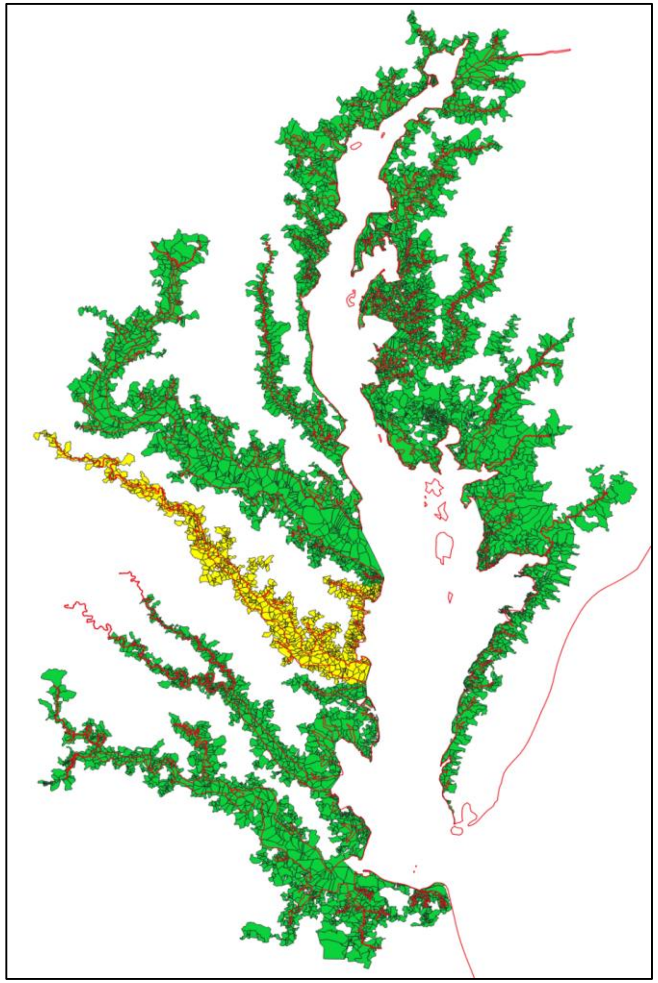
River Basin for watershed segments

- Based on P6 watershed information, we computed the river basin for P7 watershed segments
- It works OK, but not ideal. It would be better to get the information from watershed modeling team

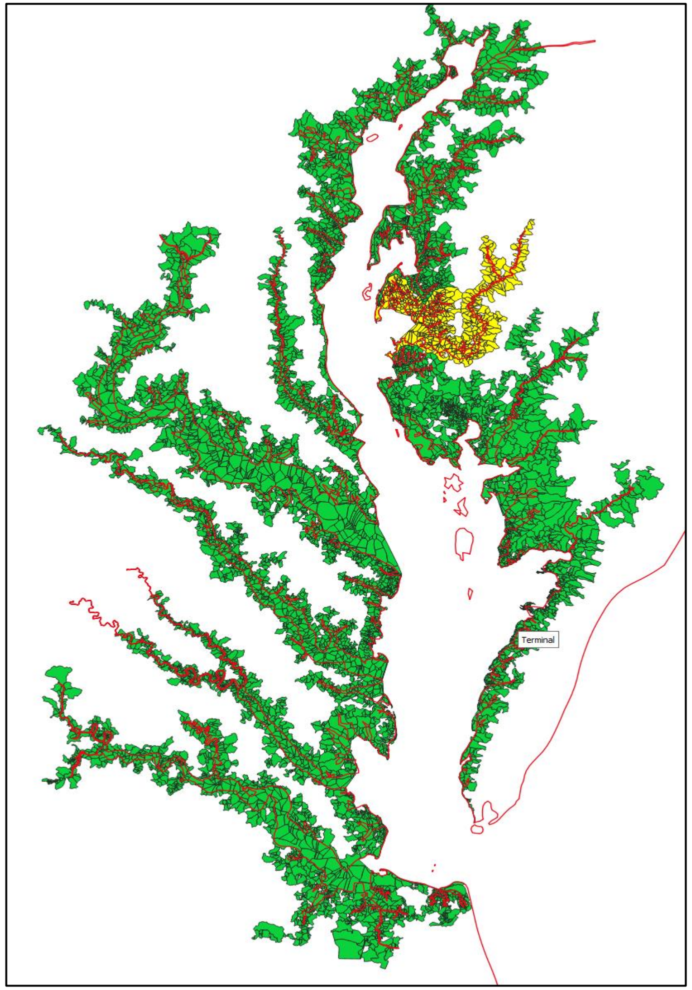
James River



Rappahannock River

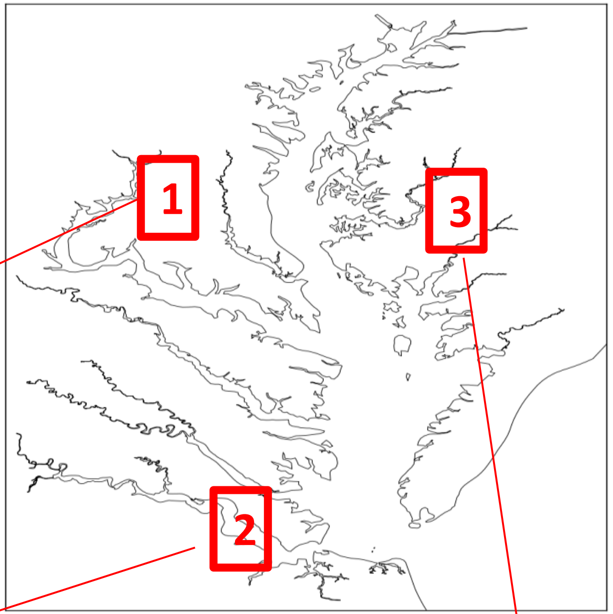


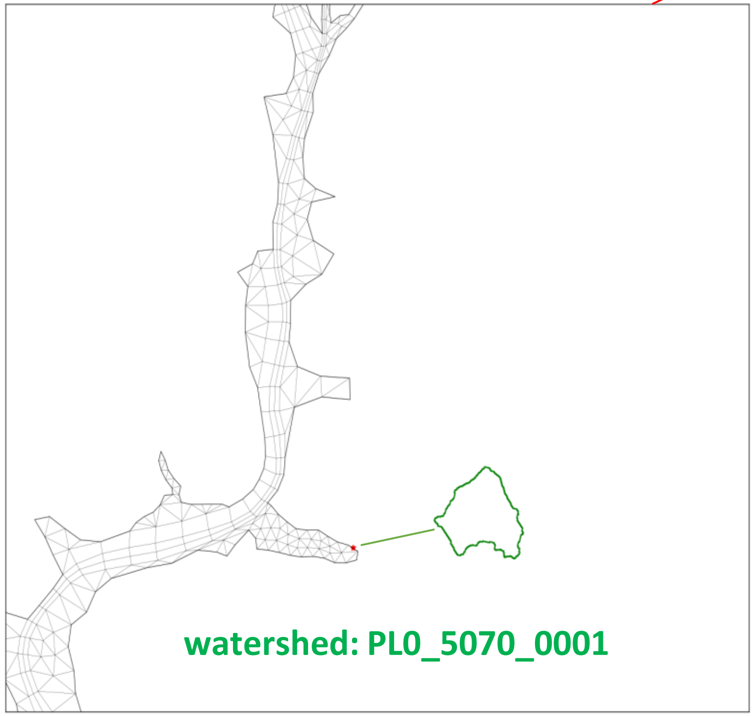
Choptank River

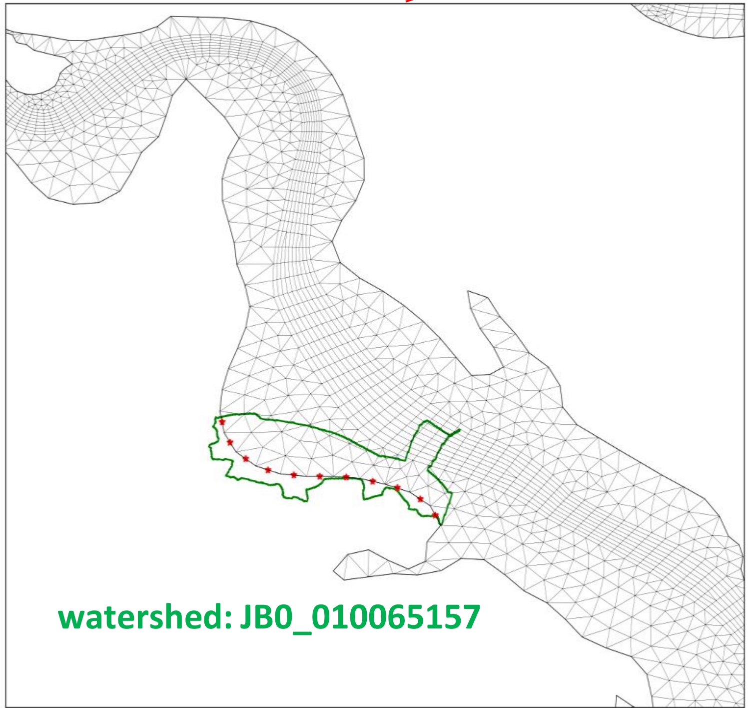


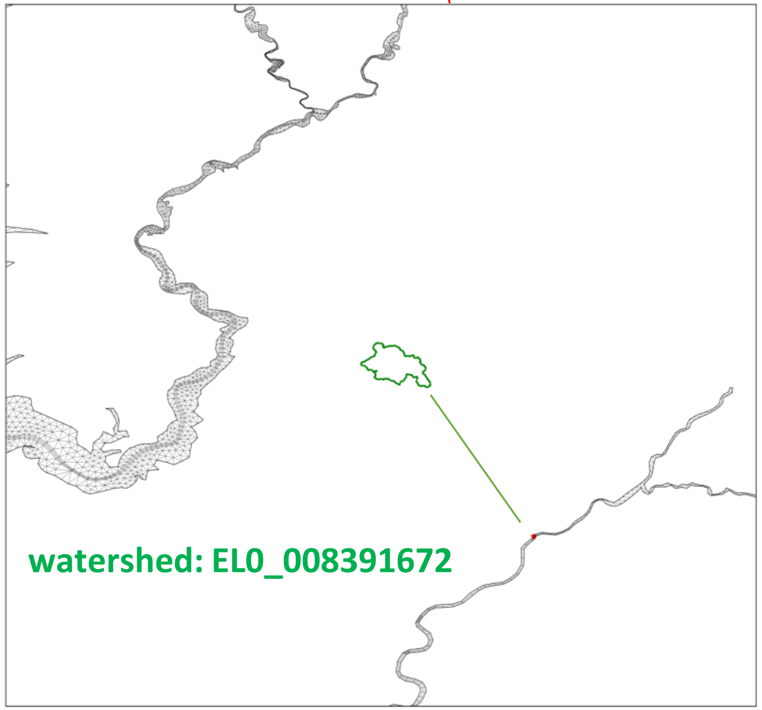
Allocation of watershed loading to MBM grid

- For watershed that intersects with MBM grid, we directly distribute its loading to the adjacent MBM cells.
- For watershed that doesn't intersect MBM grid, we search the nearby watershed with same ***cbseg*** that intersects MBM grid
- The watershed loading is distributed among MBM boundary sides, based on side length







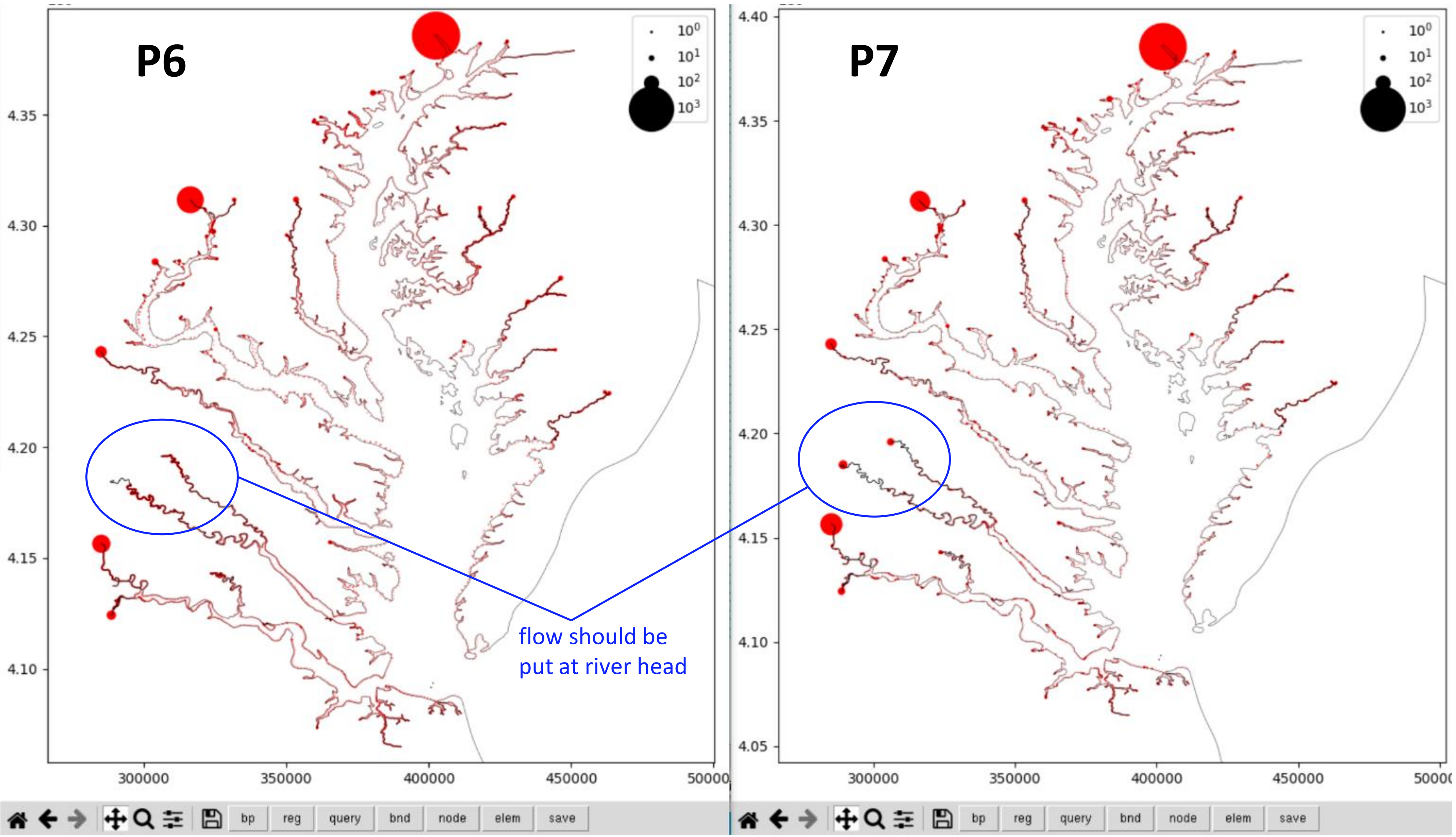


Special treatment for the RIM watershed

- ❑ For large rivers, we need to make sure the loadings are put at the river head (most upstream location)
  - SL9_2720_0001 – Susquehanna
  - PM7_4820_0001 – Potomac
  - JL7_7070_0001 – James
  - RU5_6030_0001 – Rappahannock
  - JA5_7480_0001 – Appomattox
  - YP4_6750_0001 – Pamunkey
  - YM4_6620_0001 – Mattaponi
  - XU3_4650_0001 – Patuxent
  - EM2_3980_0001 – Choptank

Flow comparison between P6 and P7

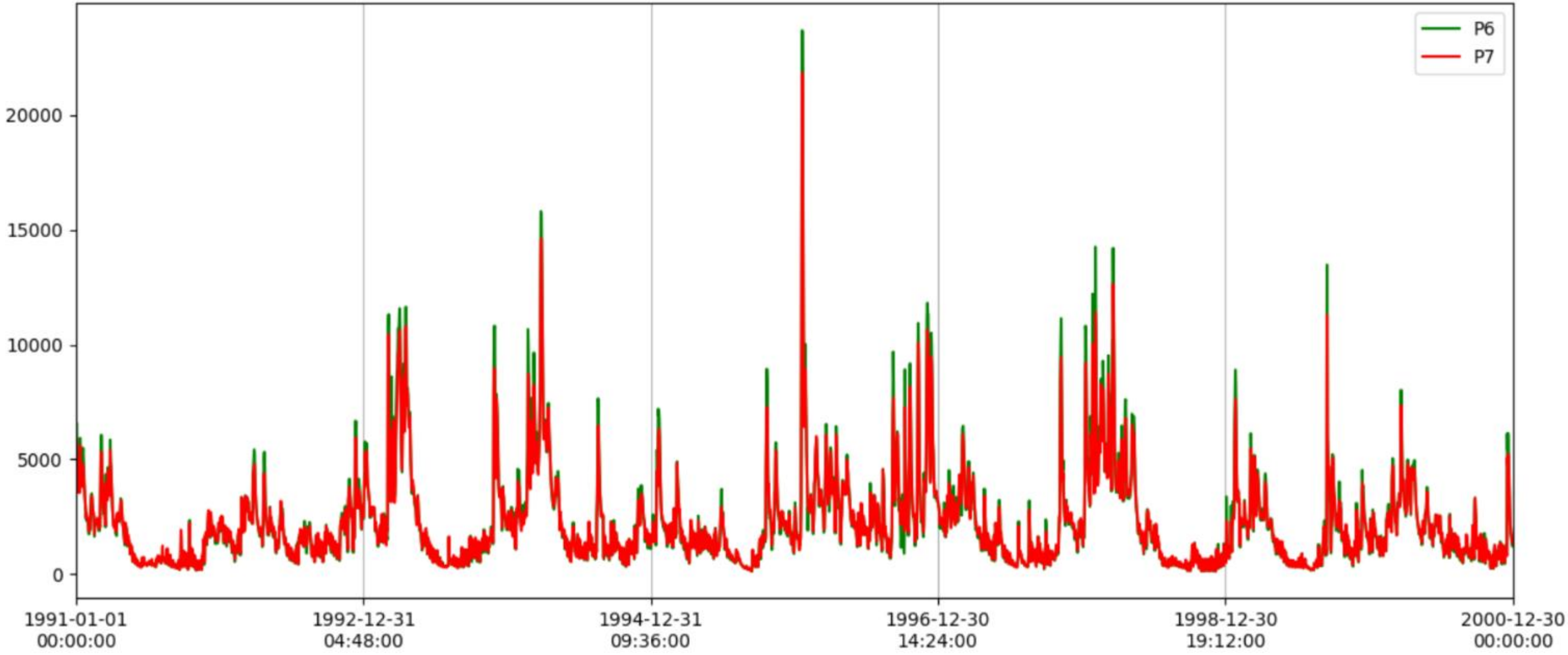
- Overall, the flow distributions are very similar between P6 and P7
- Due to the higher resolution in P7, there is some local improvement in flow distribution



Flow comparison between P6 and P7

- Total flow and variation between P6 and P7 are similar

mean flow (P6)= 2291 m^3/s **mean flow (P7)= 2249 m^3/s**

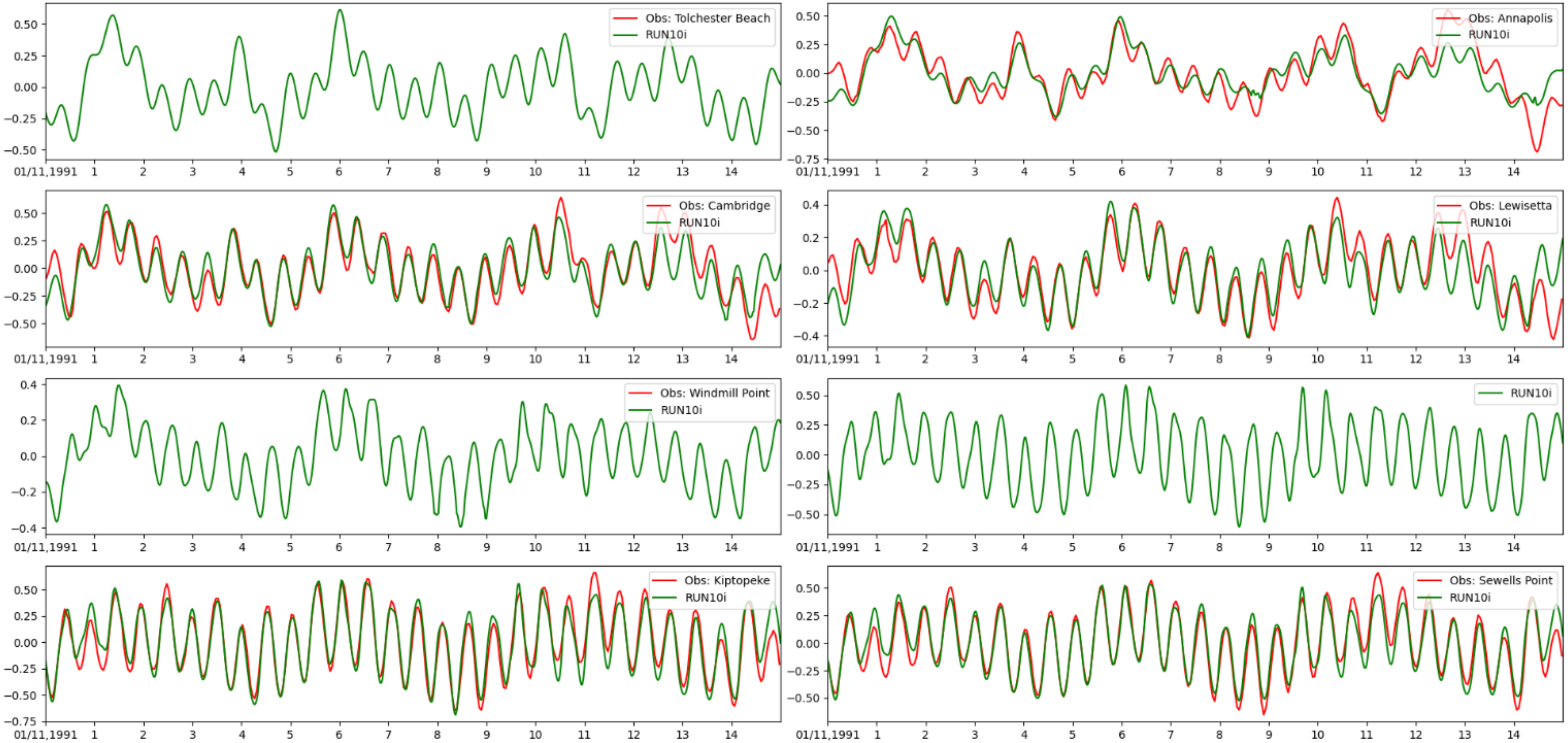


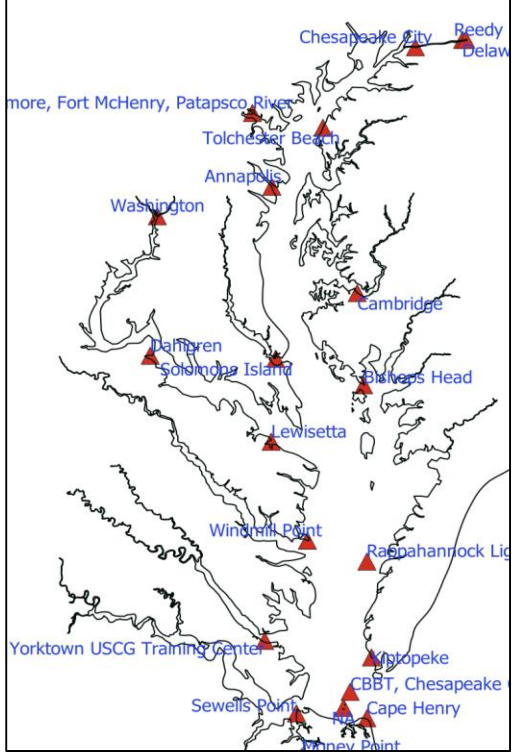
Hydrodynamics with P7 loading

Water Level: tidal signal

- Water levels match well between model and observation from upper bay to lower bay.

Obs P7

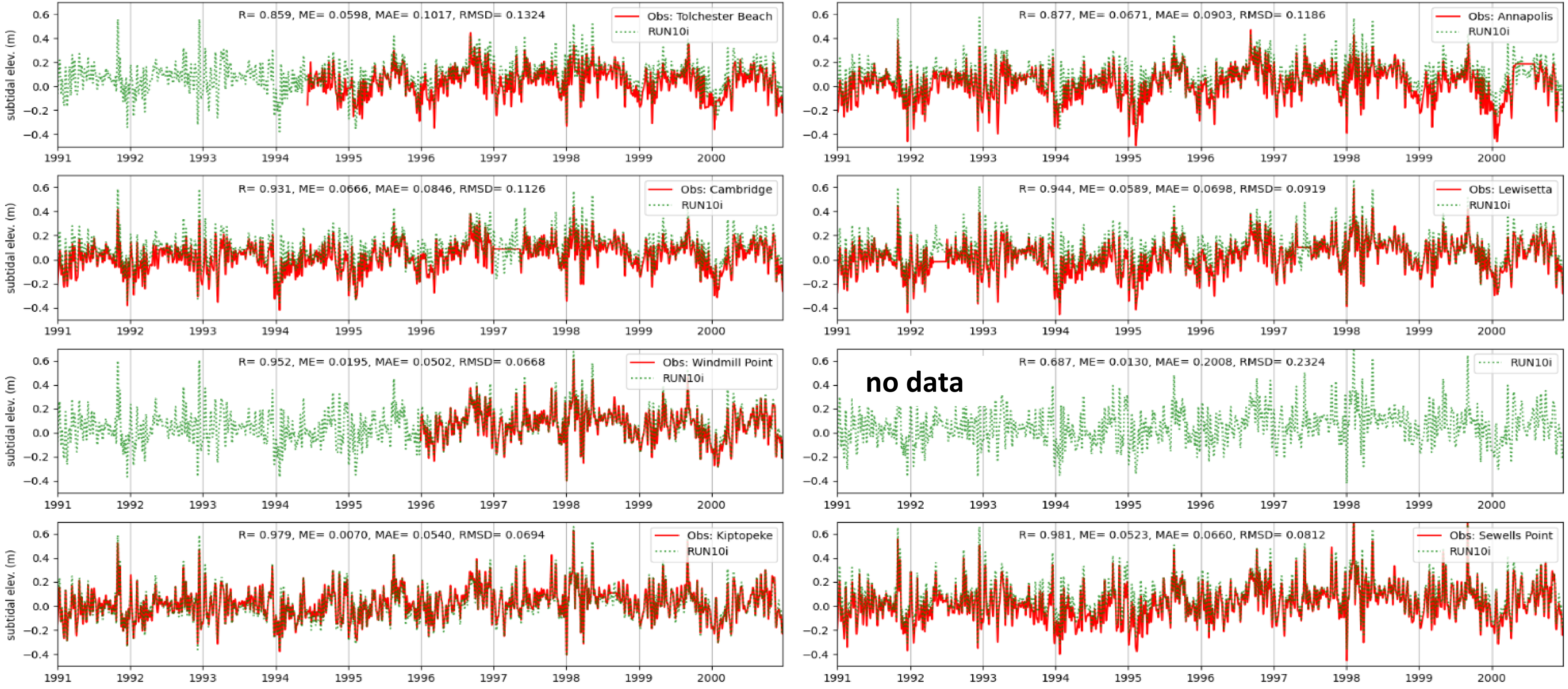




Water Level: sub-tidal signal

- The model reproduced the sub-tidal signals well inside the bay.
- RMSD varies from 0.067 m to 0.13 m

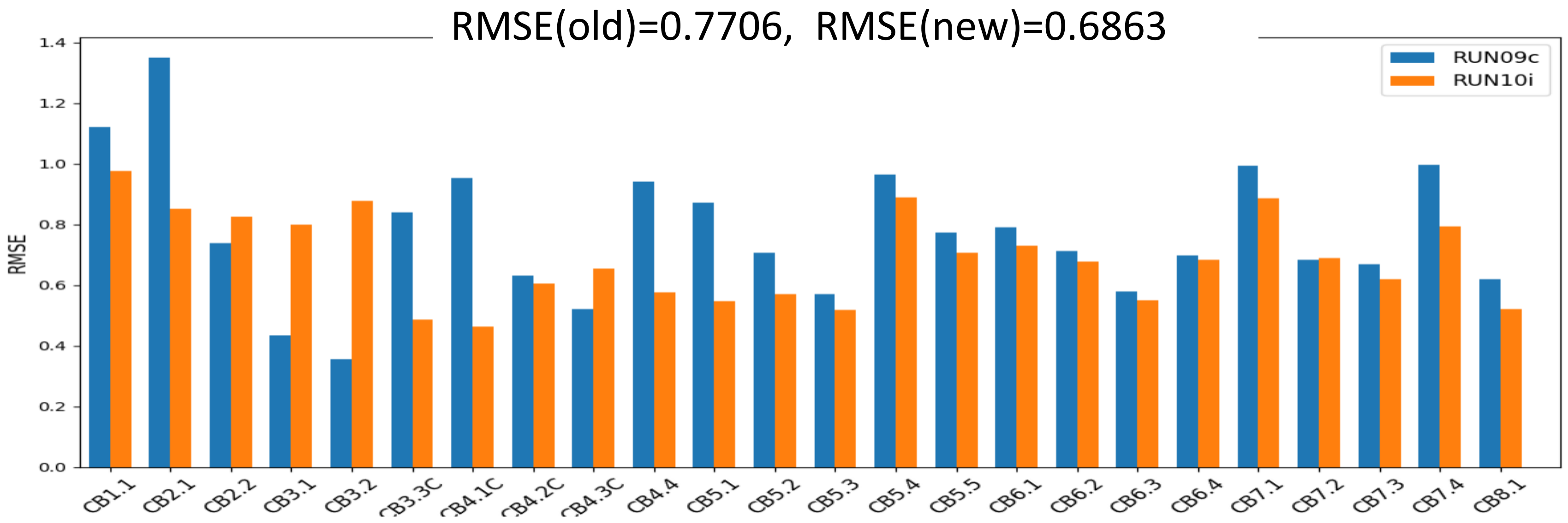
Obs P7



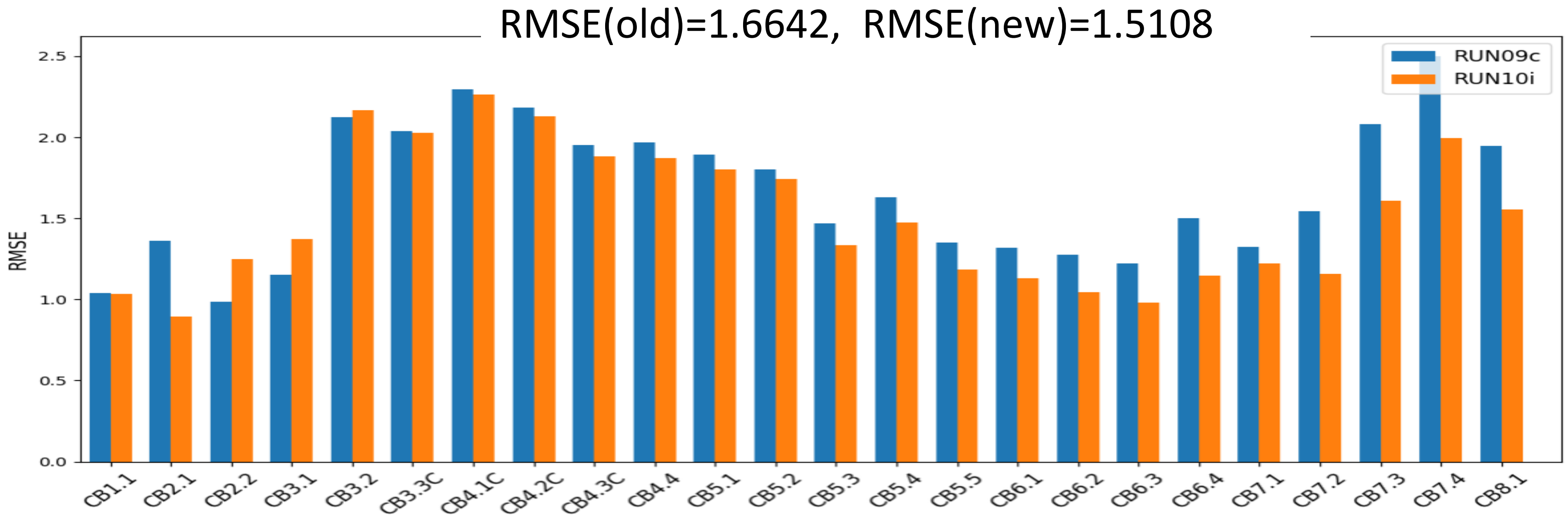
New Temperature Calibration: Main Channel

- Surface and bottom temperatures along the main bay channel are improved slightly from P6 loading

Surface Temp. (°C)

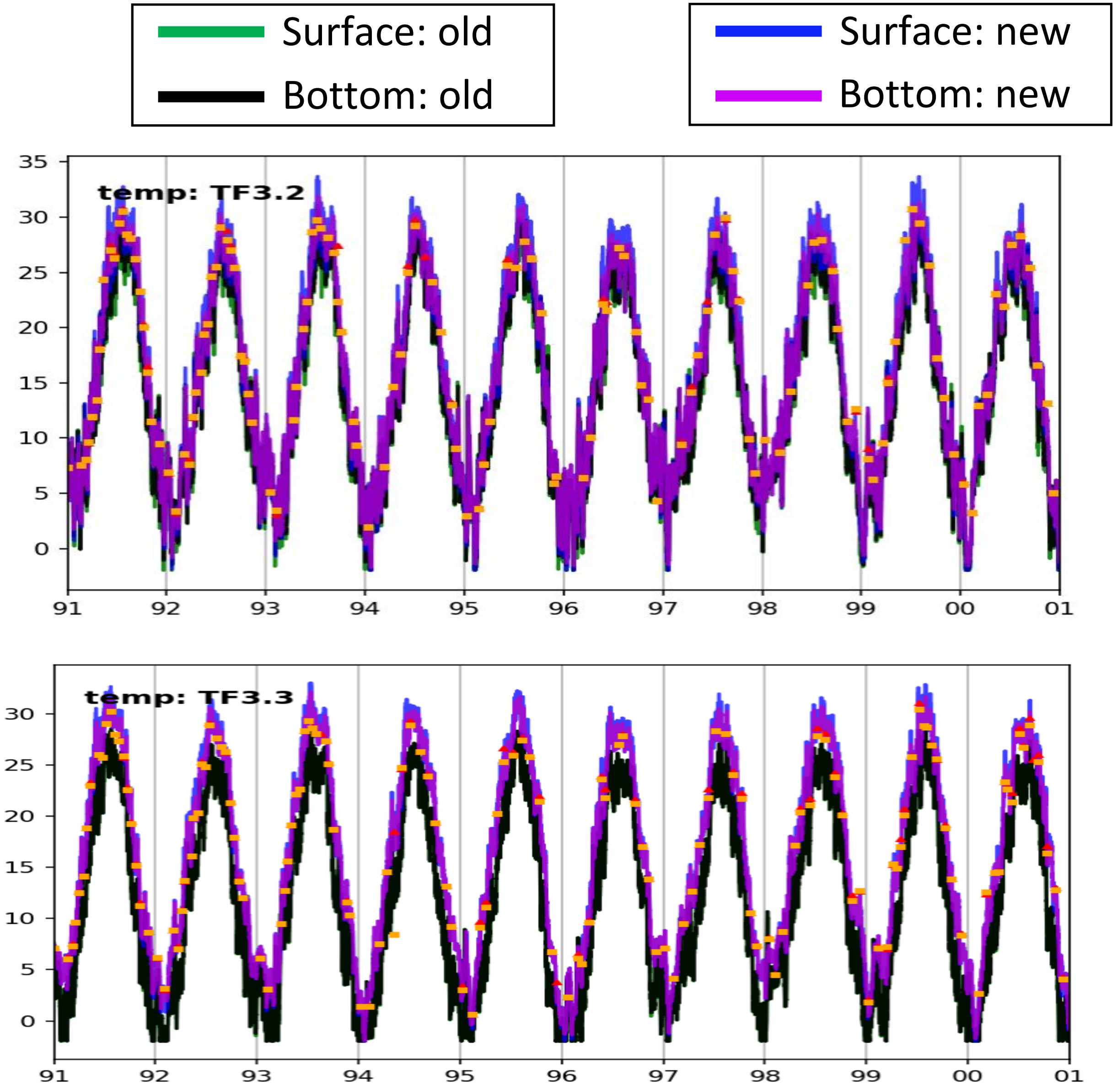


Bottom Temp . (°C)



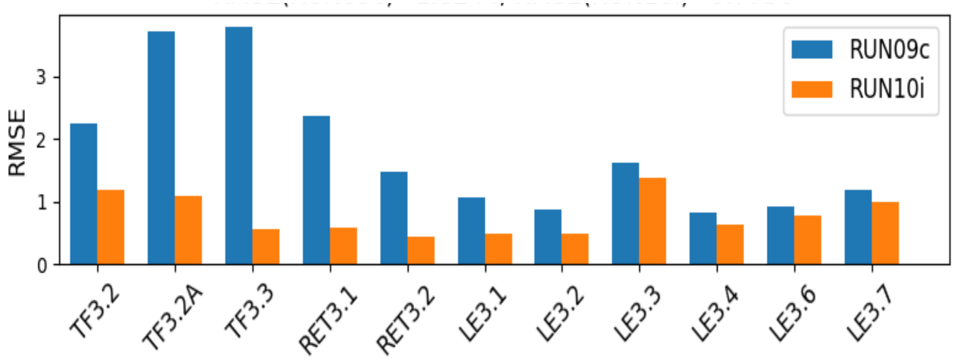
New Temperature Calibration: Rappahannock River

- Surface and bottom temperatures in the rivers are much improved in some tribs



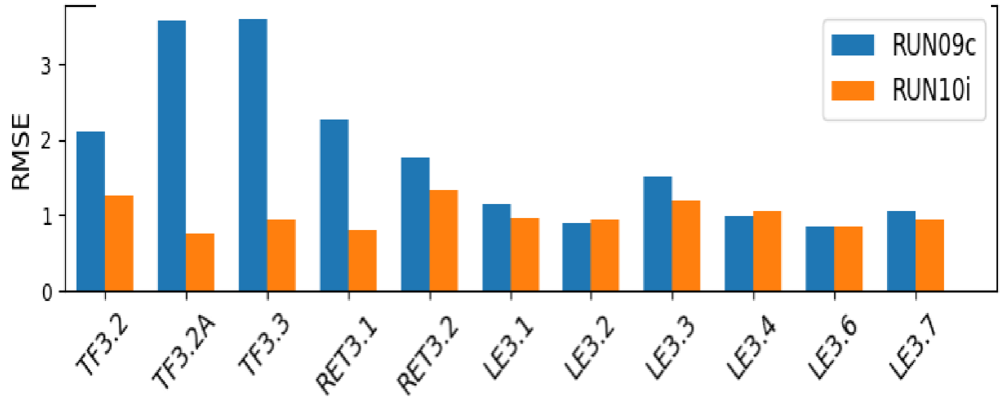
Surface

RMSE(old)=1.8244, RMSE(new)=0.7750



Bottom

RMSE(old)=1.8037, RMSE(new)=0.9999

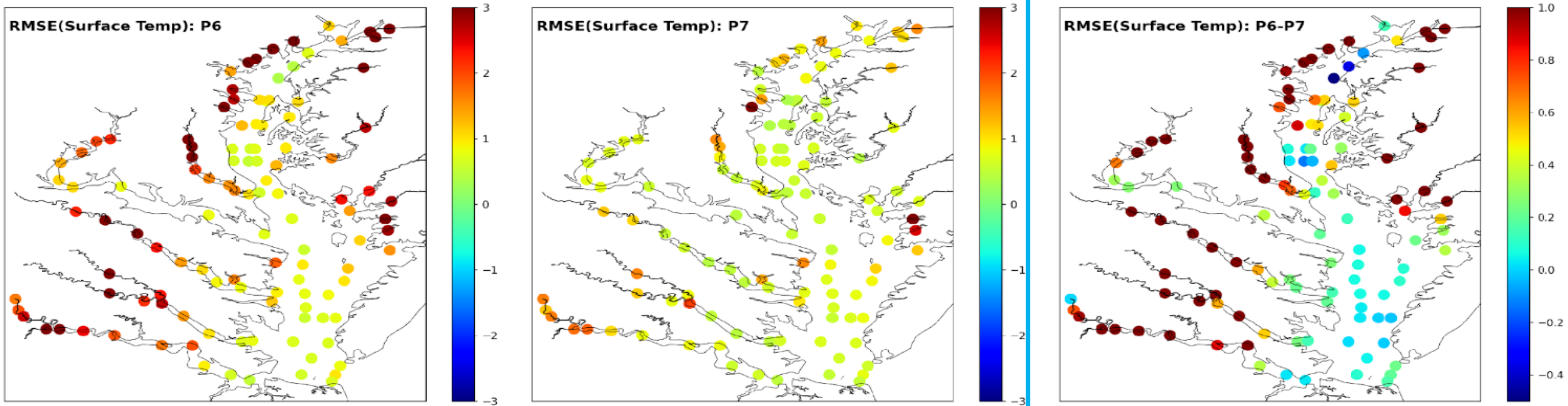


Spatial distribution of temperature error inside the bay

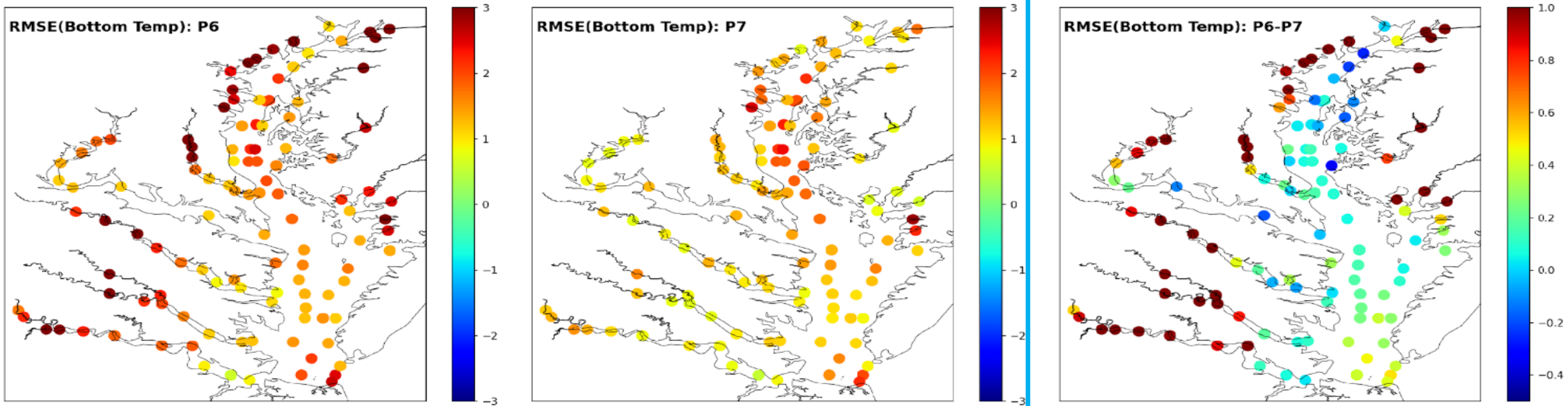
- Surface and bottom temperatures in deep regions are slightly improved.
- Surface and bottom temperatures in shallow regions are greatly improved.

- **positive values mean improvement**
- **P6: old results   P7: new results**

Surface Temp. (°C)



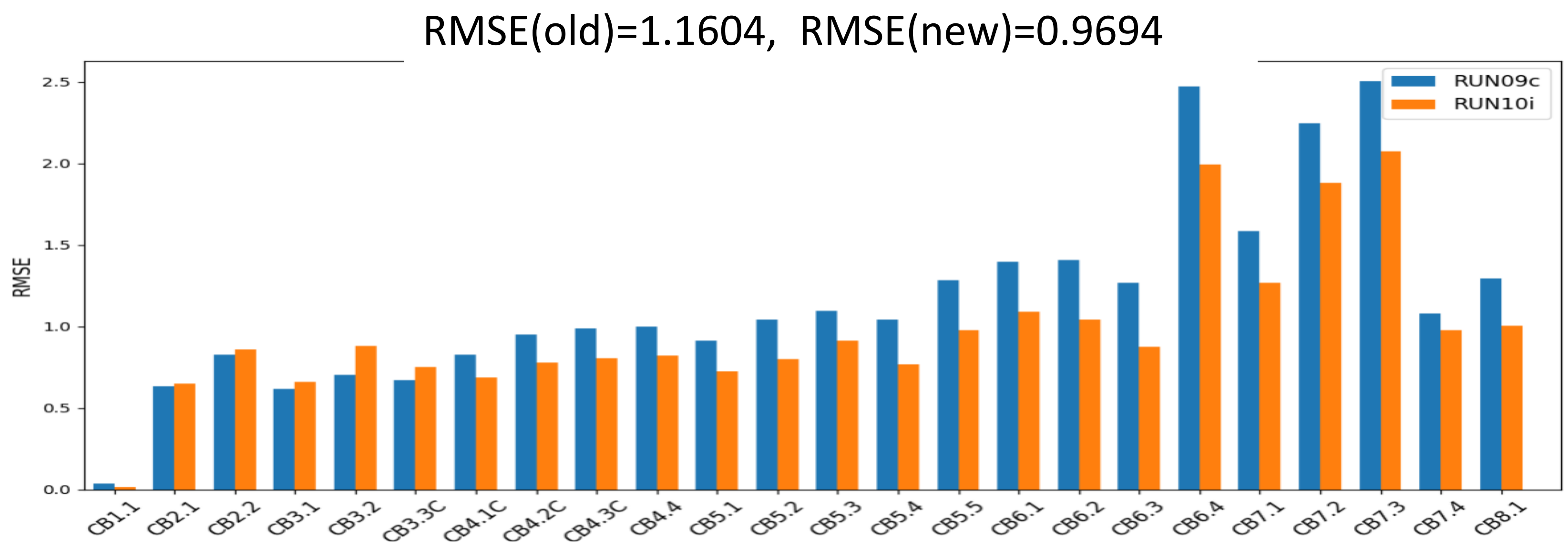
Bottom Temp . (°C)



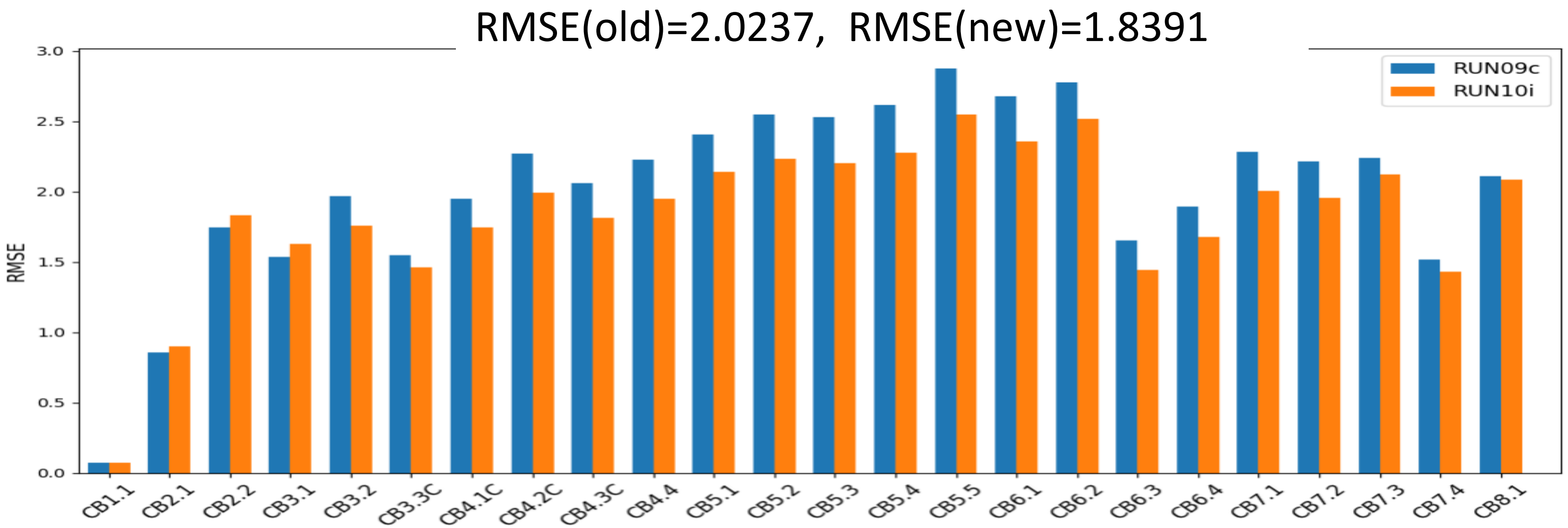
New salinity Calibration: Main Channel

- Bottom surface and bottom salinities along the main bay channel are improved slightly from P6 loading

Surface Salinity (PSU)



Bottom Salinity (PSU)



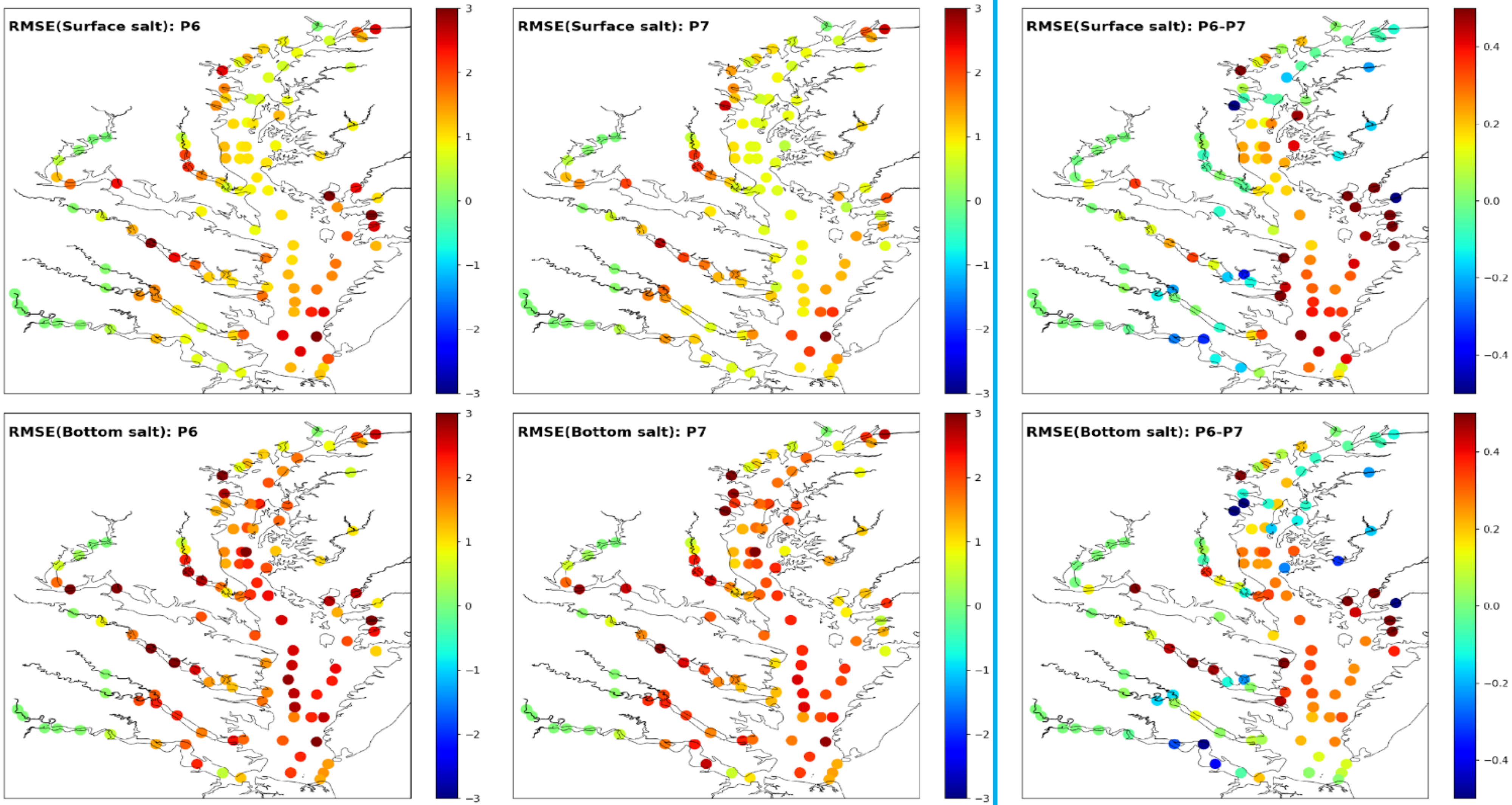
Spatial distribution of salinity error inside the bay

- Salinity in mid-bay and lower bay is improved.
- For most stations in upper bay and rivers, salinity is slightly improved
- For a few stations in the rivers, salinity gets worse and site-specific calibration may be needed

- **positive values mean improvement**
- **P6: old results   P7: new results**

Surface Salinity (PSU)

Bottom Salinity (PSU)



Summary

- We have recalibrated the oyster model, and the model results are now reasonable in different regions
- Overall, the oyster impact on water quality is small. Sensitivity experiments with higher oyster biomass led to larger impact.

- We have finished incorporating the new phase-7 watershed loading into our MBM workflow.
- The interpolation method for mapping watershed loading to MBM grid seems to work but further improvement can be made with help from GIS team.

- We have preliminarily tested the phase-7 loading for the MBM hydrodynamics
    - Temperature in the bay is much improved in the rivers; slightly improved in the main-bay channel.
    - Salinity in the mid-bay and lower-bay is improved, and slightly improved in the rivers.