Update on the Phase 7 Main Bay Model (MBM) Progress

VIMS team: Joseph Zhang, Jian Shen, Harry Wang, Marjy Friedrichs,

Zhengui Wang, Wenfan Wu, Pierre St-Laurent

CBPO: Richard Tian, Gopal Bhatt, Lew Linker et al.

UMCES team: Jeremy Testa

Advisor: Carl Cerco

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VIRGINIA INSTITUTE OF MARINE SCIENCE

Outline

- Previously: preliminarily calibrated P6 and first beta version of P7
- This quarter: calibrated baseline for MBM using a beta version P7

- Collaboration with watershed modeling team
  - Help assess beta versions of P7 WSM
- Current MBM status and latest modeling workflow
- Latest MBM modeling results
- Assessment of the sediment diagenesis and living resources
- Summary

Recap of last quarterly meeting (Apr 2025)

- ❑ **We received the 1st version of phase-7 watershed loading. We finished processing the data, and converted it into a database.**

- ❑ **We did a thorough assessment of the phase-7 nutrient loading on estuarine modeling**
  - In major rivers
  - In small embayments

- ❑ **We set up the MBM with phase-7 loading and tested the new model.**

- ❑ **We analyzed the preliminary model results**
  - Hydrodynamics: elevation, temperature, salinity
  - Water quality: Chl-a, DO, nitrogen, phosphorus, etc.
  - Primary production, and sediment nutrient fluxes

Building on previous work, in this quarter we produced first calibrated baseline for MBM using Jan25 beta version of P7

Collaboration with watershed modeling team

- We hold regular weekly meeting with watershed modeling (WSM) team and CBPO to coordinate our work on coupling between WSM and MBM.

- During the last quarter, we successfully converted the format of new watershed loading from ASCII to NetCDF, which greatly facilitated the coupling and simplifies the MBM workflow.

- MBM results are sensitive to watershed loading (Gopal), atmospheric deposition (Gopal) and shoreline erosion (Richard). We closely work with other teams to keep our MBM progress on track.

New Format of Watershed Loading

Old WSM Format: ASCII files

- One file only contains one nutrient loading from one segment
- There are over 220 K files. Parallel post-processing (multiple CPUs) is needed, and is very time consuming.
- Transfer of watershed loading is cumbersome.

```
EL0_010231687.pipx  EM0_009409082.no3x  EM4_009408266.clay
EL0_010231687.po4x  EM0_009409082.orgn  EM4_009408266.doxx
EL0_010231687.sand  EM0_009409082.orgp  EM4_009408266.flow
EL0_010231687.silt  EM0_009409082.phyt  EM4_009408266.nh4x
EL0_010231687.tocx  EM0_009409082.pipx  EM4_009408266.no3x
EL0_010231687.totn  EM0_009409082.po4x  EM4_009408266.orgn
EL0_010231687.totp  EM0_009409082.sand  EM4_009408266.orgp
EL0_010231687.tssx  EM0_009409082.silt  EM4_009408266.phyt
EL0_010231687.wtmp  EM0_009409082.tocx  EM4_009408266.pipx
EL0_010231707.chla  EM0_009409082.totn  EM4_009408266.po4x
EL0_010231707.clay  EM0_009409082.totp  EM4_009408266.sand
EL0_010231707.doxx  EM0_009409082.tssx  EM4_009408266.silt
EL0_010231707.flow  EM0_009409082.wtmp  EM4_009408266.tocx
EL0_010231707.nh4x  EM0_009409090.chla  EM4_009408266.totn
EL0_010231707.no3x  EM0_009409090.clay  EM4_009408266.totp
EL0_010231707.orgn  EM0_009409090.doxx  EM4_009408266.tssx
EL0_010231707.orgp  EM0_009409090.flow  EM4_009408266.wtmp
EL0_010231707.phyt  EM0_009409090.nh4x  EM4_009408272.chla
EL0_010231707.pipx  EM0_009409090.no3x  EM4_009408272.clay
EL0_010231707.po4x  EM0_009409090.orgn  EM4_009408272.doxx
EL0_010231707.sand  EM0_009409090.orgp  EM4_009408272.flow
EL0_010231707.silt  EM0_009409090.phyt  EM4_009408272.nh4x
EL0_010231707.tocx  EM0_009409090.pipx  EM4_009408272.no3x
```

watershed segment **nutrient**

New WSM Format: NetCDF

- One file contains everything. There is no need for post-processing. Transfer of watershed loading becomes easy.
- All nutrient variables are well organized, which allows us to perform different operations (nutrient analysis, search, mapping, etc.)

```
'file_format: "NETCDF4", string',
"sname : narray(12479,), <class 'str'>",
"stype : narray(12479,), <class 'str'>",
'time  : narray(13149,), int64',
'chla  : narray(12479, 13149), float32',
'clay  : narray(12479, 13149), float32',
'doxx  : narray(12479, 13149), float32',
'flow  : narray(12479, 13149), float32',
'nh4x  : narray(12479, 13149), float32',
'no3x  : narray(12479, 13149), float32',
'orgn  : narray(12479, 13149), float32',
'orgp  : narray(12479, 13149), float32',
'phyt  : narray(12479, 13149), float32',
'pipx  : narray(12479, 13149), float32',
'po4x  : narray(12479, 13149), float32',
'sand  : narray(12479, 13149), float32',
'silt  : narray(12479, 13149), float32',
'tocx  : narray(12479, 13149), float32',
'totn  : narray(12479, 13149), float32',
'totp  : narray(12479, 13149), float32',
'tssx  : narray(12479, 13149), float32',
'wtmp  : narray(12479, 13149), float32',
"dimname: list['time', 'nseg', 'nvar']",
```

# of watershed segment

time dimension (1985 – 2020)

New Format of Shoreline Erosion and Atmospheric Loadings

- Thanks to Richard, the nutrient loading from shoreline erosion was also converted to NetCDF format
- Gopal is still working on P7 atmospheric deposition, we will work with him to convert the final product to NetCDF format as well.

Shoreline Erosion: NetCDF

```
'file_format: "NETCDF3_64BIT_DATA", string'
'cellid: narray(9714,), int32',
'time  : narray(8764,), int32',
'sand  : narray(9714, 8764), float32',
'silt  : narray(9714, 8764), float32',
'clay  : narray(9714, 8764), float32',
'orgs  : narray(9714, 8764), float32',
'RPOC  : narray(9714, 8764), float32',
'G3OC  : narray(9714, 8764), float32',
'RPON  : narray(9714, 8764), float32',
'G3ON  : narray(9714, 8764), float32',
'RPOP  : narray(9714, 8764), float32',
'G3OP  : narray(9714, 8764), float32',
'PIP   : narray(9714, 8764), float32',
"dimname: list['cell', 'time']",
```

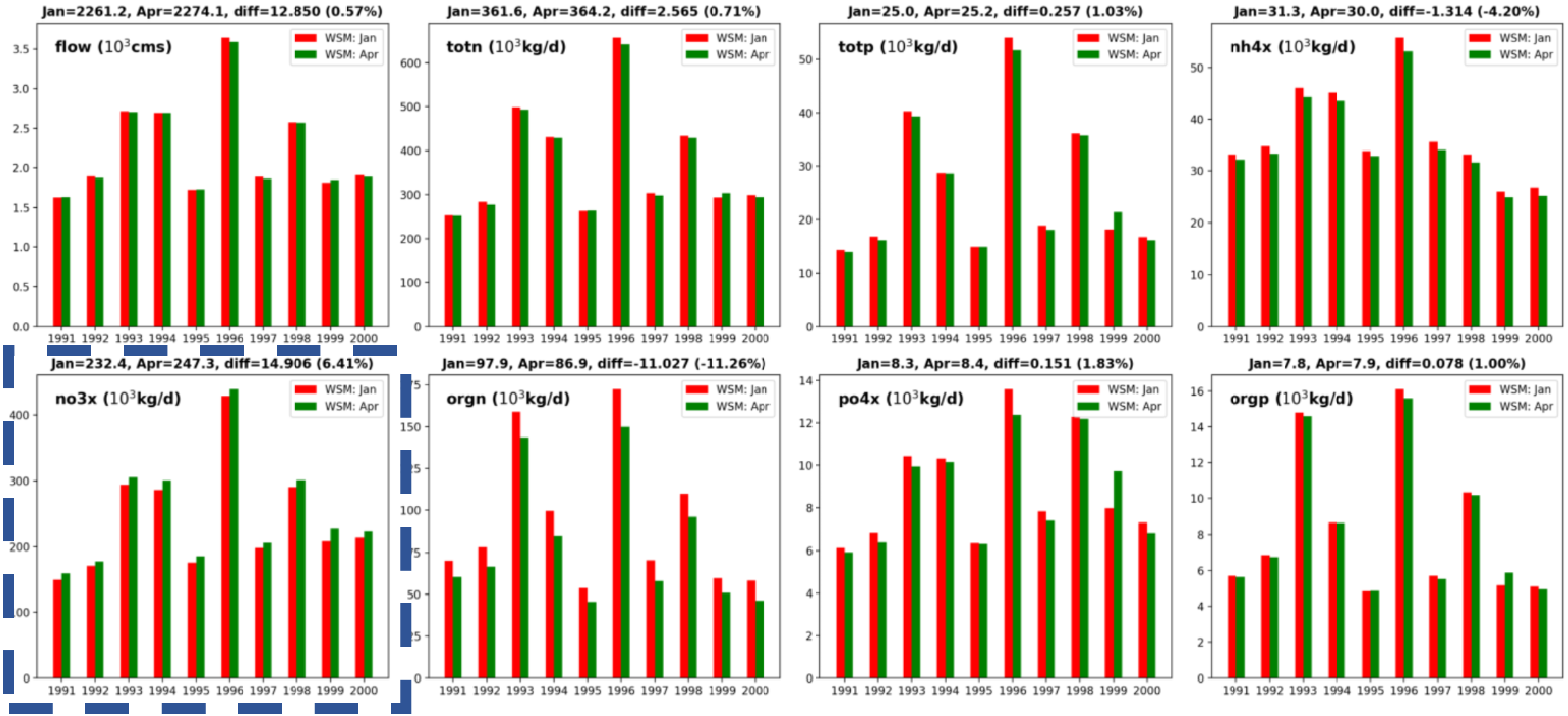
# of nutrients sources

time dimension (1991 – 2014)

nutrient variables

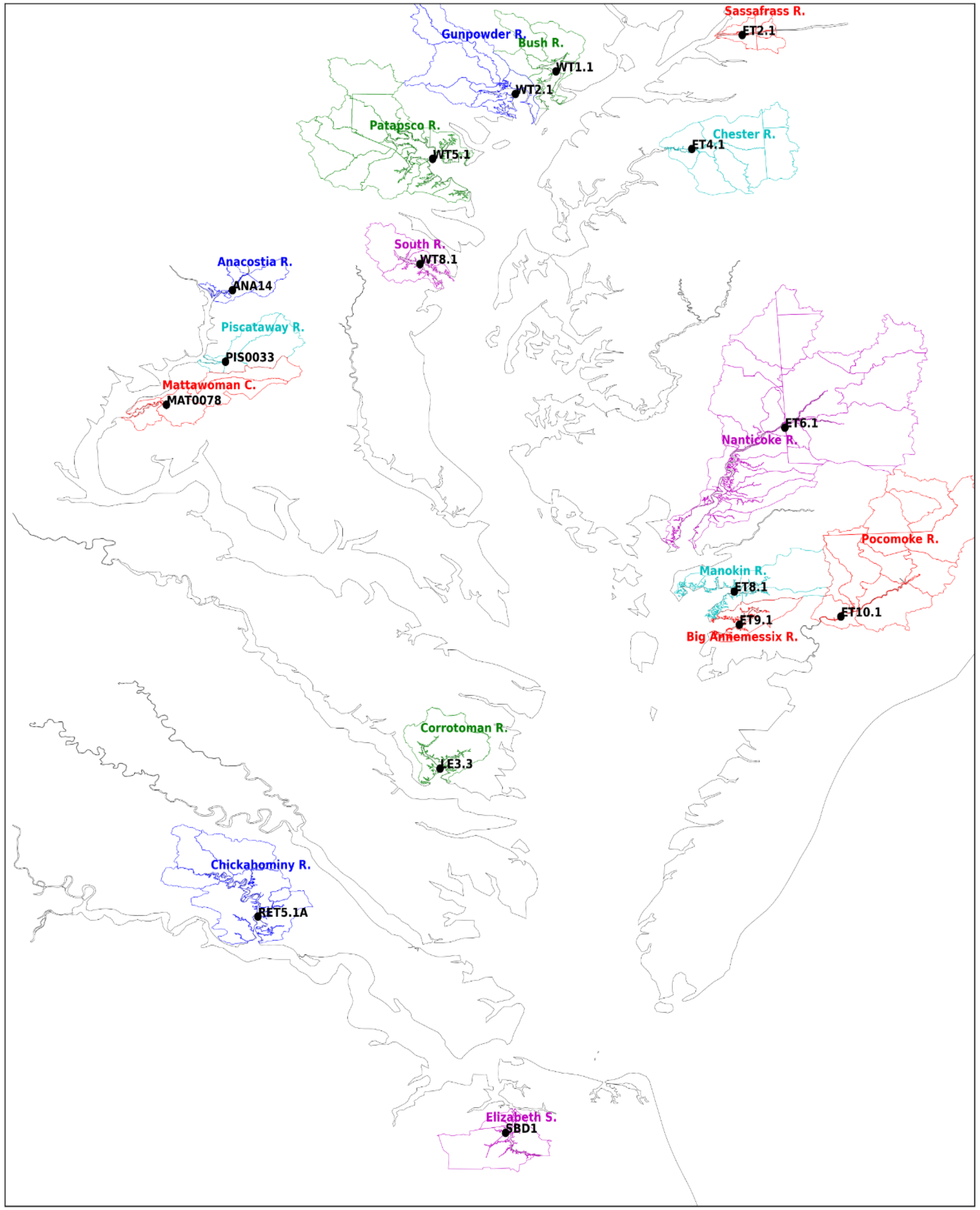
Cross Assessment of Different Beta Versions of WSM Loading

- Here, we compare the **April** WSM version with **January** version regarding flow, N and P from 1991 to 2000.
- Overall, the changes on the flow, TN and TP loadings are small.
- There is about 15% increase in NO3, accompanied with 11% decrease in organic nitrogen. This might have localized impact



Assessment of P7 WSM loading in small embayment

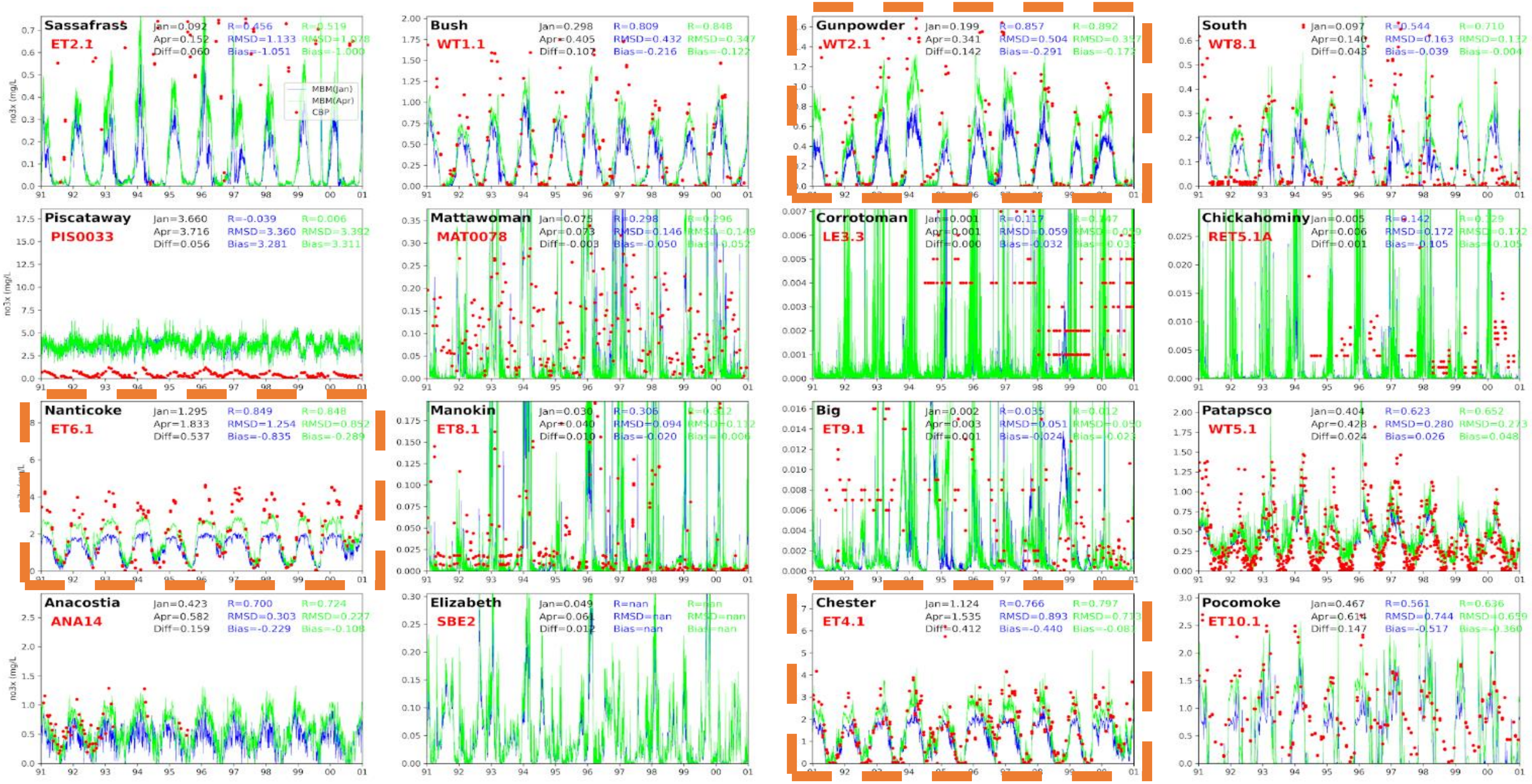
- We selected 16 small embayments to check how P7 WSM loading impacts the nearby MBM simulation.
- The assessment on WSM loading through MBM simulation provides additional information to the WSM team, which can help to further improve the WSM, and in turn improve MBM simulation (positive feedback).



Comparison of NO3 simulation between Jan and Apr WSMs

Jan Apr CBP Obs.

- Overall, NO3 simulation in MBM with April version was improved at small embayments



Comparison of nutrient simulations between Jan and Apr WSMs

- Compared with observations at nearby CBP stations, the nutrient simulations in MBM are similar for NH4, TN and TP at most locations between two WSMs.
- NO3 and PO4 are generally improved with April WSM loading.

MBM(RMSD)

	river impact	salinity	NH4	NO3	PO4	TN	TP
Sassafrass R.	99.5%	1.82	(0.1029, 0.1078)	(1.1331, 1.0776)	(0.0260, 0.0263)	(1.0504, 1.1062)	(0.1101, 0.1109)
Bush R.	95.9%	0.86	(0.2594, 0.2612)	(0.4319, 0.3468)	(0.0103, 0.0093)	(0.8290, 0.8222)	(0.0650, 0.0668)
Gunpowder R.	94.7%	1.70	(0.0675, 0.0678)	(0.5044, 0.3570)	(0.0066, 0.0066)	(0.3998, 0.4183)	(0.0547, 0.0552)
South R.	69.1%	9.96	(0.0826, 0.0834)	(0.1629, 0.1324)	(0.0365, 0.0368)	(0.3867, 0.3894)	(0.0661, 0.0663)
Piscataway R.	100.0%	0.00	(0.3084, 0.3148)	(3.3604, 3.3922)	(0.0374, 0.0371)	(3.4631, 3.4867)	(0.0829, 0.0831)
Mattawoman (	100.0%	0.01	(0.0712, 0.0675)	(0.1464, 0.1487)	(0.0211, 0.0220)	(0.3752, 0.3701)	(0.0575, 0.0568)
Corrotoman R.	56.6%	14.77	(0.0807, 0.0808)	(0.0590, 0.0588)	(0.0089, 0.0081)	(0.2779, 0.2879)	(0.0301, 0.0309)
Chickahominy	99.7%	1.19	(0.0697, 0.0699)	(0.1725, 0.1724)	(0.0203, 0.0186)	(0.4617, 0.4749)	(0.0780, 0.0800)
Nanticoke R.	99.8%	0.20	(0.0901, 0.0953)	(1.2542, 0.8523)	(0.0497, 0.0434)	(1.0435, 1.0282)	(0.0662, 0.0660)
Manokin R.	49.0%	13.99	(0.0757, 0.0763)	(0.0939, 0.1119)	(0.0440, 0.0400)	(0.5576, 0.5999)	(0.0621, 0.0623)
Big Annemessi	47.8%	15.52	(0.0876, 0.0870)	(0.0505, 0.0503)	(0.0226, 0.0199)	(0.4941, 0.5179)	(0.0382, 0.0386)
Patapsco R.	80.8%	10.37	(0.2276, 0.2292)	(0.2797, 0.2734)	(0.0209, 0.0211)	(0.7287, 0.7107)	(0.0478, 0.0481)
Anacostia R.	100.0%	0.19	(0.3146, 0.3254)	(0.3027, 0.2265)	(0.0293, 0.0273)	(0.7582, 0.8349)	(0.0718, 0.0793)
Elizabeth S.	46.9%	19.07	(0.2285, 0.2367)	(nan, nan)	(0.0430, 0.0323)	(0.4246, 0.4558)	(0.0523, 0.0418)
Chester R.	99.3%	0.54	(0.0719, 0.0723)	(0.8925, 0.7126)	(0.0438, 0.0350)	(1.1138, 1.0477)	(0.1457, 0.1480)
Pocomoke R.	100.0%	0.16	(0.0411, 0.0431)	(0.7438, 0.6588)	(0.0880, 0.0759)	(0.6024, 0.6663)	(0.1077, 0.0967)

Apr. is better (green) **Similar** (grey) **Jan. is better** (red)

Current status of MBM

- **Currently, the MBM is calibrated with P7_hybrid WSM loading (January version)**
  - P7 shoreline erosion data is applied.
  - P6 atmospheric deposition data is used.
- **The MBM has all the modeling components, and a two-step model approach is used**
  - Physical (1st step): Hydrodynamics, Wave, Sediment Transport, SAV.
  - Biological (2nd step): Water Quality (sediment diagenesis), Living resources.
- **The MBM model skill is generally satisfactory**
  - Compared with P6, salinity and temperature are better simulated.
  - For most of water quality variables, P7 model skills are comparable to P6. Bottom DO/hypoxia are improved

New MBM Workflow

- **During the last quarter, we updated the MBM workflow**
  - We updated the workflow to accommodate to the new NetCDF format of P7 WSM loading
  - We added the configurations of living resource modules (oyster, marsh, sav) into the workflow
  - We refactored the MBM workflow with better structure and more efficiency

- **The new workflow is updated with latest model configurations (e.g. watertype, drag - see Wenfan's talk)**

- **We created new databases for initial and boundary conditions, and model parameters**
  - Temperature
  - Salinity
  - Sediment Transport Model
  - Water Quality Variables
  - Sediment Nutrients Concentrations (no need 10-year warm-up)
  - Living Resources

The structure of MBM Workflow

- The python-based MBM workflow supports **from grid generation all the way to model setup**
- The workflow provides flexibility for different types of model configurations
- All functionalities are integrated in one python script, which can be launched at any location (tested on sciclone)

set simulation time →

choose model grid →

select models →

select sub-modules →

```
#---------------------------------------------------------------------------
#Inputs:
#  base:  reference run for current setup
#  flag=0:
#       if base is not None:  create link to the input file in base run
#       if base is None: skip this file
#  flag=1: re-generate input file
#---------------------------------------------------------------------------
p.StartT=datenum(1991,1,1);  p.EndT=datenum(1995,12,31) #simulation time

p.base= 'None' # reference run
p.grid_dir='/sciclone/data10/wangzg/CBP/grid/v9b' #directory of hgrid & 

#models
p.flag['ICM']= 0  #ICM   model (1: 21 variables; 10: 21-variable offline
p.flag['SED']= 0  #SED3D model
p.flag['WWM']= 0  #Wave  model

#sub-modules
p.flag['VEG'] = 0 #Hydro Vegetation module
p.flag['CLAM']= 0 #ICM: oyster/clam model
p.flag['SAV'] = 0 #ICM: SAV model
p.flag['WET'] = 0 #ICM: tidal-wetland model
```

choose your model inputs

```
#model inputs
p.flag['elev2D.th.nc']                = 0 #hydro
p.flag['TEM_3D.th.nc']                = 0 #hydro
p.flag['TEM_nu.nc']                   = 0 #hydro
p.flag['SAL_3D.th.nc']                = 0 #hydro
p.flag['SAL_nu.nc']                   = 0 #hydro
p.flag['sflux']                       = 0 #hydro
p.flag['albedo.gr3']                  = 0 #hydro
p.flag['watertype.gr3']               = 0 #hydro (1: max=
p.flag['diffmin.gr3']                 = 0 #hydro
p.flag['diffmax.gr3']                 = 0 #hydro
p.flag['shapiro.gr3']                 = 0 #hydro
p.flag['tvd.prop']                    = 0 #hydro
p.flag['windrot_geo2proj.gr3']        = 0 #hydro
p.flag['veg_*.gr3']                   = 0 #hydro: veg mod
p.flag['rough.gr3']                   = 0 #hydro,SED
p.flag['bctides.in']                  = 0 #hydro,SED,ICM
p.flag['hotstart.nc']                 = 0 #hydro,SED,ICM
p.flag['source.nc']                   = 0 #hydro,SED,ICM
p.flag['ICM_3D.th.nc']                = 0 #ICM
p.flag['ICM_nu.nc']                   = 0 #ICM
p.flag['ICM_sflux.th.nc']             = 0 #ICM
p.flag['ICM_param.nc']                = 0 #ICM
p.flag['SED_hvar_*.ic']               = 0 #SED
p.flag['bed_frac_*.ic']               = 0 #SED
p.flag['bedthick.ic']                 = 0 #SED
p.flag['hgrid_WWM.gr3']               = 0 #WWM
p.flag['wwmbnd.gr3']                  = 0 #WWM
```

databases

```
#databases
p.bdir='/sciclone/data10/wangzg/CBP/database/' #MBM database dir
p.MBM_init  = p.bdir+'MBM_init.npz'             #MBM database: multiple datasets
p.source    = p.bdir+'load_p7_v4.npz'           #CBP watershed sources
p.atmdep    = p.bdir+'atm_load.npz'             #CBP atmospheric deposition
p.hycom     = p.bdir+'hycom.nc'                 #HYCOM database
p.sflux     = p.bdir+'sflux_narr_subdomain'     #sflux database
p.WW3       = p.bdir+'WW3'                      #WW3 wave forcing
p.hydro_out = p.bdir+'hydro/RUN11/outputs'      #hydro_out for offline ICM model
p.region    = p.bdir+'region/'                  #region files
```

Summary for MBM calibration

- Overall, the MBM model skill is comparable to Phase 6 (CH3D)
- For many variables, the RMSDs in MBM are slightly better
- For most variables in both models, the errors at bottom are generally larger than those on surface
- Also, the errors in tributaries are generally larger than those in mainstem regions
  - MBM has the potential to drastically improve in shallow areas due to its gridding flexibility

Major Variables

RMSD	temp	salt	chla	DO	TN	TP
surface	(1.668, 0.970)	(2.074, 1.165)	(12.694, 12.468)	(1.413, 1.241)	(0.370, 0.380)	(0.052, 0.039)
bottom	(1.858, 1.300)	(2.193, 1.674)	(12.083, 11.618)	(1.837, 1.785)	(0.489, 0.409)	(0.066, 0.058)

Bias	temp	salt	chla	DO	TN	TP
surface	(0.140, -0.218)	(0.664, -0.221)	(-2.065, -3.236)	(0.204, -0.145)	(0.051, -0.188)	(0.011, -0.016)
bottom	(0.312, 0.072)	(-0.045, -0.293)	(-2.010, -1.318)	(0.538, 0.480)	(0.187, -0.166)	(0.002, -0.030)

Nutrient Species

RMSD	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(0.231, 0.268)	(0.069, 0.058)	(0.017, 0.016)	(1.815, 2.102)	(0.179, 0.175)	(0.018, 0.012)	(1.357, 1.267)	(0.206, 0.185)	(0.044, 0.038)
bottom	(0.207, 0.239)	(0.110, 0.088)	(0.021, 0.019)	(1.763, 2.020)	(0.180, 0.182)	(0.017, 0.012)	(1.707, 1.617)	(0.232, 0.233)	(0.066, 0.060)

Bias	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(-0.028, -0.155)	(-0.008, -0.018)	(0.002, 0.002)	(-0.926, -1.430)	(-0.025, -0.018)	(0.008, -0.001)	(-0.980, -0.779)	(-0.145, -0.095)	(-0.034, -0.025)
bottom	(-0.011, -0.125)	(0.022, -0.018)	(0.005, 0.001)	(-0.899, -1.313)	(-0.034, -0.023)	(0.006, -0.001)	(-0.916, -0.822)	(-0.123, -0.098)	(-0.047, -0.039)

1. In brackets, the 1st number is CH3D error, and 2nd number is MBM error.

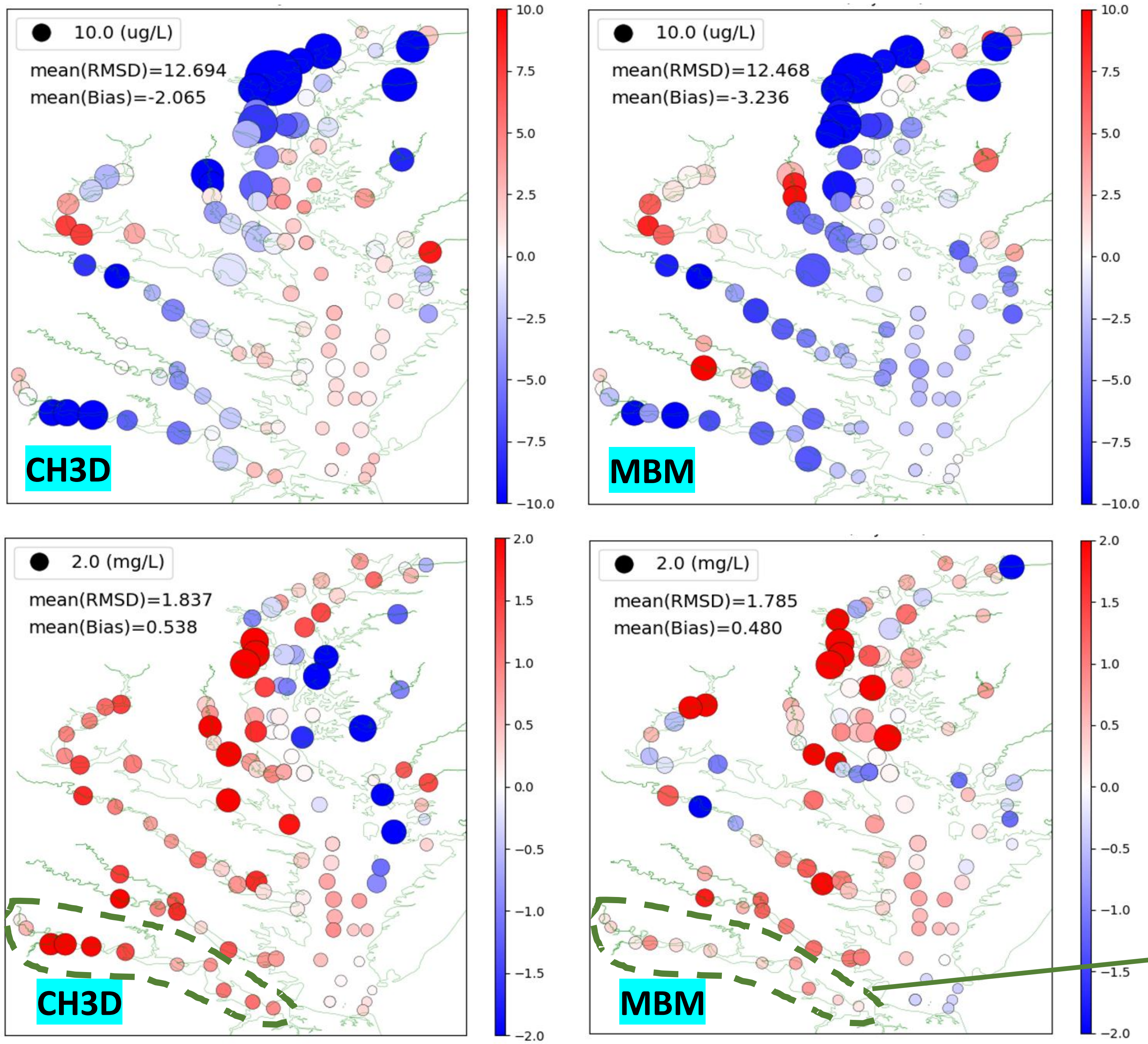
MBM is better (green) | CH3D is better (red)

Error Distribution: Surface Chla and Bottom DO

size: RMSD **color**: Bias

Surface Chla

Bottom DO



❖ **CH3D-ICM model is used for reference**

- Overall, the MBM model skill is comparable to CH3D for both surface Chla and bottom DO.
- The error distributions are also similar between these two models.
- For Chla along main-bay channel, CH3D overestimates while MBM underestimates.
- MBM has better model skills at some tribs (e.g. James River).

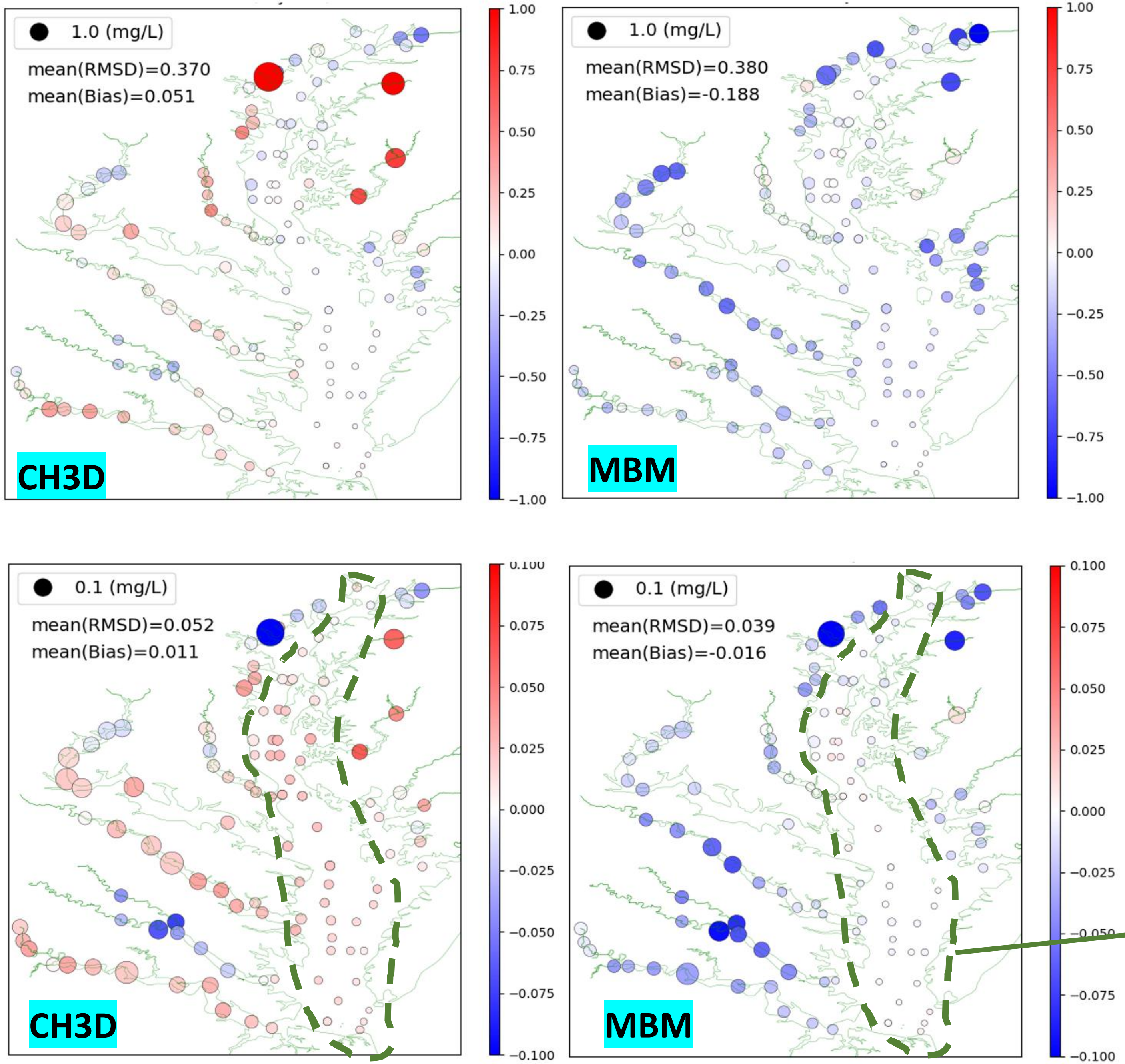
better performance in MBM: James River

Error Distribution: Surface TN and TP

size: RMSD **color**: Bias

Surface TN

Surface TP



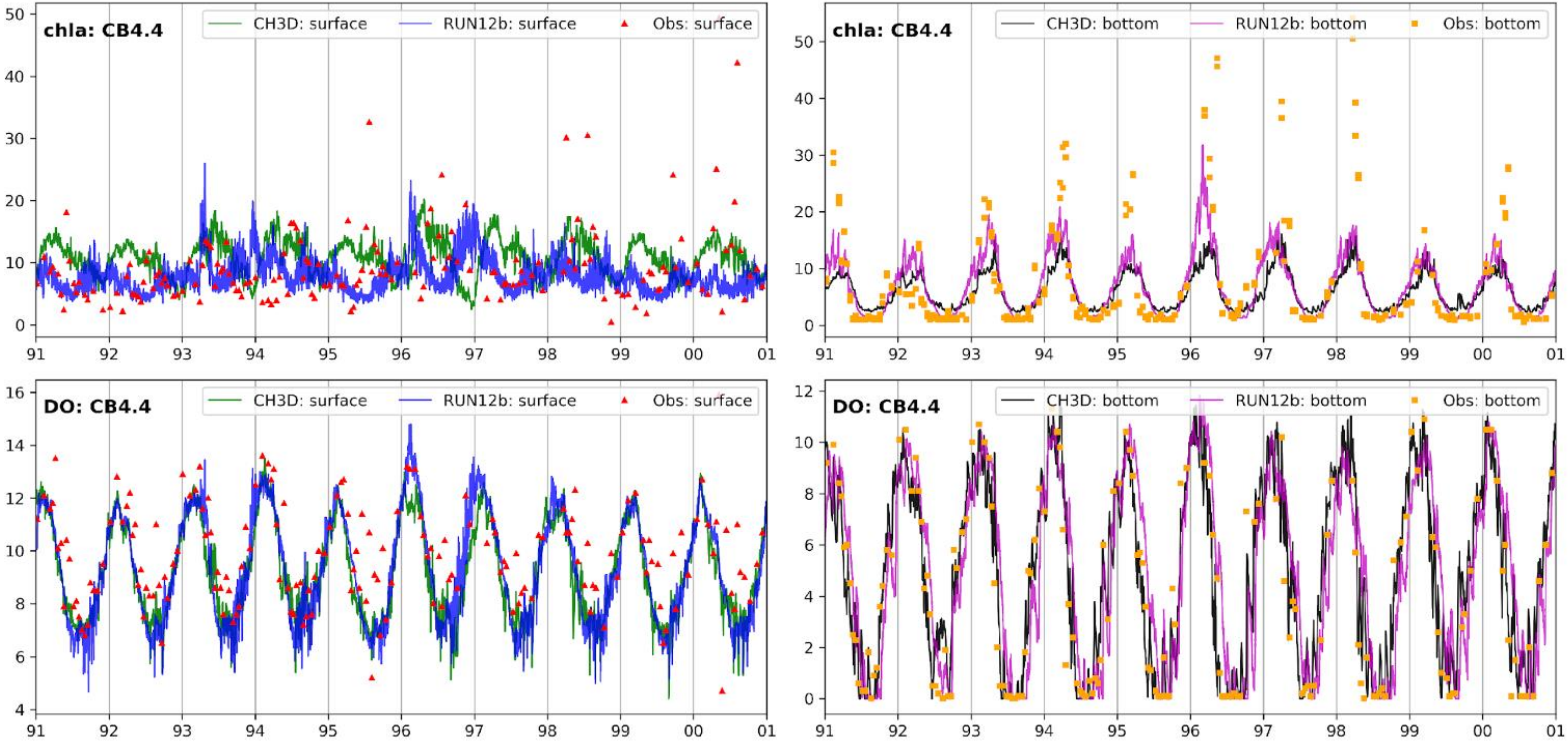
❖ **CH3D-ICM model is used for reference**

- For surface TN and TP, CH3D tends to overestimate, while MBM tends to underestimate.
- For TP in the mainstem, MBM has better model skill than CH3D.

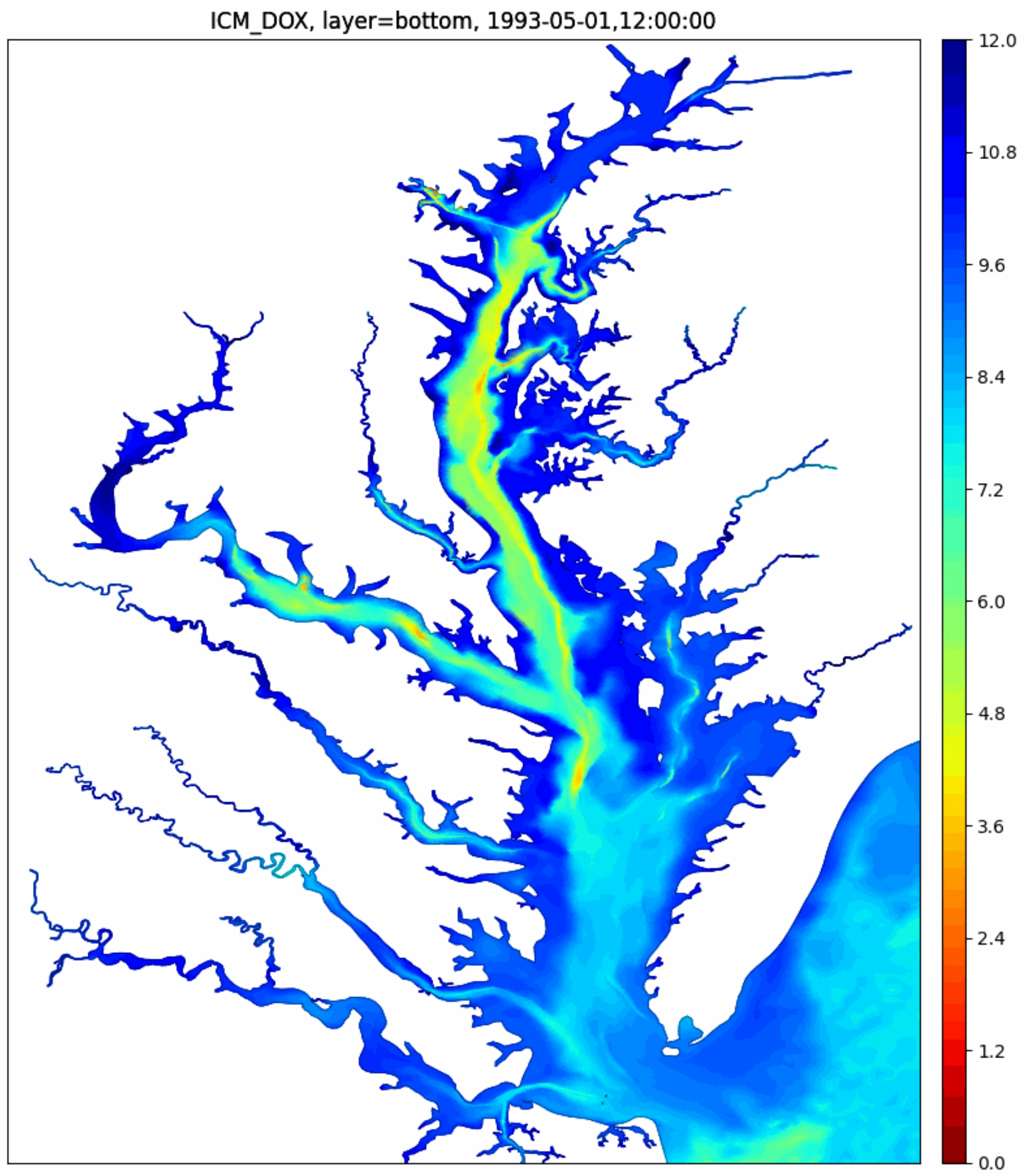
better performance in MBM

Comparison of time series of Chla and DO at CB4.4

- Both models have large errors for surface Chla, while the comparisons are better for bottom Chla
- For DO, both models did a good job in simulating the seasonal variation and hypoxia.

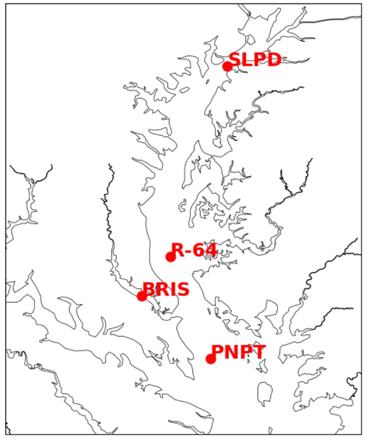


Animation of Bottom DO in summer, 1993

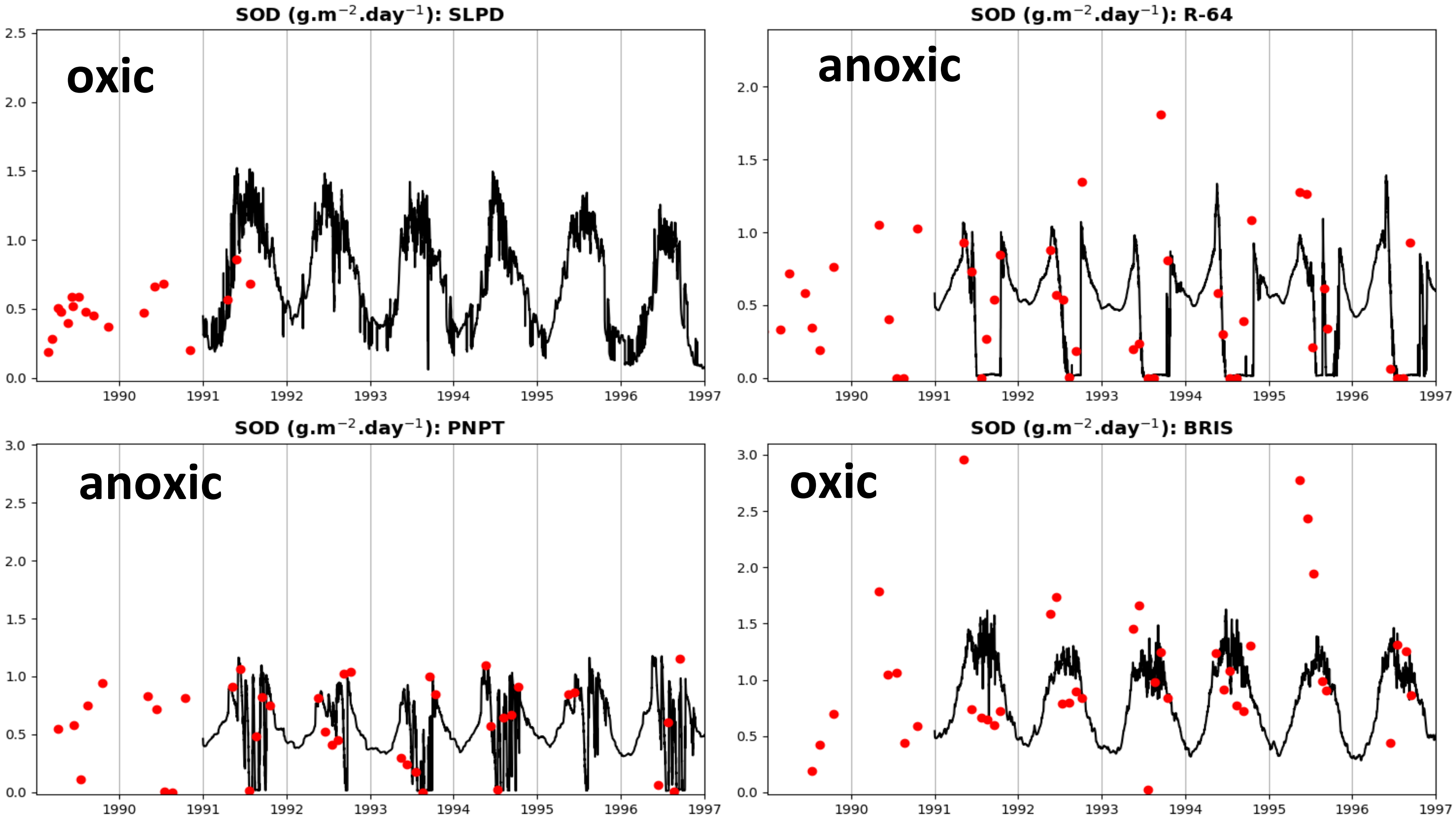


- 1993 was a high-flow year, and relatively severe hypoxic condition was observed.

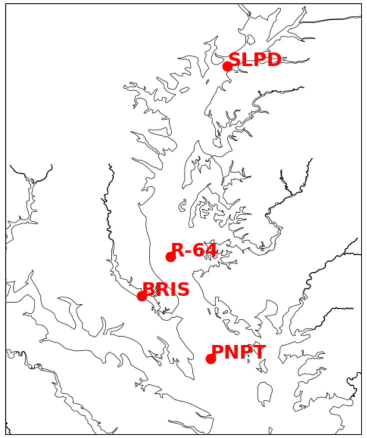
Sediment Diagenesis: SOD



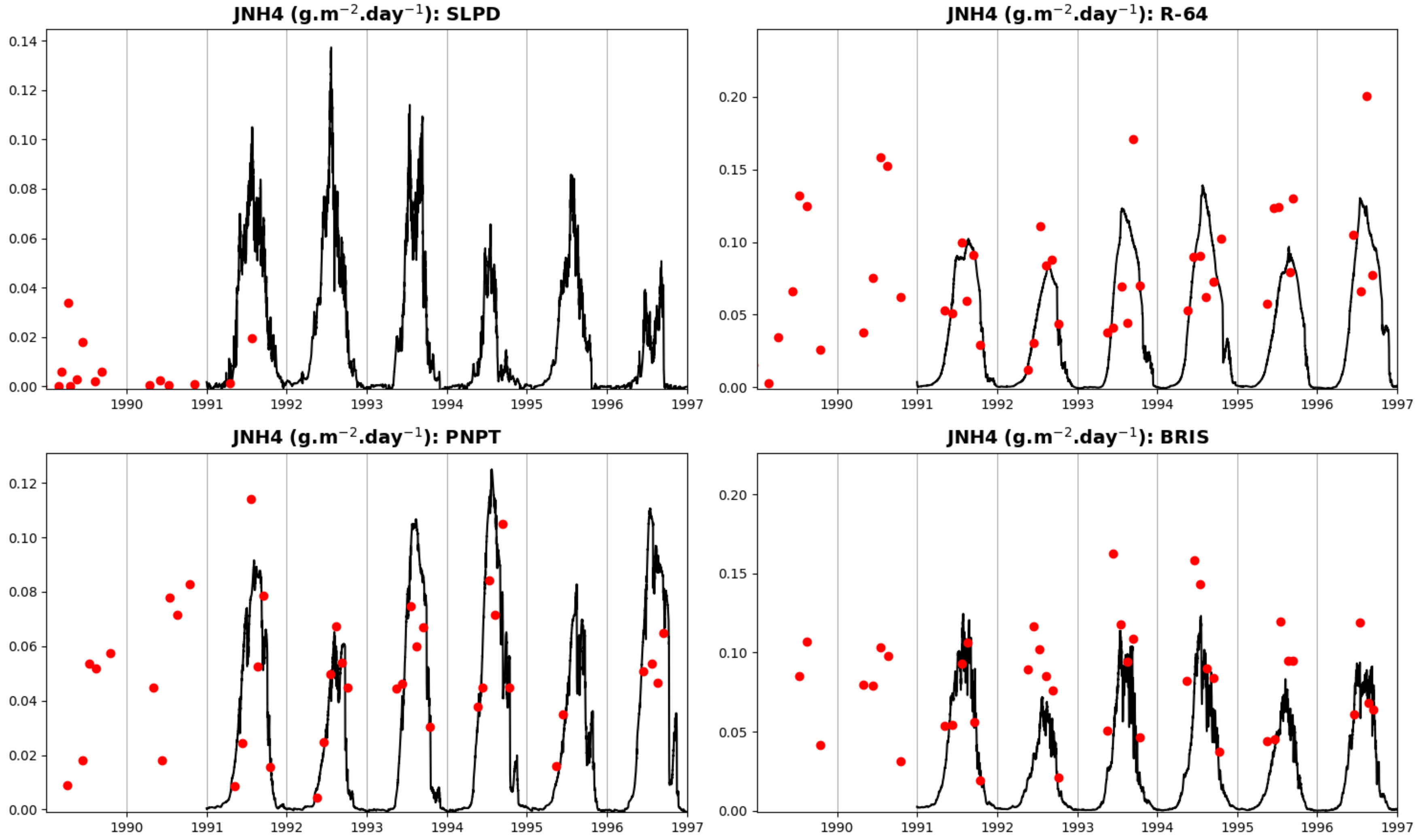
- In shallow water systems like Chesapeake Bay, the tight coupling between water column processes and sediment diagenesis processes is a fundamental process.
- Therefore, it is important to make sure the simulated SOD and sediment nutrient fluxes are correct.
- MBM correctly simulated SOD for both oxic and anoxic conditions.



Sediment Diagenesis: NH4 flux

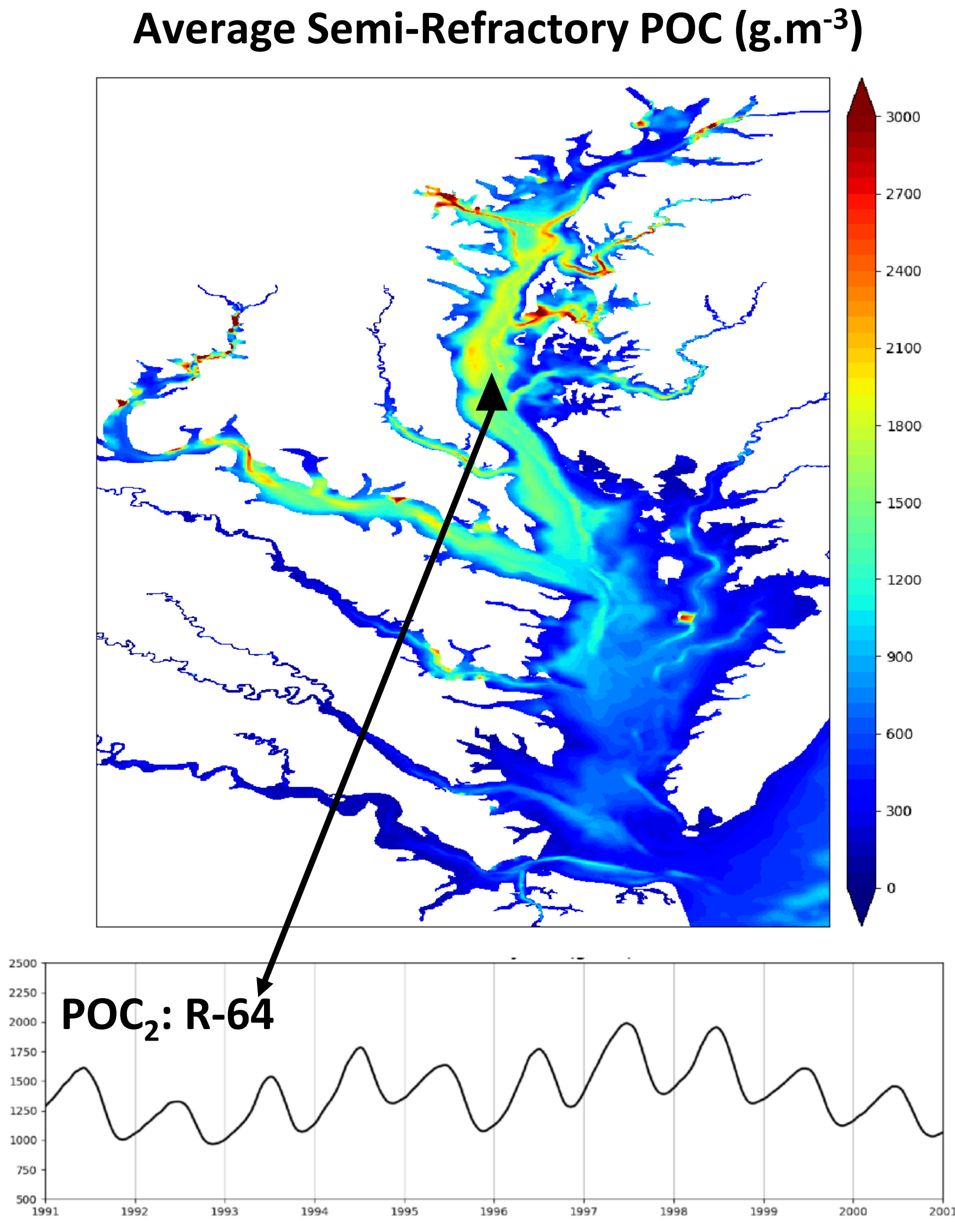


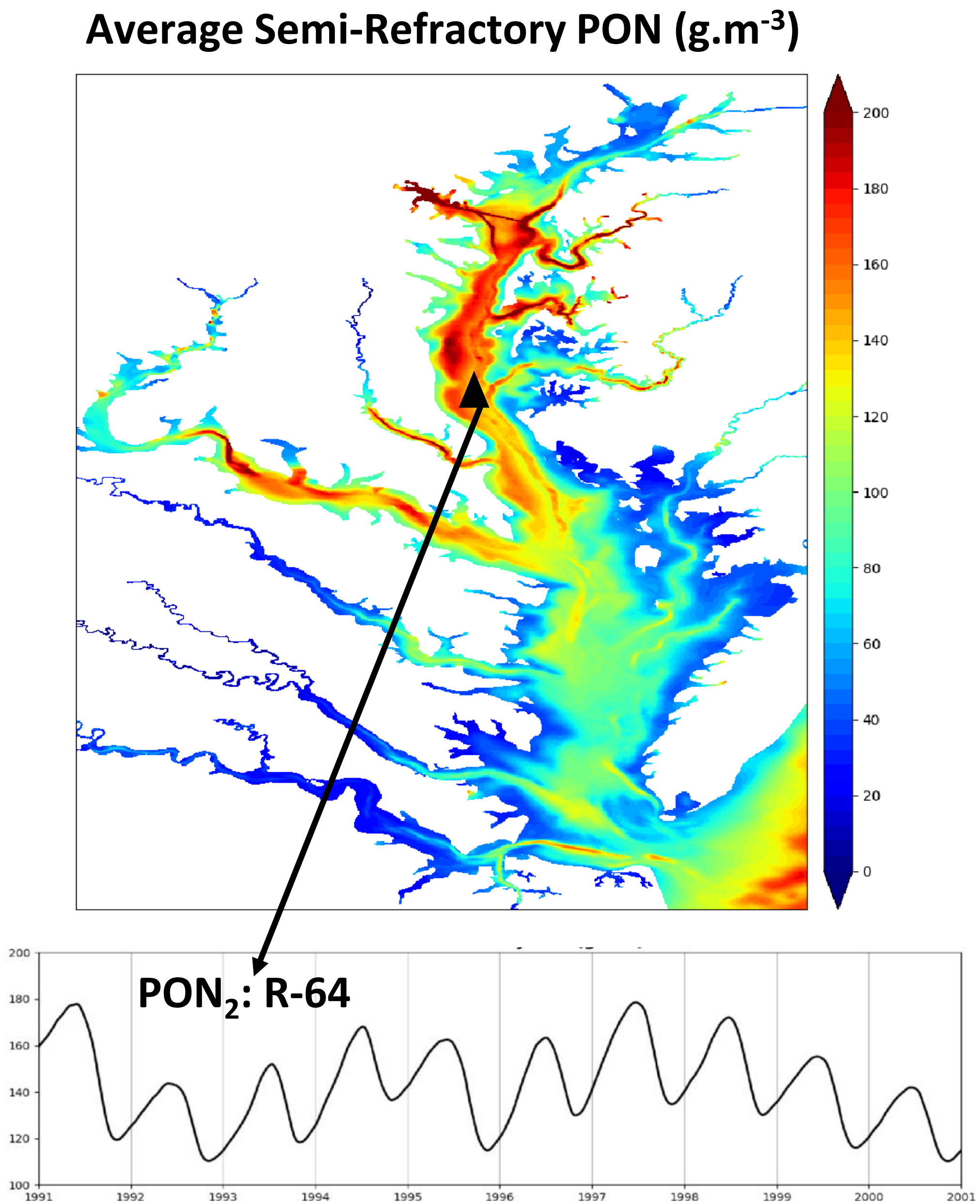
- MBM well captures the seasonal variation of sediment NH4 fluxes in Chesapeake Bay



Sediment Concentrations: POC and PON

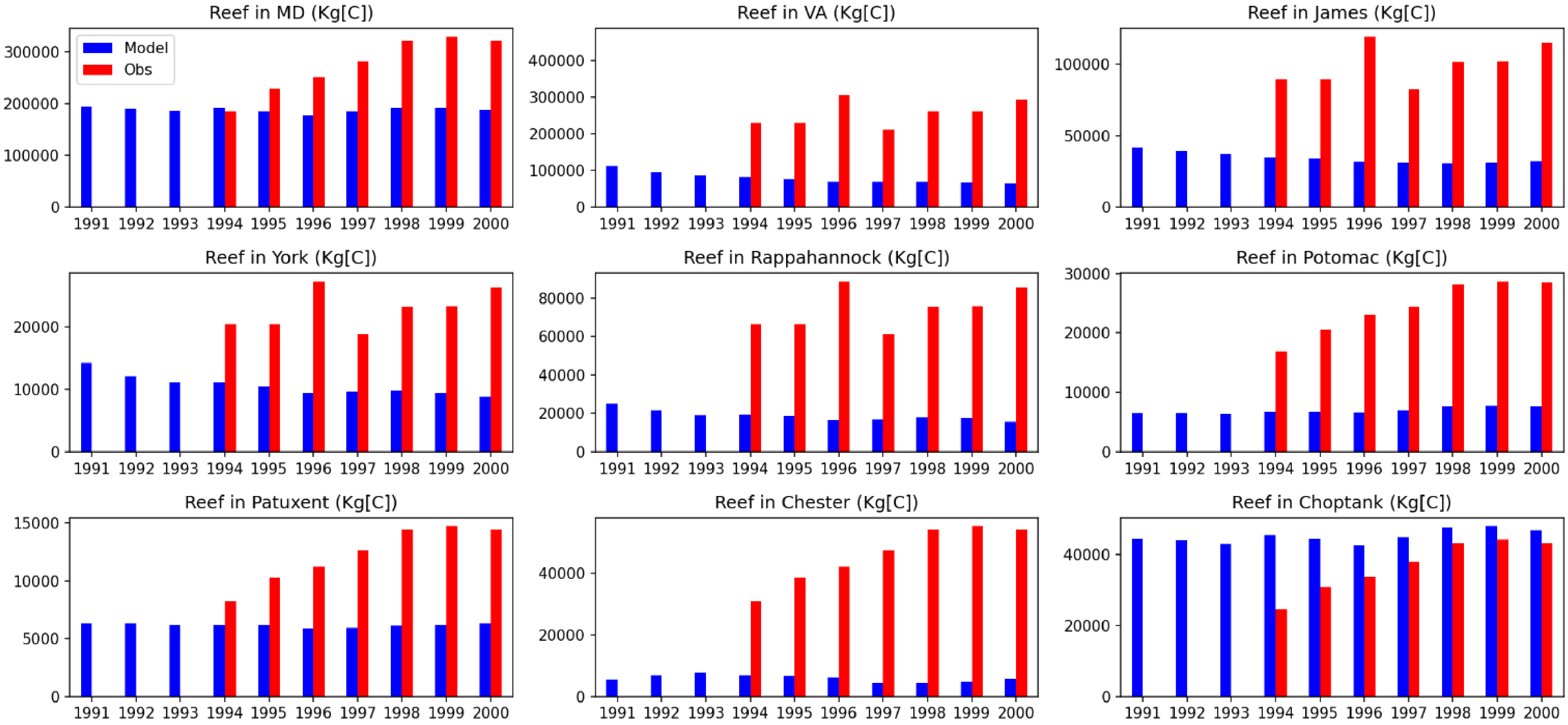
- We also checked the sediment POM concentrations to make sure they reach quasi-equilibrium state





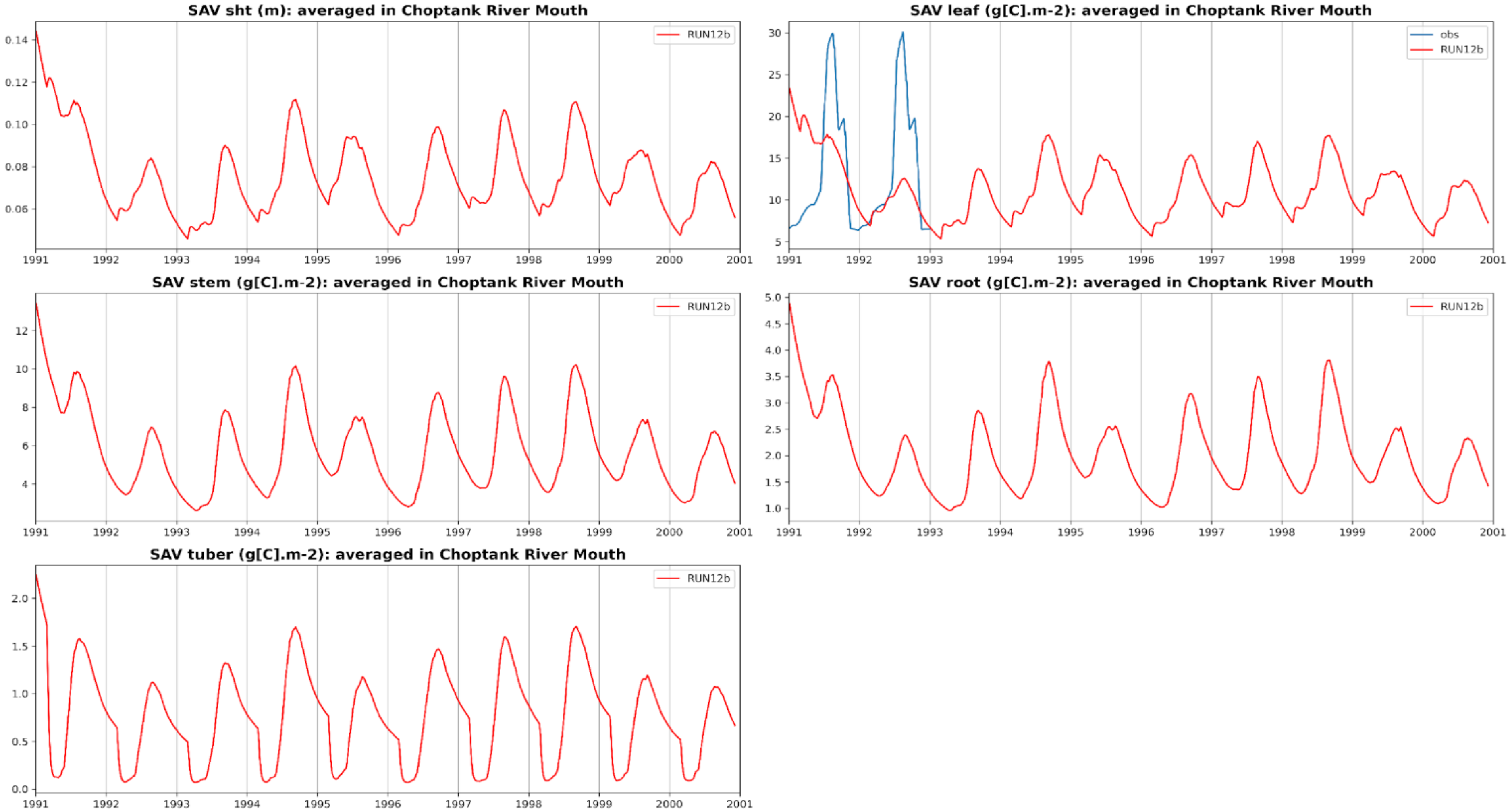
Oyster Simulation

- The new MBM workflow includes the Living resource modules. Below shows the comparison of Reef oyster with observations in different regions.
- In general, the Reef oyster is underestimated , which needs further improvement.



SAV Simulation

- MBM simulates the SAV canopy height (sht), and the biomass of SAV leaf/stem/root/tuber.
- The SAV biomass simulated at Choptank River mouth shows a reasonable seasonal pattern.
- However, it seems that SAV biomass might be underestimated. More observational data is needed to validate the model.



Summary

- We closely collaborated with WSM team on coupling between MBM and watershed loading
- We have successfully updated the MBM workflow to use the new NetCDF format of P7 WSM loading and shoreline erosion.
- MBM now includes all planned modeling components for both physical (1st step) and biological (2nd step) simulations.
- Overall, the MBM results are satisfactory, and the water quality results are comparable or better than P6, with great potential for further improvement in shallows.
- Re-assessed sediment diagenesis, primary production (not shown in this report) and living-resource modules. The results are generally reasonable, but some need further improvement.