## **Update on the Phase 7 Main Bay Model (MBM)**

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## **Outline**

- ☐ Assessment of phase-7 (beta) nutrient loading on estuarine modeling
  - Assessment in major rivers
  - ☐ Assessment in smaller embayment

- Preliminary results of MBM model with phase-7 (beta) loading
  - Hydrodynamics: elevation, temperature, salinity
  - Water quality: Chl-a, DO, nitrogen, phosphorus, etc.
  - Primary production, and sediment nutrient fluxes
- Summary

## P7 watershed loading (beta)

- We began to receive preliminary P7 watershed loading since December 2024
- We worked closely with watershed modeling (WSM) team to develop the P7 loading linkage to the MBM, and have successfully completed the new MBM workflow.

• We have tested different versions of P7 watershed loadings. We decided to use the P7 version hybridized with P6 loading (P7 beta) at RIM stations for the new MBM calibration.

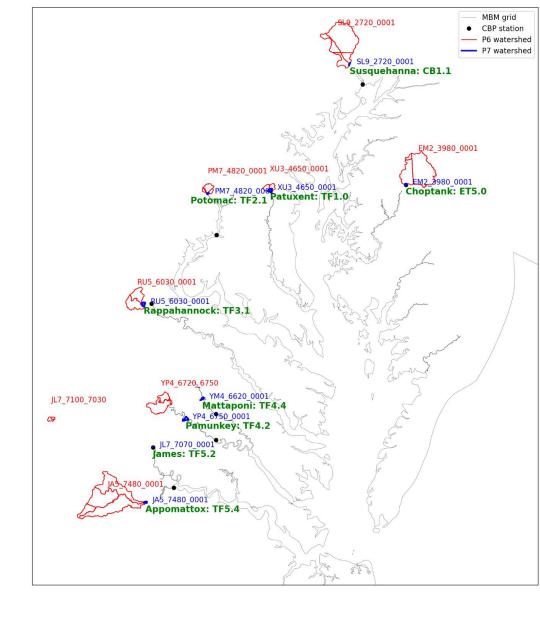
- We will continue to test updated P7 (beta) watershed inputs from WSM, and provide feedback on WSM performance
  - Assessment of WSM results in some rivers and embayment

## Assessment of P7 (beta) loading in major rivers (RIM)

- ☐ Analyzed how WSM input affects MBM simulation of nutrients near river boundary
- ☐ There are 9 big rivers with monitoring data (RIM stations)
- Compared 4 types of nutrient concentrations for these rivers
  - 1. Observations at RIM stations (on watershed side)
  - 2. Observations at CBP stations (on estuarine side)
  - 3. Simulated concentration from watershed model (WSM)
  - 4. Simulated concentration in MBM

#### Note:

**a. TF2.1, TF4.4, TF4.2, TF5.4** are downstream stations from the RIM stations



River	Susquehanna	Patuxent	Potomac	Rappahannock	James	Choptank	Mattaponi	Pamunkey	Appomattox
CBP station	CB1.1	TF1.0	TF2.1	TF3.1	TF5.2	ET5.0	TF4.4	TF4.2	TF5.4

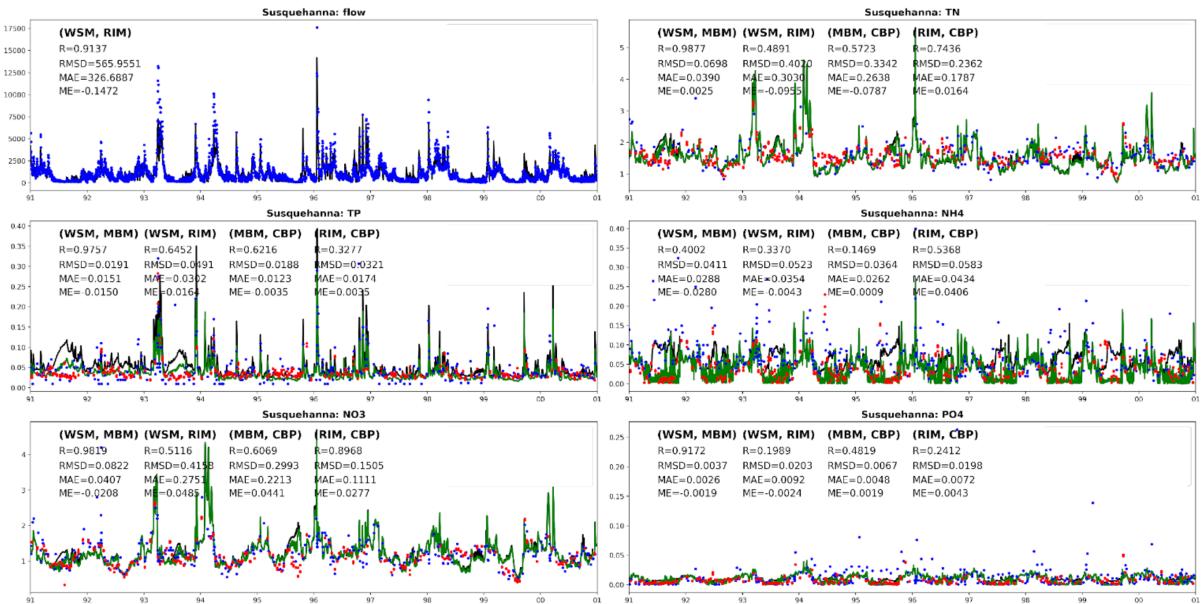
## Susquehanna River

WSM\_P7 hybrid
MBM: CB1.1

RIM Obs: Susquehanna

CBP Obs: CB1.1

- High correlation between WSM and MBM (except NH4)
- Good model skills between WSM and RIM
- Consistency between CBP and RIM data

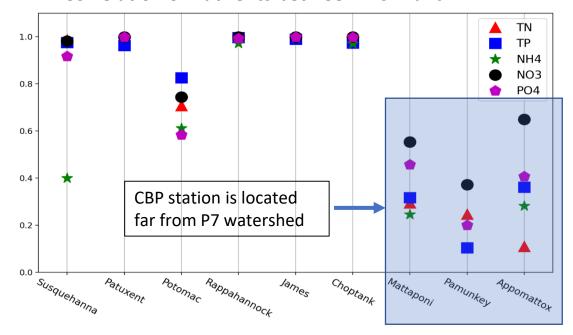


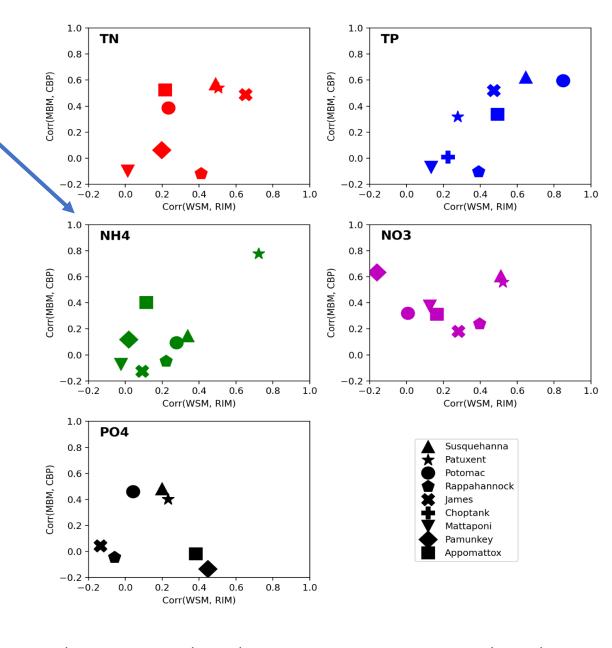
#### **Correlation between WSM and MBM**

- For TN, TP and NH4, it shows the better performance of WSM led to better performance of MBM
- No evident correlation for NO3 and PO4

High correlation between WSM and MBM nutrients shows that MBM is correctly representing the nutrient input from WSM

#### Correlation of nutrients between WSM and MBM



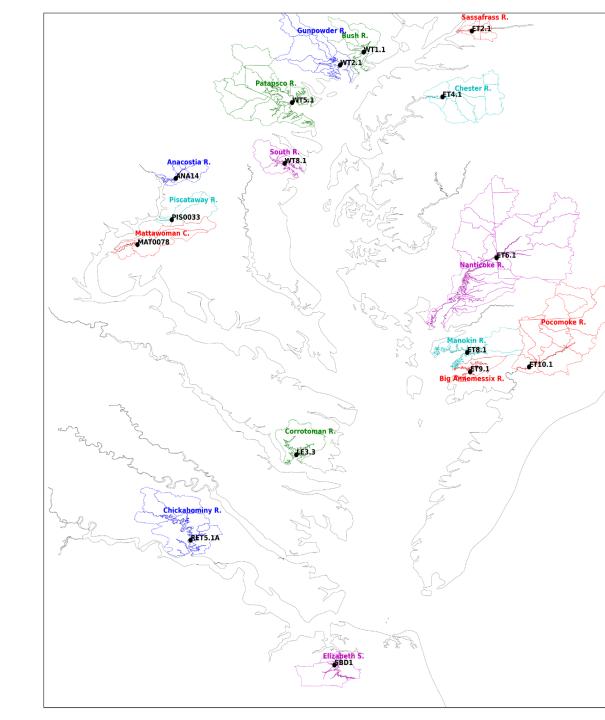


- The x-axis is correlation between WSM concentration and RIM data
- The y-axis is correlation between MBM concentration and CBP data

# Assessment of P7 loading in small embayment

☐ We selected 16 small embayments to check how P7
WSM loading are related to the nearby MBM
simulation

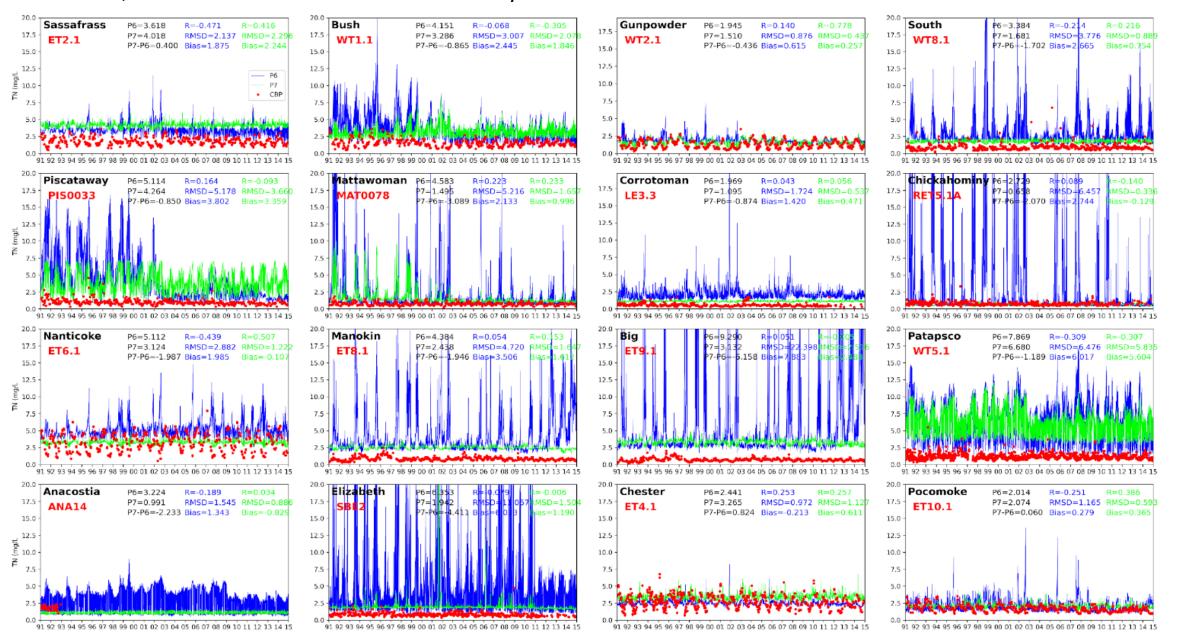
- ☐ Compared 5 types of concentrations for nutrients
  - Observations at CBP stations (on estuarine side)
  - Simulated concentration from P6 WSM
  - Simulated concentration from P7 WSM
  - Simulated concentration from MBM (driven by P6 load)
  - Simulated concentration from MBM (driven by P7 load)



## **Comparison of TN from P6 and P7 WSMs**

P6 — P7 • CBP Obs.

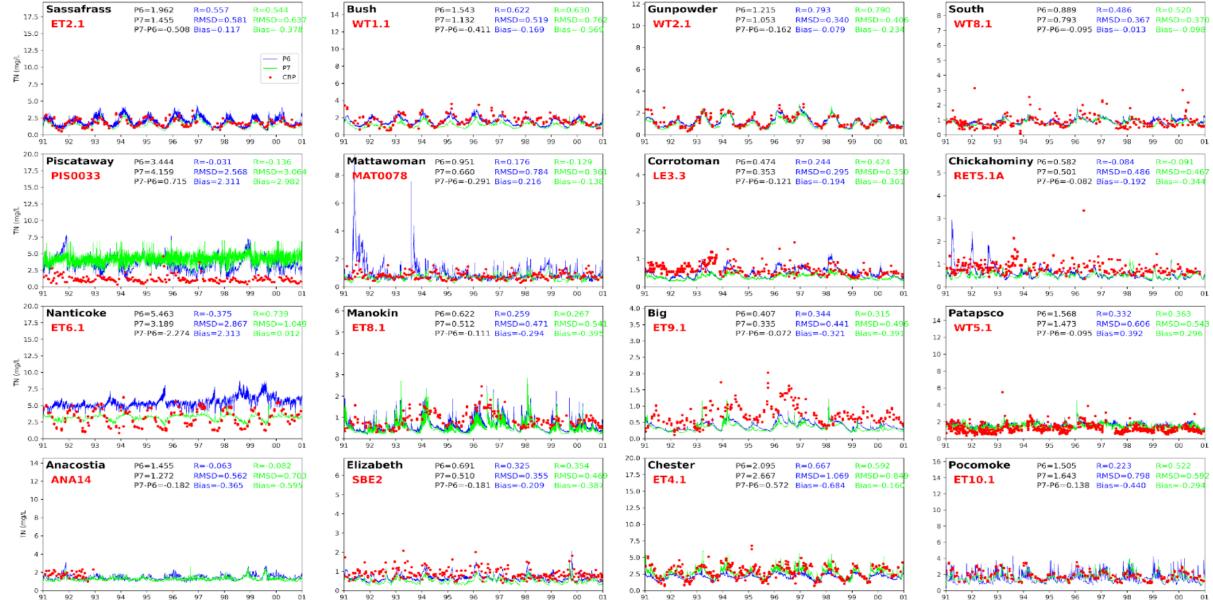
Overall, TN concentration in P7 matches nearby CBP observations better than P6



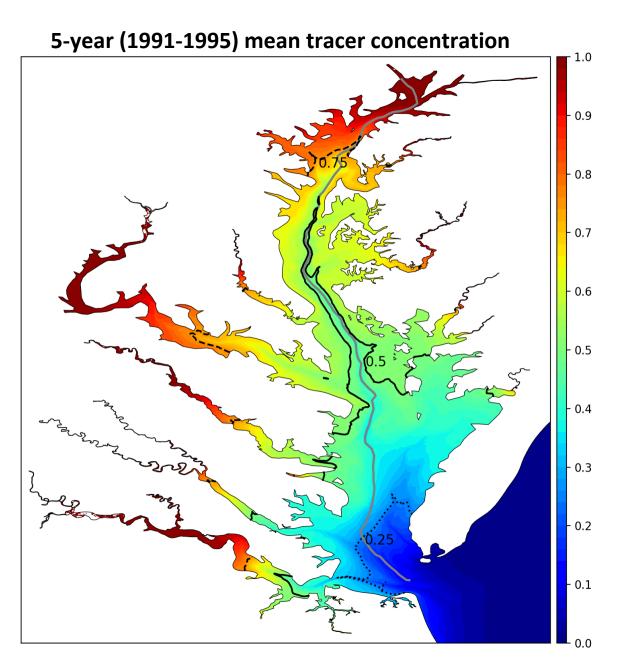
#### Comparison of TN simulated in MBM with P6 and P7 loads

-MBM(P6) ----MBM(P7) • CBP Obs.

 For most embayment, TN simulation from MBM driven by either P6 or P6 is reasonable in terms of seasonal variation and magnitude.



## Watershed influence on the Bay



 A tracer study was conducted by continuously releasing tracers (of unit concentration) along with watershed flows

- Output tracer concentrations reflect the influence from watershed flow: 1 for full influence, 0 for no influence
- The upper bay and upper reaches of tributaries are mainly controlled by watershed flows
- Tracer concentration in the 16 embayments can be used as indicator of watershed influence

## **Comparison of WSM loads**

- Compared with observations at nearby CBP stations, P7 WSM loading generally has smaller error than P6 WSM for most variables for all stations
- For most embayments, the difference of RMSD values between P6 and P7 is relatively small, which suggests that estuarine processes also play an important role besides the WSM nutrient load

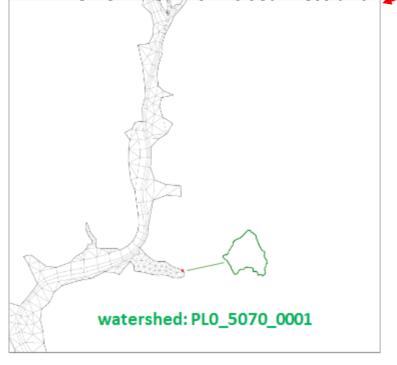
SM (RMSD)			<del> </del>	i			
<del> </del>	river impact	salinity	NH4	NO3	PO4	TN	TP
Sassafrass R.	99.5%	1.91	(0.1553, 0.1724)	(2.1799, 1.5663)	(0.0506, 0.0303)	(2.1749, 2.2918)	(0.1157, 0.0708)
Bush R.	95.9%	0.84	(1.5825, 0.8445)	(2.4744, 2.0285)	(0.1267, 0.1176)	(3.0666, 2.1254)	(0.1737, 0.1249)
Gunpowder R.	94.7%	1.63	(0.0774, 0.0722)	(1.0177, 0.4990)	(0.0122, 0.0164)	(0.8905, 0.4488)	(0.0471, 0.0442)
South R.	69.1%	9.84	(0.1297, 0.1260)	(3.9673, 1.0413)	(0.0467, 0.0570)	(3.8474, 0.8997)	(0.0784, 0.0691)
Piscataway R.	100.0%	0.00	(0.3453, 0.3234)	(5.3081, 3.5262)	(0.0381, 0.0407)	(5.3026, 3.7516)	(0.0702, 0.0805)
Mattawoman C.	100.0%	0.02	(0.2073, 0.1016)	(4.8008, 1.8416)	(0.4483, 0.1060)	(5.5305, 1.7449)	(0.7417, 0.1505)
Corrotoman R.	56.6%	14.53	(0.1101, 0.0573)	(1.8100, 0.7028)	(0.0223, 0.0406)	(1.8435, 0.5316)	(0.0785, 0.0431)
Chickahominy R.	99.7%	1.18	(0.9466, 0.0622)	(5.4596, 0.1991)	(0.0683, 0.0370)	(7.2374, 0.3392)	(0.1628, 0.0585)
Nanticoke R.	99.8%	0.19	(0.1803, 0.1174)	(2.9407, 1.4765)	(0.0436, 0.0748)	(2.8671, 1.2300)	(0.0962, 0.0807)
Manokin R.	49.0%	13.87	(1.1536, 0.1188)	(3.7258, 1.3950)	(0.0762, 0.1538)	(4.8577, 1.6415)	(0.1603, 0.1767)
Big Annemessix R.	47.8%	15.41	(10.0068, 0.2549)	(17.8570, 1.7639)	(0.4463, 0.1978)	(25.9882, 2.5115)	(0.8129, 0.2395)
Patapsco R.	80.8%	10.42	(3.5302, 3.2289)	(2.9920, 2.4831)	(0.2444, 0.2266)	(6.6460, 5.9269)	(0.3410, 0.3307)
Anacostia R.	100.0%	0.17	(0.2177, 0.2341)	(2.7501, 0.3297)	(0.0824, 0.0522)	(1.7004, 0.8990)	(0.0571, 0.0756)
Elizabeth S.	46.9%	19.08	(1.8986, 0.4678)	(4.3389, 1.0248)	(0.8990, 0.2319)	(7.6235, 1.3427)	(1.2829, 0.3256)
Chester R.	99.3%	0.49	(0.1221, 0.1062)	(1.0766, 1.2225)	(0.0301, 0.0733)	(0.9874, 1.1437)	(0.1563, 0.1110)
Pocomoke R.	100.0%	0.20	(0.2716, 0.0722)	(0.7283, 0.6284)	(0.0953, 0.0869)	(1.1926, 0.6074)	(0.1445, 0.1108)
BM(RMSD)	river impact	salinity	NH4	NO3	PO4	TN	TP
Sassafrass R.	99.5%	2.12	(0.0969, 0.0840)	(0.5650, 0.5072)	(0.0289, 0.0277)	(0.5852, 0.6393)	(0.1007, 0.1076)
Bush R.	95.9%	0.95	(0.1995, 0.2352)	(0.5606, 0.4075)	(0.0132, 0.0119)	(0.5272, 0.7612)	(0.0700, 0.0672)
Gunpowder R.	94.7%	1.91	(0.0665, 0.0666)	(0.3670, 0.4627)	(0.0075, 0.0074)	(0.3368, 0.4037)	(0.0593, 0.0594)
South R.	69.1%	10.02	(0.0799, 0.0788)	(0.2548, 0.1814)	(0.0366, 0.0365)	(0.3692, 0.3716)	(0.0642, 0.0632)
Piscataway R.	100.0%	0.00	(0.1651, 0.2608)	(2.5954, 3.1800)	(0.0471, 0.0378)	(2.5791, 3.1839)	(0.1015, 0.0955)
Mattawoman C.	100.0%	0.01	(0.0655, 0.0700)	(0.5875, 0.1995)	(0.0233, 0.0255)	(0.7926, 0.3598)	(0.0730, 0.0551)
Corrotoman R.	56.6%	14.53	(0.0729, 0.0776)	(0.1617, 0.0695)	(0.0090, 0.0084)	(0.2931, 0.3502)	(0.0329, 0.0300)
Chickahominy R.	99.7%	0.61	(0.0690, 0.0619)	(0.1521, 0.1623)	(0.0192, 0.0189)	(0.4934, 0.4674)	(0.0804, 0.0743)
Nanticoke R.	99.8%	0.19	(0.0987, 0.1370)	(3.1678, 1.2049)	(0.0315, 0.0534)	(2.9262, 1.0648)	(0.0761, 0.0646)
Manokin R.	49.0%	13.95	(0.0686, 0.0709)	(0.3022, 0.1680)	(0.0152, 0.0422)	(0.4878, 0.5558)	(0.0489, 0.0580)
Big Annemessix R.	47.8%	15.49	(0.0797, 0.0824)	(0.1130, 0.0594)	(0.0055, 0.0143)	(0.4411, 0.4971)	(0.0285, 0.0315)
Patapsco R.	80.8%	10.45	(0.2162, 0.2217)	(0.3866, 0.3704)	(0.0234, 0.0219)	(0.6135, 0.5672)	(0.0446, 0.0476)
Anacostia R.	100.0%	nan	(0.3215, 0.3077)	(0.3335, 0.2997)	(0.0269, 0.0286)	(0.5762, 0.7065)	(0.0680, 0.0735)
Elizabeth S.	46.9%	18.80	(0.2274, 0.2143)	(nan, nan)	(0.0376, 0.0436)	(0.3541, 0.4680)	(0.0424, 0.0524)
Chester R.	99.3%	0.60	(0.0843, 0.0864)	(0.9019, 0.9045)	(0.0316, 0.0497)	(1.0764, 0.8648)	(0.1862, 0.1473)
Pocomoke R.	100.0%	0.18	(0.0461, 0.0509)	(0.6085, 0.7433)	(0.0507, 0.0834)	(0.8366, 0.5998)	(0.0883, 0.1048)

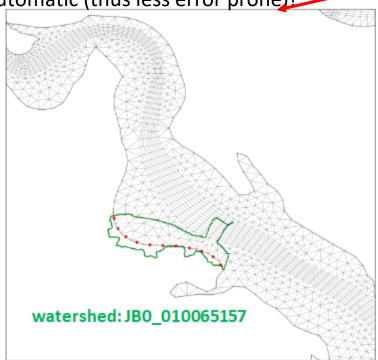
- 1. In brackets, the 1<sup>st</sup> number is RMSD for P6 WSM, and 2<sup>nd</sup> number is for P7 WSM
- 2. Green color indicates smaller P7 error, while red means larger. Gray color means that P6 and P7 errors are

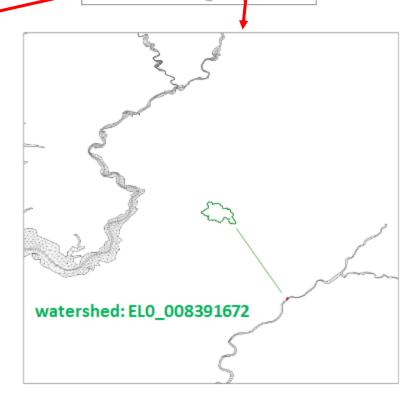
# Revised MBM workflow with P7 (beta) watershed loading

- Worked with Gopal and Richard in changing the format of WSM load to netCDF, which is self describing
- Streamlined the mapping method of WSM loading onto MBM grid, and removed the middle step using CH3D grid
- Optimized the MBM workflow by incorporating the processing of WSM loading, airshed loading and shoreline erosion

The new workflow is seamless and fully automatic (thus less error prone)!







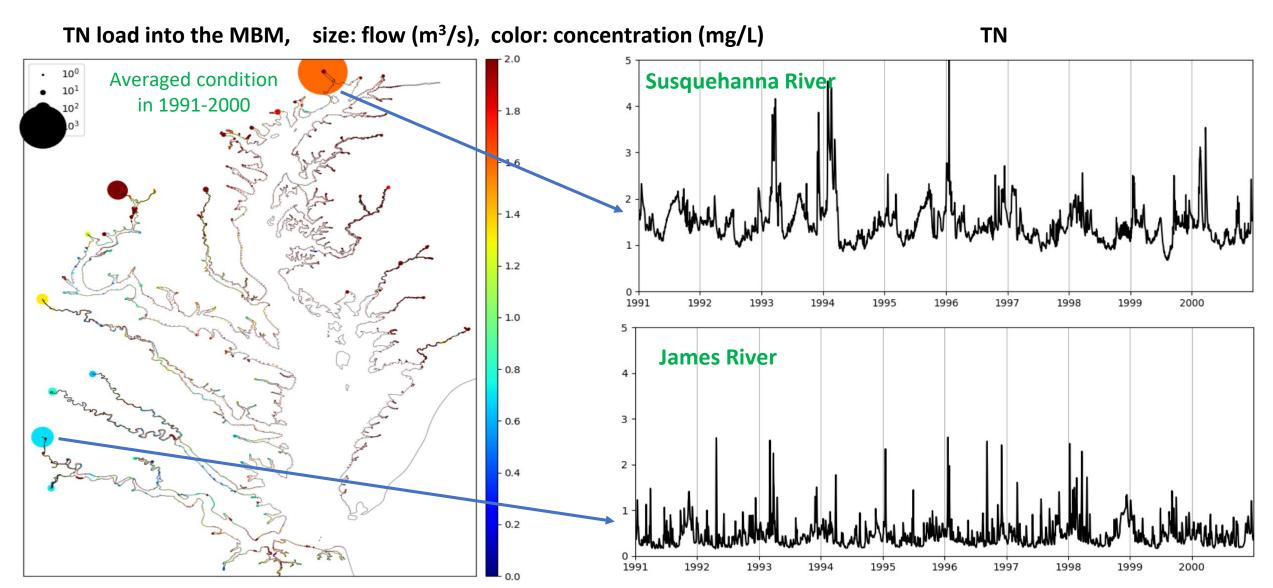
## Mapping of P7 watershed flow to MBM grid

• A robust algorithm was developed to seamlessly distribute the loading from watershed to MBM grid, without the need for intermediary as before

Watershed flow into the MBM (mean=2249m³/s) A GUI-app (schismcheck) was developed to visualize note: the loading input and other SCHISM inputs. Averaged condition in 1991-2000 Susquehanna River  $(mean=1121 m^3/s)$ **James River**  $(mean=218 m^3/s)$ 1500

## Mapping of P7 watershed nutrient loading to MBM grid

- In MBM, watershed nutrient loadings were converted to nutrient concentrations
- TN concentrations generally decrease from north to south



# MBM re-calibration with P7 (beta) watershed loading

- We have begun to re-calibrate the MBM with new P7 (beta) loading
- Results are still preliminary; we are systematically examining all WQ parameters against CBP observations at long-term monitoring stations

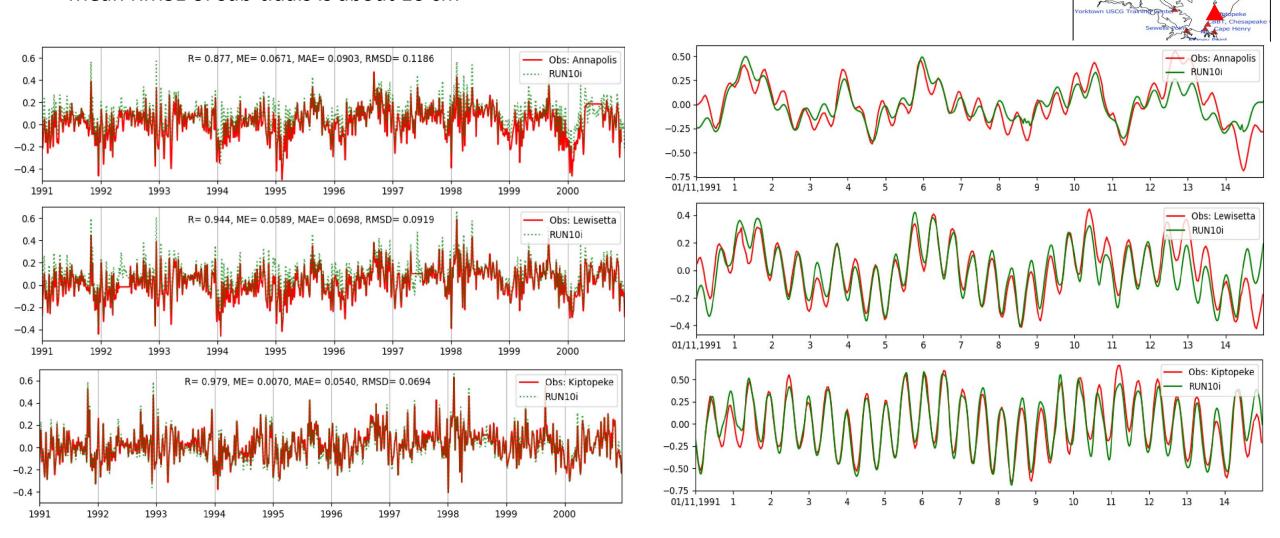
 Overall, the current model skill of P7 MBM is comparable to CH3D-ICM, consistent with previous MBM as driven by P6 loading

• We continue to improve MBM water quality simulation, particularly in the tributaries

Also, we will soon add living resources modules (Oyster, SAV, Tidal marsh) in this new version

#### MBM re-calibration: elevation

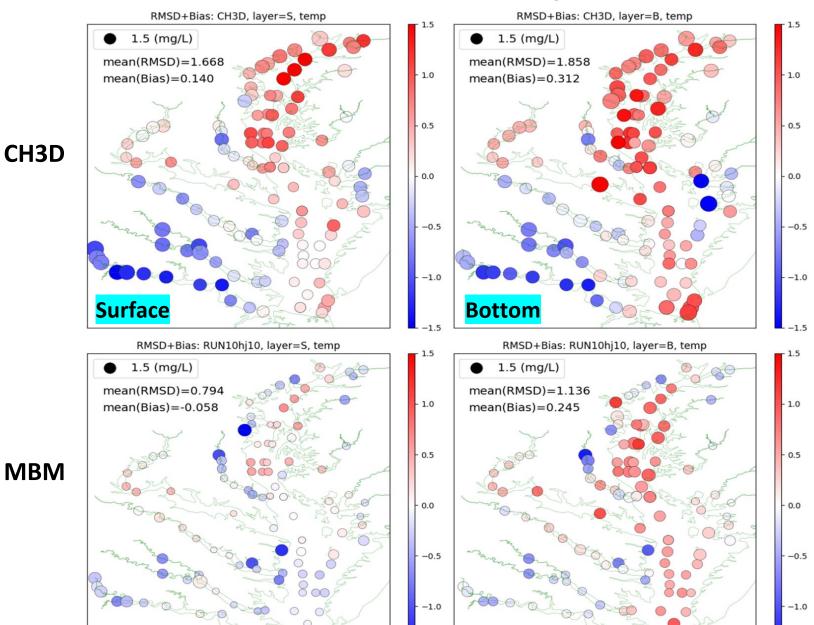
- Elevation are well simulated in both sub-tidal signals and tidal harmonics (not shown for brevity), in terms of long-term trend and event scales
  - Great potential for future inundation studies
- Mean RMSE of sub-tidals is about 10 cm



## **MBM** re-calibration: Temperature

CH<sub>3</sub>D

Surface

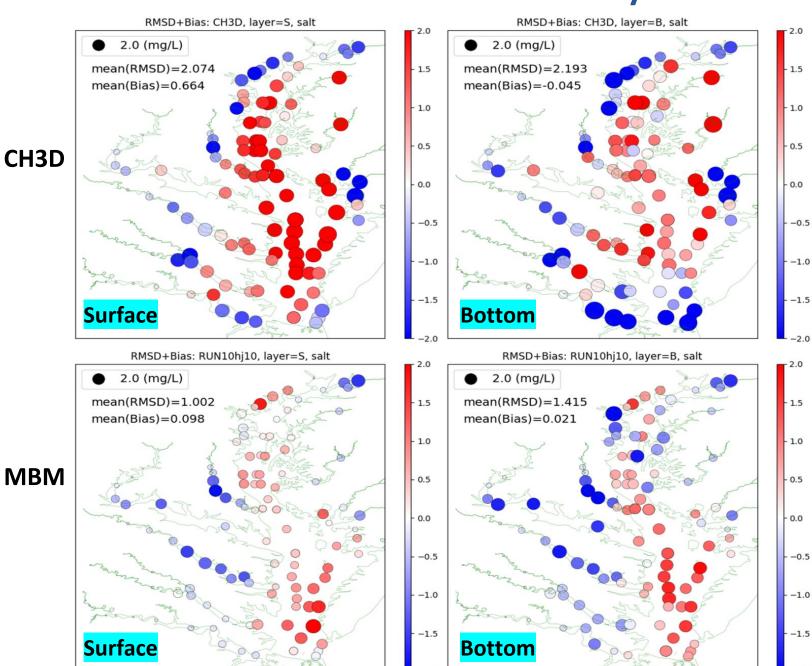


**Bottom** 

color: Bias size: RMSD

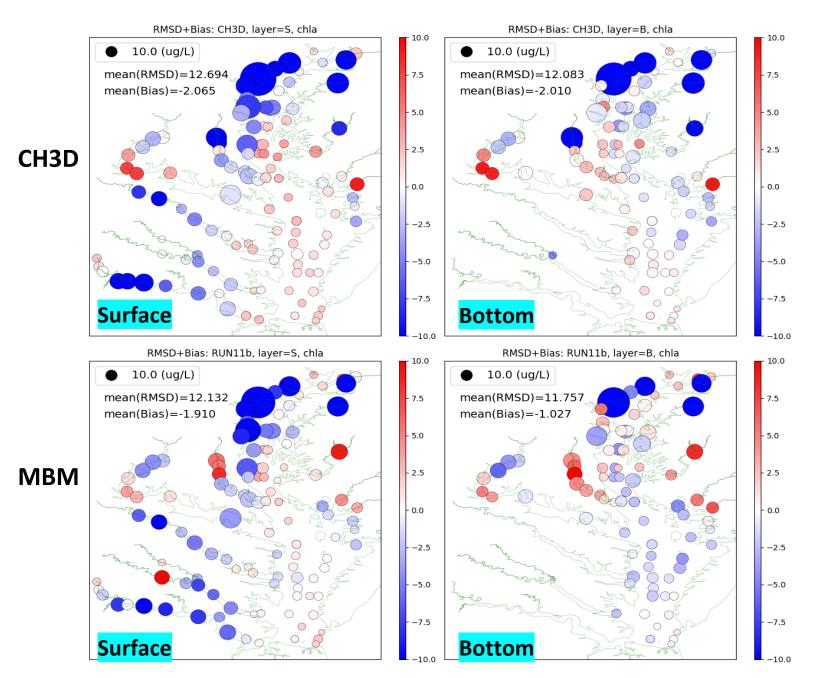
- CH3D-ICM model is used for reference
- Temperature is well simulated in MBM. The model skill is generally better than CH3D for both surface and bottom
- In MBM, bottom temperature has slightly larger error than the surface.
- Along the Bay channel, bottom temperature in MBM tends to be overestimated
- In some tributaries and shallow regions, temperature tends to underestimated.

## **MBM** re-calibration: Salinity



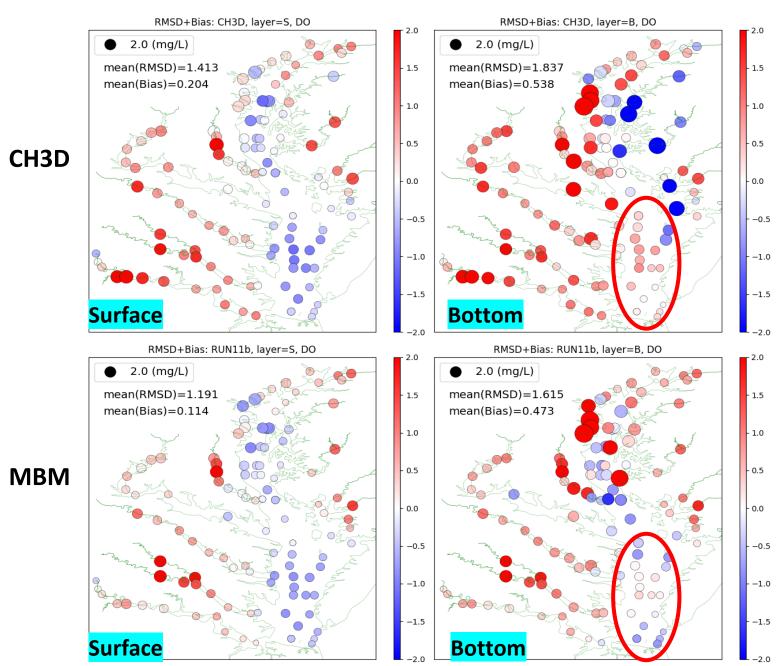
- Salinity is also well simulated in MBM. The model skill is generally better than CH3D for both surface and bottom.
- In the mainstem, salinity is overestimated, particularly towards the lower Bay.
- The bottom salinity has larger error than the surface.
- In tributaries, salinity is generally underestimated.

#### MBM re-calibration: Chl-a



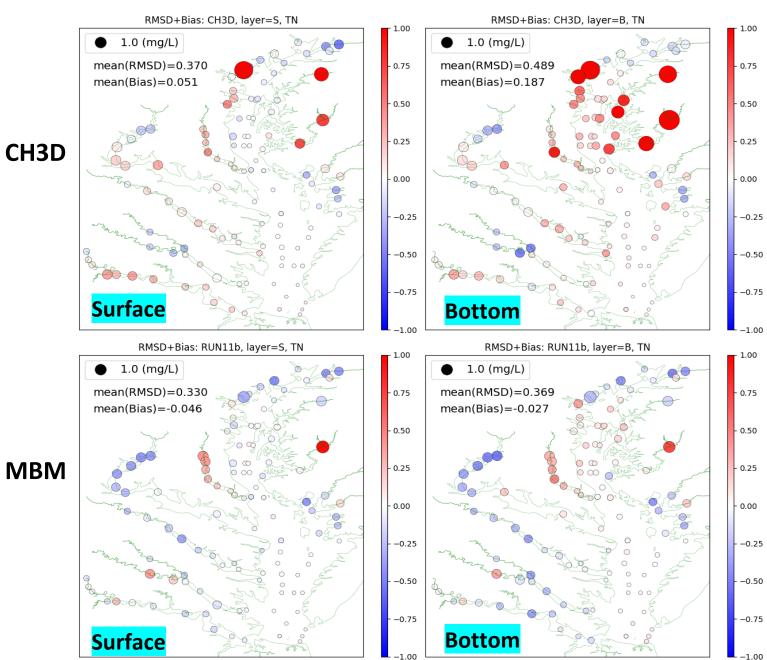
- Overall, Chl-a simulation in the MBM is comparable to CH3D in both RMSD and Bias at both surface and bottom.
- The special distributions of errors between two models are very similar with larger errors appearing in the shallow region and tributaries.
- One possible reason for the large error in shallow region is due to high bloom peaks. For example, at WT4.1 (Back River), Chl-a can be over 200 ug/L, and both models underestimated the blooms.

## MBM re-calibration: DO



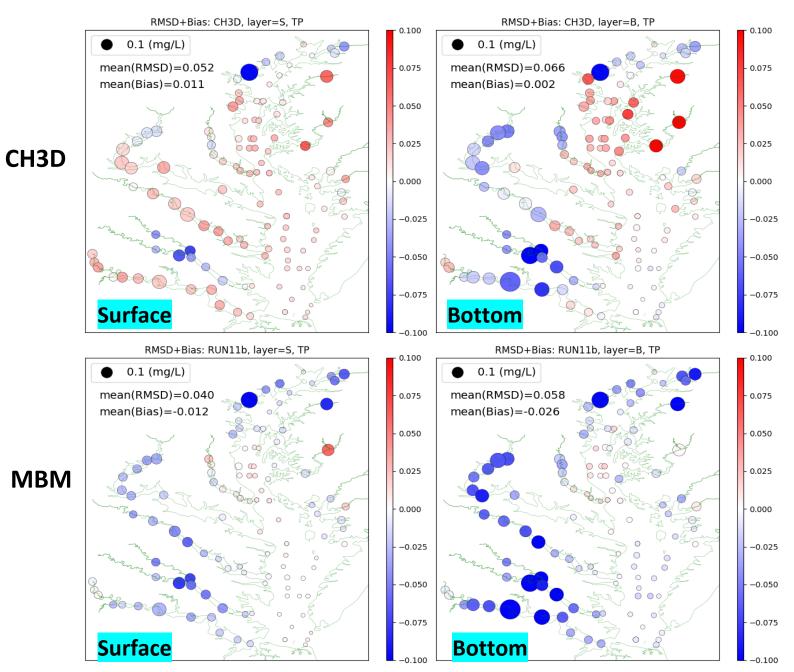
- Overall, the MBM is comparable to CH3D for DO simulation.
- The special distributions of errors between two models are similar, except in lower Bay, where MBM captured the hypoxia better
- In general, both surface and bottom DO are underestimated in MBM for mainstem stations, but overestimated in tributaries.
- On average, the RMSD of simulated DO is about 1.2 mg/L for the surface, and 1.6 mg/L for the bottom.

#### **MBM** re-calibration: TN



- MBM is comparable to CH3D for TN simulation.
- Both models well simulated the TN in the mainstem stations with small RMSD and Bias.
- MBM also performs better than CH3D in tributaries; both have slightly larger errors than at mainstem stations.
- On average, the RMSD of TN simulation is about 0.33 mg/L for the surface, and 0.37 mg/L for the bottom.

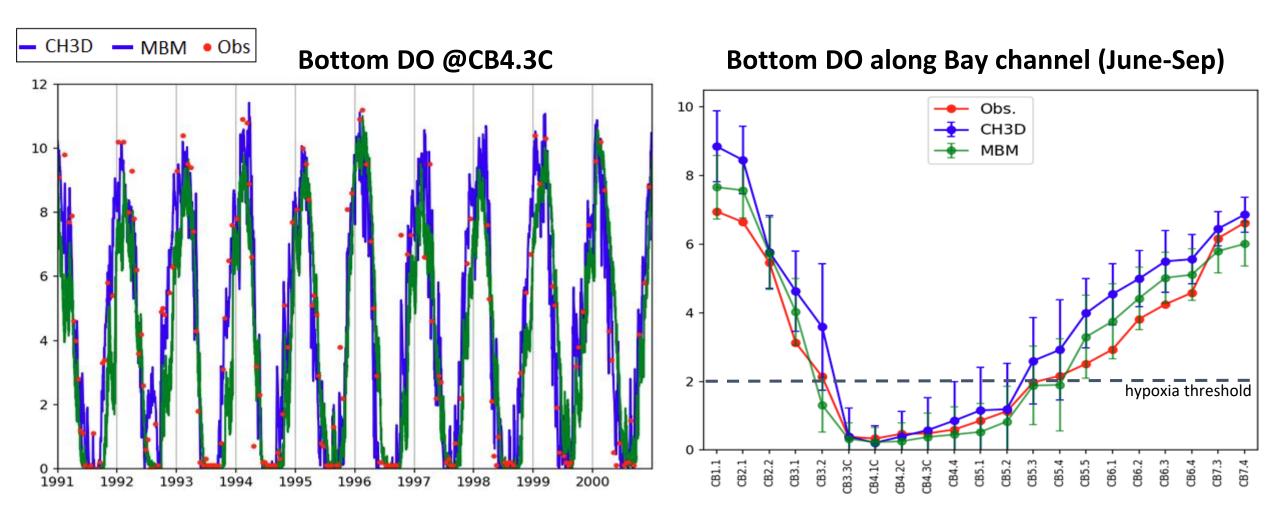
## **MBM** re-calibration: TP



- At mainstem stations, both models show good model skills. MBM seems to perform slightly better than CH3D.
- At tributary station, both models have larger errors.
- In some rivers (Potomac, Rappahannock, James), CH3D tends to overestimate the surface TP, but MBM tends to underestimate.
- On average, the RMSD of TP simulation is about 0.04 mg/L for the surface, and 0.06 mg/L for the bottom.

## **Summer Hypoxia**

- Both CH3D and MBM correctly capture the summer hypoxia at CB4.3C
- Both models also correctly capture the variation of bottom DO along bay channel
- MBM captures DO (hypoxia) better in lower bay



#### Statistics for MBM re-calibration

- ❖ Overall, the MBM model skill is comparable to 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
  - O MBM has the potential to drastically improve in shallow areas due to its flexibility

Major Variable s

RMSD	temp	salt	chla	DO	TN	TP
surface	(1.668, 0.963)	(2.074, 1.151)	(12.694, 12.132)	(1.413, 1.191)	(0.370, 0.330)	(0.052, 0.040)
bottom	(1.858, 1.324)	(2.193, 1.664)	(12.083, 11.757)	(1.837, 1.615)	(0.489, 0.369)	(0.066, 0.058)
Bias	temp	salt	chla	DO	TN	TP
surface	(0.140, -0.205)	(0.664, -0.082)	(-2.065, -1.910)	(0.204, 0.114)	(0.051, -0.046)	(0.011, -0.012)
bottom	(0.312, 0.129)	(-0.045, -0.098)	(-2.010, -1.027)	(0.538, 0.473)	(0.187, -0.027)	(0.002, -0.026)

#### Nutrients

RMSD	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(0.231, 0.258)	(0.069, 0.063)	(0.017, 0.017)	(1.815, 2.060)	(0.179, 0.178)	(0.018, 0.013)	(1.357, 1.205)	(0.206, 0.190)	(0.044, 0.037)
bottom	(0.207, 0.241)	(0.110, 0.102)	(0.021, 0.020)	(1.763, 1.919)	(0.180, 0.185)	(0.017, 0.013)	(1.707, 1.573)	(0.232, 0.226)	(0.066, 0.060)
Bias	NO3	NILIA	DO4	DOC	DON	DOD	POC	DON	POP
Dias	1403	NH4	PU4	DOC	DON	DOP	POC	PON	POP
surface	(-0.028, -0.046)		(0.002, 0.001)	(-0.926, -1.681)		(0.008, 0.001)		(-0.145, -0.093)	
	surface bottom	surface (0.231, 0.258) bottom (0.207, 0.241)	surface         (0.231, 0.258)         (0.069, 0.063)           bottom         (0.207, 0.241)         (0.110, 0.102)	surface         (0.231, 0.258)         (0.069, 0.063)         (0.017, 0.017)           bottom         (0.207, 0.241)         (0.110, 0.102)         (0.021, 0.020)	surface         (0.231, 0.258)         (0.069, 0.063)         (0.017, 0.017)         (1.815, 2.060)           bottom         (0.207, 0.241)         (0.110, 0.102)         (0.021, 0.020)         (1.763, 1.919)	surface         (0.231, 0.258)         (0.069, 0.063)         (0.017, 0.017)         (1.815, 2.060)         (0.179, 0.178)           bottom         (0.207, 0.241)         (0.110, 0.102)         (0.021, 0.020)         (1.763, 1.919)         (0.180, 0.185)	surface         (0.231, 0.258)         (0.069, 0.063)         (0.017, 0.017)         (1.815, 2.060)         (0.179, 0.178)         (0.018, 0.013)           bottom         (0.207, 0.241)         (0.110, 0.102)         (0.021, 0.020)         (1.763, 1.919)         (0.180, 0.185)         (0.017, 0.013)	surface         (0.231, 0.258)         (0.069, 0.063)         (0.017, 0.017)         (1.815, 2.060)         (0.179, 0.178)         (0.018, 0.013)         (1.357, 1.205)           bottom         (0.207, 0.241)         (0.110, 0.102)         (0.021, 0.020)         (1.763, 1.919)         (0.180, 0.185)         (0.017, 0.013)         (1.707, 1.573)	surface         (0.231, 0.258)         (0.069, 0.063)         (0.017, 0.017)         (1.815, 2.060)         (0.179, 0.178)         (0.018, 0.013)         (1.357, 1.205)         (0.206, 0.190)           bottom         (0.207, 0.241)         (0.110, 0.102)         (0.021, 0.020)         (1.763, 1.919)         (0.180, 0.185)         (0.017, 0.013)         (1.707, 1.573)         (0.232, 0.226)

<sup>1.</sup> In brackets, the 1<sup>st</sup> number is CH3D error, and 2<sup>nd</sup> number is MBM error.

2. Green color indicates MBM error is smaller, while red means larger.

## **Primary Production**

• Simulated GPP in MBM is reasonable, which resembles the seasonal and spatial variations in CH3D

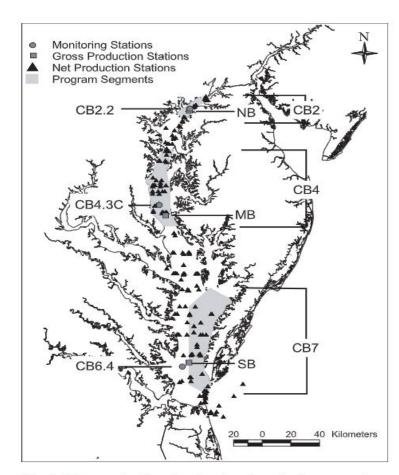


Fig. 1. Chesapeake Bay showing location of primary production sampling stations

Cerco, C. F., & Noel, M. R. (2004). Process-based primary production modeling in Chesapeake Bay. Marine Ecology Progress Series, 282, 45-58.

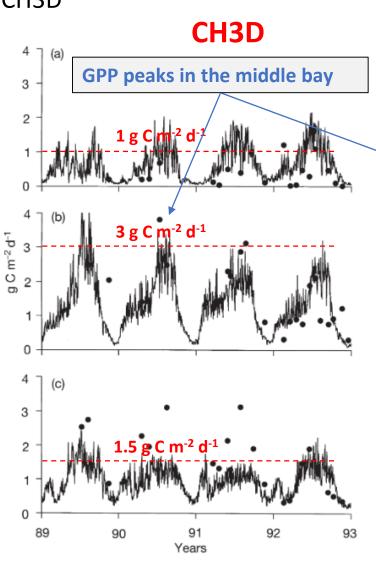
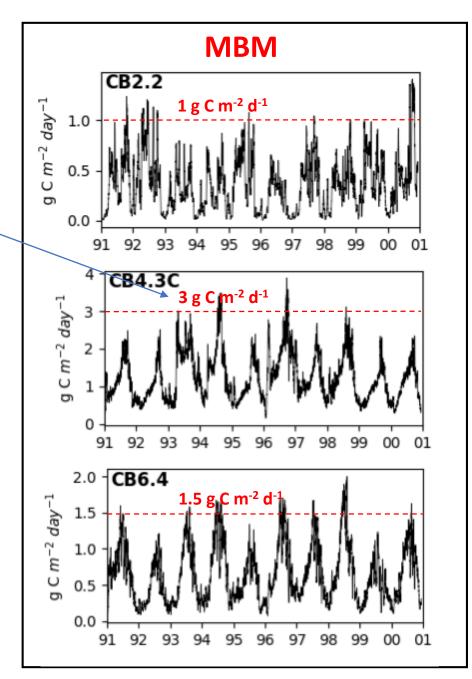
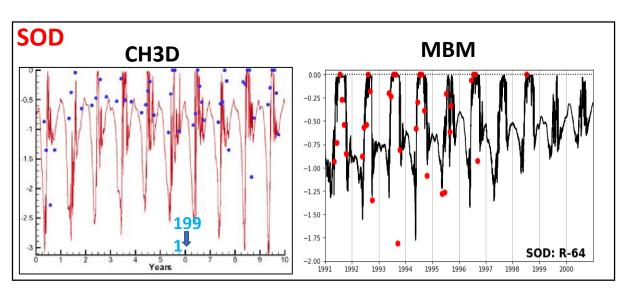


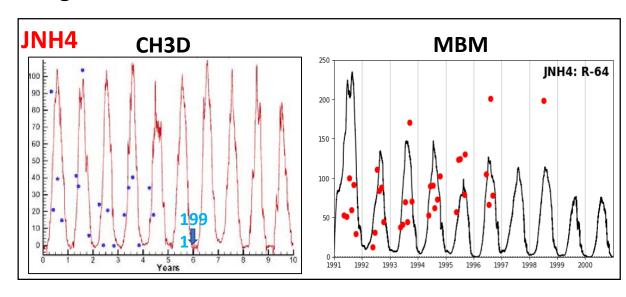
Fig. 6. Observed and computed GPP for (a) upper, (b) midand (c) lower Chesapeake Bay

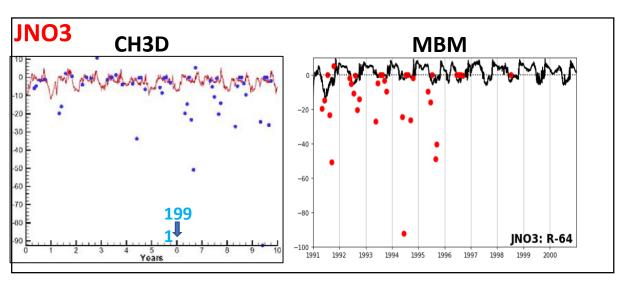


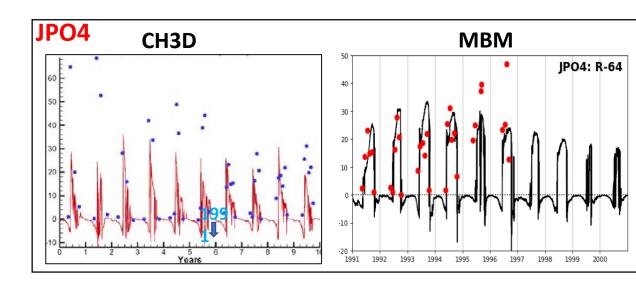
## SOD and sediment nutrient flux

- Sediment fluxes in MBM were assessed against obs from <a href="https://gonzo.cbl.umces.edu/data.htm">https://gonzo.cbl.umces.edu/data.htm</a> (Boynton)
- Generally, simulated sediment fluxes are reasonable in magnitude and seasonal variation









## **Summary**

- ☐ We have successfully upgraded the new MBM workflow with P7 loading
- ☐ An assessment on WSM nutrient loadings was conducted against CBP observation
  - At RIM stations, P7 (beta) WSM has good model skill for major rivers
  - In small embayments, the P7 (beta) WSM is generally better than P6 model
- ☐ We have begun the re-calibration of MBM hydro and water quality with P7 (beta) loading
- ☐ Water quality simulation in MBM are comprehensively assessed with CBP observations.

The preliminary results confirm that MBM is as good or better than CH3D