Update on the Phase 7 Main Bay Model (MBM)

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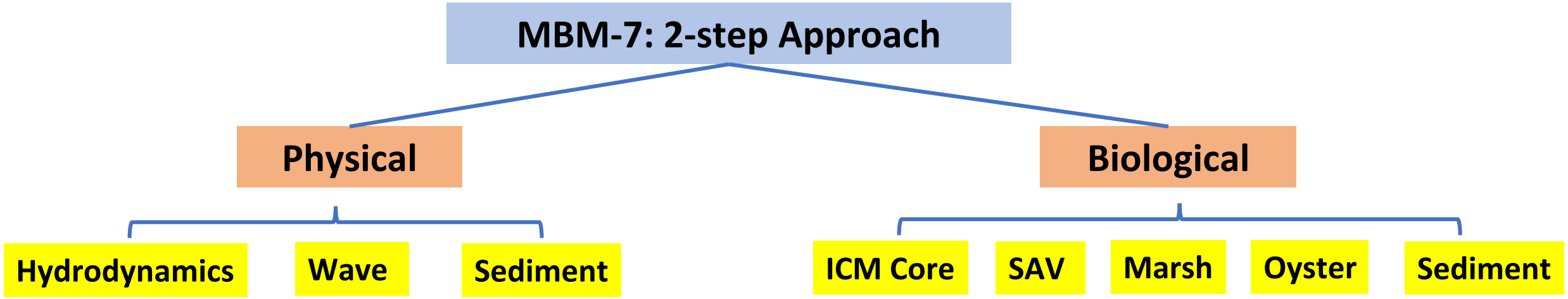
Outline

- Assessment of watershed loading between P6 and P7
  - We are switching to a pure Phase 7 loading model from now on
  - MBM-6: MBM with hybrid P6-P7 loading (RIM from P6, rest from P7)
  - MBM-7: MBM with (pure) P7 loading (WSM, ATM, SHO)
- Assessment of watershed Loading between P6 and P7
- MBM calibration
  - MBM-7 vs MBM-6
  - MBM-7 vs CH3D
- Spatiotemporal variations of Chl-a and DO in MBM-7
- Summary and future work

Overview On MBM-7 Progress

❖ **We have calibrated the MBM with pure phase-7 nutrient inputs (MBM-7)**

❖ **The model skill of MBM-7 is consistent with both CH3D and MBM-6**



- Watershed flow
- Shoreline erosion
- Boundary conditions of elevation, velocity, TS and wave inputs
- Initial conditions of hydrodynamics and sediment
- Atmospheric Forcing: ERA5

- Watershed nutrient loading
- Shoreline erosion for sediment and nutrients
- Atmospheric nutrient deposition

Assessment of Watershed Loading between P6 and P7: Major Rivers

- ❑ We assessed nutrient concentrations from watershed loadings against nearby downstream CBP observations
- ❑ P7 nutrient concentrations match better with observations at RIM stations than P6
- ❑ Note: P6 refers to the hybrid loading (20250101_P7beta_Hybrid).

RMSE between WSM nutrient conc. and the nearby CBP observations

Worse | Close | Better

Regions	NH4	NO3	PO4	TN	TP	TSS ✓
Susquehanna	(0.0432,0.0437)	(0.2875,0.2991)	(0.0089,0.0106)	(0.3310,0.3425)	(0.0280,0.0243)	(11.5428,13.6488)
Patuxent	(0.1483,0.1814)	(0.6331,0.9060)	(0.0455,0.0680)	(0.7464,1.1992)	(0.0866,0.1336)	(35.6555,32.6645)
Potomac	(0.0963,0.0931)	(0.5480,0.5792)	(0.1282,0.1275)	(0.7700,0.5674)	(0.0637,0.1044)	(16.6087,14.0334)
Rappahannock	(0.0334,0.0430)	(0.2594,0.3228)	(0.0178,0.0133)	(0.6914,0.5231)	(0.2182,0.1911)	(104.7578,97.1951)
James	(0.0370,0.0414)	(0.2161,0.1410)	(0.0683,0.0488)	(0.3482,0.3166)	(0.1287,0.1314)	(66.3107,73.1921)
Choptank	(0.0424,0.0491)	(0.7703,0.3458)	(0.0272,0.0211)	(0.6864,0.3682)	(0.0919,0.0719)	(20.3460,8.3691)
Mattaponi	(0.0344,0.0404)	(0.1240,0.1050)	(0.0145,0.0215)	(0.3505,0.2198)	(0.0650,0.0682)	(15.3698,17.6690)
Pamunkey	(0.0298,0.0534)	(0.1702,0.1721)	(0.0209,0.0356)	(0.3722,0.2859)	(0.0548,0.0755)	(47.7405,53.3133)
Appomattox	(0.0343,0.0345)	(0.1621,0.1739)	(0.0076,0.0094)	(0.3941,0.2013)	(0.0292,0.0291)	(15.6633,13.1813)

In brackets, the 1st number is P6 error, and 2nd number is P7 error.

Assessment of Watershed Loading between P6 and P7: Small Tributaries

- P7 generally matches nearby CBP data better than P6.
- For NO3, the RMSEs are mostly comparable between P6 and P7.

Worse | Close | Better

Regions	NH4 ✓	NO3 ✗	PO4 ✓	TN	TP	TSS ✓
Sassafrass R.	(0.1823,0.1320)	(1.4854,2.7223)	(0.0302,0.0273)	(2.2593,2.6860)	(0.0594,0.0598)	(49.1427,40.3539)
Bush R.	(0.8858,0.8922)	(1.8011,2.3498)	(0.1090,0.1017)	(2.1012,2.5281)	(0.1229,0.1135)	(26.4053,25.8072)
Gunpowder R.	(0.0647,0.0535)	(0.5028,0.6381)	(0.0185,0.0150)	(0.4385,0.4197)	(0.0451,0.0453)	(27.7806,26.4902)
South R.	(0.1141,0.0711)	(1.0163,1.2951)	(0.0538,0.0516)	(0.8464,0.8738)	(0.0667,0.0632)	(23.7436,14.3373)
Piscataway R.	(0.4604,0.4396)	(3.3839,3.3781)	(0.0414,0.0428)	(3.7830,3.7361)	(0.0782,0.0882)	(26.4851,24.6814)
Mattawoman C.	(0.0984,0.0919)	(1.8191,1.5988)	(0.1002,0.0977)	(1.6432,1.3970)	(0.1394,0.1345)	(18.1706,10.7982)
Corrotoman R.	(0.0605,0.0547)	(0.6748,0.7305)	(0.0414,0.0449)	(0.5454,0.5219)	(0.0429,0.0436)	(12.7431,7.3679)
Chickahominy R.	(0.0656,0.0659)	(0.1914,0.1568)	(0.0365,0.0253)	(0.3223,0.4886)	(0.0352,0.0443)	(26.0526,26.0285)
Nanticoke R.	(0.1189,0.0979)	(1.4959,1.4710)	(0.0743,0.0627)	(1.2518,1.2843)	(0.0799,0.0784)	(28.8704,26.7130)
Manokin R.	(0.1235,0.0830)	(1.4136,1.8581)	(0.1448,0.1620)	(1.6160,1.6766)	(0.1647,0.1807)	(24.0913,19.3087)
Big Annemessix R.	(0.2729,0.1772)	(1.7622,2.3882)	(0.1833,0.1897)	(2.4569,2.5141)	(0.2211,0.2241)	(15.2829,11.0865)
Patapsco R.	(3.5756,3.5692)	(2.1879,2.3088)	(0.2286,0.2232)	(5.6865,5.7518)	(0.3230,0.3106)	(23.8751,19.4416)
Anacostia R.	(0.3184,0.3556)	(0.4647,0.3999)	(0.0518,0.0492)	(1.1469,1.2848)	(0.0810,0.0730)	(90.8186,88.8498)
Elizabeth S.	(0.5307,1.0394)	(1.1256,1.9357)	(0.3627,0.9572)	(1.7113,3.0640)	(0.5050,1.3484)	(9.2259,12.2521)
Chester R.	(0.1045,0.0948)	(1.1741,2.3536)	(0.0708,0.0593)	(1.0956,1.8124)	(0.0979,0.1032)	(74.9775,73.3785)
Pocomock R.	(0.0780,0.0690)	(0.6219,1.1817)	(0.0874,0.0947)	(0.6916,1.0027)	(0.1296,0.1363)	(16.5084,14.6002)

MBM-7 vs MBM-6

Comparison between MBM-6 and MBM-7 simulations

❖ MBM-7 results are mostly comparable to MBM-6.

- ❑ For most variables, the RMSEs are very close between two MBM results.
- ❑ Compared to MBM-6, MBM-7 has slightly larger errors for TP and PO4. On the other hand, NO3, DOC and DON has some improvements.

In brackets, the 1st number is MBM (P6) error, and 2nd number is current MBM (P7) error.

Major Variables

RMSE	temp	salt	chla	DO	TN	TP
surface	(0.770, 0.770)	(1.082, 1.082)	(12.776, 12.637)	(1.192, 1.175)	(0.334, 0.319)	(0.044, 0.047)
bottom	(0.987, 0.987)	(1.602, 1.602)	(12.296, 12.595)	(1.510, 1.504)	(0.365, 0.370)	(0.060, 0.063)

Bias	temp	salt	chla	DO	TN	TP
surface	(-0.212, -0.212)	(-0.372, -0.372)	(0.174, 0.606)	(-0.210, -0.153)	(-0.095, -0.005)	(0.002, 0.007)
bottom	(0.085, 0.085)	(-0.781, -0.781)	(1.493, 2.211)	(0.469, 0.375)	(-0.079, 0.021)	(-0.011, -0.004)

MBM-7 better

Close (<5%)

MBM-6 better

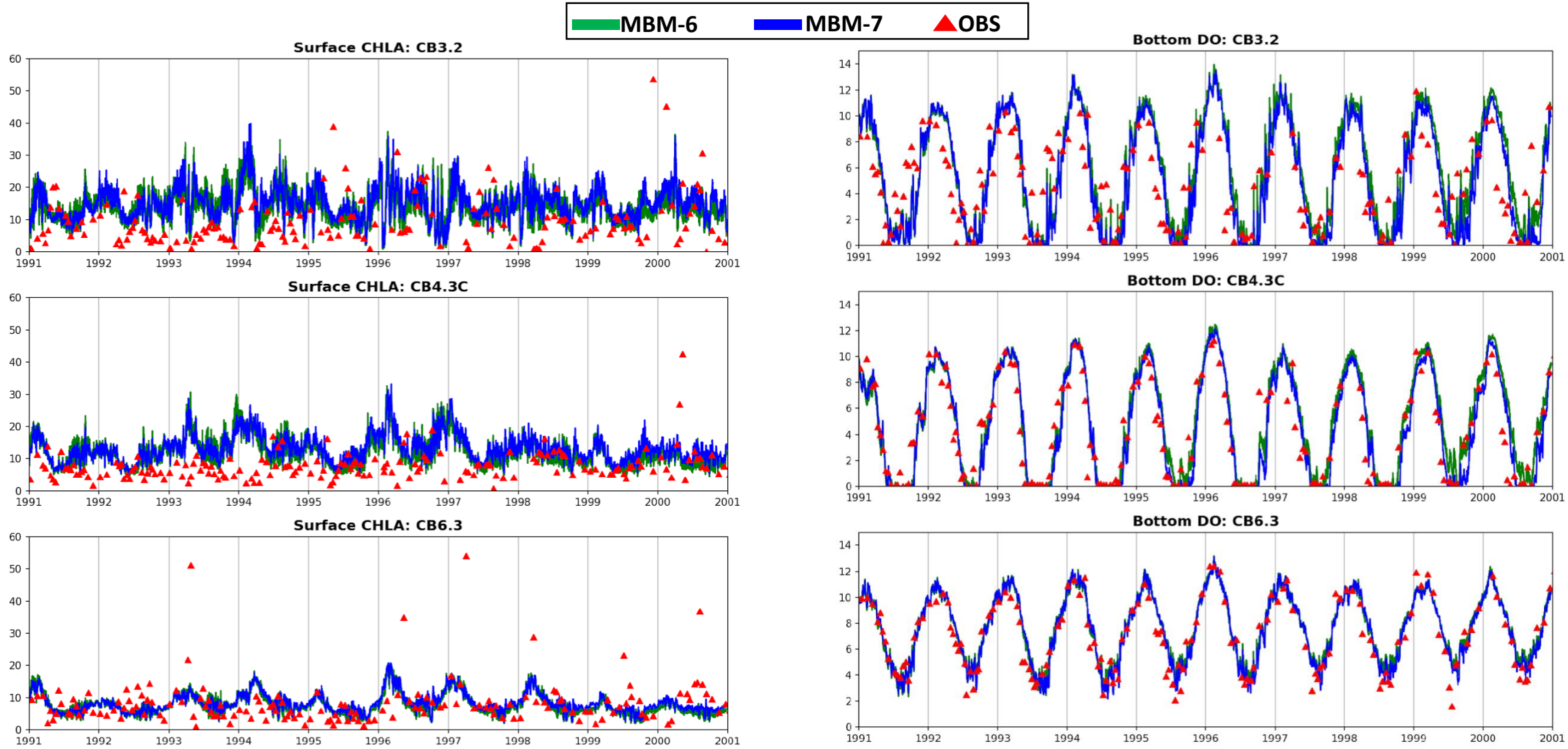
Nutrients

RMSE	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(0.234, 0.221)	(0.059, 0.059)	(0.020, 0.020)	(2.016, 1.908)	(0.170, 0.149)	(0.012, 0.012)	(1.506, 1.467)	(0.176, 0.173)	(0.036, 0.038)
bottom	(0.222, 0.216)	(0.085, 0.088)	(0.022, 0.023)	(1.932, 1.819)	(0.176, 0.155)	(0.012, 0.012)	(1.906, 1.929)	(0.220, 0.222)	(0.058, 0.058)

Bias	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(-0.082, -0.022)	(-0.013, -0.010)	(0.003, 0.004)	(-1.518, -1.552)	(-0.065, -0.053)	(-0.002, -0.002)	(-0.330, 0.177)	(-0.078, -0.061)	(-0.013, -0.010)
bottom	(-0.052, 0.006)	(-0.015, -0.002)	(0.003, 0.006)	(-1.395, -1.417)	(-0.067, -0.056)	(-0.003, -0.002)	(-0.474, 0.142)	(-0.089, -0.070)	(-0.026, -0.023)

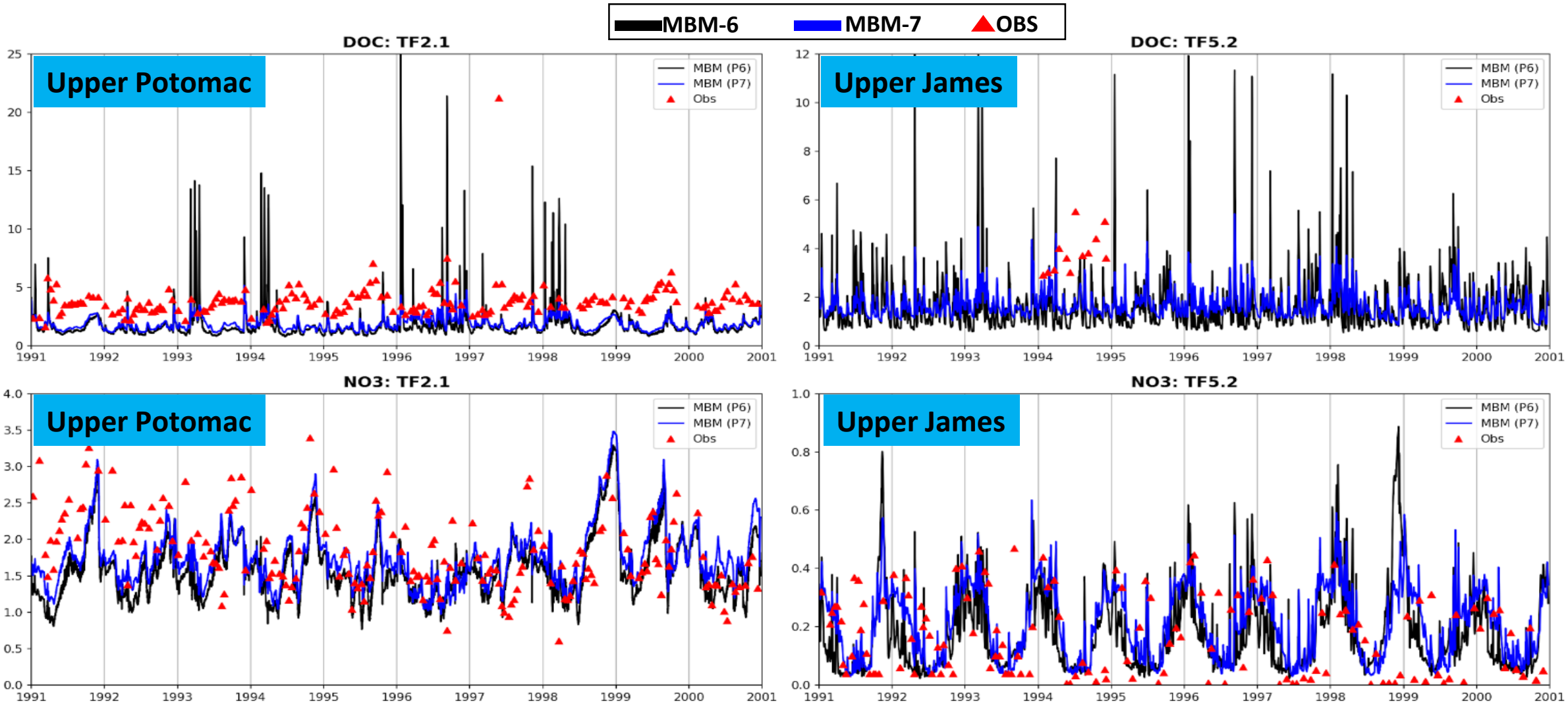
Comparison for Chl-a and DO time series

- Variabilities of Chl-a and DO are similar at most stations.
- Minor differences in the bottom DO can be identified in the MBM-7, in part due to recent calibration



Improvements in Phase-7 nutrient loadings

- Phase-7 WSM loading removes some unrealistic nutrient spikes. This improvement is evident in DOC simulation, but can be also seen for other variables in other regions (not shown here)
- Some improvement on NO3 is also observed



MBM-7 vs CH3D

Comparison between CH3D and MBM-7: Major Variables

- ❑ We comprehensively reviewed all WQ variables and processes to ensure MBM represents well the physical and WQ processes
- ❑ Overall, MBM-7 skill is satisfactory, and comparable to CH3D-ICM

MBM-7 better | **Close (<10%)** | **CH3D better**

All CBP Stations (115)

RMSE	temp	salt	chla	DO	TN	TP
surface	(1.668, 0.770)	(2.074, 1.082)	(12.694, 12.637)	(1.413, 1.175)	(0.370, 0.319)	(0.052, 0.047)
bottom	(1.858, 0.987)	(2.193, 1.602)	(12.083, 12.595)	(1.837, 1.504)	(0.489, 0.370)	(0.066, 0.063)

Bias	temp	salt	chla	DO	TN	TP
surface	(0.140, -0.212)	(0.664, -0.372)	(-2.065, 0.606)	(0.204, -0.153)	(0.051, -0.005)	(0.011, 0.007)
bottom	(0.312, 0.085)	(-0.045, -0.781)	(-2.010, 2.211)	(0.538, 0.375)	(0.187, 0.021)	(0.002, -0.004)

Main-Bay Channel stations (24)

RMSE	temp	salt	chla	DO	TN	TP
surface	(1.484, 0.588)	(2.574, 0.927)	(7.081, 6.896)	(1.238, 1.106)	(0.179, 0.195)	(0.025, 0.033)
bottom	(1.819, 0.962)	(2.256, 1.574)	(7.805, 8.044)	(1.411, 1.403)	(0.247, 0.249)	(0.029, 0.035)

Bias	temp	salt	chla	DO	TN	TP
surface	(0.505, -0.108)	(1.811, -0.017)	(1.184, 1.445)	(-0.405, -0.488)	(-0.020, 0.077)	(0.015, 0.025)
bottom	(0.753, 0.294)	(0.193, -0.263)	(-0.525, 2.002)	(0.299, -0.071)	(0.050, 0.136)	(0.005, 0.018)

In brackets, the 1st number is CH3D error, and 2nd number is MBM-7

Comparison between CH3D and MBM-7: Nutrient Species

- The two models produced comparable results for nutrient species

MBM-7 better | **Close (<10%)** | **CH3D better**

All CBP Stations (115)

RMSE	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(0.231, 0.221)	(0.069, 0.059)	(0.017, 0.020)	(1.815, 1.908)	(0.179, 0.149)	(0.018, 0.012)	(1.357, 1.467)	(0.206, 0.173)	(0.044, 0.038)
bottom	(0.207, 0.216)	(0.110, 0.088)	(0.021, 0.023)	(1.763, 1.819)	(0.180, 0.155)	(0.017, 0.012)	(1.707, 1.929)	(0.232, 0.222)	(0.066, 0.058)

Bias	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(-0.028, -0.022)	(-0.008, -0.010)	(0.002, 0.004)	(-0.926, -1.552)	(-0.025, -0.053)	(0.008, -0.002)	(-0.980, 0.177)	(-0.145, -0.061)	(-0.034, -0.010)
bottom	(-0.011, 0.006)	(0.022, -0.002)	(0.005, 0.006)	(-0.899, -1.417)	(-0.034, -0.056)	(0.006, -0.002)	(-0.916, 0.142)	(-0.123, -0.070)	(-0.047, -0.023)

Main-Bay Channel stations (24)

RMSE	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(0.152, 0.156)	(0.028, 0.028)	(0.010, 0.014)	(1.282, 1.242)	(0.110, 0.100)	(0.009, 0.007)	(0.855, 0.809)	(0.126, 0.084)	(0.019, 0.017)
bottom	(0.094, 0.142)	(0.093, 0.083)	(0.015, 0.018)	(1.203, 1.189)	(0.115, 0.115)	(0.007, 0.007)	(1.139, 1.153)	(0.155, 0.133)	(0.030, 0.022)

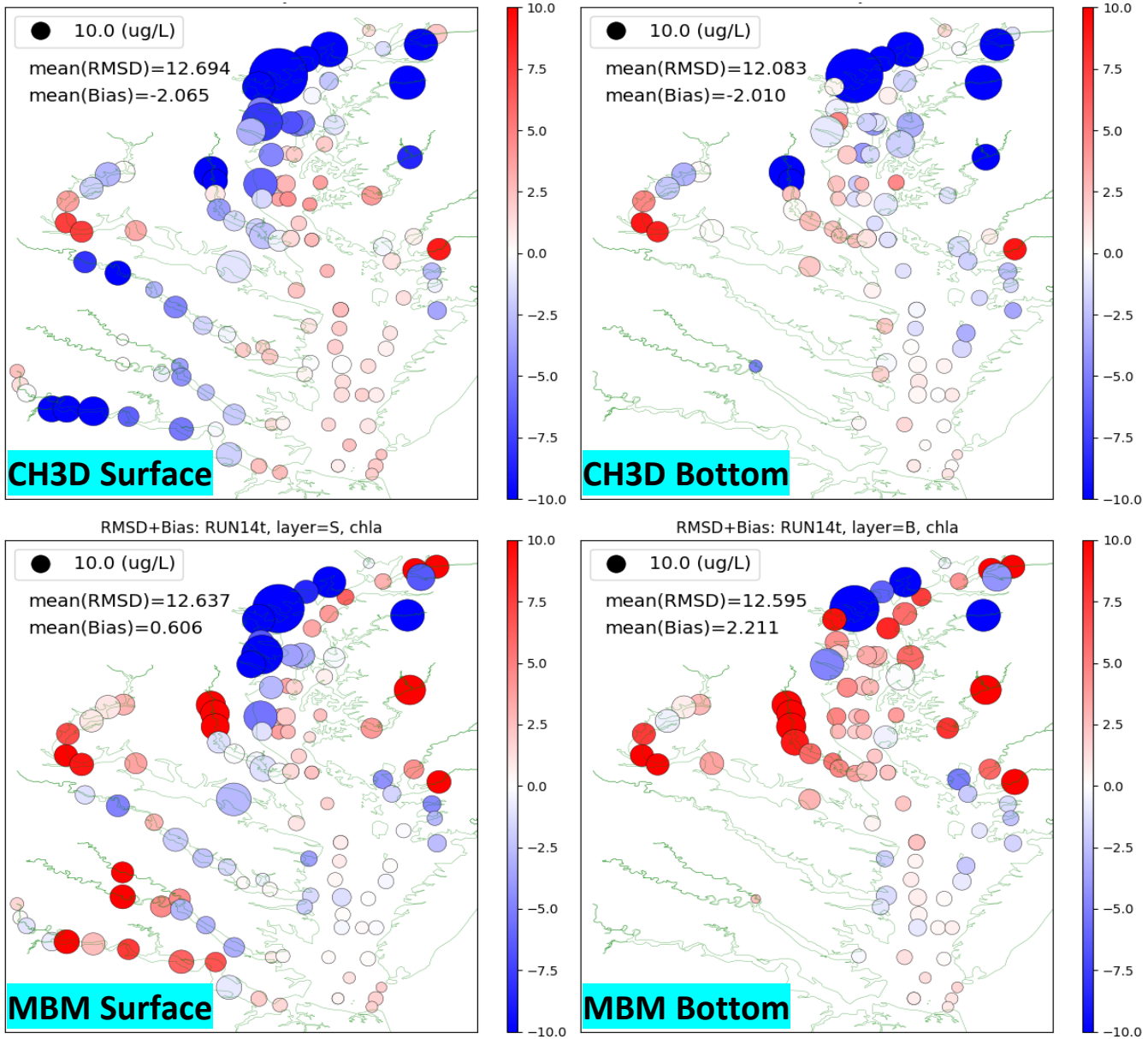
Bias	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(-0.044, -0.004)	(-0.005, 0.002)	(0.003, 0.005)	(-1.032, -1.016)	(-0.051, -0.044)	(0.005, -0.001)	(-0.678, 0.168)	(-0.100, 0.004)	(-0.016, 0.010)
bottom	(-0.009, 0.052)	(0.033, 0.030)	(0.004, 0.008)	(-0.916, -0.896)	(-0.072, -0.071)	(0.002, -0.002)	(-0.574, 0.342)	(-0.079, 0.015)	(-0.023, 0.003)

In brackets, the 1st number is CH3D error, and 2nd number is MBM-7 error

Spatial comparison between CH3D and MBM-7: Chl-a

Chl-a Error

size: RMSE **color**: Bias

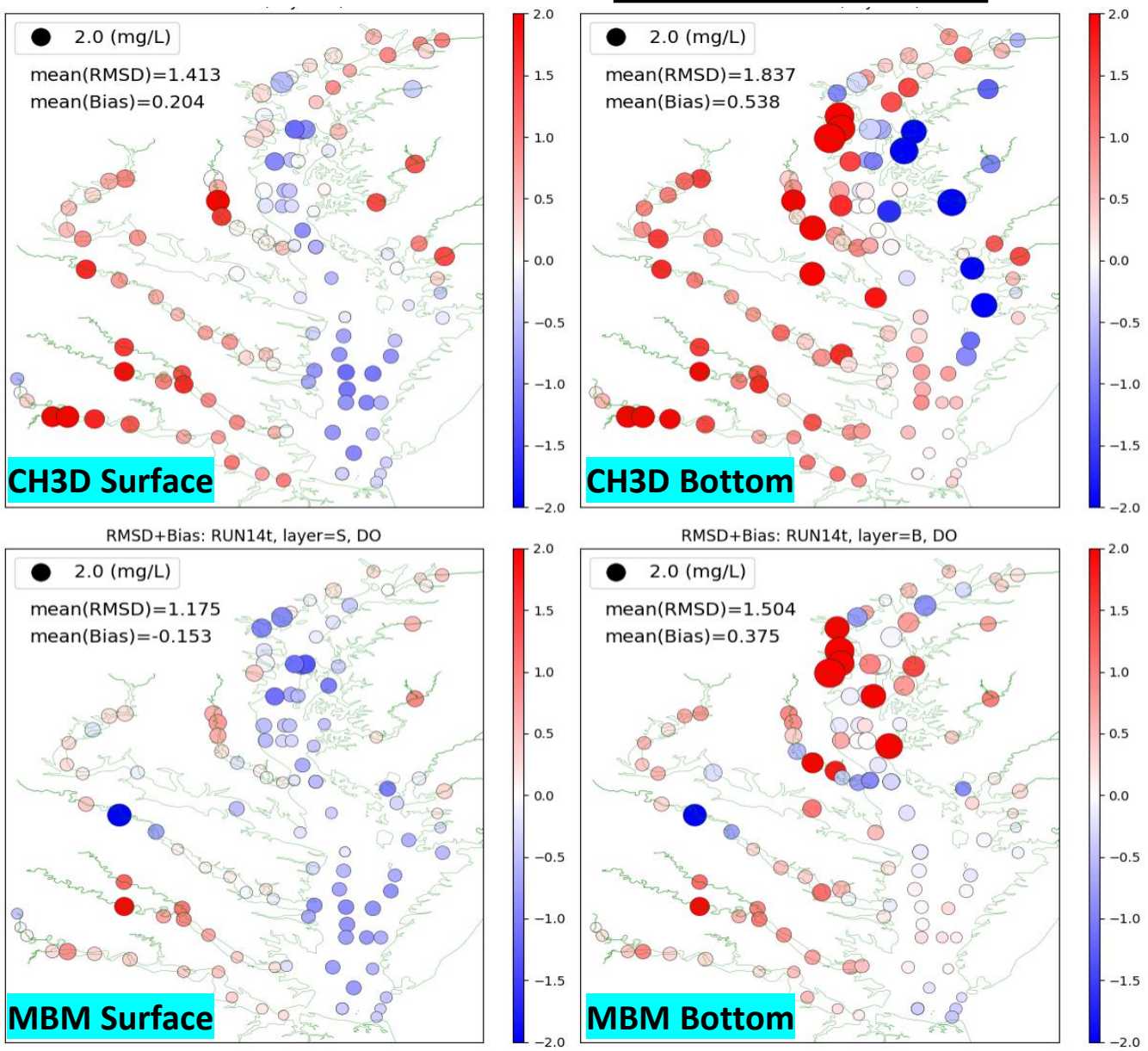


- Chl-a simulation in the MBM is comparable to CH3D both surface and bottom.
- The spatial distributions of errors between the two models are also similar.
- In the shallow regions of upper bay, large errors are found for both models.
- Along the main-bay channel, some overestimation of Chl-a is found in the CH3D surface and MBM bottom.
- In the upper reach of most tributaries, CH3D tends to underestimate, while MBM tends to overestimate.

Comparison between CH3D and MBM-7: DO

DO Error

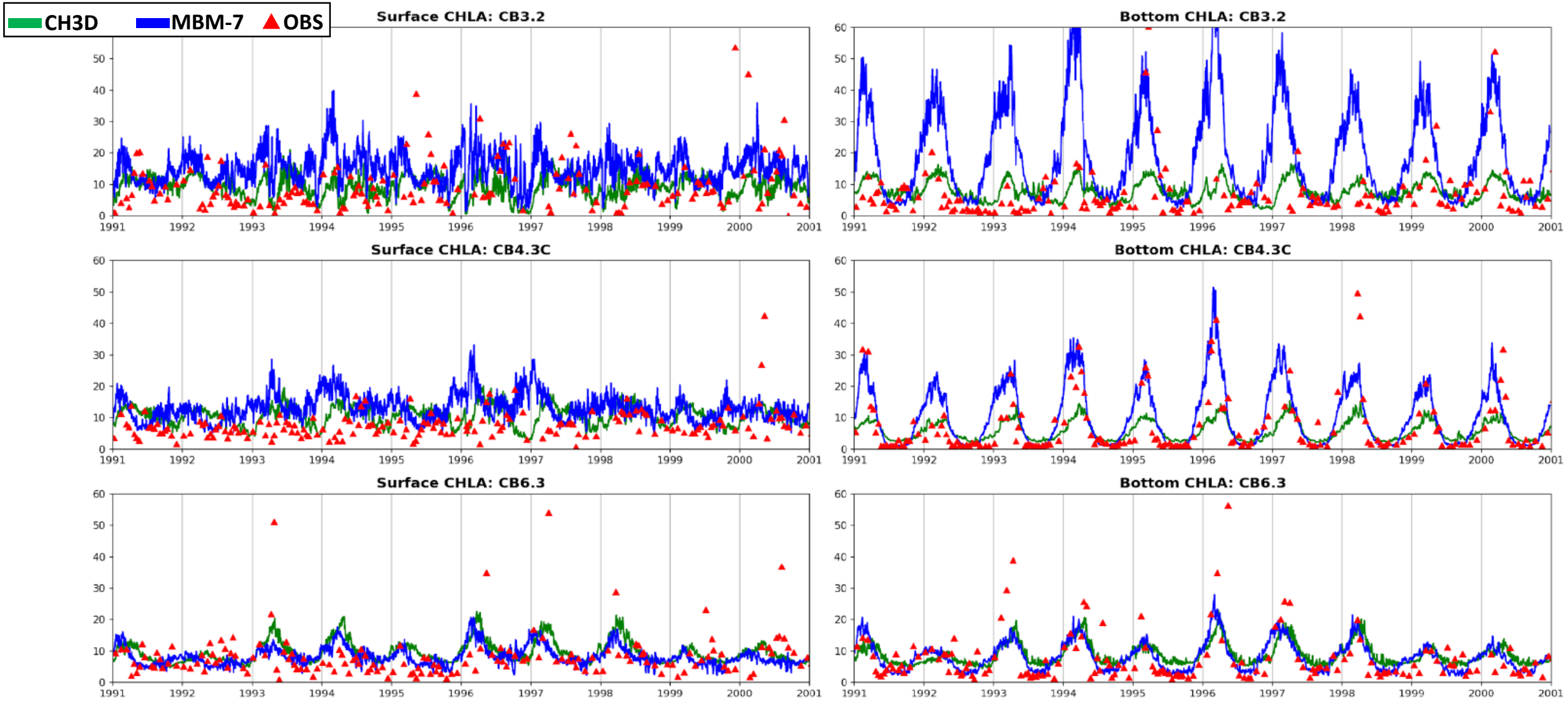
size: RMSE **color**: Bias



- Overall, MBM-7 yielded comparable DO results to CH3D. The spatial distributions of errors between two models are also similar.
- In MBM, surface DO is underestimated for mainstem stations, but overestimated in tributaries.
- In MBM, bottom DO along mainstem is well simulated.
- In most tributaries, MBM seems to have smaller errors for DO simulation compared to CH3D.

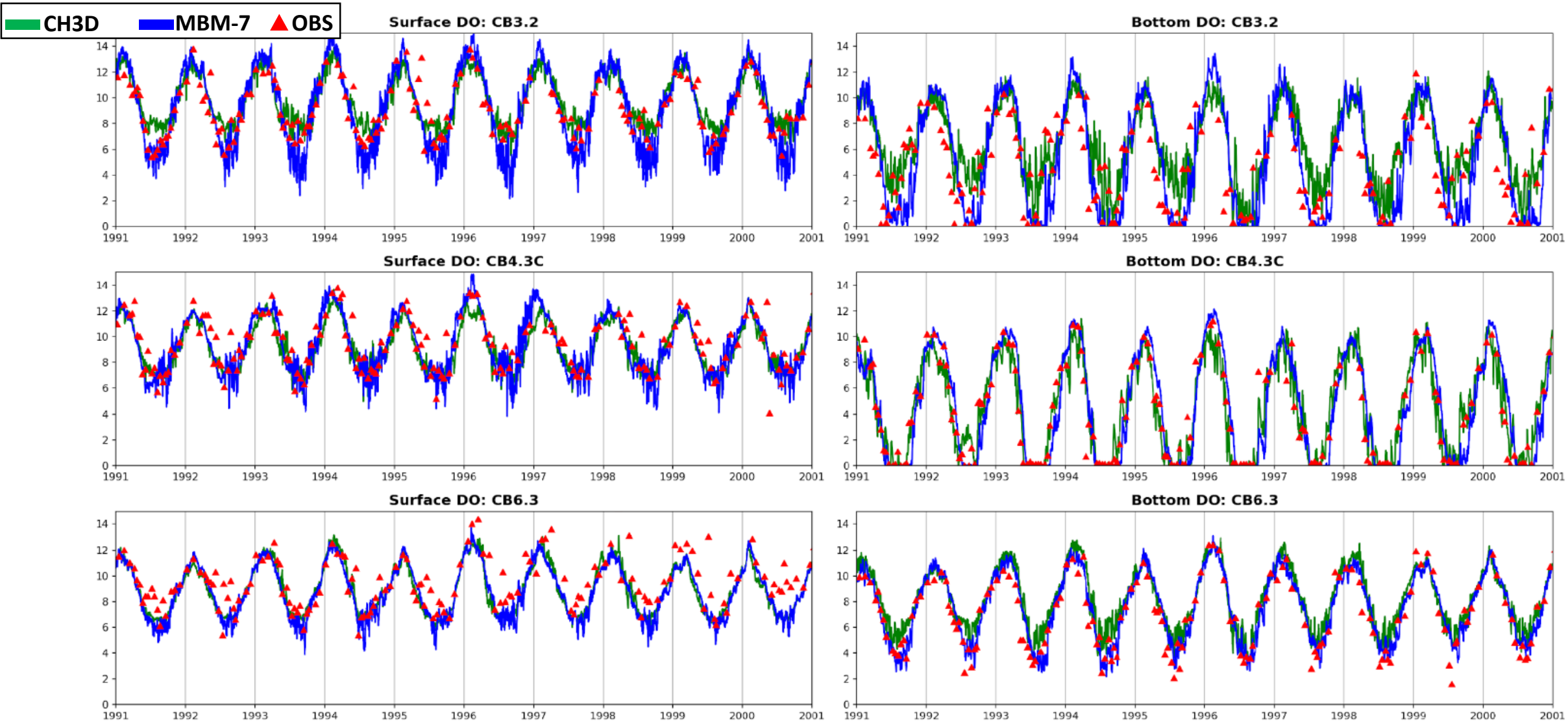
Comparison between CH3D and MBM-7 at key stations: Chl-a

- For surface Chl-a, both models got the magnitude correct, but had some challenges in capturing the variability.
- For bottom Chl-a, MBM simulates well the seasonal variation. At CB3.2, MBM overestimates. At CB4.3C and CB6.3, MBM performance is rather satisfactory.

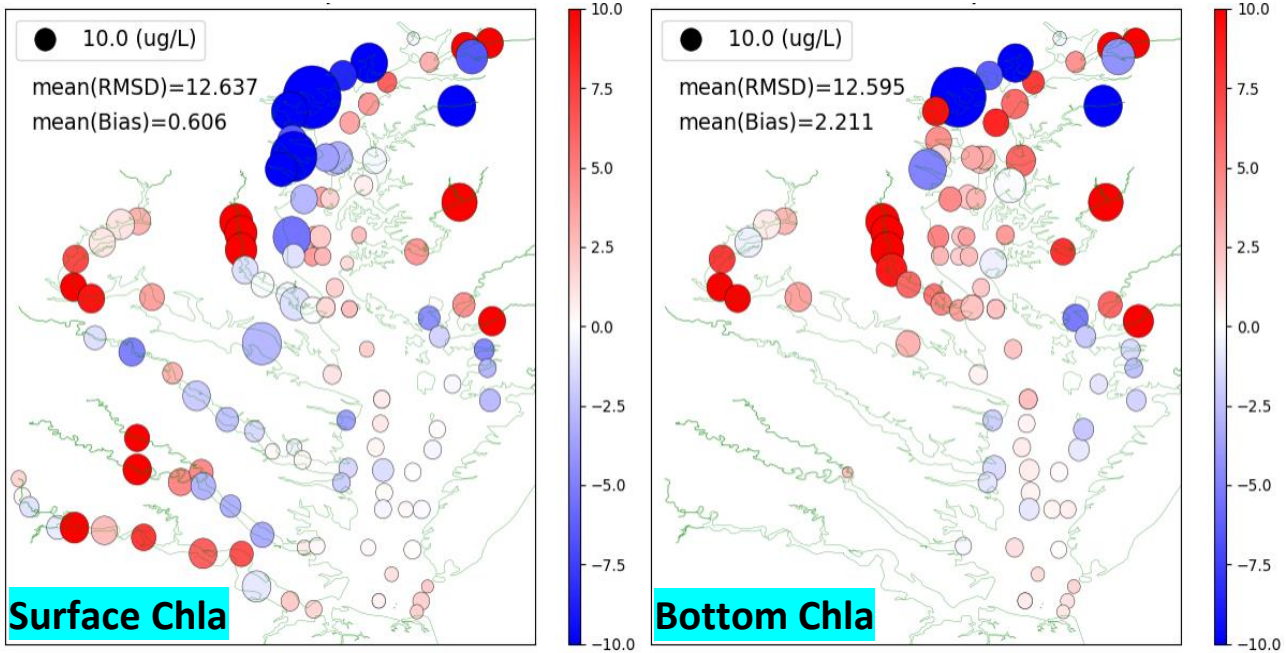


Comparison between CH3D and MBM-7 at key stations: DO

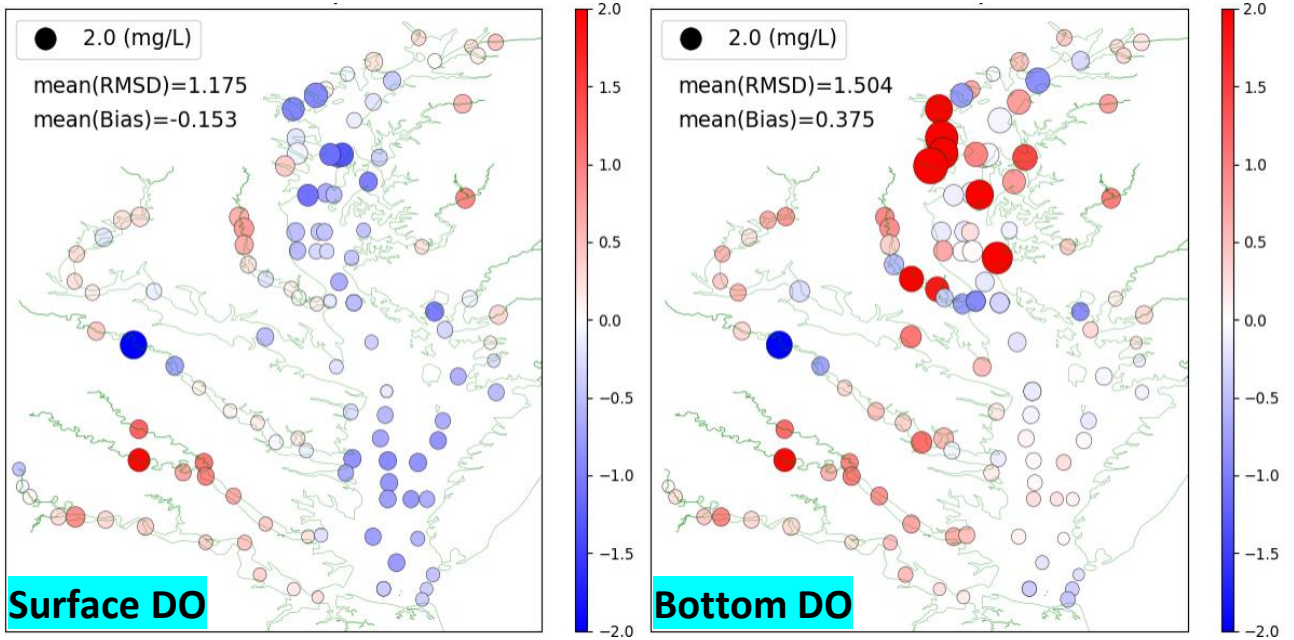
- ❑ Both models reproduced the correct seasonal variation of DO variations on the surface and bottom.
- ❑ At CB3.2, surface DO of MBM was underestimated. It is likely related to the overestimation of Chl-a simulation.
- ❑ For bottom DO at CB3.2 and CB6.3, MBM seems to capture the hypoxia better.
- ❑ For bottom DO at CB4.3C, earlier MBM had phase-lag issue for hypoxia simulation, while the current MBM-7 shows significant improvement



Spatial Distribution of MBM-7 Errors: Chl-a and DO

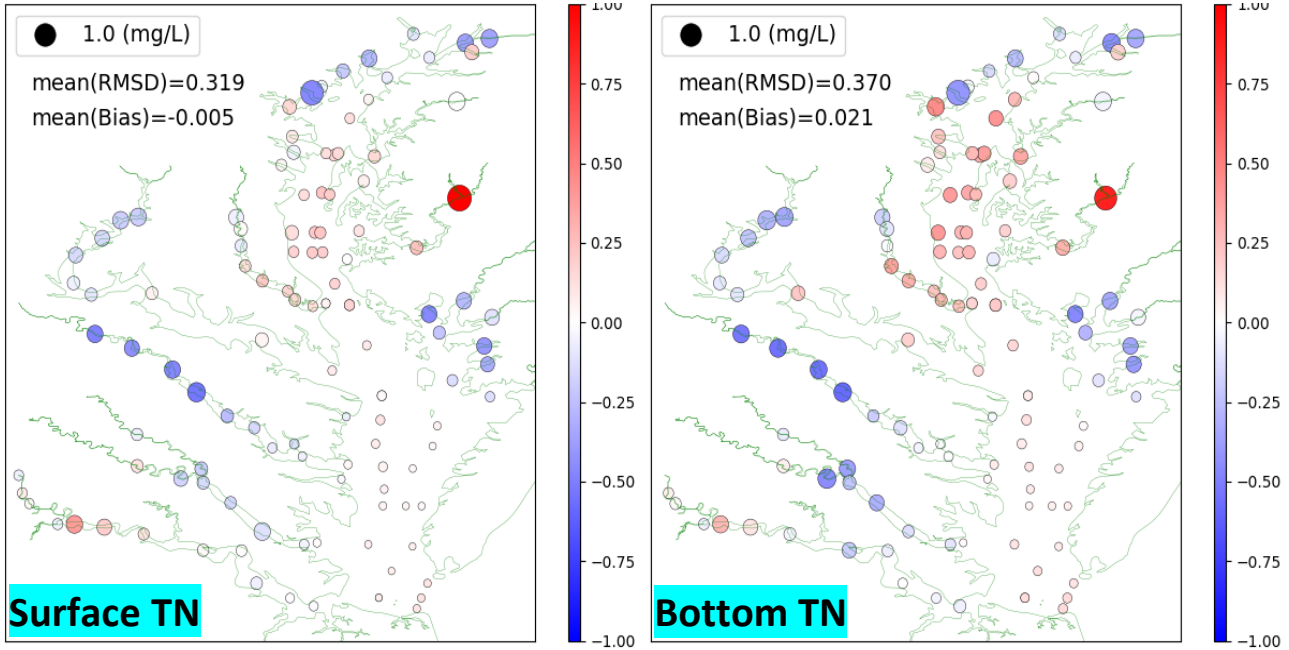


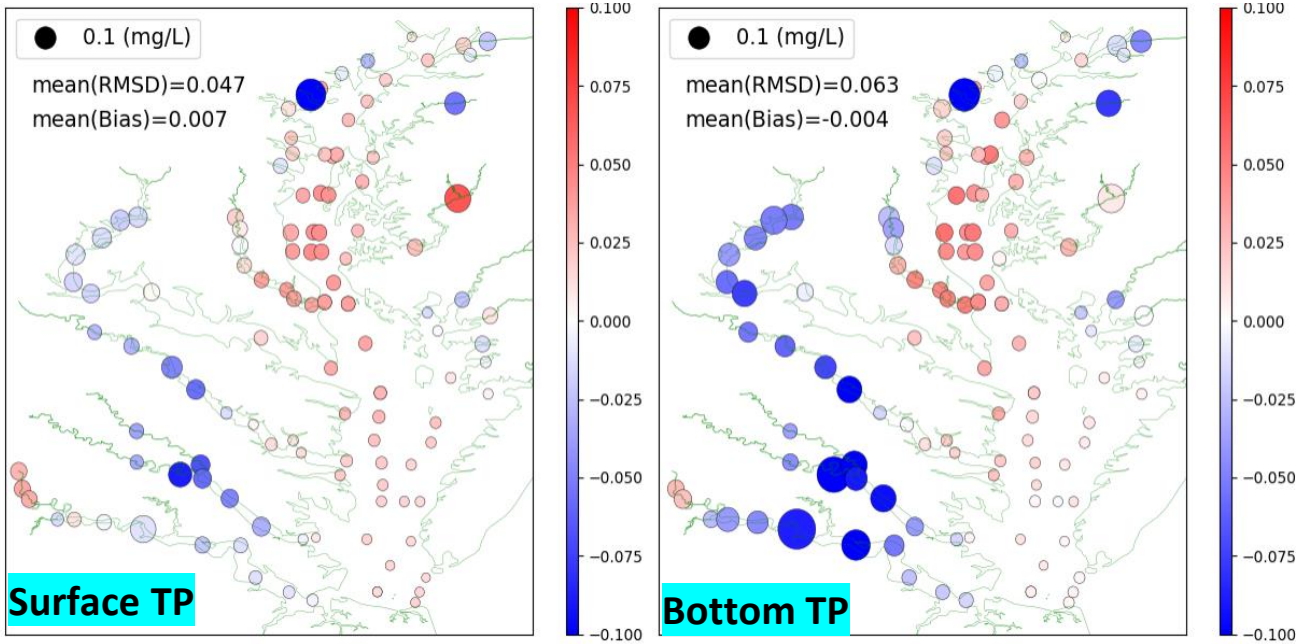
- Along main channel, Chl-a simulation has relatively small errors with some overestimation in the upper Bay region.
- Overestimation of Chl-a is found in upper tributaries. Large underestimation mainly concentrated in the shallow regions of upper Bay.



- Surface DO tends to be underestimated in the mainstem, and slightly overestimated in the tributaries.
- Overall, bottom DO is well simulated in the mainstem. In the tributaries and shallow regions, bottom DO tends to be overestimated (which may be related to living resources).

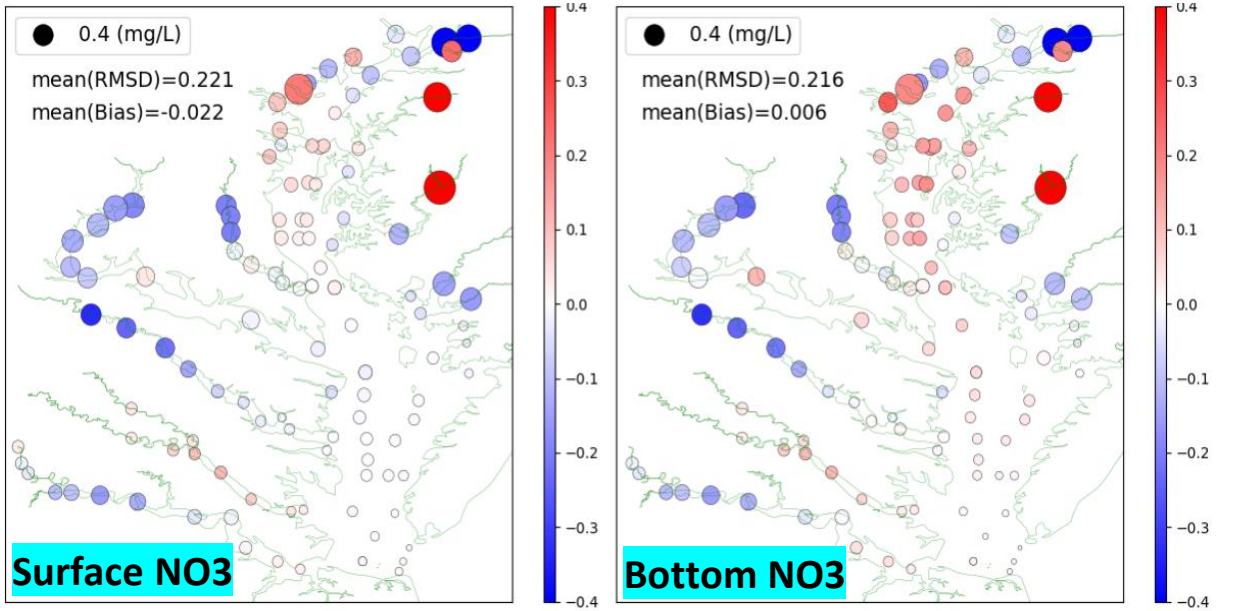
Spatial Distribution Of MBM-7 Errors: TN and TP

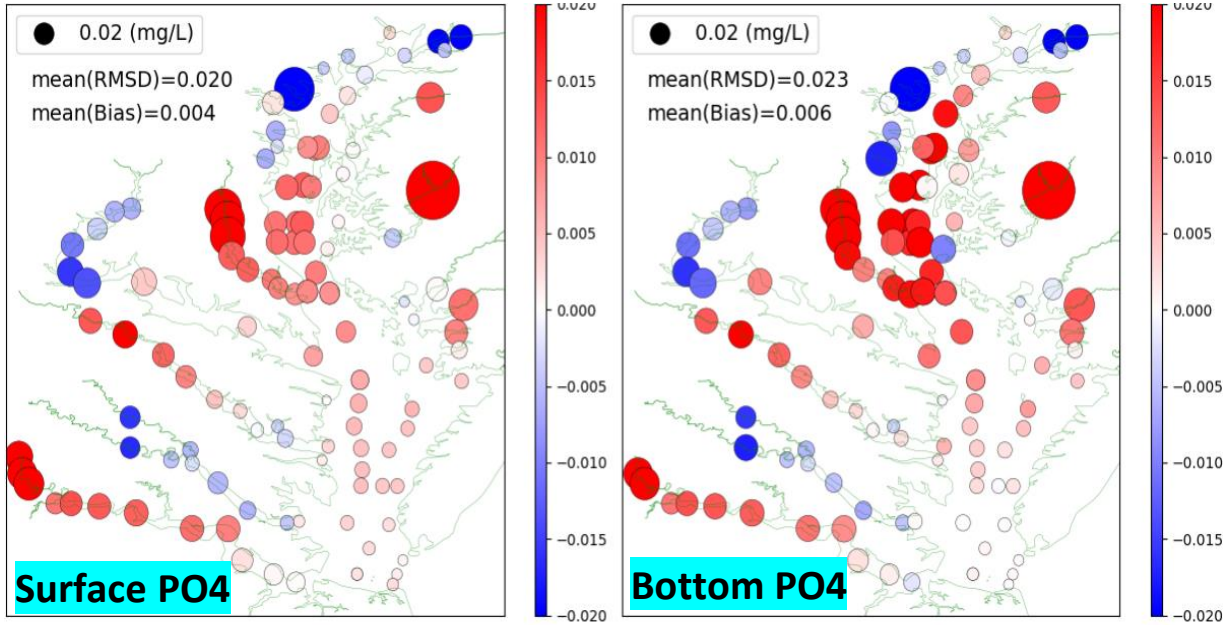


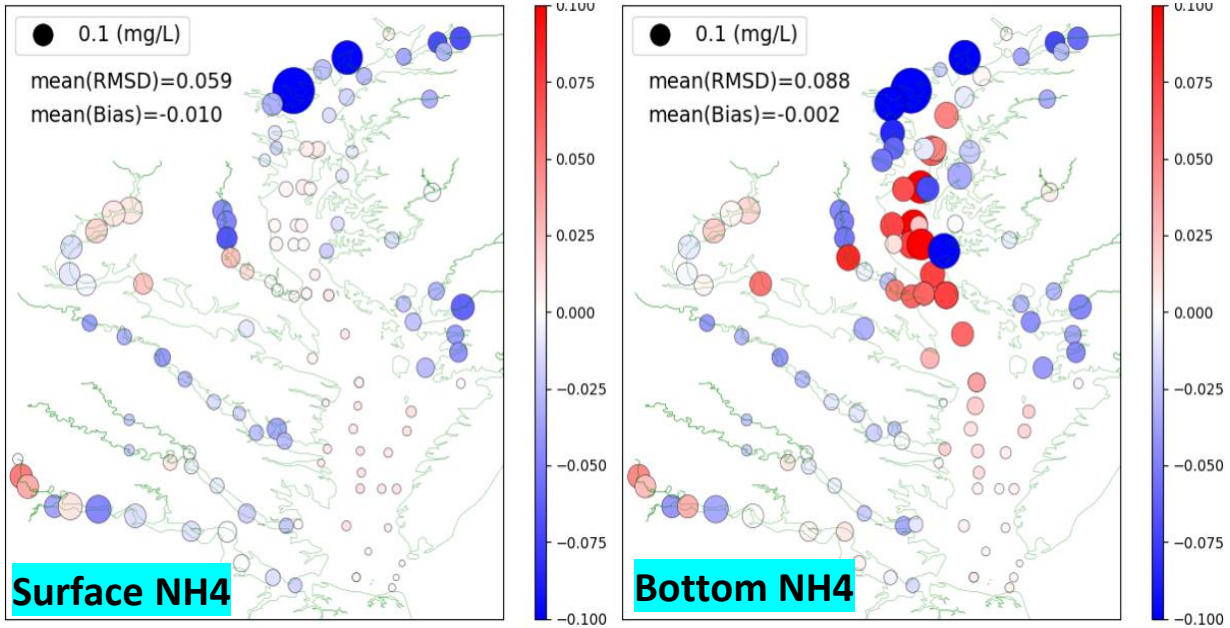


- TN simulation is satisfactory, particularly in the lower Bay region.
- TN overestimation is mainly found around upper and mid bay. TN underestimation is mainly found in the tributaries.
- TP is generally overestimated in the mainstem, and underestimated in some tributaries.

Spatial Distribution Of MBM-7 Errors: NO3, NH4, and PO4



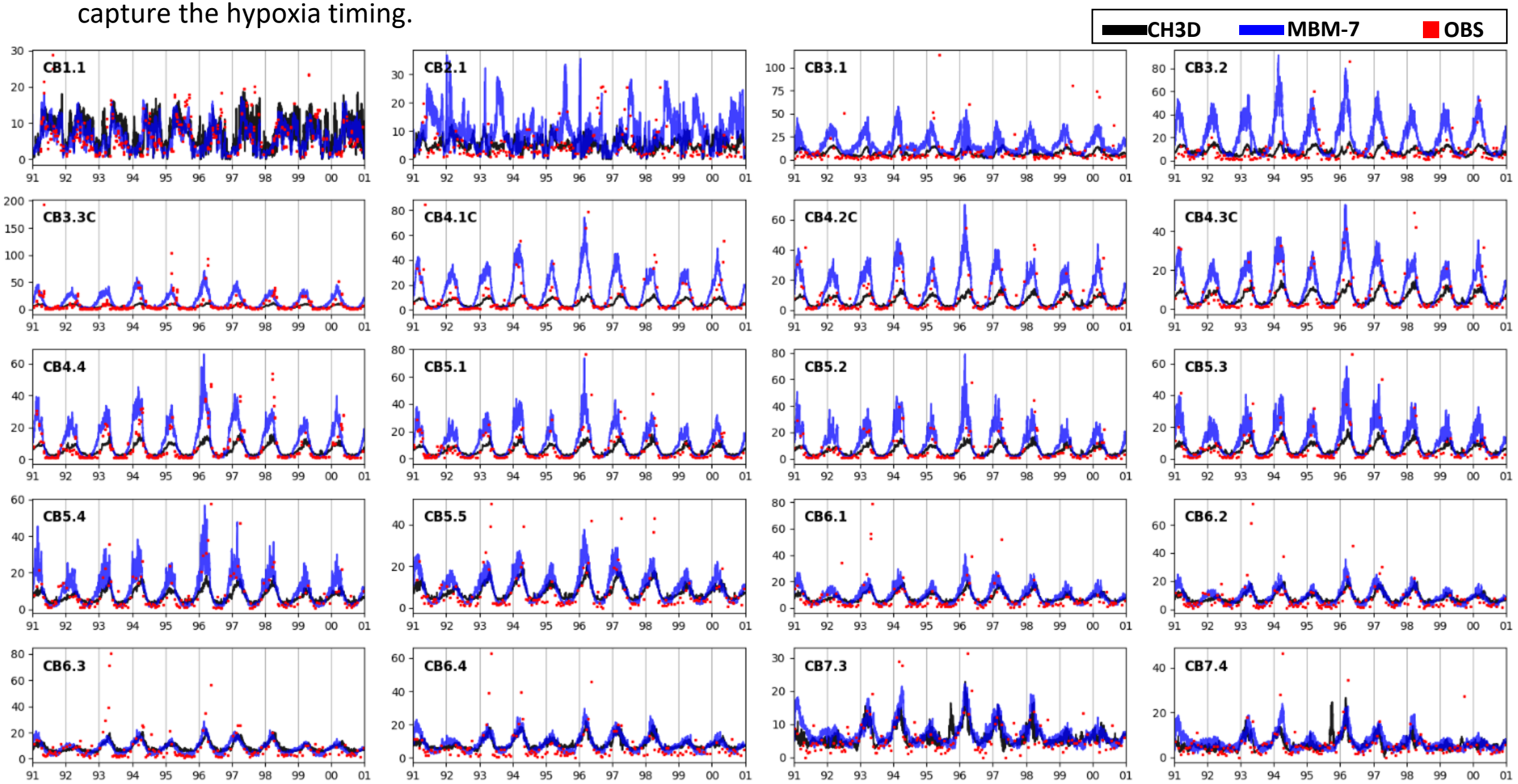




- ❑ NO3 is well simulated. Underestimation is found in some upper tributaries.
- ❑ Overestimation of bottom NH4 is found in the upper and mid bay, and underestimation is found in some shallow areas.
- ❑ For PO4, the MBM simulation tends to be generally overestimated, which warrants further investigation.

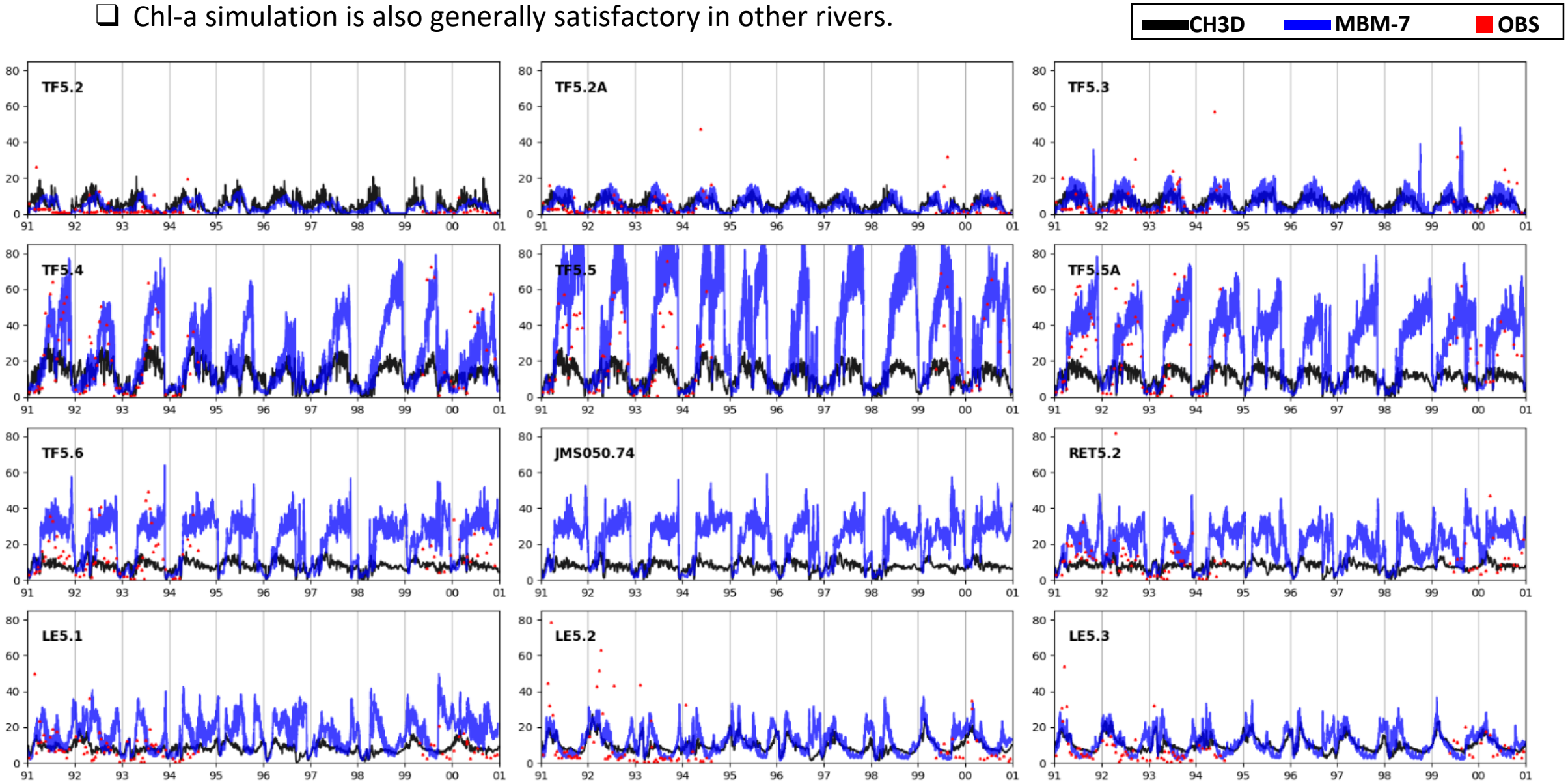
Chl-a Simulation Along Main-Bay Channel

- MBM-7 did a good job in capturing the high Chl-a concentrations in the bottom during spring, which helps capture the hypoxia timing.



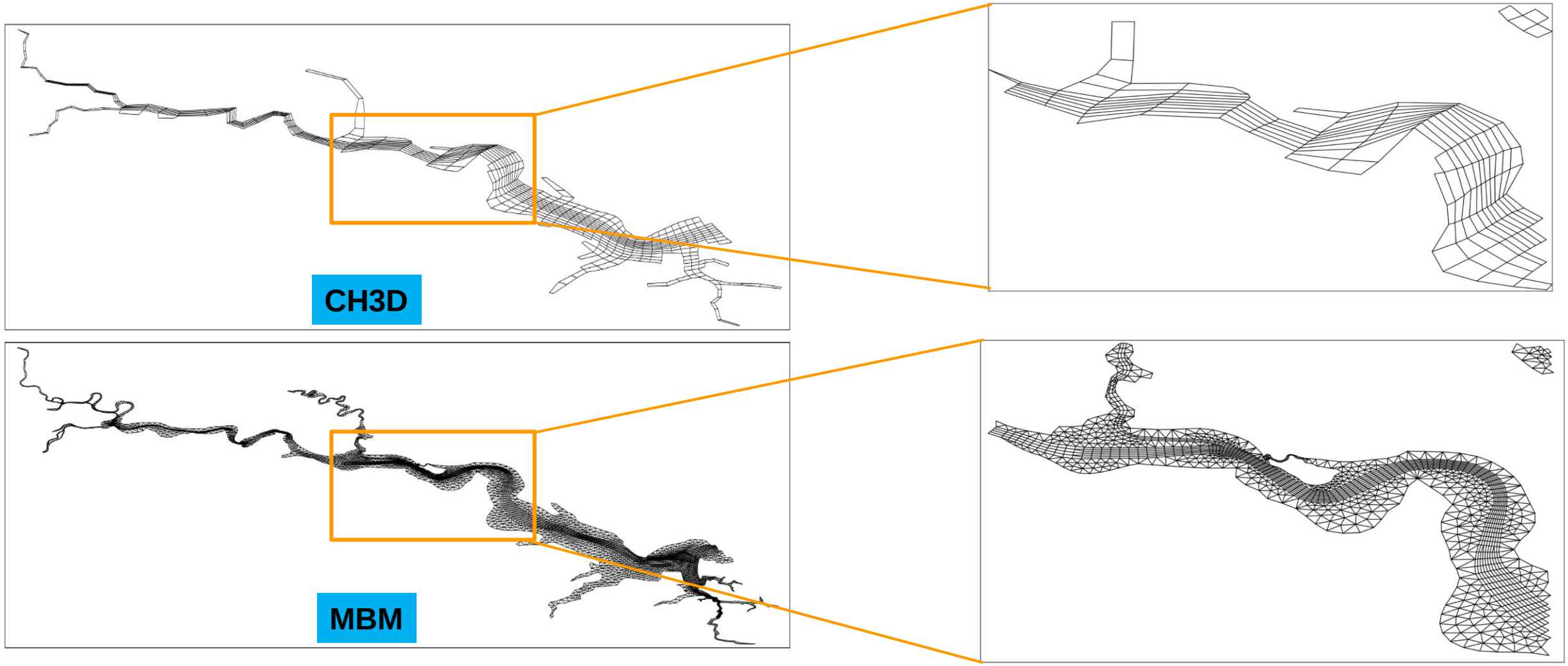
Chl-a Simulation In James River

- MBM also captured the occurrence of the large Chl-a blooms in the mid reach of James River.
- Chl-a simulation is also generally satisfactory in other rivers.



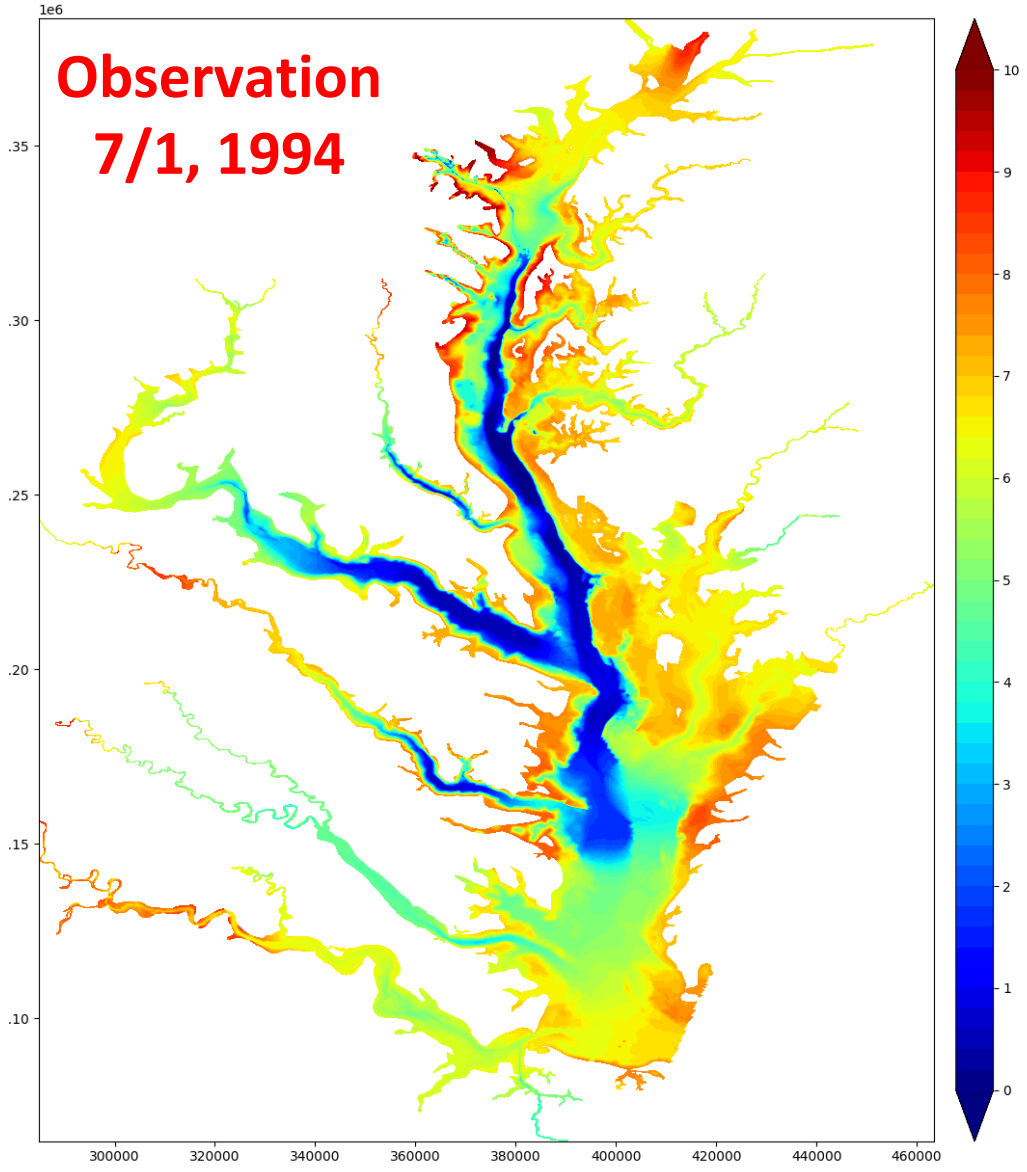
Grid comparison between CH3D and MBM in James River

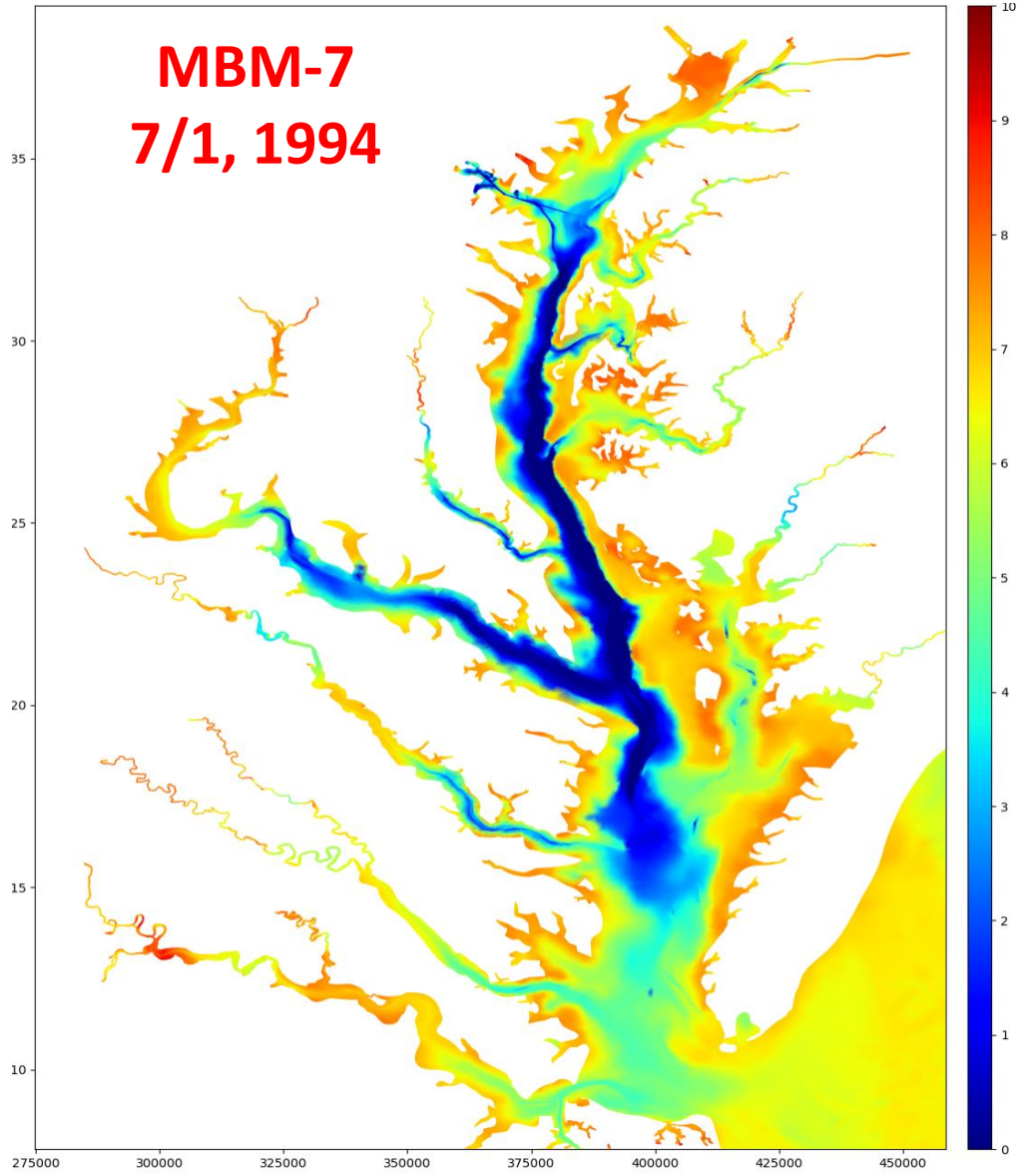
- Compared to CH3D, MBM grid has higher resolution in James River. Both the channels and shallow regions are well represented in MBM grid.
- This pays off in the simulation of productive shallows (including living resources), and helps refine the new TMDL



Spatial Distribution of Bottom DO in Chesapeake Bay

- We interpolated CBP DO observations inside the Bay, and compared with MBM simulation. Overall, the summer hypoxia pattern matches between model and data.



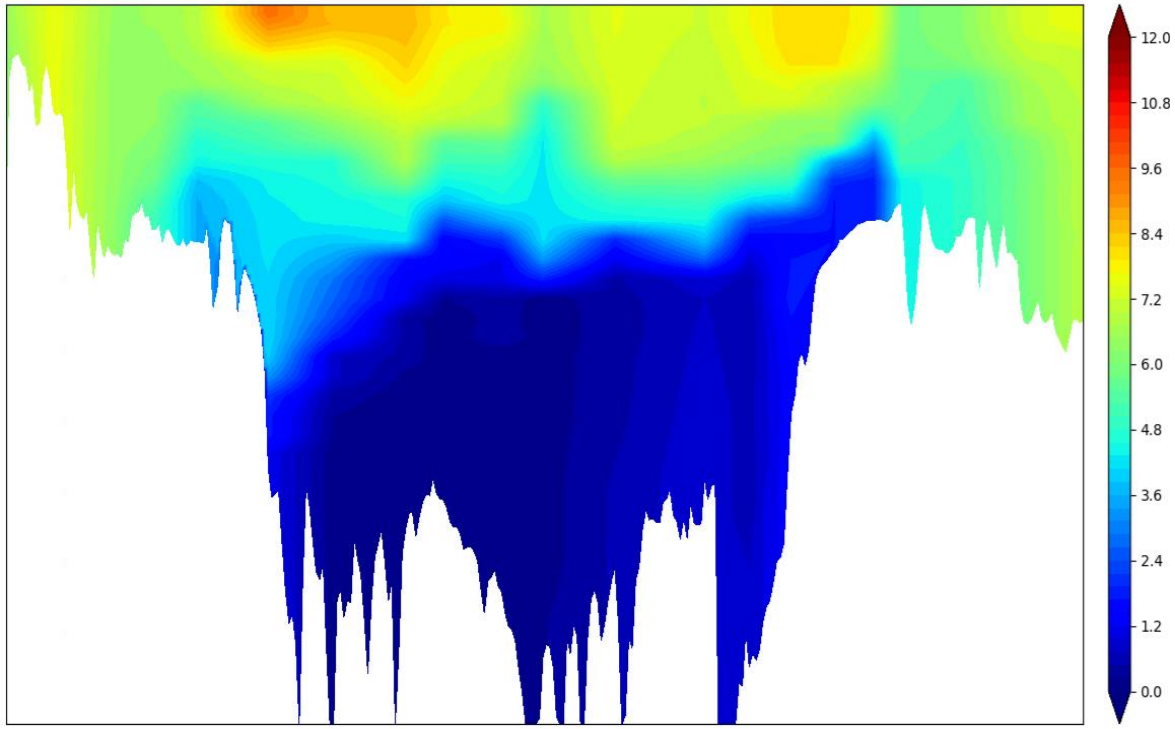


Vertical Profile Of DO Along Main-Bay Channel

- Along the main-bay channel, MBM also captures the hypoxic region fine (model has higher spatial variability due to resolution)

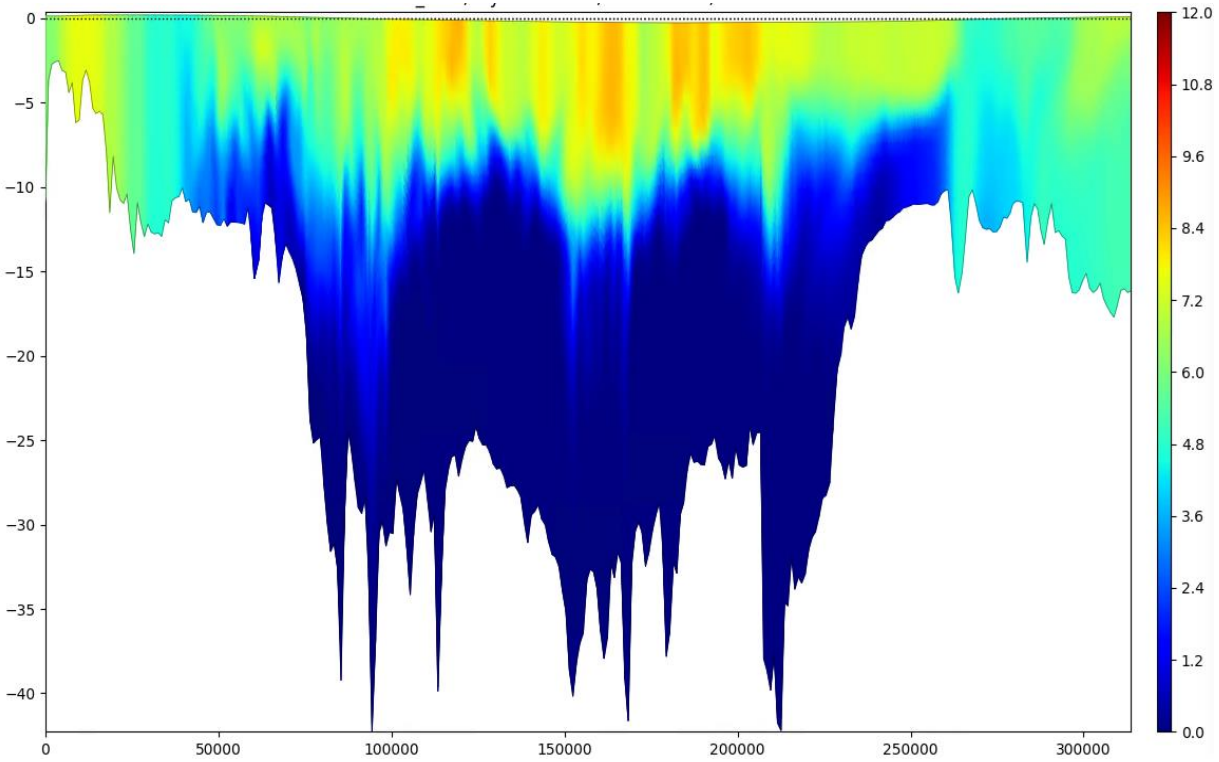
- In the upper bay, there is some underestimation.

Observation 7/1, 1994



Upper Bay ⟷ Lower Bay

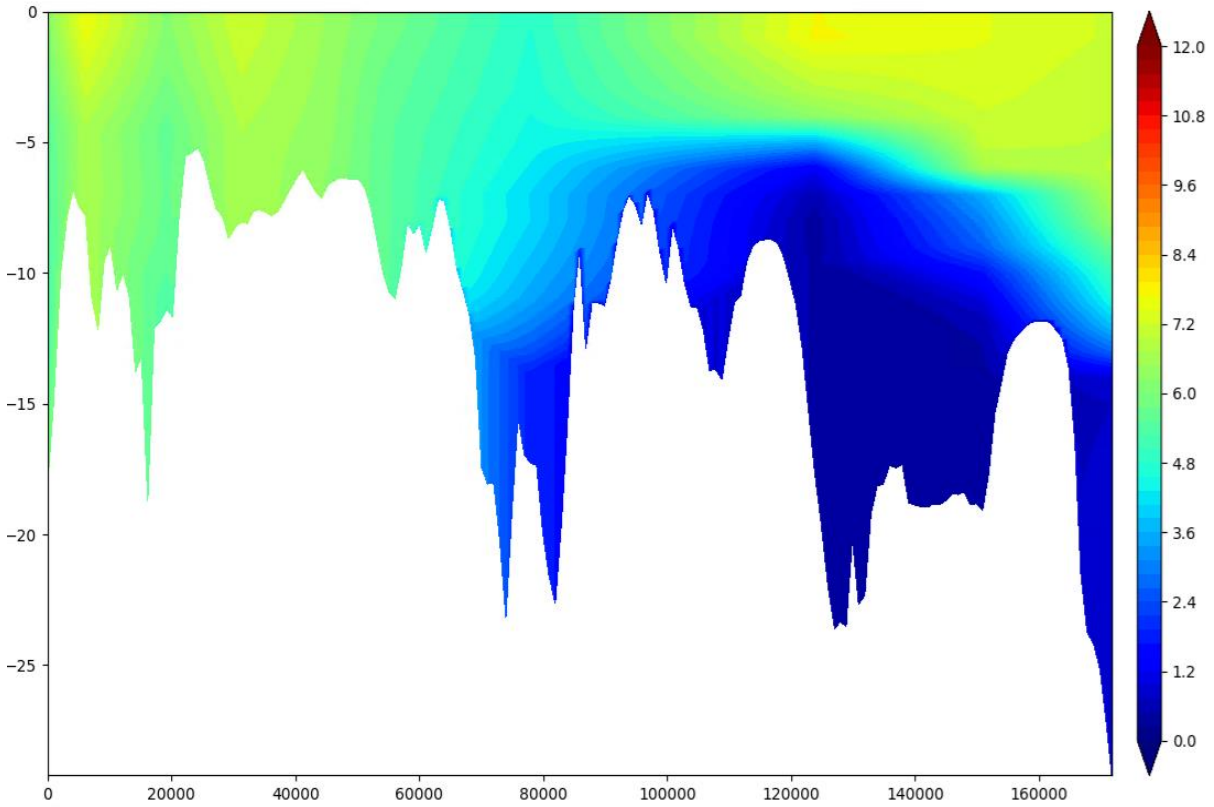
MBM 7/1, 1994



Vertical Profile Of DO Along Potomac River Channel

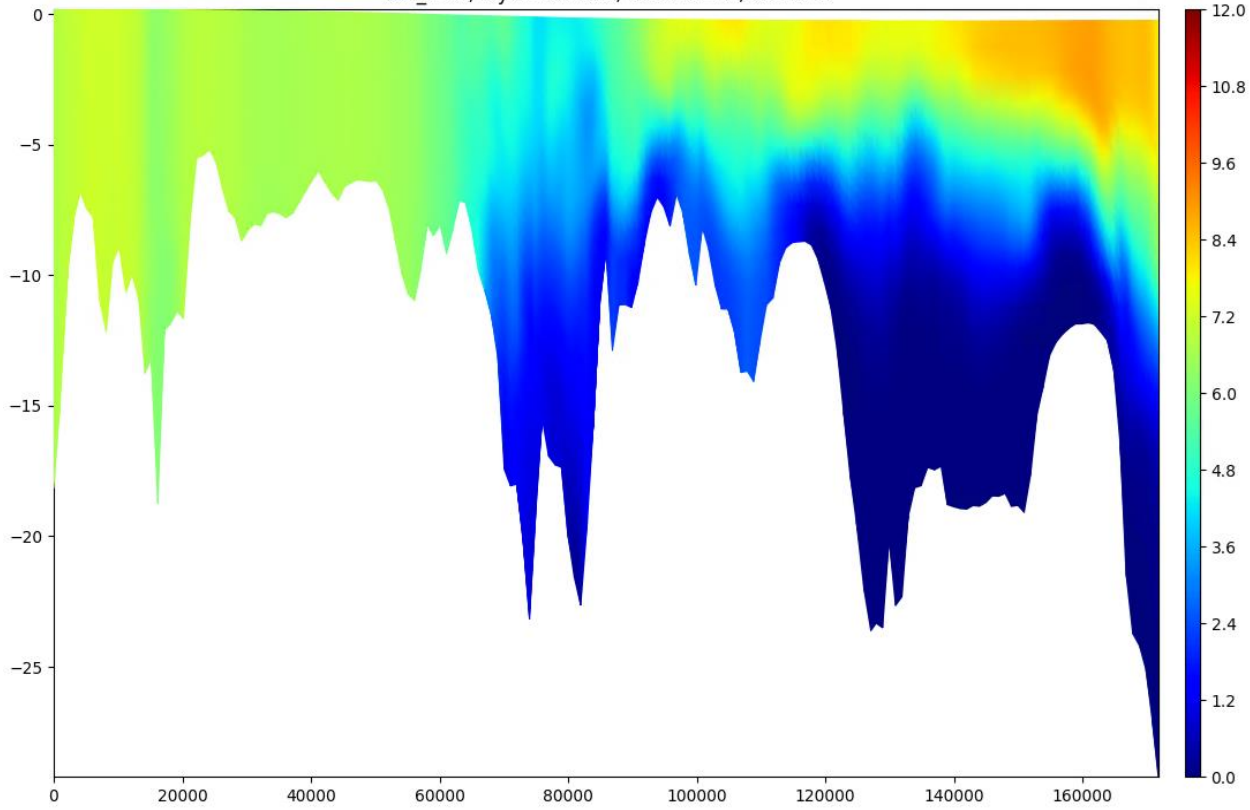
- In Potomac River, the vertical profile of DO is also well simulated

Observation 7/1, 1994



upstream ⟷ downstream

MBM 7/1, 1994



Summary and future work

- In the last quarter, we finished the calibration of the 1st baseline MBM version using a hybrid WSM loading. Then, we switched to pure Phase-7 nutrient loadings.

- The latest MBM results are satisfactory for most variables, and they are generally comparable to CH3D results.

- We compared the MBM simulations with Phase-6 and Phase-7 nutrient inputs. Overall, the results are similar. We also noticed some improvement with the “pure” Phase-7 loading.

- MBM captured the spatial variations Chl-a and DO well, and showed improvement in the tributaries and shallows

- Future work
  - MBM documentation.
  - Continue to improve MBM model skill (PO4; living resources).
  - Continue to work with WSM team to test new beta versions of WSM loadings.