

Appendix C: Verification of Transport Fidelity

This appendix is in connection with Section 3.1.3.1 in the main report – Integration with Hydrodynamic Model. In this study, transport information is calculated by the EFDC model and transferred to WASP via stored output (or linkage file) for use in simulating water column transport of constituents. Key parameters for preparing the linkage file include: (1) the coupling interval NTSMMT, i.e., the number of time steps for EFDC to average and output variables to the linkage file; and (2) the upper limit on the vertical mixing ABMAX, aiming at capping larger vertical mixing coefficient values and maintaining numerical stability in WASP. Determining these parameters needs to consider: 1) the capability for WASP to reproduce conservative tracer transports by EFDC; 2) maintaining mass balance in WASP; 3) controllable WASP computation time; and 4) a manageable linkage file size.

This appendix demonstrates: (1) the parameter selection processes, (2) WASP can reproduce transport predicted by the EFDC and mass can be conserved in WASP, with adequate values of NTSMMT and ABMAX.

1. CONSERVATIVE TRACER SIMULATIONS

Conservative tracer simulations were performed to determine proper values of key parameters that would enable WASP to reproduce transport predicted by EFDC. These simulations were conducted using both EFDC and WASP by releasing continuous and vertically uniform tracers of 100 mg/L at four primary Delaware Estuary River boundaries: Trenton, Schuylkill River, C&D Canal, and ocean (see Figure 3-1 in the main report) for the period of 2019. Benchmarking EFDC and WASP outputs ensures proper hydro-linkage from EFDC to WASP and also validates the prediction of two models under the same input conditions. Parameter NTSMMT was set to be 30; i.e., EFDC averaged and output variables to the linkage file at every 30-time steps. In this application, the time step for EFDC was 10 seconds, resulting linkage output every 300 seconds (every 5 minutes). The upper limit on the vertical mixing coefficient, ABMAX, was set to values of 0.01 and 0.001 m²/s, respectively, for the test simulations presented in this appendix.

Figure 1-1 shows the predicted surface layer tracer concentrations along the navigation channel from the four release scenarios averaged over a low flow period from September 7 to October 7, 2019. The combination of NTSMMT = 30 and ABMAX = 0.01 m²/s produced good agreement in conservative tracer transports between EFDC and WASP, as the two tracer results almost lie on top of each other in Figure 1-1. The other combination of NTSMMT = 30 and ABMAX = 0.001 m²/s generated comparable downstream transports but less desirable upstream transport as those in the first combination with ABMAX = 0.01 m²/s. In terms of computation time, WASP simulation with ABMAX = 0.01 m²/s was three times longer than the WASP simulation with ABMAX = 0.001 m²/s.

Figure 1-2 through Figure 1-17 show time series of surface and depth-averaged tracer concentration comparisons at USGS stations at Ben Franklin, Chester, Reedy Island, as well as NOAA station at Ship John Shoal, from the four release scenarios. Again, WASP tracers with ABMAX = 0.01 m²/s match well with EFDC tracers in almost all plots. WASP tracer results with ABMAX = 0.001 m²/s were in reasonable agreement with EFDC tracers in some locations (e.g., Figure 1-9) and noticeably apart from EFDC tracers in other locations (e.g., Figure 1-10).

Figure 1-1: 3D Longitudinal Profile along Navigation Channel

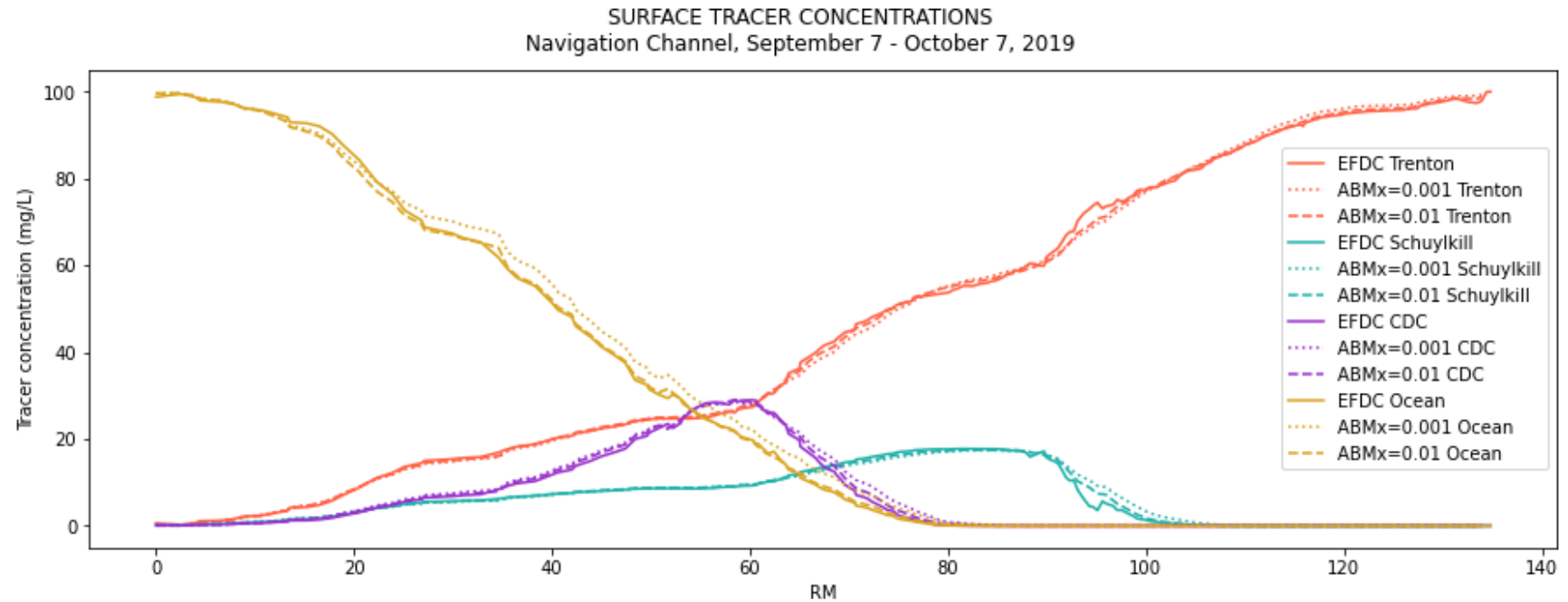
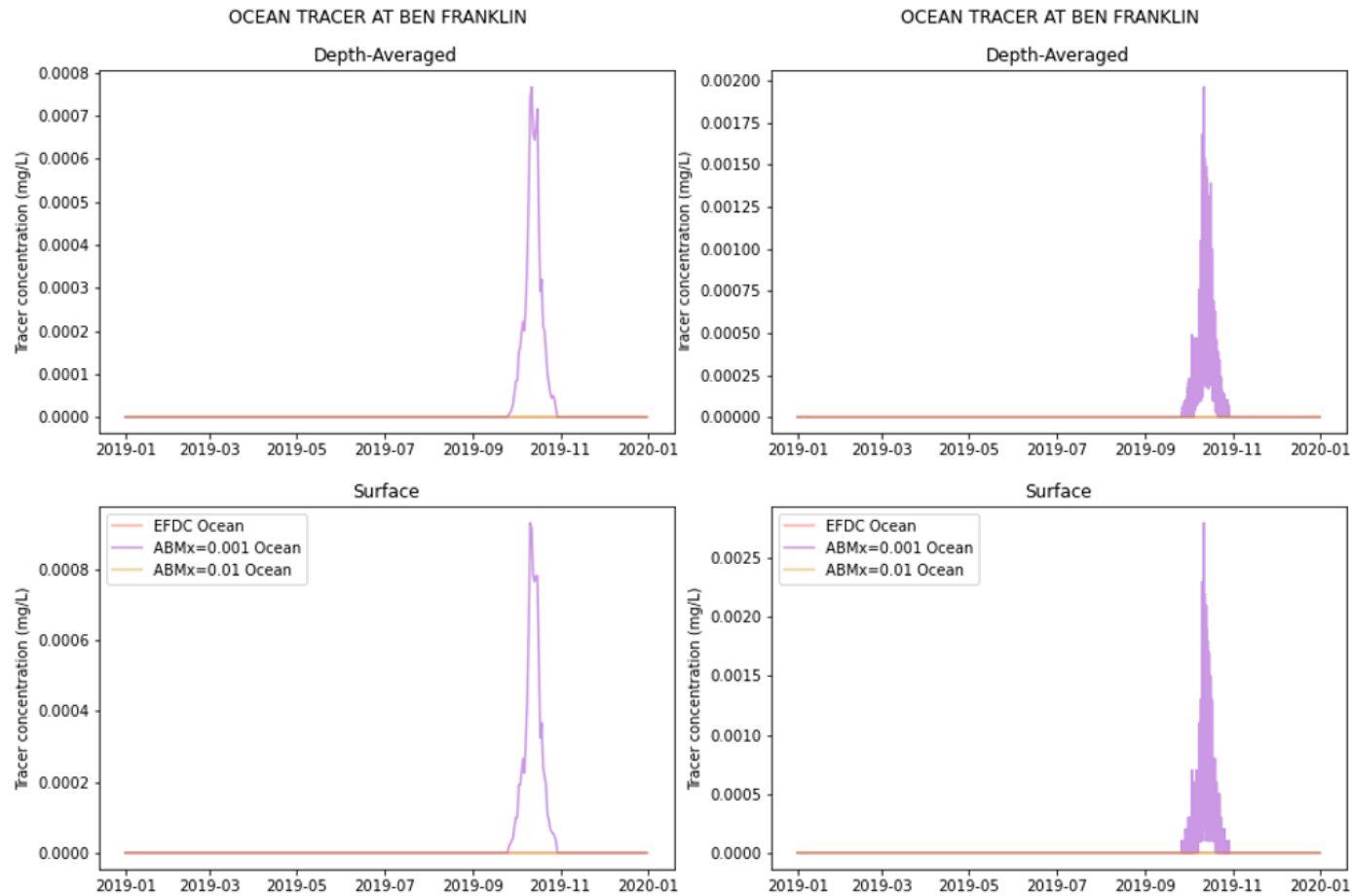


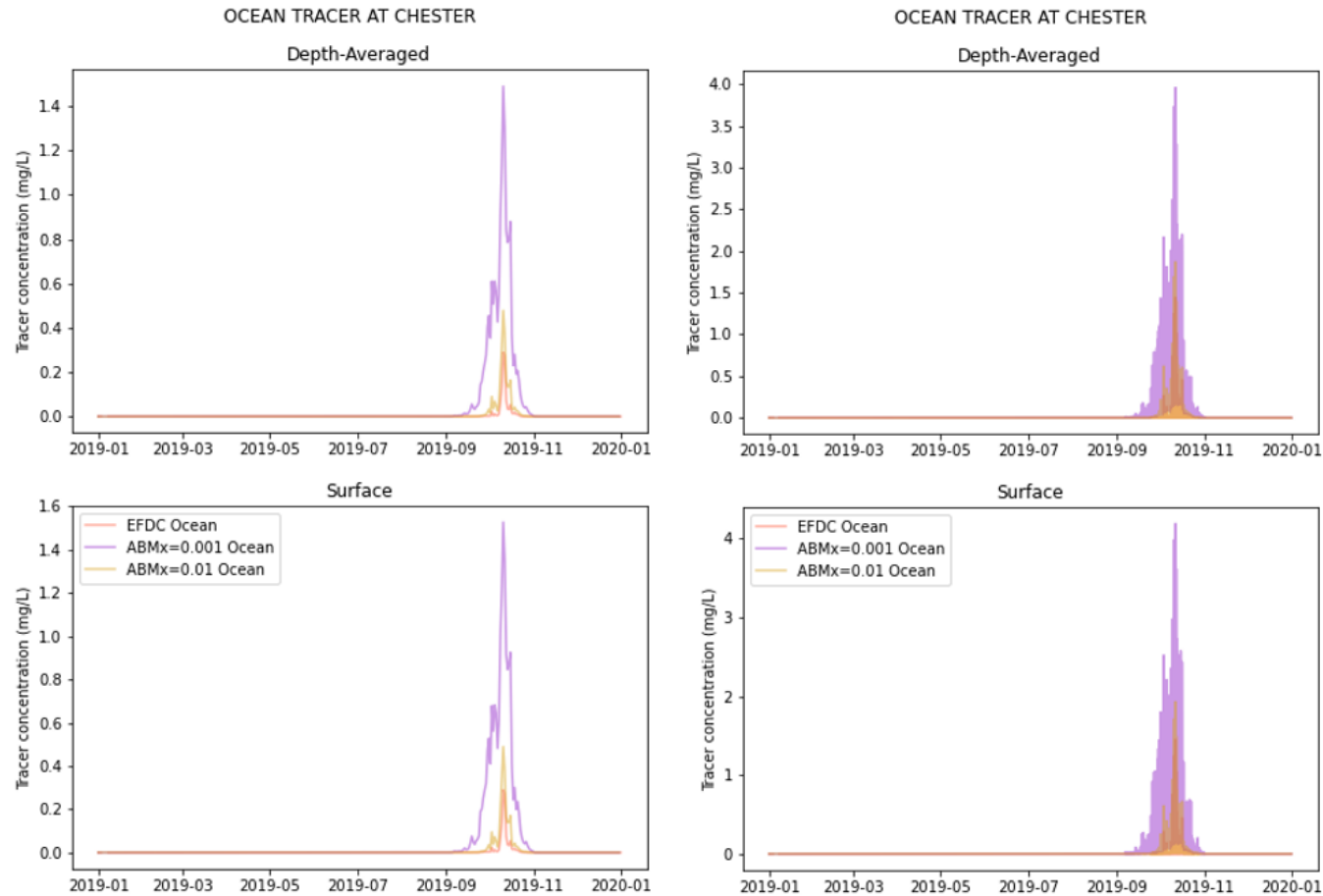
Figure 1-2: Time Series Plots of Ocean Tracer Release – Concentration at Ben Franklin Bridge (RM 100)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

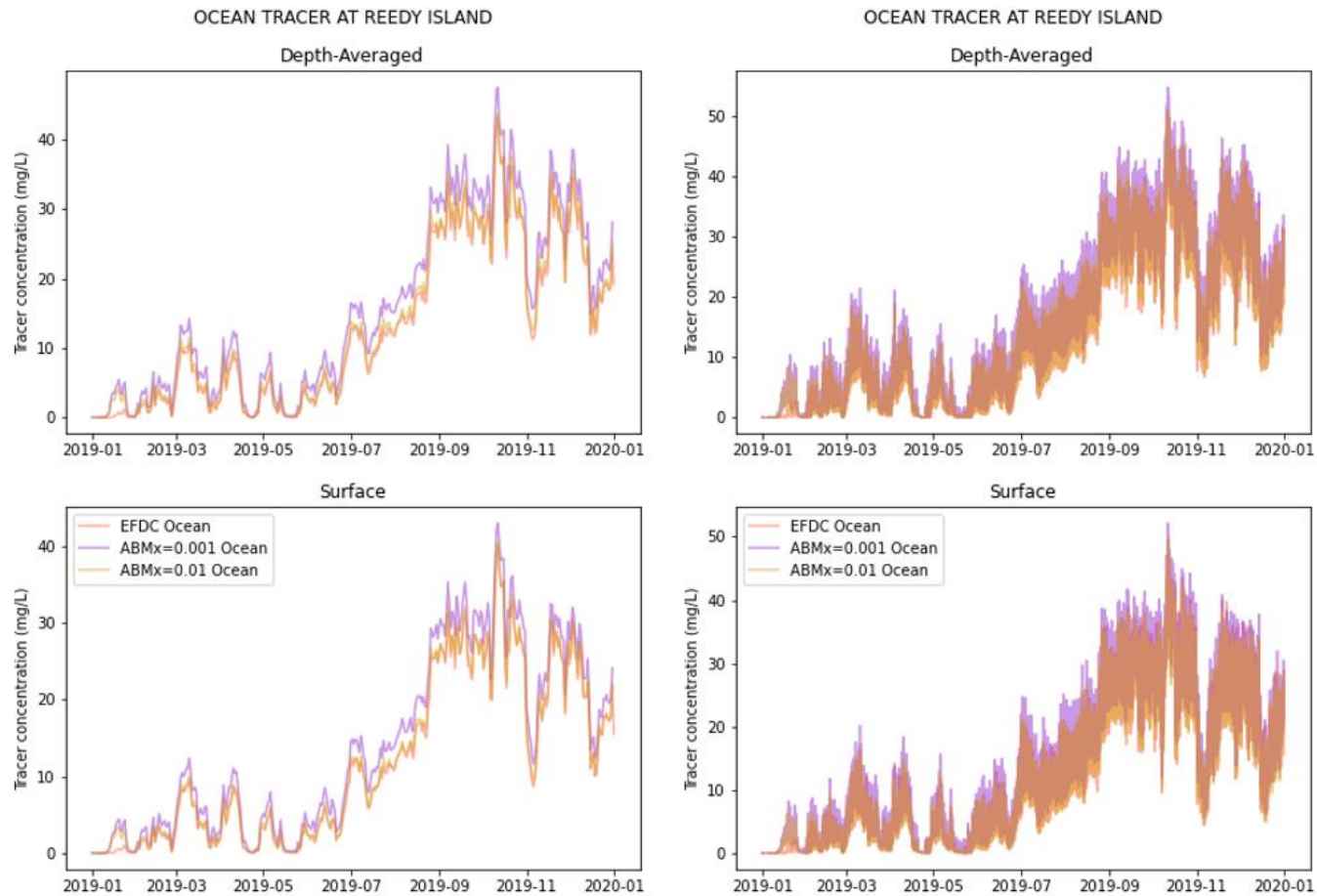
Figure 1-3: Time Series Plots of Ocean Tracer Release – Concentration at Chester (RM 84)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

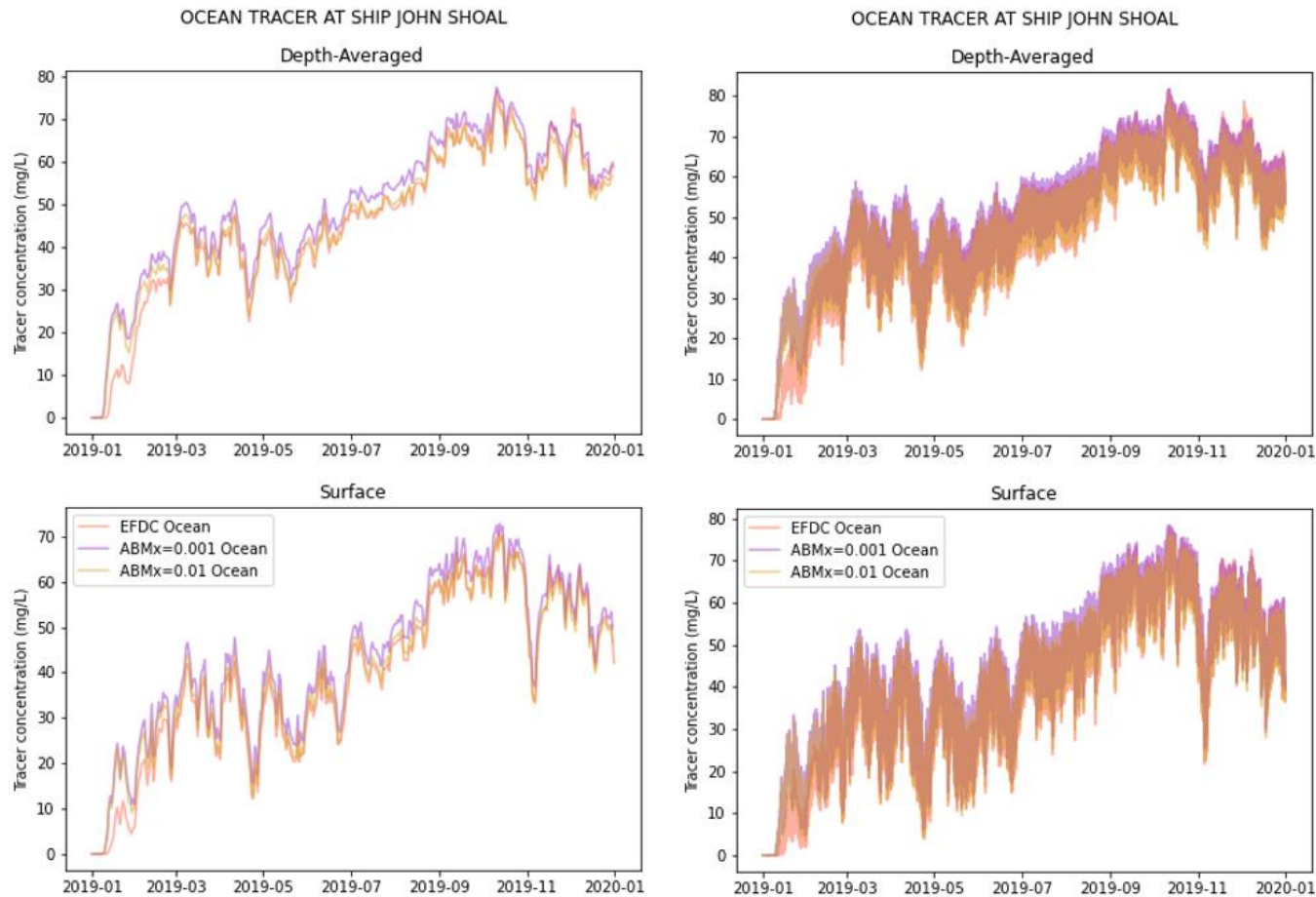
Figure 1-4: Time Series Plots of Ocean Tracer Release – Concentration at Reedy Island (RM 54)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

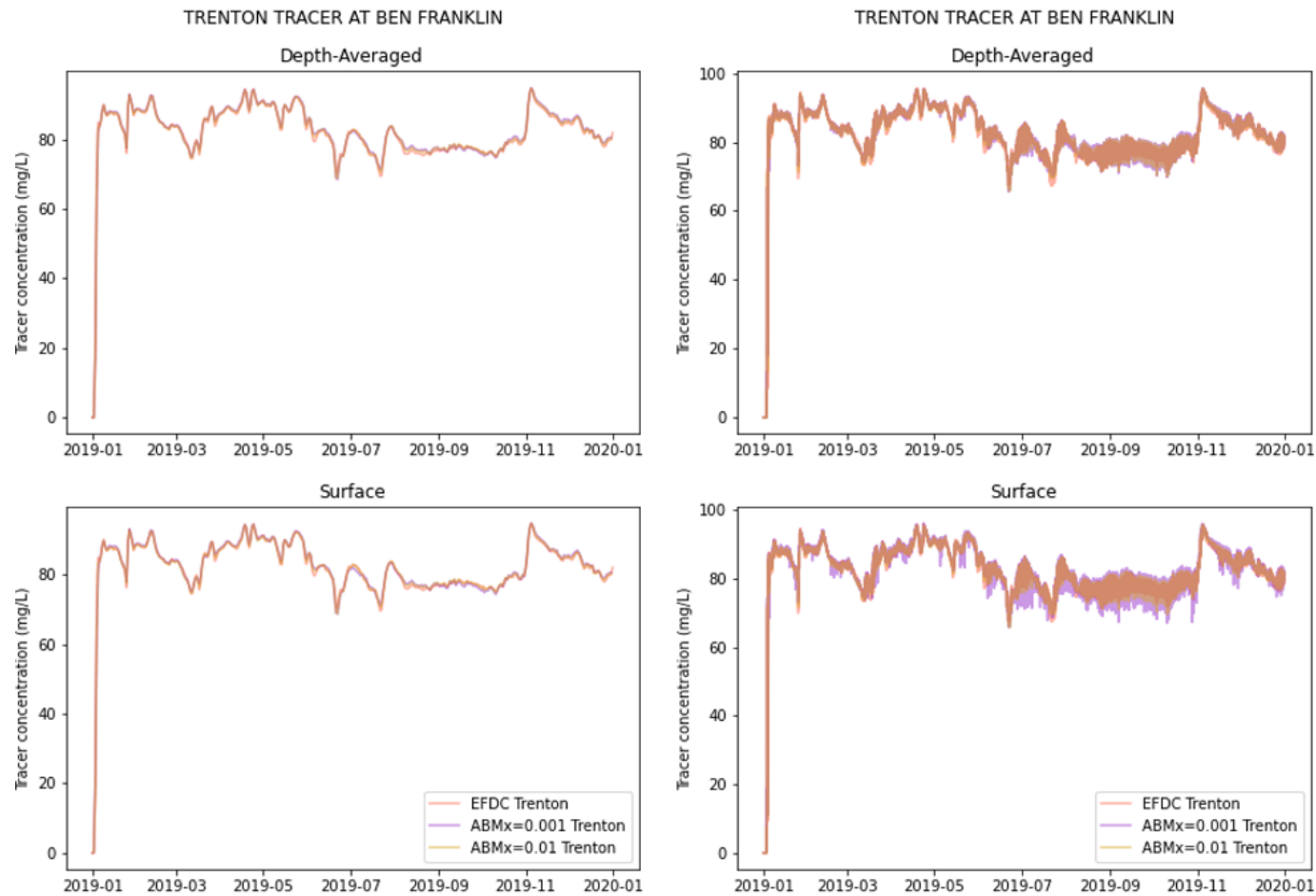
Figure 1-5: Time Series Plots of Ocean Tracer Release – Concentration at Ship John Shoal (RM 37)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

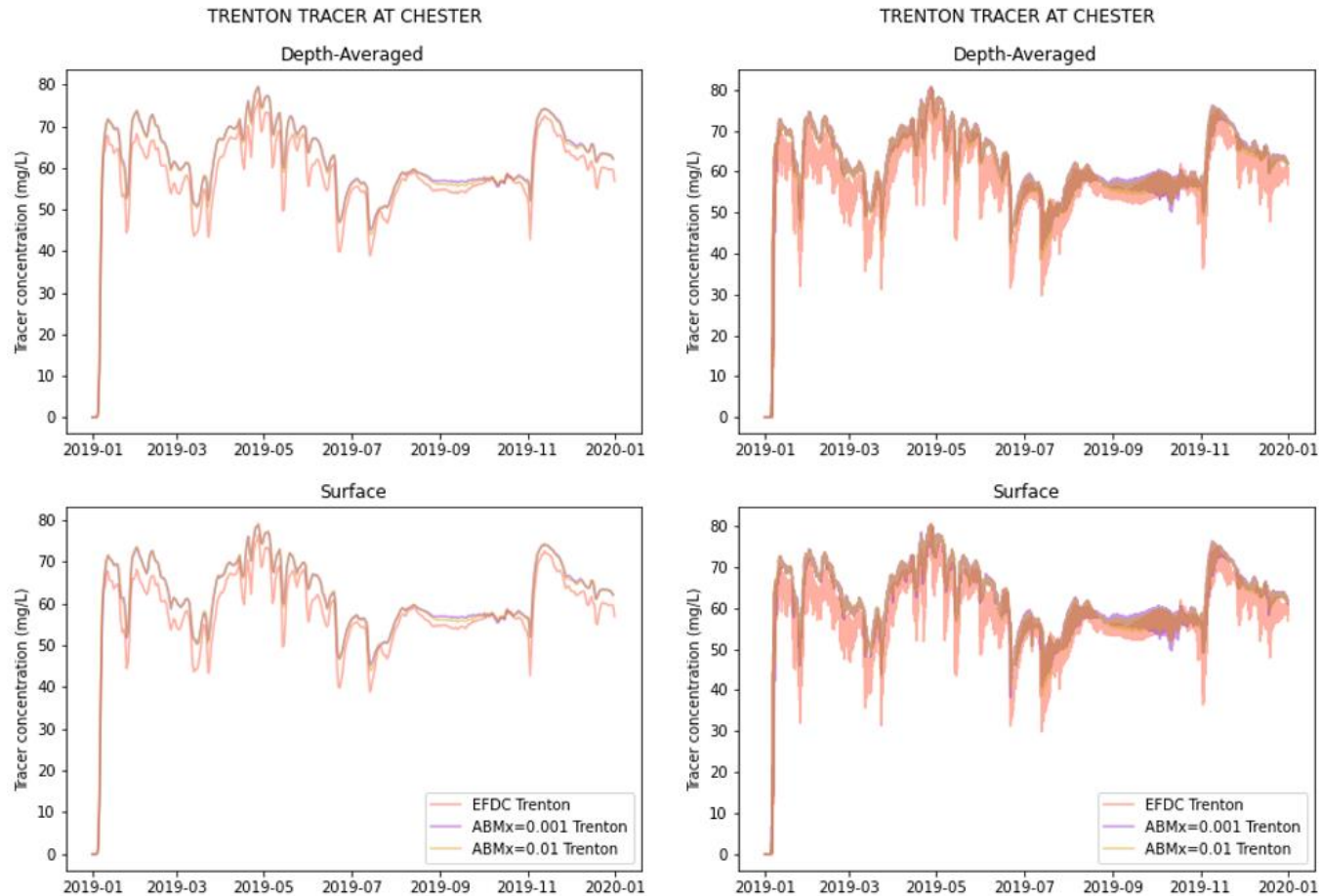
Figure 1-6: Time Series Plots of Trenton Tracer Release – Concentration at Ben Franklin Bridge (RM 100)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

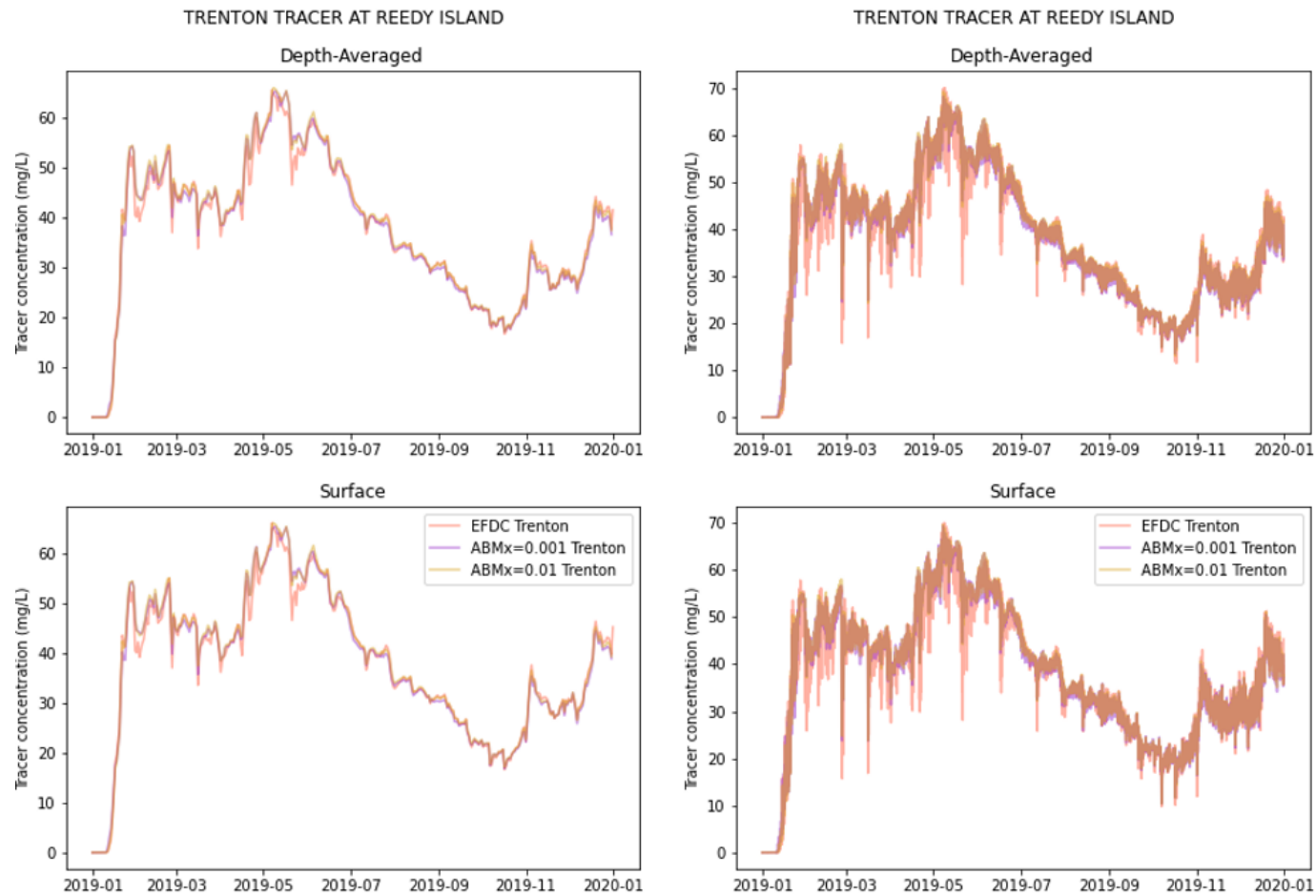
Figure 1-7: Time Series Plots of Trenton Tracer Release – Concentration at Chester (RM 84)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

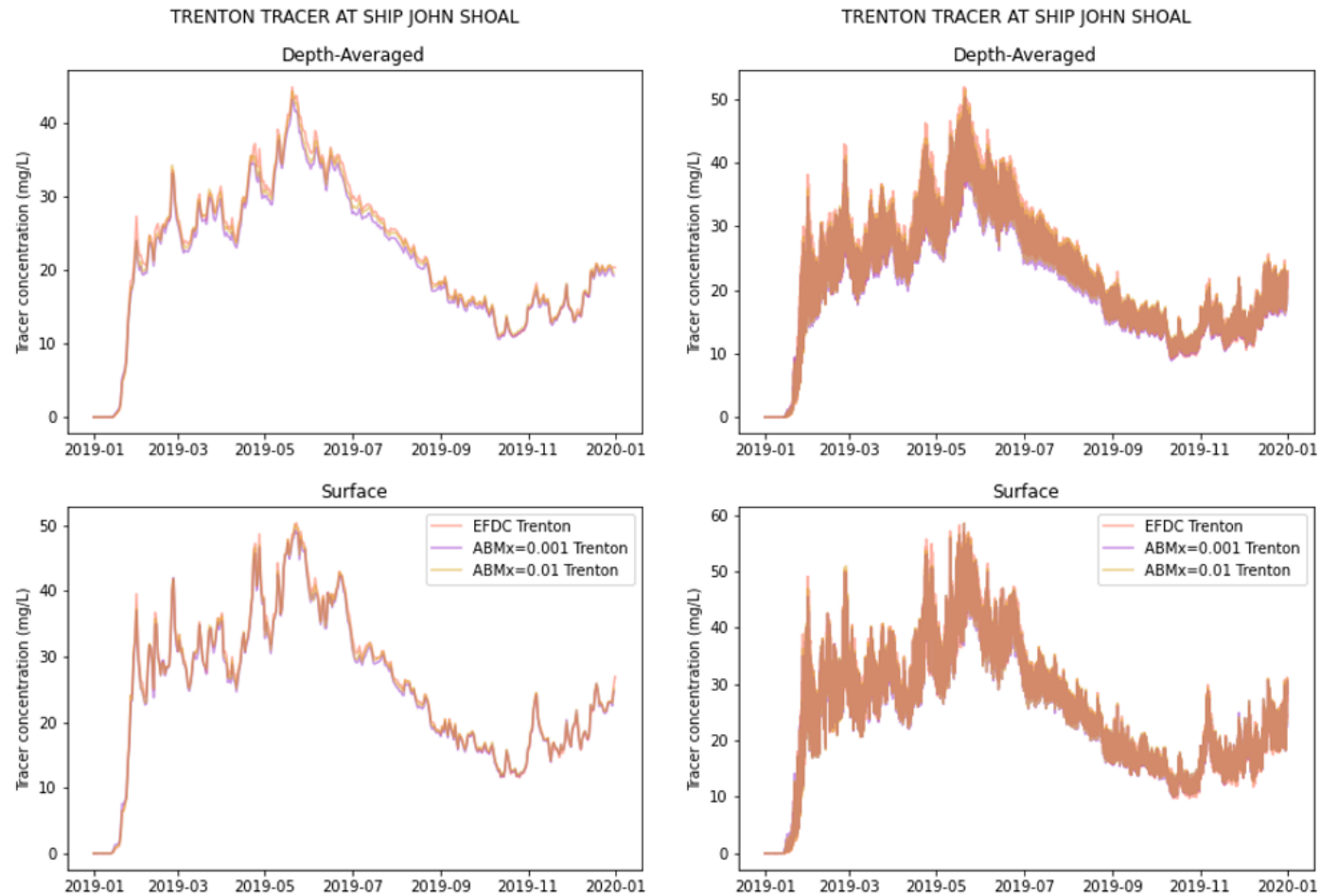
Figure 1-8: Time Series Plots of Trenton Tracer Release – Concentration at Reedy Island (RM 54)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

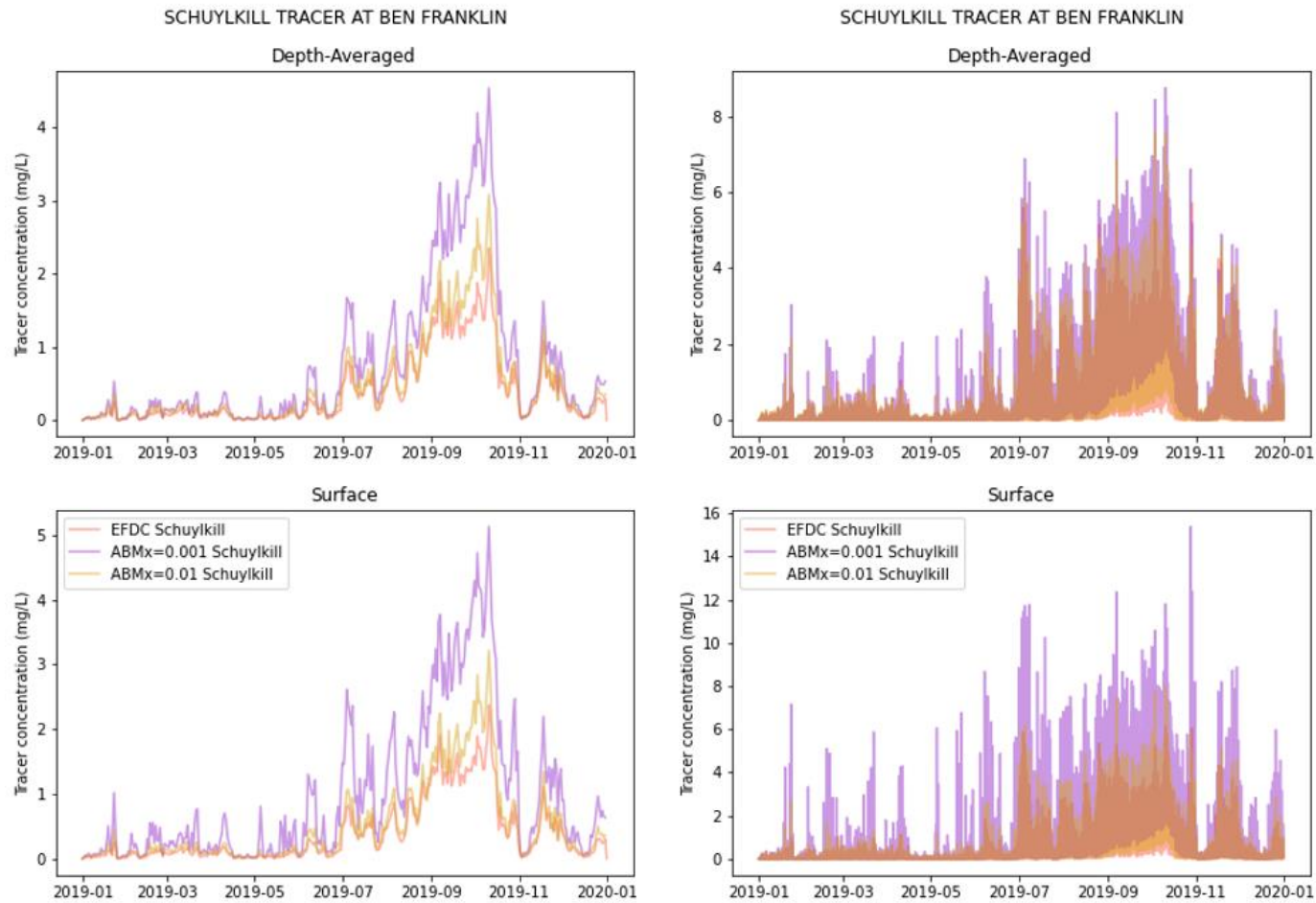
Figure 1-9: Time Series Plots of Trenton Tracer Release – Concentration at Ship John Shoal (RM 37)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

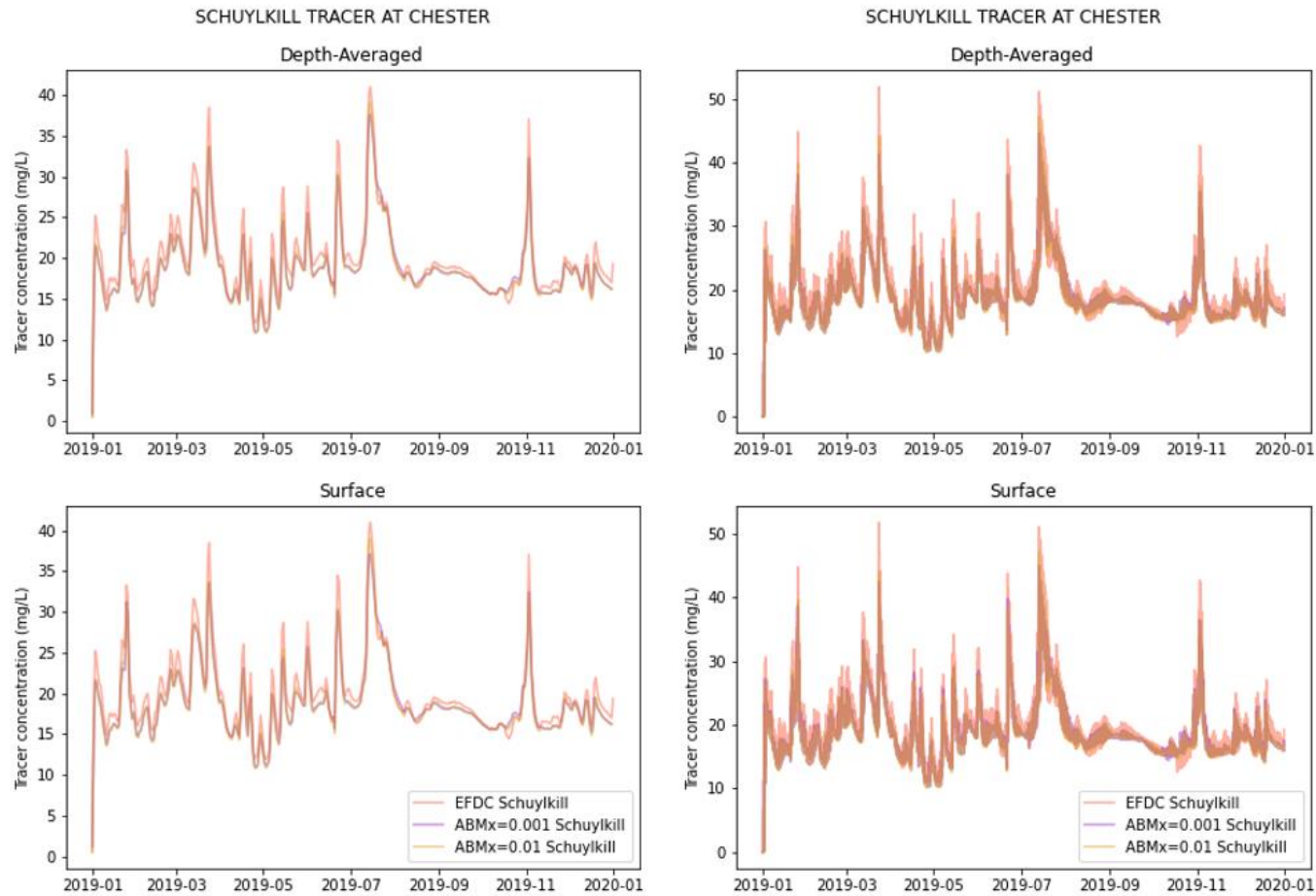
Figure 1-10: Time Series Plots of Schuylkill Tracer Release – Concentration at Ben Franklin Bridge (RM 100)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

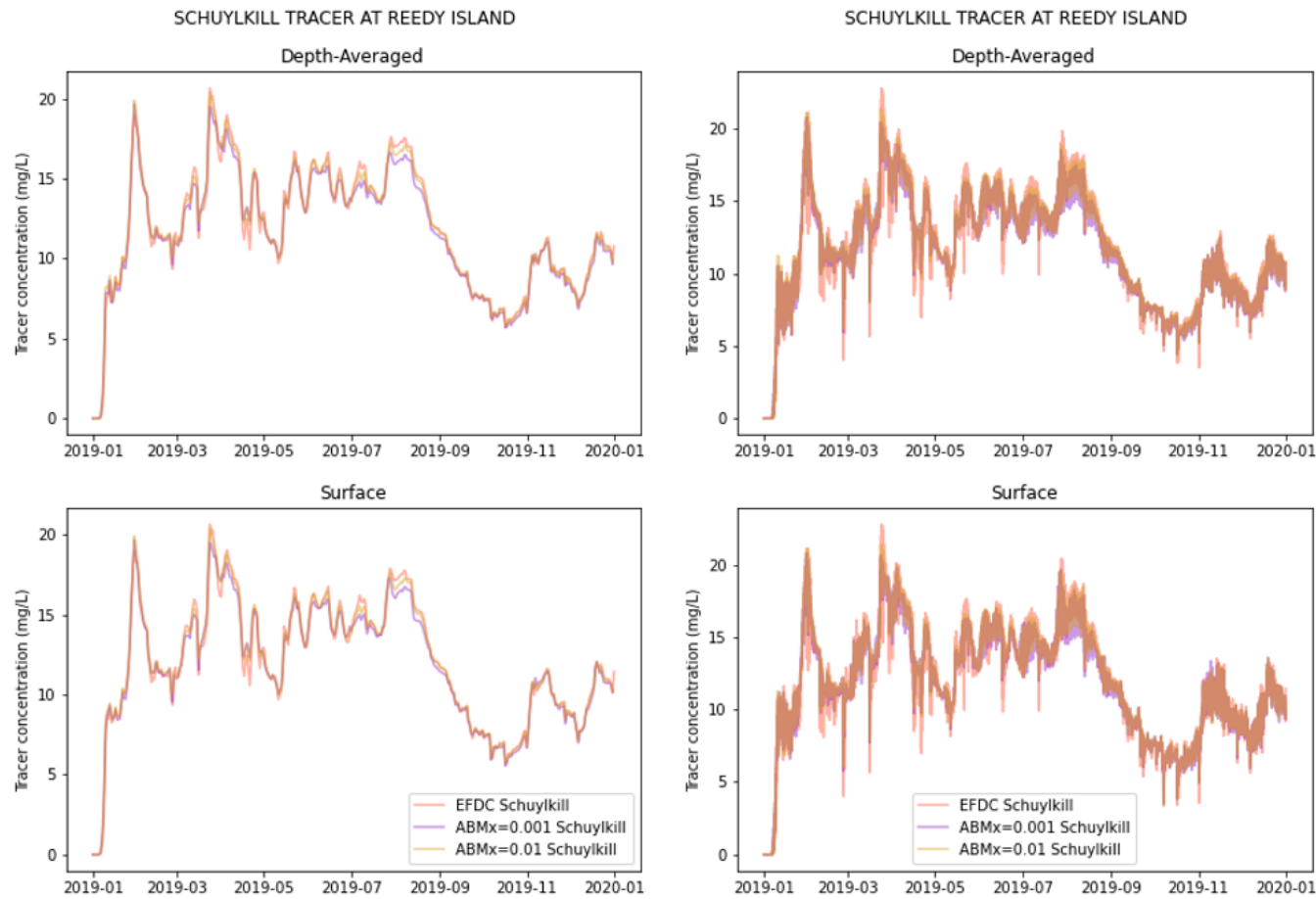
Figure 1-11: Time Series Plots of Schuylkill Tracer Release – Concentration at Chester (RM 84)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

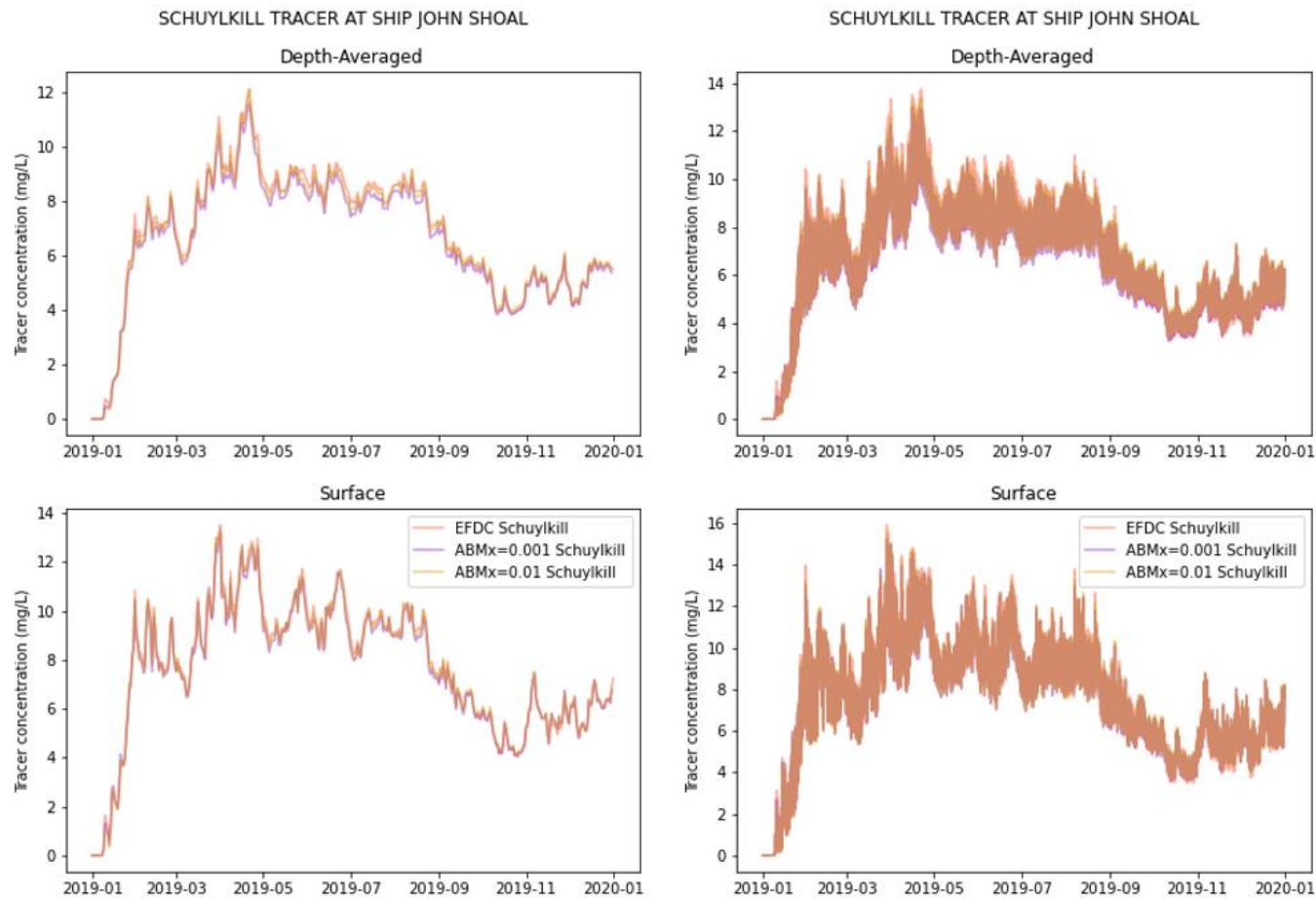
Figure 1-12: Time Series Plots of Schuylkill Tracer Release – Concentration at Reedy Island (RM 54)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

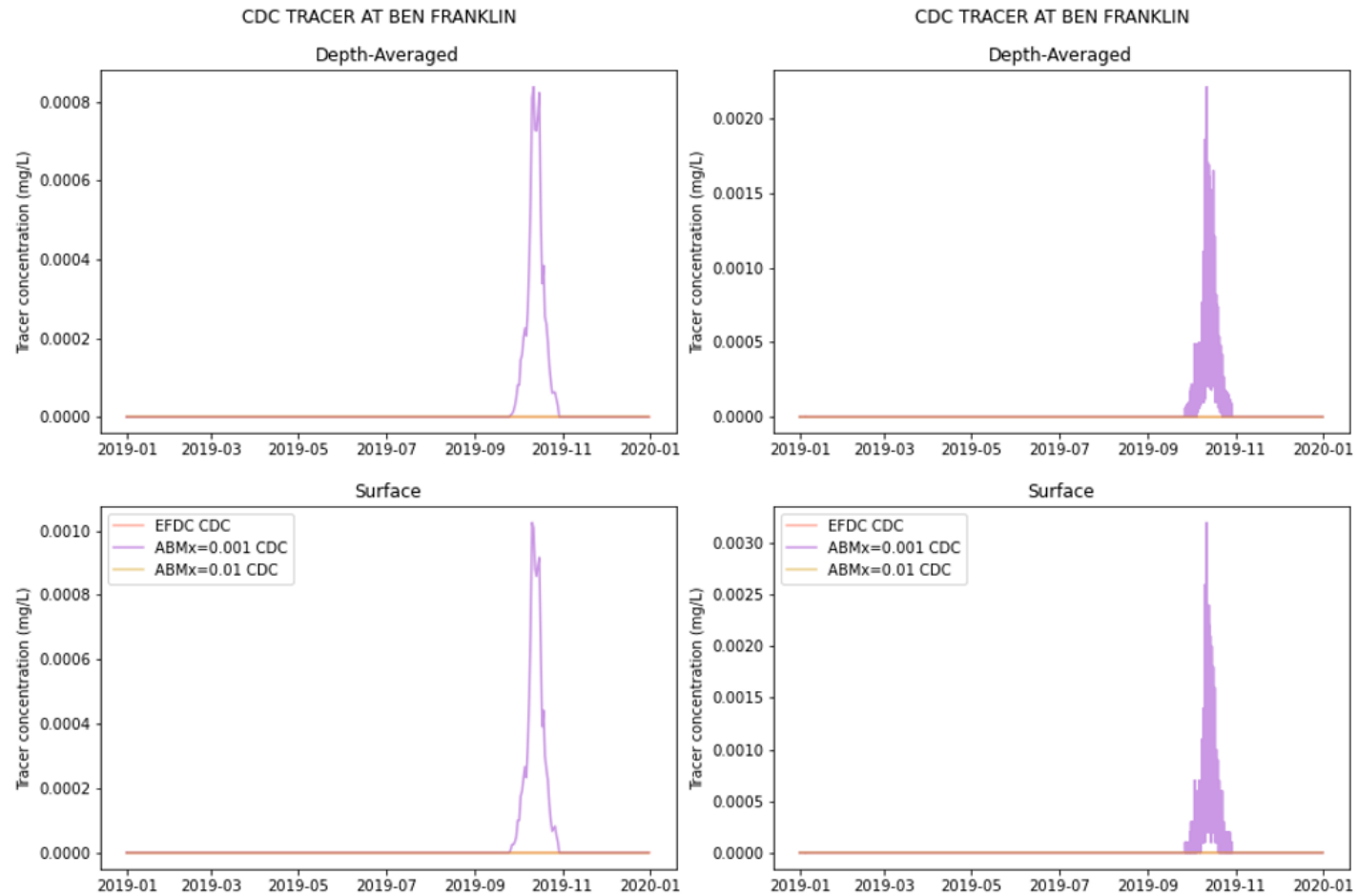
Figure 1-13: Time Series Plots of Schuylkill Tracer Release – Concentration at Ship John Shoal (RM 37)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

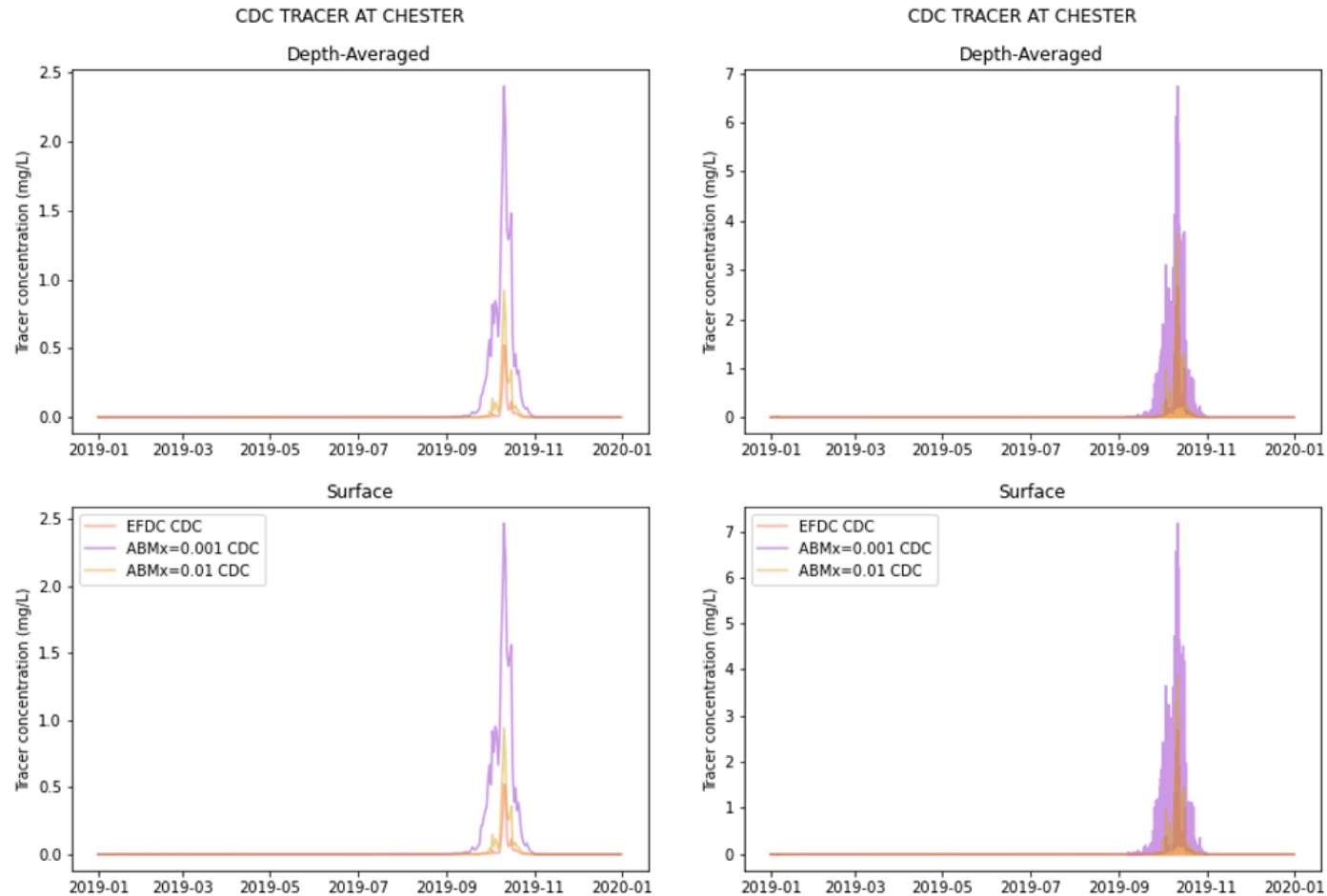
Figure 1-14: Time Series Plots of C&D Canal Tracer Release – Concentration at Ben Franklin Bridge (RM 100)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

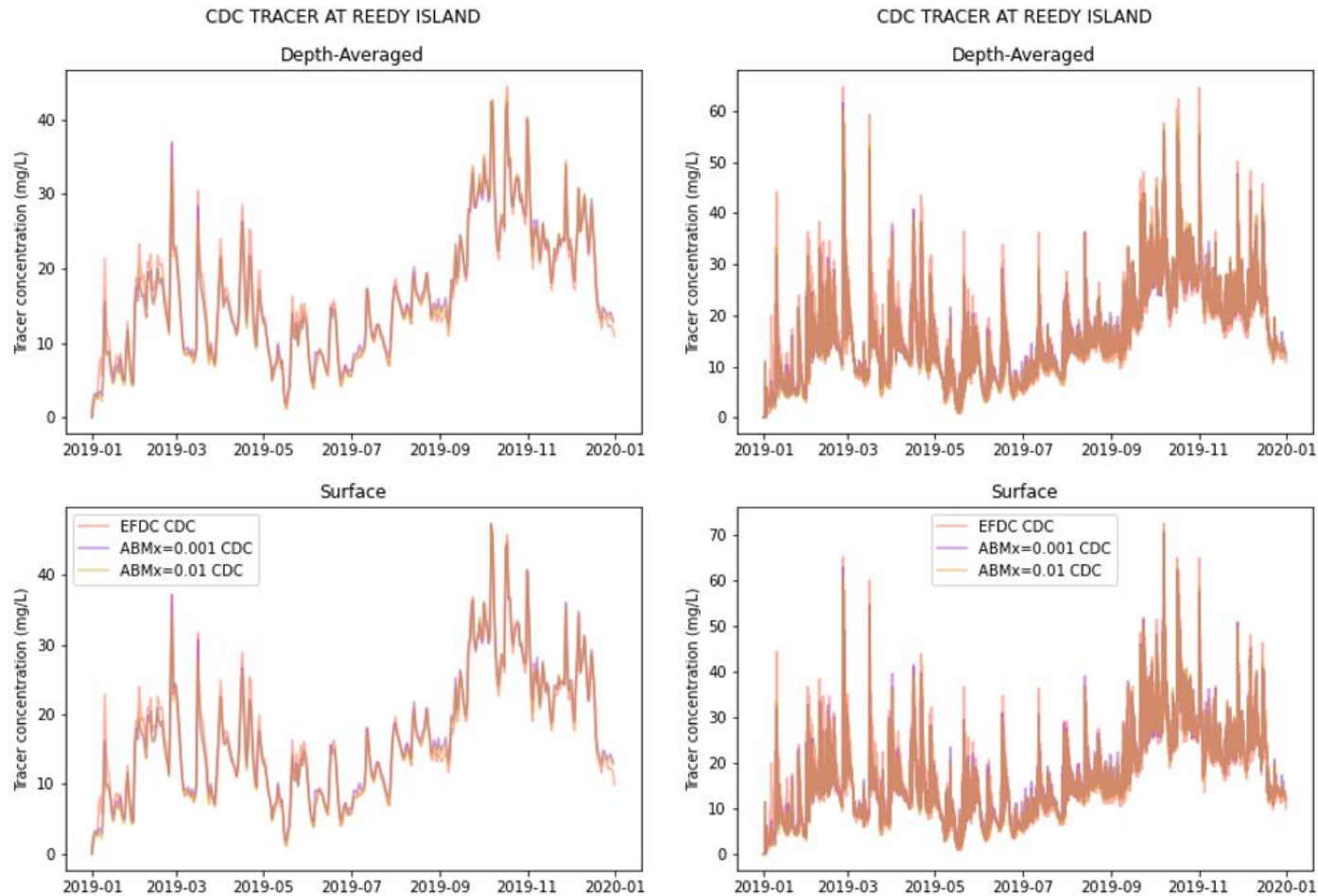
Figure 1-15: Time Series Plots of C&D Canal Tracer Release – Concentration at Chester (RM 84)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

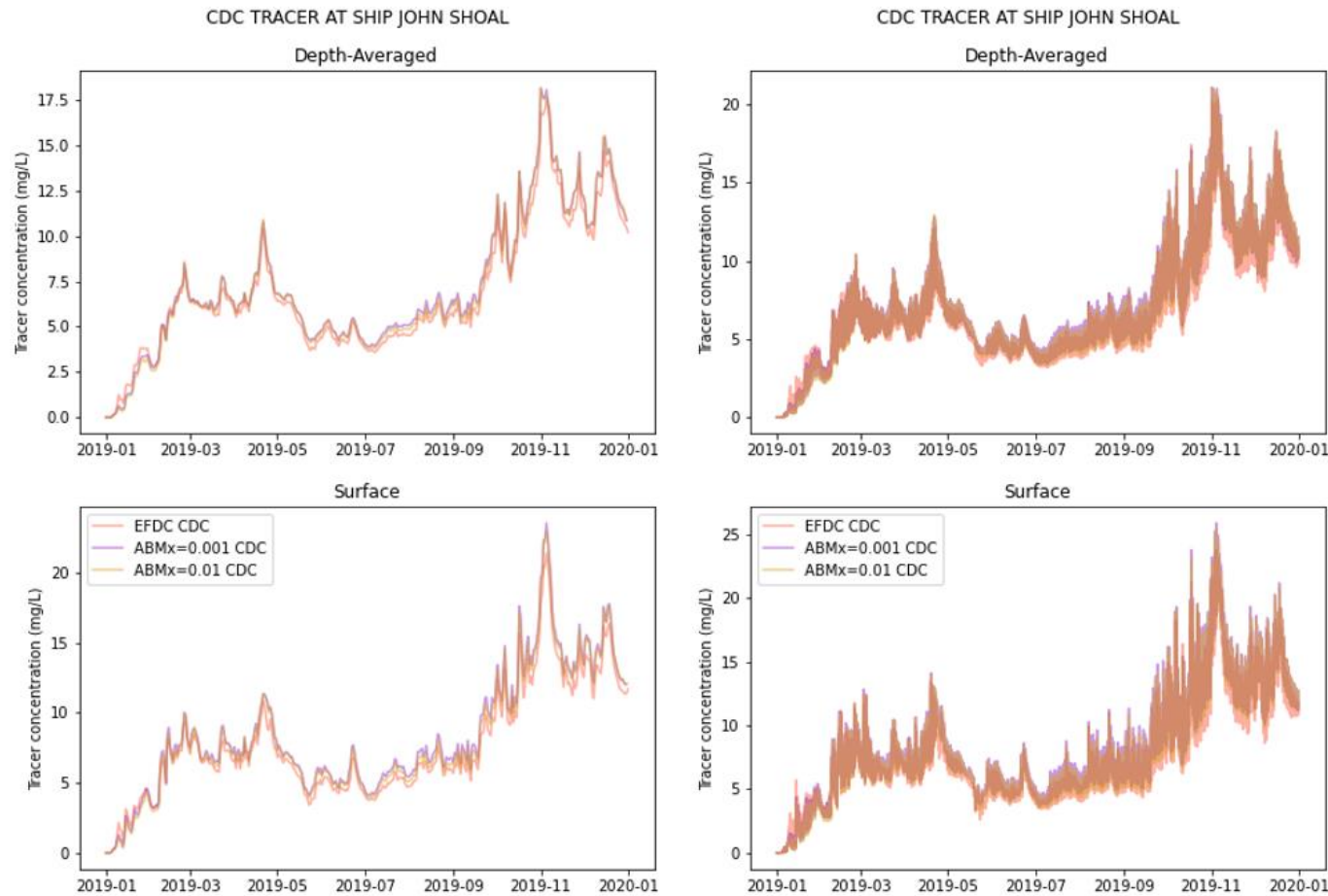
Figure 1-16: Time Series Plots of C&D Canal Tracer Release – Concentration at Reedy Island (RM 54)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

Figure 1-17: Time Series Plots of C&D Canal Tracer Release – Concentration at Ship John Shoal (RM 37)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Red: EFDC; Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

2. MASS BALANCE CHECK

WASP provides a simple way of evaluating mass balance through conservative tracer simulation by setting the initial conditions and all boundary conditions for the tracer concentration to one. If mass balance is honored, the tracer concentrations would theoretically be one everywhere, assuming precipitation and evaporation process are disabled. In other words, any deviation of tracer concentrations from one can be considered as mass balance error. In this section, mass balance checks were conducted for the period of 2019 using linkage files with ABMAX = 0.001 and 0.01 m²/s, respectively. NTSMMT was set to 30 in both scenarios to have a linkage file for every 5 minutes.

Figure 2-1 illustrates yearly- and depth-averaged mass check results along navigation channel. The maximum mass balance error with ABMAX = 0.001 m²/s was about 4.3%, whereas the maximum mass balance with ABMAX = 0.01 m²/s was about 1.9%

Figure 2-2 through Figure 2-5 depict the time series of surface and depth-averaged mass check results at NOAA station at Ship John Shoal and USGS stations at Ben Franklin Bridge, Chester, and Reedy Island during 2019. A combination of NTSMMT = 30 and ABMAX = 0.01 m²/s generated about 5% or lower instantaneous errors. Another combination of NTSMMT = 30 and ABMAX = 0.001 m²/s resulted in mass balance errors double but three times faster than the first combination.

Figure 2-6 through 2-8 show spatial contours of averaged surface mass check results from March 1 through October 31 in the areas of RM 93 – 114 for ABMAX = 0.01 and 0.001 m²/s, respectively. The scenario with ABMAX = 0.01 m²/s displayed mass balance errors up to 0.8%, compared with mass balance errors up to 1.8% for the scenario with ABMAX = 0.001 m²/s. No spikes or discontinuity of mass check results were observed for either scenario.

Figure 2-1: WASP Mass Check – Longitudinal Profile along Navigation Channel

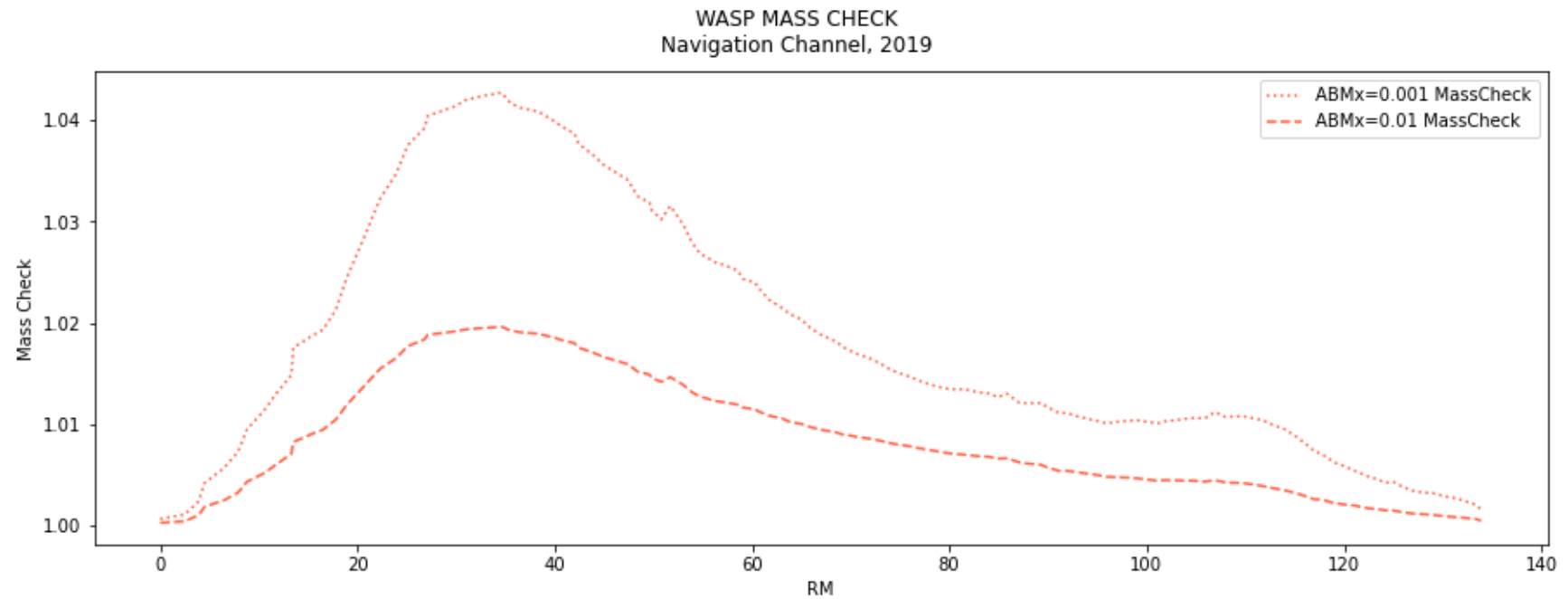
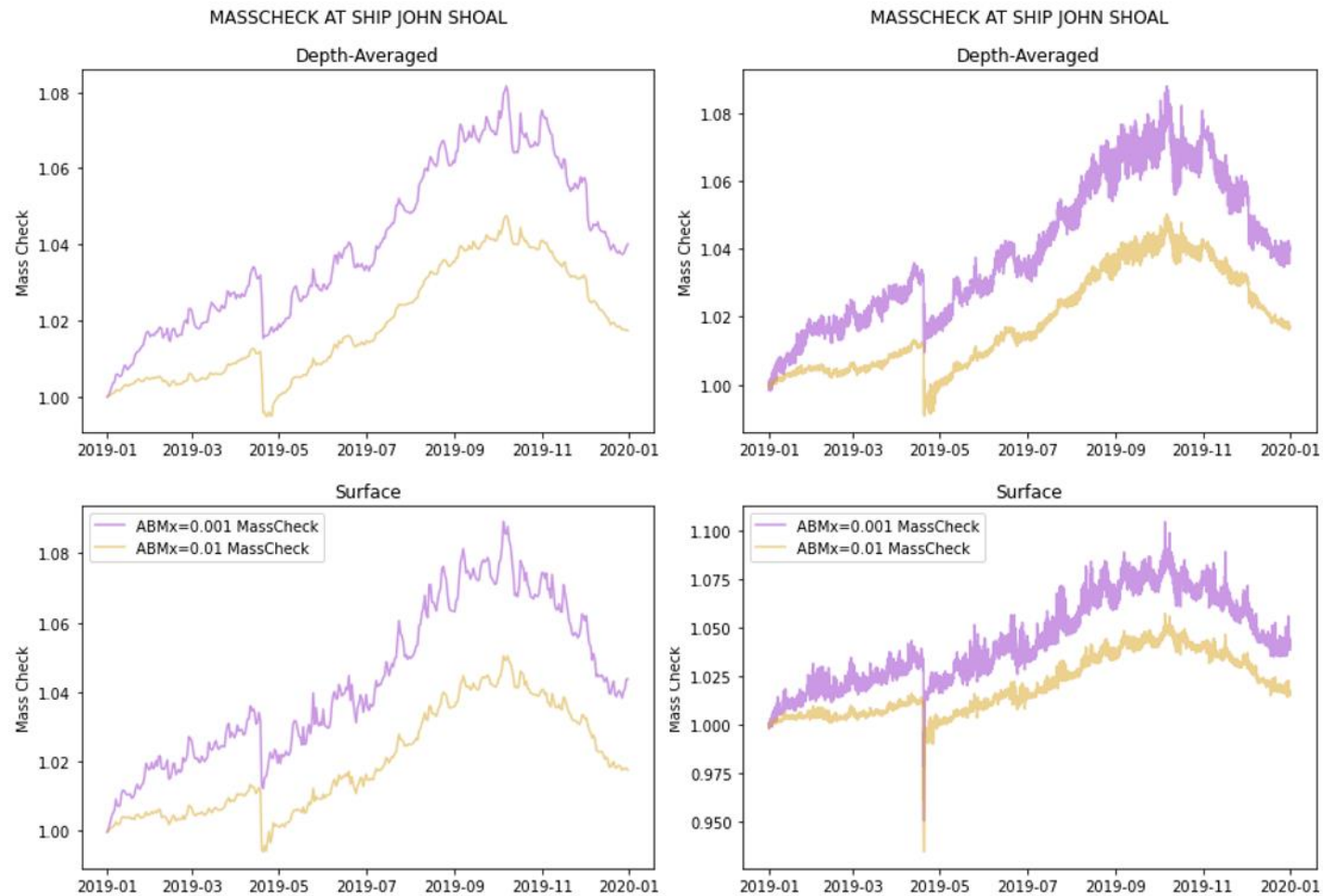


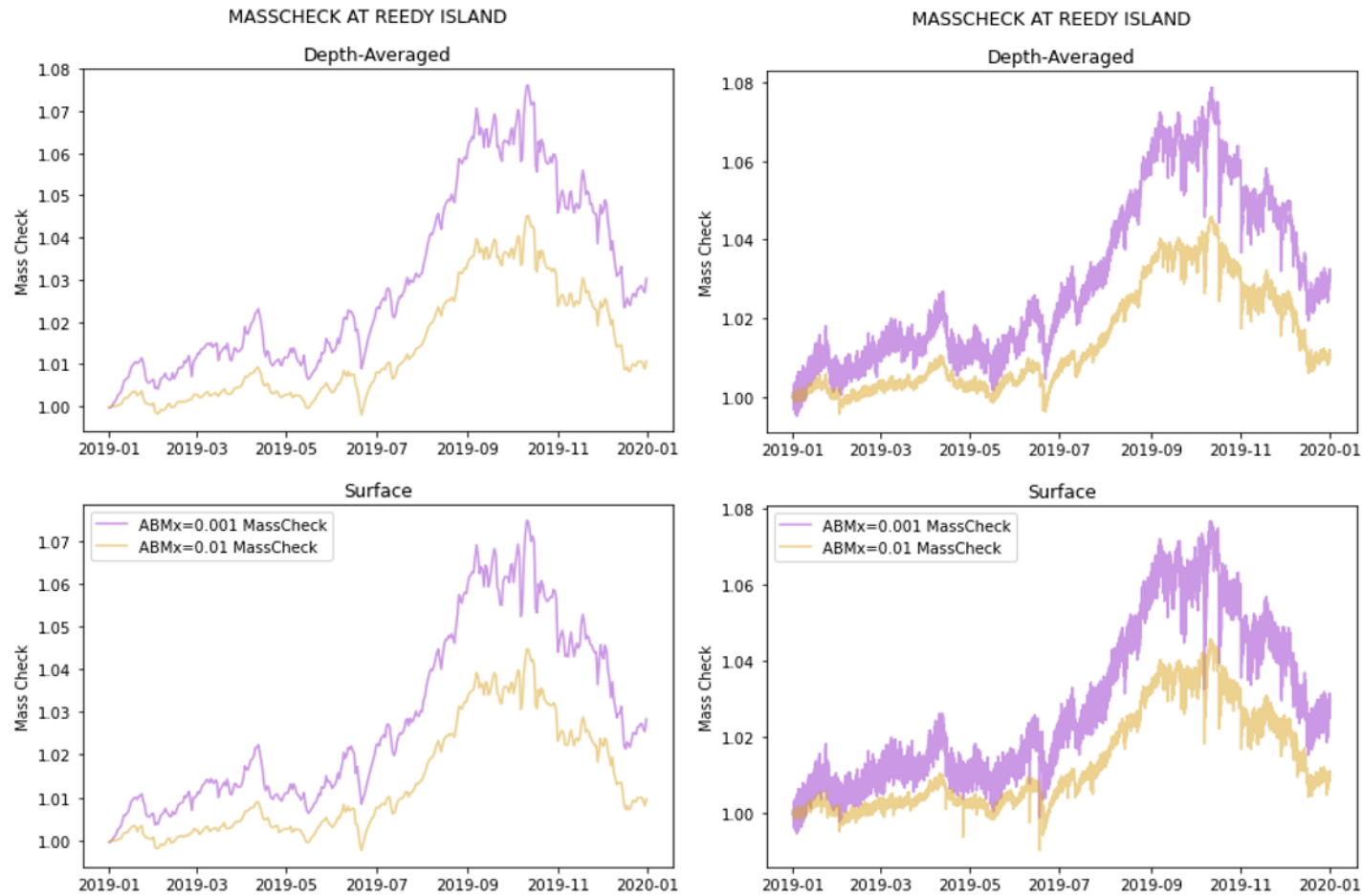
Figure 2-2: Time Series Plots of Mass Check at Ship John Shoal (RM 37)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

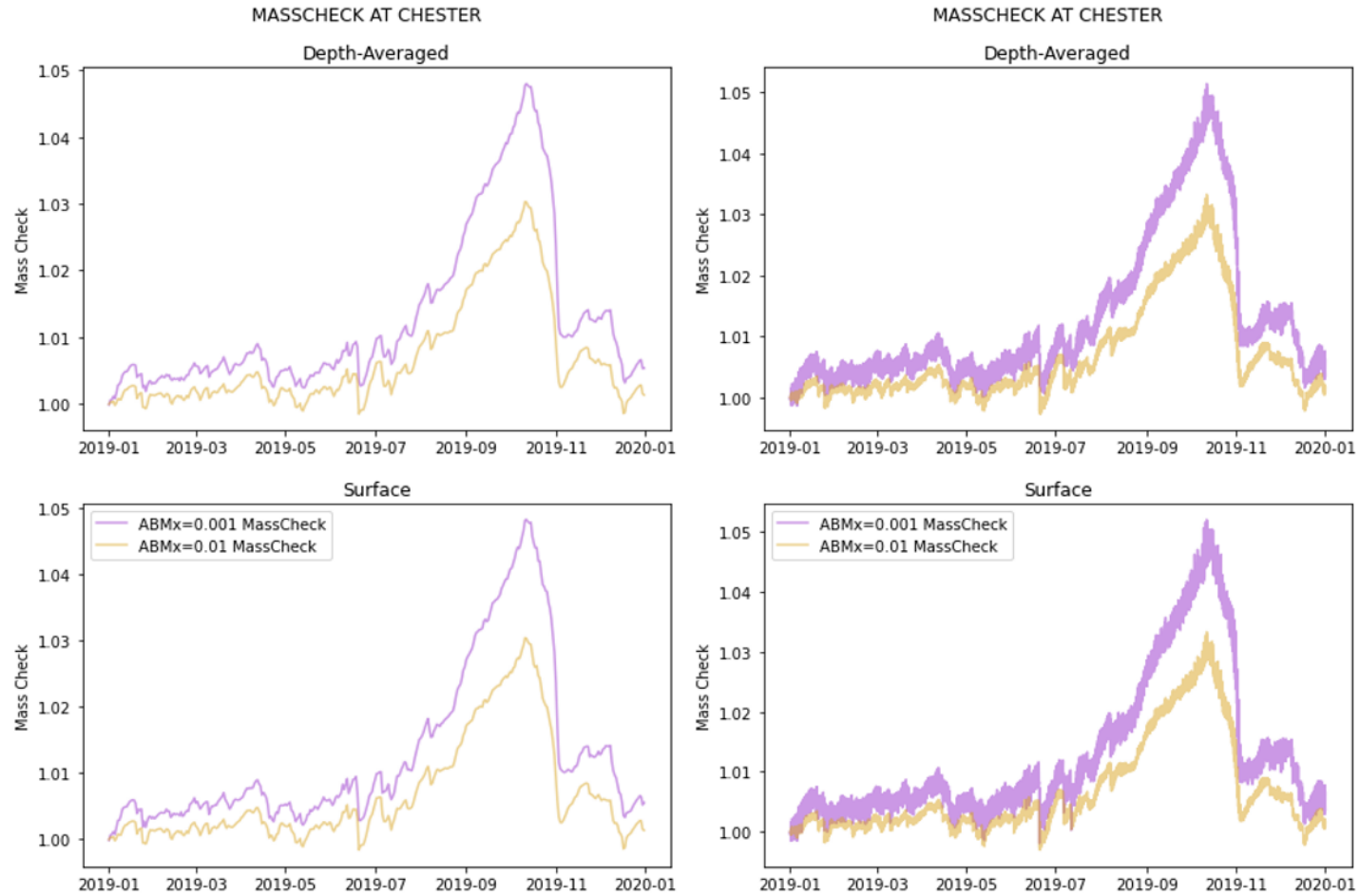
Figure 2-3: Time Series Plots of Mass Check at Reedy Island (RM 54)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

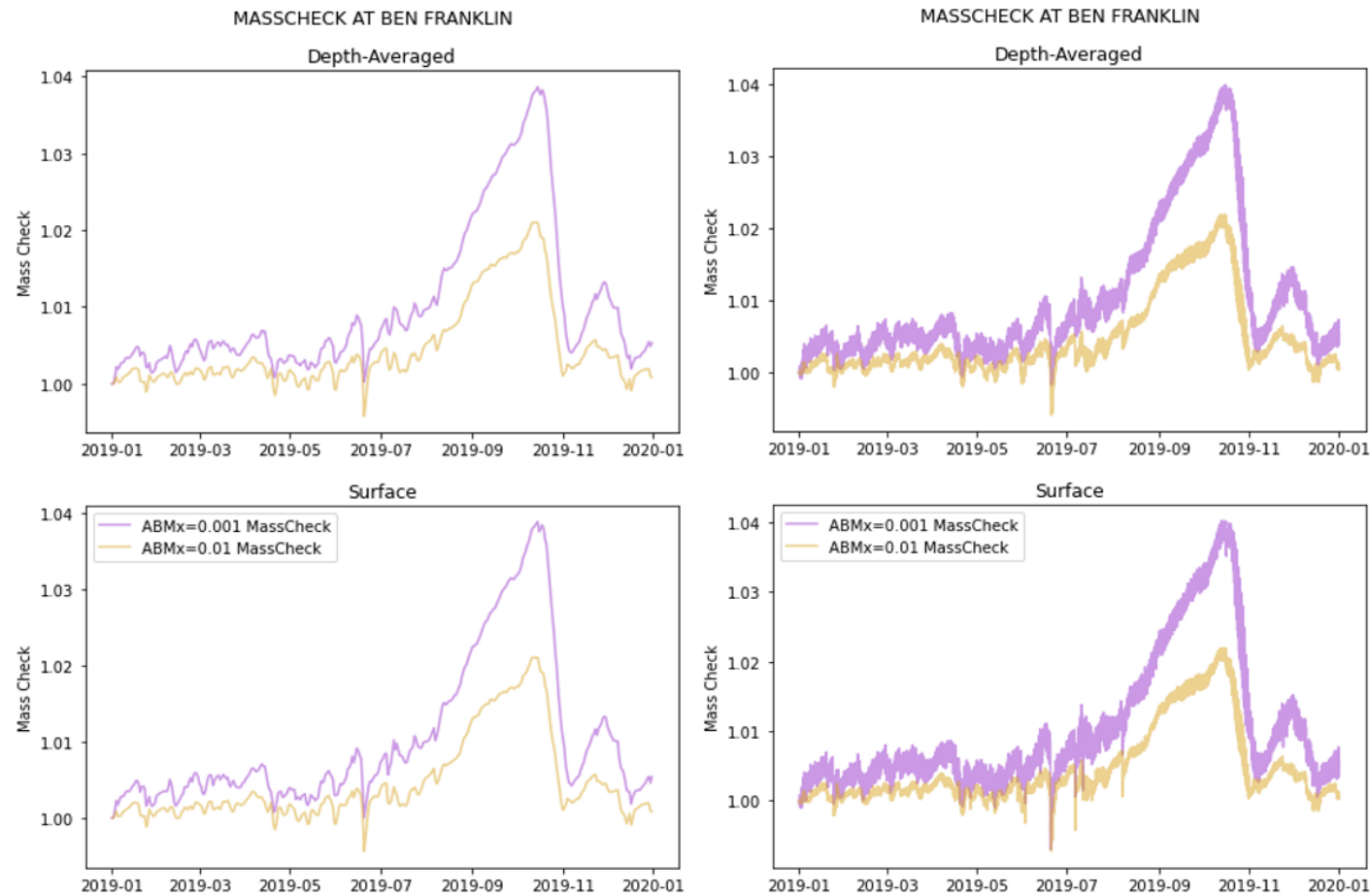
Figure 2-4: Time Series Plots of Mass Check at Chester (RM 84)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

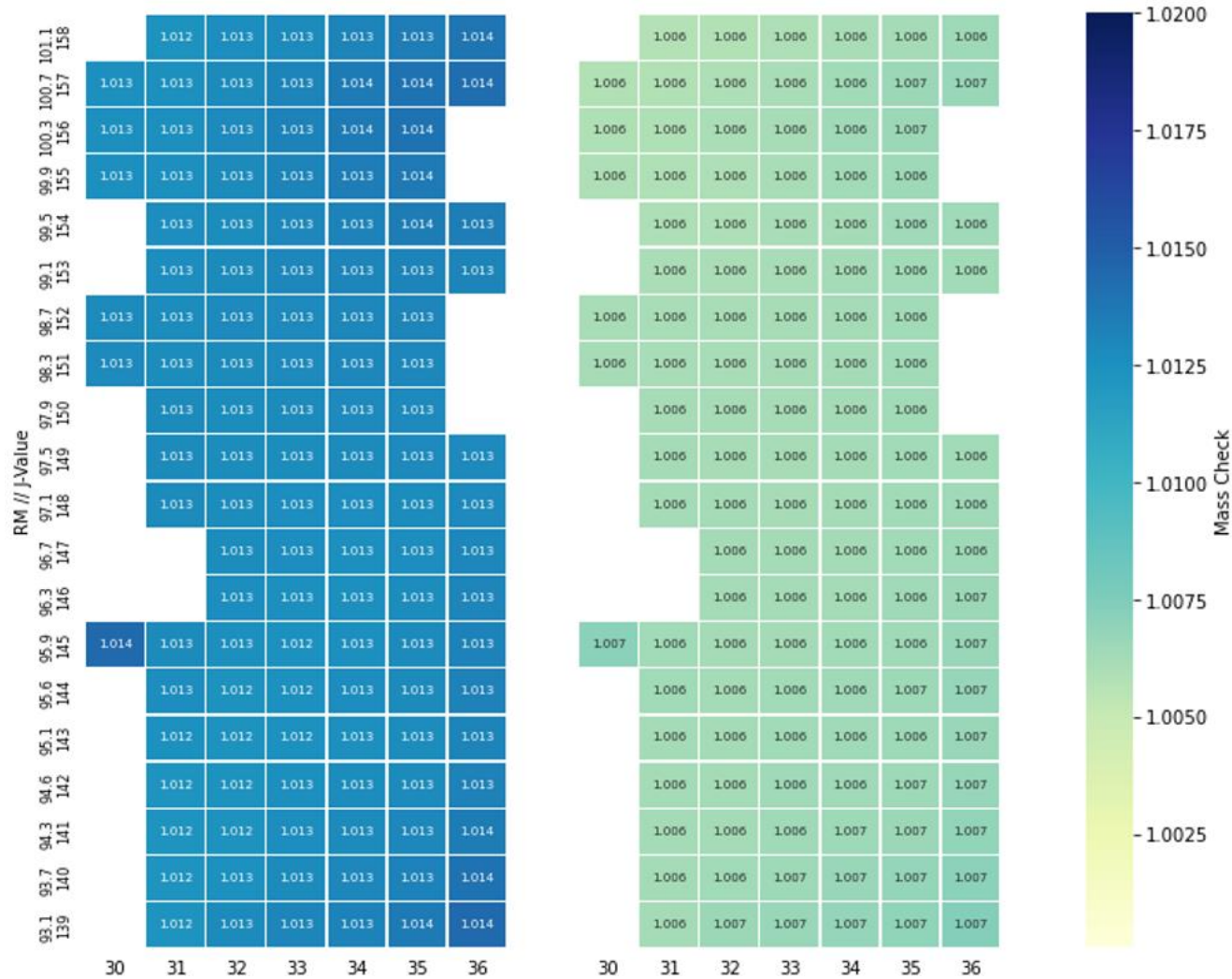
Figure 2-5: Time Series Plots of Mass Check at Ben Franklin Bridge (RM 100)



Left: Daily average; Right: Raw output; Top: Depth-averaged; Bottom: Surface cell

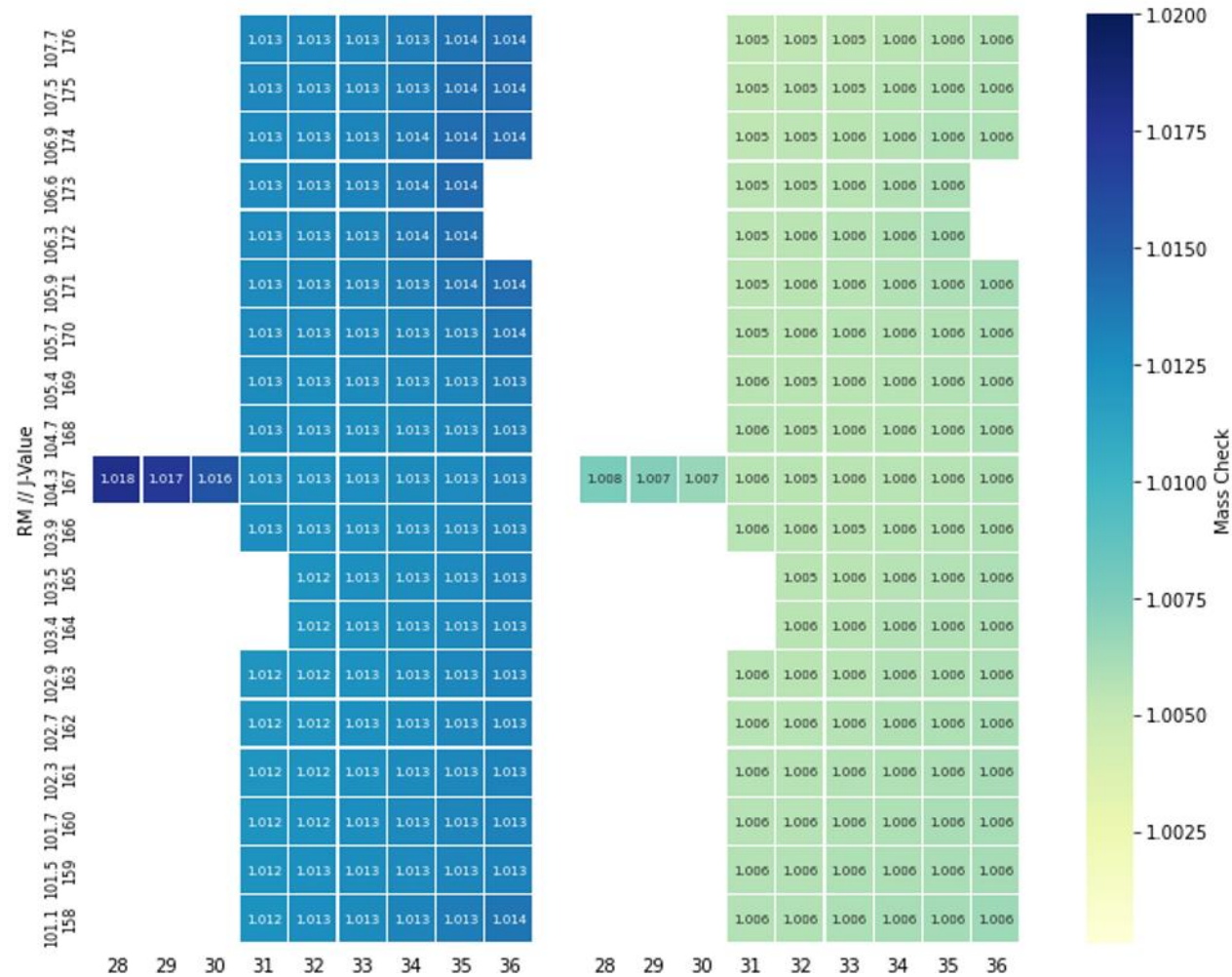
Purple: WASP, ABMax = 0.001; Yellow: WASP, ABMax= 0.01

Figure 2-6: Mass Check Spatial Plot, RM 93 – 101, Surface cells



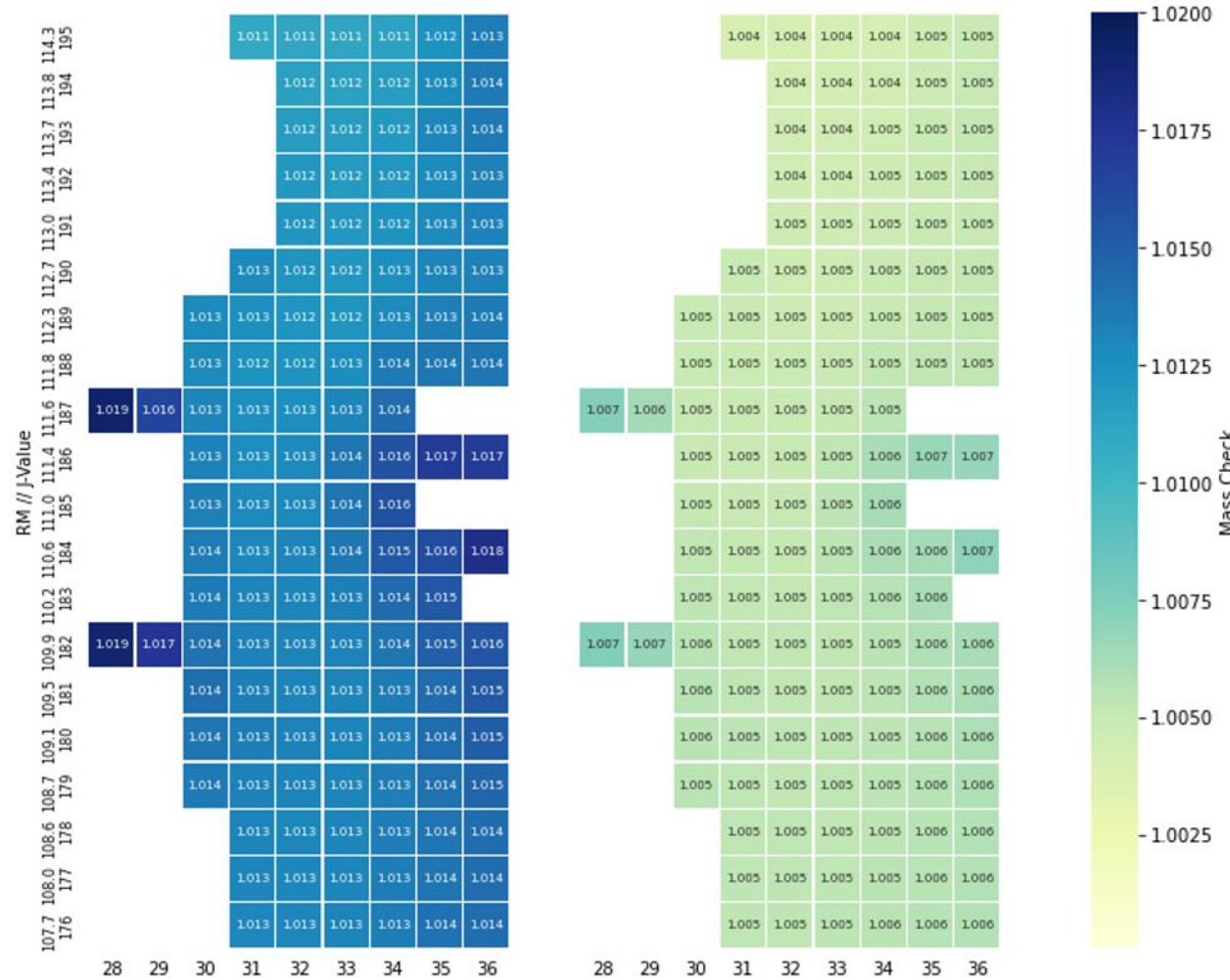
Left: ABMAX = 0.001; Right: ABMAX = 0.01, Temporally averaged from March – October 2019

Figure 2-7: Mass Check Spatial Plot, RM 101 – 108, Surface cells



Left: $ABMAX = 0.001$; Right: $ABMAX = 0.01$, Temporally averaged from March – October 2019

Figure 2-8: Mass Check Spatial Plot, RM 108 – 114, Surface cells



Left: ABMAX = 0.001; Right: ABMAX = 0.01, Temporally averaged from March – October 2019

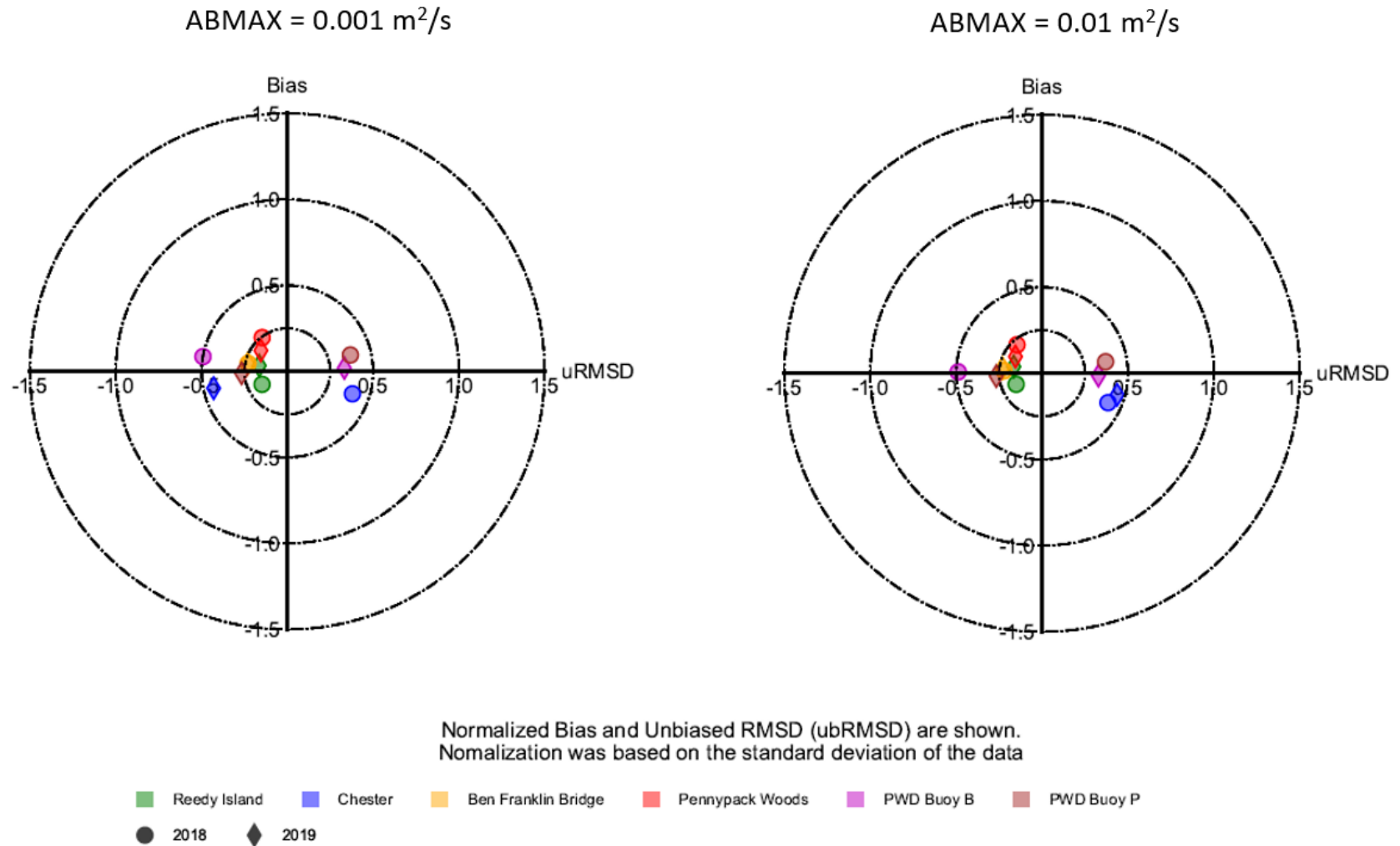
3. DO COMPARISON

Dissolved oxygen (DO) results for 2018-2019 were compared using the final calibration parameters and linkage files with ABMAX = 0.01 and 0.001 m²/s, respectively. NTSMMT was set to 30 in both scenarios. Bi-hourly DO results at four USGS stations (Pennypack Woods, Ben Franklin Bridge, Chester, and Reedy Island) and PWD Buoy-B and P (Figure 3-12 in the main report) were compared with observed data. Target diagrams, which provide a summary of model performance at all stations during multiple year period, were used to evaluate the performance of these two scenarios.

Discussions and application of target diagram were provided in Jolliff et al. (2009) and McWilliams et al. (2015). The bias and the unbiased Root Mean Square Difference (ubRMSD) described in Section 3.2.4.2 in the main report are normalized by the observed standard deviation, so the values were comparable among different variables (i.e., to compare model accuracy among group of stations, and/or among different periods, etc.). On the target diagram, the normalized bias is plotted on the Y-axis and the normalized ubRMSD is plotted on the X-axis. An ideal model result would lie on the origin of the target diagram. Predictions falling outside a radius of 1 were classified as indicating poor agreement between the model predictions and the observed data (Jolliff et al. 2009, McWilliams et al. 2015).

Target diagram for DO comparison is shown in Figure 3-1. All symbols shown on the target diagram fall within the 0.5-radius. Scenario with ABMAX = 0.01 m²/s is slightly better than the scenario with ABMAX = 0.001 m²/s, considering symbols are a little more evenly distributed around the x-axis in the first scenario. Both scenarios slightly underestimated the variability in DO concentrations, since the positive-x symbols are a little less than the negative-x ones. By and large, these results indicate: (1) the differences in predicted DO concentrations between Scenarios with ABMAX = 0.01 and 0.001 m²/s are insignificant; and (2) both scenarios reasonably predicted DO concentrations at multiple locations throughout the estuary for the calibration period.

Figure 3-1: Target Diagram for Predicted Dissolved Oxygen, ABMAX = 0.001 vs. 0.01 m²/s



4. SUMMARY

Numerical tests in Sections 1 to 2 demonstrated that (1) a combination of $NTSMMT = 30$ and $ABMAX = 0.01 \text{ m}^2/\text{s}$ generated reasonably well conservative tracer transports and mass balance; and (2) a second combination of $NTSMMT = 30$ and $ABMAX = 0.001 \text{ m}^2/\text{s}$ was three times faster than the first combination, although the results of conservative tracer transport and mass balance were less desirable. Furthermore, numerical tests in Section 3 indicated that there were insignificant differences in predicted DO concentrations using these two combinations. Therefore, we used the second combination for production runs and the first combination for the final calibration.