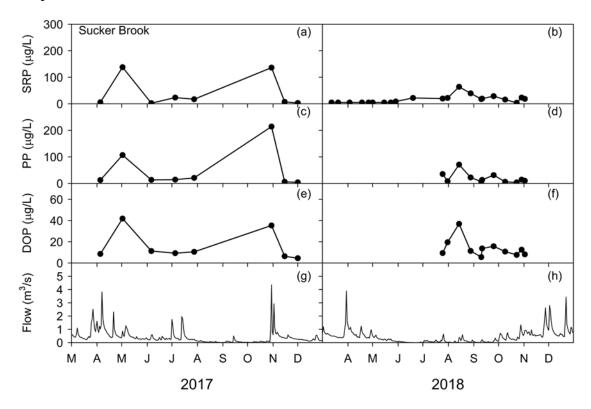
### **Appendix A: Data Matrix**

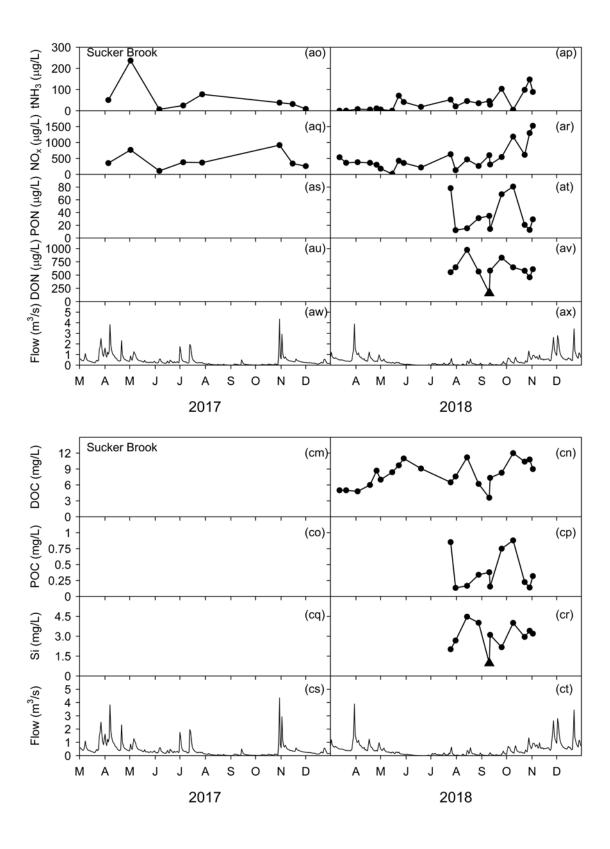
The data matrix is an Excel spreadsheet with a width greater than can be reproduced legibly on a standard 8"×11" page. For this reason a hard copy of the matrix does not appear here. Additionally, the spreadsheet contains hyperlinks to almost seventy supporting documents, including QAPPs, reports emails, and memos. These hyperlinks rely on maintenance of a fixed file directory structure. Due to the large number of linked files and overall size, this appendix is provided electronically on CD.

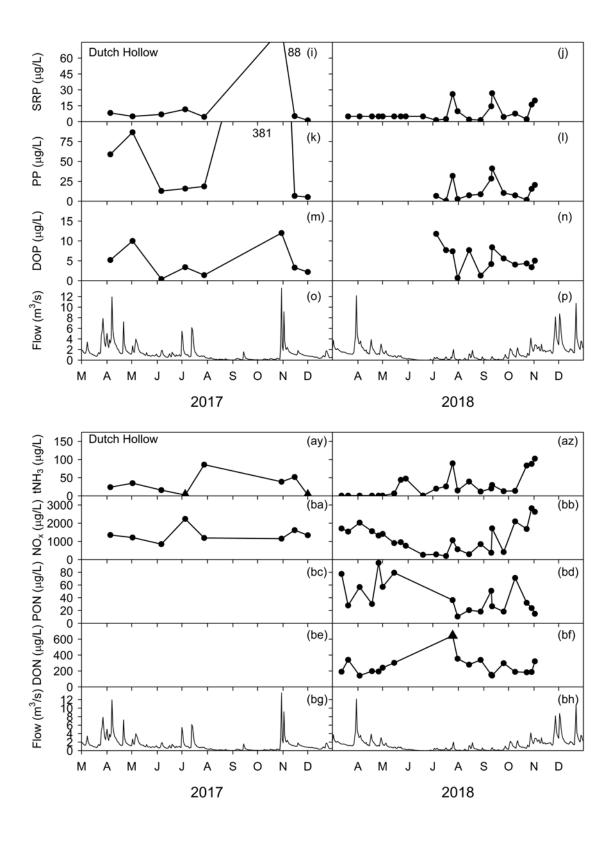
### **Appendix B: Tributaries and Loading**

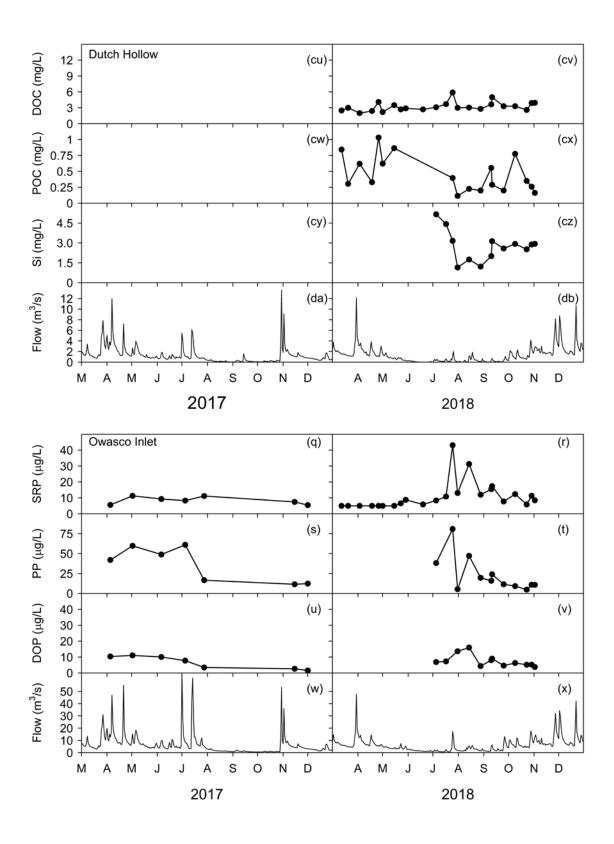
### Appendix B-1. 2017-18 Tributary Grab Sample Time series

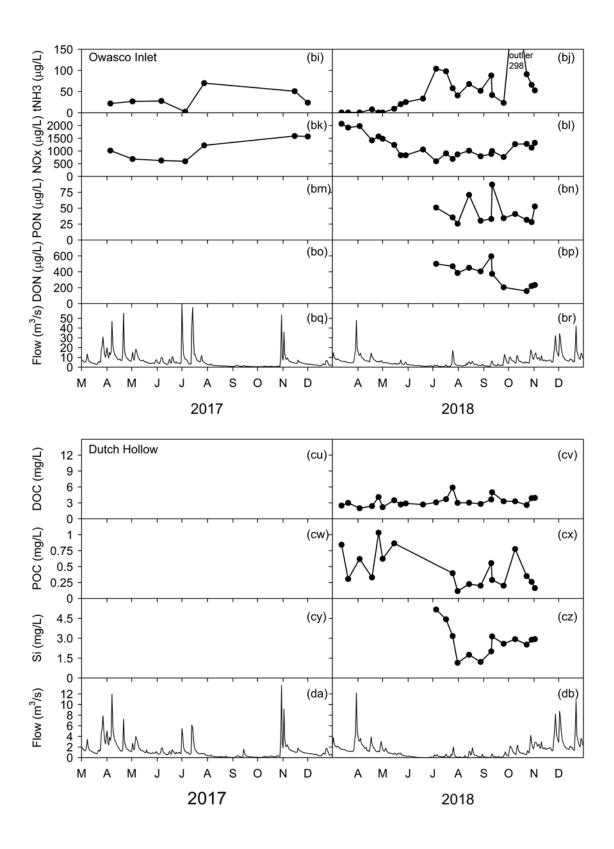
Time series of grab samples and calculated constituents required by the water quality model for Owasco Lake tributaries during 2017 and 2018 Triangles represent outliers removed from data prior to load estimation. Data are presented here as daily averages when multiple grab samples were taken on the same date.

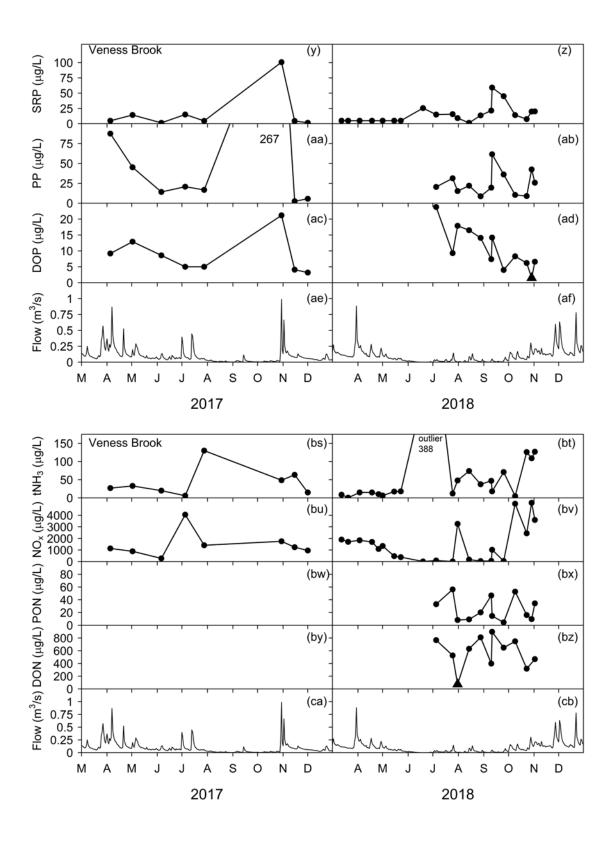


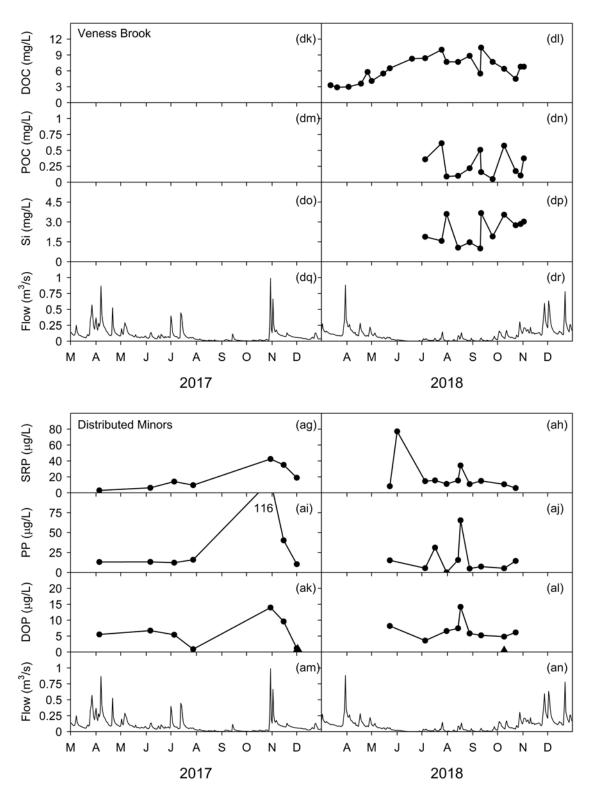




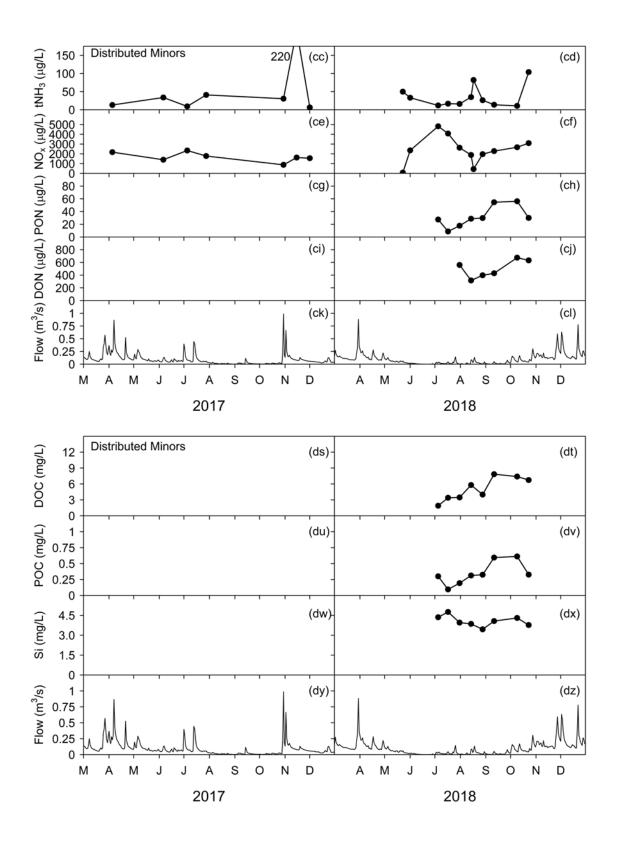








\*NOTE: The "floating" outlier is the result of data averaging.



# **Appendix B-2. Outliers Removed Prior to Load Estimation**

Table B-1. Outliers excluded from C-Q regressions used for load estimation in FLUX32.

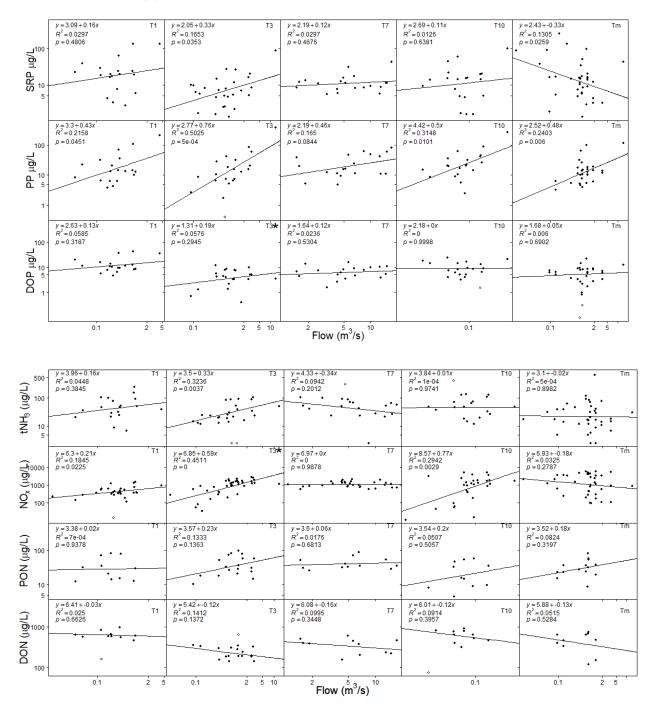
Tributary	Constituent	Date	Flow (m <sup>3</sup> /s)	Observed Concentration (µg/L)	Leverage (%) <sup>a</sup>	Reason(s) for exclusion
Sucker Brook	Silica	9/10/18	0.128	967.60	-0.05	below data trend, causes underestimation of concentration at low flow, identified as outlier by FLUX
Sucker Brook	NO <sub>x</sub>	5/15/18	0.261	13.30	-9.24	identified as unexpectedly low but verified result from lab, identified as outlier by FLUX w/ large impact on load
Sucker Brook	DON	9/10/18	0.128	160.11	-1.76	calculated constituent, low sample relative to rest of trend, also identified by FLUX
Dutch Hollow Brook	tNH <sub>3</sub>	7/5/17 12/1/17	1.147 0.828	2.50 2.50	2.52 -0.17	samples below LOD, identified as outliers by FLUX, both fall below the data trend
Dutch Hollow Brook	PP	7/17/18	0.654	0.40	-15.78	falls below the data trend, identified as outlier by FLUX
Dutch Hollow Brook	DON	7/25/18	1.243	644.07	-9.81	calculated constituent, high relative to rest of trend, identified as outlier by FLUX
Inlet	tNH <sub>3</sub>	10/9/18	4.600	298.00	-15.09	falls above data trend, associated with failed duplicate in lab, identified by FLUX as outlier
Veness	tNH <sub>3</sub>	7/5/18	0.027	388	-14.28	Identified as outlier by FLUX, large

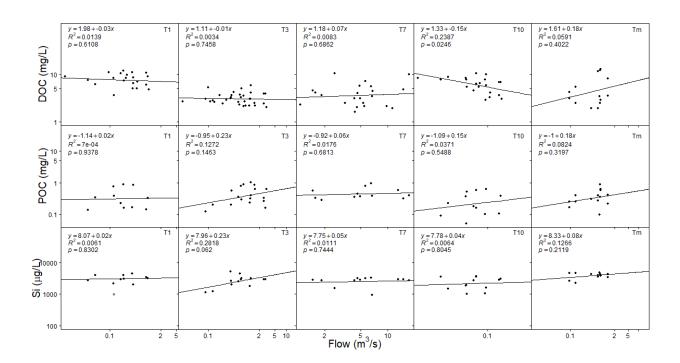
Tributary	Constituent	Date	Flow (m <sup>3</sup> /s)	Observed Concentration (µg/L)	Leverage (%) <sup>a</sup>	Reason(s) for exclusion
Brook						influence on loads, increased CV
Veness Brook	DOP	10/29/18	0.195	1.50	8.20	high flow with low concentration outside of data trend, causes underestimation of concentration at high flows, identified as outlier by FLUX
Veness Brook	DON	7/31/18	0.006	73.74	-37.17	very low compared to data trend, causes underestimation at low flow and overestimation at high flows, calculated constituent identified as outlier by FLUX
distribute d minors	DOP	12/1/17 10/9/18	0.909 0.762	0.30 0.10	-1.99 -12.49	falls outside of data trend, calculated constituent, both identified as outliers by FLUX

<sup>&</sup>lt;sup>a</sup> Determined using jackknife routine in FLUX32; represents change in load when specified data point is excluded

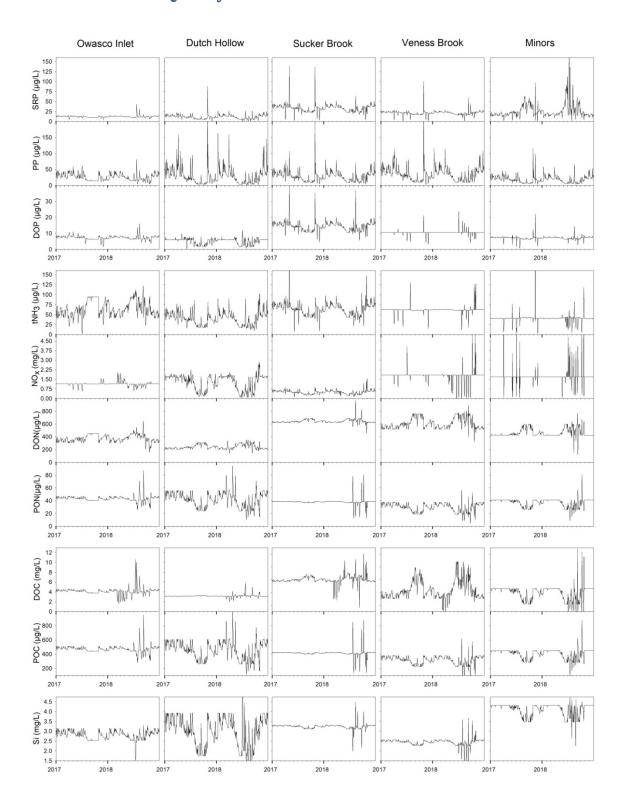
# Appendix B-3. Concentration Flow Relationships for Constituent Grab Samples

All relationships are presented as a single regression line after the removal of any data deemed outliers, which are plotted as open circles. If multiple regression lines were used to estimate loads, such as stratification based on flow, those relationships are presented in Section 2 and denoted with a (\*) below.





Appendix B-4. Daily Constituent Concentration Inputs to the Water Quality Model for 2017 and 2018



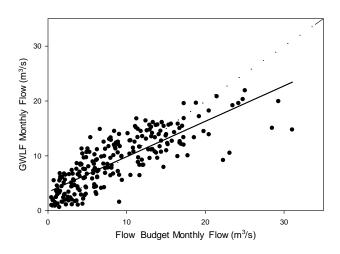
### Appendix B-5. Full GWLF-E Watershed Modeling Report

Use of data from multiple projects, each with a unique goal, can introduce variability into load estimation using observed samples. Sample size for some constituent load and concentration estimates was quite low for Owasco Lake Tributaries, especially calculated constituents. Although the use of actual observed samples is the most desirable, watershed modeling can also provide estimates of constituent loading. For this project, estimates were available through the use of the Enhanced Generalized Watershed Loading Functions (GWLF-E) model. GWLF-E is a combined distributed/lumped parameter watershed model, allowing for multiple land use/land cover scenarios. The most recent version utilizes data from the National Land Cover Database 2011.

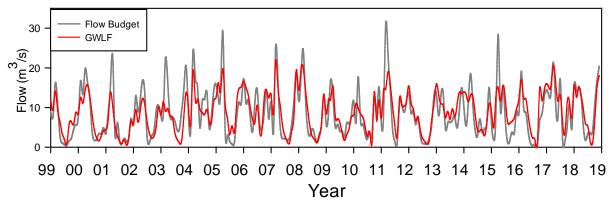
As of the writing of this report, GWLF-E is integrated with an open source online application maintained by the Stroud Water Research Center (Model My Watershed, www.modelmywatershed.org) that allows users to define an area of interest and model water quality and hydrology. The online tool uses available geospatial information system (GIS) layers to derive inputs for the area of interest and local meteorological data for 1961 through 1990 to model water quality. The model input file was exported from the online platform and calibration of the GWLF-E completed using updated meteorological data for the period of interest.

CE-QUAL-W2 uses hour meteorological data as a driver. The temperature and precipitation data was daily average for the years of interest (1999-2018) and were used to drive GWLF-E using a custom built data manipulation program for correct formatting. Other changes to model inputs were completed using the GWLF-E desktop program which provides six model driver categories with coefficients that can be edited manually.

Initial hydrology calibration was completed in smaller tributary watersheds with active stream gages, including the Owasco Inlet to the USGS gage in Moravia, and Dutch Hollow Brook. These efforts demonstrated good agreement between modeled and observed monthly flows after minor calibration of model inputs. Hydrology of the entire Owasco Lake watershed was calibrated using this projects flow budget and lessons learned from the smaller watersheds with stream gages. Modeled hydrology agreed well with the flow budget derived as part of the water quality modeling effort when monthly mean flows were compared (Figures B-1, B-2). Slight underestimation of modeled flows at the high end of the observed flow range was present throughout all testing and final model runs, and exists in other studies utilizing GWLF-E (i.e. Tetra Tech, 2007).



**Figure B-1.** Mean monthly flow ( $m^3/s$ ) from the Owasco Lake flow budget developed as part of this project, compared to monthly mean modeled flow from the GWLF-E model for 1999-2018 ( $R^2 = 0.675$ , NSE = 0.760).



**Figure B-2.** Timeseries of mean monthly flow (m<sup>3</sup>/s) from the Owasco Lake flow budget and modeled flows from GWLF-E from 1999-2018.

The GWLF-E model provides estimated loads of total and dissolved phosphorus and nitrogen as well as total suspended solids. A summary of the sources from which the model derives these estimated loads is available as well. Although these constituents aren't drivers for the water quality model, comparing load estimates derived using FLUX32 to a watershed model provided an approximation of variability in load estimation using different methodologies. Load estimates for comparison to GWLF-E that were derived using FLUX32 were the annual sum of constituent parts. Total phosphorus was the sum of daily mass (kg) of SRP, PP, and DOP; dissolved phosphorus was the sum of SRP and DOP. Total nitrogen was the sum of tNH<sub>3</sub>, NO<sub>x</sub>, DON, and PON; dissolved nitrogen was the sum of tNH<sub>3</sub>, NO<sub>x</sub>, and DON. The relative contribution of the dissolved portion of phosphorus and nitrogen varied between methodologies (Table B-2). This disparity likely is the result of how GWLF-E characterizes solid state nutrients as associated with sediment erosion and point source inputs without consideration for

compounds dissolving once they are in an aqueous environment (Haith, 1992). For this reason only loads of total phosphorus and nitrogen were compared as part of this project.

Table B-2. Percent of TP and TN made up of dissolved constituents as determined by FLUX32 software and the GWLF-E watershed model.

Method	FLUX32		GWL	F-E
Constituent	TDP (%)	TDN (%)	TDP (%)	TDN (%)
Mean	40	97	31	35
Minimum	37	97	25	33
Maximum	44	98	38	36

Constituent loading is dependent upon concentration and is a function of flow, with increases in flow resulting in an increased load if concentration remains the same. Assumptions made when setting up the GWLF-E driver file can significantly alter modeled constituent loading for a given flow regime due to the impacts of soil erodibility, attenuation, alteration of nutrient values from various land cover types, as well as the use of rural and urban best management practices which can alter either side of the concentration flow relationship. In the Owasco Lake watershed, initial model runs demonstrated a significant deficit of nitrogen loading compared to estimates using FLUX32 software. The agricultural land around Owasco Lake, and much of the Finger Lakes Region of New York State, contains tile drainage; a system of perforated piping to improve growing conditions for crops. Nitrogen constituents, especially nitrate, are labile in soil, and tile drainage contributes a significant amount of nitrogen loads downstream. After discussion with local Soil and Water Conservation Districts, a coefficient was included in the GWLF-E driver file that allotted 10% of all agricultural area with tile drainage. This addition resulted in similar loading estimates for total nitrogen between GWLF-E and FLUX32.

After hydrology and nitrogen calibration, the annual average total phosphorus loads using GWLF-E were nearly three times higher than those derived using FLUX32 software. Multiple reasons were identified that could impact the model estimates of phosphorus loading to be higher than observed values. First, the large wetland area at the mouth of the Owasco Inlet might alter the character of constituents as they move through. Particulate matter is deposited and dissolved constituents can be taken up within wetlands during the growing season. To account for these processes the "percent drainage" coefficient was adjusted within GWLF-E. The Owasco Inlet tributary watershed makes up approximately 57% of the total Owasco Lake watershed area, so a coefficient of 0.57 was applied. Second, a lot of effort has been placed in developing and implementing best management practices (BMP's) within the Owasco Lake watershed. BMP's linked with improved water quality from the watershed can play an important role in nutrient load reductions. An agricultural census for Cayuga County by the United Stated Department of Agriculture lists the use of no till agriculture (20%), reduced till agriculture (22%), and cover crops (21%) (USDA, 2019). In GWLF-E coefficients were applied under the BMP category to

include these inputs as well as some assumed values based off of reports of streambank stabilization efforts in the watershed (Ecologic, 2015). Finally, sediment loading (TSS) was compared between FLUX32 and GWLF-E, demonstrating a similar disparity to that observed for phosphorus. This suggests that much of the difference is due to high particulate loads derived through GWLF-E. To adjust this, under the "Transport" tab, an adjustment was made to decrease the amount of erosion along streambanks. This change was suggested in a report on the use of GWLF-E in the northeastern United States as a result of lower erodibility of glaciated soils, compared to the default value which is set for highly erodible soils. All changes to model inputs are listed in Table B-3.

**Table B-3**. Driver calibration for GWLF-E model for the entire Owasco Lake watershed.

Category	Driver	Downloaded value from MMW	Calibrated value	Justification
Transport	% tile drainage	0.0	0.1*	Conversations with local SWCD
Transport	Sed A Adjustment	1.5	0.3	{Penn State, 2007}
Nutrient	Dissolved runoff coefficient for Hay/Pasture	0.52	0.2	{Haith, 1992} Table B-15
Nutrient	Dissolved runoff coefficient for Crops	0.52	0.3	{Haith, 1992} Table B-15
Animal	Dairy Cows Grazing	Yes	No	Conversations with local dairy farmers
Delivery	Percent Drainage	0.00	0.57*	This study
BMP	Cover Crop	0.0	0.2*	{USDA, 2019}
BMP	Conservation Tillage	0.0	0.3*	{USDA, 2019}
BMP	Conservation Plan	0.0	0.3*	{Cayuga County, 2015} Table 5-2
BMP	Nutrient Management	0.0	0.3*	{Cayuga County, 2015} Table 5-2
BMP	Grazing land management/Ag- land retirement	0.0	0.1*	Assumption based on {Cayuga County, 2015} Table 5-2
BMP	Animal waste management system	0.0	0.1*	Assumption based on {Cayuga County, 2015} Table 5-2
BMP	Runoff Control	0.0	0.1*	Assumption based on {Cayuga County, 2015} Table 5-2

BMP	Phytase in Feed	0.0	0.1*	Assumption based on {Cayuga County, 2015} Table 5-2
BMP	Stream length w/ vegetated buffer (km)	0.0	25.0	Assumed length based on {Cayuga County, 2015} Table 5-2
BMP	Stream length w/ fencing (km)	0.0	10.0	Assumed length based on {Cayuga County, 2015} Table 5-2
BMP	Stream length w/ bank stabilization (km)	0.0	25.0	Assumed length based on {Cayuga County, 2015} Table 5-2

<sup>\*</sup>Represents a percentage as a decimal number

Watershed modeling of a large, complex system such as the entire Owasco Lake watershed proved challenging, however, lessons learned throughout the process are useful to understand what drives estimates of loads from a watershed model and how it compares to those estimated using FLUX32 software. Further fine tuning of the model might result in even better agreement between the two methods, but there is need for published data to back up any further calibration of model inputs. Annual total phosphorus load estimates were consistently higher from GWLF-E even after calibration of model inputs. Total nitrogen and sediment load estimates compared more closely but with a high amount of variability from year to year (Table B-4).

The year 2003 represents the worst comparison for TN and TSS (corresponding to the only year where TP estimates were higher using FLUX32) which lined up with the worst hydrograph fit. During this period the modeled flow were consistently low with respect to this projects flow budget highlighting the importance of hydrology in driving the GWLF-E model. Even though four meteorological stations were used to create the weather inputs used in GWLF-E, localized storms might have played a role in the disparity in flow during some years.

Table B-4. Comparison of annual load estimates from the Owasco Lake watershed (kg) using the GWLF-E model and FLUX32 software

Year	TP GWLF	TP FLUX	TN GWLF	TN FLUX	TSS GWLF	TSS FLUX
1999	21,173	9,378	357,373	293,222	3,780,300	3,033,917
2000	21,669	16,990	390,745	485,445	4,256,280	5,597,652
2001	16,969	12,018	254,079	345,644	3,103,740	3,848,485
2002	19,677	15,142	337,832	462,224	4,098,350	5,049,930
2003	19,110	21,504	336,242	601,766	3,652,460	7,151,953
2004	28,817	23,039	489,556	644,832	5,938,130	7,637,964
2005	32,805	19,141	567,918	513,511	5,825,580	6,062,978
2006	29,926	18,588	513,145	548,148	5,844,870	6,186,096
2007	26,428	17,953	476,660	497,745	4,268,610	5,848,442
2008	26,149	17,027	471,824	484,696	4,174,900	5,572,335
2009	21,714	12,192	365,081	397,286	4,369,970	4,023,776
2010	26,804	15,026	405,495	453,783	4,984,500	4,920,819
2011	32,869	22,292	558,181	613,881	6,934,740	7,412,168
2012	19,450	10,156	323,412	336,240	3,643,010	3,391,223
2013	29,681	16,092	519,664	501,924	5,924,250	5,381,310
2014	24,049	14,910	424,668	467,691	4,521,750	4,958,936
2015	27,376	15,800	474,724	444,020	5,624,690	5,149,478
2016	26,600	12,521	478,387	375,725	4,401,960	4,163,866
2017	32,072	20,047	603,876	550,001	5,606,700	6,962,387
2018	29,874	19,554	513,437	575,942	4,778,950	6,449,809
Mean	25,661	16,469	443,115	479,686	4,786,687	5,440,176
Min	16,969	9,378	254,079	293,222	3,103,740	3,033,917
Max	32,869	23,039	603,876	644,832	6,934,740	7,637,964
Range	15,899	13,661	349,796	351,610	3,831,000	4,604,047

References:

Ecologic LLC. 2015. Owasco Lake Watershed Management and Waterfront Revitilization Plan; Watershed and Waterbody Inventory Report.

Haith, D., Mandel, R., Shyan Wu, R. 1992. Generalized Watershed Loading Functions User's Manual Version 2.0. Cornell University Department of Agricultural & Biological Engineering.

Tetra Tech Inc. 2007. Limberlost Creek Watershed Sediment and Nutrient TMDL Development; Draft for U.S. EPA Approval. Accessed at:

 $\underline{https://www.in.gov/idem/nps/files/tmdl\_limberlost\_draftreport.pdf}$ 

United States Department of Agriculture (USDA). 2019. 2017 Census of Agriculture County Profile Cayuga County New York. Accessed at:

https://www.nass.usda.gov/Publications/AgCensus/2012/Online\_Resources/County\_Profiles/New\_York/cp36011.pdf

# **Appendix C: Limnology**

### Owasco Lake In-Lake Model

Biological Components Final Report Dreissenid Mussel, Plankton, and Mussel Bed Nutrient Survey Components Final Report

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### 1 I. Overview of Biological Component – Project Justification and Objectives:

### 1.1 Overview

Owasco Lake, NY, is one of a number of lakes in the Northern Temperate Zone that has shown increases in algal blooms and harmful algal blooms (HABs). A number of factors may contribute to these blooms, including nutrient loading (e.g., nitrogen and phosphorus), changes in climate that alter runoff timing and frequency, reduce ice cover duration and may increase surface water temperatures and the invasion of non-native species (e.g., Jöhnk at al. 2008, Pendergrass, A.G. and R. Knutti. 2018. Rantala et al. 2017, Sinha et al 2017).

Zooplankton, especially large species in the genus *Daphnia*, as well as invasive dreissenid mussels, both are efficient grazers of phytoplankton; both plankton and mussels have the ability to reduce algal concentrations at any given nutrient level (e.g., Sarnelle et al. 2005). However, zooplankton and mussels can exhibit selective feeding and may avoid consuming cyanobacteria, and they also excrete nutrients that may stimulate algal growth, including growth of HAB-producing species(e.g., Sarnelle 2005).

The invasions of predatory zooplankton such as *Cercopagis*, the fish-hook waterflea, and the two species of benthic Mollusca, zebra and quagga mussels (*Dreissena polymorpha* and *Dreissena rostriformis bugensis*) to many lakes in New York State may be altering nutrient recycling and the grazing of phytoplankton, potentially contributing to increases in HABs.

Upstate Freshwater Institute has developed an in-lake model that has been applied in other systems, such as Cayuga Lake, and the overall goal of this project is to parameterize a similar model for Owasco Lake, which has experienced a number of HABs in recent years (<a href="https://www.dec.ny.gov/chemical/83332.html">https://www.dec.ny.gov/chemical/83332.html</a>).

The primary tasks of this biological component of the project were to assist Upstate Freshwater Institute with collection of data to allow parameterization of these biological components for an in-lake model for Owasco Lake that includes biological parameters.

Specifically, data on the spatial/depth distributions of: (1) dreissenid populations, and characterization of the (2) phytoplankton and (3) zooplankton assemblages were collected and analyzed for input to the UFI in-lake model. In addition, nutrient samples from above mussel beds were collected and provided to UFI for analysis to inform estimates of nutrient recycling by mussels.

To support the application of a dreissenid module to the Owasco Lake In-lake Model, a dreissenid mussel survey in Owasco Lake therefore was required. The most recent benthic survey was completed in 2007 (Watkins et al. 2007). During that survey it was determined that zebra mussels had invaded the lake, primarily in shallow regions (<20 m), but quagga mussels had not yet invaded Owasco Lake. Quagga mussels were reported as having invaded Owasco Lake subsequently, but the extent of that invasion had not been quantified. Assessing the distribution of mussels at different depths of Owasco Lake was needed to parameterize UFI's 2-D nutrient modeling effort.

To that end, we collected both images of the benthos (sediment-water interface) and mussel samples from sites around the lake using a rig that was constructed to allow sampling of a standardized area of sediment that was also sampled for mussels, which were identified and counted in the laboratory. The goals of this dreissenid

task were to estimate the current dreissenid mussel composition (zebra and quagga mussels) in different depths and regions of the lake as well as to test the efficacy of using images to monitor benthic mussels.

In addition, a number of nutrient samples were collected by divers above mussel beds at differing depths, substrate types and mussel densities for analysis by Upstate Freshwater Institute (UFI) to estimate and validate model predictions for nutrient release from the mussel beds.

To parametrize the plankton components of the model, phytoplankton grab samples and zooplankton tows also were collected by UFI during their regular nutrient monitoring, and provided to SUNY ESF for analysis. These samples were enumerated and the taxonomic composition was quantified. The phytoplankton and zooplankton data were converted to summary parameters, including number and mass of zooplankton grazers, omnivores and predators over the summer season, and the biovolume of specific taxonomic groups of phytoplankton, that then could be input directly into the UFI water quality model.

This report summarizes the methods and results for the biological components of the Owasco In-Lake Model Project.

As listed in the initial project outline, the specific responsibilities for biological components were as follows:

- 1. Coordinate biological and nutrient sampling with Upstate Freshwater Institute.
- 2. Determine site locations; review parameter selection, and sampling frequency needs with UFI.
- 3. Work with the State University of New York's Dive Safety Officer to establish dive safety procedures and ensure adequate training of divers.
- 4. Oversee, train, and supervise field sampling and field assistants.
- 5. Oversee and supervise transfer of field nutrient samples to Upstate Freshwater Institute and receipt of plankton samples from Upstate Freshwater Institute.
- 6. Oversee training and supervision of mussel samplers and undergraduate student counters.
- 7. Organize, enter, and validate field data, images, and mussel survey counts.
- 8. Count plankton and zooplankton in samples received from Upstate Freshwater Institute.
- 9. Organize and analyze mussel and plankton data and deliver data and report to Upstate Freshwater Institute.

These objectives have been accomplished, although we were unsuccessful in finding a method that enabled quantification of mussels using image analysis.

### 1.2 Summary of delays in start and effect on completion of project, as well as additional delays

Although all of these components have been completed, because the contractual start of the project was delayed until June 2018, we were unable to recruit the graduate student to the project, and the biological components relied on summer undergraduate employees and the biological component PI (Schulz) as field hands and analysts, along with undergraduate volunteers in Fall 2018 and Spring 2019.

In addition, a delay in purchase of dive equipment at SUNY ESF's Purchasing office due to difficulty in obtaining alternate vendor bids pushed the dive plan approval back even further. Nonetheless, submission of dive protocols to the divemaster for approval was completed by the mid-June 2018. The necessary equipment

for divers was ordered and received in late June/early July, and training of personnel for diving on this project was co-ordinated by the SUNY ESF dive master from June through August. Preliminary dives and method testing for this project were approved by August 2018 and completed in August and September 2018. However, the delay prevented the dive master from being able to complete the three deep dives he had been planning to perform with another trained dive master (deep dives require special certifications and safety protocols), so we were unable to collect voucher mussel samples from deeper than the ~25 meter depth that our protocols permitted for the faculty and student divers.

Upstate Freshwater Institute also began their sampling for biological parameters later than expected, and our first plankton samples were received in July 2018. Plankton samples were collected by UFI from July through September 2018 and delivered to SUNY ESF for processing.

In addition, the PI was hindered in completing laboratory work due to a serious family injury that resulted in hospitalization, surgery, and rehabilitation, which made overtime work impossible from January-April 2019. Health issues in mid-2019 through early 2020 and then the extra work associated with the COVID-19 pandemic's effect teaching in March-May 2020 (moving to remote instruction and redesigning a large course with five lab sections) greatly interfered with progress as the project analysis was being completed. Nonetheless, despite these many setbacks, the required analyses and are now completed and a summary of the data collection, analyses and results are included in this project.

Due to delay in receiving all the required components from Schulz, UFI is still completing the modeling effort. All components of the originally conceived project have been analyzed and the Owasco Lake Model can be parameterized with the needed mussel, phytoplankton and zooplankton components to inform the consideration of factors contributing to HABs in Owasco Lake.

### 1.3 Summary of Personnel Involved in the Biological Component

**Primary Investigator for the Biological Components**: Kimberly L. Schulz, Associate Professor Department of Environmental and Forest Biology,

State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13215 (315) 470-6808 kschulz@esf.edu

### **Dive Safety Officer**

Jason Meany, Deep Stop SCUBA, 150 Township Blvd, Suite 20, Camillus, NY 13031; 315-378-7175, jmeany@deepstopscuba.com

### Responsibilities:

- 1. Approved all gear for use in the underwater imaging and scuba dive surveys.
- 2. Worked with PM Schulz and the research divers to certify that the dive methods are appropriate and train all dive personnel on the protocols and safety training.
- 3. Was contracted to collect 3-5 deep (>80-100+ feet) calibration samples

### Research Divers – late summer 2018

Alexander Romer (alexromer2@gmail.com) and Robert Pedian (bob.pedian@gmail.com)

### Responsibilities:

- 1. Learn dive protocols and be tested and cleared for project protocols by Dive Safety Officer, Jason Meany.
- 2. Assist with constructing field gear; checking and cleaning gear daily.
- 3. Along with PM Schulz, serve as surface tender or two-person dive crew for each sample collection site.

### **Volunteer Student Assistants and Researchers**

In the field: Tyler Duby, Matthew Cowen, Lydia Pleasants, Alexandra Cormack

In the lab: Lydia Pleasants, Alexandra Cormack, Carrick Palmer, Kyla Watson, Jack Zeng

Volunteer responsibilities in the field included:

- 1. Cowen, a former U.S. Navy sonar operator, was responsible for initial sonar setup and calibration with PM Schulz.
- 2. Student volunteers assisted as surface tenders during field sampling under supervision of PM Schulz (Duby and Cowen).
- 3. Cowen also assisted PM Schulz with sonar data collection.

### Volunteer responsibilities in the laboratory included:

- 1. Students were trained by PM Schulz to identify dreissenid mussels and to distinguish zebra and quagga mussels (Duby and Pleasants)
- 2. Students assisted PM Schulz in counting frozen mussel samples, previously collected in the field, by separating into empty mussel shells versus live mussels (Cormack, Duby, Palmer, Pleasants, Watson, Zeng).
- 3. Students assisted PM Schulz in identifying collected mussels as zebra or quagga (Duby and Pleasants).
- 4. Cowen assisted PM Schulz with sonar data and plotting data.

### II. Methods and Results

### 1.4 Part A: Mussel Objectives

The main objectives of the mussel component of the project were:

- 1. To survey mussel distribution and investigate patterns of mussel distribution with depth.
- 2. To provide nutrient samples collected above mussel beds where mussels would be quantified

A decade-old survey of Owasco Lake in 2007 (Watkins et al. 2010), approximately a decade after zebra mussels had invaded the lake, used an Ekman dredge to sample the organisms living on the surficial sediment in a transect on a centerline from the north to the south end of the lake. This survey indicated that zebra mussels,

(*Dreissena polymorpha*), but not quagga mussels (*Dreissena rostriformis bugensis*) were present in the lake at that time, reaching densities of 3,000-4,000 mussels per m<sup>2</sup> and reaching maximum abundances in the 10 m depth samples. They expressed concern that invasion quagga mussels would pose a risk to endemic benthic invertebrates that were persisting in a deeper water refuge in the lake at the time of that survey.

However, reports on iMap invasives and qualitative observations by Finger Lakes Institute and others indicated that quagga mussels have since invaded Owasco Lake. While zebra mussels tend to be most abundant on hard substrates and shallower regions of lakes, quagga mussels are able to thrive on soft sediments and are able to survive in deep waters, having been found to dominate the benthos in profundal areas of deep lakes (Karatayev et al. 2015).

Therefore the first objective was to resurvey the lake to quantify the presence and current distribution of invasive mussels in Owasco Lake, so that UFI could parameterize that portion of their 2D lake model.

### 1.4.1 A. 1. Survey of Mussel Distribution and Nutrients Above Mussel Beds – Field Sampling

After several test dives, UFI and ESF personnel agreed on a sampling strategy of sampling six transects, two each on the north and south end of the lake (Table 1; Figures 1A-D), one on the west shore on a rocky steep area about 1/3 of the way up the lake, and one near frequent HAB blooms on the sediment-rich and shallower-sloped east side of the lake, about 2/3 up the east shore (Figure 2).

In consultation with UFI, we established 6 transects from shallow (~2 m) to deep (~23 m) water to quantify mussel distribution in the lake, with the goals of determining the patterns of zebra and quagga mussel distributions with depth around the lake (Table 1; Figures 1A-D). These are the same sites for which nutrient samples were provided to UFI for analysis (see Part A.2).

Depth and site locations were geo-referenced using a high-end commercial side-scan sonar (Hummingbird Helix 5; SI.GPS).

We used underwater photography to take images of the mussels at the bottom of Owasco Lake and sampled known areas of the benthos with SCUBA for laboratory analysis (identification and quantification) to determine how many and what types of these dreissenid mussels are currently found at different locations in the lake, and how extensively these mussels cover the lake bottom. We imaged, collected water from above these mussel beds, and sampled the mussels at geo-referenced locations along the transects.

Quantification of zebra and quagga mussel distributions on the bottom of Owasco Lake was performed by use of a combination of direct sample collection by divers at known locations determined with sonar (and depth confirmed with dive computers) in conjunction with imaging of these reference sites. The hope was that images could be used to survey mussels on additional sites around the lake bottom quickly, as taking images and having an automated method for analyzing the images potentially would be less laborious than direct collect and counting, and would allow greater resolution for estimating coverage of the lake bottom with mussels if many photos could be collected from around the lake and analyzed quickly with imaging software.

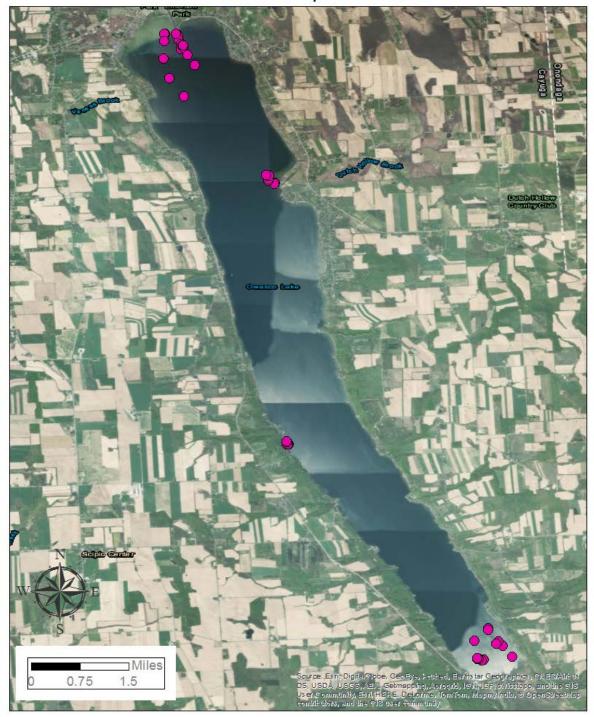
**Table 1.** Site numbers, depths, GPS locations, and whether a nutrient sample was collected (nutrient samples were not collected in conditions such as high plant density or the sediments being disturbed). The site locations are indicated with purple dots on Figures 1 A-D.

Mussel	Waypoint	Latitude	Longitude	<b>Depth in meters</b>	Nutrient
Site		(sonar)	(sonar)	(sonar or dive	Sample
Number				watch)	Provided to
					UFI
OW11A*	47	42 45.517	76 28.163	3.0	Yes
OW11B*	47	42 45.517	76 28.163	1.8	Yes
OW12A*	48	42 45.535	76 28.226	5.9	Yes
OW12B*	48	42 45.535	76 28.226	4.1	Yes
OW12C*	48	42 45.535	76 28.226	7.1	Yes
OW13**	between 48-49	N/A	N/A	10.9	No
OW14**	49	42 45.540	76 28.225	16.8	Yes
OW15**	50	42 45.540	76 28.225	11.8	Yes
OW16	53	42 53.913	76 32.413	1	Yes
OW17	54	42 53.819	76 32.415	4.9	Yes
OW18	55	42 53.583	76 32.424	9.9	Yes
OW19	56	42 53.315	76 32.346	13.8	Yes
OW20	57	42 53.070	76 32.160	21.6	Yes
OW21	58	42 45.560	76 27.759	1	Yes
OW22	59	42 45.705	76 27.881	6.0	Yes
OW24	62	42 45.920	76 28.078	21.9	Yes
OW25	63	42 45.773	76 27.944	14.1	Yes
OW26	64	42 45.740	76 27.966	11.2	Yes
OW27	66	42 51.907	76 30.946	1	Yes
OW28	67	42 51.946	76 31.020	4.8	Yes
OW29	69	42 52.008	76 31.038	16.4	Yes
OW30	70	42 52.014	76 31.014	8.2	Yes
OW31	71	42 52.018	76 31.053	22.9	Yes
OW32	72	42 48.410	76 30.782	1.0	Yes
OW33	73	42 48.413	76 30.748	11.9	Yes
OW34	74	42 48.416	76 30.761	4.5	Yes
OW35	75	42 48.439	76 30.770	17.9	Yes
OW36	76	42 48.446	76 30.783	20.6	Yes

<sup>\*</sup>Sites marked with an asterisk were collected while the boat was moored at the same sample site as another sample collection location. These sites were in close proximity (<5m) to each other, and given the wind conditions, movement of the boat, and/or the slight angle of the line on the camera rig (due to wind) their location could not be resolved to greater precision. The depth at these sites was determined with the dive watch depth reading. Note: at all sites, not just these, the sonar depth reading also was confirmed with the dive watch reading.

<sup>\*\*</sup>Three sites at which 'deep' mussel samples were collected in a smaller quadrat after the standard sampling of surface mussels was completed

## Owasco Lake Sample Locations

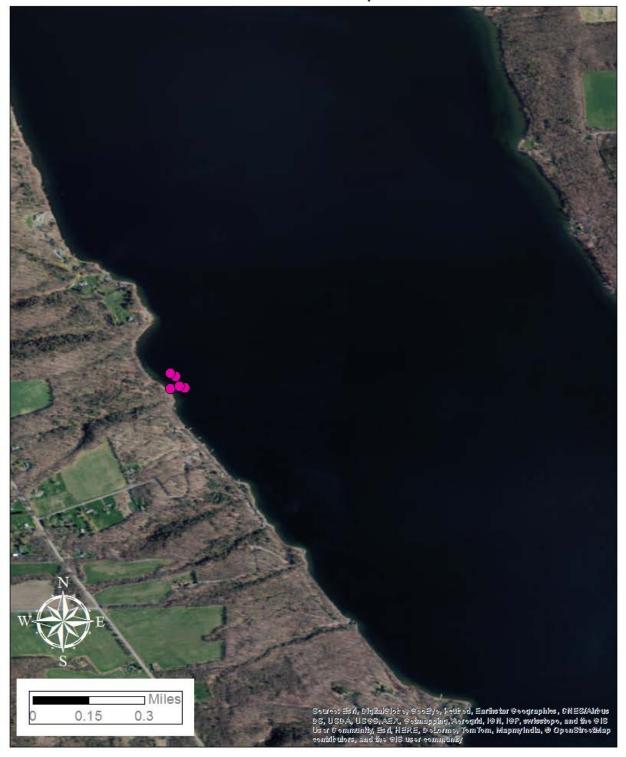


Figures 1A. Sampling transects and quadrat locations selected for this survey of Owasco Lake. Two shallow to deep transects were performed at both the North and South ends of the lake, one on the Northeast side, near the site of many HAB reports, and one on the southwest side. Note: the points on the Southwest side survey are close together due to the steep topography at this transect. See Table 1 for the coordinates and other site information.

# Owasco Lake Northern Sample Locations Miles

**Figure 1B.** Locations of the one eastern and two northern and transects and sites. See Table 1 for the coordinates and other site information.

# Owasco Lake Central Sample Locations



**Figure 1C.** Locations of Central/Western Owasco Lake transects and sites. See Table 1 for the coordinates and other site information.

# Owasco Lake Southern Sample Locations



**Figure 1D.** Locations of Southern Owasco Lake transects and sites. See Table 1 for the coordinates and other site information.

Lewis MacCaffrey (DEC) has demonstrated that mounting an underwater camera to a milk crate could allow imaging of lake sediments and dreissenid mussels. Because a milk crate has a closed top and so cannot be sampled by divers, we constructed a different version of a mussel camera rig to allow for imaging and collection of the imaged sample for laboratory analysis.(Figure 2a). This rig was constructed by Schulz and the undergraduate research divers with help from the machine shop at SUNY ESF. The frame was made from PVC and consisted of a standard 0.5 x 0.5 meters PVC dive sampling quadrat (a sampling square of known area) as the bottom of a PVC cube, with a GoPro attached to a crossbar at the top end of the cube, and lines connecting the corners of the top piece to a line for lowering the rig from the boat. The machine shop constructed attachments for two high-intensity dive lights so they could be attached to side struts to illuminate the entire bottom quadrat. The dive lights provided excellent illumination, but also were limited in battery life (~2 hours run time on a charge).

The GoPro was enclosed in a deep dive waterproof case and was set to record pulsed images, so the least disturbed image could be used for analysis. In cases where the GoPro image was slightly askew due to currents or bending of the frame, the dimensions of the quadrat in a partial image could be calibrated with the length of known PVC pieces in the image (e.g., Figure 2b). The open top and sides allowed for divers to access the imaged site.





Figure 2. (a) View from the GoPro of the sample quadrat while still on the boat. The camera is mounted with dive lights above the rig. (b) Typical view of the quadrat at the bottom of the lake with soft sediments and visible mussels covering much of the sediment surface.

The dive plan for sampling was approved by the Dive Safety Officer, Jason Meany, and he trained all of the divers on the protocol using blackout masks in a pool, until the sampling could be carried out in the zero visibility conditions that were present once sampling of mussels began, due to the stirring of the sediments.

According to the plan, at each station, an electronic dive slate with the site number was first be displayed under the camera before lowering over the side, so that the series of images that followed could be matched with the site/quadrat number. Then the rig was lowered slowly to the bottom and allowed to sit until any plume suspended by the quadrat was seen to dissipate on the sonar image. In calm conditions, sediment disturbance was minimal, but in windy conditions, if the tender vessel was pulling on the anchor, sampling the quadrat, and

interpretation of images was not always possible, as the sampling rig was dragged along this bottom. This necessitated limiting mussel and nutrient sample collection to calm days.

Dive lights were generally left off during the descent of the dive rig to the bottom of the lake, so those images are often greenish or dark in hue depending on the depth.

As mentioned, at times, such as in Figure 2 above, the camera would become slightly skewed due to movement on the trip down, but the known length of the PVC pieces could then be used to determine the image sizes for potential calibration. All images were uploaded to a Google Drive and images and movie clips from the GoPro can be accessed at a folder containing all raw images collected during the dive surveys: <a href="https://drive.google.com/drive/folders/119AwPQoICqr\_jAZFkTtmXb-4Ri4X4wql?usp=sharing">https://drive.google.com/drive/folders/119AwPQoICqr\_jAZFkTtmXb-4Ri4X4wql?usp=sharing</a>.

Lowering the rig to the sediments stirred up sediment if the area was covered in soft mud (most of the Owasco Lake bottom). We could visualize any sediment disturbance on the sonar after the rig was deployed and reached the bottom. The divers waited at least 5 minutes to descend slowly down the line to the sample site. The two divers had distinct tasks. Diver 1 carried an acid-washed re-sealable plastic bag labeled with the site number. Diver 2 carried a double plastic mesh sampling bag, gloves and trowel, Before either diver touched the bottom and disturbed sediments, the nutrient sample was collected by Diver 1 from 0.5-1 m above the quadrat in an acid-rinsed bag.

Upon Diver 1's completion of that task, Diver 2 descended to the bottom of the lake and knelt at the edge of the quadrat. Diver 2 turned off the dive lights to save batteries and because once sampling commenced, suspended sediments reduced visibility to 0 meters even with the light on. Diver 1 remained about 1 meter above the quadrat, watching the progress of Diver 1 and monitoring air bubble release to ensure safety of Diver 2. If any concern about safety had been observed, Diver 1 would have signaled the tender on the vessel by a pre-arranged number of pulls on the line and proceeded to assist Diver 2 and follow safety protocols to abort the dive if necessary.

Diver 2, provisioned with a doubled plastic mesh collecting bag, trowel and gloves, was responsible for collecting all surface mussels for identification and counting after Diver 1 had finished collecting the nutrients and had then become established in the safety observer position.

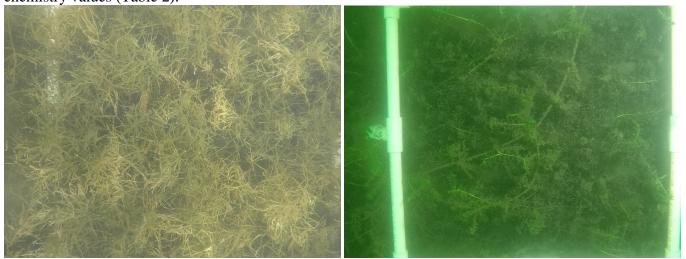
Once collection of mussels began, the sediment was disturbed by the movements of Diver 2, resulting in zero visibility, so all collection was done by hand/feel. This was one of the tasks practiced in a pool in advance, with the dive master giving the divers blackout masks and requiring them to collect small objects and verifying that they were able to collect *all* the small objects from within a quadrat with zero visibility.

Collection at the site continued until all mussels were removed from the surface of the site. The mussel-collecting diver (Diver 2) then signaled completion, and joined the tending diver (Diver 1) who was hovering and observing ~one meter above the collector, and the two surfaced in accordance with safe diving protocols. On the deeper dives, dive logs and dive watches were monitored closely to ensure dive safety and perform any required decompression.

As soon as the diver surfaced, the boat tender labeled the mussel bag with the site number, made sure it was drained, and immediately put it on ice in a cooler. The boat tender also collected the nutrient bag from Diver 1 and carefully used some of the water to rinse the acid-washed nutrient sample bottles provided by UFI, and then filled the bottle with the rest of the sample and immediately placed it in a separate cooler.

Fortunately, there were no safety issues on any of the dives.

The test dives and five sampling survey transects from shallow (1 m) to deeper water (~25 m) were completed around the lake (including transects on south, east, west and north shores) in August and September 2019. At several sites, the nutrient sample bags did not contain enough water to rinse and fill the bottles, or were spilled accidentally by the tender, accounting for the sites with mussel samples, but lacking corresponding water chemistry values (Table 2).



**Figure 3A and 3B.** Examples of images of sites with plants (3A - Site OW21; 3B – Site OW22)

At sites with macrophytes, the images just showed plants, and mussels were not visible. Note the tendency of the GoPro to become uncentered during some descents. Different camera rig attachments were tested to reduce this tendency, but none of the tested standard attachments was completely stable in all conditions, again requiring reliance on the known size PVC connectors to calibrate image sizes (e.g., Figure 3). Although we realized that images would not be useful in macrophyte beds, we still collected some samples in these shallow regions so we could characterize the mussel populations and nutrients in these areas.

We collected mussel samples at the bottom of the lake from shallow (~1-3 m) to deep (~20 m) sites along the five transects and collected water as described above from above these mussel beds. Upon return to shore after a day of diving, nutrient samples were delivered to UFI, or UFI personnel picked them up within 12 hours of sampling completion. Sample days often extended past normal business hours, in which case samples were stored in a portable cooler in the field and in a walk-in cooler (0-2°C) at SUNY ESF upon return to the laboratory, until UFI could receive the samples the next morning.

We anticipated that deep dives by the ESF diversaster would be completed in Spring/Early Summer of 2018, but the lack of funding and approval for these dives in early summer when the dive master was available (before the commercial dive shop he runs was operating at full-capacity for the season) made this impossible. The delay in project start prevented him from being able to collect those samples.

Upon return to the lab, mussel samples were frozen until counting.

### 1.4.2 A.2. Observation and Preliminary Estimation of Live Mussels Below the Surficial Sediments

During collection of mussels from the first sites at approximately 10 m depth, we (Schulz and Pedian) made the surprising observation that the sediments were very unconsolidated in composition, and it was possible without

much effort for a diver to extend his or her arm into the sediments past the elbow and to the shoulder. The best analogy we could make about the consistency of the sediments was that they were equivalent to the thickness of a milkshake or smoothie. In addition, it was observed (tactilely, since visibility is zero after sediments have been disturbed) that there seemed to be intact (closed) and possibly live mussels present beneath the surface sediments.

The presence of these mussels was intriguing, but beyond the scope of this study. We didn't want to include these deeper mussels in the counts of the mussels at the site, since that would be a change in sampling protocol. In addition, these deeper mussels, even if alive, would obviously not be visible from images of surface sediments and would complicate comparison of counts with image analysis. Therefore, we continued to collect surficial mussels according to standard protocol at these sites and all other sites.

However we realized that if there were mussels alive deep in the sediments, their potential movements and respiration might have an influence on sediment mixing and the release of nutrients from deep sediments to the sediment surface. After convening onboard the vessel, we decided to take pilot samples of deeper mussels after collection of the standard surface mussel samples.

Accordingly, after the standard nutrient and surface mussel sampling at sites 13, 14 and 15, we collected deeper mussels from a smaller quadrat (0.25 m X 0.25 m) placed within the sample grid after the surficial mussels had been removed according to the standard protocols. We attempted to keep the depth of sampling for these separate collections somewhat consistent, by marking a spot on each of our arms at approximately 50 cm depth and collecting mussels to that depth, and only sampled these deep mussels at these three sites. These deeper mussels were also returned to the lab and frozen until analysis.

Counts revealed that there were substantial numbers of live mussels deep in the sediments of these sites (Figure 4). About 75% of the intact mussels deep in the sediments were quagga mussels. It is unclear if these mussels are metabolically active or if they can move up and down in the sediments. Their presence deep in the sediments is intriguing and perhaps warrants further investigation, especially related to the potential for sediment movement and oxygen consumption or effects on redox potential in the sediments, which also may affect nutrient release from sediments.

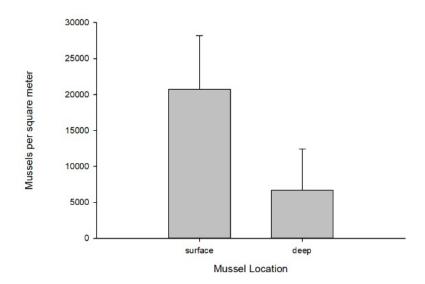


Figure 4. Number of live mussels per square meter at the surface and below the surface to ~50 cm depth at 3 test sites.

## 1.4.3 <u>A.3. Survey of Mussel Distribution and Nutrients Above Mussel Beds - Nutrient composition</u> above mussel beds

Upstate Freshwater Institute analyzed the water samples collected above the sediment water interface at the sampling quadrats parameterized the in-lake model (Table 2).

Not every site with mussel counts had nutrient concentration data, and many sites with nutrient concentrations did not have mussel counts (see mussel-counting section for more details). Higher concentrations above mussel beds might suggest nutrients are being released from the beds to the overlying water. The data from 13 sites with mussel counts and nutrient data (Table 3) did not show any simple significant linear regression relationships between mussel density and any of the nutrient concentrations. Benthic nutrient concentrations are influenced by numerous factors including water depth, water oxygen concentrations, sediment composition, as well as the possible relationship with mussel concentrations.

**Table 2.** Results of water chemistry analysis from water samples collected ~0.5 m above the sediment surface by the SUNY ESF scientific divers and analyzed within 24 hours of collection by Upstate Freshwater Institute.

Sampling	Depth (m)	tNH3	TP	TDP	SRP
Date	dive watch	(µgN/L)	(µgP/L)	(µgP/L)	(µgP/L)
08/20/2018	16.8	48	14.9	8.6	5.8
08/20/2018	11.8	86	12.6	5.8	0.8
08/20/2018	3	43	39.3	8	0.3
08/20/2018	1.8	38	72.1	7.4	0.3
08/20/2018	5.9	74	57.2	15.2	5
08/20/2018	4.1	54	25.1	8.2	1
08/20/2018	7.1	93	62.6	10.2	5.3
09/01/2018	0.93	43	14.5	5.7	0.7
09/15/2018	5.1	19	11.7	2.1	0.3
09/15/2018	10.14	27	12.2	0.5	0.3
09/15/2018	13.8	40	35.7	5.3	3.7
09/15/2018	21.5	5	10	3.5	1
09/15/2018	1	22	14.6	3.2	0.3
09/15/2018	6	36	39.8	0.5	0.6
09/15/2018	No sample				
09/15/2018	21.9	24	14.8	3.6	0.6
09/15/2018	14.1	99	19.5	0.5	4.9
09/15/2018	11.2	37	13.1	2.3	0.3
09/16/2018	1	31	11.3	6.3	0.9
09/16/2018	4.8	35	10.1	2.4	0.3
09/16/2018	16.4	19	17.7	0.5	0.3
09/16/2018	8.2	35	10.4	2.5	0.3
09/16/2018	22.9	17	12.1	1.4	0.3
09/16/2018	1	22	13.9	2.2	1
09/16/2018	11.9	34	13.5	1.1	0.3
09/16/2018	4.5	18	18.8	0.5	0.3
09/16/2018	17.9	11	15.8	2	0.3
09/16/2018	20.6	5	16.1	3.9	0.7

**Table 3.** Inorganic nutrient chemistry data for sites with both mussel counts and nutrient chemistry

Site	Depth (m)	tNH3 (μgN/L)	TP	TDP	SRP	Mussels per m <sup>2</sup>
OW11 A	3	43	39.3	8	0.3	812
OW11 B	1.8	38	72.1	7.4	0.3	392
OW12 A	5.9	74	57.2	15.2	5	6484
OW12 B	4.1	54	25.1	8.2	1	7032
OW 14	16.8	48	14.9	8.6	5.8	16148
OW 15 B	11.8	86	12.6	5.8	0.8	29336
OW19	13.8	40	35.7	5.3	3.7	8980
OW26	11.2	37	13.1	2.3	0.3	6472
OW29	16.4	19	17.7	0.5	0.3	21500
OW30	8.2	35	10.4	2.5	0.3	19628
OW31	22.9	17	12.1	1.4	0.3	3644
OW33	11.9	34	13.5	1.1	0.3	5440
OW36	20.6	5	16.1	3.9	0.7	9364

## 1.4.4 A. 4. Counting of mussel samples and image analysis

We counted the frozen mussels that were collected at each site to estimate the number of mussels in the lake. Samples were kept frozen and small subsamples removed for processing each day. Because the delay in funding prevented recruitment of a graduate student to the project, and funds were not available for a student in 2019, counting was performed by the PI and a group of undergraduate volunteers who were trained to identify zebra and quagga mussels. This small army of volunteers was dedicated and reliable, but only able to work 4-8 hours per week for credit. Much of the counting was therefore performed by Schulz.

For each sample, mussels were each identified as zebra or quagga mussels, and dead shells were separated from the mussels that had been alive (were intact) at the time of sampling. Because there were so many shells on the sediment surface, the process of separation of mussels that had been alive at the time of sampling from the loose shells was laborious and time consuming.

We spent some time (several weeks) trying to develop a protocol for subsampling the mussels, but were unable to achieve subsamples that had similar species composition and body masses by various types of mixing/homogenization, and did not find a protocol in our literature survey. So we proceeded with counting the entire sample. Some of the larger samples required many tens of hours of labor to identify to species and count. We would recommend that future surveys use smaller quadrats to reduce the large time commitment of sample identification and processing.

In total, surface mussel samples from 14 sites were completely processed and sorted to species of mussel (Table 4). Shells of the zebra and quagga mussels that had been collected alive were placed in separate bags for each sample and re-frozen. Later these samples were used to measure the lengths of each type of mussel at each site to help parameterize the filtration rates. At each site a subset of 25 mussels of each species (when present) was measured with a digital micrometer to estimate the size composition of mussels at each site for parameterization of mussel filtration rates for the UFI model (Appendix 1).

We used images from five of the sites during Spring and early Summer 2019 in the open source ImageJ software package and attempted various methods for automating counting from images, with the goal mentioned previously of being able to increase resolution of mussel density estimates through image analysis.

Schulz uses ImageJ to automatically count microscope images of DAPI stained bacteria taken using epifluorescence microscopy on a compound microscope, and we have found this method agree with 99% accuracy to manual user counts of bacteria, so we were optimistic about the potential efficacy of this approach.

Despite concerted attempts to adjust contrast and other parameters to increase the ability of the software to identify and count mussels, we did not succeed in getting the program to identify the mussels automatically. In fact, even with manual counting of mussels in the images, it was often hard to identify mussels because they are not a 2-dimensional surface (unlike the bacteria), but are packed in clumps. In addition, the mussels are found in different orientations and it is hard or impossible to distinguish live from dead mussels. We concluded that our image analysis would not provide an accurate indication of mussel abundance. However, we know Lewis McCaffrey (DEC) is attempting a similar analysis, and perhaps he will have more success. In that event, or if someone wants to investigate other software or machine learning for estimation, the images are available at the link provided earlier in this document. In our investigations, it seemed potentially possible to determine a relative abundance of the mussels with image analysis, but we were discouraged about the likelihood of obtaining quantitative mussel estimates from this method. Unfortunately, that means that rapid surveying of exact numbers of mussels from additional photographic imaging may not be successful. However, such a survey might allow a *qualitative* estimation of the mussel density over the lake bottom.

Based on our manual counted samples, we determined that at many locations in Owasco Lake, there are now thousands of mussels per unit of m<sup>2</sup> of sediment area (Table 4; Figure 5). We also found that compared with the previous 2007 survey (Watkins et al. 2010), quagga mussels in the lake now extend down to the deepest sites we sampled (~25 m). It is unfortunate the dive master was unable to sample deeper sites in 2019 as that would have been informative for determining mussel extent. Perhaps Lewis McCaffrey's sampling can help inform that distribution. Since oxygen concentrations in the hypolimnion of Owasco Lake in summer are low, it is likely that the metalimnetic sediment samples we collected may represent the maximal extent of the mussel distribution, but it is possible that mussels persist in deeper water. The deepest sites we sampled were below the thermocline and still contained substantial numbers of mussels.

We determined that in many locations there are thousands to tens of thousands of mussels per square meter of benthic surface area. We also found that there are now quagga mussels in the lake that extend down to at least 25 m, while zebra mussels remain in the lake, but are mostly on hard bottom, steep areas on the west shore. Many mussels are also present on the aquatic plants in the lake, and their feeding may also influence nutrients in the water or HAB formation, but this has not been investigated extensively previously. We also found that in the soft sediment areas, live mussels extend deep in to the sediments, which is surprising as this has not been reported previously; we are uncertain the role that these mussels may play in resuspending nutrients from deep sediments.

While zebra mussels remain in the lake, they are more common on hard bottom, steep areas on the western shore, and on shallow sites with plants (Table 4; Figure 4). Similar observations of zebra mussels dominating in shallow areas and quagga mussels in deep areas have been made in other systems (e.g., Karatayev et al. 2010). The depth at which quagga mussels begin to dominate the mussel assemblage appears to occur at around 7 meters (Figure 4).

Many mussels were present on the aquatic plants in the lake (Table 4). These are likely not counted during sampling with Ekman or other dredges. Although macrophyte samples are also laborious to process -- as the mussels need to be separated from the plant material, many small mussels recruit to plants. The high proportion of juvenile mussels on the plants also makes it harder to identify species and to measure lengths. The role of these mussels in the water column may be more substantial than appreciated, and the synergistic effect of mussel filtration increasing light penetration, which may increase macrophyte growth, likely promotes both plant growth and recruitment of zebra mussels nearshore.

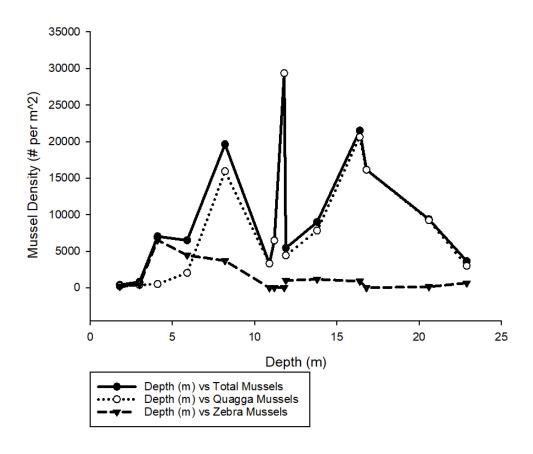
However, the presence of these mussels on plants and their feeding – not just in the sediments, but also in the water column while attached to plants – may also influence nutrients in the water or HAB formation. Further investigation of the water column feeding selectivity and processes on the nearshore phytoplankton might be informative.

We also found that in the soft sediment areas, live mussels extend deep into the sediments, which is surprising as this has not been reported previously and we are uncertain the role that these mussels may play in resuspending nutrients from deep sediments.

**Table 4**. Total zebra and quagga mussels in the **0.25 m<sup>2</sup>** samples collected from Otisco Lake in summer 2018 that were alive when sampled

SITE	Total per m <sup>2</sup>	Depth (m)	Total Mussels Alive (# per 0.25 m^2)	Total Quagga Mussels Alive (# per 0.25 m^2)	Total Zebra Mussels Alive (# per 0.25 m^2)	Habitat notes
OW11 A	812	3	203	99	104	in macrophyte bed
OW11 B	392	1.8	98	60	38	in macrophyte bed
OW12 A	6484	5.9	1621	510	1111	
OW12 B	7032	4.1	1758	127	1631	in macrophyte bed
OW13	3316	10.9	829	829	0	
OW 14	16148	16.8	4037	4033	4	
OW 15 B	29336	11.8	7334	7332	2	
OW19	8980	13.8	2245	1956	289	
OW26	6472	11.2	1618	1615	3	
OW29	21500	16.4	5375	5154	221	
OW30	19628	8.2	4907	3983	924	
OW31	3644	22.9	911	749	162	
OW33	5440	11.9	1360	1108	251	
OW36	9364	20.6	2341	2308	33	

Summary of Total Mussel Density and Density of QM vs ZM with Depth



**Figure 5**. Distribution of mussels with depth for all quadrats sampled

### 1.5 Part B: Phytoplankton Objectives

The primary objectives of the phytoplankton component of this project were to parameterize the seasonal phytoplankton distribution component of the model. Specifically, these were to:

- B1. Identify and count phytoplankton in samples collected by UFI from their monitoring station during the 2018 season
  - B2. Convert the phytoplankton densities to biovolumes using species-specific conversion factors
- B3. Create a summary table for each of the major groupings of phytoplankton used in UFI's in-lake model, ready for input to the model
- B4. Summarize results of phytoplankton counts from samples collected from nearshore stations in Owasco Lake in 2016, where UFI did not sample with fluoroprobes (and so biovolume and taxonomic group summaries were not compiled). Not surprisingly, the nearshore phytoplankton and zooplankton compositions vary significantly from those of the offshore 2018 sampling sites. Because the goal of this analysis was not for model input per se, but to fully characterize the phytoplankton assemblage, more subsamples (10 per sample) were enumerated for these samples than for the 2018 samples. The methods for sample processing also varied slightly. The 2016 summary and methodological differences are elaborated briefly in section B1/B2. The biomass summaries for 2016 phytoplankton are provided in Appendix 6.

## 1.5.1 B.1/B.2. Identification and Counting Methods and Conversion to Biovolumes

Phytoplankton samples were collected by UFI according to their standard protocols, and preserved with Lugol's solution. UFI collected samples with a Kemmerer bottle from 0.5 m depth at their monitoring site. Samples were provided to SUNY ESF after collection.

Methods were standard for phytoplankton analysis and generally paralleled those of the Cayuga Lake modelling project performed by Cornell University. Upon receipt of the phytoplankton samples at ESF, they were stored at 4°C in the dark until counting. Every 1-2 months, samples were checked for color and additional Lugol's solution was added if necessary (only one sample required addition of more Lugol's solution, on one date). One sample was observed on the first check-in date to have had a cracked lid, resulting in sample loss and loss of color, so this sample was not processed due to sample volume loss and likelihood of inconsistent preservation.

In order to count the phytoplankton sample, it was first concentrated using the Utermöhl method, which allows phytoplankton to settle out of a larger volume and be concentrated on a coverslip for counting on an inverted microscope. In this process, the sample bottles were inverted 10X to homogenate, and then concentrated by settling for at least 2 hours in a 1 cm (10 mL) Utermöhl chamber constructed by Aquatic Research Instruments.

Counting was performed using a Leica DMB IRB inverted microscope, generally using a 10X objective, with a 1.5 x side magnifier and a 10X HG Plan ocular. For one sample in 2018, when there was a humungous bloom of small *Microcystis*-like cells, the subsamples were counted with the higher magnification ocular, so a different concentration factor was applied to calculate biovolume, as described next.

The field of view dimensions for each ocular were confirmed with a stage micrometer. For the 10X objective the diameter of a complete field of view was 1.368 mm, so given the 1 cm height of the settling chamber each complete field of view counted the cells in 0.0137 mL. For the few samples counted at higher power, the diameter of the field of view was 0.32 mm, so the complete sample enumerated was 0.0008 mL.

All the phytoplankton in replicate complete fields of view were enumerated, using a method in which random fields along a diagonal transect from upper right to lower left of the counting chamber were fully enumerated, with every cell within the field or touching a set half of the field identified and counted as being within the field.

Phytoplankton were identified to Genus when possible, or to the lowest taxonomic group possible with the limitations of the Utermöhl method, but always at least to Phylum. (Note: formerly 'Division' was standard for phytoplankton, as in the Cayuga Lake report. The current convention is to use 'Phylum' rather than 'Division' for phytoplankton, to be consistent with other organisms).

Cell numbers were converted to biomass using biovolume conversion factors for the same taxa at similar seasons from the Cayuga Lake study or literature values, and reported as  $\mu m^3$  cell volume per mL of water. Biovolumes from major taxonomic groups were summed for input by UFI into their in-lake model. The conversion factors and their sources are given in Appendix 2.

This process was repeated for each sample, and seasonal patterns in biomass for the major taxonomic groups used in the modeling effort were provided to UFI, along with the count data from the microscopic analysis.

In 2016, when the goal was taxonomic enumeration of the sample, 10 fields were enumerated and the entire chamber was searched for rare taxa.

In 2018, when the goal was to parameterize the in-lake model, three or 4 fields were enumerated, making sure sample size was at least 200 identified individuals. On one sampling date in 2018, there was a massive bloom of single-celled cyanobacteria that were categorized as *Microcystis* based on shape, but obviously it would have required genetic analysis to determine the actual strain of cyanobacteria. For purposes of biovolume correction, this distinction is unimportant. The bloom was so dense that the microscope field was packed with cells and very difficult/impossible to enumerate at the normal objective/power. Therefore, for these samples, magnification was switched to a higher power objective to make counting feasible. These counts were than adjusted for the smaller volume of sample counted, and the cells were highlighted in yellow to make the distinction clear, and a comment entered into the spreadsheet. All other phytoplankton samples for both 2016 and 2018 were enumerated at the magnification listed as standard.

Because of the current state of flux of phytoplankton taxonomy, taxonomic names were checked after counting in February and March, but before sample data analysis, for Phylum and Family accuracy on the taxonomy browser function in AlgaeBase.com (accessed in June 2020).

Detailed summary tables of the taxonomic composition and biovolume conversions for samples from each field collection date in 2018 are provided in Appendices 2 and 3.

## 1.5.2 B.3. Summary tables for model input

After identification and enumeration were complete, the densities and biovolumes of species for the taxonomic group's use in the in-lake model were pooled for each date, and provided to UFI in a tabular form for input into the lake model (Tables 5 and 6 below).

**Table 5**. Phytoplankton density (#/mL) summarized for major taxonomic groups (Cynanophyta, Chlorophyta [including taxa currently reclassified as Charophyta], Bacillariophyta, Chrysophyta, Cryptophyta, Euglenophyta, and Dinoflagellates) in 2018 for input to the Owasco Lake model

Date	Cyano.	Chlorop.	Bacill.	Chryso.	Crypto.	Eugleno.	Dino
5-Jul-18	6065	1754	913	73	37	0	0
18-Jul-18	25089	4238	3946	0	49	0	0
2-Aug-18	408116	4238	3946	0	49	0	0
31-Aug-18	8477	2972	1364	0	0	0	49
12-Sep-18	30301	3215	4287	0	49	0	0
27-Sep-18	5213	974	633	1705	49	0	244

**Table 6.** Phytoplankton biovolumes (μm³mL¹) summarized for major taxonomic groups (Cynanophyta, Chlorophyta [including taxa currently reclassified as Charophyta], Bacillariophyta, Chrysophyta, Cryptophyta, Euglenophyta, and Dinoflagellates) in 2018 for input to the Owaco Lake model.

Date	Cyano.	Chloro.	Bacill.	Chryso.	Crypto.	Eugleno.	Dino.
5-Jul-18	2.48E+05	1.39E+05	7.99E+05	6.85E+03	1.30E+04	0.00E+00	0.00E+00
18-Jul-18	2.30E+05	8.40E+05	1.48E+06	0.00E+00	1.74E+04	0.00E+00	0.00E+00
2-Aug-18	5.01E+06	8.40E+05	1.48E+06	0.00E+00	1.74E+04	0.00E+00	0.00E+00
31-Aug-18	1.92E+05	2.01E+05	1.23E+06	0.00E+00	0.00E+00	0.00E+00	2.05E+05
12-Sep-18	1.33E+05	9.26E+04	3.92E+06	0.00E+00	1.74E+04	0.00E+00	0.00E+00
27-Sep-18	3.51E+04	2.79E+04	5.49E+05	1.60E+05	1.74E+04	0.00E+00	1.03E+06

## 1.5.3 <u>B.4. Summary tables for taxonomic enumeration of 2016 phytoplankton assemblage on each sampling date and from each sampling location</u>

Summary tables of the composition of the phytoplankton assemblage and cell counts on each sampling date were made from the count data and compiled in Appendix 6.

## 1.6 Part C: Zooplankton Objectives

The primary objectives of the zooplankton component of this project were to parameterize the seasonal zooplankton distribution component of the model. Specifically, these were to:

- C.1. Identify and count zooplankton in samples collected by UFI from their monitoring station during the 2018 season
- C2. Estimate the size and biomass of the zooplankton in the samples and convert the zooplankton densities to biomass
- C3. Create two summary tables, with values for each sampling date for the zooplankton to be used in UFI's in-lake model, ready for input into the model. The first table needed was the estimated biomass ( $\mu$ g/L) for the major taxonomic groups on each sample date. The second table pooled individual species or genera in terms of functional group (predator, omnivore, herbivore) and provided summed biomass for each of these functional groups on each date.

# 1.6.1 <u>C.1. Identify and count zooplankton in samples collected by UFI from their monitoring station during the 2018 season</u>

Samples were collected by Upstate Freshwater Institute using a 0.5 m diameter zooplankton net and a tow depth from 15 meters to the surface at their primary sampling site. These zooplankton samples were preserved in ethanol, delivered to Schulz, and stored in cool, dark conditions until enumeration.

Before processing, samples were poured through a 20 sample into a known volume. The zooplankton samples were rinsed gently with filtered tap water and suspended in a measured 100 mL total volume for counting. Using a calibrated wide-bore pipette, the samples were homogenized with a star-shaped mixing pattern to avoid a centrifugation effect, and a subsample was rapidly removed and placed in a zooplankton counting tray. Each subsample was completely enumerated under a Leica MZ 12.5 dissecting scope. Complete subsamples were enumerated until over 200 animals from a known volume of sample were counted and identified.

The invasive predatory cladoceran, *Cercopagis pengoi*, commonly known as the fish-hook flea, forms clumps and cannot be subsampled accurately. In samples where *C. pengoi* was present (based on a scan of the sample at low power), the entire sample was scanned for Cp and the entire population in the sample was enumerated. This is, unfortunately, the only way to assess this organism's abundance accurately. *C. pengoi* was

 $\square$  m m

one of the few predatory zooplankton in this zooplankton assemblage, so its accurate assessment was necessary to quantify composition of trophic functional groups.

Generally we found a small-bodied zooplankton assemblage with low abundances of large bodied zooplankton such as *Daphnia*. Rotifers and smaller Cladocera, such as *Chydorus* were more abundant, and these taxa have low grazing impact on the phytoplankton and are unlikely to promote clear water phases in the lake.

**Table 7**. Genera of zooplankton found in Owasco Lake samples from summer 2018, along with their functional feeding groups.

Genus/species	Taxonomic group	Herbivore/Predator/Omnivore
Collotheca	Rotifer	herbivore
Lecane	Rotifer	herbivore
Pompholyx	Rotifer	herbivore
Asplanchna	Rotifer	predator
Trichocerca	Rotifer	herbivore
Synchaeta	Rotifer	herbivore
Polyarthra	Rotifer	herbivore
Keratella	Rotifer	herbivore
Brachionus	Rotifer	herbivore
Ascomorpha	Rotifer	herbivore
Testudinella	Rotifer	herbivore
Kellicottia	Rotifer	herbivore
Ploesoma	Rotifer	herbivore
Conochilis	Rotifer	herbivore
Ceriodaphnia	Cladoceran	herbivore
Bosmina longirostris	Cladoceran	herbivore
Eubosmina	Cladoceran	herbivore
Daphnia retrocurva	Cladoceran	herbivore
Cercopagis pengoi	Cladoceran	predator
Leptodora kindtii	Cladoceran	predator
Alona	Cladoceran	herbivore
Chydorus	Cladoceran	herbivore
Daphnia galeata mendotae	Cladoceran	herbivore
Diacyclops thomasi female	Copepod	omnivore
Diacyclops thomasi male	Copepod	omnivore
Diacyclops thomasi copepodid	Copepod	herbivore
Diacyclops thomasi nauplii	Copepod	herbivore
Difflugia	Arcellinida	herbivore
Veliger	Mollusca	herbivore

## 1.6.2 <u>C2. Estimate the size and biomass of the zooplankton in the samples and convert the zooplankton densities to biomass values</u>

Methods for zooplankton analysis were modelled on the zooplankton methods used by Cornell to analyze Cayuga Lake zooplankton samples for use by UFI for the Cayuga Lake model. The sources of the zooplankton biomass conversion factors are provided in Appendix 7. Sizes of common taxa were determined using a calibrated ocular micrometer at known magnifications, and biomass was estimated with standard length-weight regressions taken from these measurements, or from the literature for rarer taxa (where finding sufficient individuals for measurement would have been impractical or impossible). When literature values were needed for length estimations, values from Finger Lakes or standard Great Lakes regressions were used. In other cases, such as for rare or small rotifers, general literature values were used, if available.

# 1.6.3 C3. Create two summary tables, with values for each sampling date for the zooplankton to be used in UFI's in-lake model, ready for input to the model.

After identification and enumeration were complete, the densities and biovolumes of species for the taxonomic group's use in the in-lake model were pooled for each date, and provided to UFI in a tabular form for input into the lake model (Tables 8 and 9 below).

One interesting observation is that not a single calanoid copepod was observed in any sample. In addition, while *Cercopagis pengoi*, an invasive predator to the region (commonly known as the fish-hook flea), was at times abundant in the lake, a related invader, *Bythotrophes*, the spiny water flea, was not found in any sample and apparently has still not invaded the Finger Lakes from Lake Ontario.

**Table 8.** Biomass of zooplankton in each taxonomic group at each sampling date during summer 2018. Units are mass ( $\mu$ g/L)

Date	Daphnia	Non-daphnid Cladocera	Copepods	Rotifers	Other
5-Jul-18	0.08	1.32	5.54	1.64	0.38
18-Jul-18	0.00	1.78	0.39	1.33	0.38
2-Aug-18	0.20	11.56	0.72	1.63	0.04
15-Aug-18	2.35	40.37	1.86	1.49	0.19
31-Aug-18	2.10	16.13	1.05	1.81	0.11
12-Sep-18	1.55	8.58	0.72	0.73	0.04
27-Sep-18	2.63	10.01	1.49	0.06	0.04

**Table 9.** Biomass of zooplankton in functional feeding groups during summer 2018. Units are mass  $(\mu g/L)$ .

Date	Predator	Omnivore	Herbivore
5-Jul-18	1.54	5.06	2.36
18-Jul-18	1.69	0.10	2.09
2-Aug-18	4.58	0.21	9.35
15-Aug-18	10.13	0.44	35.70
31-Aug-18	4.12	0.31	16.77
12-Sep-18	2.96	0.31	8.35
27-Sep-18	0.90	1.39	11.94

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## Appendix 1. Size distribution of zebra and quagga mussels at different sites in Owasco Lake in 2018

All values in mi													in the sample from this site			Z ZIVI	in the sample from this site		_				i in the sampi									
Site 11A		Site 1	L1B	Site 12	A	Site		Site 13 A	Site 13 Deep Mussels (subsurface,	but alive	Site 14 A	S	Site 14 Deep Mussels (subsurface, bu	rt alive)	Site15 A		Site 15 Deep Mussels (subsurface, but alive)		Site 1	19	Site	26	Site 2	9	Site	30	Site	31	Site	£ 33	Site	36
Quagga Zebr	ra C	Quagga Z	Zebra	Quagga Ze	bra	Quagga	Zebra	Quagga Zebra	Quagga	ebra Q	uagga Zebra	ı q	Quagga Ze	bra	Quagga Zebra		Quagga Zebra	Qua	gga Z	ebra	Quagga	Zebra	Quagga Ze	ebra	Quagga 2	Zebra	Quagga	Zebra	Quagga	Zebra	Quagga Z	Zebra
10.32	11.48	12.91	5.67	5.87	7.79	9.09	13.45	25.93 none	9.20	10.22	19.31 1	2.17	8.78	12.43	10.76 16	6.78	9.56 14.51	1	22.68	22.46	11.60	17.01	18.61	13.01	7.57	8.80	19.06	12.24	15.94	14.43	5.54	10.84
8.07	8.60	11.30	11.52	6.79	10.28	10.76	13.29	13.00	19.99		9.21	5.74	6.77	14.54	6.78 18	8.41	20.17 17.73	3	7.75	13.95	13.49	7.95	10.62	10.32	17.60	7.74	9.06	19.49	15.03	17.17	17.28	14.83
6.86	11.17	11.47	8.99	9.41	5.74	6.40	11.20	21.32	11.16		18.12 1	1.96	15.57	11.93	7.11		10.81 15.54	4	9.19	16.15	10.82	10.80	15.31	9.46	14.71	10.78	11.93	10.58	9.22	14.62	11.00	8.94
6.85	12.80	11.56	7.81	8.25	9.45	9.95	7.65	11.25	13.76		6.79	6.98	19.66	19.21	9.93		11.74 13.69	9 :	12.12	13.43	6.61		5.93	5.34	16.58	8.01	5.84	5.97	11.08	9.06	11.70	10.02
6.98	11.93	9.94	13.46	10.38	8.08	6.73	12.10	7.85	11.69		1.33		8.75	15.49	6.79		8.94 9.06	6	26.93	18.47	17.78		12.91	7.51	7.48	8.06	7.60	10.24	12.74	13.89	7.55	
7.93	9.83	7.10	11.41	7.20	5.00	8.90	10.03	7.32	11.45		5.06		7.85	12.26	10.53		21.90 22.99	9	14.03	16.42	18.70		19.53	9.37	9.70	10.10	14.51	10.88	10.09	10.95	10.07	12.18
11.93	11.61	6.42	13.97	11.96	9.14	9.94	11.59	11.19	10.00		10.26		8.39	14.72	22.44		13.52 10.71	1	20.00	16.94	10.02		14.67	12.80	10.12	6.25	7.41	10.60	14.76	10.38	16.81	6.84
	11.63	8.97	10.01	7.10	8.84		9.00	19.89	8.72		7.41		12.43	12.51	12.63		17.74 16.98		11.95	13.91	13.34		14.10	11.84	9.45	6.60	12.29	13.48	14.84		13.78	
	10.06	9.25	11.15	10.19	7.04	12.36	10.97	19.65	22.52		11.22		9.89	13.01	11.12		6.76 14.20		9.40	15.71	22.50		17.19	8.03	18.41	10.38	5.71	15.57	8.96	18.52	21.67	
6.92	8.66	5.82	13.20	6.68	6.68		14.41	7.14	13.91		7.69		10.14	15.75	8.19		8.49 14.35	-	21.83	15.95	10.04		16.71	11.13	12.00	7.55	15.77	11.01	16.12		12.59	
	10.82	10.19	5.64	8.89	7.78	8.65	10.40	12.61	9.85		6.71		6.67	14.44	5.68		21.79 16.02		17.48	16.60	10.01		9.70	11.01	5.24	9.29	10.27	18.56	15.27	9.40	21.58	
	8.54	11.80	9.64	5.09	9.28		12.96	10.74	11.95		4.38		8.71	19.46	7.75		7.97 14.66		19.43	15.79	11.22		12.90	9.56	13.14	9.61	8.89	16.61	9.44	15.14	23.71	6.65
	12.53	7.58	12.31	7.50	11.45		7.88	14.83	11.93		20.35		13.25	11.61	8.37		17.83 16.27		9.34	16.79	10.85		13.64	6.96	7.75	6.83	15.52	16.48	11.68		23.06	
	10.27	7.32	10.51	6.30	7.66		10.65	21.31	19.80		6.27		8.37	14.05	15.70		12.27 9.95		17.11	17.50	15.67		10.45	5.71	14.99	8.46	22.26	10.52	15.64		16.68	
6.69	9.90	11.79	8.82	6.42	7.52		16.35		11.49		8.11		10.00	13.31	11.52		7.23 14.54		17.91	15.25	7.75		9.78	11.73	9.76	7.35	9.86	9.12	15.83		6.75	
	10.09	10.12	11.57	10.85	11.75		12.50	10.71	11.51		5.87		8.12	11.35	6.74		19.54 9.51		5.36	15.22	11.93		14.84	8.36	13.82	8.26	9.78	13.99	10.00		20.15	
6.68	8.77	4.19	12.19	7.19	10.57		9.59	24.42	12.14		22.25		19.46	17.94	8.08		10.53 16.71		11.92	15.44	9.83		14.46	7.82	7.13	6.76	8.76	15.86	14.00		14.35	
	10.68	6.66	8.80	8.39	5.97		12.54	16.61	20.42		9.46		10.94	16.29	6.80		18.55 14.79		10.39	21.62	12.59		13.88	10.36	12.24	11.39	9.12	14.10	16.32		11.96	
6.78	7.75	12.44	11.63	5.96	7.75	4.75	13.31	10.89	6.84		10.91	_	8.33	20.56	9.62		19.30 14.07		18.98	13.88	16.07		14.46	9.03	7.76	9.31	11.73	11.83	8.44		10.91	
10.18	9.13	10.96	10.13	6.72	9.32		11.88	13.29	10.79		12.40	_	9.10	14.62	12.72	_	20.42 11.75		18.89	15.86	11.54		19.02	12.44	16.15	11.95	8.10	6.92	8.45		9.14	
	10.07	8.99	12.12	6.28	9.93		6.78	13.38	8.57		6.88	_	9.64	18.43	22.92		13.32 13.62		9.64	15.03	10.95		11.96	11.39	14.03	10.35	7.51	9.94	13.45		7.40	
5.76	9.18	11.16	12.31	12.23	6.15		12.28	6.21	9.85		11.60		9.81	14.43	7.14		6.03 17.09		12.39	18.07	11.86		14.62	7.76	11.54	6.69	12.73	17.61	18.76		6.32	
13.93	7.69	8.60	13.24	5.45	9.39	6.25	10.23	10.70	13.38		12.09		7.88	20.69	3.79	-	12.92 14.70		20.62	16.32	7.37		12.84	7.10	9.77	6.53	8.62	12.76	9.87	14.61	16.44	
8.82	8.32	7.07	10.76	6.36	7.56	0.02	8.73	8.17	13.73		5.60	_	9.39	14.18	7.72		9.53 13.16		12.95	12.63	13.17		14.94	10.31	11.54	8.53	10.20	12.81	8.63		7.40	
7.40	7.74	7.81	12.32	7.00	9.30	9.99	12.44	12.71	18.92		8.62	_	11.38	18.62	8.24		19.52 18.25	١-	6.74	15.03	10.56		13.01	10.25	12.23	9.20	8.80	14.86	13.46	10.43	17.41	7.14
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## 2 Appendix 2. Biovolume conversions used to calculate biovolumes of Owasco Lake phytoplankton, with data source

<b>hylum/Larger taxonomic</b> န acillariophyta acillariophyta	measurements of phytoplankto  Class  Bacillariophyceae		June to Septem	ber measurement	in Cayuga Lake	cell Biovo							
acillariophyta acillariophyta		Estimate 1				Cell Biovo	olume Es	timonto I I c					
acillariophyta acillariophyta		Estimate 1				UC D.U.U		umate os	ed				
acillariophyta	Bacillariophyceae		Estimate 2	Estimate 3	Estimate 4	um^3			Source				
		506	422	2 1430	86	4	134		Schaffner				
acillariophyta	Bacillariophyceae	506	422	2 1430	86	4	806		Schaffner				
	Coscinodiscophyceae	600	750	0 480			610		Schaffner				
acillariophyta	Mediophyceae	393					393		Schaffner N	Note: fron	n centric re	cord	
acillariophyta	Bacillariophyceae	85	135	5			110		Schaffner N	Note: also	from gene	ric record	
acillariophyta	Bacillariophyceae	59					59		Schaffner				
acillariophyta	Bacillariophyceae	65					65		Schaffner N	Note: fron	n generic re	ecord	
acillariophyta	Bacillariophyceae	155					155		Schaffner				
acillariophyta	Bacillariophyceae	1296	1500	0 1080	187	5	1438		Schaffner				
acillariophyta	Bacillariophyceae	2492	2860	0			2676		diatom.ansp	o.org	(not just d	iatom values)	
		1104					1104				from gene	ric record in Cayuga	
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chrophyta	Synurophyceae	733	785	5			759		Schaffner				
a a a a a a a a h h h h h h h h h h h r y y y y y y y y	acillariophyta alorophyta	acillariophyta Bacillariophyceae acillariophyta Capperatophyta allorophyta * allorophyta Chlorophyceae allorophyta Chlorophycea allorophytea allorophyta Chlorophycea allorophytea allorophyta Chlorophycea allorophytea allorophyta Chlorophycea allorophycea allorophyta Chlorophycea allorophytea allorophyta Chlorophycea allorophyta Ch	acillariophyta Bacillariophyceae 155 acillariophyta Bacillariophyceae 155 acillariophyta Bacillariophyceae 1296 acillariophyta Bacillariophyceae 1296 acillariophyta Bacillariophyceae 1104 acillariophyta Bacillariophyceae 1104 acillariophyta Bacillariophyceae 1227 acillariophyta Bacillariophyceae 1227 acillariophyta Bacillariophyceae 1227 acillariophyta Bacillariophyceae 1227 acillariophyta Bacillariophyceae 14379 acillariophyta Bacillariophyceae 14379 acillariophyta Bacillariophyceae 14379 acillariophyta Bacillariophyceae 14379 acillariophyta 14 acillariophyta 2ygnematophyceae 14379 acillariophyta 15 acillariophyta 2ygnematophyceae 153 alorophyta 15 al	acillariophyta Bacillariophyceae 155 acillariophyta Bacillariophyta Bacillariophyceae 155 acillariophyta Bacillariophyceae 1296 150 acillariophyta Bacillariophyceae 1292 286 acillariophyta Bacillariophyceae 1104 acillariophyta Bacillariophyceae 1104 acillariophyta Bacillariophyceae 1104 acillariophyta Bacillariophyceae 625 acillariophyta Bacillariophyceae 942 88 acillariophyta Bacillariophyceae 942 88 acillariophyta Bacillariophyceae 944 88 acillariophyta Bacillariophyceae 1913 187 acillariophyta Bacillariophyceae 4379 462 acillariophyta Bacillariophyceae 681 acillariophyta 8 acillariophyceae 350770 acillorophyta Chlorophyceae 350770 acillorophyta Chlorophyceae 64 66 acillorophyta Chlorophyceae 64 66 acillariophyta Chlorophyceae 64 67 acillorophyta Chlorophyceae 357 acillariophyta Chlorophyceae 357 acillariophyceae 358 acillariophyce	acillariophyta Bacillariophyceae 155 acillariophyta Bacillariophyceae 155 acillariophyta Bacillariophyceae 155 acillariophyta Bacillariophyceae 1296 1500 1080 acillariophyta Bacillariophyceae 2492 2860 acillariophyta Bacillariophyceae 1104 acillariophyta Bacillariophyceae 1104 acillariophyta Bacillariophyceae 625 acillariophyta Bacillariophyceae 227 acillariophyta Bacillariophyceae 227 acillariophyta Bacillariophyceae 327 acillariophyta Bacillariophyceae 342 880 980 acillariophyta Bacillariophyceae 34379 4625 acillariophyta Bacillariophyceae 34379 4625 acillariophyta Bacillariophyceae 681 acillariophyta 2ygnematophyceae 681 acillariophyta 2ygnematophyceae 681 acillariophyta 8 acillariophyceae 333 16 acillariophyta 8 acillariophyceae 655 21 180 acillariophyta Chlorophyceae 350770 acillariophyta 6 acillariophyceae 350770 acillariophyta Chlorophyceae 64 67 acillariophyta Chlorophyceae 64 67 acillariophyta Chlorophyceae 64 67 acillariophyta Chlorophyceae 357 acillariophyta Chlorophycea 357 acillariophyceae 355 acill	Bacillariophyta   Bacillariophyceae   155   Bacillariophyta   Bacillariophyta   Bacillariophyceae   155   Bacillariophyta   Bacillariophyceae   1296   1500   1080   187:	Secillariophyta   Bacillariophyceae   155	Scillariophyta   Bacillariophyceae   65   155	Secolariophyta   Bacillariophycae   Secolariophyta   Bacillariophycae   Secolariophyta   Bacillariophycae   Secolariophyta   Secolariophyta   Bacillariophycae   Secolariophyta   Secolariophyta   Bacillariophycae   Secolariophyta   Secolariophyta   Bacillariophycae   Secolariophyta   Secolariophyta   Bacillariophycae   Secolariophyta   Secolariophycae   Secolariophyta   Secolariophycae   Secolariophyta   Secolariophycae   Secolariophyta   Secolariophycae   Secolariophyta   Secola	Schaffner   Scha	Schaffner   Note: Front   Schaffner   Note	Schaffner   Note: from generic reciliariophyta   Bacillariophyceae   155   150   1090   1875   1438   Schaffner   Schaffner	Schaffrer   Note: from generic record

**Appendix 3A.** Detailed taxonomic composition of phytoplankton and biovolume calculations for Owasco Lake Phytoplankton, 5 July 2018

Sample 1	5-Jul-18					Cyanob.	Chlorop.	Bacill.	Chyrsop.	Cryptop.	Euglenop.	Dino/Pyrrop.	
Site: UFI Owasco Site 2		Depth on bottle	none (but should be 0.5m	density	(#/mL)	6065		913					
UFI ID: OW SITE 2	site 2	units are # of cells unless					1.39E+05					0.00E+00	
					<u> </u>					Cell Density		Total biovolume	
Genus or Lowest Taxonomic Unit	Phylum/Larger taxonomic group	Class	Additional Information	Field 1	Field 2	Field 3	Field 4	# Cells	mL sample	#/mL	um^3	um^3/mL	Note
Asterionella (cells total)	Bacillariophyta	Bacillariophyceae		0				0	0.055	0	134	0.00E+00	)
Asterionella (colonies)	Bacillariophyta	Bacillariophyceae		0	) 0	0	0	0		0	806	0.00E+00	
Aulacoseira	Bacillariophyta	Coscinodiscophyceae		0	) 0			0		0	610	0.00E+00	
Cyclotella	Bacillariophyta	Mediophyceae		0	) 0			0		0	393	0.00E+00	
Cocconeis	Bacillariophyta	Bacillariophyceae		1		0	0	1		37	110	4.01E+03	
Cymbella	Bacillariophyta	Bacillariophyceae		0	1	0	0	1		37			
Diatoma	Bacillariophyta	Bacillariophyceae		0	_		_	1		37	65	2.39E+03	
Fragilaria (cells)	Bacillariophyta	Bacillariophyceae		0		0	_	0		0	155	0.00E+00	
Fragilaria (filaments)	Bacillariophyta	Bacillariophyceae		0		0	0	0		0	1438	0.00E+00	
Gyrosigma	Bacillariophyta	Bacillariophyceae		0		0	ŭ	0		0	2676	0.00E+00	
Navicula	Bacillariophyta	Bacillariophyceae		0	_			0		0	1104	0.00E+00	
Nitzschia	Bacillariophyta	Bacillariophyceae		4		. 0		8		292	625	1.83E+05	
Surirella	Bacillariophyta	Bacillariophyceae		0	=			0		0	227	0.00E+00	
Synedra	Bacillariophyta	Bacillariophyceae		3		. 3		13		475	934	4.44E+05	
Tabellaria	Bacillariophyta	Bacillariophyceae		0		_	_	0		0	1894	0.00E+00	
Urosolenia	Bacillariophyta	Bacillariophyceae		0				1	0.055	37	4502	1.64E+05	
Cosmarium	Charophyta	Zygnematophyceae		0		<u> </u>		0		0	681	0.00E+00	_
eukaryotic oval cell non-flagellate*	Chlorophyta	*	Most are likely in Chloroph	ŭ			_	4		146			
eukaryotic round cell non-flagellate	Chlorophyta	*	Most are likely in Chloroph			~	15	31	0.055	1133	-		
eukaryotic round flagellate	Chlorophyta	*	Most are likely in Chloroph					0		0	89	0.00E+00	
Pediastrum	Chlorophyta	Chlorophyceae	Wost are likely in emoroph	0				0		0	350770	0.00E+00	
Scenedesmus (cells)	Chlorophyta	Chlorophyceae		1		ŭ		4	0.055	146		3.58E+03	
Scenedesmus (filaments)	Chlorophyta	Chlorophyceae		1		~		1	0.055	37	_	2.40E+03	
Sphaerocystis	Chlorophyta	Chlorophyceae		0		~		0		0		0.00E+00	
Selenastrum				0		·		0		0	67	0.00E+00	
	Chlorophyta	Chlorophyceae		4	·	ŭ	ŭ	8		292	357	1.04E+05	
Tetraspora Cryptomonas-like flagellate	Chlorophyta	Chilorophyceae		0						37		1.30E+04	
,,		Cryptomonas		0	_					37			
Anabaena Anabaena (filaments)	Cyanobacteria Cyanobacteria	Cyanophycea		0				0		0	117 117	0.00E+00 0.00E+00	
Anabaena (maments) Anabaena flosaguae morph (oval cell		Cyanophycea		0				0		0	117	0.00E+00 0.00E+00	
Anabaena nosaquae morph (ovai ceii Aphanizomenon	Cyanobacteria	Cyanophycea		0				0		0		0.00E+00 0.00E+00	
Apnanizomenon Calothrix	Cyanobacteria	Cyanophycea		0				0		0	196	0.00E+00 0.00E+00	
	Cyanobacteria	Cyanophysea		18	Ĭ	8		37		1352	85 170	0.00E+00 2.29E+05	
Chroococcus		Cyanophycea		18				37 0		1352	1/0	2.29E+05 0.00E+00	
Coelosphaerium Gleocapsa	Cyanobacteria	Cyanophycea		0	Ĭ	ŭ	ŭ	0		0	7	0.00E+00 0.00E+00	
	Cyanobacteria	Cyanophysea		0			ŭ	0		0	,	0.00E+00 0.00E+00	
Merismopedia Microcyctic	Cyanobacteria	Cyanophycea	cells	16				99		3617	9	1.23E+04	
Microcystis Oscillatoria	Cyanobacteria	Microcystaceae	filaments	16				99		3617	43		
	Cyanobacteria	Cyanophysea	maments	9				30		ŭ	43	6.52E+03	
Synechococcus	Cyanobacteria	Cyanophysea		9						1096 0	32	0.00E+00	
Synecocystis	Cyanobacteria	Cyanophycea		0						0	32 1728	0.00E+00 0.00E+00	
Euglenoid		Euglenophyceae		0						0			-
Peridinium	Miozoa	Dinophyceae		-	_	ŭ	•	0		Ŭ	4211	0.00E+00	
Dinobryon	Ochrophyta	Chrysophyceae		0	_	_	_	2		73		6.85E+03	
Mallomonas	Ochrophyta	Synurophyceae		0	0	0	0	0	0.055	0	759	0.00E+00	J

Appendix 3B . Detailed taxonomic composition of phytoplankton and biovolume calculations for Owasco Lake Phytoplankton, 18 July 2018

Asterionella (cells total) Asterionella (colonies) Asterionella (colonies) Aulacoseira Bacillar Cyclotella Bacillar Cocconeis Bacillar Cocconeis Bacillar Diatoma Bacillar Fragilaria (cells) Bacillar Fragilaria (filaments) Bacillar Suricula Bacillar Bacillar Bacillar Suricula Bacillar Surirella Bacillar Surirella Bacillar Tabellaria Bacillar Cosmarium Eukaryotic round cell non-flagellate Eukaryotic round flagellate Eukaryotic round flagellate Eukaryotic round flagellate Chlorop Scenedesmus (filaments) Chlorop Scenedesmus (filaments) Chlorop Coccondia Chlorop	um/Larger taxonomic group lariophyta	Depth on bottle units are # of cells unless Class Bacillariophyceae Bacillariophyceae Mediophyceae Bacillariophyceae		biovolum	Field 2	25089	# Cells	Volume Cou mL sample 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041		0.00E+00	Dino/Pyrrop.  0 0.00E+00  Total biovolume um^3/mL 0.00E+00 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Site: UFI Owasco Site 2  UFI ID: OW SITE 2  Senus or Lowest Taxonomic Unit Asterionella (cells total) Asterionella (colonies) Adacoseira  Socyolotella  Socyolotella  Socyonella  Socyonella  Socyonella  Socillar  Sorrosigma  Socyonella  Socyonella  Socyonella  Socyonella  Socillar  Sorrosigma  Socillar  Sorrosigma  Socillar  Socyonella  Socillar  Socyonella  Socillar  Socyonella  Socillar  Socyonella  Socillar  Socyonella  Socillar  Socyonella  Bacillar  Socyonella  Bacillar  Socyonella  Bacillar  Socyonella  Bacillar  Socillar  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Socinedesmus  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Chlorop  Socinedesmus  Socinedesmus  Chlorop  Socinedesmus  Socinedesmus  Chlorop  So	um/Larger taxonomic group ariophyta lariophyta	Depth on bottle units are # of cells unless Class Bacillariophyceae Bacillariophyceae Mediophyceae Bacillariophyceae	listed as filament	Field 1 0 0 0 0 0 0 0 0 0 0 0 48 4 4	Field 2  0 0 0 0 0 0 0 0 0 0 0	2.30E+05  Field 3  0 0 0 0 0 0 0 0 0	# Cells	Volume Cou mL sample 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041	1.74E+04  Cell Density #/mL  0 0 0 0 0 0	0.00E+00  Cell biovolum^3  134  806 610 393 110	Total biovolume um^3/mL 0.00E+00 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Genus or Lowest Taxonomic Unit Asterionella (cells total) Asterionella (colonies) Asterionella (colonies) Bacillar Asterionella (colonies) Bacillar Aulacoseira Cyclotella Bacillar Cocconeis Bacillar Bacillar Cocconeis Bacillar Bacillar Bacillar Bacillar Bacillar Bacillar Bacillar Cocconeis Bacillar Bacillar Bacillar Bacillar Bacillar Cocconeis Bacillar Bacillar Bacillar Cocconeis Bacillar Cocconeis Bacillar Cocconeis Bacillar Cocconeis Bacillar Bacillar Cocconeis Bacillar Bacillar Bacillar Bacillar Cocconeis Bacillar Bac	um/Larger taxonomic group lariophyta	units are # of cells unless Class Bacillariophyceae Bacillariophyceae Coscinodiscophyceae Mediophyceae Bacillariophyceae	listed as filament	0 0 0 0 0 0 0 48 4	0 0 0 0 0 0	0 0 0 0 0		mL sample 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041	#/mL 0 0 0 0 0	um^3 134 806 610 393 110	um^3/mL 0.00E+00 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Asterionella (cells total) Asterionella (colonies) Ast	ariophyta lariophyta	Class Bacillariophyceae Bacillariophyceae Coscinodiscophyceae Mediophyceae Bacillariophyceae		0 0 0 0 0 0 0 48 4	0 0 0 0 0 0	0 0 0 0 0		mL sample 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041 0 0.041	#/mL 0 0 0 0 0	um^3 134 806 610 393 110	um^3/mL 0.00E+00 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Asterionella (cells total)  Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Bacillar  Ascillar  Asterionella Bacillar  Asterionella Bacillar  Asterionella Bacillar  Cosmarium  Charop  Bukaryotic oval cell non-flagellate*  Chlorop  Bukaryotic round cell non-flagellate  Chlorop  Celiastrum  Chlorop  Celicenedesmus (cells)  Chlorop  Celenastrum  Chlorop  Chlorop  Celenastrum  Chlorop  Chlorop  Cryptomonas-like flagellate  Cryptog  Anabaena  Anabaena (filaments)  Anabaena flosaquae morph (oval cells Cyanob  Chrococcus  Cyanob  Chrococcus  Cyanob	ariophyta lariophyta	Bacillariophyceae Bacillariophyceae Coscinodiscophyceae Mediophyceae Bacillariophyceae	Additional Information	0 0 0 0 0 0 0 48 4	0 0 0 0 0 0	0 0 0 0 0		0.041 0.041 0.041 0.041 0.041 0.041	0 0 0 0	134 806 610 393 110	0.00E+00 0.00E+00 0.00E+00 0.00E+00 0.00E+00
Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Asterionella (colonies)  Bacillar  Cosmarium  Charop  Bukaryotic round cell non-flagellate*  Chlorop  Bukaryotic round flagellate  Chlorop  Cukaryotic round flagellate  Chlorop  Cucenedesmus (cells)  Chlorop  Chlor	ariophyta lariophyta	Bacillariophyceae Coscinodiscophyceae Mediophyceae Bacillariophyceae		0 0 0 0 0 0 48 4	0 0 0 0 0 0	0 0 0 0 0		0.041 0.041 0.041 0.041 0.041	0 0	806 610 393 110	0.00E+00 0.00E+00 0.00E+00 0.00E+00
ulacoseira yclotella bacillar yclotella bacillar yclotella bacillar yclotella bacillar ymbella lascillar iatoma bacillar ragilaria (cells) bacillar ragilaria (filaments) bacillar iatoria lavicula lavic	lariophyta	Coscinodiscophyceae Mediophyceae Bacillariophyceae		0 0 0 0 0 48 4	0 0 0 0 0	0 0 0 0	( ( (	0.041 0.041 0.041 0.041	0 0	610 393 110	0.00E+00 0.00E+00 0.00E+00
yclotella Bacillar occoneis Bacillar ymbella Bacillar ymbella Bacillar iatoma Bacillar ragilaria (cells) Bacillar ragilaria (filaments) Bacillar yrosigma Bacillar iavicula Bacillar ivicula Ba	lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta	Mediophyceae Bacillariophyceae		0 0 0 0 48 4	0 0 0 0	0 0 0 0	(	0.041 0 0.041 0 0.041	0	393 110	0.00E+00 0.00E+00
occoneis ymbella probella sacillar ymbella sacillar sacillar ragilaria (cells) ragilaria (filaments) sacillar ragilaria (filaments) sacillar ragilaria (filaments) sacillar sa	ariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta	Bacillariophyceae		0 0 0 48 4	0 0 0 0	0 0	(	0.041 0.041	0	110	0.00E+00
ymbella Bacillar ymbella Bacillar ragilaria (cells) Bacillar ragilaria (filaments) Bacillar ragilaria (filaments) Bacillar yrorsigma Bacillar lavicula Bacillar lavicula Bacillar urirella Bacillar ynedra Bacillar abellaria Bacillar losolenia Bacillar losolenia Bacillar ukaryotic oval cell non-flagellate* Ukaryotic round cell non-flagellate Ukaryotic round flagellate Chlorop ukaryotic round flagellate Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Chlorop phaerocystis Chlorop phaerocystis Chlorop etraspora Chlorop ryptomonas-like flagellate Cryptop nabaena Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob hroococcus	lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta	Bacillariophyceae		0 0 48 4	0	0	(	0.041			
latoma Bacillar ragilaria (cells) Bacillar ragilaria (cells) Bacillar ragilaria (filaments) Bacillar yrosigma Bacillar avicula Bacillar Bacillar urirella Bacillar urirella Bacillar abellaria Bacillar rosolenia Bacillar osmarium Charop ukaryotic oval cell non-flagellate* Chlorop ukaryotic round cell non-flagellate Chlorop ukaryotic round flagellate Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob alothrix Cyanob	lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta	Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae		0 48 4	0	0			0	59	
agilaria (cells) agilaria (filaments) agilaria (filaments) agilaria (filaments) ayrosigma Bacillar avrosigma Bacillar avicula Bacillar altzschia Bacillar arriella Bacillar abellaria Bacillar abellaria Bacillar assarilar assari	lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta	Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae		48 4	0		,	0.041			0.00E+00
ragilaria (filaments) ragilaria (filaments) ryrosigma avicula Bacillar avicula Bacillar avicula Bacillar Bacillar Bacillar abellaria Bacillar rosolenia Bacillar osmarium Ukaryotic oval cell non-flagellate* Ukaryotic round cell non-flagellate Chlorop ukaryotic round flagellate Chlorop chaerocystis Chlor	ariophyta Iariophyta Iariophyta Iariophyta Iariophyta Iariophyta Iariophyta	Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae		4	ŭ	12	(	0.041	0	65	0.00E+00
yrosigma Bacillar avicula Bacillar itzschia Bacillar itzschia Bacillar itzschia Bacillar itzschia Bacillar abellaria Bacillar rosolenia Bacillar osmarium Charop ukaryotic oval cell non-flagellate* Chlorop ukaryotic round cell non-flagellate Chlorop charyotic round flagellate Cryptop charyotic round flagellate Chlorop chlorop charyotic round flagellate chlorop chloro	lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta	Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae			0	12	60	0.041	2923	155	4.53E+05
avicula Bacillar itzschia Bacillar itzschia Bacillar urirella Bacillar ynedra Bacillar ynedra Bacillar abellaria Bacillar rosolenia Bacillar osmarium Charop ukaryotic oval cell non-flagellate* Chlorop ukaryotic round cell non-flagellate Chlorop ukaryotic round flagellate Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Cyanob nabaena (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob chroococcus Cyanob	lariophyta lariophyta lariophyta lariophyta lariophyta lariophyta	Bacillariophyceae Bacillariophyceae Bacillariophyceae Bacillariophyceae		0	U	2	6	0.041	292	1438	4.20E+05
itzschia Bacillar urirella Bacillar urirella Bacillar ynedra Bacillar abellaria Bacillar rosolenia Bacillar osmarium Charop ukaryotic oval cell non-flagellate* Chlorop ukaryotic round cell non-flagellate Chlorop ukaryotic round flagellate Chlorop cheediastrum Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Chlorop chaerocystis Chlorop chaerocystis Chlorop ceraspora Chlorop ryptomonas-like flagellate Cryptop nabaena Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob	lariophyta lariophyta lariophyta lariophyta lariophyta	Bacillariophyceae Bacillariophyceae Bacillariophyceae			0	0	(	0.041	0	2676	0.00E+00
urirella Bacillar ynedra Bacillar ynedra Bacillar ynedra Bacillar abellaria Bacillar Chlorop Ukaryotic oval cell non-flagellate Chlorop Ukaryotic round cell non-flagellate Chlorop Chlorop Cenedesmus (cells) Chlorop Cenedesmus (filaments) Chlorop Cenedesmus (filaments) Chlorop Cenedesmus (filaments) Chlorop Cenedesmus (filaments) Chlorop	ariophyta ariophyta ariophyta	Bacillariophyceae Bacillariophyceae		0	0	0	(	0.041	0	1104	0.00E+00
ynedra Bacillar abellaria Bacillar abellaria Bacillar abellaria Bacillar abellaria Bacillar osmarium Charop ukaryotic oval cell non-flagellate Chlorop ukaryotic round cell non-flagellate Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Chlorop cenadesmus Chlorop cenadesmus Chlorop cenadesmus Chlorop cenade con control control cenadesmus Chlorop cenadesmus (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob hroococcus Cyanob	ariophyta ariophyta	Bacillariophyceae		5	0	0			244	625	1.52E+05
abellaria Bacillar rosolenia Bacillar rosolenia Bacillar osmarium Charop ukaryotic oval cell non-flagellate* Chlorop ukaryotic round cell non-flagellate Chlorop ukaryotic round flagellate Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Cyanob nabaena Cyanob nabaena (filaments) Cyanob phanizomenon Cyanob phanizomenon Cyanob alothrix Cyanob	ariophyta			0	0	0	(	0.041	0	227	0.00E+00
rosolenia Bacillar osmarium Charop ukaryotic oval cell non-flagellate* Chlorop ukaryotic round cell non-flagellate Chlorop ukaryotic round flagellate Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Chlorop chaerocystis Chlorop cha				1	3	6	10	0.041	487	934	4.55E+05
osmarium Charop ukaryotic oval cell non-flagellate* Chlorop ukaryotic round cell non-flagellate Chlorop ukaryotic round flagellate Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Chlorop chaerocystis Chlorop c		Bacillariophyceae		0	0	0	(	0.041	0	1894	0.00E+00
ukaryotic oval cell non-flagellate* Ukaryotic round cell non-flagellate Ukaryotic round flagellate Ukaryotic round flagellate Chlorop Chlorop Cenedesmus (cells) Chlorop Cyanob Cyanob Cyanob Inabaena (filaments) Cyanob Inabaena flosaquae morph (oval cells Cyanob Inabaena flosaquae morph Cyanob Inabaena Cyanob	ariophyta	Bacillariophyceae		0	0	0	(	0.041	0	4502	0.00E+00
ukaryotic round cell non-flagellate ukaryotic round flagellate chlorop dediastrum chlorop cenedesmus (cells) chlorop chenedesmus (filaments) chlorop chaerocystis chlorop cleneatrum chlorop etraspora cyntomonas-like flagellate cyanob nabaena cyanob nabaena flosaquae morph (oval cells cyanob phanizomenon alothrix cyanob cyanob cyanob cyanob	ophyta	Zygnematophyceae		0	0	0	(	0.041	0	681	0.00E+00
ukaryotic round flagellate Chlorop ediastrum Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Chlorop chaerocystis Chlorop elenastrum Chlorop elenastrum Chlorop cetraspora Chlorop ryptomonas-like flagellate Cryptop nabaena (filaments) Cyanob nabaena filosaquae morph (oval cells Cyanob phanizomenon Cyanob phanizomenon Cyanob alothrix Cyanob	ophyta	*	Most are likely in Chlorophy	10	2	4	16	0.041	779	25	1.91E+04
ediastrum Chlorop cenedesmus (cells) Chlorop cenedesmus (filaments) Chlorop chaerocystis Chlorop elenastrum Chlorop etraspora Chlorop nabaena Cyanob nabaena (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob	ophyta	*	Most are likely in Chlorophy	2	3	3	8	0.041	390	22	8.67E+03
cenedesmus (cells)  cenedesmus (filaments)  chaerocystis  clelenastrum  Chlorop  cetraspora  Chlorop  ryptomonas-like flagellate  Cyanob  nabaena (filaments)  nabaena flosaquae morph (oval cells Cyanob  phanizomenon  clelis Cyanob  phanizomenon  clelis Cyanob  phococcus  Cyanob	ophyta	*	Most are likely in Chlorophy	0	0	0			0	89	0.00E+00
cenedesmus (filaments) chaerocystis clenastrum chlorop cetraspora chlorop ryptomonas-like flagellate cyanob nabaena (filaments) cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon cyanob phanizomenon cyanob	ophyta	Chlorophyceae		0	0	0	(	0.041	0	350770	0.00E+00
chaerocystis clenastrum chlorogetenastrum chlorogeteraspora cryptomonas-like flagellate cryptog nabaena nabaena (filaments) nabaena flosaquae morph (oval cells Cyanob phanizomenon cloromenon cloromenon cloromenon cloromenon cloromenon cloromenon cloromenon cyanob phococcus cyanob	ophyta	Chlorophyceae		4	6	4	14	0.041	682		1.67E+04
elenastrum Chloropetraspora Chloropryptomonas-like flagellate Cryptomabaena Cyanob nabaena (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob nalothrix Cyanob chroococcus Cyanob chroococcus Cyanob	ophyta	Chlorophyceae		1	2	1	4	0.041	195	66	1.28E+04
etraspora Chlorogryptomonas-like flagellate Cryptognabaena Cyanob nabaena (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob cyanob cyanob	ophyta	Chlorophyceae		0	0	0	(	0.041	0	184	0.00E+00
ryptomonas-like flagellate Cryptop nabaena Cyanob nabaena (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob hroococcus Cyanob	ophyta	Chlorophyceae		0	0	0			0	67	0.00E+00
nabaena Cyanob nabaena (filaments) Cyanob nabaena (filaments) (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob hroococcus Cyanob	ophyta	Chlorophyceae	colony	18	13	14	45	0.041	2192	357	7.83E+05
nabaena (filaments) Cyanob nabaena flosaquae morph (oval cells Cyanob phanizomenon Cyanob alothrix Cyanob nroococcus Cyanob	ophyta	Cryptomonas		0	0	1	1		49		1.74E+04
nabaena flosaquae morph (oval cells' Cyanob phanizomenon Cyanob alothrix Cyanob hroococcus Cyanob	obacteria	Cyanophycea		0					0	117	0.00E+00
phanizomenon Cyanob alothrix Cyanob hroococcus Cyanob	obacteria	Cyanophycea		0	0	0	(		0	117	0.00E+00
alothrix Cyanob hroococcus Cyanob		Cyanophycea		0	0	0	(		0	117	0.00E+00
hroococcus Cyanob	obacteria	Cyanophycea		0	0	ŭ	(		0	196	0.00E+00
	obacteria	Cyanophycea		2	1	0	3		146		1.24E+04
oolocphagrium Cyanob	obacteria	Cyanophycea		5	2	4	11		536	170	9.09E+04
	obacteria	Cyanophycea		0	0		(		0	7	0.00E+00
	obacteria	Cyanophycea		0	0				0	7	0.00E+00
	obacteria	Cyanophycea	cells	0	0		8		390	6	2.32E+03
	obacteria	Microcystaceae	cells	44	350	18			20071	3	6.82E+04
	obacteria	Cyanophycea	filaments	0		0			0	43	0.00E+00
	obacteria	Cyanophycea		16					2679	6	1.59E+04
	obacteria	Cyanophycea		26					1267	32	4.03E+04
uglenoid Eugleno		Euglenophyceae		0					0	1728	0.00E+00
eridinium Miozoa		Dinophyceae		0		0	-		0	4211	0
Dinobryon Ochrop	oa	Chrysophyceae		0	0	0			0	94	0
Mallomonas Ochrop	oa ophyta	Synurophyceae		0	0	0	(	0.041	0	759	0

Appendix 3C. Detailed taxonomic composition of phytoplankton and biovolume calculations for Owasco Lake Phytoplankton, 2 August 2018

						Cyanob	Chlorop.	Bacill.	Chyrsop.	Cryptop.	Euglenop.	Dino/Pyrrop.
				density	(#/mL)	408116		3946	Cnyrsop.			
Sample 3	2 Au	ıg-18					8.40E+05				0.00E+00	
Site: UFI Owasco Site 2	Z-A0	Depth on bottle	none (but should be 0.5m		t unii-3/iiiL	J.01L+00	0.40L+03	1.461700	0.00E+00	1.742+04	0.002+00	0.002+00
JFI ID: OW SITE 2	site 2	units are # of cells unles		)								
						4 hinbau aa		# C-II-	Values Car	Cell Density	Call biassals	Tatal historia
	(MC) in sample; counted the highlighted t			etalala			wer; volume	# Cells		-		Total biovolume
enus or Lowest Taxonomic Unit	Phylum/Larger taxonomic group	Class	Additional Information	Field 1	Field 2	Field 3		0	mL sample	#/mL	um^3	um^3/mL
sterionella (cells total)	Bacillariophyta	Bacillariophyceae		0	_	_		0		0	134	0.00E+00
sterionella (colonies)	Bacillariophyta	Bacillariophyceae		0		ŭ		0	0.041	0	806	0.00E+00
ulacoseira	Bacillariophyta	Coscinodiscophyceae		0				0	0.041	0	610	0.00E+00
yclotella	Bacillariophyta	Mediophyceae		0	_	_		0	0.041	0	393	0.00E+00
occoneis	Bacillariophyta	Bacillariophyceae		0		ŭ		0	0.041	0	110	0.00E+00
ymbella	Bacillariophyta	Bacillariophyceae		0	_	ŭ		0	0.041	. 0	59	0.00E+00
atoma	Bacillariophyta	Bacillariophyceae		0		_		0	0.041	. 0	65	0.00E+00
agilaria (cells)	Bacillariophyta	Bacillariophyceae		48				60	0.041	2923	155	4.53E+05
agilaria (filaments)	Bacillariophyta	Bacillariophyceae		4	•	-		6	0.041	292	1438	4.20E+05
yrosigma	Bacillariophyta	Bacillariophyceae		0	0	0	)	0	0.041	0	2676	0.00E+00
avicula	Bacillariophyta	Bacillariophyceae		0	0	0	)	0	0.041	. 0	1104	0.00E+00
itzschia	Bacillariophyta	Bacillariophyceae		5	0	0	)	5	0.041	244	625	1.52E+05
ırirella	Bacillariophyta	Bacillariophyceae		0	0	0	)	0	0.041	. 0	227	0.00E+00
ynedra	Bacillariophyta	Bacillariophyceae		1	. 3	6	i	10	0.041	487	934	4.55E+05
abellaria	Bacillariophyta	Bacillariophyceae		0	0	0	)	0	0.041	0	1894	0.00E+00
rosolenia	Bacillariophyta	Bacillariophyceae		0	0	0	)	0	0.041	. 0	4502	0.00E+00
osmarium	Charophyta	Zygnematophyceae		C	0	0	)	0	0.041	. 0	681	0.00E+00
ukaryotic oval cell non-flagellate*	Chlorophyta	*	Most are likely in Chloroph	10	) 2	4		16	0.041	779	25	1.91E+04
ukaryotic round cell non-flagellate	Chlorophyta	*	Most are likely in Chloroph	2 ر	. 3	3		8	0.041	390	22	8.67E+03
ukaryotic round flagellate	Chlorophyta	*	Most are likely in Chloroph	, 0	0	0	)	0	0.041	0	89	0.00E+00
ediastrum	Chlorophyta	Chlorophyceae		O	0	0	)	0	0.041	0	350770	0.00E+00
cenedesmus (cells)	Chlorophyta	Chlorophyceae		4	6	4		14	0.041	682	25	1.67E+04
enedesmus (filaments)	Chlorophyta	Chlorophyceae		1	. 2	. 1		4	0.041	195	66	
phaerocystis	Chlorophyta	Chlorophyceae		O	0	0	)	0	0.041	0	184	0.00E+00
elenastrum	Chlorophyta	Chlorophyceae		0		0	· )	0	0.041	0	67	0.00E+00
etraspora	Chlorophyta	Chlorophyceae	colony	18				45	0.041	2192	357	7.83E+05
ryptomonas-like flagellate	Cryptophyta	Cryptomonas	Colony	0	1			1	0.041	49	356	1.74E+04
nabaena	Cyanobacteria	Cyanophycea		0				0		-19	117	0.00E+00
nabaena (filaments)	Cyanobacteria	Cyanophycea		0				0	0.041	0	117	0.00E+00
nabaena (maments) nabaena flosaquae morph (oval cells		Cyanophycea		0				0	0.041	0	117	0.00E+00
phanizomenon	Cyanobacteria	Cyanophycea	filaments	75		ŭ		207	0.041	10084	196	1.98E+06
alothrix	Cyanobacteria		Haments	2				3	0.041	146		1.24E+04
nroococcus	Cyanobacteria	Cyanophycea		5		ŭ		11	0.041	9118	85 170	1.24E+04 1.55E+06
		Cyanophycea		0	_			0		9118	1/0	
pelosphaerium	Cyanobacteria	Cyanophycea		0	Ŭ	ŭ		0		0	7	0.00E+00
leocapsa	Cyanobacteria	Cyanophycea	II-		_				0.041	300	/	0.00E+00
erismopedia ·	Cyanobacteria	Cyanophycea	cells	0	Ŭ	Ŭ		8	0.041	390	6	2.32E+03 1 c
icrocystis	Cyanobacteria	Microcystaceae	cells	44				412	0.002	341520	3	1.16E+06 rep
scillatoria	Cyanobacteria	Cyanophycea	filaments	0	_			0	0.041	0	43	0.00E+00
rnechococcus	Cyanobacteria	Cyanophycea		16				55		45591	6	2.71E+05
rnecocystis	Cyanobacteria	Cyanophycea		26				26	0.041	1267	32	4.03E+04
ıglenoid	Euglenozoa	Euglenophyceae		0				0		0	1728	0.00E+00
eridinium	Miozoa	Dinophyceae		0				0	0.041	0	4211	0.00E+00
inobryon	Ochrophyta	Chrysophyceae		0		_		0	0.041	0	94	0.00E+00
allomonas	Ochrophyta	Synurophyceae		0	) 0	0	)	0	0.041	0	759	0.00E+00

Appendix 3 D. Detailed taxonomic composition of phytoplankton and biovolume calculations for Owasco Lake Phytoplankton, 31 August 2018

						Cyanob.	Chlorop.	Bacill.	Chyrsop.	Cryptop.	Euglenop.		
ample 4	31-Aug-18			density	(#/mL)	8477	2972	1364	0	0	-		
ite: UFI Owasco Site 2					um^3/mL	1.92E+05	2.01E+05	1.23E+06	0.00E+00	0.00E+00	0.00E+00	2.05E+05	
JFI ID: OW SITE 2	site 2	Depth on bottle	none (but should be 0.5m	)									
		units are # of cells unless	listed as filament										
									Volume Cou	•		Total biovolume	
ienus or Lowest Taxonomic Unit	Phylum/Larger taxonomic group	Class	Additional Information	Field 1	Field 2	Field 3			mL sample	#/mL	um^3	um^3/mL	
sterionella (cells total)	Bacillariophyta	Bacillariophyceae		0	0	, ,		0	0.041	0	134	0.00E+00	
sterionella (colonies)	Bacillariophyta	Bacillariophyceae		0	-	·		0		0	806	0.00E+00	
ulacoseira	Bacillariophyta	Coscinodiscophyceae		0	·	, ,		0		0	610	0.00E+00	
yclotella	Bacillariophyta	Mediophyceae		0	-	·		0		0	393	0.00E+00	
occoneis	Bacillariophyta	Bacillariophyceae		0	ď	0		0		0	110	0.00E+00	
ymbella	Bacillariophyta	Bacillariophyceae		0	-	·		0		0	59		
Diatoma	Bacillariophyta	Bacillariophyceae		0	-	· -		1	0.041	49	65	3.19E+03	
ragilaria (cells)	Bacillariophyta	Bacillariophyceae		0	-	·		0		0	155	0.00E+00	
ragilaria (filaments)	Bacillariophyta	Bacillariophyceae		0	-	, ,		0		0	1438	0.00E+00	
iyrosigma	Bacillariophyta	Bacillariophyceae		0	-	·		0		0	2676	0.00E+00	
lavicula	Bacillariophyta	Bacillariophyceae		0	-	·		0		0	1104	0.00E+00	
litzschia	Bacillariophyta	Bacillariophyceae		0	·	·		0		0	625	0.00E+00	
urirella	Bacillariophyta	Bacillariophyceae		0	-	·		0		0	227	0.00E+00	
ynedra	Bacillariophyta	Bacillariophyceae		9				27		1315	934	1.23E+06	
abellaria	Bacillariophyta	Bacillariophyceae		0	-	_		0		0	1894	0.00E+00	
rosolenia	Bacillariophyta	Bacillariophyceae		0				0		0	4502	0.00E+00	
osmarium	Charophyta	Zygnematophyceae		0		0		0		0	681	0.00E+00	
ukaryotic oval cell non-flagellate*	Chlorophyta	*	Most are likely in Chloroph		_	! 0		5		244	25		
ukaryotic round cell non-flagellate	Chlorophyta	*	Most are likely in Chloroph		_	. 6		9	0.041	438	22		
ukaryotic round flagellate	Chlorophyta	*	Most are likely in Chloroph			0		0		0	89	0.00E+00	
ediastrum	Chlorophyta	Chlorophyceae		0	0	· · · · · · · · · · · · · · · · · · ·		0		0	350770	0.00E+00	
cenedesmus (cells)	Chlorophyta	Chlorophyceae		8	8	16		32		1559	25	3.82E+04	
cenedesmus (filaments)	Chlorophyta	Chlorophyceae		2	2	. 4		8		390	66	2.56E+04	
phaerocystis	Chlorophyta	Chlorophyceae		0	0	0		0	0.041	0	184	0.00E+00	
elenastrum	Chlorophyta	Chlorophyceae		0	0	0		0	0.041	0	67	0.00E+00	
etraspora	Chlorophyta	Chlorophyceae	colony	2	3	2		7	0.041	341	357	1.22E+05	
ryptomonas-like flagellate	Cryptophyta	Cryptomonas		0	0	0		0	0.041	0	356	0.00E+00	
nabaena	Cyanobacteria	Cyanophycea		8	0	0		8	0.041	390	117	4.56E+04	
nabaena (filaments)	Cyanobacteria	Cyanophycea		1	. 0	_		1		49		5.70E+03	
nabaena flosaquae morph (oval cells		Cyanophycea		0	Ŭ	Ŭ		0		0	117	0.00E+00	
phanizomenon	Cyanobacteria	Cyanophycea	filaments	0	2	_		3		146	196	2.86E+04	
alothrix	Cyanobacteria	Cyanophycea		0	0	0		0		0	85	0.00E+00	
hroococcus	Cyanobacteria	Cyanophycea		4	2	. 4		10		487	170	8.26E+04	
oelosphaerium	Cyanobacteria	Cyanophycea		0	0	0		0		0	7	0.00E+00	
ileocapsa	Cyanobacteria	Cyanophycea		2	3	0		5		244	7	1.61E+03	
1erismopedia	Cyanobacteria	Cyanophycea	cells	0	Ŭ	Ŭ		0		0	6	0.00E+00	
/licrocystis	Cyanobacteria	Microcystaceae	cells	41	41	. 51		133		6479	3	2.20E+04	
Scillatoria	Cyanobacteria	Cyanophycea	filaments	0	1	. 0		1	0.041	49	43	2.09E+03	
ynechococcus	Cyanobacteria	Cyanophycea		6	1	. 6		13		633	6	3.76E+03	
ynecocystis	Cyanobacteria	Cyanophycea		0	0	0		0	0.041	0	32	0.00E+00	
uglenoid	Euglenozoa	Euglenophyceae		0				0		0	1728	0.00E+00	
eridinium	Miozoa	Dinophyceae		0	1	. 0		1	0.041	49	4211	2.05E+05	
inobryon	Ochrophyta	Chrysophyceae		C	0	0		0	0.041	0	94	0.00E+00	
Mallomonas	Ochrophyta	Synurophyceae		0	0	0		0	0.041	0	759	0.00E+00	
·													

Appendix 3E. Detailed taxonomic composition of phytoplankton and biovolume calculations for Owasco Lake Phytoplankton, 12 September 2018

						Cyanob.	Chlorop.	Bacill.	Chyrsop.	Cryptop.	Euglenop.	Dino/Pyrrop.
				density	(#/mL)	30301		4287	Citytsop.			
ample 5	12-Sc	ep-18					9.26E+04			1.74E+04		-
ite: UFI Owasco Site 2		Depth on bottle	none (but should be 0.5m									
JFI ID: OW SITE 2	site 2	units are # of cells unles	•	ĺ								
									Volume Cou	Cell Density	Cell biovol	Total biovolum
enus or Lowest Taxonomic Unit	Phylum/Larger taxonomic group	Class	Additional Information	Field 1	Field 2	Field 3		# Cells	mL sample	#/mL	um^3	um^3/mL
sterionella (cells total)	Bacillariophyta	Bacillariophyceae		C	0	0		0	0.041	0	134	0.00E+00
sterionella (colonies)	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	806	0.00E+00
ulacoseira	Bacillariophyta	Coscinodiscophyceae		(	) 0	0		0	0.041	0	610	0.00E+00
yclotella	Bacillariophyta	Mediophyceae		(	0	0		0	0.041	0	393	0.00E+00
Cocconeis	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	110	0.00E+00
Cymbella	Bacillariophyta	Bacillariophyceae		(	) 1	. 0		1	0.041	49	59	2.87E+03
Diatoma	Bacillariophyta	Bacillariophyceae		1	0 ا	0		1	0.041	49	65	3.19E+03
ragilaria (cells)	Bacillariophyta	Bacillariophyceae		C	0	0		0	0.041	0	155	0.00E+00
ragilaria (filaments)	Bacillariophyta	Bacillariophyceae		C	0	0		0	0.041	0	1438	0.00E+00
Syrosigma	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	2676	0.00E+00
lavicula	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	1104	0.00E+00
litzschia	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	625	0.00E+00
urirella	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	227	0.00E+00
ynedra	Bacillariophyta	Bacillariophyceae		27	7 28	31		86	0.041	4190	934	3.91E+06
abellaria	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	1894	0.00E+00
Irosolenia	Bacillariophyta	Bacillariophyceae		(	0	0		0	0.041	0	4502	0.00E+00
osmarium	Charophyta	Zygnematophyceae		(	) 0	0	1	0	0.041	0	681	0.00E+00
ukaryotic oval cell non-flagellate*	Chlorophyta	*	Most are likely in Chloroph	r 3	3 1	. 3		7	0.041	341	25	8.37E+03
ukaryotic round cell non-flagellate	Chlorophyta	*	Most are likely in Chloroph	r 9	7	5		21	0.041	1023	22	2.28E+04
ukaryotic round flagellate	Chlorophyta	*	Most are likely in Chloroph	r C	0	0		0	0.041	0	89	0.00E+00
ediastrum	Chlorophyta	Chlorophyceae		(	0	0		0	0.041	0	350770	0.00E+00
cenedesmus (cells)	Chlorophyta	Chlorophyceae		12	2 12	6		30	0.041	1461	25	3.58E+04
cenedesmus (filaments)	Chlorophyta	Chlorophyceae		3	3	2		8	0.041	390	66	2.56E+04
phaerocystis	Chlorophyta	Chlorophyceae		(	) 0	0		0	0.041	0	184	0.00E+00
elenastrum	Chlorophyta	Chlorophyceae		(	) 0	0		0	0.041	0	67	0.00E+00
etraspora	Chlorophyta	Chlorophyceae	colony	C	0	0		0	0.041	0	357	0.00E+00
ryptomonas-like flagellate	Cryptophyta	Cryptomonas		(	) 1	0		1	0.041	49	356	1.74E+04
nabaena	Cyanobacteria	Cyanophycea		C	) 0	0		0	0.041	0	117	0.00E+00
nabaena (filaments)	Cyanobacteria	Cyanophycea		C	) 0	0		0	0.041	0	117	0.00E+00
nabaena flosaquae morph (oval cells	s Cyanobacteria	Cyanophycea		C	) 0	0		0	0.041	0	117	0.00E+00
phanizomenon	Cyanobacteria	Cyanophycea	filaments	(	) 0	0		0	0.041	0	196	0.00E+00
alothrix	Cyanobacteria	Cyanophycea		(	) 0	0		0	0.041	0	85	0.00E+00
Chroococcus	Cyanobacteria	Cyanophycea		C	) 2	0		2	0.041	97	170	1.65E+04
oelosphaerium	Cyanobacteria	Cyanophycea		C	) 0	0		0	0.041	0	7	0.00E+00
ileocapsa	Cyanobacteria	Cyanophycea		C	0	0		0	0.041	0	7	0.00E+00
1erismopedia	Cyanobacteria	Cyanophycea	cells	C	) 0	0		0	0.041	0	6	0.00E+00
icrocystis	Cyanobacteria	Microcystaceae	cells	17	7 30	460		507	0.041	24699	3	8.40E+04
cillatoria	Cyanobacteria	Cyanophycea	filaments	C	) 0	0		0	0.041	0	43	0.00E+00
ynechococcus	Cyanobacteria	Cyanophycea		16	5 6	91		113	0.041	5505	6	3.27E+04
ynecocystis	Cyanobacteria	Cyanophycea			,			0	0.041	0	32	0.00E+00
uglenoid	Euglenozoa	Euglenophyceae		(	0	0		0	0.041	0	1728	0.00E+00
eridinium	Miozoa	Dinophyceae		C	) 0	0		0	0.041	0	4211	0.00E+00
Dinobryon	Ochrophyta	Chrysophyceae		C	0	0		0	0.041	0	94	0.00E+00
Mallomonas	Ochrophyta	Synurophyceae		(	) 0	0		0	0.041	0	759	0.00E+00

Appendix 3F. Detailed taxonomic composition of phytoplankton and biovolume calculations for Owasco Lake Phytoplankton, 27 August 2018

						Cvanob.	Chlorop.	Bacill.	Chyrsop.	Cryptop.	Euglenop.	Dino/Pyrrop.
				density	(#/mL)	5213	•		1705	49		244
ample 6	27-Se	p-18 much less dense sampl	le visually			3.51E+04	2.79E+04		1.60E+05	1.74E+04		
ite: UFI Owasco Site 2		Depth on bottle	none (but should be 0.5m	)								
JFI ID: OW SITE 2	site 2	units are # of cells unle	ss listed as filament									
									Volume Cou	Cell Density	Cell biovol	Total biovolume
Genus or Lowest Taxonomic Unit	Phylum/Larger taxonomic group	Class	<b>Additional Information</b>	Field 1	Field 2	Field 3		# Cells	mL sample	#/mL	um^3	um^3/mL
sterionella (cells total)	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	134	0.00E+00
sterionella (colonies)	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	806	0.00E+00
ulacoseira	Bacillariophyta	Coscinodiscophyceae		0	0	0		0	0.041	0	610	0.00E+00
Cyclotella	Bacillariophyta	Mediophyceae		0	0	0		0	0.041	0	393	0.00E+00
Cocconeis	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	110	0.00E+00
Cymbella	Bacillariophyta	Bacillariophyceae		0	0	) 1		1	0.041	49	59	2.87E+03
Diatoma	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	65	0.00E+00
ragilaria (cells)	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	155	0.00E+00
ragilaria (filaments)	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	1438	0.00E+00
Gyrosigma	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	2676	0.00E+00
lavicula	Bacillariophyta	Bacillariophyceae		0	0	) 0		0	0.041	0	1104	0.00E+00
litzschia	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	625	0.00E+00
urirella	Bacillariophyta	Bacillariophyceae		0	0	) 0		0	0.041	0	227	0.00E+00
ynedra	Bacillariophyta	Bacillariophyceae		4	2	! 6		12	0.041	585		5.46E+05
abellaria	Bacillariophyta	Bacillariophyceae		0	0	0		0	0.041	0	1894	0.00E+00
Jrosolenia	Bacillariophyta	Bacillariophyceae		0	0	) 0		0	0.041	0	4502	0.00E+00
Cosmarium	Charophyta	Zygnematophyceae		0	0	) 0		0	0.041	0	681	0.00E+00
ukaryotic oval cell non-flagellate*	Chlorophyta	*	Most are likely in Chloroph	r 9	3	. 0		12	0.041	585		
ukaryotic round cell non-flagellate	Chlorophyta	*	Most are likely in Chloroph					0	0.041	0	22	
ukaryotic round flagellate	Chlorophyta	*	Most are likely in Chloroph			) 0		0	0.041	0	89	0.00E+00
ediastrum	Chlorophyta	Chlorophyceae	most are interval are emeropi.	. 0	0	) 0		0	0.041	0	350770	0.00E+00
cenedesmus (cells)	Chlorophyta	Chlorophyceae		2	~			6	0.041	292		
cenedesmus (filaments)	Chlorophyta	Chlorophyceae		1	0	•		2	0.041	97	_	6.40E+03
phaerocystis	Chlorophyta	Chlorophyceae		0	-	_		0	0.041	0	184	0.00E+00
elenastrum	Chlorophyta	Chlorophyceae		0	~	•		0	0.041	0	67	0.00E+00
etraspora	Chlorophyta	Chlorophyceae	colony	0	-	_		0	0.041	0	357	0.00E+00
ryptomonas-like flagellate	Cryptophyta	Cryptomonas	colony	0				1	0.041	49		1.74E+04
nabaena	Cyanobacteria	Cyanophycea		0				0	0.041	40	117	0.00E+00
nabaena (filaments)	Cyanobacteria	Cyanophycea		0	ď			0	0.041	0	117	0.00E+00
anabaena flosaquae morph (oval cells		Cyanophycea		0	0			0	0.041	0	117	0.00E+00
uphanizomenon	Cyanobacteria	Cyanophycea	filaments	0	ď	Ŭ		0	0.041	0	196	0.00E+00
Calothrix	Cyanobacteria	Cyanophycea	Manients	0	ď	•		0	0.041	0	85	0.00E+00 0.00E+00
Chroococcus	Cyanobacteria			0	0	•		1	0.041	49	85 170	8.26E+03
Coelosphaerium	Cyanobacteria	Cyanophycea		0	ď	_		0	0.041	49	1/0	0.00E+00
	Cyanobacteria	Cyanophycea		0	0	•		0	0.041	0	7	0.00E+00 0.00E+00
ileocapsa Aorismonadia		Cyanophycea	colle	0	ď	Ŭ		0	0.041	0	- /	0.00E+00 0.00E+00
Merismopedia  Micro custic	Cyanobacteria	Cyanophycea	cells	32		_		75	0.041	3654	6	
Microcystis	Cyanobacteria	Microcystaceae	cells	32 1							3	1.24E+04
Oscillatoria	Cyanobacteria	Cyanophycea	filaments	_	0			3	0.041	146	43	6.28E+03
ynechococcus	Cyanobacteria	Cyanophycea		10		11		28	0.041	1364	6	8.11E+03
ynecocystis	Cyanobacteria	Cyanophycea		0		_		0	0.041	0	32	0.00E+00
uglenoid	Euglenozoa	Euglenophyceae		0				0	0.041	0	1728	0.00E+00
Peridinium	Miozoa	Dinophyceae		2				5	0.041	244		1.03E+06
Dinobryon	Ochrophyta	Chrysophyceae		20				35	0.041	1705.057548	94	1.60E+05
//allomonas	Ochrophyta	Synurophyceae		0	0	) 0		0	0.041	0	759	0.00E+00

## **Appendix D: Model Drivers**

## **Appendix D-1 Meteorology**

The meteorological drivers have a tremendously important impact on the hydrothermal/transport water quality sub-models. Therefore considerable effort was expended in selecting the best source of these data. The ideal data source would located on or near the lake, provide year-round, hourly (or more frequent) measurements, provide historical data (1999 or early), and be freely available. Two autonomous buoys located near site 10 measured meteorological from 2005-2008 and 2014-present. The early buoy was maintained by UFI and latter was maintained the Finger Lake Institute (FLI). These buoys although ideally located, have several important limitations: (1) large data gap between 2008 and 2014, (2) only available from April-October with occasional seasonal data gaps, and (3) unavailable before 2005. These limitations clearly limit using these data directly as model inputs, however these data can be used to evaluate and possibly improve (i.e., adjust) onshore metrological data. We evaluated other sites (Figure 5-3), we selected the National Weather Service station located at the Syracuse Airport (KSYR) as the primary source of meteorological data. Paired measurements between KSYR, UFI and FLI data are shown in Figures D-1—Figures D-11. We found that Tair, Tdp, and incident light were adequately correlated between the lake buoys and KSYR (Table D-1), while there were considerable differences between wind velocities (Figure 5-4). With exception of wind velocity, these data were merged and used without modification.

The KSYR wind velocity was transformed as described in Section 5.3.1 using the coefficients (A, B, C, D) from Eq. 5-1 and 5-2 shown in the Table D-2.

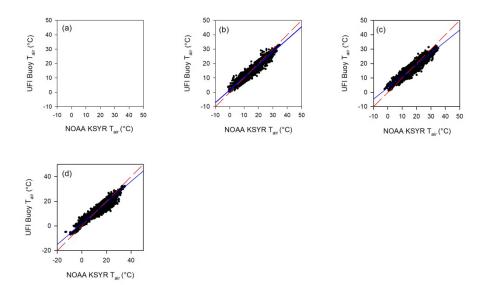


Figure D-1. Air temperature (°C) hourly regressions for Owasco Lake UFI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2005, (b) 2006, (c) 2007, (d) 2008. The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference. \*Note that no temperature was available from the UFI buoy in 2005.

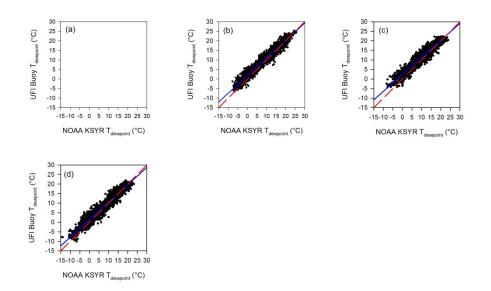


Figure D-2. Dew point temperature (°C) hourly regressions for Owasco Lake UFI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2005, (b) 2006, (c) 2007, (d) 2008. The regressions are shown as a solid blue line The dashed red line is a 1:1 relationship for reference. \*Note that due to lack of temperature data for 2005 no dew point could be calculated for the UFI buoy.

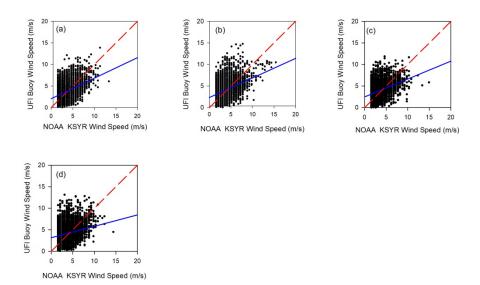


Figure D-3. Wind speed (m/s) hourly regressions for Owasco Lake UFI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2005, (b) 2006, (c) 2007, (d) 2008. The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference.

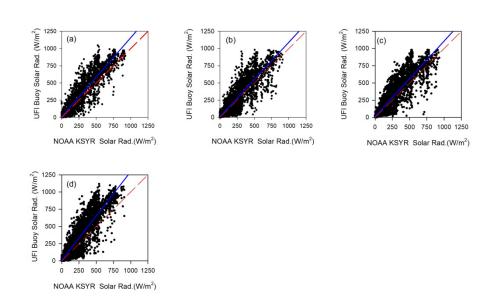


Figure D-4. Solar radiation (W/m²) hourly regressions for Owasco Lake UFI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2005, (b) 2006, (c) 2007, (d) 2008. The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference.

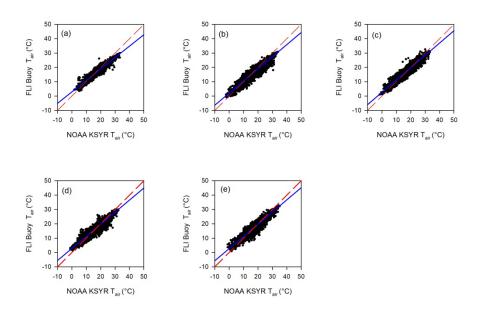


Figure D-5. Air temperature (°C) hourly regressions for Owasco Lake FLI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2014, (b) 2015, (c) 2016, (d) 2017, (e) 2018. The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference.

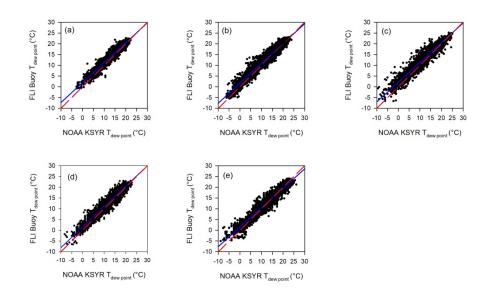


Figure D-6. Dew point temperature (°C) hourly regressions for Owasco Lake FLI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2014, (b) 2015, (c) 2016, (d) 2017, (e) 2018. The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference.

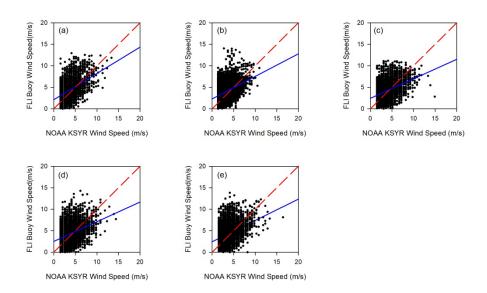
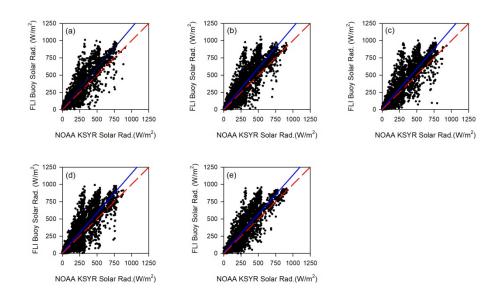
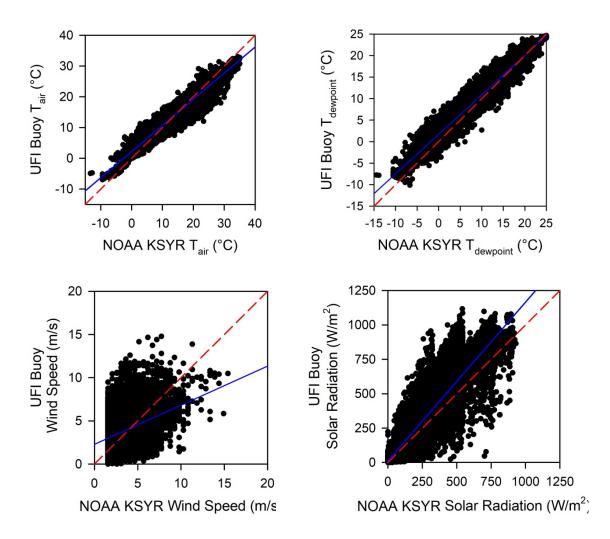


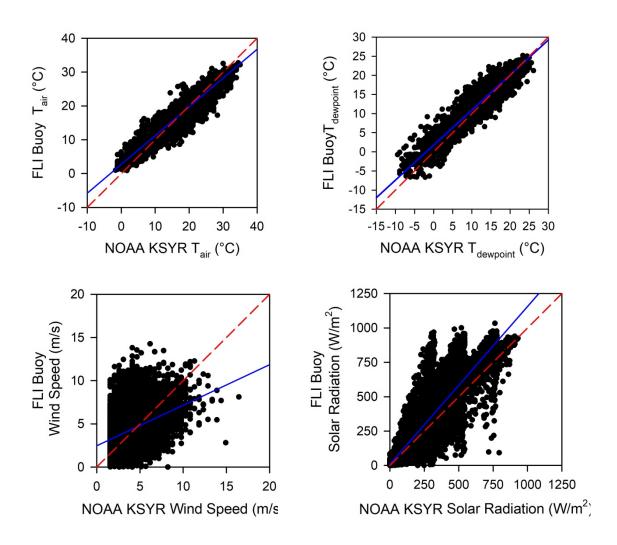
Figure D-7. Wind speed (m/s) hourly regressions for Owasco Lake FLI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2014, (b) 2015, (c) 2016, (d) 2017, (e) 2018. The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference.



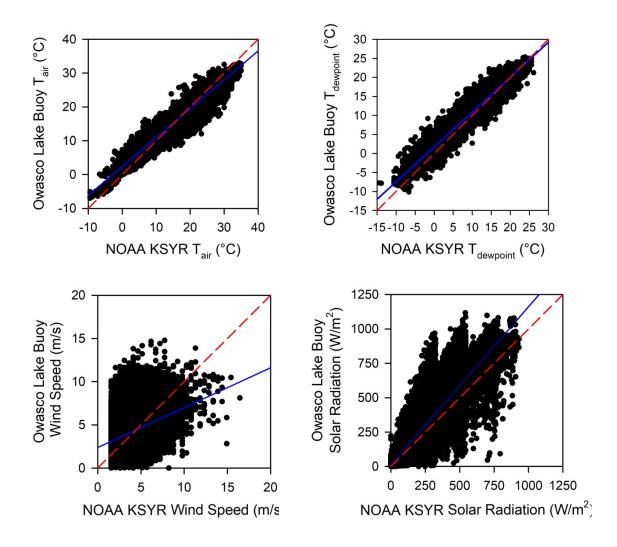
**Figure D-8**. Solar radiation (W/m²) hourly regressions for Owasco Lake FLI buoy met station versus NOAA Hancock Airport (KSYR) for (a) 2014, (b) 2015, (c) 2016, (d) 2017, (e) 2018. The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference.



**Figure D-9**. Lumped hourly regressions (2005-2008) for Owasco Lake UFI buoy met station versus NOAA Hancock Airport (KSYR). The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference. The windspeed regression excludes 2008 data which was determined to be an outlier.



**Figure D-10.** Lumped hourly regressions (2016-2018) for Owasco Lake FLI buoy met station versus NOAA Hancock Airport (KSYR). The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference. FLI buoy data from 2014-2015 is excluded (not collected under an approved QAPP).



**Figure D-11**. Lumped hourly regressions of all available data (2005-2008 + 2016-2018) for Owasco Lake buoy met stations versus NOAA Hancock Airport (KSYR). The regressions are shown as a solid blue line. The dashed red line is a 1:1 relationship for reference. FLI buoy data from 2014-2015 is excluded (not collected under an approved QAPP), and UFI buoy wind speed data from 2008 is excluded (determined to be an outlier).

**Table D-1**. Regressions statistics for Owasco Lake UFI and FLI buoy MET Hourly Average Data verses KSYR.

Year	T <sub>air</sub> (°C)			$T_{ m dew} \ (^{\circ}C)$				ar Radiat Watts/m²		Wind Speed (m/s)			
	slope	int.	r2	slope	int.	r2	slope	int.	r2	slope	int.	r2	
UFI Buoy							-		•	-			
2005	N/A	N/A	N/A	N/A	N/A	N/A	1.15	10.86	0.88	0.49	2.00	0.17	
2006	0.88	1.65	0.93	0.92	1.77	0.95	1.08	10.22	0.83	0.45	2.35	0.16	
2007	0.80	3.30	0.92	0.89	2.42	0.92	1.09	16.75	0.85	0.42	2.49	0.13	
2008	0.85	2.04	0.94	0.91	1.32	0.95	1.29	9.52	0.87	0.27	3.13	0.08	
FLI Buoy													
2014	0.80	2.96	0.93	0.93	1.97	0.93	1.18	8.75	0.84	0.61	2.13	0.22	
2015	0.85	2.10	0.91	0.92	1.65	0.94	1.18	9.78	0.85	0.52	2.30	0.16	
2016	0.86	2.62	0.93	0.92	2.14	0.93	1.16	11.61	0.86	0.45	2.45	0.15	
2017	0.84	2.83	0.90	0.95	1.48	0.93	1.15	9.99	0.83	0.46	2.52	0.14	
2018	0.85	2.76	0.92	0.90	1.45	0.94	1.13	6.43	0.87	0.50	2.43	0.16	
Overall lumped regression UFI <sup>2</sup>	0.85	2.18	0.93	0.92	1.70	0.94	1.15	12.17	0.85	0.45	2.29	0.15	
Overall lumped regression FLI <sup>1</sup>	0.85	2.74	0.92	0.92	1.77	0.93	1.15	9.25	0.85	0.47	2.47	0.15	
ALL DATA <sup>1,2</sup>	0.85	2.41	0.93	0.92	1.73	0.94	1.15	10.79	0.85	0.46	2.39	0.15	

 Table D-2.
 KSYR wind velocity transformation coefficients.

θ≥	θ<	Α	В	С	D
0	45	0.485	-0.205	-1.31	0.765
45	90	0.895	-1.2	-0.75	-0.325
90	135	0.33	-0.155	-1.145	1.035
135	180	0.825	0.05	-0.285	1.38
180	225	0.505	-0.095	-0.3	1.275
225	270	0.62	-0.165	-0.215	1.245
270	315	1.01	0.99	-0.135	1.22
315	360	0.55	-0.025	-0.195	0.82

## **Appendix E: Hydrothermal Model**

## **Appendix E-1 Hydrothermal Model Equations**

#### 1.1.1 Horizontal momentum

(**Eq. 4-1**). 
$$\frac{\partial UB}{\partial t} + \frac{\partial UUB}{\partial x} + \frac{\partial WUB}{\partial z} = -\frac{1}{\rho} \frac{\partial BP}{\partial x} + \frac{\partial \left[BA_X \frac{\partial U}{\partial x}\right]}{\partial x} + \frac{\partial B\tau_x}{\partial z}$$

where

U = longitudinal, laterally averaged velocity, m/sec

B = waterbody width, m

t = time, sec

x = longitudinal Cartesian coordinate: x is along the lake centerline at the water surface, positive to the right

z = vertical Cartesian coordinate: z is positive downward

W = vertical, laterally averaged velocity, m/sec

 $\rho$  = density, kg/m<sup>3</sup> P = pressure, N/m<sup>2</sup>

 $A_x = longitudinal momentum dispersion coefficient, m<sup>2</sup>/sec$ 

 $\tau_x$  = shear stress per unit mass resulting from the vertical gradient of the horizontal velocity, U, m<sup>2</sup>/sec2

The first term represents the time rate of change of horizontal momentum, and the second and third terms are the horizontal and vertical advection of momentum. The first term on the right hand side (RHS) of Eq. 4-5 is the force imposed by the horizontal pressure gradient. The second term on the RHS is the horizontal dispersion of momentum, and the third term is the force due to shear stress.

### 1.1.2 Constituent transport

(**Eq. 4-2**). 
$$\frac{\partial B\phi}{\partial t} + \frac{\partial UB\phi}{\partial x} + \frac{\partial WB\phi}{\partial z} - \frac{\partial \left[BD_x \frac{\partial \phi}{\partial x}\right]}{\partial x} - \frac{\partial \left[BD_z \frac{\partial \phi}{\partial z}\right]}{\partial z} = q_{\phi}B + S_{\phi}B$$

where

 $\phi$  = laterally averaged constituent concentration, g/m<sup>3</sup>

 $D_x =$ longitudinal temperature and constituent dispersion coefficient, m<sup>2</sup>/sec

 $D_z$  = vertical temperature and constituent dispersion coefficient, m<sup>2</sup>/sec

 $q_{\phi}$  = lateral inflow or outflow mass flow rate of constituent per unit volume, g/m<sup>3</sup>/sec

 $S_0$ =kinetics source/sink term for constituent concentrations, g/m<sup>3</sup>/sec

Each constituent has a balance as in Eq. 4-6 with specific source and sink terms. The first term in Eq. 4-6 represents the time rate of change of constituent concentrations and the second and third terms are the horizontal and vertical advection of constituents. The fourth and fifth terms are the horizontal and vertical diffusion of constituents. The first term on the RHS is the

lateral inflow/outflow of constituents, and the second term represents kinetic source/sink rates for constituents.

#### 1.1.3 Free water surface elevation

(**Eq. 4-3**). 
$$\frac{\partial B_{\eta}\eta}{\partial t} = \frac{\partial}{\partial x} \int_{\eta}^{h} UBdz - \int_{\eta}^{h} qBdz$$

where

 $B_{\eta}$  = time and spatially varying surface width, m

 $\eta$  = free water surface location, m

h = total depth, m

q = lateral boundary inflow or outflow, m<sup>3</sup>/sec

### 1.1.4 Hydrostatic pressure

(**Eq. 4-4**). 
$$\frac{\partial P}{\partial z} = \rho g$$

where

g = acceleration due to gravity, m/sec<sup>2</sup>

## 1.1.5 Continuity

(**Eq. 4-5**). 
$$\frac{\partial UB}{\partial x} + \frac{\partial WB}{\partial z} = qB$$

### 1.1.6 Equation of state

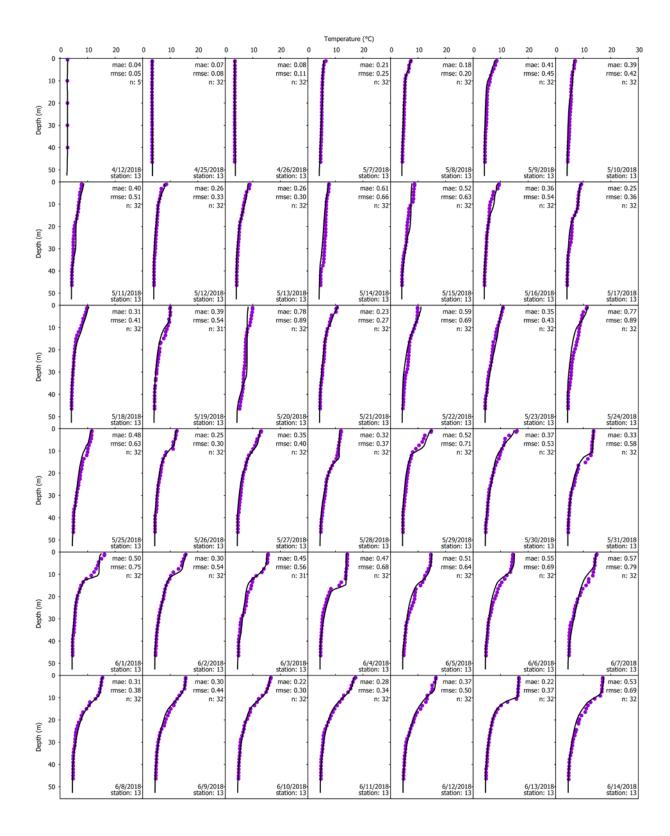
(Eq. 4-6). 
$$\rho = f(T_{W_s} \phi_{TDS}, \phi_{SS})$$

where

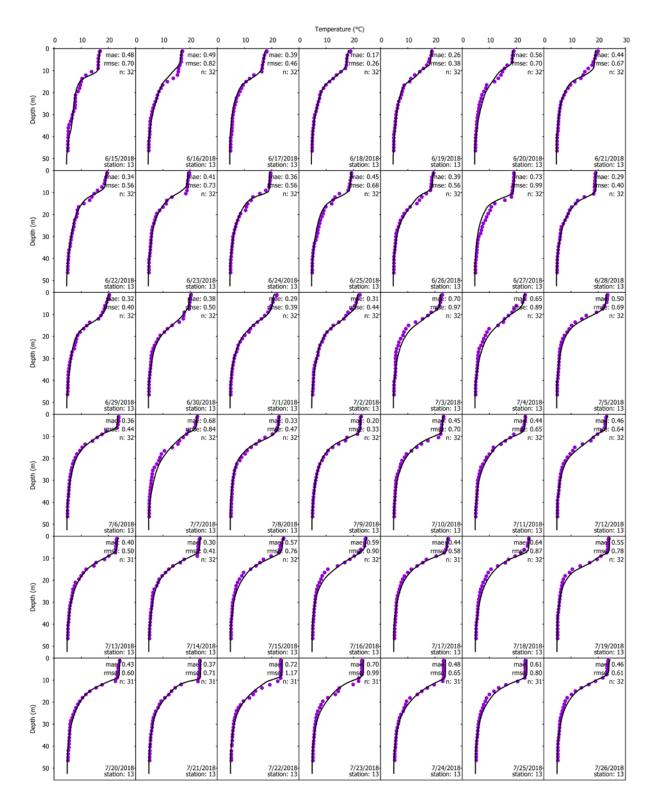
 $f(T_w, \phi_{TDS}, \phi_{SS})$  = density function dependent upon temperature, total dissolved solids or salinity, and suspended solids.

The six equations result in six unknowns: (1) free water surface elevation,  $\eta$ ; (2) pressure, P; (3) horizontal velocity, U; (4) vertical velocity, W; (5) constituent concentration,  $\phi$ ; and (6) density,  $\rho$ . Lateral averaging eliminates the lateral momentum balance, lateral velocity, and Coriolis acceleration. The solution of the six equations for the six unknowns forms the basic model structure.

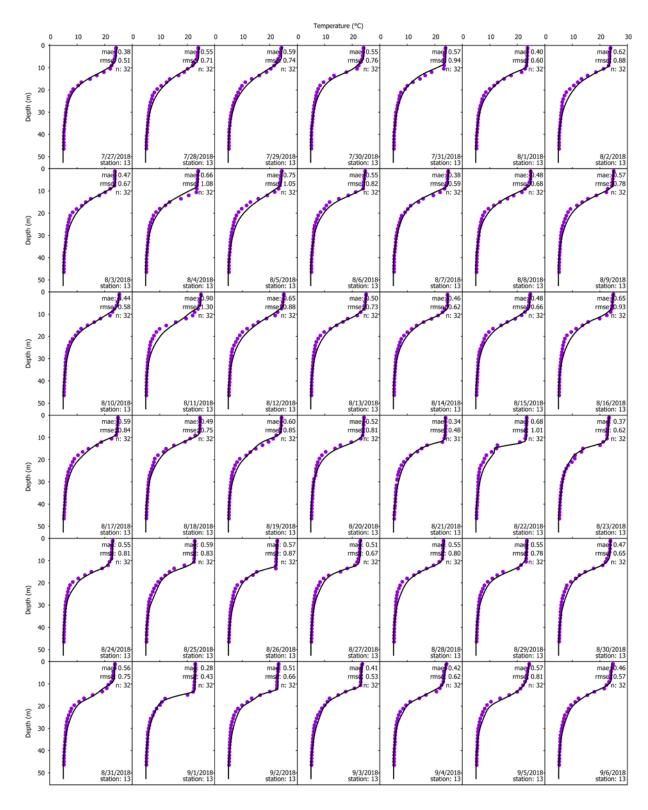
## Appendix E-1 Calibration, 2018



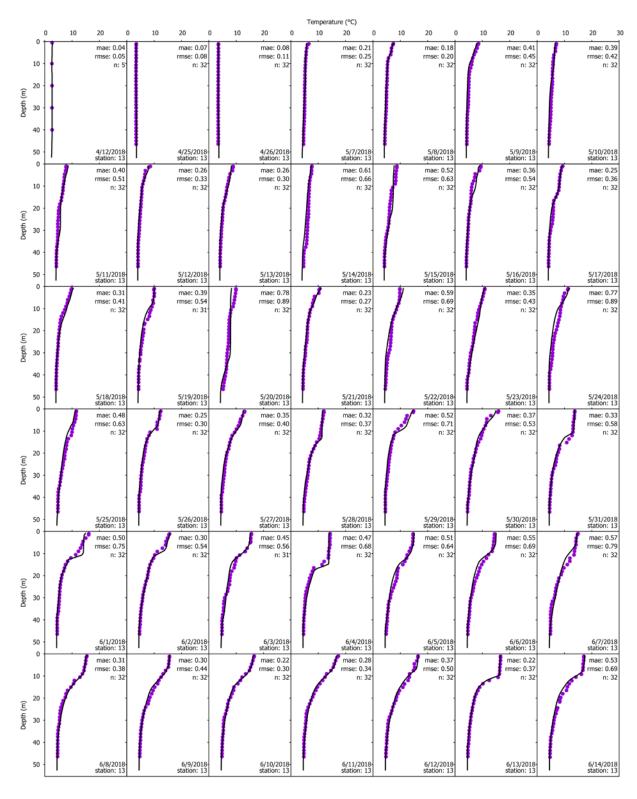
**Figure E-1.** Hydrothermal Model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for calibration year, 2018 page 1 of 5.



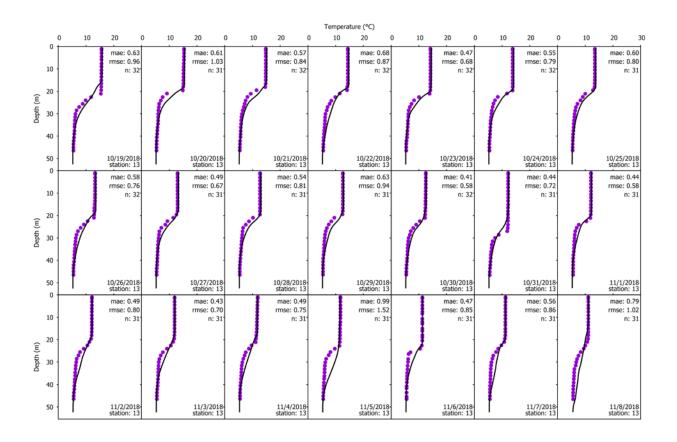
**Figure E-1.** Hydrothermal Model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for calibration year, 2018 page 2 of 5.



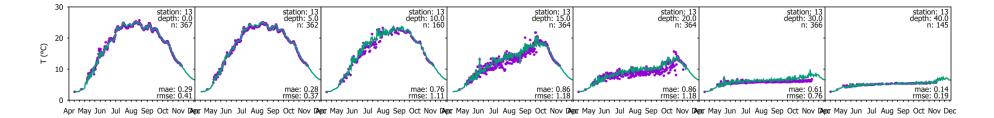
**Figure E-1**. Hydrothermal Model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for calibration year, 2018 page 3 of 5.



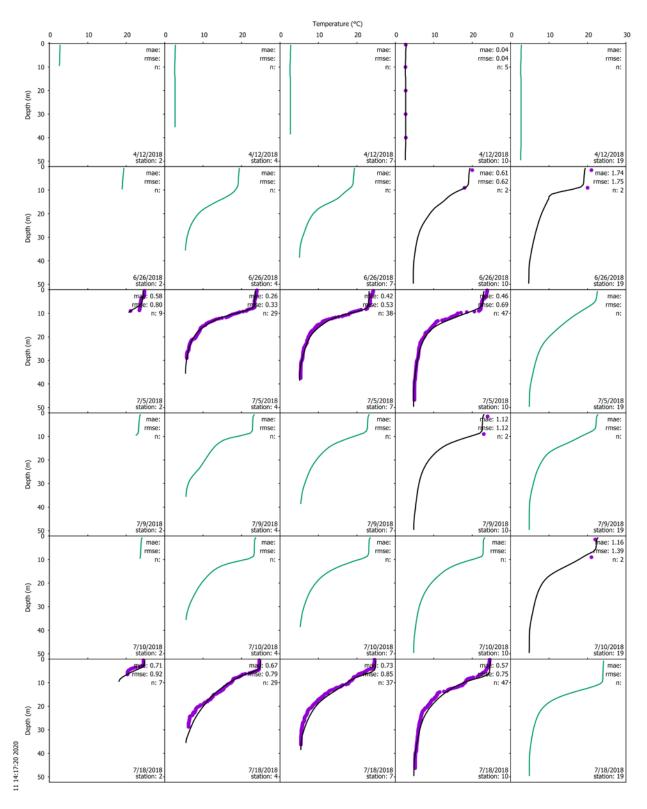
**Figure E-1**. Hydrothermal Model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for calibration year, 2018 page 4 of 5.



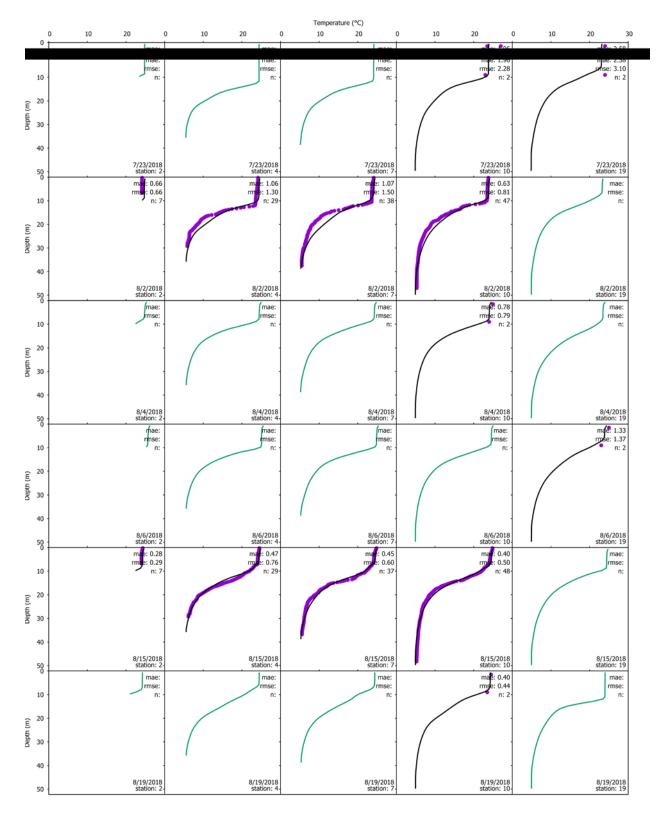
**Figure E-1**. Hydrothermal Model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for calibration year, 2018 page 5 of 5.



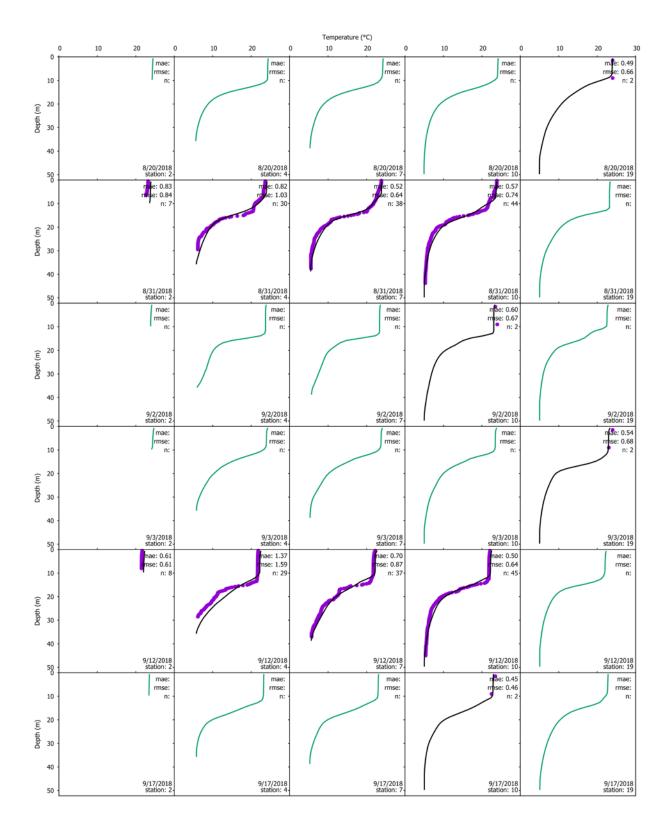
**Figure E-2**. Time series of hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for calibration year, 2018 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.



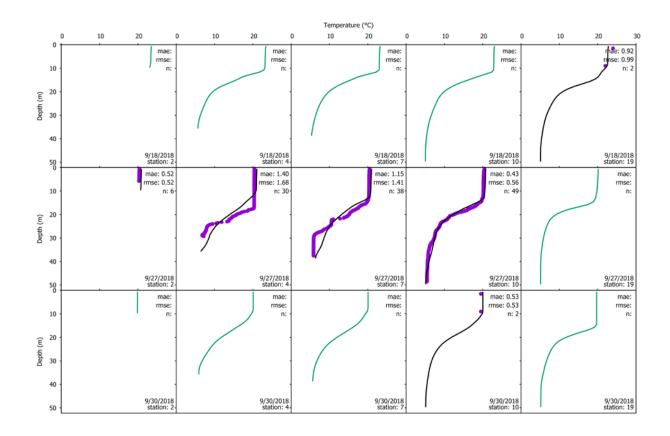
**Figure E-3**. Hydrothermal Model fit to daily UFI SeaBird profiles and CSLAP temperature measurements at multiple sites (Figure 5-14) down the longitudinal axis of Owasco Lake for calibration year, 2018 page 1 of 4



**Figure E-3.** Hydrothermal Model fit to daily UFI SeaBird profiles and CSLAP temperature measurements at multiple sites (Figure 5-14) down the longitudinal axis of Owasco Lake for calibration year, 2018 page 2 of 4

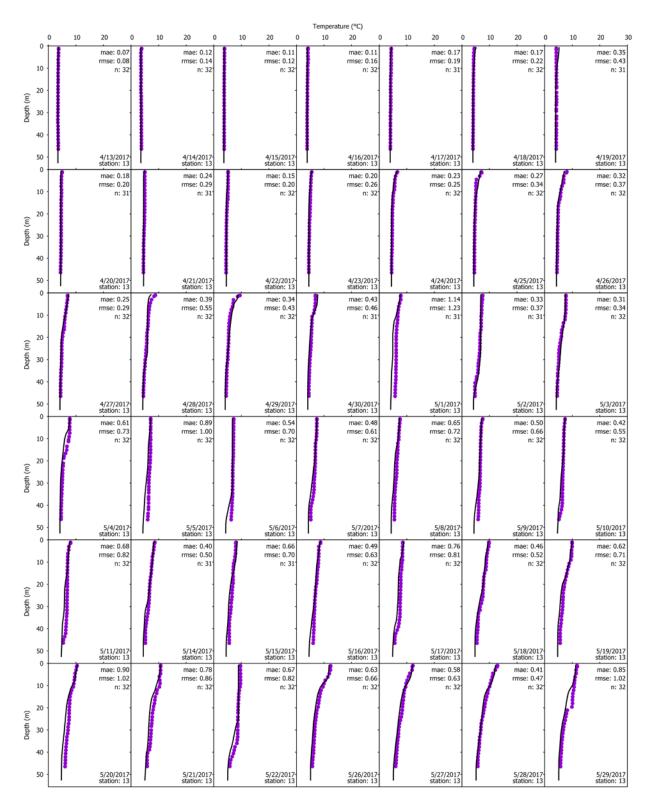


**Figure E-3**. Hydrothermal Model fit to daily UFI SeaBird profiles and CSLAP temperature measurements at multiple sites (Figure 5-14) down the longitudinal axis of Owasco Lake for calibration year, 2018 page 3 of 4

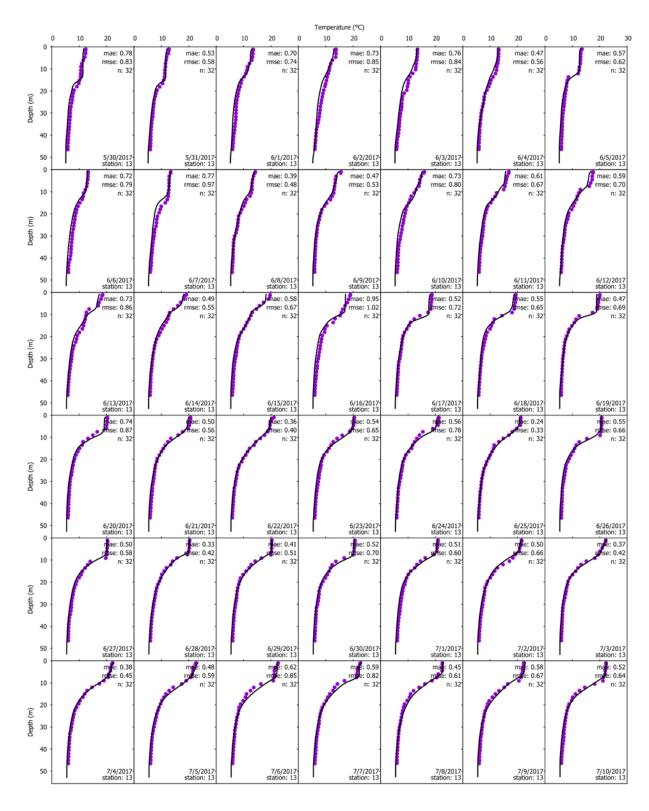


**Figure E-3**. Hydrothermal Model fit to daily UFI SeaBird profiles and CSLAP temperature measurements at multiple sites (Figure 5-14) down the longitudinal axis of Owasco Lake for calibration year, 2018 page 4 of 4

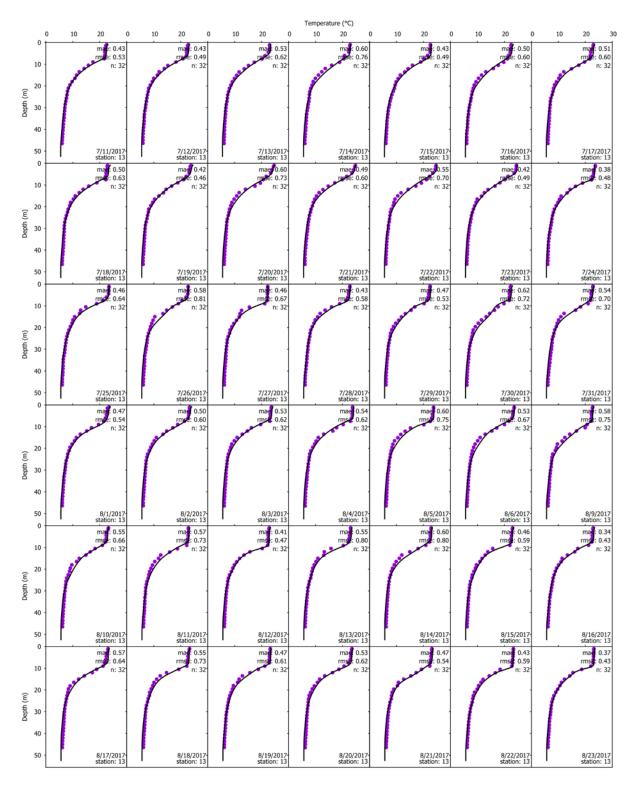
## **Appendix E-2 Confirmation, 2017**



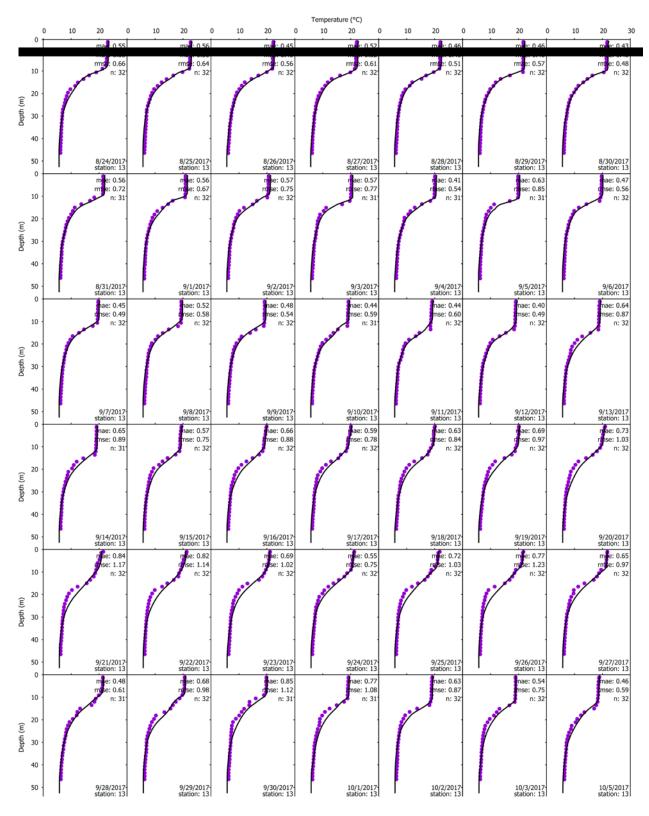
**Figure E-4**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2017 page 1 of 5.



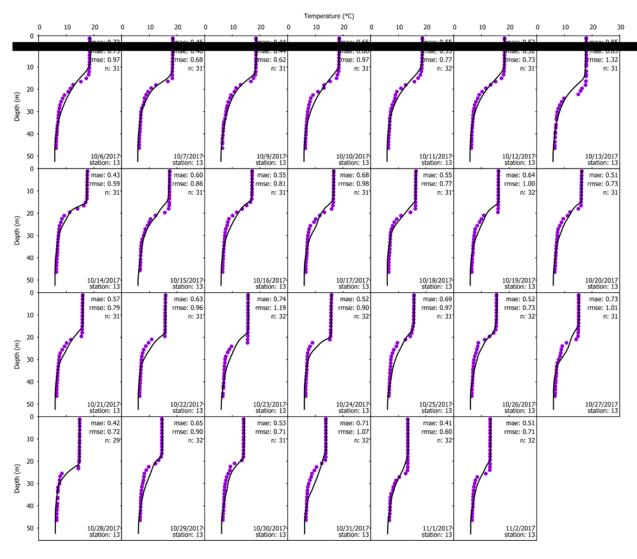
**Figure E-4**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2017 page 2 of 5.



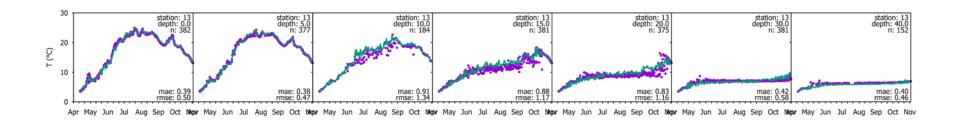
**Figure E-4**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2017 page 3 of 5



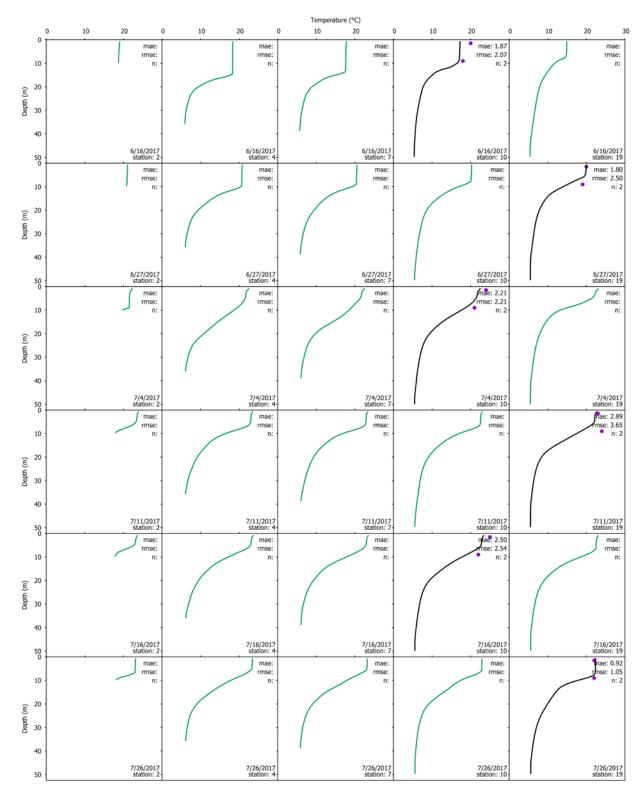
**Figure E-4.** Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2017 page 4 of 5



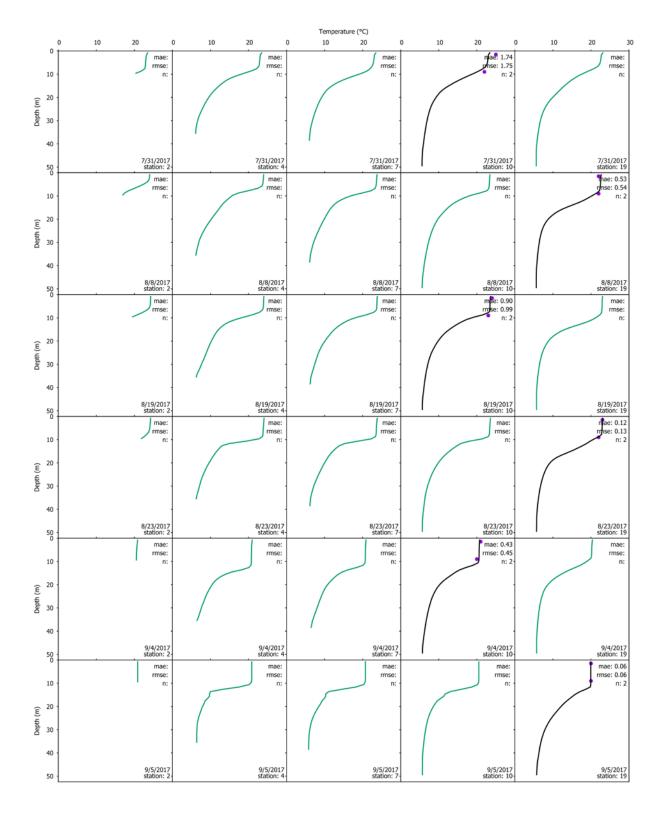
**Figure E-4.** Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2017 page 5 of 5



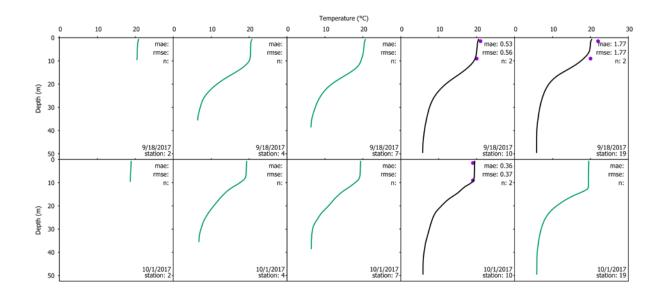
**Figure E-5**. Time series of hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2017 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.



**Figure E-6.** Hydrothermal model fit to daily CSLAP temperature measurements at two sites (Figure 5-14) down the longitudinal axis of Owasco Lake for the primary confirmation year, 2017 page 1 of 3

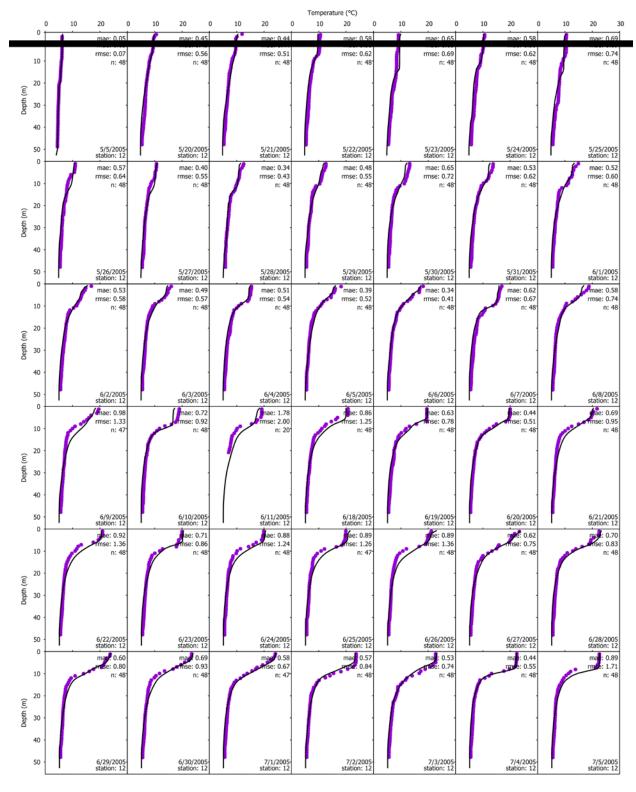


**Figure E-6.** Hydrothermal model fit to daily CSLAP temperature measurements at two sites (Figure 5-14) down the longitudinal axis of Owasco Lake for the primary confirmation year, 2017 page 2 of 3.

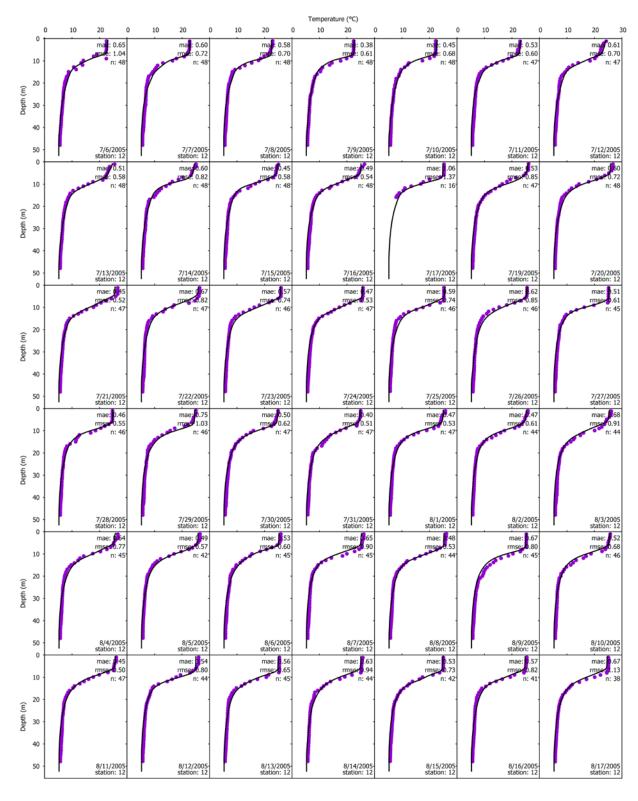


**Figure E-6.** Hydrothermal model fit to daily CSLAP temperature measurements at two sites (Figure 5-14) down the longitudinal axis of Owasco Lake for the primary confirmation year, 2017 page 3 of 3.

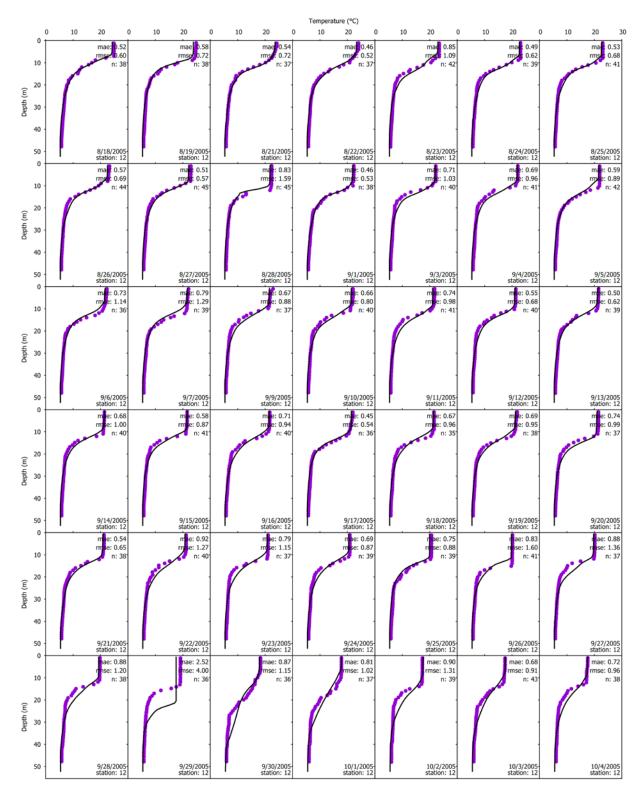
## Appendix E-3 Further Confirmation, 2005-2008, 2014-2016



**Figure E-7**. Hydrothermal model fit to daily buoy profiles at site 12 (Figure 5-14) on Owasco Lake for confirmation year, 2005 page 1 of 4



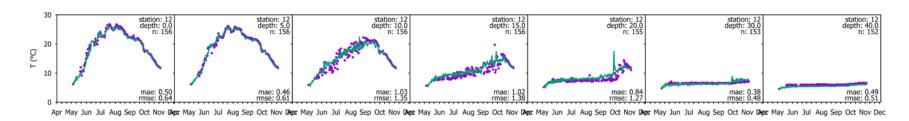
**Figure E-7**. Hydrothermal model fit to daily buoy profiles at site 12 (Figure 5-14) on Owasco Lake for confirmation year, 2005 page 2 of 4



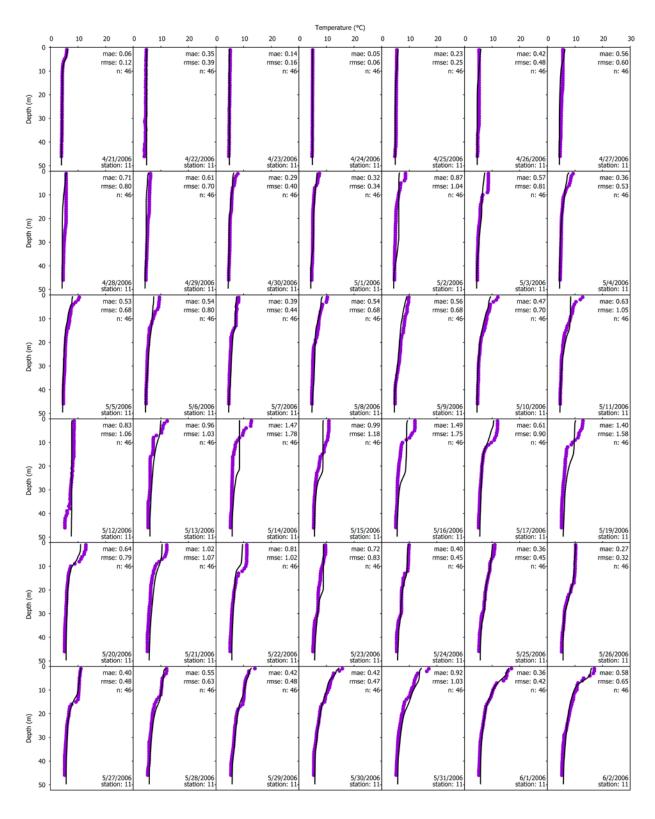
**Figure E-7**. Hydrothermal model fit to daily buoy profiles at site 12 (Figure 5-14) on Owasco Lake for confirmation year, 2005 page 3 of 4



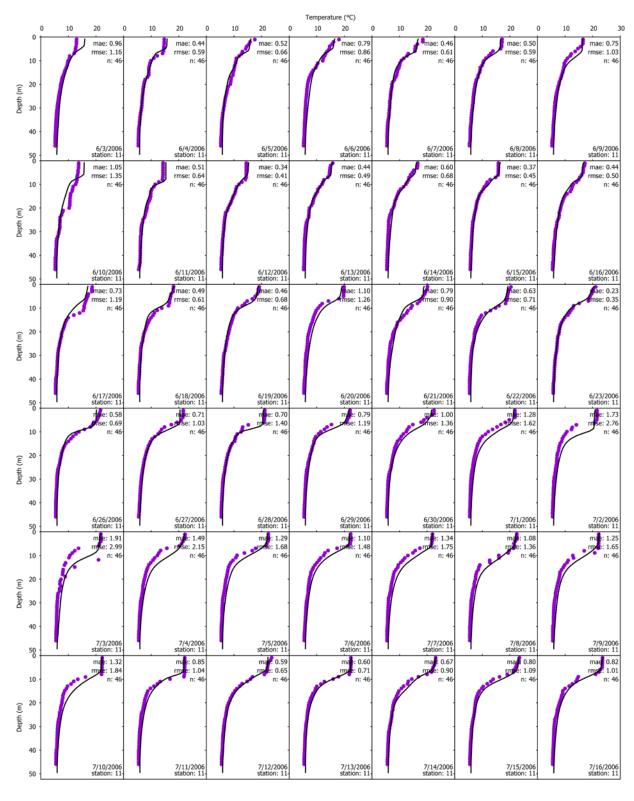
**Figure E-7**. Hydrothermal model fit to daily buoy profiles at site 12 (Figure 5-14) on Owasco Lake for confirmation year, 2005 page 4 of 4



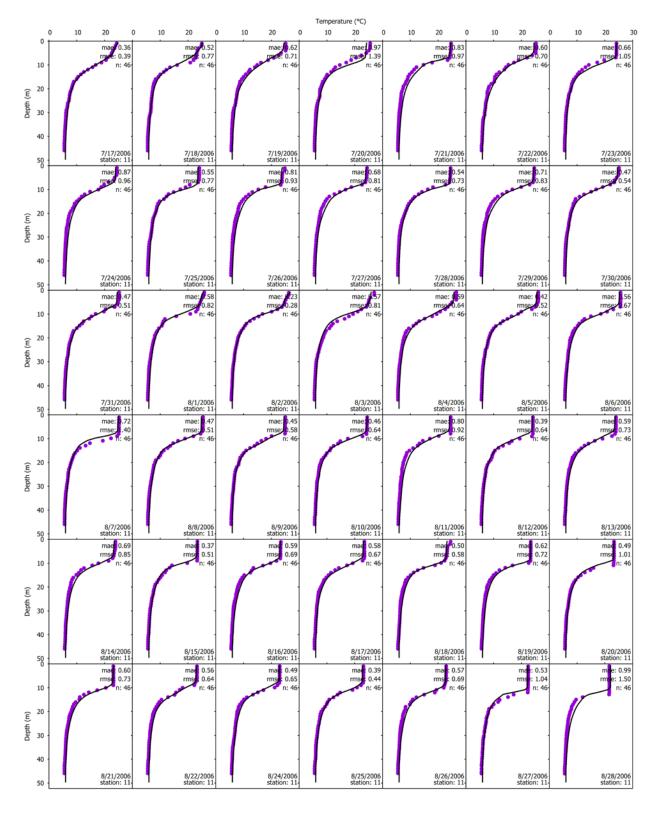
**Figure E-8**. Time series of hydrothermal model fit to daily buoy profiles at site 12 (Figure 5-14) on Owasco Lake for primary confirmation year, 2005 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.



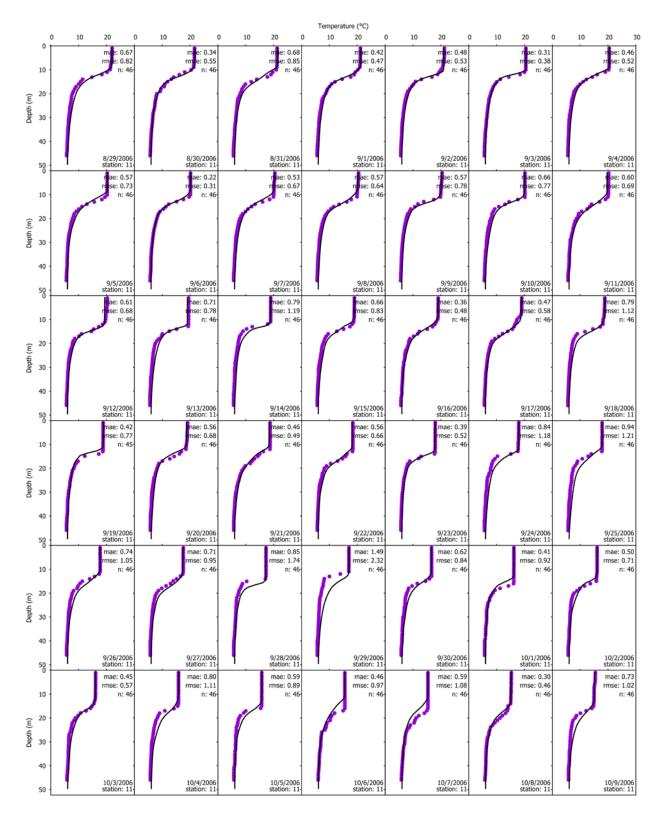
**Figure E-9**. Hydrothermal model fit to daily buoy profiles at site 11 (Figure 5-14) on Owasco Lake for confirmation year, 2006 page 1 of 5.



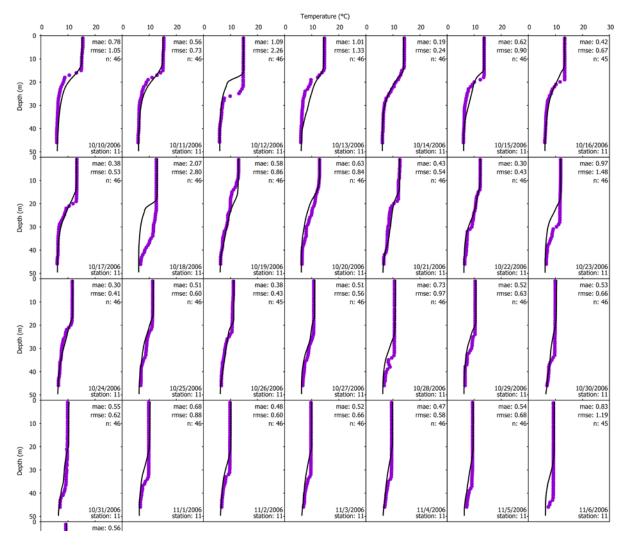
**Figure E-9**. Hydrothermal model fit to daily buoy profiles at site 11 (Figure 5-14) on Owasco Lake for confirmation year, 2006 page 2 of 5.



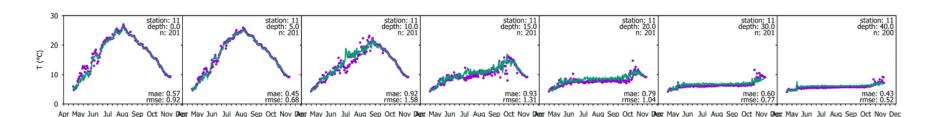
**Figure E-9**. Hydrothermal model fit to daily buoy profiles at site 11 (Figure 5-14) on Owasco Lake for confirmation year, 2006 page 3 of 5.



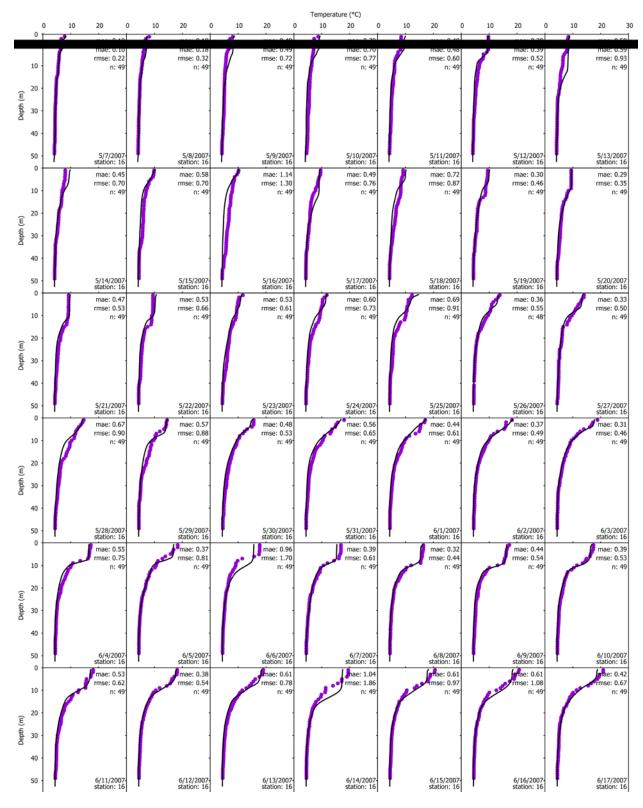
**Figure E-9**. Hydrothermal model fit to daily buoy profiles at site 11 (Figure 5-14) on Owasco Lake for confirmation year, 2006 page 4 of 5.



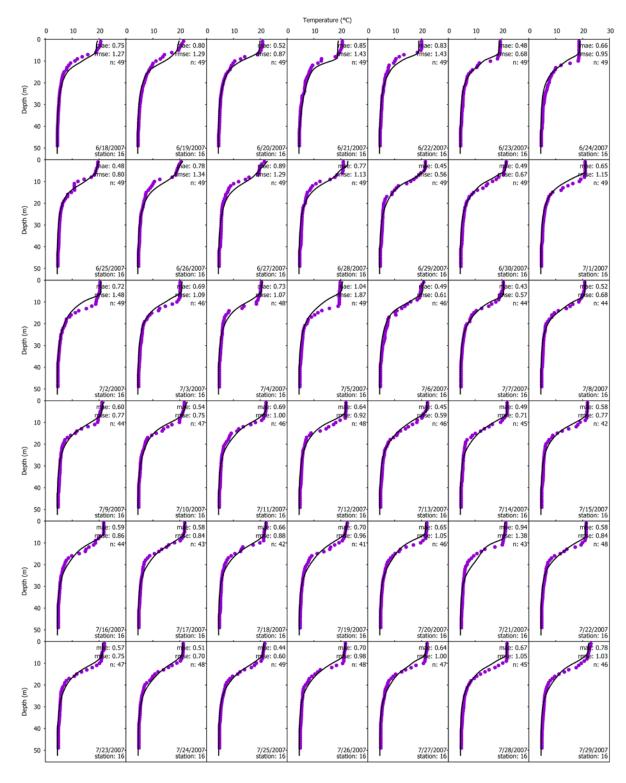
**Figure E-9**. Hydrothermal model fit to daily buoy profiles at site 11 (Figure 5-14) on Owasco Lake for confirmation year, 2006 page 5 of 5.



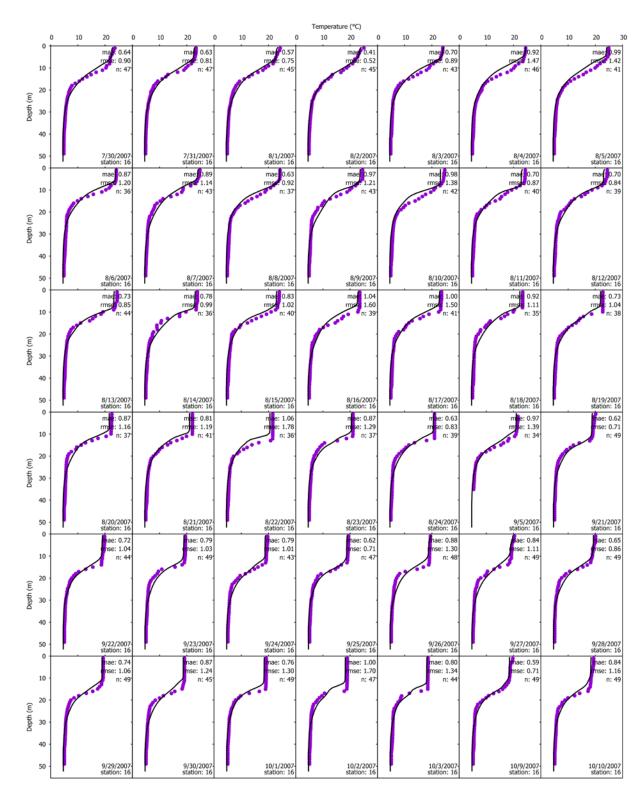
**Figure E-10**. Time series of hydrothermal model fit to daily buoy profiles at site 11 (Figure 5-14) on Owasco Lake for primary confirmation year, 2006 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.



**Figure E-11**. Hydrothermal model fit to daily buoy profiles at site 16 (Figure 5-14) on Owasco Lake for confirmation year, 2007 page 1 of 4.



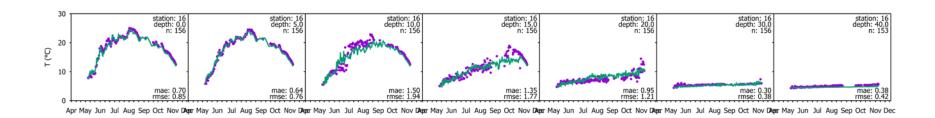
**Figure E-11**. Hydrothermal model fit to daily buoy profiles at site 16 (Figure 5-14) on Owasco Lake for confirmation year, 2007 page 2 of 4.



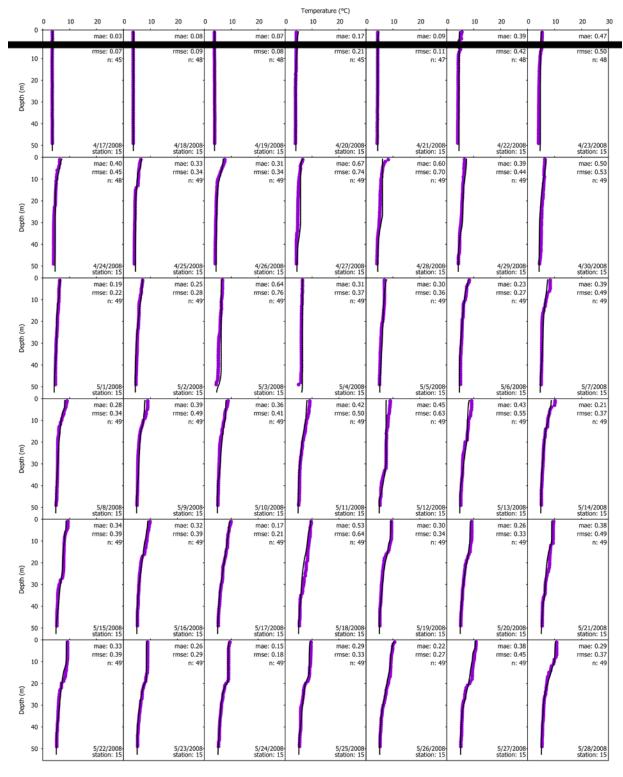
**Figure E-11**. Hydrothermal model fit to daily buoy profiles at site 16 (Figure 5-14) on Owasco Lake for confirmation year, 2007 page 3 of 4.



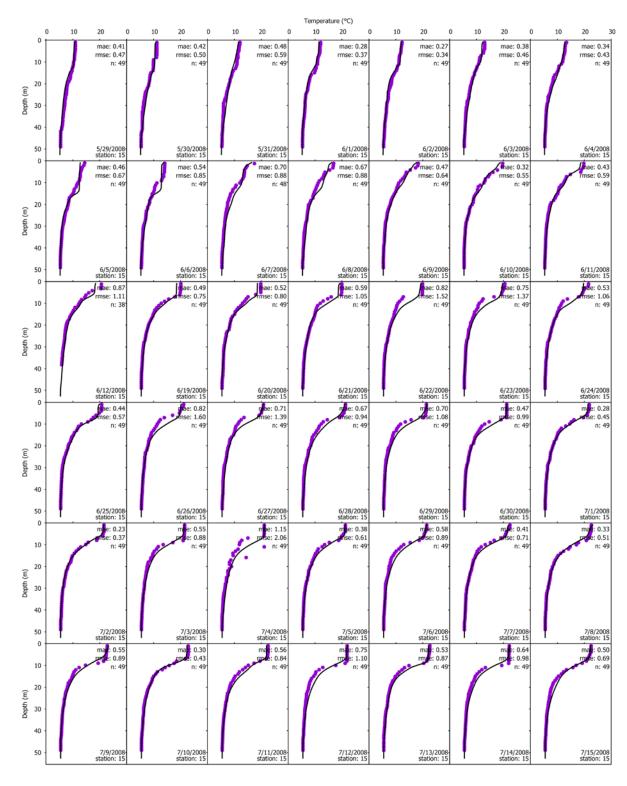
**Figure E-11**. Hydrothermal model fit to daily buoy profiles at site 16 (Figure 5-14) on Owasco Lake for confirmation year, 2007 page 4 of 4.



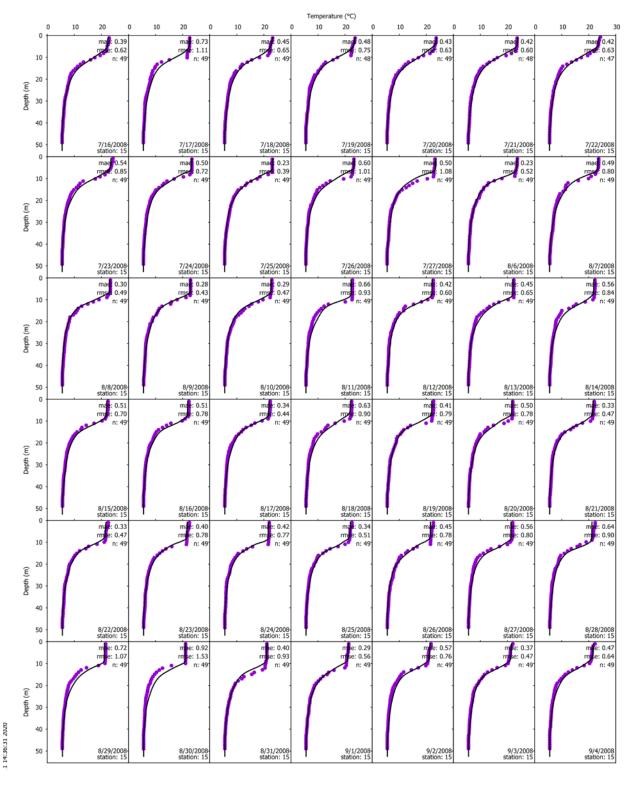
**Figure E-12**. Time series of hydrothermal model fit to daily buoy profiles at site 16 (Figure 5-14) on Owasco Lake for primary confirmation year, 2007 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.



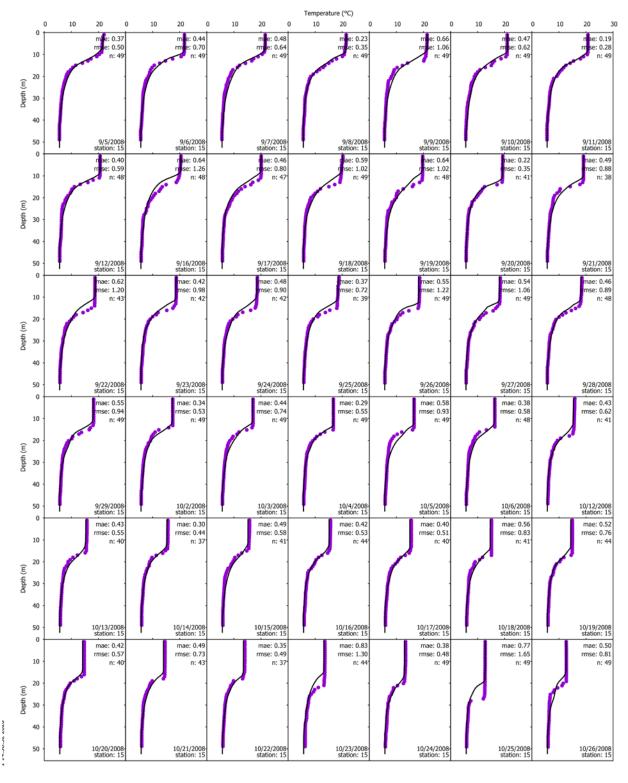
**Figure E-13.** Hydrothermal model fit to daily buoy profiles at site 15 (Figure 5-14) on Owasco Lake for confirmation year, 2008 page 1 of 5.



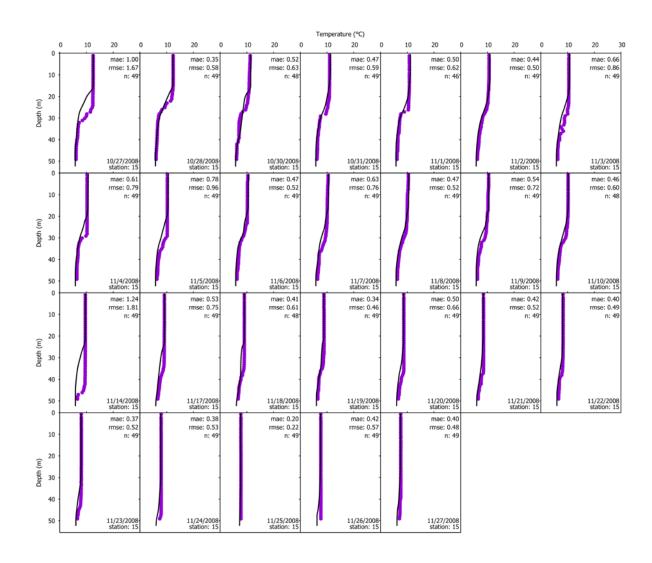
**Figure E-13.** Hydrothermal model fit to daily buoy profiles at site 15 (Figure 5-14) on Owasco Lake for confirmation year, 2008 page 2 of 5.



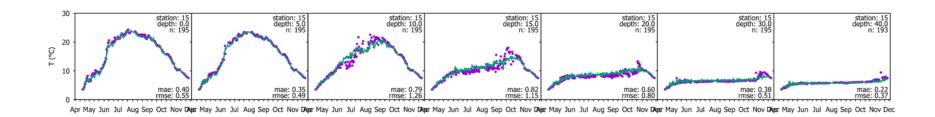
**Figure E-13.** Hydrothermal model fit to daily buoy profiles at site 15 (Figure 5-14) on Owasco Lake for confirmation year, 2008 page 3 of 5.



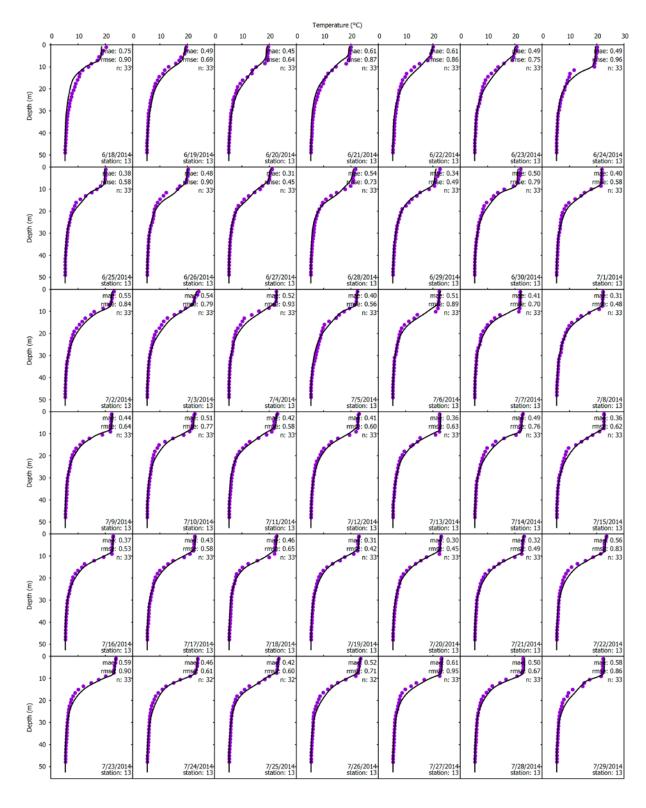
**Figure E-13.** Hydrothermal model fit to daily buoy profiles at site 15 (Figure 5-14) on Owasco Lake for confirmation year, 2008 page 4 of 5.



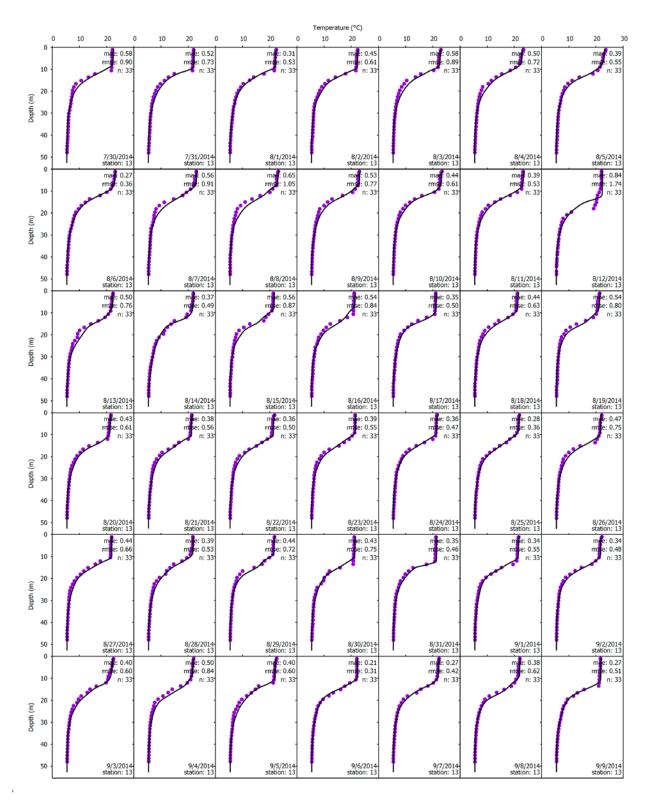
**Figure E-13.** Hydrothermal model fit to daily buoy profiles at site 15 (Figure 5-14) on Owasco Lake for confirmation year, 2008 page 5 of 5.



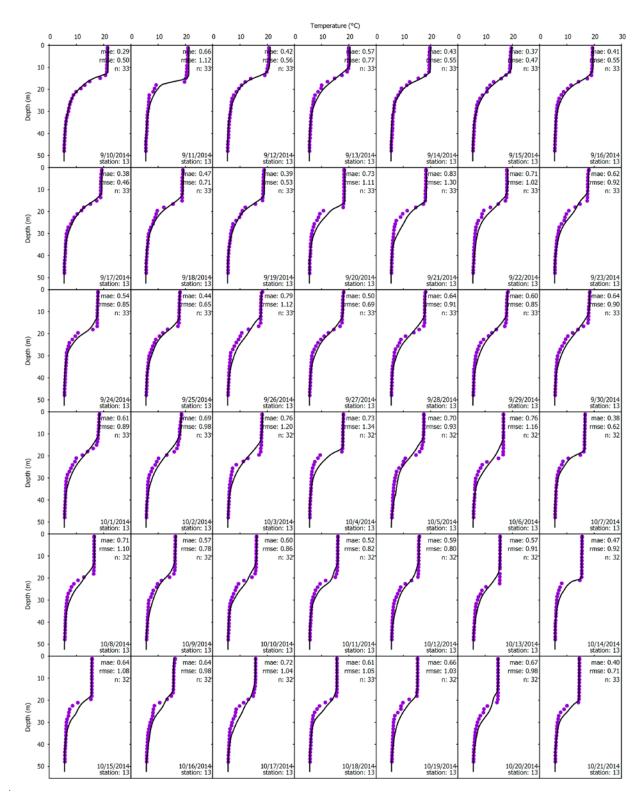
**Figure E-14**. Time series of hydrothermal model fit to daily buoy profiles at site 15 (Figure 5-14) on Owasco Lake for primary confirmation year, 2008 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.



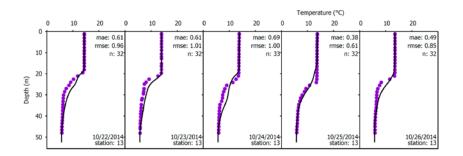
**Figure E-15**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2014 page 1 of 4.



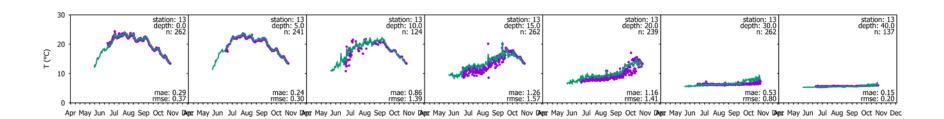
**Figure E-15**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2014 page 2 of 4.



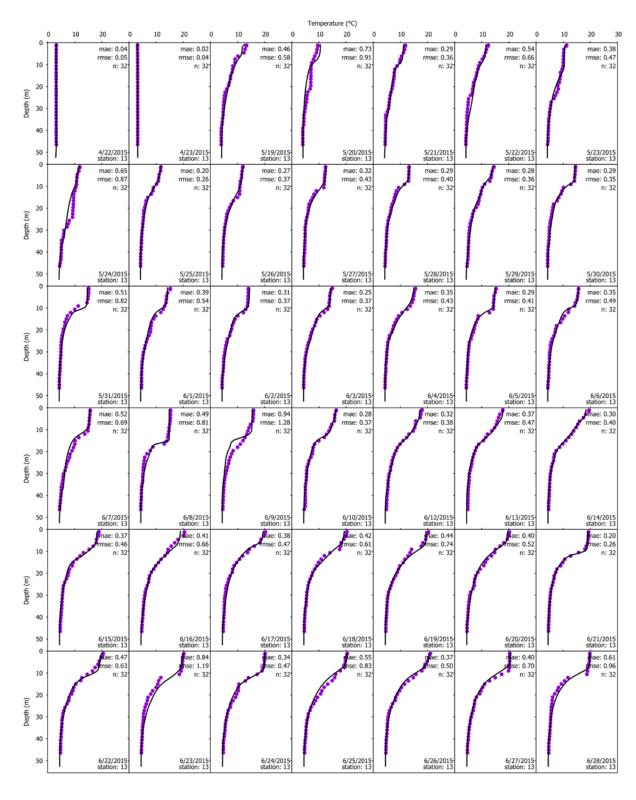
**Figure E-15**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2014 page 3 of 4.



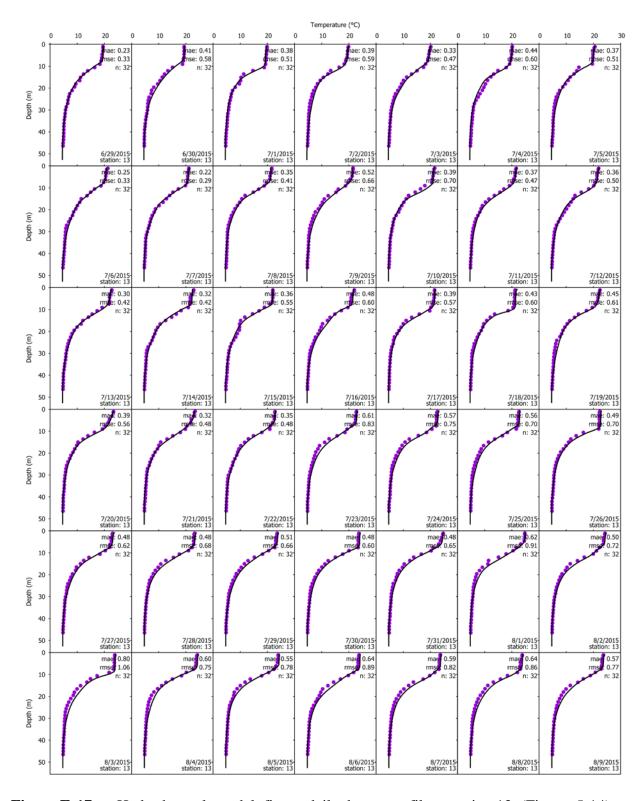
**Figure E-15**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2014 page 4 of 4.



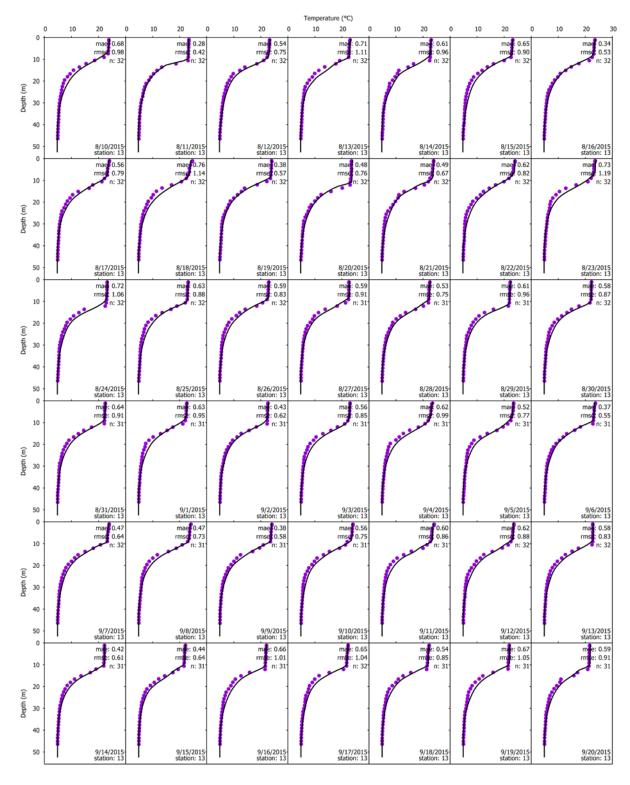
**Figure E-16**. Time series of hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2014 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.



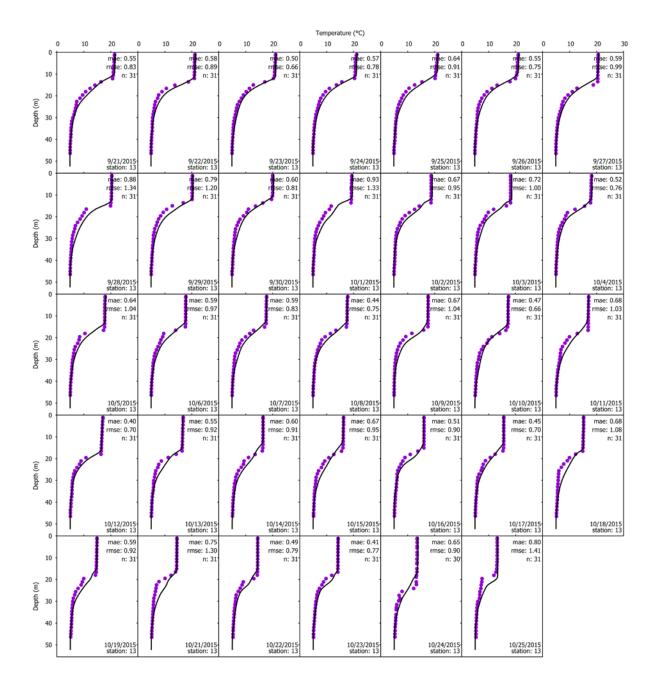
**Figure E-17**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2015 page 1 of 4.



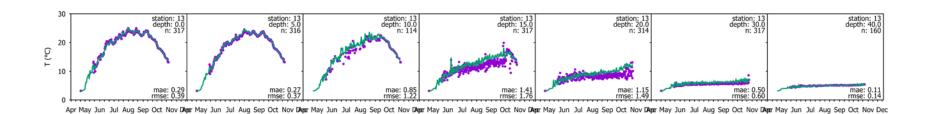
**Figure E-17**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2015 page 2 of 4.



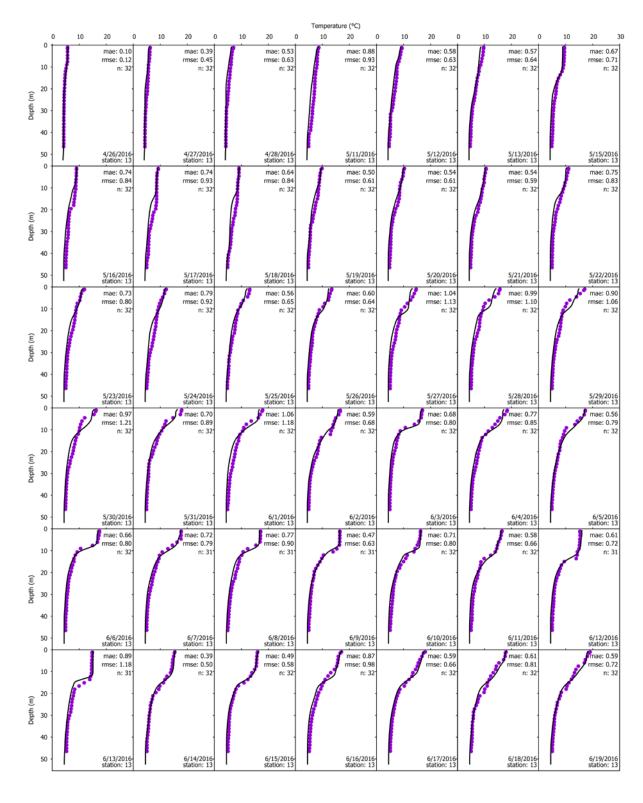
**Figure E-17**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2015 page 3 of 4.



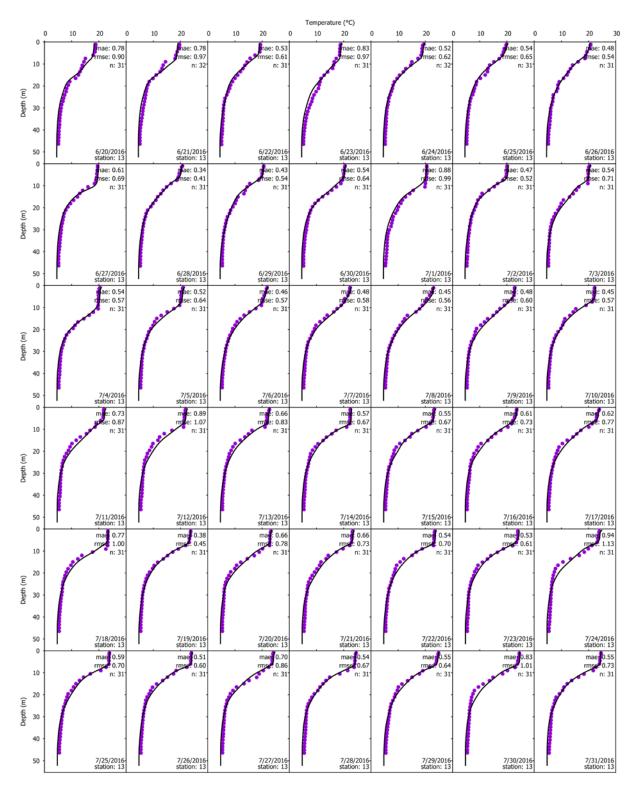
**Figure E-17**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2015 page 4 of 4.



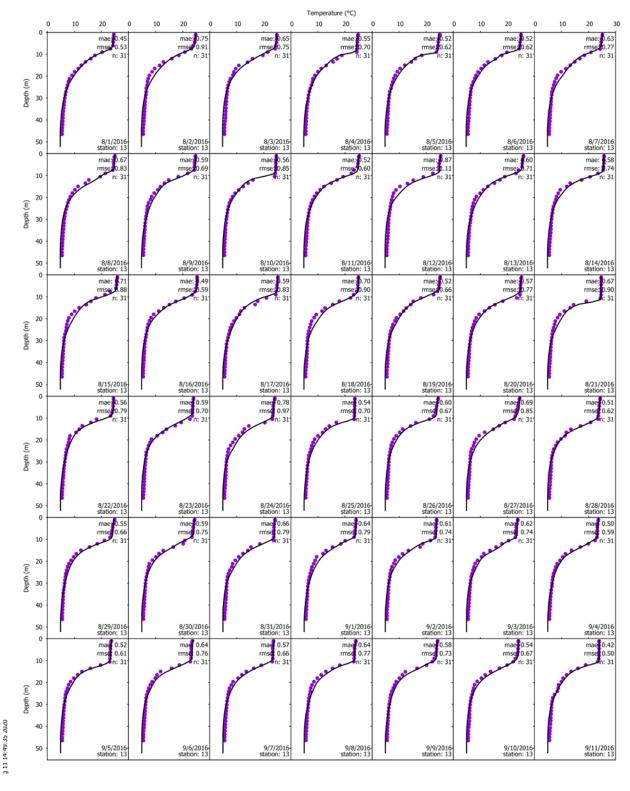
**Figure E-18**. Time series of hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2015 at seven depths, 0, 5, 10, 15, 20, 30, and 40 m.



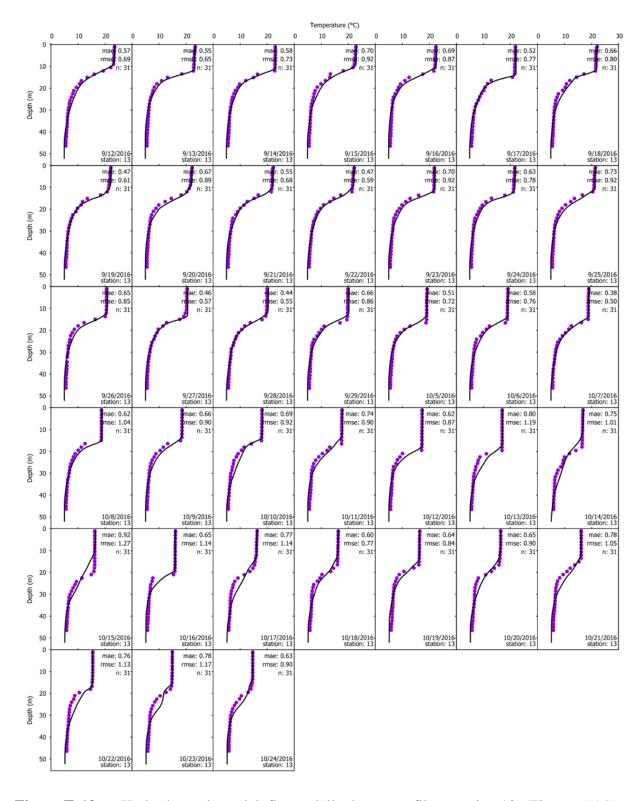
**Figure E-19**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2016 page 1 of 4.



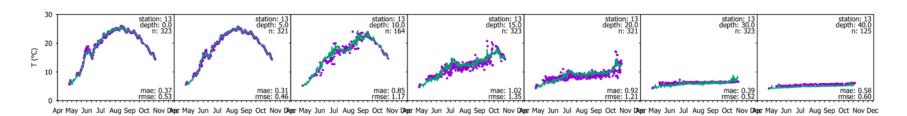
**Figure E-19**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2016 page 2 of 4.



**Figure E-19**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2016 page 3 of 4.



**Figure E-19**. Hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for confirmation year, 2016 page 4 of 4.



**Figure E-20**. Time series of hydrothermal model fit to daily buoy profiles at site 13 (Figure 5-14) on Owasco Lake for primary confirmation year, 2016 at seven depths, 0, 5, 10, 15, 20, 30, and 40m.

## **Appendix F: Water Quality**

## **Appendix F-1 Model Coefficients**

**Table F-1**. Algal kinetics for calibration/confirmation of the Owasco Lake water quality sub-model (A1 is diatoms, A2 is others (not diatoms or cyanobacteria), A3 is cyanobacteria).

Coefficient	:4	Abbrevi	W2	Calibration		
Coefficient	unit	ation	default	Algal group A1 A2 A3		A3
maximum algal grayith rate	1/d	AG	2.0	A1 2.5	2.75	1.75
maximum algal growth rate maximum algal respiration rate	1/d 1/d	AG	0.04	0.04	.04	0.04
	1/d 1/d	AR AE	0.04	0.04	0.02	0.04
maximum algal excretion rate maximum algal mortality rate	1/d 1/d	AE	0.04	0.02	0.02	0.02
•						
algal settling rate algal half-saturation for phosphorus	m/d	AS	0.1	0.20	0.10	-0.50
limited growth	mg/L	AHSP	0.003	0.003	0.003	0.003
algal half-saturation for nitrogen limited growth	mg/L	AHSN	0.014	0.04	0.04	0.04
algal half-saturation for silica limited growth	mg/L	AHSSI	0.0	0.30	0	0
light saturation intensity at maximum photosynthetic rate	W/m2	ASAT	100	40	120	100
lower temperature for algal rates (AG, AR, AE, AM)	°C	AT1	5	4	10	18
lower temperature for maximum algal rates (AG, AR, AE, AM)	°C	AT2	25	12	16	26
upper temperature for maximum algal rates (AG, AR, AE, AM)	°C	AT3	35	16	28	30
upper temperature for algal rates (AG, AR, AE, AM)  AR, AE, AM)	°C	AT4	40	30	35	40
fraction of algal rates at AT1	unitless	AK1	0.1	0.1	0.1	0.1
fraction of maximum algal rate at AT2	unitless	AK2	0.99	0.99	0.99	0.99
fraction of maximum algal rate at AT3	unitless	AK3	0.99	0.99	0.99	0.99
fraction of algal rate at AT4	unitless	AK4	0.1	0.1	0.1	0.1
stoichiometric equivalent between algal phosphorus and algal biomass	mg P/mg algal biomass	ALGP	0.005	0.005	0.005	0.005
stoichiometric equivalent between algal nitrogen and algal biomass	mg N/mg algal biomass	ALGN	0.08	0.15	0.15	0.15
stoichiometric equivalent between algal carbon and algal biomass	mg C/mg algal biomass	ALGC	0.45	0.45	0.45	0.45
stoichiometric equivalent between algal silica and algal biomass	mg Si/mg algal biomass	ALGSI	0.18	0.26	0	0
ratio between algal biomass and chlorophyll- <i>a</i>	mg algal biomass/µg Chl-a	ACHLA	0.05	0.10	0.10	0.10
fraction of algal biomass that is converted to particulate organic matter when algae die	unitless	ALPOM	0.8	0.8	0.8	0.8
equation number for algal ammonium preference (1 = simple, 2 = complex)	unitless	ANEQN	2	2	2	2
half saturation constant for ammonium preference	mgN/L	ANPR	0.001	0.02	0.02	0.02

**Table F-**2. Zooplankton kinetics for calibration/confirmation of the Owasco Lake water quality sub-model (one zooplankton group - herbivores).

Coefficient	Unit	Abbreviati on	W2 default	Calibration Zooplankton group Z1
maximum zooplankton growth rate or ingestion rate	1/d	ZG	1	0.7
maximum zooplankton respiration rate	1/d	ZR	0.1	0.15
maximum zooplankton mortality (non-predatory) rate	1/d	ZM	0.1	0.15
zooplankton assimilation efficiency or proportion of food assimilated to food consumed	unitless	ZEFF	0.5	0.5
preference factor of zooplankton for detritus or IPOM	unitless	PREFP	0.5	0.5
threshold food concentration at which zooplankton feeding begins	mg alg bio/L	ZOOMIN	0.01	0.02
zooplankton half saturation constant for food (includes LPOM, algae and zoops.)	mg alg bio/L	ZS2P	0.3	0.30
preference factor of zooplankton for algae	unitless	PREFA	0.5	1, 1, 0.1
preference factor of zooplankton for zooplankton	unitless	PREFZ	0.0	0
lower temperature for zooplankton rates (ZG, ZR, ZM)	°C	ZT1	5	4
lower temperature for maximum zooplankton rates (ZG, ZR, ZM)	°C	ZT2	25	16
upper temperature for maximum zooplankton rates (ZG, ZR, ZM)	°C	ZT3	35	26
upper temperature for zooplankton rates (ZG, ZR, ZM)	°C	ZT4	40	35
fraction of zooplankton rates (ZG, ZR, ZM) at ZT1	unitless	ZK1	0.1	0.1
fraction of zooplankton rates (ZG, ZR, ZM) at ZT2	unitless	ZK2	0.99	0.99
fraction of zooplankton rates (ZG, ZR, ZM) at ZT3	unitless	ZK3	0.99	0.99
fraction of zooplankton rates (ZG, ZR, ZM) at ZT4	unitless	ZK4	0.1	0.1
stoichiometric equivalent between zooplankton phosphorus and zooplankton biomass	gP/g Zoo biomass	ZP	0.005	0.005
stoichiometric equivalent between zooplankton nitrogen and zooplankton biomass	gN/g Zoo biomass	ZN	0.08	0.08
stoichiometric equivalent between zooplankton carbon and zooplankton biomass	μgC/μg zoo biomass	ZC	0.45	0.45

 Table F-3.
 Organic matter coefficients.

Coefficient	unit	Abbreviation	W2 default	Calibration/ Confirmation
labile DOM decay rate	1/d	LDOMDK	0.1	0.07
refractory DOM decay rate	1/d	RDOMDK	0.001	0.001
labile to refractory DOM decay rate	1/d	LRDDK	0.01	0.005
labile POM decay rate	1/d	LPOMDK	0.08	0.1
refractory POM decay rate	1/d	RPOMDK	0.001	0.001
labile to refractory POM decay rate	1/d	LRPDK	0.01	0.005
POM settling rate	m/d	POMS	0.1	0.1
stoichiometric equivalent between phosphorus and organic matter	μgP/μg OM	ORGP	0.005	0.005
stoichiometric equivalent between nitrogen and organic matter	μgN/μg OM	ORGN	0.08	0.08
stoichiometric equivalent between carbon and organic matter	μgC/μg OM	ORGC	0.45	0.45
stoichiometric equivalent between silica and organic matter	μgSi/μg OM	ORGSI	0.18	0.18
lower temperature for organic matter decay	°C	OMT1	4	5
upper temperature for organic matter decay	°C	OMT2	25	25
fraction of organic matter decay rate at OMT1	unitless	OMK1	0.1	0.1
fraction of organic matter decay rate at OMT2	unitless	OMK2	0.99	0.99

 Table F-4.
 Phosphorus, nitrogen and silica coefficients.

Coefficient	unit	Abbreviat ion	W2 default	Calibration/ confirmation
sediment release rate of phosphorus, fraction of SOD	unitless	PO4R	0.001	0
phosphorus partitioning coefficient for suspended solids	unitless	PARTP	0	0
sediment release of ammonium fraction of SOD	unitless	NH4R	0.001	0.001
ammonium decay (nitrification - requires DO)	1/d	NH4DK	0.12	0.08
lower temperature for ammonia decay	°C	NH4T1	5	5
upper temperature for ammonia decay	°C	NH4T2	25	24.5
fraction of nitrification rate at NH4K1	unitless	NH4K1	0.1	0.1
fraction of nitrification rate at NH4K2	unitless	NH4K2	0.99	0.99
water column denitrification rate or nitrate decay rate (requires DO to be gone)	1/d	NO3DK	0.03	0.03
denitrification rate from sediments	m/d	NO3S	0.001	0.006
fraction of the NO <sub>X</sub> that diffused into the sediments that become part of ON in sediments (rest denitrified)	unitless	FNO3SED	0	1
lower temperature for nitrate decay	°C	NO3T1	5	5
upper temperature for nitrate decay	°C	NO3T2	25	24
fraction of denitrification rate at NO3T1	unitless	NO3K1	0.1	0.1
fraction of denitrification rate at NO3T2	unitless	NO3K2	0.99	0.99
dissolved silica sediment release rate, fraction of SOD	unitless	DSIR	0.1	0.1
particulate biogenic silica settling rate	m/d	PSIS	1	1.0
particulate biogenic silica decay rate	1/d	PSIDK	0.3	0.3
dissolved silica partitioning coefficient	unitless	PARTSI	0	0

 Table F-5.
 Dissolved oxygen coefficients.

Coefficient	unit	Abbreviati on	W2 default	Calibration/ confirmation
sediment carbon dioxide release rate, fraction of sediment oxygen demand (p C-215)	gC/gO2	CO2Rel	0.358	0.358
oxygen stoichiometry for nitrification (ammonia decay)	mg O <sub>2</sub> /mg N <sub>2</sub>	O2NH4	4.57	4.57
oxygen stoichiometry for organic matter decay	mg O <sub>2</sub> /mg organic matter	O2OM	1.4	1.4
oxygen stoichiometry for algal respiration	mgO2/mg algal biomass	O2AR	1.1	1.1
oxygen stoichiometry for algal primary production	mg O2/mg algal biomass	O2AG	1.4	1.8
oxygen stoichiometry for zooplankton respiration	g O2/g dry wt zoo biomass	O2ZR	1.1	1.1
half saturation constant $K_{do}$ in manual O2IIM in control file (concentration at which aerobic processes are at 50%)	mg/L or g/m3	O2LIM (KDO)	0.1	0.4
fraction of zero order SOD rate used	fSOD		1	1
lower temperature for zero order SOD	°C	SODT1	4	4
upper temperature for zero order SOD	°C	SODT2	25	25
T correction rising limb; fraction of SOD at SODT1	unitless	SODK1	0.1	0.1
fraction of SOD at SODT2	unitless	SODK2	0.99	0.99
Sediment oxygen demand by segment	g/m2/d	SOD	0.2	2-8, 14-22 =0 9-13 0.8
Waterbody type	unitless	REARC	2	2
reaeration equation # see page C-227 or 595	unitless	EQN#	6	9

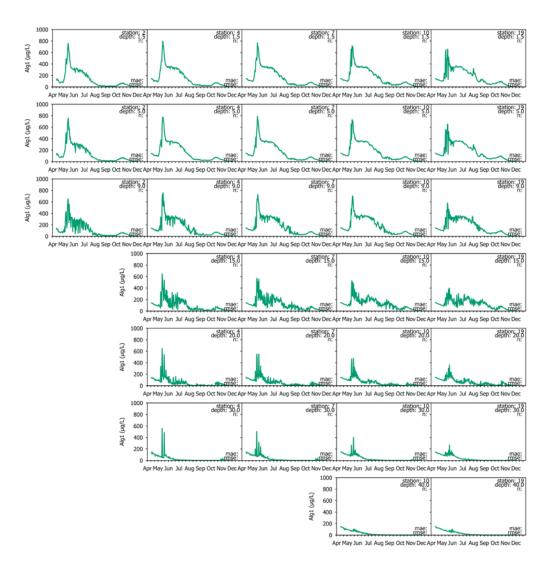
**Table F-6**. Dreissenid mussel coefficients.

Coefficient	unit	Abbreviation	Calibration/ confirmation
Turn on mussels	unitless	MUSSELC	ON
phosphorus excretion rate	umol/gDW/hr	PEXCR	0.18
nitrogen excretion rate	umol/gDW/hr	NEXCR	2.70
oxygen respiration rate	umol/gDW/hr	O2con	54.0
zebra mussel filtering rate	ml/mg DW/hr	FILTER	5.0
temperature correction rate for all zebra mussel reactions(Pex,Nex,O2)	unitless		1.08
mussel conversion of IPOM to IDOM	unitless	frMUSLD	0.45
fraction of algal biomass that is converted to IDOM from mussels filtering of algea	unitless	frMUSPF	0.45
preference for mussel filtering of Alg1	unitless	perfa	1.0
preference for mussel filtering of Alg2	unitless	perfa	1.0
preference for mussel filtering of Alg3	unitless	perfa	0.2

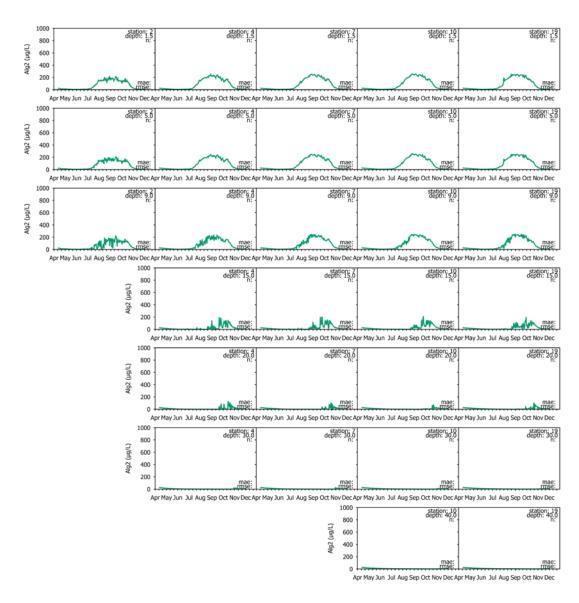
**Table F-7**. Other revisions to CE-QUAL-W2.

Coefficient	unit	Abbreviation	Calibration/ confirmation
Algae minima set for Alg1 used in long-term runs	unitless	minAlg1	0.001
Algae minima set for Alg2 used in long-term runs	unitless	minAlg2	0.001
Algae minima set for Alg3 used in long-term runs	unitless	minAlg2	0.001
SRP loss rate (hypolimnion)	mgP/L/d	SRPrate	0.001
half saturation on loss	μgP/L	1/2Sat	0.002
Fraction of SRP to labile particulate (remainder to refractory)	unitless	frPO4LP	0.5

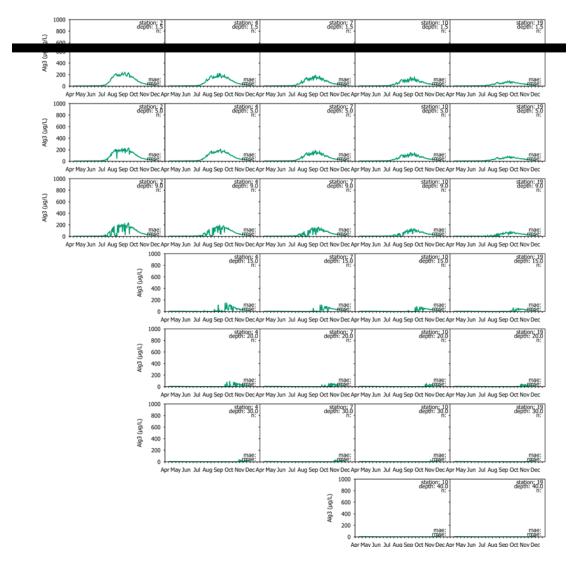
Appendix F-2 Calibration of the Water Quality Sub-model, 2018					



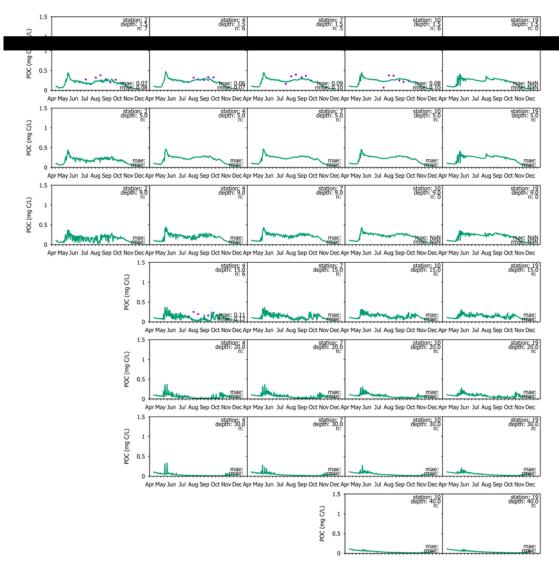
**Figure F-1**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Alg1.



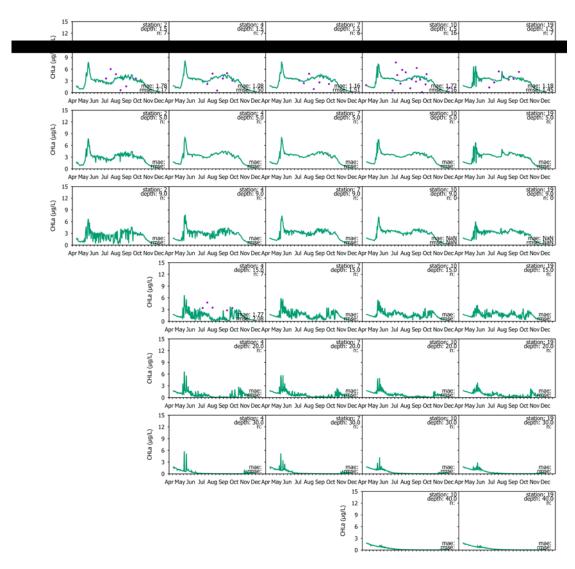
**Figure F-2**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Alg2.



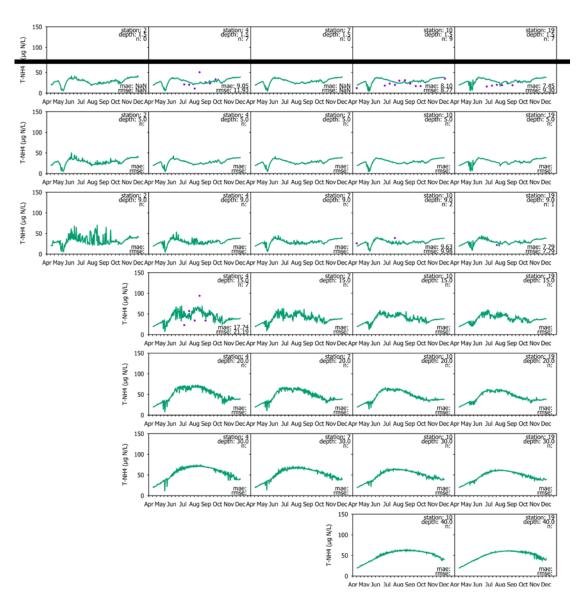
**Figure F-3**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Alg3.



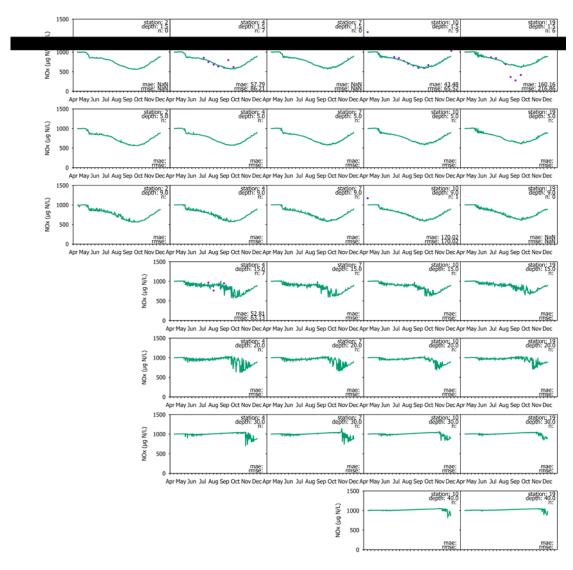
**Figure F-4**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for POC.



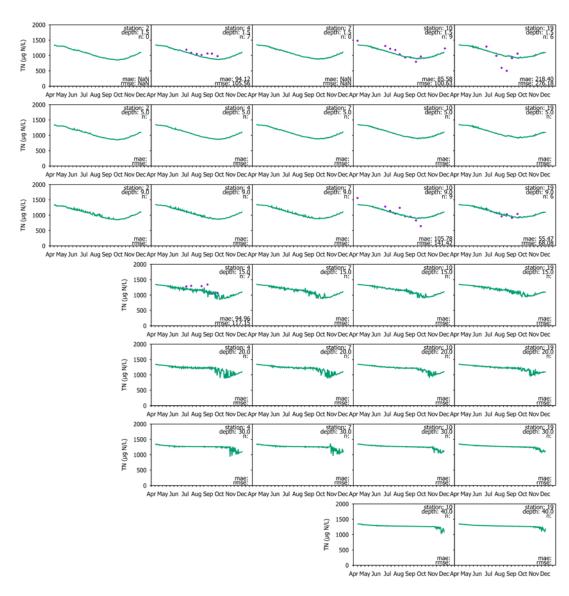
**Figure F-5**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Chl-*a*.



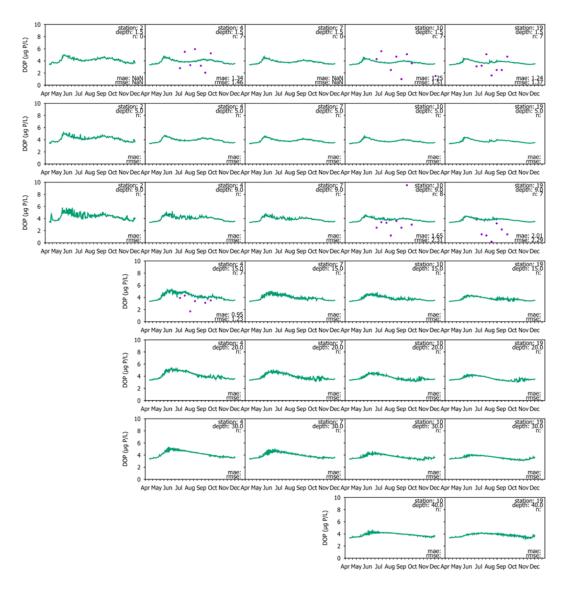
**Figure F-6**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for  $tNH_3$ .



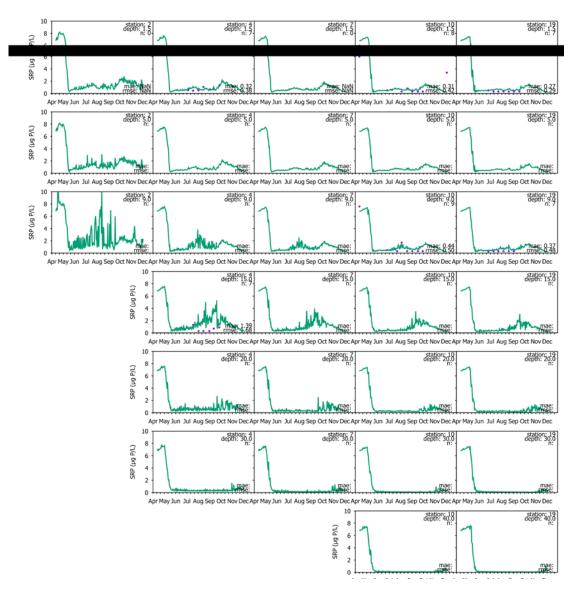
**Figure F-7**. Time series of 2018 model predictions and observations when available at multiple sites  $(2, 4, 7, 10 \text{ and } 19 \text{ and } at \text{ multiple depths } (1, 5, 9, 15, 20, 30 \text{ and } 40 \text{ m}) \text{ for NO}_X$ .



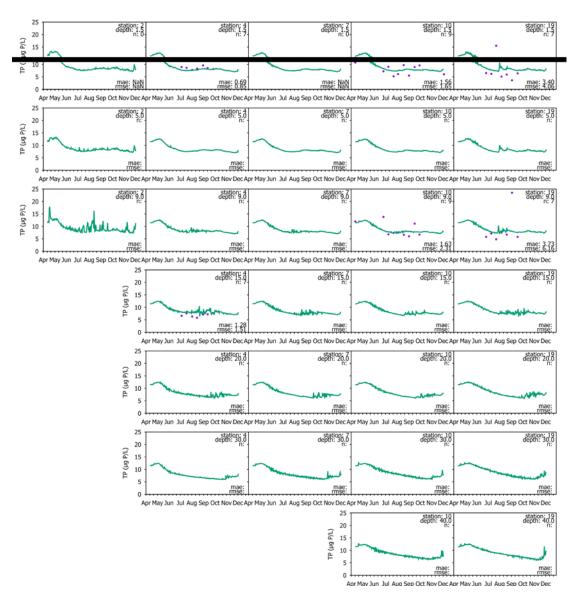
**Figure F-8**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for TN.



**Figure F-9**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for DOP.

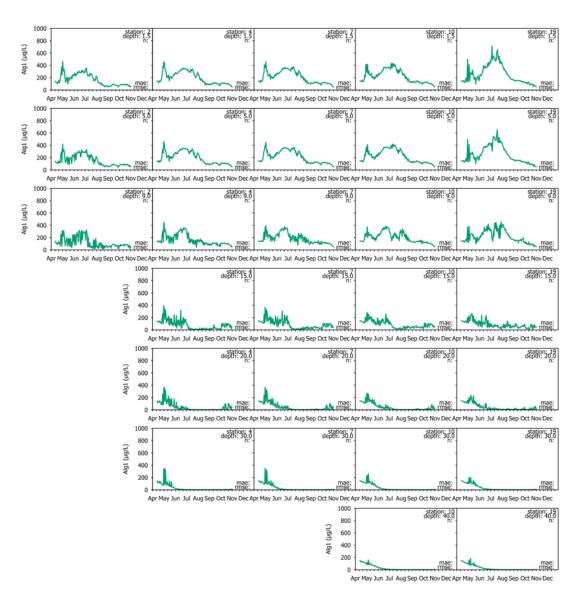


**Figure F-10**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for SRP.

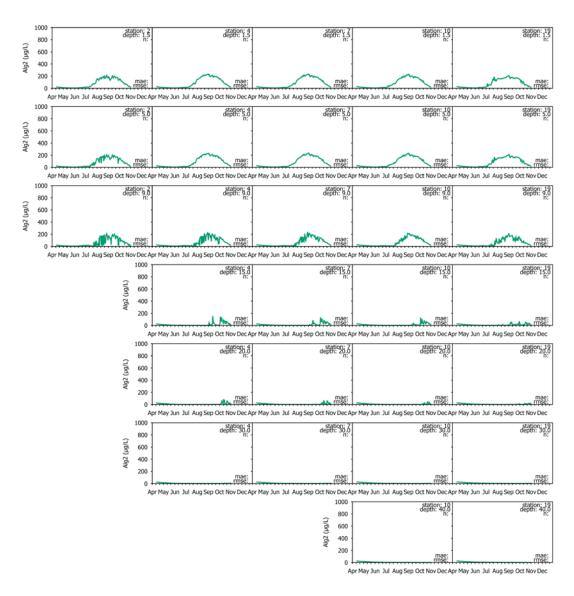


**Figure F-11**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for TP.

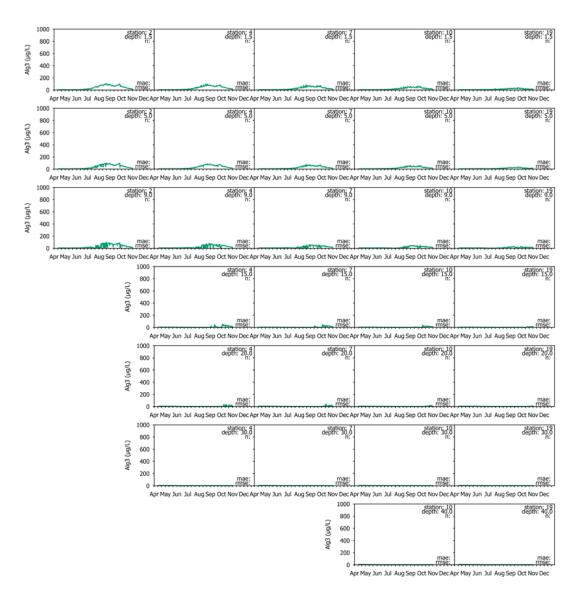
Appendix F-2 Confirmation of the Water Quality Sub-model, 2017



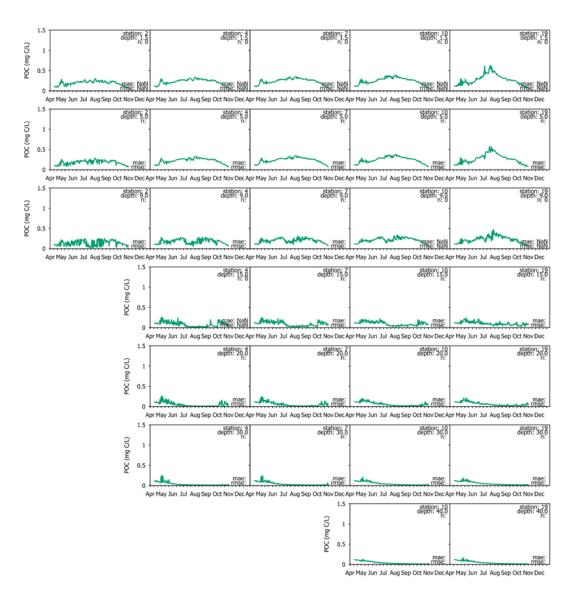
**Figure F-12**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Alg1.



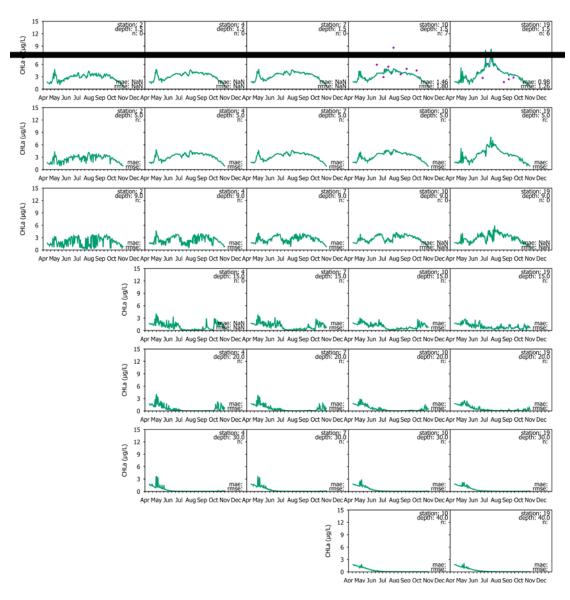
**Figure F-13**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Alg2.



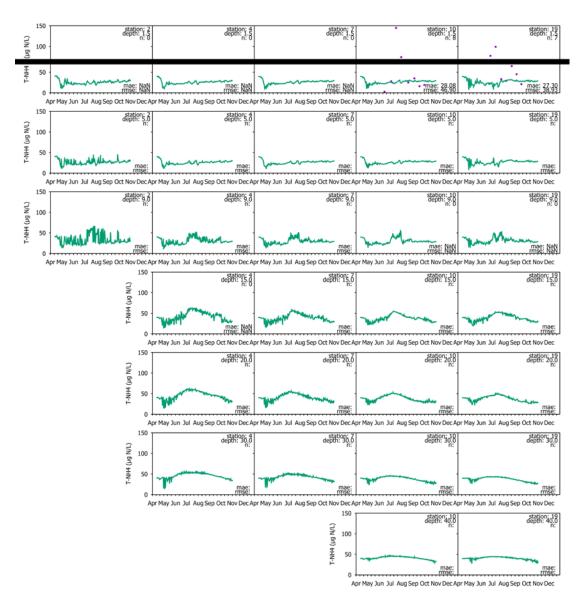
**Figure F-14**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Alg3.



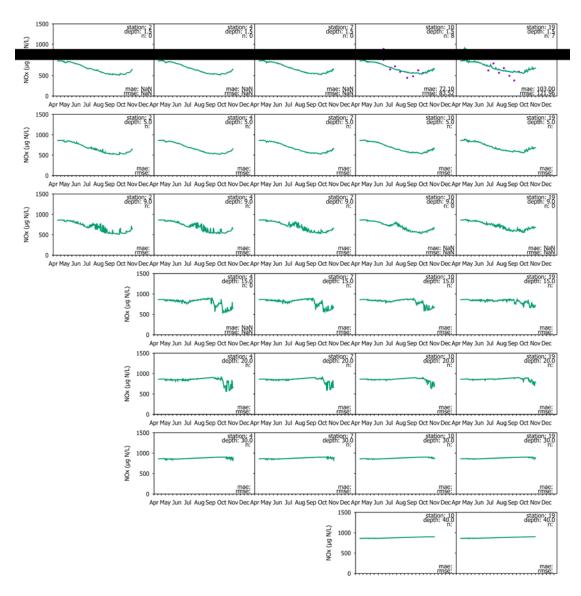
**Figure F-15**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for POC.



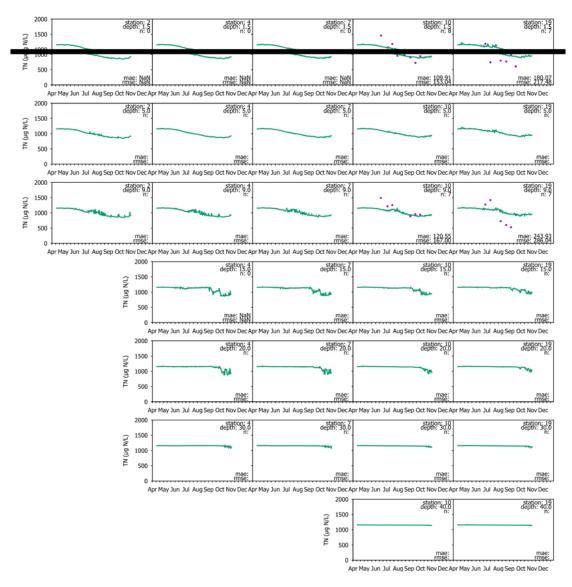
**Figure F-16**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for Chl-a.



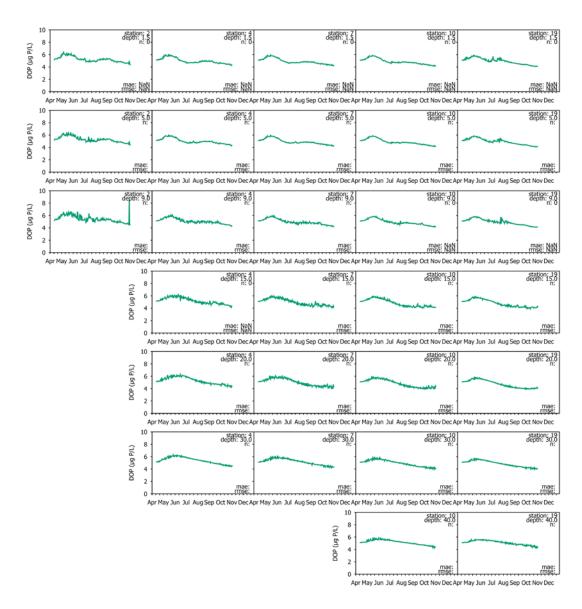
**Figure F-17**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for  $tNH_3$ .



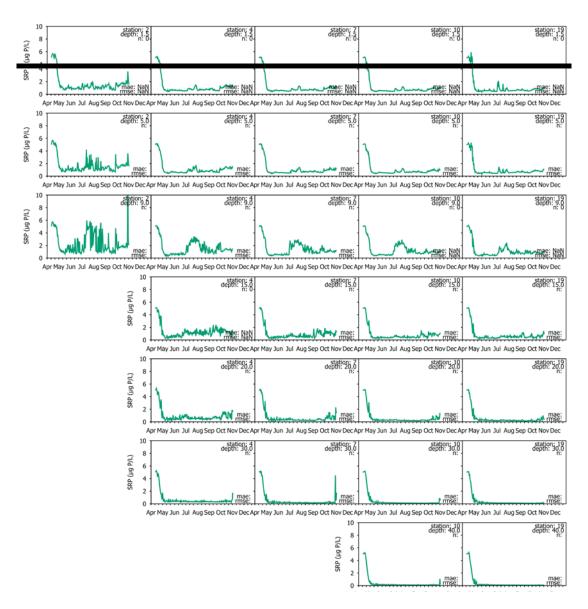
**Figure F-`18**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for  $NO_X$ .



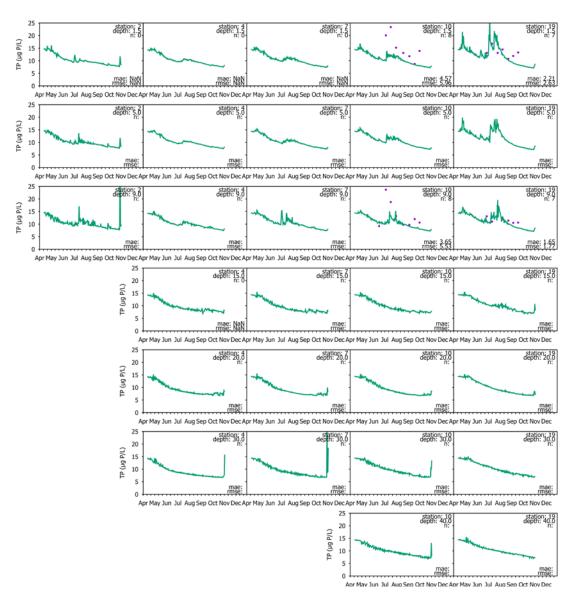
**Figure F-19**. Time series of 2018 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for TN.



**Figure F-20**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for DOP.



**Figure F-21**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for SRP.



**Figure F-22**. Time series of 2017 model predictions and observations when available at multiple sites (2, 4, 7, 10 and 19 and at multiple depths (1, 5, 9, 15, 20, 30 and 40 m) for TP.