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1 **River Discharge Mediates Extent of Phytoplankton and Harmful Algal Bloom Habitat in**  
2 **the Columbia River Estuary (USA) During North Pacific Marine Heat Waves**

3

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10

11

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20 Time (DART) for the use of publicly available data.

21

1 **Abstract**

2 Marine heat waves (MHW) have been associated with extensive harmful algal blooms (HABs) in  
3 the northeast Pacific Ocean, but the degree to which these large-scale oceanographic events are  
4 mirrored in nearshore environments has not been well established. We compared phytoplankton  
5 assemblages in the Lower Columbia River Estuary (LCRE) during two Pacific MHWs that took  
6 place in 2015 and 2019, with observations from 2017, a year with no MHW. These data were  
7 paired with environmental data from the summers of 2015 - 2019 to characterize differences in  
8 estuarine conditions during MHWs that promote phytoplankton assemblage transitions, and  
9 identify HAB-conducive conditions. Bloom densities of HAB taxa, *Pseudo-nitzschia* spp. ( $4.16$   
10  $\times 10^6$  cells  $L^{-1}$ ) and *Gymnodinium catenatum* ( $5.66 \times 10^6$  cells  $L^{-1}$ ), were noted in the estuary  
11 during 2015 and 2019, respectively, two years where Pacific MHWs occurred during the summer  
12 months. These blooms coincided with estuary temperatures that were 1-2 °C above and river  
13 discharge volumes 46-48% lower than decadal daily averages. We identified patterns in the  
14 densities of several algal taxa associated with MHW-mediated low discharge in the LCRE, such  
15 as declines in tythropelagic diatoms and increasing abundance of pelagic marine taxa. We  
16 conclude that low river discharge, through extension of saline habitat area and longer residence  
17 times, likely contributed to the development of the observed marine HABs in the estuary. MHWs  
18 and associated declines in discharge are projected to become more common in the Pacific  
19 Northwest with climate change, which may alter late summer phytoplankton assemblages in the  
20 LCRE.

21 **Key words:** Harmful algal blooms, marine heat waves, estuarine ecology, discharge,

22 *Gymnodinium catenatum*, *Pseudo-nitzschia*

23

## 1 **Introduction**

2 Harmful algal blooms (HABs) are occurring more frequently on a global scale, a phenomenon  
3 connected to climate change (Hallegraeff 1993, 2010; Van Dolah 2000; Lewitus et al. 2012).  
4 HABs often result in fishery closures due to the production of algal toxins, which can accumulate  
5 in consumers. Closures aid in protecting public health, but can destabilize commercial and  
6 recreational fisheries, create declines in fisheries and tourism revenue, and impact residents' food  
7 security, cultural activities, and quality of life (Dyson and Huppert 2010; Poe et al. 2015;  
8 Berdalet et al. 2016; Ritzman et al. 2018). The northeast Pacific Ocean experienced a long-lived,  
9 persistent MHW, commonly called "The Blob", that began in the winter of 2013, peaked in  
10 2014-2015, and dissipated in 2016 (Bond et al. 2015; Di Lorenzo and Mantua 2016). A shorter-  
11 lived MHW (given the name "Blob 2.0") appeared during the summer of 2019 and disappeared  
12 after approximately four months (Amaya et al. 2020). Negative ecosystem effects, including a  
13 massive marine HAB, associated with The Blob have been extensively documented in the  
14 northeast Pacific Ocean (Du et al. 2016; McCabe et al. 2016; Brodeur et al. 2019; Rogers-  
15 Bennett and Catton 2019; von Biela et al. 2019; Piatt et al. 2020). Previous temperature  
16 anomalies in the Northeast Pacific coastal ocean have resulted in impacts to phytoplankton  
17 biomass, productivity, and community composition (Kudela et al. 2006). MHWs can also alter  
18 estuarine ecosystems, but HAB studies along the U.S. West Coast have focused on offshore and  
19 coastal habitats, leaving gaps in our knowledge of how atmospheric phenomena impact estuaries.  
20 Several studies on estuaries outside the Pacific Northwest suggest heat waves negatively affect  
21 estuarine water quality (e.g., increased biological oxygen demand, cyanobacteria blooms, low  
22 DO, low pH, and microbial pathogen growth) (Wetz and Yoskowitz 2013; Tassone et al. 2022).  
23 To our knowledge there is only one published observation of a localized heat wave linked to a

1 HAB within a U.S. west coast estuary (Cloern et al. 2005). Other than this event, the 2015 and  
2 2019 events are the only recorded MHWs associated with estuarine HABs for the region.  
3 Though MHW-associated HABs have been observed globally (Roberts et al. 2019; Gao et al.  
4 2021), this field of study is relatively young and events where these phenomena are linked are  
5 somewhat sparse (Hobday et al. 2018). Other HABs have been documented in Pacific Northwest  
6 estuaries, but were not linked to heat waves and were associated with transport from coastal  
7 waters (Lewitus et al. 2012). In the LCRE, algal blooms are relatively rare, with the exception of  
8 a recurring late summer *Mesodinium rubrum* bloom (Herfort et al. 2011). In this study, we refer  
9 to phytoplankton cell concentrations on the order of  $10^4$  cells  $L^{-1}$  or greater as a bloom. We set  
10 this quantitative definition because both *Pseudo-nitzschia australis* and *Gymnodinium catenatum*  
11 are known to produce levels of domoic acid and saxitoxins, respectively, that result in consumer  
12 contamination at this density (Lefebvre et al. 2002; Costa et al. 2010). This threshold identifies  
13 algal densities impactful for fisheries management due to toxin contamination of harvested  
14 species.

15         The LCRE, like the majority of large Pacific Northwest estuaries, is freshwater-  
16 dominated (Heady et al. 2014), and therefore thought to be less impacted by oceanographic  
17 events like MHWs. Columbia River hydrology is largely influenced by snowpack in low-  
18 elevation mountain ranges, with plentiful winter precipitation that falls as rain or snow  
19 depending on temperatures, a spring freshet, and dry summers (Tohver et al. 2014). Atmospheric  
20 influences such as the position of the deep Aleutian low of the Pacific/North American  
21 circulation pattern, El Nino/Southern Oscillation (ENSO) and disruptions of the jet stream,  
22 which can contribute to the formation of MHWs, have a large influence on snowpack, and the  
23 resulting timing and volume of snowmelt runoff to the LCRE (Cayan 1996; Clark et al. 2001;

1 Mote 2006). The flow regime of the Columbia River is also influenced by a series of storage and  
2 run-of-the-river dams (Federal Columbia River Power System 2001). Flow rates to the LCRE  
3 may be altered during drought years due to lower snowpack [e.g. 2014-2015 Pacific Northwest  
4 “snowpack drought” (Boniface et al. 2016)], warmer temperatures, and exceptionally low  
5 summer flows; all characteristics projected under climate change for the region (Hamlet and  
6 Lettenmaier 1999). Although the LCRE is river-dominated for much of the year, oceanographic  
7 conditions develop during the summer months when river flow is at its lowest (Chawla et al.,  
8 2008), creating an inverse relationship between discharge and salinity. Oceanographic inputs to  
9 the estuary affect water quality, for example, delivery of upwelling-derived nitrate through tidal  
10 exchange (Bruland et al. 2008). The shifts from freshwater-dominated to brackish-marine  
11 conditions is reflected in the seasonal succession of estuarine plankton (Rollwagen-Bollens et al.  
12 2020). Therefore, the vulnerability of the LCRE to the ecological effects of MHWs could differ  
13 significantly depending on the timing of their occurrence.

14 In this study, we compare phytoplankton assemblages of the LCRE during two MHWs  
15 (2015 and 2019) that differed in extent and timing with those in 2017 without MHW. Our study  
16 objectives are to (1) characterize differences in estuarine conditions during MHWs that may  
17 promote HABs, and (2) identify phytoplankton assemblage characteristics to aid in identifying  
18 transitions to HAB-conducive conditions. This work provides insight into the LCRE’s algal  
19 community response to two MHWs of differing persistence, and evaluates how hydrologic  
20 forcing could play an important role in mediating the impact of MHWs in the LCRE. Particularly  
21 during anomalous oceanographic events, understanding the degree and timing of ocean-estuary  
22 connectivity is crucial to predicting algal community shifts in estuarine habitat.

23

1 **Methods**

2 *Study area*

3           The LCRE is a river-dominated, drowned river mouth estuary (Heady et al. 2014), with  
4 the fourth largest river volume in the United States (Baptista et al. 2015) (Fig. 1). The LCRE  
5 food web is largely detritus-driven, and phytoplankton grazing makes up the main living  
6 component of food resources for primary consumers (Simenstad et al. 1990). Haertel and  
7 Osterberg (1967) described three main groups of plankton in the LCRE: those associated with  
8 freshwater, marine plankton that are transported into the estuary from the coast, and plankton  
9 indigenous to the estuary that are associated with brackish waters. The study took place at a site  
10 in Ilwaco Harbor in Baker Bay, a shallow (<15 m depth) bay just upstream of the river mouth  
11 (~5 km) on the northern side of the estuary. We also sampled two nearby sites in the mainstem of  
12 the LCRE on the southern side of the estuary during a research cruise aboard the R/V *Oceanus*  
13 (Fig. 1a).

14

15 *Sample collection and analyses*

16           The majority of phytoplankton samples (total  $n = 24$ ) were collected from the surface at  
17 Ilwaco Harbor ( $n=18$ ), with additional samples collected in September-October 2015 ( $n=6$ )  
18 aboard the R/V *Oceanus*, which provided data on the depth distribution of phytoplankton in the  
19 LCRE (surface, mid-depth, and bottom). Surface samples at the Ilwaco site in 2015 and 2017  
20 were collected approximately monthly during the spring and summer of these years, while  
21 samples were collected monthly June - July of 2019 and fortnightly August - October of 2019  
22 (Fig. 1b). Whole water samples were collected for algal identification and enumeration using  
23 clean glass French square bottles. Samples were preserved in Lugol's Iodine solution (final

1 concentration, 1%). Samples were homogenized and settled in an Utermöhl sedimentation  
2 chamber for 24 h and cells were identified and enumerated using a Leica DMIL inverted  
3 microscope. Cells were enumerated up to 400 counting units, using 100X, 200X, and 400X  
4 magnification, each for several of fields of view per sample in order to adequately capture both  
5 smaller cells and rarer, larger taxa. Where replicate samples were available, counts were  
6 averaged. Where possible, cells were identified to genus or species, and in some cases complexes  
7 or groups that were more practical for identification using light microscopy. For example,  
8 species within the genus, *Pseudo-nitzschia*, cannot be identified to species with a light  
9 microscope alone; individuals were therefore classified into complexes of *Pseudo-nitzschia* c.f.  
10 *australis/fraudulenta*, *P. c.f. pungens/multiseries*, or *P. c.f. pseudodelicatissima/delicatissima*,  
11 which can be differentiated by cell size and shape (e.g., length: width ratio) (Trainer and  
12 Suddleson 2005). Phytoplankton abundances are reported as cell concentrations or as a  
13 proportion of the total cells counted in the sample. Simpson's Diversity Index (D) was calculated  
14 using the 'vegan' package in R (Simpson 1949).

15

#### 16 *Collection and analysis of environmental data*

17 Environmental data were collected using continuous sensors at the SATURN-03  
18 endurance station (Fig. 1; www.stccmop.org), including salinity (every 15 s), temperature (every  
19 15 s), chlorophyll (every 3 min), and nitrate (every hour) at three depths (2.4 m, 8 m, and 13 m).  
20 Chlorophyll fluorescence was measured using an *in situ* fluorometer (Turner Designs AlgaeWatch  
21 in 2015 and a Turner Designs Cyclops in 2019) and calibrated against extracted chlorophyll a (S.  
22 Riseman, pers. comm.), and nitrate was measured using an *in situ* ultraviolet spectrophotometer  
23 (ISUS Satlantic in 2015, SUNA Seabird Scientific in 2019). Although the SATURN-03 sensor is



1 located across the channel from the water sampling site, we determined that data collected from  
2 this sensor suite (i.e., salinity, temperature, nitrate) were highly similar to measurements from  
3 grab samples collected at Ilwaco Harbor (data not shown). Discharge data were downloaded  
4 from the USGS river gauge at Quincy Washington/Beaver Army Terminal at river mile 53 (river  
5 km 85), a point downstream from major tributaries (USGS 2022). Upwelling index data were  
6 obtained from the DART Pacific Ocean Coastal Upwelling Index Dataset, courtesy of the  
7 National Marine Fisheries Service, Pacific Fisheries Environmental Laboratory (Columbia River  
8 DART, Columbia Basin Research, and University of Washington 2021). Upwelling index values  
9 were derived from estimated Ekman transport based on mean surface atmospheric pressure fields  
10 for every 6 h at the Lincoln City, OR standard location. This index summarizes the direction and  
11 velocity of water movement, with positive values representing offshore water movement  
12 (upwelling), and negative values representing onshore movement (downwelling). Data for each  
13 environmental variable were initially averaged hourly, and were used to calculate day  
14 equivalents of elevated temperature and salinity conditions by adding all hours above a certain  
15 threshold together and dividing by 24 h (Tables 1, 2). To limit noise from diurnal tidal action, all  
16 data for each environmental variable were averaged daily for the generalized additive mixed  
17 model analysis. Sensor data were smoothed by calculating 14-d rolling daily averages to capture  
18 conditions in the window leading up to each phytoplankton sampling event prior to use in the  
19 gradient forest analysis.

20

### 21 *Algal toxin analysis*

22 A whole water sample for toxin analysis was collected concurrently with each algal  
23 sampling event, filtered onto GF/F filters (400 – 1000 mL per sample, depending on algal

1 density), and frozen at -20°C, pending analysis. Samples in which toxic algal species were  
2 present, as determined using light microscopy, were prioritized for toxin analysis of seston (total:  
3  $n=10$ , October 2015:  $n=6$ , August-October 2019:  $n=4$ ). Analytes were extracted from filters in  
4 deionized water with sonication as in Lefebvre et al. (2008), and four analytical replicates per  
5 sample were analyzed. We used ELISA kits (Mercury Science Inc.) and a Molecular Devices  
6 Spectra Max M2<sup>e</sup> plate reader with the necessary toxin standards and controls to assess  
7 concentrations of domoic acid (typically reported in  $\text{ng L}^{-1}$ ) and total saxitoxins (typically  
8 reported in ppb), the toxins produced by *Pseudo-nitzschia* spp. and *G. catenatum*, respectively.  
9 We did not collect shellfish samples during the study to understand whether the algal toxin  
10 production translated to accumulation of toxins in shellfish tissues.

11

## 12 *Statistical analyses*

13 We used generalized additive mixed models (GAMMs) to characterize the environmental  
14 conditions during May through October of 2015 - 2019, the season when HABs most commonly  
15 occur, while reducing the variation of environmental variables due to well-documented seasonal  
16 changes (Rollwagen-Bollens et al. 2020). We identified periods of statistically significant  
17 environmental change in a time series of daily averages of multiple water quality variables using  
18 the ‘*mgcv*’ package in R, with Gaussian probability distributions of the variables, and the  
19 restricted maximum likelihood (REML) method for smoothness selection (Wood 2017, Simpson  
20 2018). Temporal autocorrelation was explicitly modeled in the GAMM, and model selection was  
21 determined by comparing Bayesian Information Criterion (BIC) of models with different error  
22 correlation structure and checking for autocorrelation among model residuals.

1 We used a non-metric multidimensional scaling (NMDS) analysis with the Bray-Curtis  
2 dissimilarity index to assess patterns in species composition (Clarke 1993). Species count data  
3 were square-root-transformed prior to the NMDS, which was done using the R package ‘*vegan*’  
4 (Oksanen et al. 2011). Vectors of environmental variables were fitted to the NMDS plot using  
5 the *envfit* function in the same package. We used agglomerative hierarchical clustering with  
6 average linkage on a Bray-Curtis dissimilarity matrix to find grouping patterns in the  
7 phytoplankton assemblage dataset.

8 We used gradient forest analysis to identify thresholds separating components of  
9 phytoplankton assemblages along major environmental gradients. This analysis was performed  
10 using the ‘*extendedForest*’ and ‘*gradientForest*’ packages in R (v3.6.2; Ellis et al. 2012). A  
11 gradient forest fits a random forest model for each taxon in the phytoplankton assemblage, in  
12 which each of 500 trees is fit to a bootstrapped sample and splits are made using a random subset  
13 of predictors. Goodness-of-fit  $R^2$  values for each taxon can be distributed in proportion to the  
14 importance of each predictor to generate the overall importance of a predictor to phytoplankton  
15 species composition. Split density plots show where (on the scale of the predictor) a predictor is  
16 splitting trees, and indicate the importance of each predictor based on how much of the variance  
17 in the data it explains. Compositional turnover plots show cumulative importance of predictors  
18 for each species over gradients of predictor variables. Taxa present in <5% of samples or at very  
19 low cell concentrations ( $< 10 \text{ cells ml}^{-1}$ ) were excluded from the gradient forest analysis.

20

## 21 **Results**

22 *Estuarine conditions*

1 Daily average surface water temperatures in the LCRE were elevated by ~1-2 °C in July-  
2 December of 2015 and July-September of 2019, relative to the decadal average at the SATURN-  
3 03 site (Fig. 2). For summers included in the study period, temperatures typically increased most  
4 rapidly through May and June, peaked in the window of July-September, and began to decrease  
5 in September or October (Fig. 2).

6 Elevated surface temperatures were sustained for a longer period of time during 2015 and  
7 2019 than for any other year during the study period (approximately 49.0 and 47.4 day  
8 equivalents >18 °C; 18.3 and 12.8 day equivalents >20 °C, respectively) (Table 2). In addition,  
9 temperatures did not drop as rapidly during the summer-autumn transition in 2015 as was  
10 observed during 2016-2019 (Fig. 3).

11 Hydrographs for the LCRE varied greatly among the five years. In 2017, a non-MHW  
12 year with a strong spring freshet and high discharge throughout the growing season, peak  
13 discharge was 111% higher and minimum discharge was 4% lower than the decadal average  
14 (Fig. 2). Discharge in 2018 and 2019 also displayed a large freshet pattern, with peak daily  
15 average discharges 83% and 92% higher than the decadal average, respectively. The spring  
16 freshet was smaller in 2015 and 2016; peak flows were 53% and 5% higher than the decadal  
17 average, respectively. For all study years but 2017, minimum discharge was 42 - 76% lower than  
18 the decadal average minimum (Fig. S1).

19 Salinity in the LCRE increased throughout May - October each year, with daily averages  
20 <5 PSU typical in May, and >10 PSU typical of late summer. In 2015, however, the smoothed  
21 daily average salinity in June was >10 PSU (Fig. 3). The summer of 2015 also had the highest  
22 number of day equivalents (7.1 d) of salinity >25 PSU at 2.4 m, compared to a range of 3.8 - 4.4  
23 d for the other years studied (Table 1), showing an extended period of strong marine influence on

1 the surface waters of the LCRE. We observed an extended period of brackish surface water in  
2 2019, which had 72.5 day equivalents of salinity >15 PSU at 2.4 m, compared to a range of 45.5  
3 - 60 d in 2015 – 2018 (Table 1).

4 Upwelling patterns were similar among years, with the exception of a significant shift  
5 toward downwelling in late summer of 2016 ( $> 0 \text{ m}^3 \text{ s}^{-1} 100 \text{ m}^{-1}$ ), and an earlier peak in  
6 upwelling ( $\sim 120 \text{ m}^3 \text{ s}^{-1} 100 \text{ m}^{-1}$  in June) and a significant decline in the rate of offshore transport  
7 throughout the summer of 2019 (Fig. 3). The highest nitrate concentrations ( $>20 \text{ } \mu\text{M}$  in May  
8 2016-2018) were observed in early summer, with some fortnightly fluctuations. Nitrate  
9 concentrations were lower on average in 2015 than other study years, especially earlier in the  
10 season ( $<10 \text{ } \mu\text{M}$  in May). No nitrate data were collected in 2019 (Fig. 3). Chlorophyll showed  
11 fortnightly variation, with higher overall chlorophyll levels earlier in the summer that decreased  
12 as the summer progressed. We observed a small peak in chlorophyll during the 2015 bloom of  
13 *Pseudo-nitzschia* spp. and the 2019 *G. catenatum* bloom (z-scores of 1.8 and 2.8, respectively)  
14 (Fig. 3).

#### 16 *Algal species composition*

17 We identified 168 species or species complexes and 112 genera, with a mean richness of  
18 25 taxa per sampling date and average sample diversity D of 0.70 (range = 0.17 to 0.91) over the  
19 three years for which phytoplankton samples were collected. We identified six phyla  
20 (Bacillariophyta, Chlorophyta, Cryptophyta, Cyanophyta, Dinoflagellata, Euglenophyta) and two  
21 taxonomically amalgamated groups to capture other less common taxa (small flagellates, and  
22 other). Bacillariophyta typically dominated the assemblages, with an average relative abundance  
23 of 56%. Among phylum Bacillariophyta, *Navicula* spp. were abundant on all sampling dates,

1 peaking at 69% of total cells in April 2017. *Melosira varians*, *Skeletonema* spp., and c.f.  
2 *Cyclotella/Thalassiosira* spp. were the next most abundant diatoms in spring/early summer.  
3 Dinoflagellata had an average relative abundance of 29%, and each of the other taxonomic  
4 groups had an average relative abundance of <10% (Fig. 2). A NMDS analysis (stress = 0.12)  
5 indicated that phytoplankton samples varied most along the first NMDS axis (Fig. 4) with greater  
6 separation of samples among years (i.e., 2015 and 2019 vs. 2017) and seasons (i.e., late summer  
7 vs. early summer samples from 2015 and 2019).

8         Hierarchical cluster analysis indicated that the two algal blooms observed in the study  
9 were distinctly different in composition. In 2015, the toxigenic marine diatoms, *Pseudo-nitzschia*  
10 spp. (mostly from the *P. c.f. australis/fraudulenta* group), dominated the phytoplankton  
11 assemblage in early October (average of 56% on 10/1/2015; Fig. 2), in contrast to other sampling  
12 dates, which had either undetectable or low (March 2017, August-September 2019) *Pseudo-*  
13 *nitzschia* spp. concentrations. Particulate domoic acid (pDA) was measured at relatively low, but  
14 detectable, levels during the *Pseudo-nitzschia* spp. bloom (Fig. 6). Average toxin concentrations  
15 ranged from 41 – 86 ng L<sup>-1</sup> from samples taken at the bottom (~13 m), middle (~8 m) and  
16 surface of the water column on October 1 and mid water column on October 2, 2015. Although  
17 domoic acid was detected at ~8 m, it was not detected at the bottom or surface on October 2. In  
18 2019, the chain-forming marine dinoflagellate, *Gymnodinium catenatum*, peaked at 91% of the  
19 total assemblage in mid-August; the bloom persisted through late September. It was not detected  
20 in our light microscopy analyses any time outside this bloom period. Once the bloom began to  
21 decline (ca. 9/12/2019), *G. catenatum* was accompanied by *Euglena* sp. (24%), *Cryptomonas*  
22 *erosa* (16%), and *Mesodinium rubrum* (5%). Overall, species diversity during the peak of the  
23 2019 bloom was very low (D = 0.17) compared to the highest reported diversity from earlier that

1 year ( $D = 0.80$  on 7/10/2019). Saxitoxins were detected during the *G. catenatum* bloom, ranging  
2 from 1.14–1.79 ppb, with the highest toxin level detected during the height of the bloom in late  
3 August (Fig. 6).

#### 5 *Environmental drivers of phytoplankton assemblage composition*

6 Ordinations with overlaid environmental vectors with points scaled by the relative  
7 abundance of phytoplankton taxa (Fig. 5) indicated that densities of the marine planktonic  
8 diatoms like *Ditylum brightwellii*, *Thalassionema nitzschoides*, *Nitzschia longissima*, and  
9 *Pseudo-nitzschia* spp., as well as the planktonic dinoflagellate *G. catenatum* were generally  
10 associated with more saline, low-discharge, low-nitrate conditions. Of these, *D. brightwellii*, *T.*  
11 *nitzschoides*, *N. longissima*, and *Pseudo-nitzschia* spp. were also associated with high  
12 temperatures and upwelling. On the other hand, the abundance of the freshwater taxa  
13 *Ankistrodesmus* sp. and the tythropelagic *Navicula* spp. declined later in the growing season, with  
14 higher counts of these taxa observed in samples associated with lower temperatures, higher  
15 flows, and low salinity. This is consistent with the gradient forest cumulative density plots (Fig.  
16 7A-E), which indicate a sharp change in cumulative importance of salinity at 13-14 PSU and of  
17 discharge at approximately  $3,400 \text{ m}^3 \text{ s}^{-1}$  to the abundance of the coastal diatom species, *D.*  
18 *brightwellii*, which increased under low discharge and high salinity. *Navicula* spp. showed an  
19 increase in cumulative importance of discharge at approximately  $3,500 \text{ m}^3 \text{ s}^{-1}$  and of salinity at  
20 approximately 13 PSU, with its abundance decreasing under low discharge and high salinity.  
21 *Ankistrodesmus* sp. showed a sharp change in the importance of discharge at approximately  
22  $7,079 \text{ m}^3 \text{ s}^{-1}$ , with its abundance decreasing when discharge declined. Temperature, upwelling,  
23 and nitrate all contributed to the abundance of c.f. *Cyclotella/Thalassiosira* spp., with increases

1 in cell densities weakly associated with elevated temperature and upwelling index. Cumulative  
2 importance of upwelling index to the density of *N. longissima* increased at approximately 50 m<sup>3</sup>  
3 s<sup>-1</sup> 100 m<sup>-1</sup>, with an increase in abundance during upwelling. *T. nitzschoides* showed an increase  
4 in cumulative importance of nitrate at approximately 18 μM, with increasing abundance at lower  
5 nitrate concentrations. The gradient forest analysis indicated that the environmental variables of  
6 overall greatest importance in defining the phytoplankton assemblage in order were discharge,  
7 salinity, temperature, nitrate, and upwelling index (Fig. 7F).

## 8 **Discussion**

### 9 **Transition to brackish-marine phytoplankton assemblage in MHW years**

10 Every year, shifts in LCRE phytoplankton assemblages accompany the transition from  
11 riverine to marine influence in late summer (Rollwagen-Bollens et al, 2020; this study).  
12 However, oceanographic conditions accompanying MHWs – temperatures exceeding daily  
13 decadal averages by 1-2 °C and anomalously low discharge volumes - were associated with the  
14 only blooms of toxigenic species observed in the LCRE during the study period. In a study that  
15 temporally overlaps with ours, Rose et al. (2021) observed spikes in cyanobacterial biomass in  
16 late summer of 2017 and 2018 at a site 170 river km upstream of the mouth, though we only  
17 observed a muted elevation in cyanobacteria in the summer of 2017 at our downstream site.  
18 Although harmful cyanobacteria blooms do occur in parts of the Columbia River, we have not  
19 found records of HABs in the lower estuary area of interest for this study with the exception of  
20 those discussed herein. *Pseudo-nitzschia* spp. have been observed in the LCRE previously, but  
21 did not dominate the assemblage or reach bloom concentrations (Frame and Lessard 2009).  
22 Interestingly, the dominant HAB taxon differed between MHWs occurring in 2015 and 2019,  
23 with *Pseudo-nitzschia* spp. dominating the former and *G. catenatum* dominating the latter. Both



1 of these taxa occupy marine-brackish habitats; thus, our discussion focuses on drivers of marine  
2 and brackish HABs at the LCRE site.

3 Our results may suggest two different potential mechanisms contributing to bloom  
4 development in the LCRE. In 2015, the estuary more closely resembled the coastal ocean in  
5 bloom composition; that is, the prolonged period of marine influence in the LCRE resulting from  
6 reduced river discharge provided sufficient habitat opportunity to allow offshore *Pseudo-*  
7 *nitzschia* spp. to persist at relatively high densities following tidal exchange. The importance of  
8 low discharge in creating appropriate conditions for a bloom is suggested by the timing of the  
9 bloom in the LCRE. Offshore, toxic *Pseudo-nitzschia australis* associated with the 2015 North  
10 Pacific MHW (National Centers for Coastal and Ocean Science 2015) was prevalent during the  
11 summer, while the *P. c.f. australis/fraudulenta* complex was not detected in the LCRE at  
12 significant concentrations until October 2015 when river flows declined below  $\sim 3,400 \text{ m}^3 \text{ s}^{-1}$  and  
13 salinity was elevated ( $>14$  PSU). More broadly, the samples collected in October of 2015  
14 revealed higher abundances of marine phytoplankton, including *Pseudo-nitzschia* spp., at deeper  
15 depths where salinities were highest in association with the salt wedge (Kärnä and Baptista  
16 2016). Particulate domoic acid (pDA) was detected ( $<100 \text{ ng L}^{-1}$ ) when *P. c.f.*  
17 *australis/fraudulenta* was present, although toxin levels were less than half the concentration that  
18 leads to accumulation in shellfish (ORHAB 2021).

19 In 2019, *G. catenatum* also bloomed during a period of low discharge ( $\sim 2,800 \text{ m}^3 \text{ s}^{-1}$  -  
20  $3,400 \text{ m}^3 \text{ s}^{-1}$  14-d average) with anomalously elevated temperature relative to the site decadal  
21 average. Particulate saxitoxins in water were observed during this bloom, but concentrations  
22 were lower than recreational alert levels ( $10 \text{ ppb}$  or  $\mu\text{g L}^{-1}$ ) for freshwater systems in Oregon,  
23 which does not currently have seawater saxitoxin health guidelines (Oregon Department of

1 Agriculture 2021). This bloom did not appear to have been transported into the estuary from a  
2 nearshore marine site like the 2015 *Pseudo-nitzschia* spp. bloom. Rather, it is likely to have  
3 developed *in situ* nearby the Ilwaco sampling site in Baker Bay, based on its absence in samples  
4 concurrently collected from the Columbia River South Jetty, and several other open coast sites in  
5 Oregon and Washington (data not shown, M. Rogers pers. comm., 2019). *Pseudo-nitzschia* spp.  
6 were present in very low concentrations in the LCRE during the 2019 *G. catenatum* event, but  
7 nearby coastal sites had higher abundances (data not shown), indicating a lesser degree of  
8 transport into the LCRE than observed during the 2015 bloom event. Given that many  
9 dinoflagellates including *G. catenatum* can form resistant cysts to sustain populations through  
10 long periods in marginal environments (Blackburn et al. 1989; Hallegraeff et al. 2012), it is  
11 possible that cysts transported from an unknown seed area (either offshore or within the estuary)  
12 could have seeded the bloom in the LCRE during conditions that favored its proliferation.

13         We identified clear shifts in phytoplankton assemblages associated with thresholds of  
14 discharge and salinity, but the mechanism by which these shifts occur is not clear from this  
15 analysis, particularly in explaining the emergence of two different HABs during the transition to  
16 marine dominance of the LCRE under low-flow conditions. The observed association of *Pseudo-*  
17 *nitzschia* spp. abundance in the LCRE with upwelling may be due to the effect of wind stress on  
18 the movement of the Columbia River plume, which can act as a barrier to onshore transport of  
19 marine plankton during downwelling. During upwelling winds, offshore plankton may become  
20 entrained within it or subduction may occur (Hickey et al. 2005). The *G. catenatum* bloom did  
21 not show the same association with upwelling, and occurred during a significant decreasing trend  
22 in upwelling index. Upwelling also supplies inorganic nutrients to surface coastal waters and has  
23 a proportionally greater impact on nutrient inputs to the LCRE under low flow conditions

1 (Bruland et al. 2008). Du et al. (2016) documented enhanced *Pseudo-nitzschia* spp. growth in  
2 coastal waters during stronger upwelling in 2015, likely due to increased nutrient availability.  
3 Nitrate in the LCRE was low in early summer of 2015 compared to other years, which is likely a  
4 result of very low discharge during this time, combined with periods of weakened upwelling.  
5 During the late summer time frame when the *Pseudo-nitzschia* spp. bloom occurred, nitrate (the  
6 preferred N source for *Pseudo-nitzschia* spp. (Cochlan et al. 2008)) increased in the LCRE  
7 during a period of stronger upwelling (Du et al. 2016). We did not collect nutrient data beyond  
8 nitrate concentrations in the LCRE for 2015-2018 so we rely on previous work in this system to  
9 interpret the impact of nutrient conditions during our study period, particularly for 2019.

10 In contrast, *G. catenatum* is a poor competitor for inorganic nutrients, is not likely to  
11 bloom without a source of organic nutrients, and is capable of phagotrophy (Yamamoto et al.  
12 2004; Jeong et al. 2010)). This is consistent with our finding that *G. catenatum* was not  
13 associated with inorganic-nutrient-rich marine upwelling, despite being associated with brackish  
14 waters in the LCRE. When saline waters extend into the LCRE under low flow conditions,  
15 freshwater plankton from upriver may die from osmotic stress when they encounter salinities of  
16 1-5 PSU (Lara-Lara 1990), and contribute to available particulate organic matter (POM) (Small  
17 et al. 1990). Long residence time during low flows may slow the flushing of these resources,  
18 particularly from lateral bays, creating an optimal food source for a phagotrophic dinoflagellate,  
19 which co-occurred with other mixotrophic plankton (e.g., *Mesodinium rubrum*, *Euglena* spp.).  
20 Renewing water age in the LCRE is about 20 hours during high discharge conditions, but may  
21 exceed 120 hours under low discharge and neap tide conditions in bays with weak circulation,  
22 such as our study site in Baker Bay (Kärnä and Baptista 2016). This longer flushing time

1 observed in the late summer may retain POM and provide refuge for plankton (either transported  
2 from offshore or grown within the LCRE) that may not establish under faster flowing conditions.

3 Both HAB taxa observed are also well-adapted to the anomalously warm, saline habitat  
4 available in the LCRE during the MHWs that was not present under higher discharge conditions.  
5 *Pseudo-nitzschia* spp. are able to grow at temperatures up to 30 °C (Zhu et al. 2017). They are  
6 rarely found in low salinity waters, and exhibit high mortality rates when exposed to salinity  
7 outside 30-35 PSU (Thessen et al. 2005; Ayache et al. 2019). *G. catenatum* can grow at  
8 temperatures as high as 29 °C, though temperate ecotypes grow optimally at temperatures  
9 between 12-18 °C (Hallegraeff et al. 2012), and will tolerate salinities in the range of 15-40 PSU  
10 (Blackburn et al. 1989; Band-Schmidt et al. 2004).

11 Our analyses suggest that declining river influence during the late summer period of two  
12 anomalously warm years (2015 and 2019) was a shared driver in creating a window of habitat  
13 availability for two different HABs. Each likely occupied this habitat through a different  
14 discharge-related mechanism – an upwelling-fed coastal bloom with tidal advection into an  
15 unusually saline LCRE and *in situ* bloom development promoted by long water renewal times  
16 and a source of POM in a brackish LCRE.

### 17 **Characteristics of phytoplankton assemblage transitions**

18 Discharge and salinity were identified as the primary predictors of phytoplankton  
19 assemblage composition in the LCRE in the gradient forest analysis. This highlights the  
20 importance of the seasonally driven environmental gradient of river dominance vs. ocean  
21 influence, and takes a further step in identifying the thresholds at which the resulting  
22 phytoplankton transition occurs. The HAB taxa observed during the study period did not exhibit  
23 large changes in the cumulative importance of environmental variables in the gradient forest

1 analysis, possibly because they were present at undetectable or low abundance prior to the onset  
2 of the HABs. However, several assemblage shifts (e.g., declines in tythropelagic *Navicula* spp.  
3 and freshwater taxa, increasing marine pelagic taxa like *Ditylum brightwellii*) may be used to  
4 demarcate estuarine niche transitions associated with elevated risk of marine and brackish HABs  
5 to help focus monitoring efforts. It should be noted that our species composition dataset is  
6 relatively sparse compared to the continuous environmental data from the LCRE. Higher  
7 resolution plankton assemblage data may improve environmental threshold estimates of plankton  
8 niche transitions, and a larger dataset would allow validation of the gradient forest model. In  
9 addition, we only analyzed phytoplankton assemblage data for one year that did not have a  
10 MHW, and therefore cannot determine how representative the 2017 community is of typical non-  
11 MHW years. In order to better understand how MHWs influence phytoplankton assemblages,  
12 more baseline assemblage data are needed to compare anomalous events with normal variability.  
13 Although our study captures two HABs during two MHWs, the lack of historical documentation  
14 of either MHWs or marine/brackish HABs in the LCRE necessitates continued monitoring to  
15 understand the relationship between MHW and HABs in this unique habitat.

#### 16 **Environmental drivers of phytoplankton shifts**

17 Our NMDS analysis with environmental vector overlay indicated that *Navicula* spp. and  
18 the freshwater *Ankistrodesmus* sp. were strongly negatively associated with salinity. Although  
19 some *Navicula* species in the LCRE are thought to be tolerant of brackish conditions (Simenstad  
20 et al. 1984), it is possible that salinity exceeded the preferred range of less salt tolerant species  
21 during the extreme low flow conditions experienced in 2015 and 2019. Changes in resuspension  
22 of tythropelagic diatoms may also influence the observed shifts in phytoplankton assemblages in  
23 our surface water samples. Mixing in the LCRE is governed by complex interactions between

1 tidal transitions, river flow, and density gradient. During the summer low flow period, neap-  
2 spring tide transitions in stratification are less disrupted by high flow events, indicating that  
3 mixing may be more governed by tidal action. During this time, hydrodynamic models suggest  
4 the LCRE is strongly or weakly stratified for most of the tidal cycle, but experiences brief  
5 periods (1-2 days) of partial mixing during the transition between the neap-tide and the rest of  
6 the tidal month (Jay 1990). Reduced vertical mixing is one possible explanation for the observed  
7 decline in tychopeagic taxa during low flow conditions. However, studies on particle movement  
8 (Stevens et al. 2017) have focused on the main channel of the LCRE, and flow dynamics are less  
9 well understood in the LCRE lateral bays.

10 This analysis also showed that *Pseudo-nitzschia* spp., *T. nitzschoides*, and *N. longissima*,  
11 and *D. brightwellii* (marine pelagic taxa) were positively associated with upwelling and  
12 temperature, negatively associated with nitrate, and strongly negatively associated with  
13 discharge. *G. catenatum* and *D. brightwellii* (brackish and marine pelagic taxa) were most  
14 strongly positively associated with salinity. We observed peaks in chlorophyll in late summer of  
15 2015 and 2019, associated with the growth of these brackish and marine taxa. In contrast,  
16 chlorophyll declined significantly throughout the study period during 2017, with very low values  
17 in late summer. This may indicate a lack of a transition to marine dominance and the associated  
18 phytoplankton assemblage that increased chlorophyll in late summer of MHW years.

19 As climate change is expected to alter the hydrology of the Columbia River (Hamlet and  
20 Lettenmaier 1999), the conditions observed during the described MHW years may become more  
21 common in the future. It is likely that low-snowpack, high temperature years will become more  
22 frequent, low-flow timeframes may be extended, and flows may be lower during drought  
23 conditions, creating potential for a longer, geographically larger window of ocean-influenced

1 LCRE. Currently this LCRE habitat is ephemeral, but has the potential to increase spatially  
2 (upriver) and temporally. Our study is limited by the number of years of LCRE phytoplankton  
3 monitoring data, making mechanistic explanation of the two different HABs observed during  
4 climatically anomalous events challenging.

5         Despite the increasing occurrence of algal toxin closures for Pacific Northwest beaches,  
6 most bays and estuaries remain open to shellfish harvest all year and many are not monitored for  
7 HABs to provide early warning of toxin events. Although strong freshwater flows during the  
8 winter and spring generally preclude the need for marine and brackish HAB monitoring in river-  
9 dominated west coast estuaries, we show that these HABs can develop during anomalously low  
10 summer discharge. Sustained monitoring will be essential to understand mechanisms driving  
11 estuarine HAB development in a changing climate.

12

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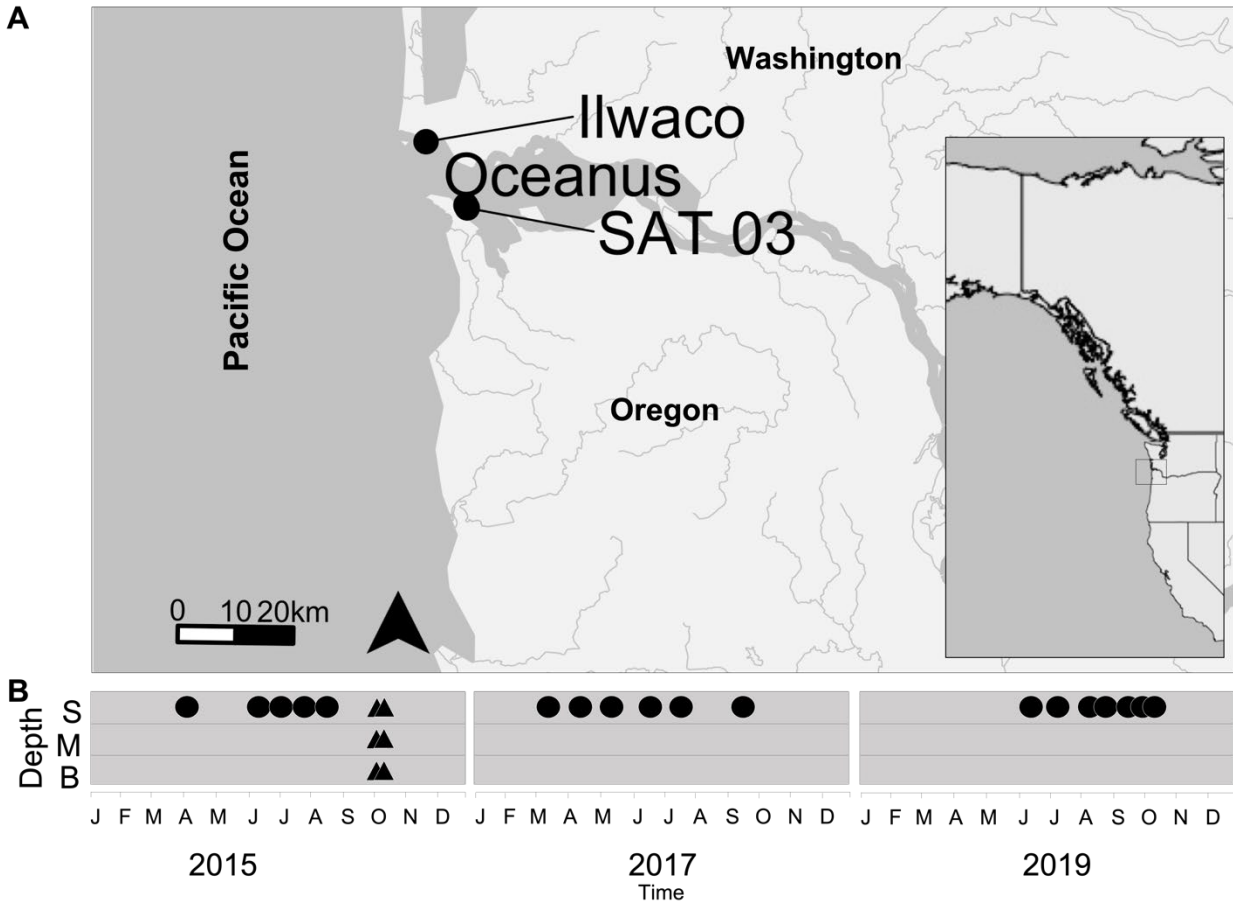
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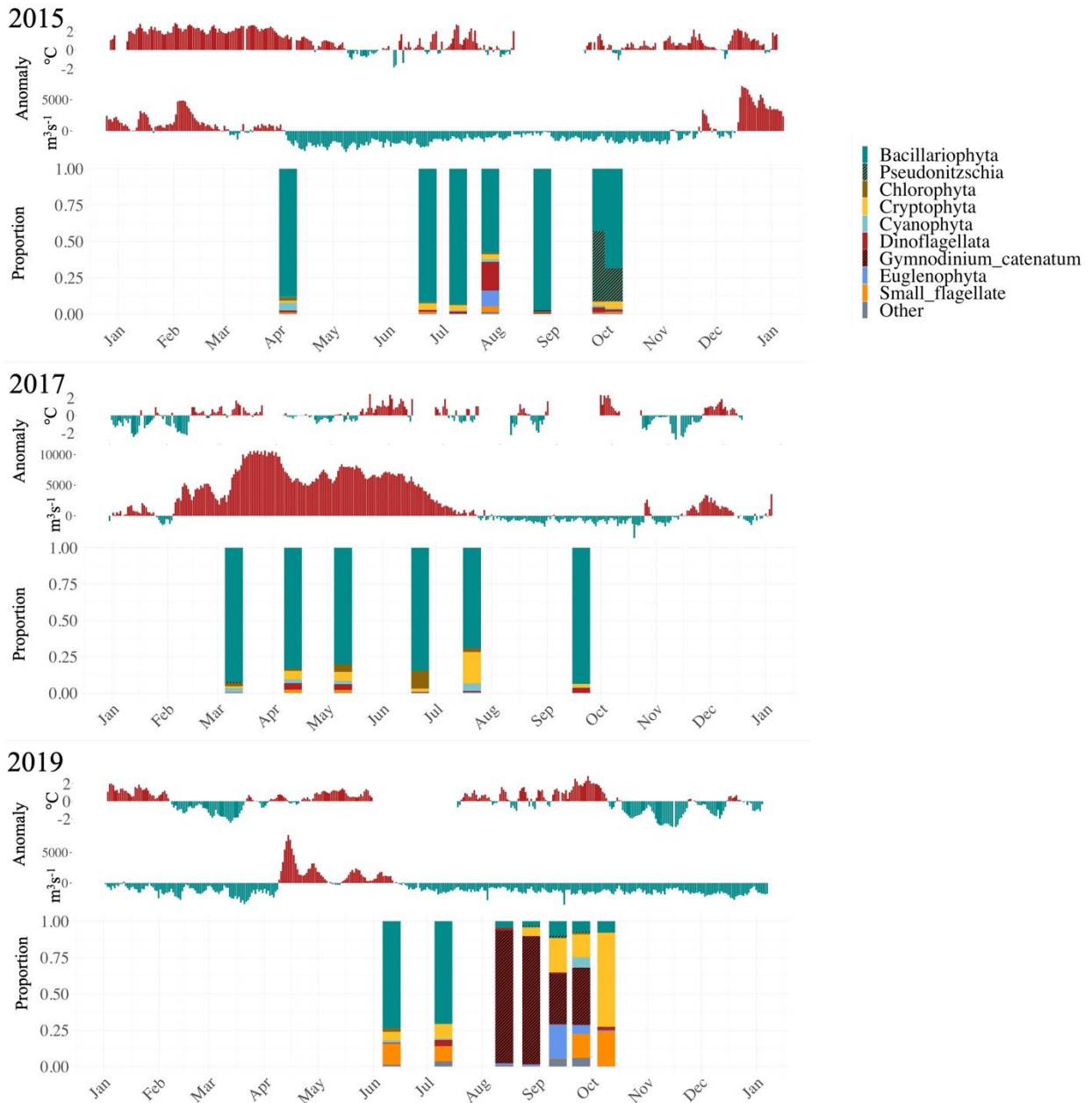
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2 **Fig. 1** Map of Lower Columbia River Estuary with regional inset (A) and phytoplankton sampling scheme (B). (A)  
3 The Columbia River forms part of the Oregon-Washington border. Phytoplankton and nutrient samples were  
4 collected from Ilwaco and Oceanus sites. Environmental data were collected from sensors at Saturn 03 site.  
5 Discharge data were collected upstream of the close-up map, and upwelling index was reported for Lincoln City  
6 (Oregon Coast). (B) Each point on the timeline represents a phytoplankton sampling event, with the depth of the  
7 sample specified on the y-axis (S = surface, M= mid-water column, B = bottom). Circles represent sampling from  
8 the Ilwaco site and triangles represent sampling from the R/V Oceanus. Our sampling scheme combined long-term,  
9 low frequency, surface samples with short-term, high-frequency, samples of the whole water column. This allowed  
10 for characterization of phytoplankton assemblages at multiple temporal and spatial scales.

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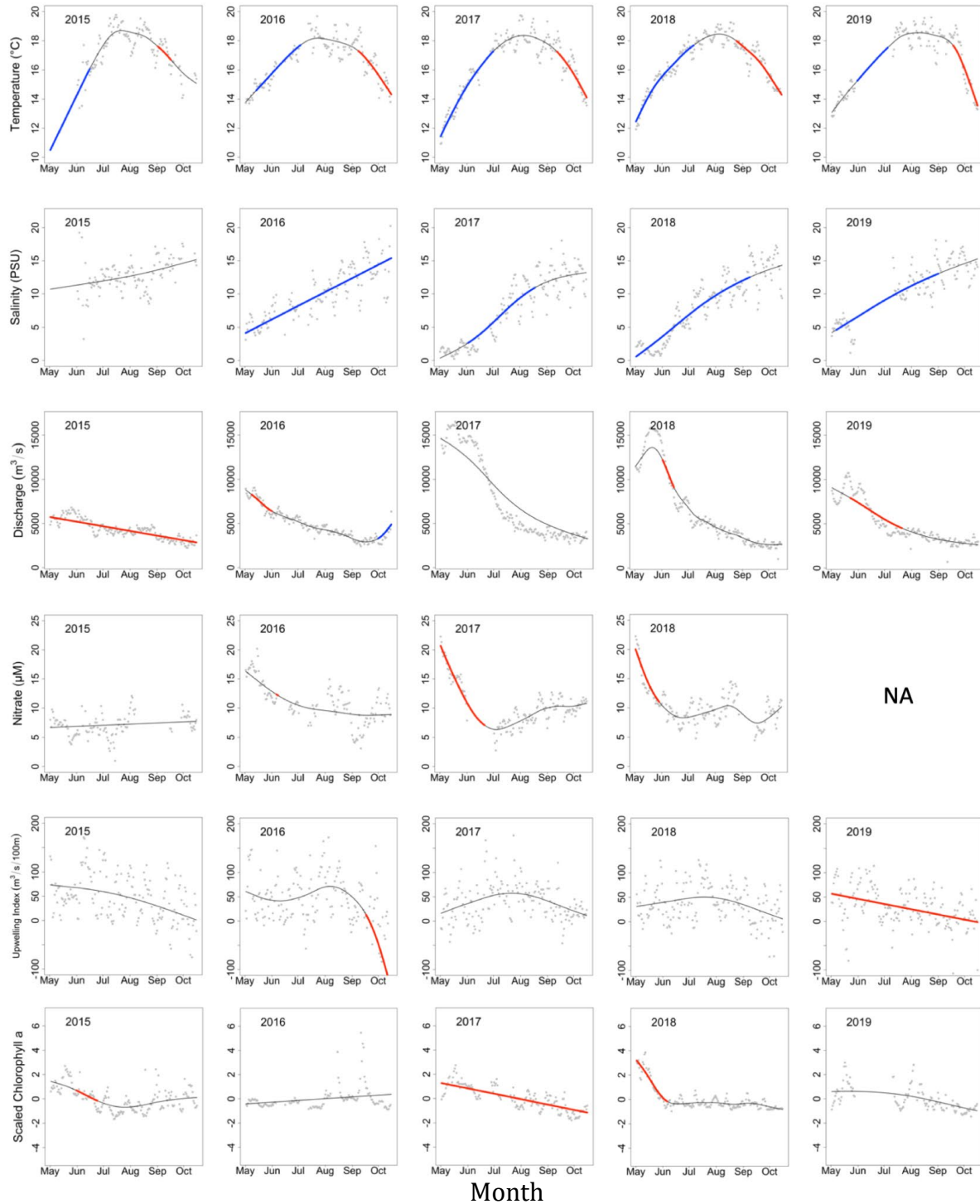
**Fig. 2** Bar plots of phytoplankton assemblage composition (bottom) with temperature anomaly in degrees Celsius (top) for 2015, 2017, and 2019. Phytoplankton taxa are divided into phyla (Bacillariophyta Chlorophyta, Cryptophyta, Cyanophyta, Dinoflagellata, Euglenophyta) and agglomerative groups (Small flagellates and Other, which includes a combination of other phyla that were relatively rare). All phytoplankton samples were taken at the surface, except for the October 2015 samples, which are shown as an average of phytoplankton samples from the surface, middle and bottom of the water column. The harmful algal blooms observed during the study period

1 (*Pseudo-nitzschia* spp. and *Gymnodinium catenatum*) are given their own group and color (striped). Temperature  
2 anomaly (difference from decadal daily average at Saturn-03 site) is shown on the same time-scale as phytoplankton  
3 bar plots, with warmer-than-average days shown in red, cooler-than-average days shown in blue, and gaps in the  
4 time series indicating missing values.

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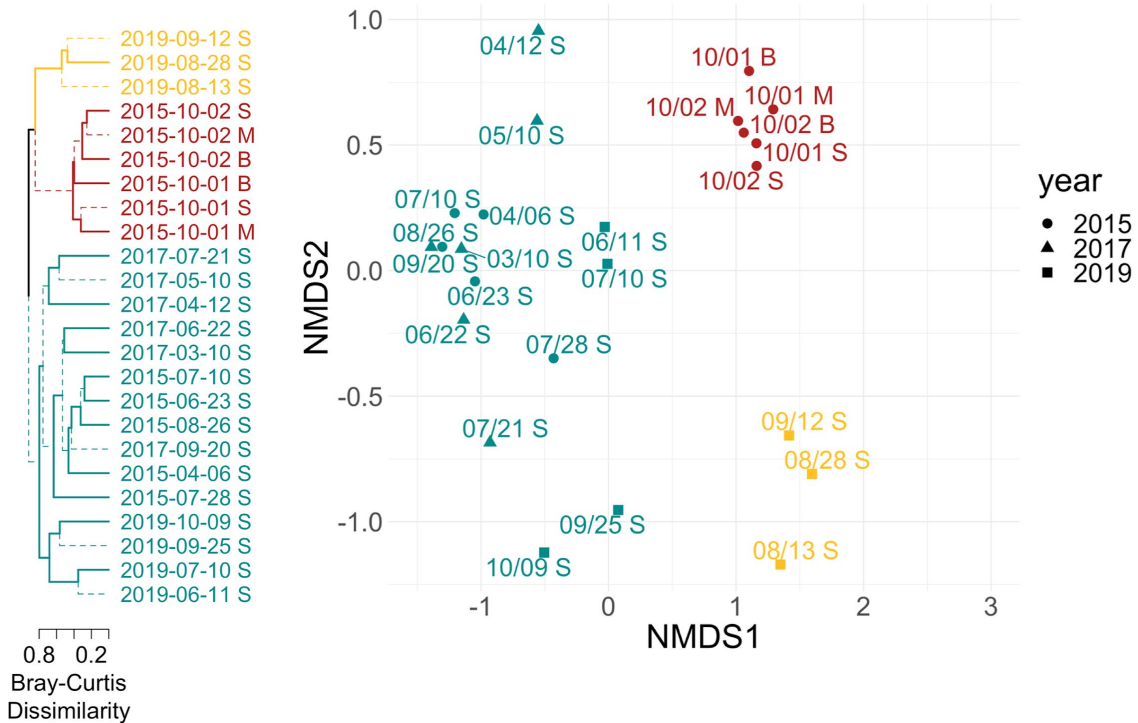




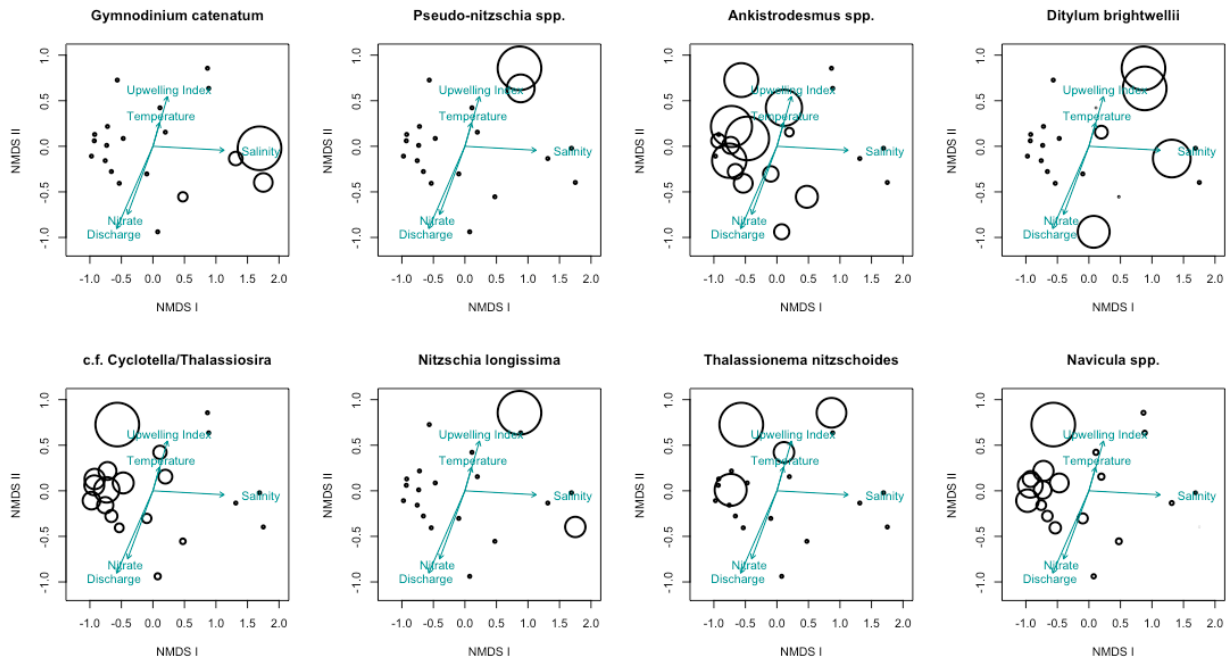
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 2 **Fig. 3** GAMMs provide a characterization of environmental conditions during the growing season (May-October) of  
 3 each year from 2015 - 2019, with significantly increasing modeled time frames displayed in blue, and significantly

1 decreasing periods shown in red. Chlorophyll a values for each year were scaled (z-scores) to account for inter-  
 2 annual differences in sensor calibration. NA: Nitrate data in 2019 was missing.

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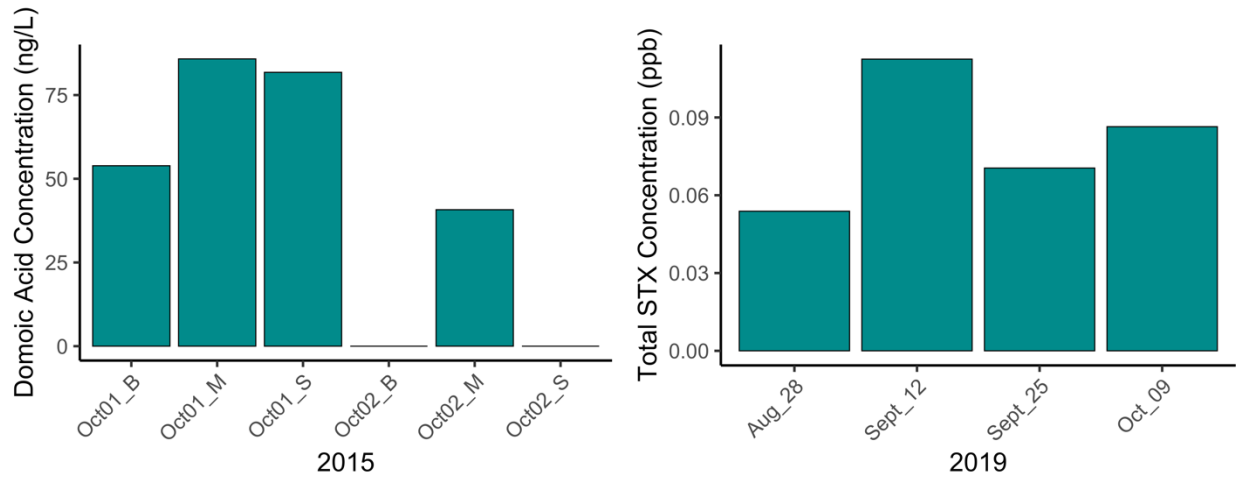


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 6 **Fig. 4** Two-dimensional ordination using non-metric multidimensional scaling (NMDS) of phytoplankton  
 7 assemblage data with hierarchical clustering analysis. Each point represents a phytoplankton sampling date and  
 8 depth (S = surface, M = mid-water column, B = bottom), with more similar communities placed closer to each other.  
 9 Stress value for the NMDS is 0.12. Shapes depict sampling year (circle = 2015, triangle = 2017, square = 2019).  
 10 Colors depict cluster identity and dashed lines indicate branches leading to distinct sub-trees.



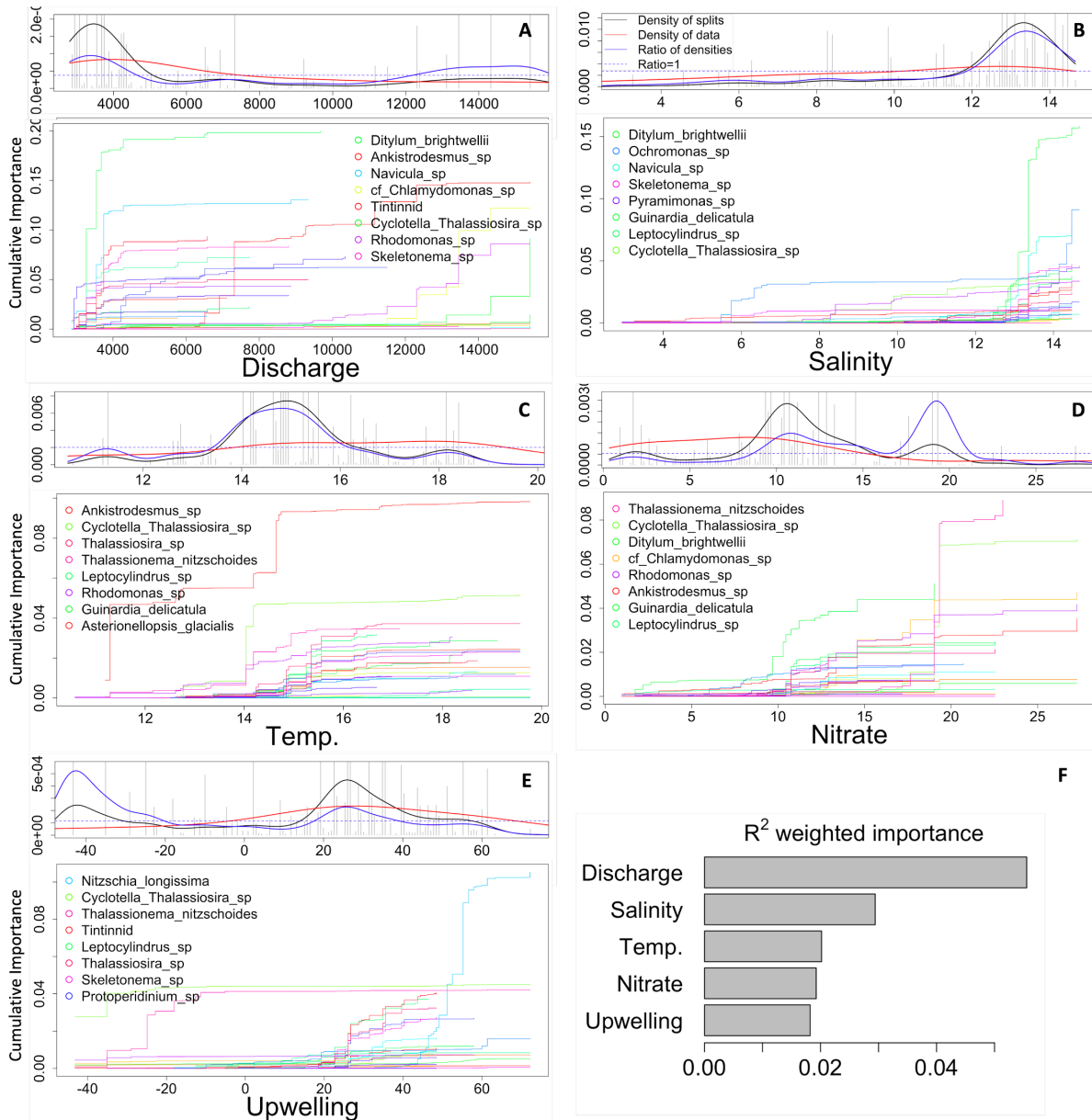
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**Fig. 5** Non-metric multidimensional scaling plots of phytoplankton assemblage from Ilwaco Harbor samples from 2015, 2017, and 2019, with bubble size proportional to the relative abundance of the selected taxa. Environmental vectors that correspond to the important physical drivers in the gradient forest analysis are overlaid. Phytoplankton taxa were selected either for toxin-production potential (*Pseudo-nitzschia spp.* and *Gymnodinium catenatum*) or because of a notable shift in cumulative importance over the gradient range of environmental predictors in the gradient forest analysis. Where multiple samples were taken (i.e. at different depths) on the same day, phytoplankton abundances were averaged. All measurements of environmental variables corresponding to phytoplankton sampling dates are 14-day moving averages leading up to the date of phytoplankton sampling. Units corresponding to the environmental vectors are: discharge ( $\text{m}^3\text{s}^{-1}$ ), temperature ( $^{\circ}\text{C}$ ), salinity (PSU), nitrate ( $\mu\text{M}$ ), upwelling index ( $\text{m}^3 \text{ s}^{-1}$  100m offshore transport).



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**Fig. 6** Concentrations of particulate algal toxins, domoic acid (ng/L) and total saxitoxins (ppb). Domoic acid samples were taken aboard the R/V Oceanus on October 1st and 2nd of 2015 during a bloom of *Pseudo-nitzschia* spp. and total saxitoxin samples were collected from Ilwaco Harbor in August-October of 2019. For each date and depth  $n=1$ .



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2 **Fig. 7** Gradient forest analysis shown as split density (top, A-E) and cumulative density (bottom, A-E) plots, and  
3 overall weighted importance of each predictor (F). (Top panel, A-E) Y axis shows density, x axis shows scale of  
4 corresponding predictor variable. Black line shows density of splits from regression trees, red line and gray bars  
5 show density of data. Blue line shows the ratio of split density to data density – above dotted blue line indicates that  
6 split density is higher than data density. (Bottom panel, A-E) Y axis shows cumulative importance of each variable  
7 to the abundance of several phytoplankton taxa ((A) Discharge ( $\text{m}^3\text{s}^{-1}$ ), (B) Salinity (PSU), (C) Temperature ( $^{\circ}\text{C}$ ),  
8 (D) Nitrate ( $\mu\text{M}$ ), (E) Upwelling Index ( $\text{m}^3 \text{s}^{-1}$  100m offshore transport) to a given species. Different taxa are  
9 designated by different colored lines. (F) Overall importance,  $R^2$  for each predictor of the physical drivers.

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Number of day equivalents of Salinity Exceeding 15, 25, 30 PSU (d)					
	2015	2016	2017	2018	2019
<b>&gt;15 PSU</b>					
2.4m	59.83	53.96	45.50	60.00	72.46
8.2m	18.29	5.00	11.04	10.79	12.75
13.0m	156.75	186.88	174.33	215.25	162.67
<b>&gt;25 PSU</b>					
2.4m	7.13	3.75	4.38	3.88	3.88
8.2m	17.38	29.21	36.04	42.13	29.33
13.0m	18.04	47.46	51.13	64.75	55.42
<b>&gt;30 PSU</b>					
2.4m	0.33	0.00	0.13	0.04	0.21
8.2m	1.88	0.54	4.96	2.79	0.54
13.0m	2.42	1.88	15.38	14.71	4.88

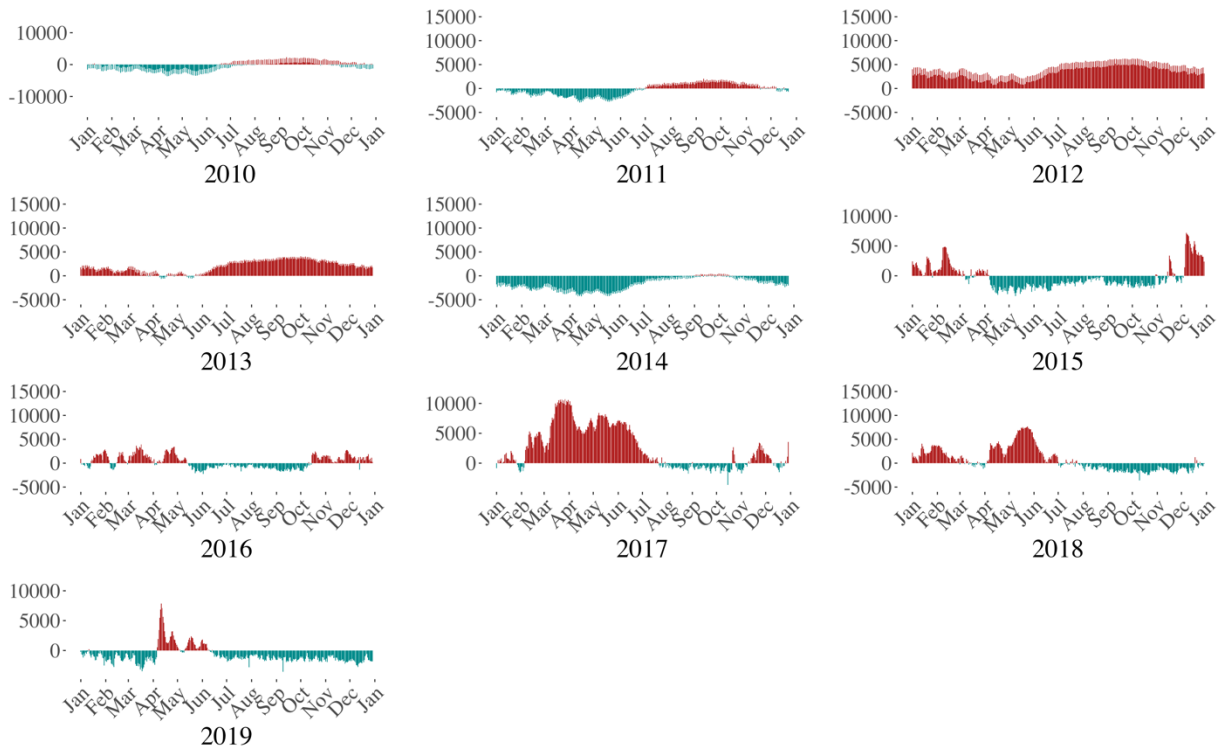
Hourly averages of salinity used to calculate number of day equivalents during June-September.

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**Table 1** Day equivalents of salinity exceeding 15, 25, and 30 PSU during summer season (June 1st - September 30th) at the Saturn 03 station. Salinity measured at 2.4 m, 8.2 m, and 13.0 m depth. Hourly averages used to calculate day equivalents, with missing hourly salinity measurements imputed using seasonal decomposition-based imputation.

Number of day equivalents of Temperature Exceeding 15, 18, 20 °C (d)					
	2015	2016	2017	2018	2019
<b>&gt;15 °C</b>					
2.4m	89.04	76.63	92.08	106.25	73.46
8.2m	24.46	45.54	43.29	55.08	68.04
13.0m	15.75	39.75	19.13	35.50	49.63
<b>&gt;18 °C</b>					
2.4m	48.96	38.29	46.25	45.88	47.38
8.2m	3.21	8.13	7.54	8.96	14.08
13.0m	2.50	4.58	2.25	3.88	6.00
<b>&gt;20 °C</b>					
2.4m	18.29	5.00	11.04	10.79	12.75
8.2m	0.54	0.04	0.04	1.08	1.00
13.0m	0.25	0.63	0.25	0.75	0.25
Hourly averages of temperature used to calculate number of day equivalents during June-September.					

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2 **Table 2** Day equivalents of temperature exceeding 15, 18, and 20 °C during summer season (June 1st - September  
3 30th) at the Saturn 03 Station. Temperature measured at 2.4 m, 8.2 m, and 13.0 m depth. Hourly averages used to  
4 calculate day equivalents, with missing hourly temperature measurements imputed using seasonal decomposition-  
5 based imputation.



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**S1** Daily discharge anomaly for 2010 – 2019 compared to daily decadal average. Discharge data from USGS Quincy Station. Red bars indicate a positive discharge anomaly, blue bars indicate a negative anomaly.