Supplementary materials

1. Different grouping of certain organisms

Table S1. Multiple diatom and dinoflagellate species, which contributed <1% (absolute) to the biomass (sum for a cruise) for most of the cruises or were only observed rarely, were summarized to "DIATOMS_other" and "DINOs_other", respectively. Heterotrophic nanoflagellates (HNF) ≤20 µm were summarized to "HNFcomplex" and autotrophic / mixotrophic flagellates to "FlagellateComplex".

DIATOMS_other	DINOs_other	HNFcomplex	FlagellateComplex
Actinocyclus spp.	*Amphidinium* spp.	*Katablepharis* spp.	*Prymnesiophyceae*
Attheya spp.	*Amylax* sp.	Choanoflagellates	Unidentified autotrophic flagellates
Aulacoseira sp.	*Cladopyxis* sp.	Unidentified heterotrophic flagellates	*Prasinopheceae*
Centrales (unidentified)	*Dinophyceae* (unidentified)	*Leucocryptos marina*	*Chrysophyceae*
Cylindrotheca closterium	*Dinophysis* spp.	*Telonema* spp.	
Cyclotella sp.	*Glenodinium* sp.		
Diatoma sp.	*Gyrodinium* spp.		
Leptocylindrus minimus	*Katodinium* sp.		
Licmophora sp.	*Oblea rotunda*		
Nitzschia sp.	Peridiniales (unidentified)		
Pseudonitzschia sp.			
Pennales (unidentified)			

2. Relative proportions of all 22 taxa considered for the final analyses

Table S2. Summary of relative contributions to the C-biomass of the 22 different plankton taxa considering all the 119 stations.

Taxonomic unit	Relative proportion [%]
Achnanthes taeniata	4.70
Cyanobacteria	0.70
Chaetoceros spp.	3.90
Cryptophyta	0.90
Ebria tripartita	1.17
Heterocapsa spp.	1.14
Melosira arctica	0.79
Mesodinium rubrum	16.08
Peridiniella catenata	14.33
Protoperidinium spp.	1.24
DinoComplex	12.47
Skeletonema marinoi	3.31
Thalassiosira baltica	9.02
Thalassisira levanderi	3.25
DIATOMS_other	1.24
DINOs_other	1.80
Chlorophyta	0.34
Euglenoideae	0.48
Ciliates (heterotrophic)	13.26
HNFcomplex	3.92
FlagellateComplex	2.60
Gymnodiniales	3.35

3. Environmental variables considered for the redundancy analysis (RDA)

Table S3. List of environmental parameters, including Chl *a* as a proxy for the bloom phases, that were considered for the RDA forward selection and the labels of significant parameters in the corresponding plot (Fig. 3A). The "x" indicates non-significant results. The distance to the shore (nautical miles) was determined based on the coordinates (WGS84 format) of the sampling stations using ArcGIS and shores of islands with an area of >100km^2 were considered.

Environmental variable	Significance (*p* values)	Label in RDA plot
Upper mixed layer depth	0.002	UMLD
Sampling time	x	
Wind speed	x	
Bottom depth	0.004	Depth_max
Chlorophyll *a*	0.002	Chl *a*
Latitude	0.002	Lat
Longitude	0.002	Long
Distance to shore	x	
Temperature	0.002	Temp
Salinity	x	
Nitrite	x	
Nitrite + Nitrate	0.006	NO2_3
Ammonium	0.038	NH4
Phosphate	0.022	PO4
Dissolved silicate	0.002	DSi

4. Determination of the upper mixed layer depth (UMLD) – Examples for different water columns

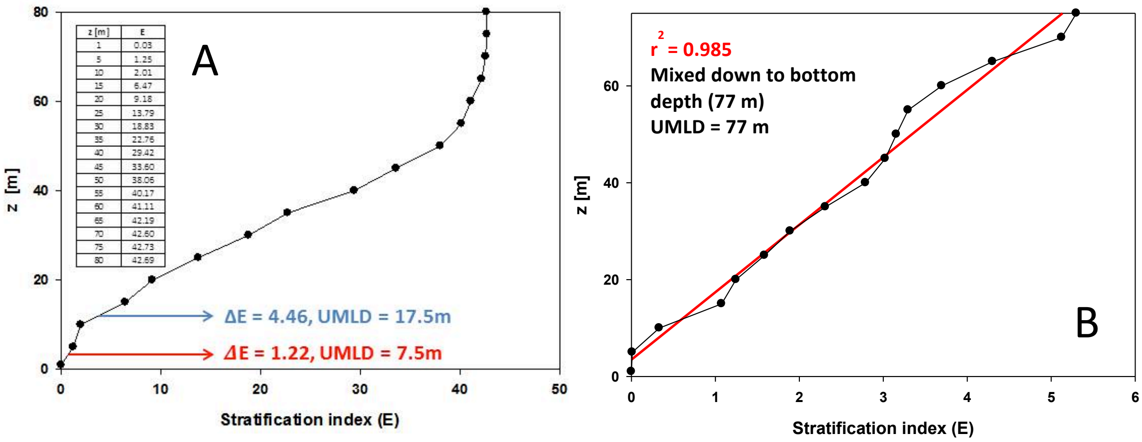

Fig. S1. Depth profiles (y-axis: water depth (z) in m; x-axis: stratification index E) of the stratification index E determined in 5 m increments. A) An example for a stratified water column (Gulf of Finland). The table included in the figure shows the actual E values considered to determine the data ΔE values to determine the two different UMLD´s at this station indicated by the arrows (ΔE=1.22, temporary UMLD at z = 7.5 m; ΔE = 4.46, stable UMLD at z = 17.5 m). B) An example for a completely mixed water column. In cases where the depth profile of E did not show a ΔE of at least 0.9 and thus, featured a linear trend (see red trend line, $r^2 = 0.985$), it was decided to set the UMLD to the bottom depth of the station.

5. Non-metric multidimensional scaling (NMDS) – Shepard (stress) plots

The stress value for the NMDS plot (Fig. 5) was ~0.20 and thus, indicates a good representation in the reduced dimensions (NMDS tutorial in R, Lefcheck 2012). The corresponding Shepard plot (stress plot, Fig. S2) did not show a large scatter around the line, indicating that the original dissimilarities were well preserved in the reduced dimensions.

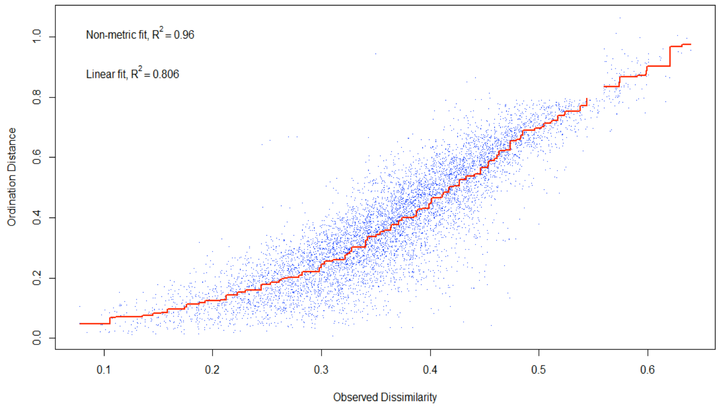

Fig. S2. The Shepard plot (stress plot) for the community ordination (NMDS) including GAM´s (Fig. 5): Non-metric fit: r^2 = 0.960, linear fit: r^2 = 0.806.

The selected function is independent of both, the number of parameters chosen, as well as the ordination method used.

6. ANOVA reports – Seston stoichiometry & gross primary production in different bloom phases (Table 3 in submitted manuscript)

Chl a:POC

All the data was log transformed first (natural log – LN in excel)
One Way Analysis of Variance
Data source: Data 2 in Notebook1
Normality Test (Shapiro-Wilk): Passed (P = 0.647)
Equal Variance Test (Brown-Forsythe): Passed (P = 0.629)

Group Name	N	Missing	Mean	Std Dev	SEM
Growth	45	26	-3.853	0.320	0.0734
Peak	45	6	-3.966	0.285	0.0457
Decline	45	0	-4.345	0.382	0.0569
Post-bloom	45	29	-4.901	0.358	0.0896

Source of Variation	DF	SS	MS	F	P
Between Groups	3	13.185	4.395	38.067	<0.001
Residual	115	13.277	0.115		
Total	118	26.463			

The differences in the mean values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = <0.001).
Power of performed test with alpha = 0.050: 1.000
All Pairwise Multiple Comparison Procedures (Tukey Test):
Comparisons for factor:

Comparison	Diff of Means	p	q	P	P<0.050
Growth vs. Post-bloom	1.047	4	12.848	<0.001	Yes
Growth vs. Decline	0.492	4	7.485	<0.001	Yes
Growth vs. Peak	0.113	4	1.681	0.635	No
Peak vs. Post-bloom	0.934	4	13.100	<0.001	Yes
Peak vs. Decline	0.379	4	7.210	<0.001	Yes
Decline vs. Post-bloom	0.555	4	7.942	<0.001	Yes

POC:PON

One Way Analysis of Variance
Data source: Data 2 in POC-PON.JNB
Normality Test (Shapiro-Wilk): Passed (P = 0.425)
Equal Variance Test (Brown-Forsythe): Failed (P < 0.050)
Test execution ended by user request, ANOVA on Ranks begun
Kruskal-Wallis One Way Analysis of Variance on Ranks.
Data source: Data 2 in POC-PON.JNB

Group	N	Missing	Median	25%	75%
Growth	46	27	1.978	1.950	2.010
Peak	46	7	2.100	2.027	2.214
Decline	46	1	2.065	1.953	2.204
Post-bloom	46	30	2.014	1.900	2.116

H = 13.068 with 3 degrees of freedom. (P = 0.004)
The differences in the median values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = 0.004)
To isolate the group or groups that differ from the others use a multiple comparison procedure.
All Pairwise Multiple Comparison Procedures (Dunn's Method):

Comparison	Diff of Ranks	Q	P	P<0.050
Peak vs Growth	32.381	3.355	0.005	Yes
Peak vs Post-bloom	22.163	2.164	0.183	No
Peak vs Decline	8.961	1.187	1.000	Do Not Test
Decline vs Growth	23.420	2.481	0.079	No
Decline vs Post-bloom	13.203	1.315	1.000	Do Not Test
Post-bloom vs Growth	10.217	0.873	1.000	Do Not Test

Note: The multiple comparisons on ranks do not include an adjustment for ties.

POC:POP

One Way Analysis of Variance
Data source: Data 2 in POC-PON.JNB
Normality Test (Shapiro-Wilk): Passed (P = 0.647)
Equal Variance Test (Brown-Forsythe): Failed (P < 0.050)
Test execution ended by user request, ANOVA on Ranks begun
Kruskal-Wallis One Way Analysis of Variance on Ranks.
Data source: Data 2 in POC-PON.JNB

Group	N	Missing	Median	25%	75%
Growth	46	27	4.692	4.560	4.798
Peak	46	7	5.088	4.711	5.259
Decline	46	1	4.976	4.720	5.251
Post-bloom	46	30	4.793	4.495	5.109

H = 17.163 with 3 degrees of freedom. (P = <0.001)
The differences in the median values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = <0.001)
To isolate the group or groups that differ from the others use a multiple comparison procedure.
All Pairwise Multiple Comparison Procedures (Dunn's Method):

Comparison	Diff of Ranks	Q	P	P<0.050
Peak vs Growth	35.366	3.664	0.001	Yes
Peak vs Post-bloom	22.603	2.207	0.164	No
Peak vs Decline	3.747	0.496	1.000	Do Not Test
Decline vs Growth	31.619	3.350	0.005	Yes
Decline vs Post-bloom	18.856	1.878	0.362	Do Not Test
Post-bloom vs Growth	12.763	1.090	1.000	No

Note: The multiple comparisons on ranks do not include an adjustment for ties.

PON:POP

One Way Analysis of Variance
Data source: Data 2 in POC-POP.JNB
Normality Test (Shapiro-Wilk): Passed (P = 0.679)
Equal Variance Test (Brown-Forsythe): Failed (P < 0.050)
Test execution ended by user request, ANOVA on Ranks begun
Kruskal-Wallis One Way Analysis of Variance on Ranks
Data source: Data 2 in POC-POP.JNB

Group	N	Missing	Median	25%	75%
Growth	46	27	2.685	2.597	2.787
Peak	46	7	2.934	2.715	3.148
Decline	46	1	2.895	2.673	3.117
Post-bloom	46	30	2.749	2.540	2.997

H = 11.757 with 3 degrees of freedom. (P = 0.008)
The differences in the median values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = 0.008)
To isolate the group or groups that differ from the others use a multiple comparison procedure.
All Pairwise Multiple Comparison Procedures (Dunn's Method):

Comparison	Diff of Ranks	Q	P	P<0.050
Peak vs Growth	29.186	3.024	0.015	Yes
Peak vs Post-bloo	17.736	1.732	0.500	No
Peak vs Decline	2.323	0.308	1.000	Do Not Test
Decline vs Growth	26.863	2.846	0.027	Yes
Decline vs Post-bloom	15.412	1.535	0.749	Do Not Test
Post-bloom vs Growth	11.451	0.978	1.000	No

Note: The multiple comparisons on ranks do not include an adjustment for ties.

POC:BSi

One Way Analysis of Variance
Data source: Data 2 in PON-POP.JNB
Normality Test (Shapiro-Wilk): Failed (P < 0.050)
Test execution ended by user request, ANOVA on Ranks begun
Kruskal-Wallis One Way Analysis of Variance on Ranks.
Data source: Data 2 in PON-POP.JNB

Group	N	Missing	Median	25%	75%
Growth	46	27	2.574	2.407	3.068
Peak	46	7	2.235	1.819	2.717
Decline	46	1	2.599	2.261	3.317
Post-bloom	46	30	2.496	2.359	3.065

H = 10.953 with 3 degrees of freedom. (P = 0.012)
The differences in the median values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = 0.012)
To isolate the group or groups that differ from the others use a multiple comparison procedure.
All Pairwise Multiple Comparison Procedures (Dunn's Method):

Comparison	Diff of Ranks	Q	P	P<0.050
Growth vs Peak	23.238	2.408	0.096	No
Growth vs Post-bloom	1.638	0.140	1.000	Do Not Test
Growth vs Decline	1.130	0.120	1.000	Do Not Test
Decline vs Peak	22.108	2.929	0.020	Do Not Test
Decline vs Post-bloom	0.508	0.0506	1.000	Do Not Test
Post-bloom vs Peak	21.599	2.109	0.210	Do Not Test

Note: The multiple comparisons on ranks do not include an adjustment for ties.

PON:BSi

One Way Analysis of Variance
Data source: Data 2 in POC-BSi.JNB
Normality Test (Shapiro-Wilk): Failed (P < 0.050)
Test execution ended by user request, ANOVA on Ranks begun
Kruskal-Wallis One Way Analysis of Variance on Ranks.
Data source: Data 2 in POC-BSi.JNB

Group	N	Missing	Median	25%	75%
Growth	46	27	0.626	0.423	1.075
Peak	46	7	0.190	-0.374	0.502
Decline	46	1	0.557	0.192	1.281
Post-bloom	46	30	0.543	0.325	0.952

H = 14.599 with 3 degrees of freedom. (P = 0.002)
The differences in the median values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = 0.002)
To isolate the group or groups that differ from the others use a multiple comparison procedure.
All Pairwise Multiple Comparison Procedures (Dunn's Method):

Comparison	Diff of Ranks	Q	P	P<0.050
Growth vs Peak	30.530	3.163	0.009	Yes
Growth vs Decline	8.151	0.864	1.000	No
Growth vs Post-bloom	4.434	0.379	1.000	Do Not Test
Post-bloom vs Peak	26.096	2.548	0.065	No
Post-bloom vs Decline	3.717	0.370	1.000	Do Not Test
Decline vs Peak	22.379	2.965	0.018	Do Not Test

Note: The multiple comparisons on ranks do not include an adjustment for ties.

Gross primary production (GPP)

One Way Analysis of Variance
Data source: Data 2 in POC-BSi.JNB
Normality Test (Shapiro-Wilk): Failed (P < 0.050)
Test execution ended by user request, ANOVA on Ranks begun
Kruskal-Wallis One Way Analysis of Variance on Ranks.
Data source: Data 2 in POC-BSi.JNB

Group	N	Missing	Median	25%	75%
Growth	46	27	0.0790	-0.757	0.715
Peak	46	7	-0.143	-3.919	0.438
Decline	46	1	-0.732	-5.151	0.0677
Post-bloom	46	30	-1.423	-5.323	-1.030

H = 17.805 with 3 degrees of freedom. (P = <0.001)
The differences in the median values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = <0.001)
To isolate the group or groups that differ from the others use a multiple comparison procedure.
All Pairwise Multiple Comparison Procedures (Dunn's Method):

Comparison	Diff of Ranks	Q	P	P<0.050
Growth vs Post-bloom	44.681	3.817	<0.001	Yes
Growth vs Decline	29.324	3.107	0.011	Yes
Growth vs Peak	16.086	1.667	0.573	No
Peak vs Post-bloom	28.595	2.792	0.031	Yes
Peak vs Decline	13.238	1.754	0.477	No
Decline vs Post-bloom	15.357	1.529	0.757	No

Note: The multiple comparisons on ranks do not include an adjustment for ties.

7. Community ordination (NMDS) – The effect of different community compositions on seston nutrient stoichiometry

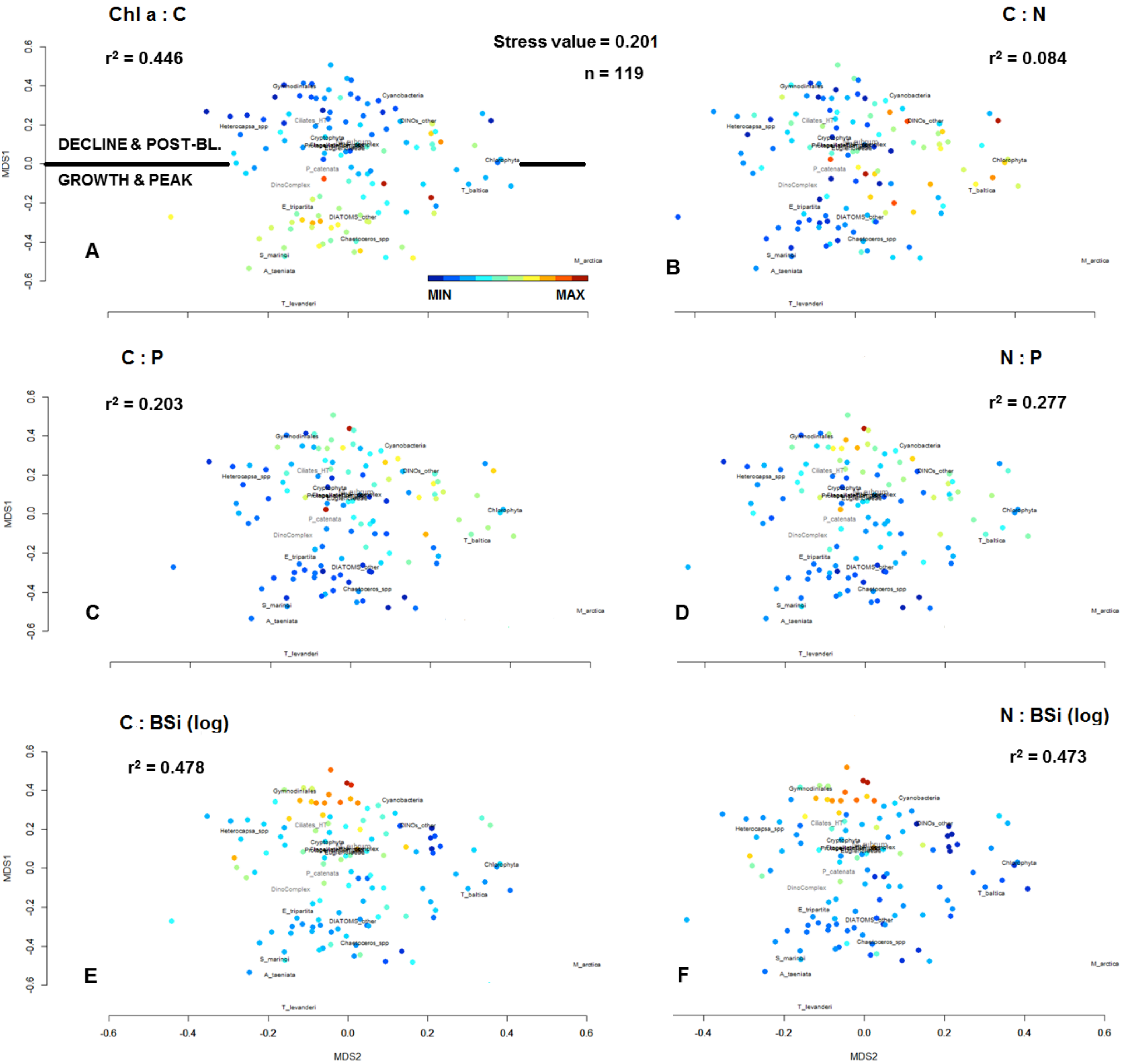

Fig. S3. Community ordination (NMDS) based on the C-biomass of the 22 taxa. A-F: The six seston ratios. Note, E and F are based on log-transformed C/N:BSi data. Symbols are colored by the corresponding ratio and the color scale in A (MIN = minimum, MAX = maximum) is valid for A-F. The black horizontal line separates bloom phases growth and peak from decline and post-bloom based on the community composition and applies to A-F. The four most relevant taxa (based on relative proportions) are represented by grey labels and the font size is equivalent to the biomass-contribution (*M. rubrum* has the largest font size). The other taxa are shown in black with the same font size for all. Stress value and number of observations (n) are valid for A-F. All coefficients of correlation (r^2) derive from GAM´s using the coordinates of each community along the MDS1 as explanatory variables. Seston ratios were the response variables. *p* values (GAM´s) were < 0.0001 for A, C, D, E, F and 0.01 for B.

8. References:

Lefcheck J (2012) NMDS tutorial in R. https://jonlefcheck.net/2012/10/24/nmds-tutorial-in-r/ (accessed 10 December 2019)