Oikos

OIK-05361
Barraquand, F., Picoche, C., Maurer, D., Carassou, L. and Auby, I. 2018. Coastal phytoplankton community dynamics and coexistence driven by intragroup density-dependence, light and hydrodynamics. – Oikos doi: 10.1111/oik.05361

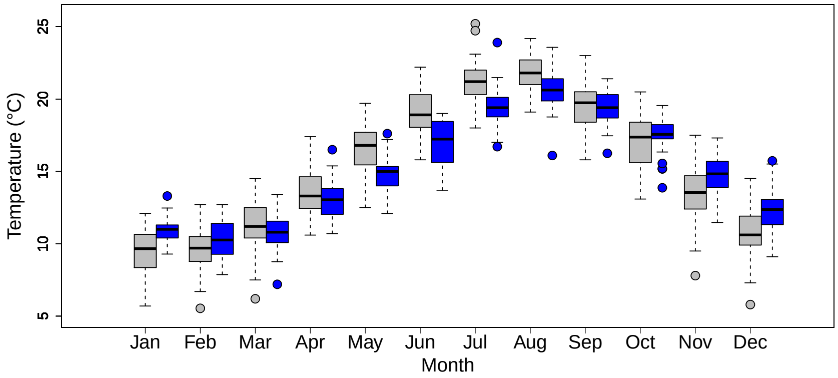
Appendix 1. Data collection and exploratory analyses

A1.1 Collection, pre-processing and selection of abiotic variables

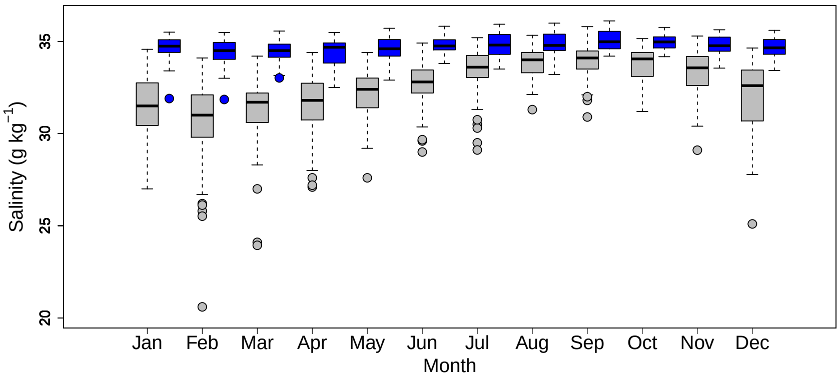
A1.1.1 Hydrological and biogeochemical functioning of Arcachon Bay

Arcachon Bay is characterized by a semi-diurnal tide ranging between 1.4 m and 4.7 m, with a strong water-level and current asymmetry. The two study sites, Teychan and Buoy 7 (B7), differ in their biogeochemical functioning (Fig. A1.1). Annual seasonality leads to a larger range of temperature over the year at Teychan. Conversely, salinity is more variable at the monthly scale at Teychan. The monthly average salinity at Teychan ranges between 30.6 g kg^{-1} (in February) and 34.0 g kg^{-1} (in September) with minimum and maximum values over the whole time series reaching 20.6 and 35.8 g kg^{-1}, respectively. The salinity range is narrower at Buoy 7: monthly average salinity ranges between 34.4 g kg^{-1} (in April) and 35.1 g kg^{-1} (in October), with extrema of 31.9 and 36.1 g kg^{-1}. On the other hand, both sites have similar turbidity values, below 5 NTU for more than 90% of water samples. These conditions lead to an average chlorophyll *a* concentration at Teychan around 2.1 µg L^{-1} and around 1.8 µg L^{-1} at Buoy 7. Hence, AB can be classified as a mesotrophic ecosystem (Glé *et al.* 2008), corresponding to a low-to-medium productivity and low eutrophication (Nixon 1995) compared to other land-sea interfaces (Cloern *et al.* 2014).

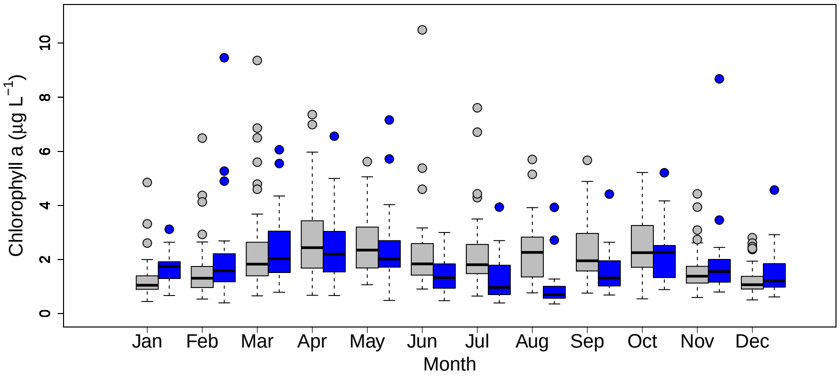
Stratification is low at both sites. The average difference of salinity between surface and bottom sampling is around 0.5 g kg^{-1}, and the average temperature difference is around 0.14°C (Fig. A1.2). Such differences are low when compared to the variability of both salinity and temperature (Fig. A1.1). The water column can therefore be considered well-mixed at Teychan and Buoy 7.



(a) Temperature



(b) Salinity



(c) Chlorophyll *a*

Figure A1.1: Distribution of salinity, temperature and chlorophyll *a* at Teychan (grey) and Buoy 7 (blue). Outliers (values above 1.5 times the interquartile range) are indicated with dots.

A1.1.2 Plankton ecology in Arcachon Bay

There is a wide temporal variability in AB, with an early phytoplankton bloom in spring and usually a late one in autumn. Based on a five-year spatialized field study of microphytoplank-

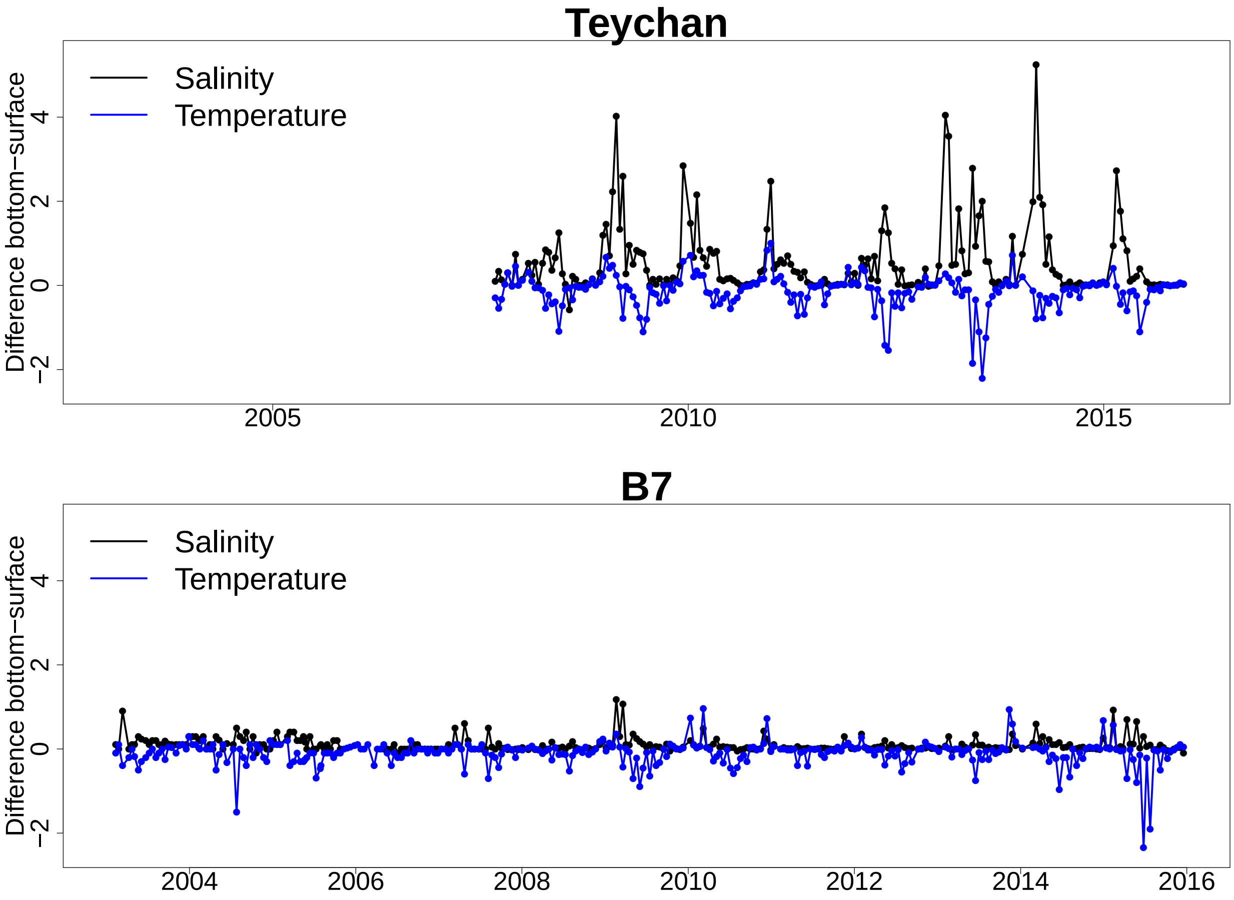


Figure A1.2: Difference between surface and bottom measures of salinity (black) and temperature (blue) at Teychan (top panel) and Buoy 7 (B7, bottom panel).

ton primary production, Glé *et al.* (2007) concluded that part of the marine plankton in AB may be coming from the adjacent Bay of Biscay oceanic waters, and the bloom within the lagoon could therefore be "seeded" by the ocean. According to their study, marine plankton find favorable conditions in AB as nutrient stocks from freshwater inflows are higher than in the ocean. A low turbidity, associated with a well-mixed water column (Fig A1.2), improves light penetration and favors a rapid population growth in response to elevated irradiance happening as early as the end of February, depending on climatic variability. According to Glé *et al.* (2008), increases in plankton abundance lead to nutrient depletion that is reflected in a lower productivity during summer. Both experimental (Glé 2007) and modeling (Plus *et al.* 2015) studies have shown so far that N might be limiting during summer in the interior of AB, while P restriction might be the main driver of productivity in external waters (Glé *et al.* 2008). On a shorter timescale, daily ebb and flow participate in nutrient cycling (amounting to 55% P and 15% N in the bay according to Deborde *et al.* 2008) while annual plankton loss to the ocean is estimated between 383 and 857 tC year^{-1} by Plus *et al.* (2015). A switch from early, large plankton assemblage with low biodiversity to a more diverse and smaller-bodied community has been noticed by Glé *et al.* (2008) although the latter study was restricted to a single year (2003), characterized by a dry winter and a strong summer heat wave. AB is also characterized by a higher average salinity and lower turbidity than other French Atlantic coastal bays where biotic and abiotic factors are similarly monitored (David *et al.* 2012).

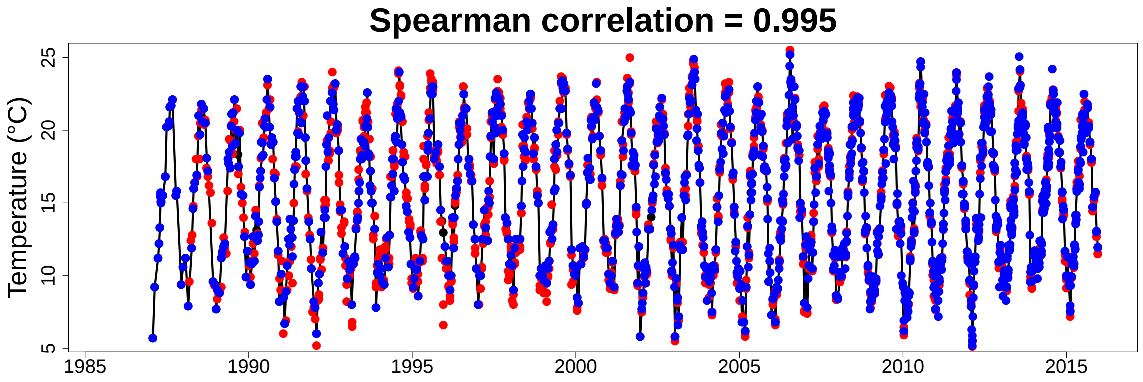
A1.1.3 Full sampling methods

Water samples were collected every two weeks, directly from the boat within the two hours around high tide. All samples were collected 1 m below the surface using a 2L Niskin bottle. Pre-filtrations were made on board with a 48 µm mesh for all nutrients (ammonia NH_4^+, phosphates PO_4^{3-} and nitrates-nitrites NO_2+NO_3^-) plus a 0.45 µm mesh for silicates ($Si(OH)_4$), which were immediately protected from light. Back at the laboratory, samples taken for nutrients were frozen or refrigerated. Before analysis, samples were centrifugated (2500 rpm, 5min, 15°C). Analyses were done with a Seal analytical Autoanalyzer III, according to the method described in Aminot & Kérouel (2007). Particulate matter samples were filtered through pre-combusted (450°C for 1 h) and pre-weighed Whatman GF/F filters, rinsed with distilled water to remove salts and stored at -20°C until analysis. Filters were dried at 70°C for at least 2 h and weighed for suspended particulate matter (SPM, mg dry mass L^{-1}). Inorganic matter (SPIM, mg ash dry mass L^{-1}) was given by the mass of ash remaining after burning at 450 °C for 5 h. Organic matter (SPOM, mg ash free dry mass/L) was given by losses at ignition.

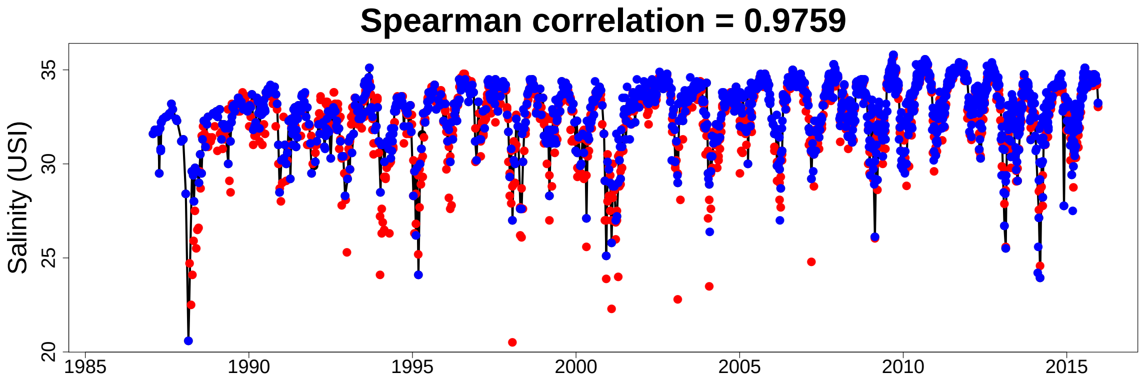
For chlorophyll *a*, samples were filtered through Whatman GF/F filters which were frozen at -25°C for no longer than 3 weeks. Pigments were extracted in 90 % acetone for 12h and analyzed with the fluorimetric method described in Aminot & Kérouel (2004).

Samples collected for phytoplankton counts (one 10 mL sample was extracted from each 2L bottle) were fixed in a Lugol's solution and the fraction above 20 µm was later identified and counted in 10 ml tanks with the Utermöhl method (Utermöhl 1958) using a phase-contrast inverted microscope (Olympus IMT2 or IX71).

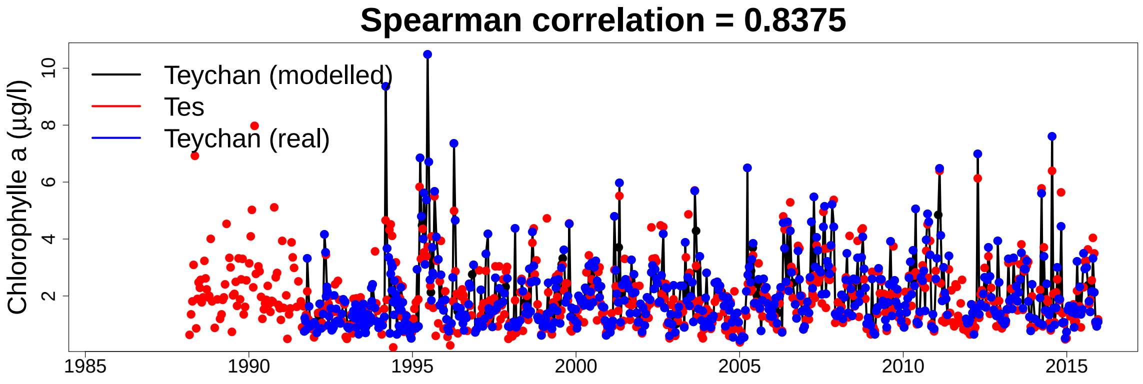
A1.1.4 Tès and Teychan biogeochemical cycles



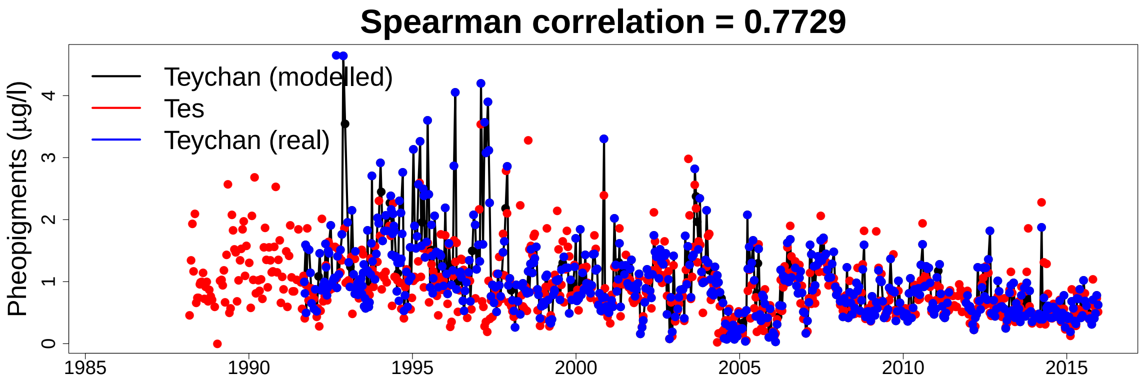
(a) Temperature



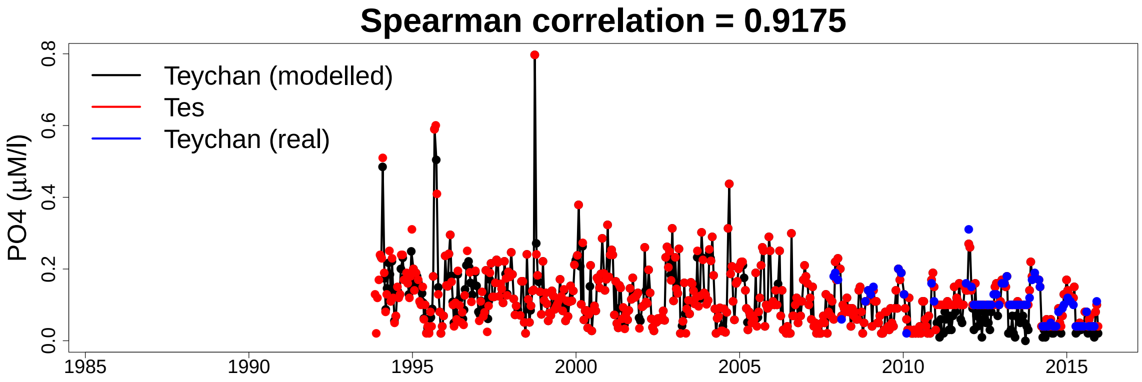
(b) Salinity



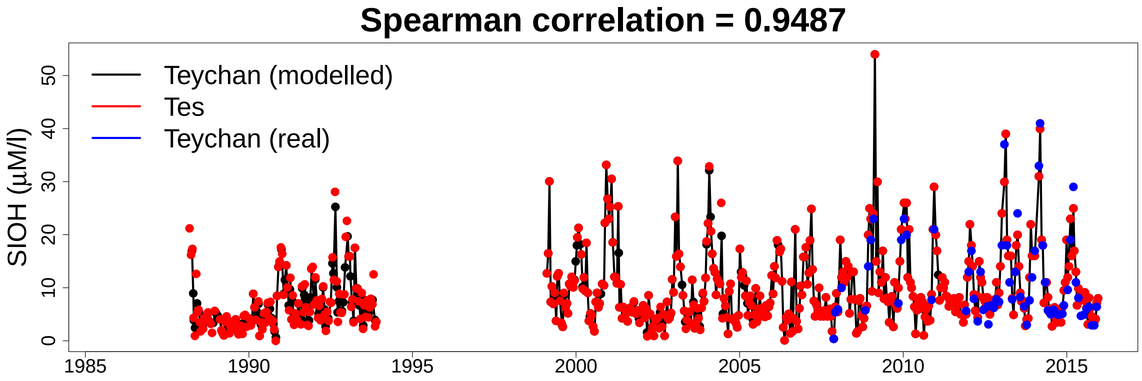
(c) Chlorophyll *a*



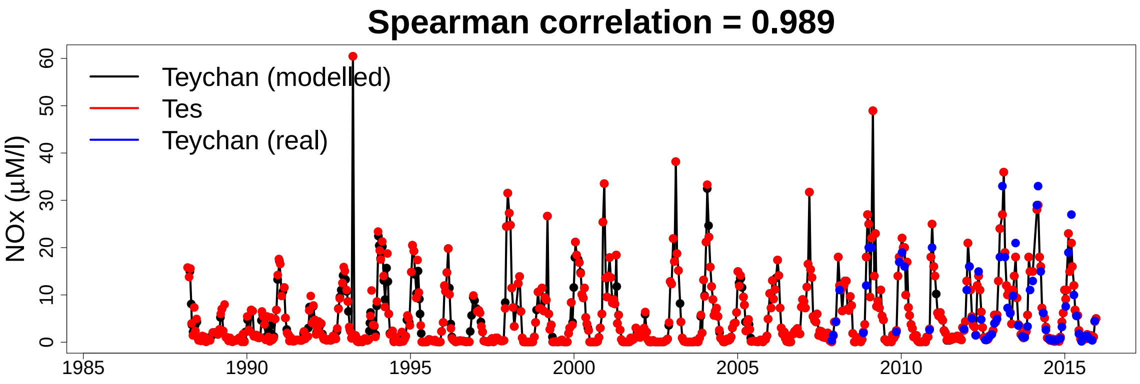
(d) Phaeopigment



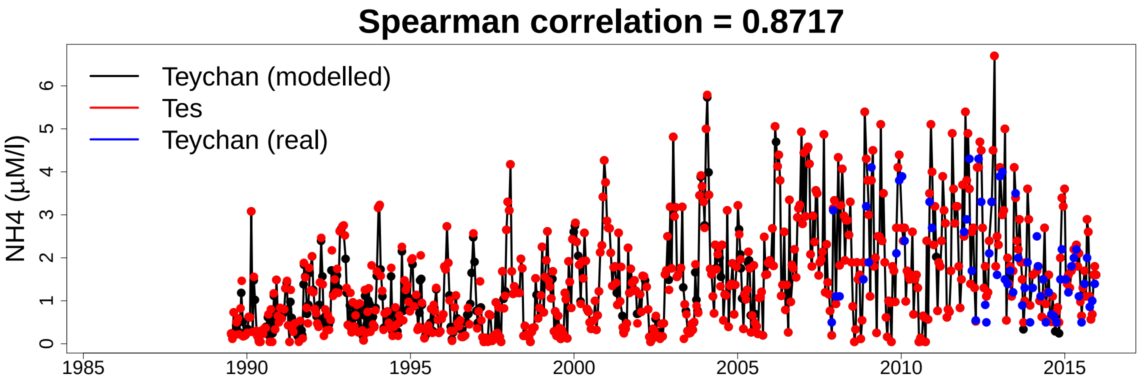
(e) PO_4^{3-}



(f) $Si(OH)_4$


Spearman correlation = 0.989

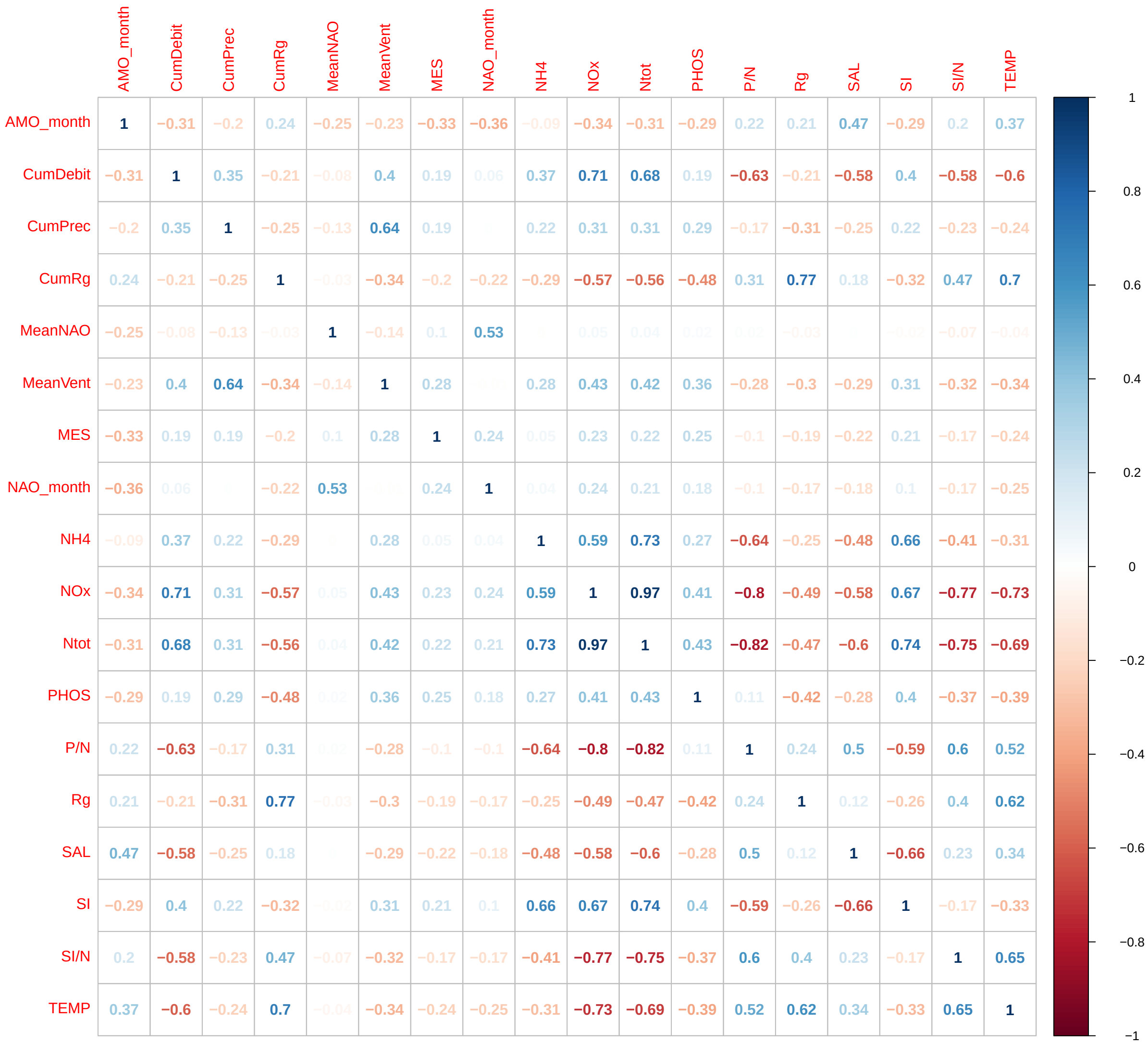
(g) $\mathrm{NO_x}$


Spearman correlation = 0.8717

(h) $\mathrm{NH_4^+}$

Figure A1.3: Comparison of water temperature, salinity, chlorophyll *a*, phaeopigment and nutrient contents at Teychan (blue dots) and Tès (red dots) sites. The title shows the probability associated to the Spearman correlation coefficient between the two sites. Such a similarity allows the modeling of Teychan environmental values after Tès measurements and linear interpolation when data are missing (black lines). Black dots correspond to the sampling dates of phytoplanktonic data.

A1.1.5 Correlation between abiotic variables



	AMO_month	CumDebit	CumPrec	CumRg	MeanNAO	MeanVent	MES	NAO_month	NH4	NOx	Ntot	PHOS	P/N	Rg	SAL	SI	SI/N	TEMP
AMO_month	1	−0.31	−0.2	0.24	−0.25	−0.23	−0.33	−0.36	−0.09	−0.34	−0.31	−0.29	0.22	0.21	0.47	−0.29	0.2	0.37
CumDebit	−0.31	1	0.35	−0.21	−0.08	0.4	0.19	0.06	0.37	0.71	0.68	0.19	−0.63	−0.21	−0.58	0.4	−0.58	−0.6
CumPrec	−0.2	0.35	1	−0.25	−0.13	0.64	0.19	0	0.22	0.31	0.31	0.29	−0.17	−0.31	−0.25	0.22	−0.23	−0.24
CumRg	0.24	−0.21	−0.25	1	−0.03	−0.34	−0.2	−0.22	−0.29	−0.57	−0.56	−0.48	0.31	0.77	0.18	−0.32	0.47	0.7
MeanNAO	−0.25	−0.08	−0.13	−0.03	1	−0.14	0.1	0.53	0	0.05	0.04	0.02	0.02	−0.03	0	−0.02	−0.07	−0.04
MeanVent	−0.23	0.4	0.64	−0.34	−0.14	1	0.28	−0.01	0.28	0.43	0.42	0.36	−0.28	−0.3	−0.29	0.31	−0.32	−0.34
MES	−0.33	0.19	0.19	−0.2	0.1	0.28	1	0.24	0.05	0.23	0.22	0.25	−0.1	−0.19	−0.22	0.21	−0.17	−0.24
NAO_month	−0.36	0.06	0	−0.22	0.53	−0.01	0.24	1	0.04	0.24	0.21	0.18	−0.1	−0.17	−0.18	0.1	−0.17	−0.25
NH4	−0.09	0.37	0.22	−0.29	0	0.28	0.05	0.04	1	0.59	0.73	0.27	−0.64	−0.25	−0.48	0.66	−0.41	−0.31
NOx	−0.34	0.71	0.31	−0.57	0.05	0.43	0.23	0.24	0.59	1	0.97	0.41	−0.8	−0.49	−0.58	0.67	−0.77	−0.73
Ntot	−0.31	0.68	0.31	−0.56	0.04	0.42	0.22	0.21	0.73	0.97	1	0.43	−0.82	−0.47	−0.6	0.74	−0.75	−0.69
PHOS	−0.29	0.19	0.29	−0.48	0.02	0.36	0.25	0.18	0.27	0.41	0.43	1	0.11	−0.42	−0.28	0.4	−0.37	−0.39
P/N	0.22	−0.63	−0.17	0.31	0.02	−0.28	−0.1	−0.1	−0.64	−0.8	−0.82	0.11	1	0.24	0.5	−0.59	0.6	0.52
Rg	0.21	−0.21	−0.31	0.77	−0.03	−0.3	−0.19	−0.17	−0.25	−0.49	−0.47	−0.42	0.24	1	0.12	−0.26	0.4	0.62
SAL	0.47	−0.58	−0.25	0.18	0	−0.29	−0.22	−0.18	−0.48	−0.58	−0.6	−0.28	0.5	0.12	1	−0.66	0.23	0.34
SI	−0.29	0.4	0.22	−0.32	−0.02	0.31	0.21	0.1	0.66	0.67	0.74	0.4	−0.59	−0.26	−0.66	1	−0.17	−0.33
SI/N	0.2	−0.58	−0.23	0.47	−0.07	−0.32	−0.17	−0.17	−0.41	−0.77	−0.75	−0.37	0.6	0.4	0.23	−0.17	1	0.65
TEMP	0.37	−0.6	−0.24	0.7	−0.04	−0.34	−0.24	−0.25	−0.31	−0.73	−0.69	−0.39	0.52	0.62	0.34	−0.33	0.65	1

Figure A1.4: Spearman correlation coefficients between environmental variables, sampled every two weeks at Teychan site. $\text{AMO}_{\text{month}}$ = monthly value of the Atlantic Multidecadal Oscillation index, CumDebit = integrated (cumulated) inflow, CumPrec = integrated (cumulated) rainfall, CumRg = integrated (cumulated) irradiance, MeanNAO=mean value of the North Atlantic Oscillation index, MeanVent = integrated wind energy, MES = Suspended Particulate Matter, $\text{NAO}_{\text{month}}$ = monthly value of the North Atlantic Oscillation index, NH4 = NH_4^+, NOx = $NO_2 + NO_3^-$, Ntot = $NH_4^+ + NOx$, PHOS = PO_4^{3-}, P/N=PHOS/Ntot, Rg = daily value of irradiance, SAL = salinity, SI = $\text{Si}(OH)_4$, SI/N = SI/Ntot, TEMP=temperature.

A1.1.6 Comparison between N and Si cycles

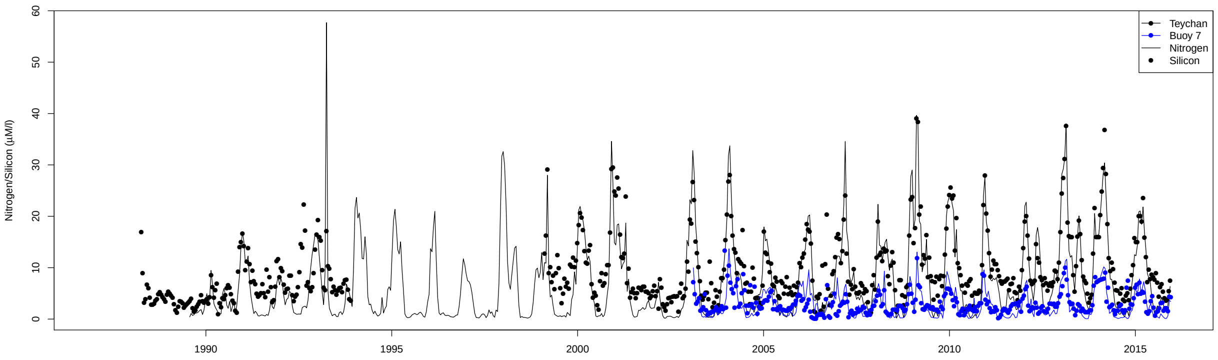


Figure A1.5: Nitrogen (lines) and silicate (dots) water concentrations sampled every two weeks at Teychan (black) and Buoy 7 (blue) sites

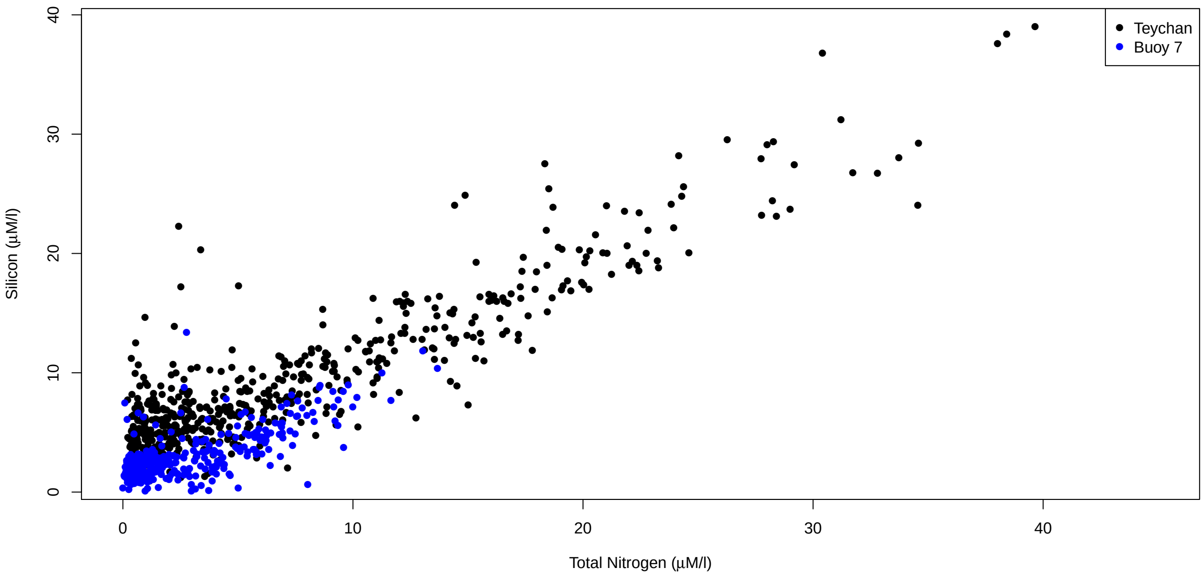
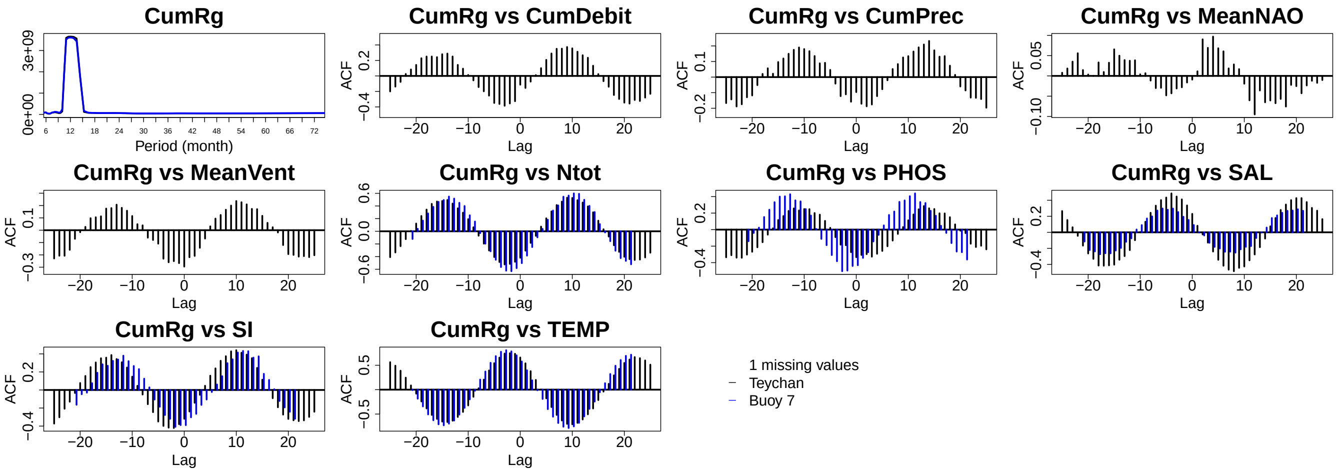
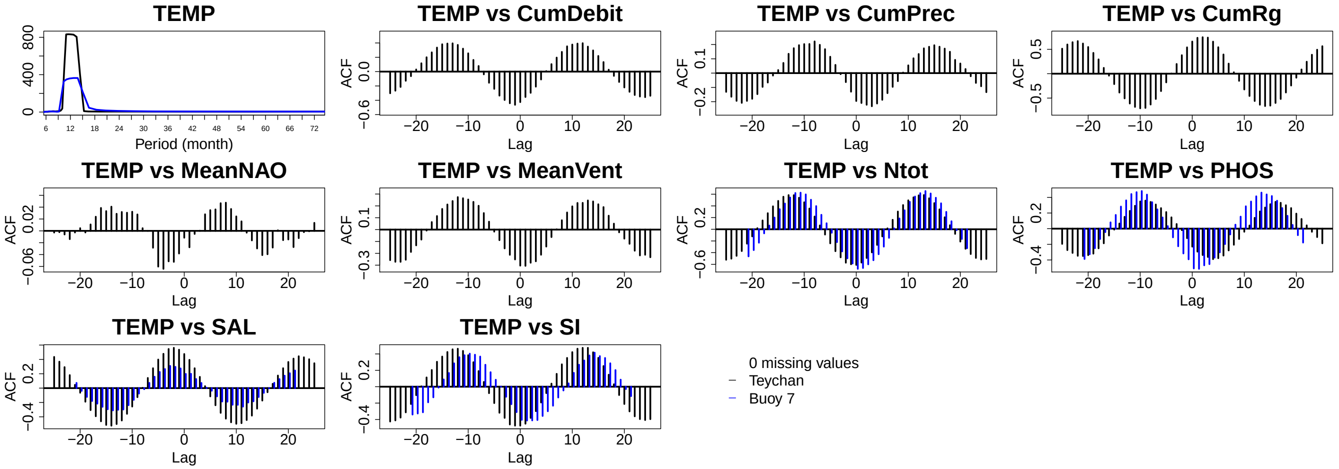


Figure A1.6: Silicate concentration against nitrogen concentration at Teychan (black) and Buoy 7 (blue) sites, sampled every two weeks between 1990 and 2015

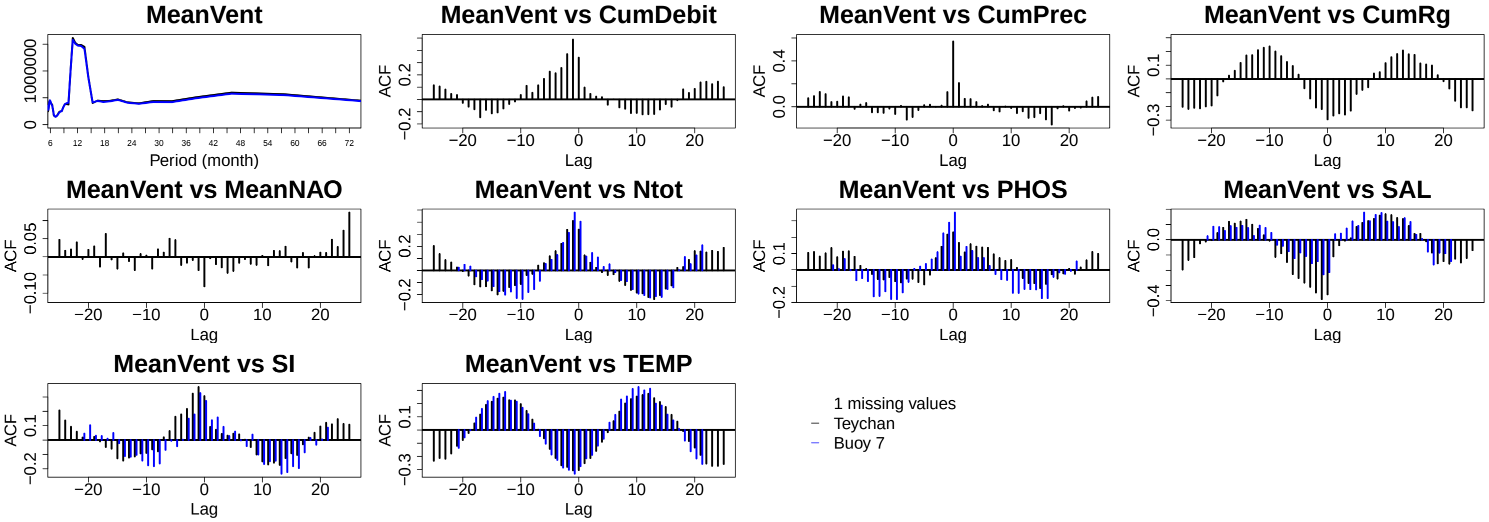
A1.1.7 Spectrum analysis of abiotic variables



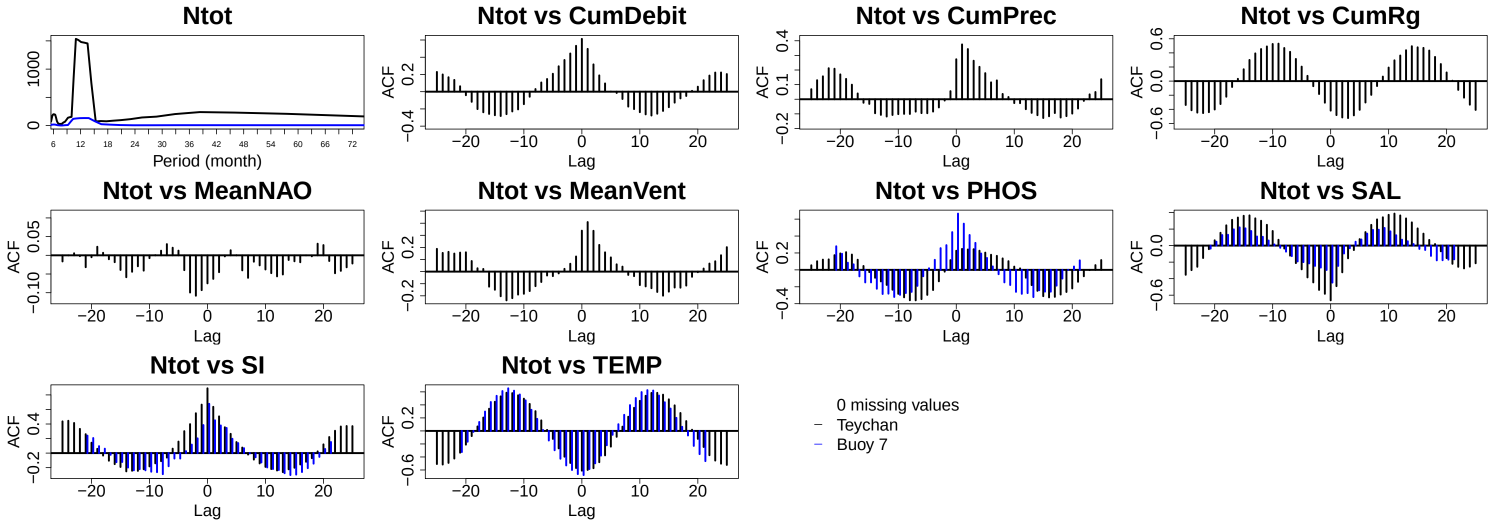
(a) Integrated irradiance



(b) Temperature



(c) Wind energy



(d) Nitrogen

Figure A1.7: Periodogram (first plot, top left) and cross-correlation (remaining plots) between abiotic variables: integrated (cumulated) irradiance (CumRg), water temperature (TEMP), mean wind energy (MeanVent) and total nitrogen content (Ntot). Spectrum analyses are shown for both Teychan (black) and Buoy 7 (blue) sites. Integrated values are taken between two sampling points, i.e. every two week. Wind energy is averaged over 3 days. For other variables (integrated (cumulated) inflow (CumDebit), integrated (cumulated) precipitation (CumPrec), phosphate concentration (PHOS), salinity (SAL), silicate concentration (SI) and mean North Atlantic Oscillation index (MeanNAO)), see Fig. A6.1 in Supplementary Material Appendix 6.

A1.1.8 Half-saturation constants for nutrient uptake

We used recently published half-saturation values for both marine diatoms and dinoflagellates found in Litchman *et al.* (2007). Concentrations were considered saturating when twice superior to 0.65 µM L^{-1}, 1.25 µM L^{-1} and 1.0 µM L^{-1} for P, N and Si, respectively, for diatoms, and 1.4 µM L^{-1} and 7.0 µM L^{-1} for P and N, respectively, for dinoflagellates. We averaged values for cryptophytes from two models (Hood *et al.* 2006; Rigosi *et al.* 2011): saturating values were twice above 1.2 µM L^{-1} and 2.7 µM L^{-1} for N and P, respectively. Based on available literature, nutrient requirements for the euglenophytes could not be so thoroughly assessed: average half-saturation values from Fisher *et al.* (1988) were used for N (2.0 µM L^{-1}) and from Chisholm & Stross (1976) for P (1.4 µM L^{-1}).

A1.1.9 Seasonal component for all variables

We chose to use temperature as the leading seasonal factor, as clearly most abiotic variables were correlated (Fig. A1.4). However, we could detect phase shifts between different variables (Fig A1.8). Irradiance increases earlier than temperature, which implies that the seasonal component would reach its maximum earlier than the one extracted from temperature. There is therefore some rationale for choosing a variable that varies in phase or in opposition to most other abiotic variables. For instance, the comparison with nitrogen shows a phase-shift with temperature close to π (Fig. A1.8 and A1.9): cycle timing remains consistent with data, the only thing that may change in that case is the sign of the coefficient attributed to the seasonal component. Temperature was therefore used instead of irradiance as the seasonal factor (Eq. 2 in main text).

We also attempted to use the `decompose` and `stl` functions in order to extract the same seasonality with a lag (see Fig. A1.13). However, these functions are sensitive to sampling frequencies: with a sampling every other week, the number of samples vary every year, which is not adapted to the way R time series objects are handled. This explains the small shift in Fig. A1.13 between a seasonal component extracted with linear modeling, and similar seasonal components obtained with the `decompose` and `stl` functions.

Finally, we also tried to build a signal averaging the multiyear trends to produce a typical yearly temperature signal from temperature data without forcing a cosine signal. Results were similar enough (Fig A1.14) to keep the first trigonometric formulation (Eq. 2 in main text).

There are divergent arguments regarding the relevance of a dedicated seasonal component extracted from other abiotic variables. On the one hand, it reduces correlations between covariates (Fig. A1.15) and leads to a slight improvement of AICc values for the univariate autoregressive log-linear models (Table 3 in the main text). On the other hand, it does not change the condition index (i.e., the measure of collinearity) of the whole system (Table A1.1). Finally, we chose to keep this component in further equations. Indeed, more than half of the autoregressive studies focusing on planktonic dynamics have an explicit seasonal component, whether it is through a qualitative variable such as the month (Griffiths *et al.* 2015), or a quantitative, sometimes complex value, such as the week, or squared week or day number (Ives *et al.* 1999), or even the fitting of different splines for seasonal covariates (Feng *et al.* 2014). When used, this dedicated variable always have a significant effect (Klug & Cottingham 2001; Hampton *et al.* 2008; Hampton & Schindler 2006; Griffiths *et al.* 2015; Gsell *et al.* 2016). We therefore remained consistent with our model choice philosophy, based on information criteria, that included a seasonal component. Results from the first linear models without a dedicated “season” variable can be found in Tables A1.2 and A1.3.

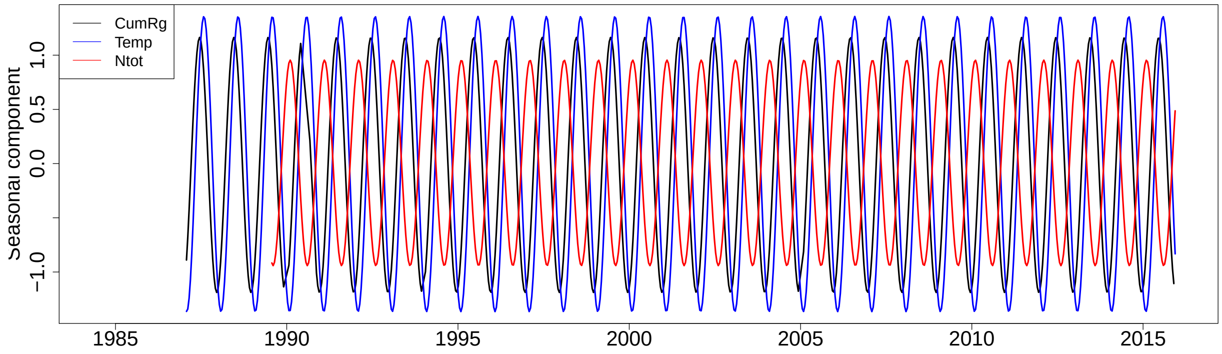


Figure A1.8: Different seasonality components extracted from three abiotic variables (irradiance in black, water temperature in blue and nitrogen content in red), by fitting a linear model to trigonometric functions according to eq. 2 in the main text.

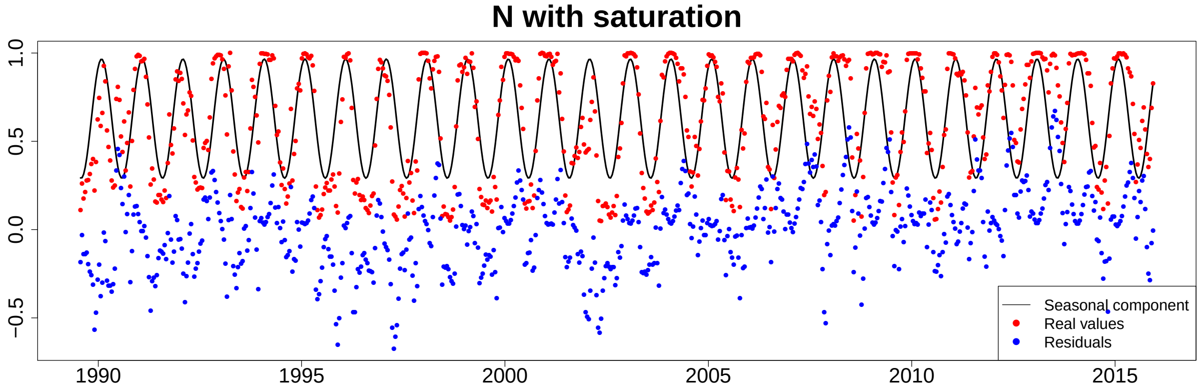


Figure A1.9: Nitrogen water content over time at Teychan site, with a saturating value corresponding to twice the half-saturation value for diatoms, decomposed between a cosine component (described in eq. 2 in the main text) with an annual frequency and its residuals. In further linear models, when seasonality is taken into account with a dedicated variable, only the residuals (in blue) are used to assess the nitrogen effect on planktonic growth rates.

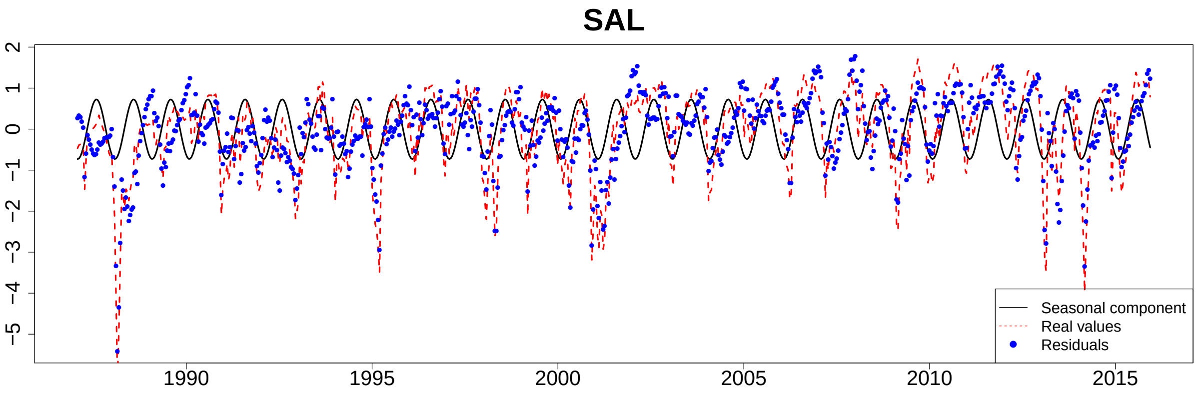


Figure A1.10: Salinity over time at Teychan site decomposed between a cosine component (described in eq. 2 in the main text) with an annual frequency and its residuals. In further linear models, when seasonality is taken into account with a dedicated variable, only the residuals (in blue) are used to assess the salinity effect on planktonic growth rates.

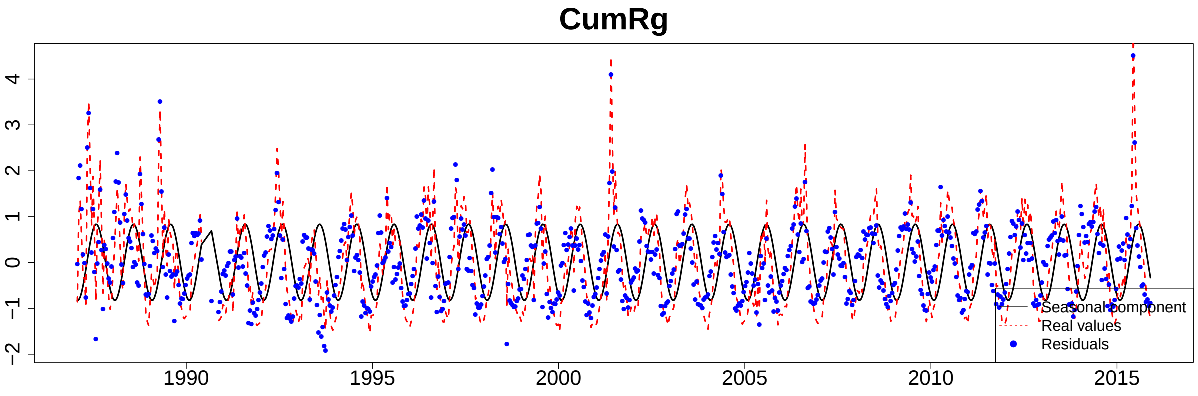


Figure A1.11: Integrated (cumulated) irradiance between two sampling dates (i.e. every other week) at Teychan site, decomposed between a cosine component (described in eq. 2 in the main text) with an annual frequency and its residuals. In further linear models, when seasonality is taken into account with a dedicated variable, only the residuals (in blue) are used to assess the irradiance effect on planktonic growth rates.

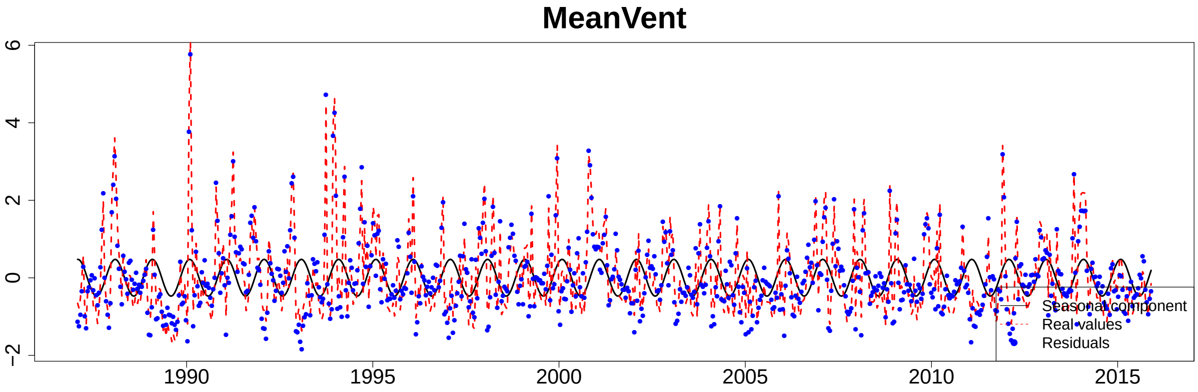


Figure A1.12: Wind energy as squared velocity averaged over 3 days at Teychan site, decomposed between a cosine component (described in eq. 2 in the main text) with an annual frequency and its residuals. In further linear models, when seasonality is taken into account with a dedicated variable, only the residuals (in blue) are used to assess the wind effect on planktonic growth rates.

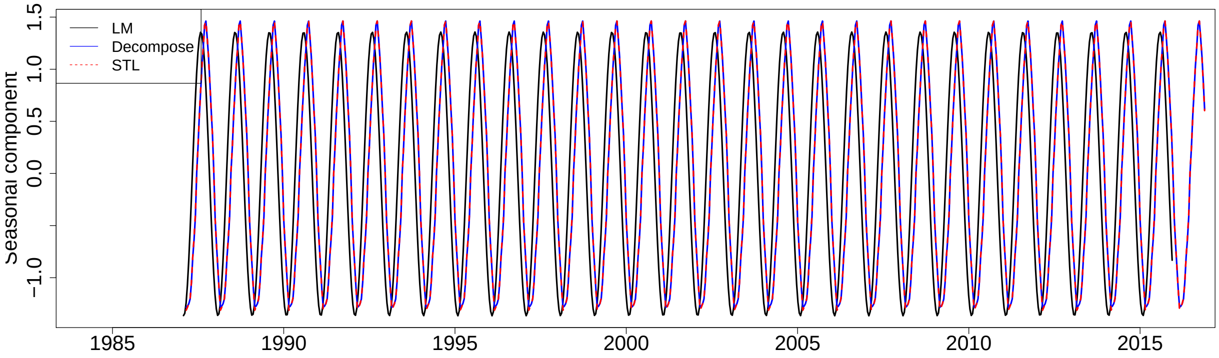


Figure A1.13: Seasonal component extracted from water temperature values, using a linear regression (black) fitted to a cosine component with an annual frequency (eq. 2 in the main text), or with `decompose` (blue) or `stl` (red) methods already available in R

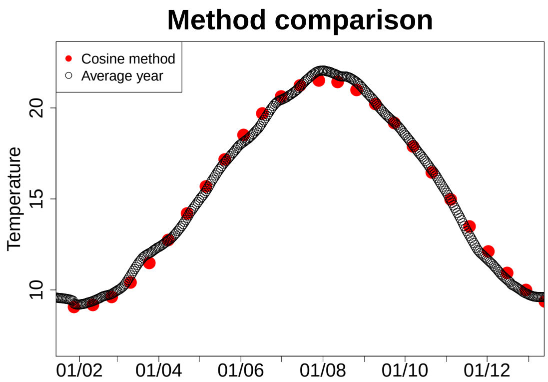


Figure A1.14: Seasonal component extracted from water temperature values, averaged over a year (black), compared to a linear model fitted to a cosine component (red) with an annual frequency (eq. 2 in the main text)

	Season	SAL	CumRg	MeanVent
Season	1	0.54	0.61	−0.33
SAL	−0.06	1	0.11	−0.19
CumRg	−0.01	−0.31	1	−0.32
MeanVent	0.08	−0.03	−0.16	1

Figure A1.15: Spearman correlation coefficients between variables sampled at Teychan that are most significant for phytoplanktonic growth (a dedicated seasonal component -Season-, salinity -SAL-, integrated (cumulated) irradiance - CumRg- and wind energy -MeanVent). Coefficients above the diagonal correspond to raw values while coefficients below the diagonal are shown after removing the seasonality according to eq. 2 in the main text.

Table A1.1: Mean condition index of the equation system relating phytoplanktonic growth to environmental variables, using a physics-only model (with integrated (cumulated) irradiance, salinity and wind energy as explanatory variables), a nutrient-only model (with phosphate and nitrogen concentrations as explanatory variables) and a model taking both sets of variables into account, with and without the extraction of a dedicated seasonal variable

	No season	Season
Nutrient only model	27.8	27.9
Physics only model	28.1	28.1
Full model	28.8	28.3

Table A1.2: AICc for models explaining phytoplankton dynamics using physical variables only (irradiance, wind energy, salinity) and nutrients only (nitrogen and phosphorus concentration) and a model using both variable sets. Composition of planktonic groups is described in Table 1 in the main text.

	Full model	Physics only	Nutrients only
AST	1430	1427	1432
CHA	1708	1716	1771
CRY	1187	1184	1191
EUG	1005	1002	1011
GUI	1268	1270	1268
GYM	1269	1266	1279
LEP	1115	1113	1130
NIT	1564	1561	1573
PRP	1128	1125	1152
PSE	1571	1567	1582
RHI	894	893	895
SKE	804	807	809

Table A1.3: Values of the coefficients and adjusted R^2 from a linear regression of physics-based model explaining phytoplankton dynamics with integrated (cumulated) irradiance, wind energy and salinity. Composition of planktonic groups is described in Table 1 in the main text.

	Irradiance	Wind energy	Salinity	R^2
AST	-0.25	-0.17	-0.10	0.17
CHA	0.31	-0.24	-0.12	0.25
CRY	0.09	0.00	-0.04	0.27
EUG	0.08	-0.08	-0.05	0.16
GUI	0.03	-0.13	0.03	0.17
GYM	0.06	-0.10	0.02	0.19
LEP	0.39	-0.06	0.03	0.24
NIT	0.19	0.00	0.01	0.19
PRP	0.21	-0.04	-0.06	0.22
PSE	-0.09	-0.32	-0.02	0.25
RHI	0.03	-0.10	-0.08	0.23
SKE	0.10	-0.10	-0.12	0.13

A1.2 Biotic variable

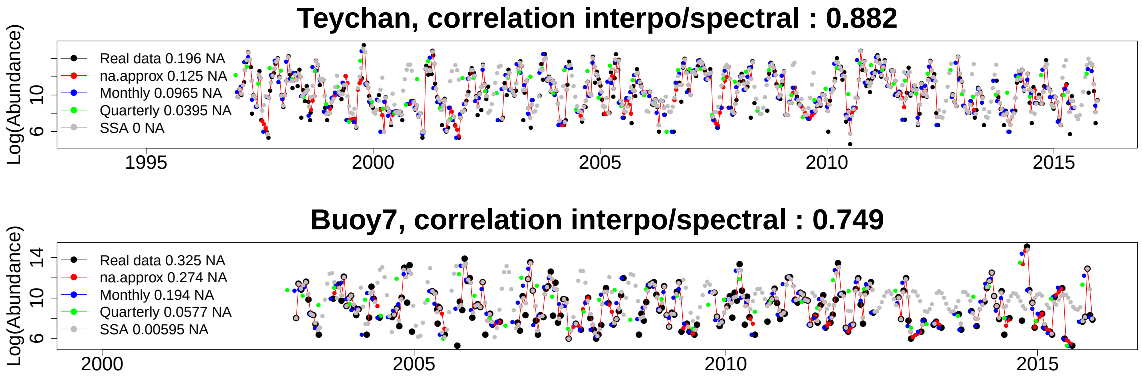
A1.2.1 Missing values

Some zeroes appearing in the time series ("false zeroes") may actually reflect a lack of detection rather a real absence or even Poisson-like sampling of small densities. Usual treatments include binning data into longer periods (first method, as in Hampton *et al.* 2008) or replacing them by a small random value between 0 and the observed minimum of the time series (second method, as done by Hampton & Schindler 2006).

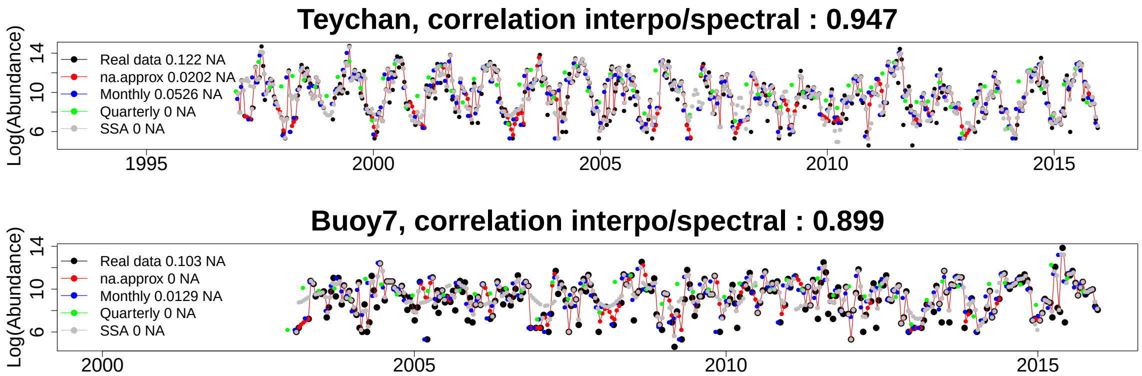
The second method may artificially increase the total variability of the time series while the former may on the contrary decrease it, especially if we use a 2-week time step, and reduce our capacity to detect short-term variations (Vasseur & Gaedke 2007). A third method consists in linearly interpolating the data - which works only for small gaps - (Hampton *et al.* 2008) and more refined methods use spectral analysis to infer the likely missing points (Kondrashov & Ghil 2006). These methods are however still sensitive to a long lack of detection and may introduce regularities which do not exist in the data (see SKE in Supplementary Material Appendix 6: Fig. A6.2(j)).

In Fig. A1.16, we therefore compare time series obtained with different reconstruction methods: linear interpolation between two dates, only replacing values for small gaps, averaging over month or season, or spectrum analysis (Kondrashov & Ghil 2006). Monthly and seasonal averaging are not sufficient to replace all missing values as there can be no observation for certain genera for long periods of time. Linear interpolation between reasonably close dates (no more than 2 consecutive missing values), followed by random sampling between zero and the minimum for the remaining, longer gaps, following Hampton & Schindler (2006), remains the closest to observed dynamics. Nonetheless, we note that Fig. A1.17 shows that spectra can be modified by differences in random draws for some genera, such as AST, EUG, GUI, PRP and RHI. For instance, AST periodicity could be either detected as mostly annual with periods less than 3 months and a biannual component, or could be described with only one period between 12 and 18 months. These discrepancies between spectra may be worth exploring in the future.

Other, more complicated reconstruction methods involve state-space modeling and an observation-error model. Unfortunately, these work best when one knows the estimation error (Knape 2008; Auger-Méthé *et al.* 2016), which is not the case here. We nonetheless know it is far from either Poisson or Binomial, which would make estimating this unknown error very difficult.

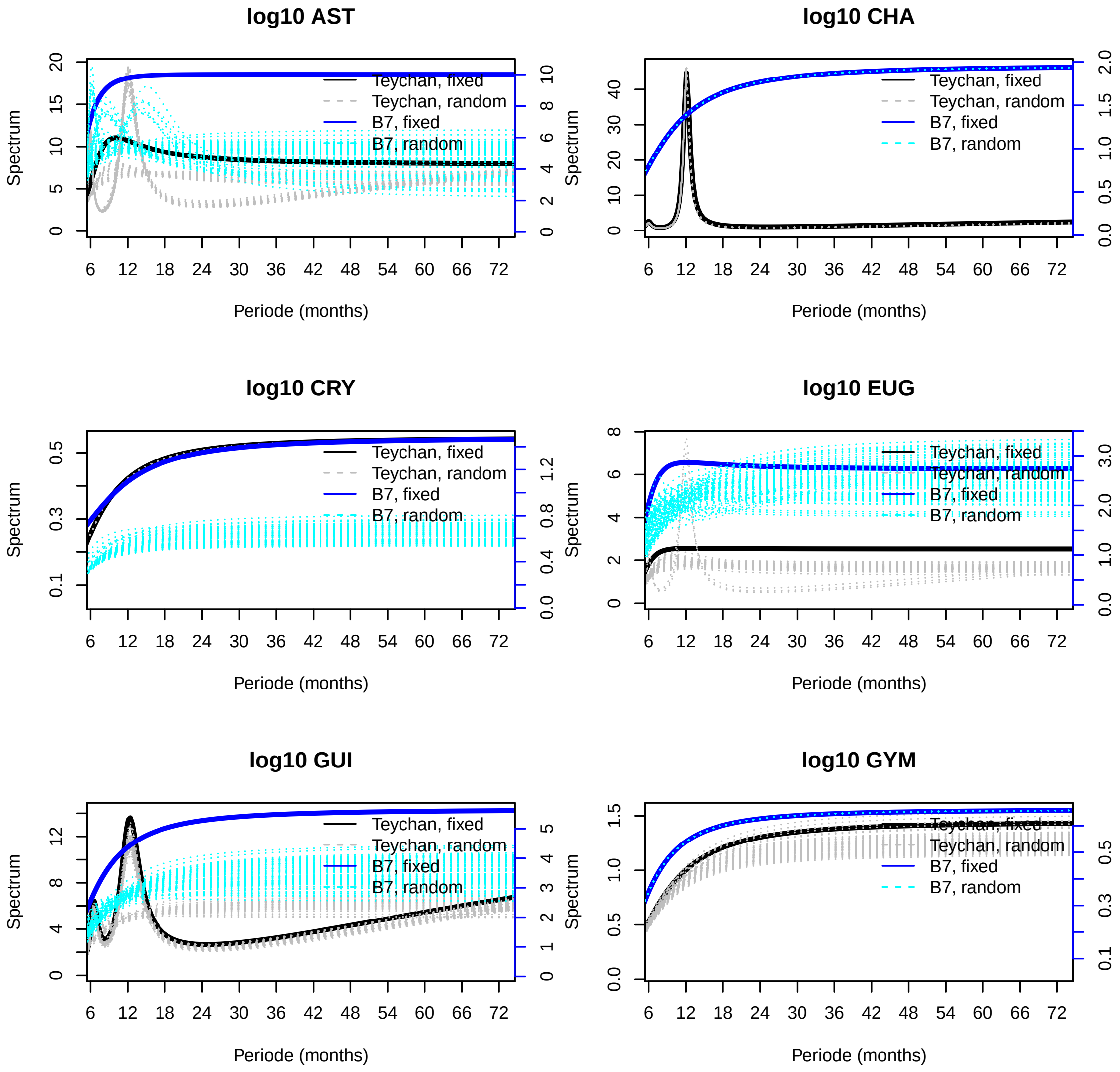


(a) AST

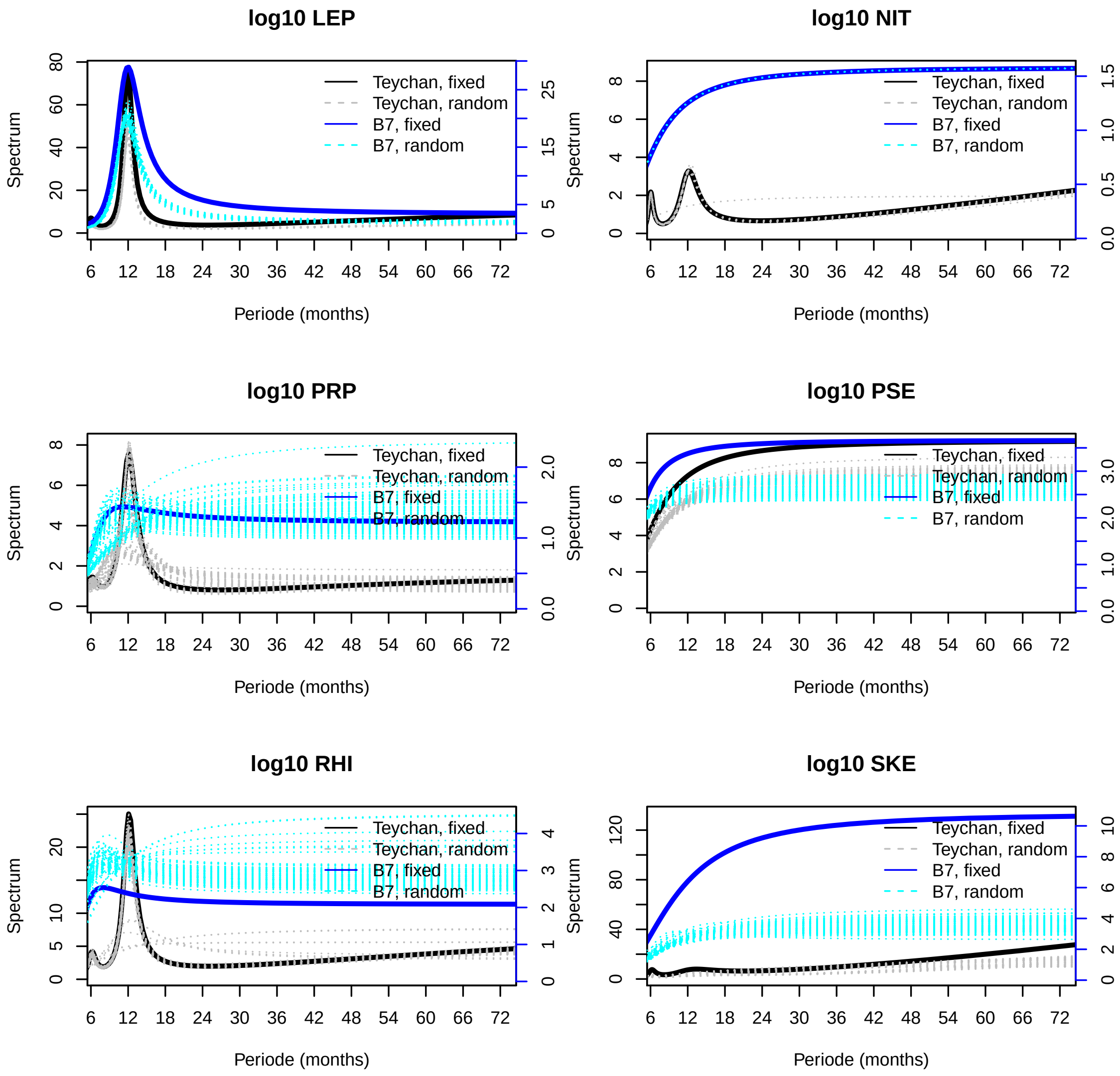


(b) CHA

Figure A1.16: Comparison between different reconstruction methods for the two main genera (*Asterionellopsis* and *Chaetoceros*) considered in our models. Red dots correspond to a linear interpolation between values separated by less than a month, which is the method we finally used in the analysis. Monthly (blue) and quarterly (green) values correspond to average values over a month or a season, respectively (described as the first method in the text above). Grey dots correspond to Singular Spectral Analysis, relying on Kondrashov & Ghil (2006) methods to estimate missing values from nonparametric spectral methods. Composition of planktonic groups is described in Table 1 in the main text. For other groups of genera, see Fig. A6.2 in Supplementary Material Appendix 6.


log10 AST
log10 CHA
log10 CRY
log10 EUG
log10 GUI
log10 GYM
Spectrum
Periode (months)
6
12
18
24
30
36
42
48
54
60
66
72
Teychan, fixed
Teychan, random
B7, fixed
B7, random

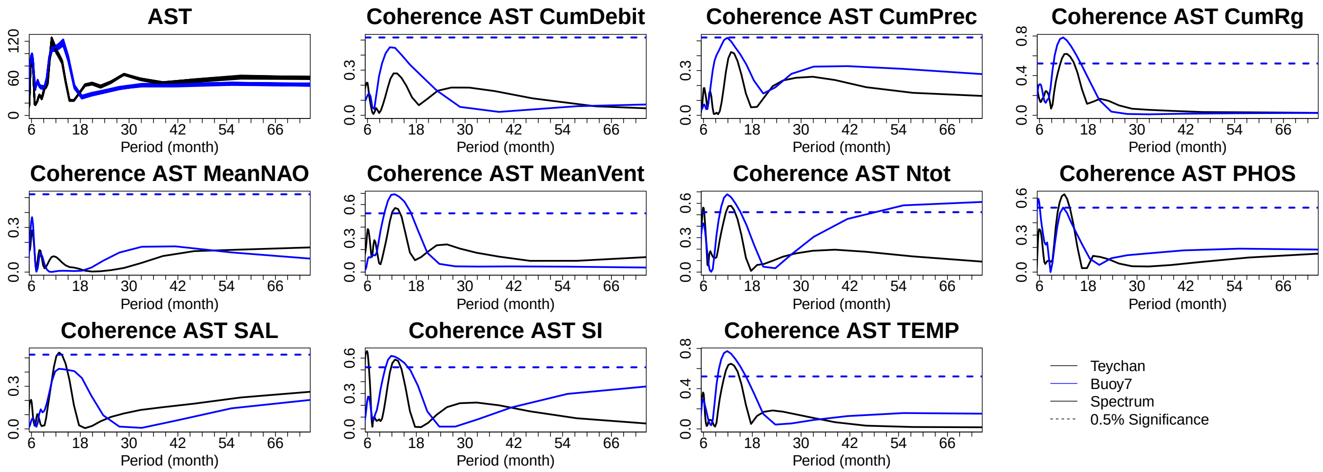
(a)



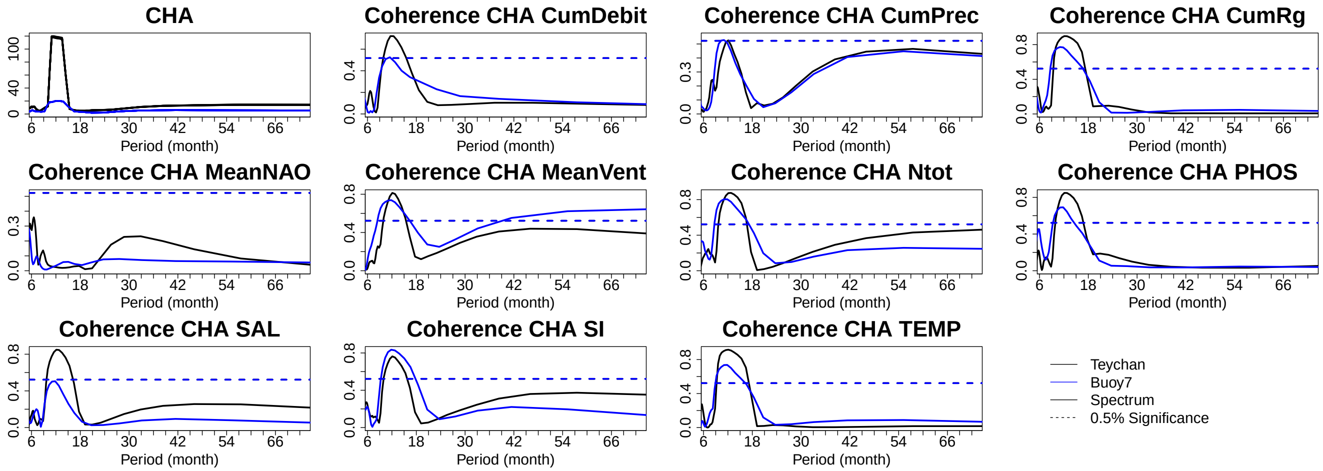
(b)

Figure A1.17: Periodogram for plankton genera log abundance at both study sites (Teychan, in black and grey, and Buoy 7, in blue and cyan), where zeroes have been replaced by either a fixed minimal value corresponding to the minimal detection threshold (plain, darker line) or a random draw between zero and the minimum values observed for the time series (dashed, lighter lines). In the second case, 100 times series are generated at random. Composition of planktonic groups is described in Table 1 in the main text. Buoy 7 site is characterized by shorter time series, which leads to a decreased ability to detect periodicity with the same algorithm, and differing spectra.

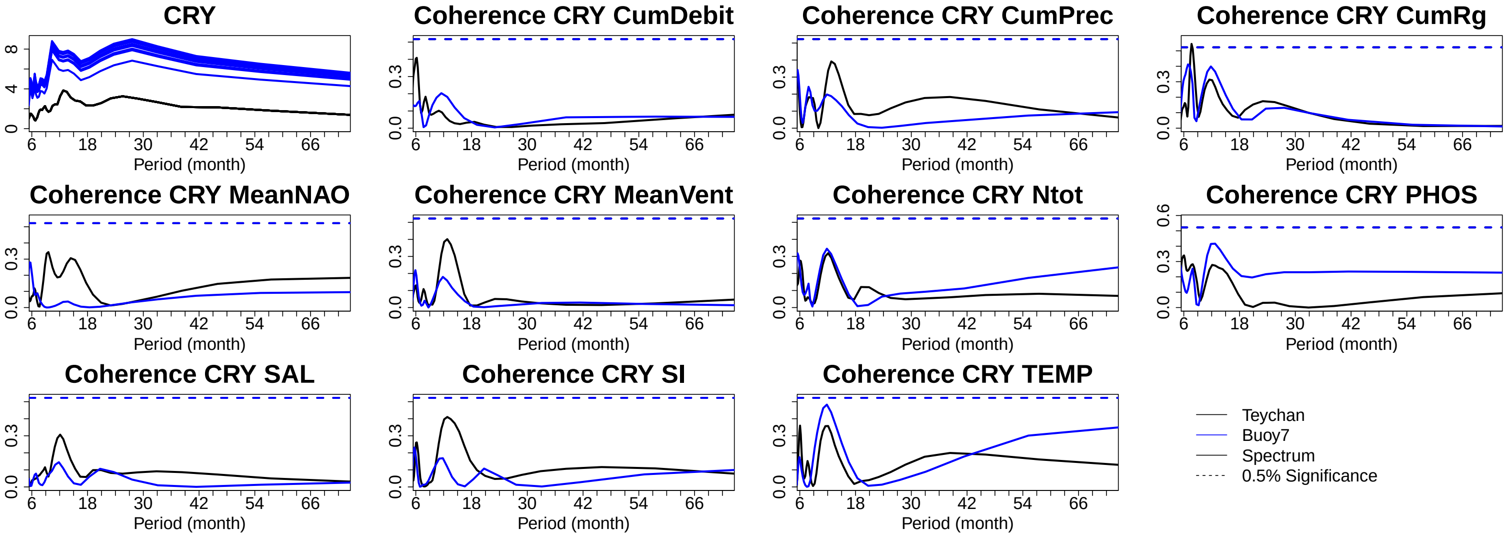
A1.2.2 Cross-spectrum (coherence) exploratory analysis between biotic and abiotic variables



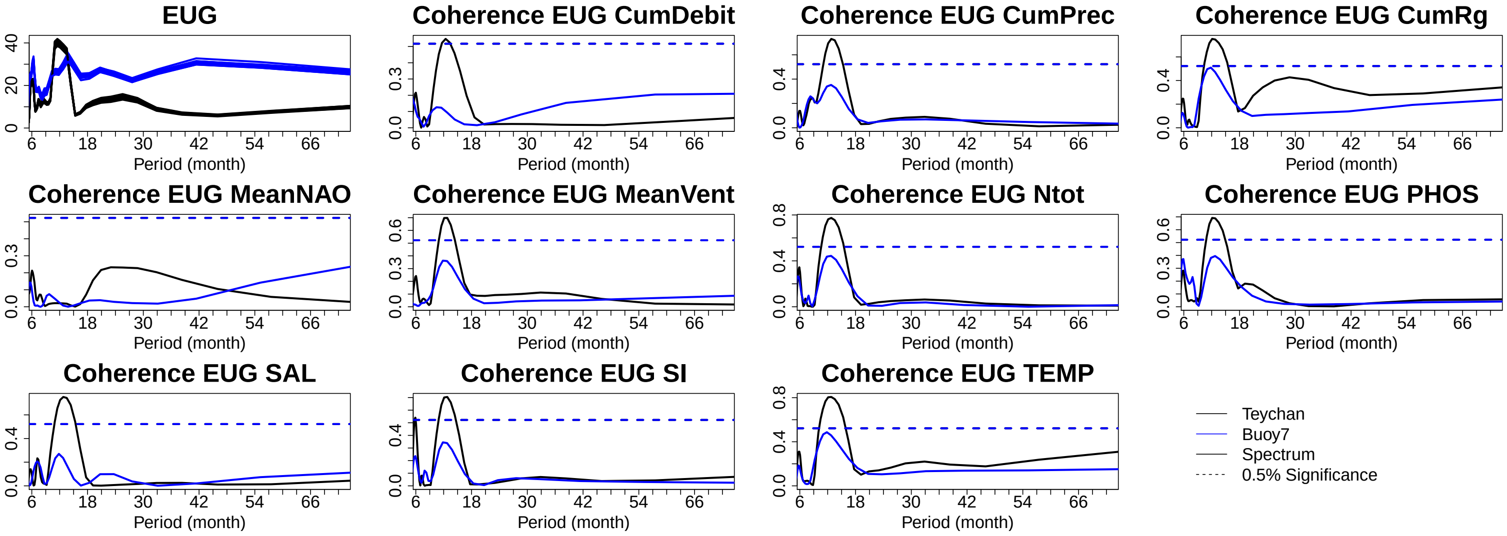
(a) AST



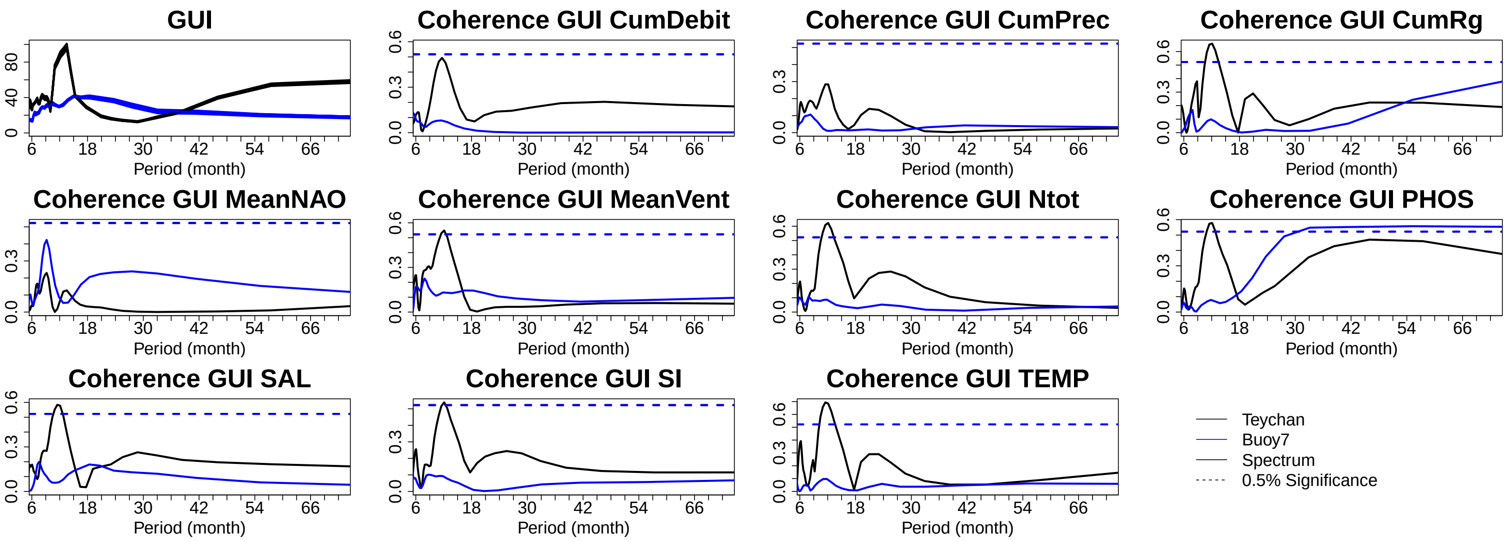
(b) CHA


CRY
Coherence CRY CumDebit
Coherence CRY CumPrec
Coherence CRY CumRg
Coherence CRY MeanNAO
Coherence CRY MeanVent
Coherence CRY Ntot
Coherence CRY PHOS
Coherence CRY SAL
Coherence CRY SI
Coherence CRY TEMP
0
4
8
0.0
0.3
0.6
6
18
30
42
54
66
Period (month)
Teychan
Buoy7
Spectrum
0.5% Significance

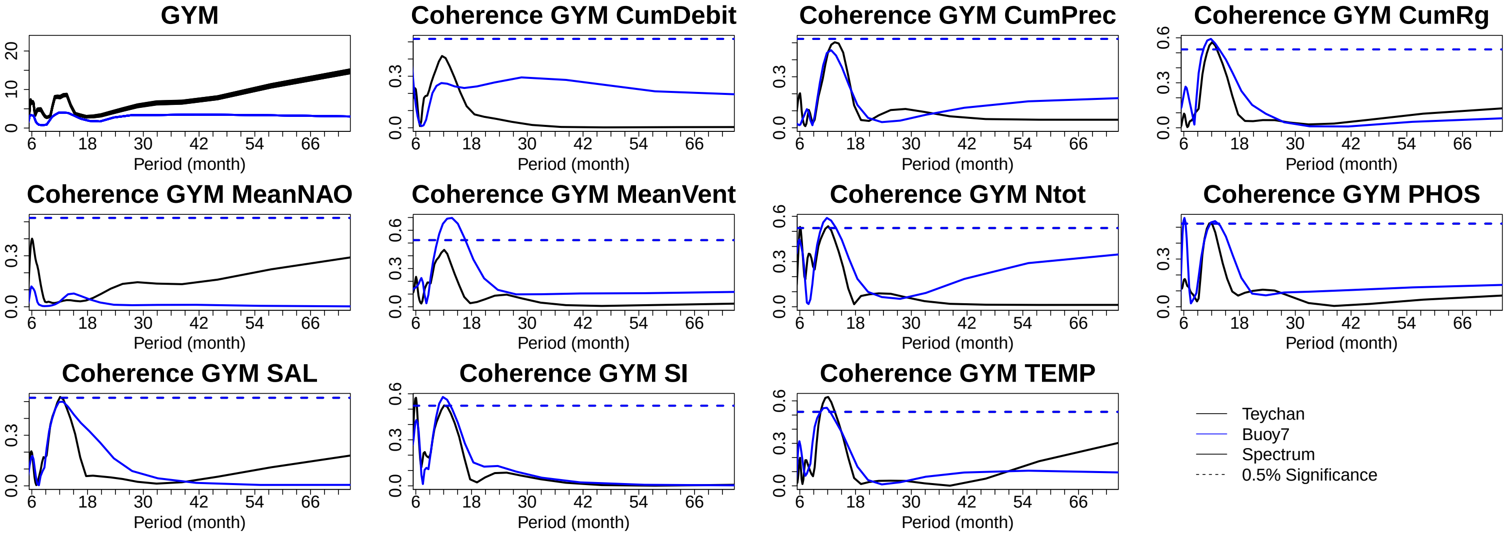
(c) CRY


EUG
Coherence EUG CumDebit
Coherence EUG CumPrec
Coherence EUG CumRg
Coherence EUG MeanNAO
Coherence EUG MeanVent
Coherence EUG Ntot
Coherence EUG PHOS
Coherence EUG SAL
Coherence EUG SI
Coherence EUG TEMP
0
20
40
0.0
0.3
0.4
0.6
0.8
6
18
30
42
54
66
Period (month)
Teychan
Buoy7
Spectrum
0.5% Significance

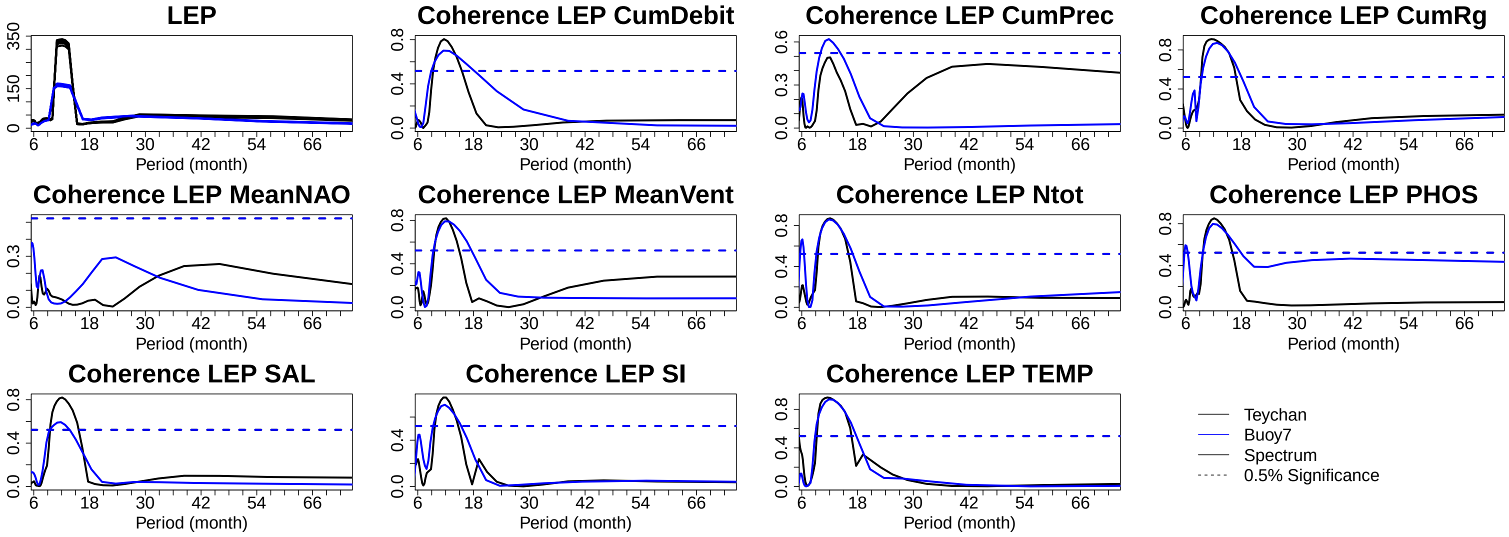
(d) EUG


GUI
Coherence GUI CumDebit
Coherence GUI CumPrec
Coherence GUI CumRg
Coherence GUI MeanNAO
Coherence GUI MeanVent
Coherence GUI Ntot
Coherence GUI PHOS
Coherence GUI SAL
Coherence GUI SI
Coherence GUI TEMP
Period (month)
6
18
30
42
54
66
0
40
80
0.0
0.3
0.6
Teychan
Buoy7
Spectrum
0.5% Significance

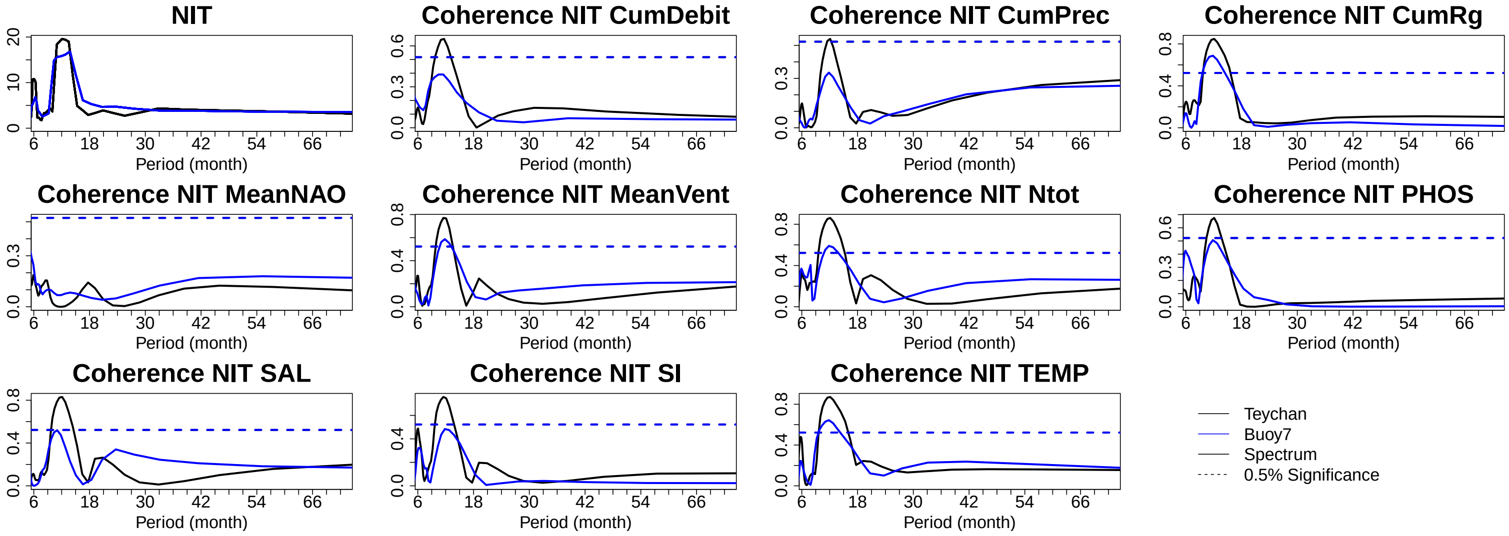
(e) GUI


GYM
Coherence GYM CumDebit
Coherence GYM CumPrec
Coherence GYM CumRg
Coherence GYM MeanNAO
Coherence GYM MeanVent
Coherence GYM Ntot
Coherence GYM PHOS
Coherence GYM SAL
Coherence GYM SI
Coherence GYM TEMP
Period (month)
6
18
30
42
54
66
0
10
20
0.0
0.3
0.6
Teychan
Buoy7
Spectrum
0.5% Significance

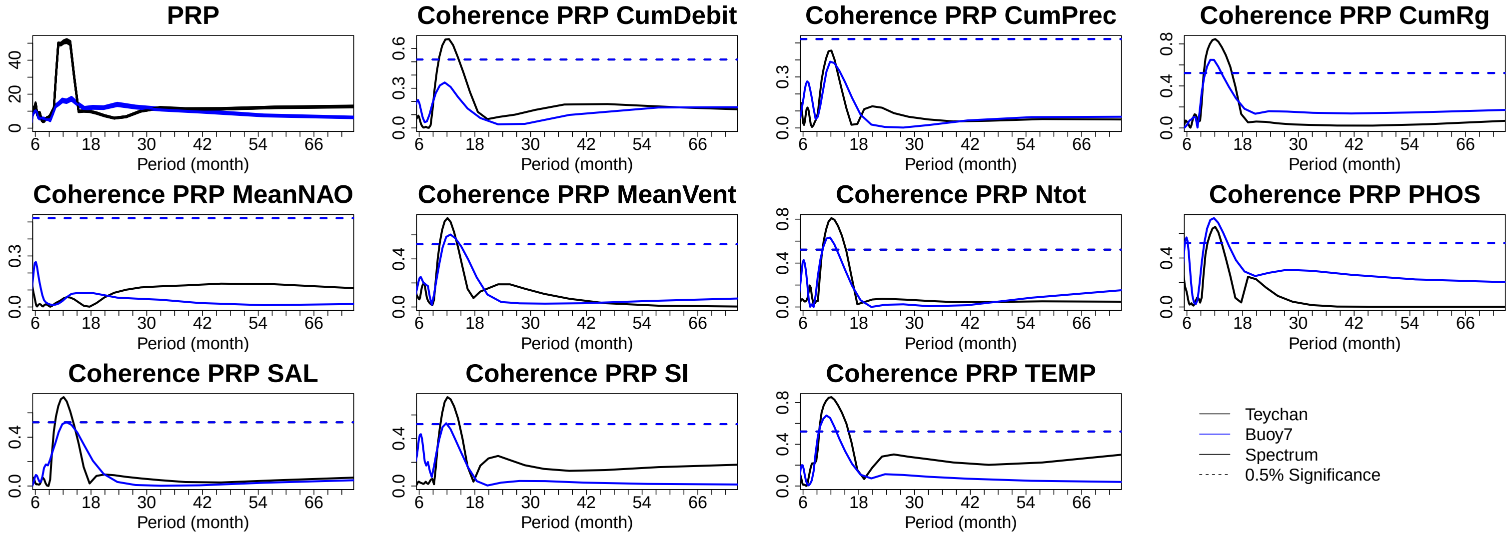
(f) GYM


LEP
Coherence LEP CumDebit
Coherence LEP CumPrec
Coherence LEP CumRg
Coherence LEP MeanNAO
Coherence LEP MeanVent
Coherence LEP Ntot
Coherence LEP PHOS
Coherence LEP SAL
Coherence LEP SI
Coherence LEP TEMP
Period (month)
6 18 30 42 54 66
Teychan
Buoy7
Spectrum
0.5% Significance

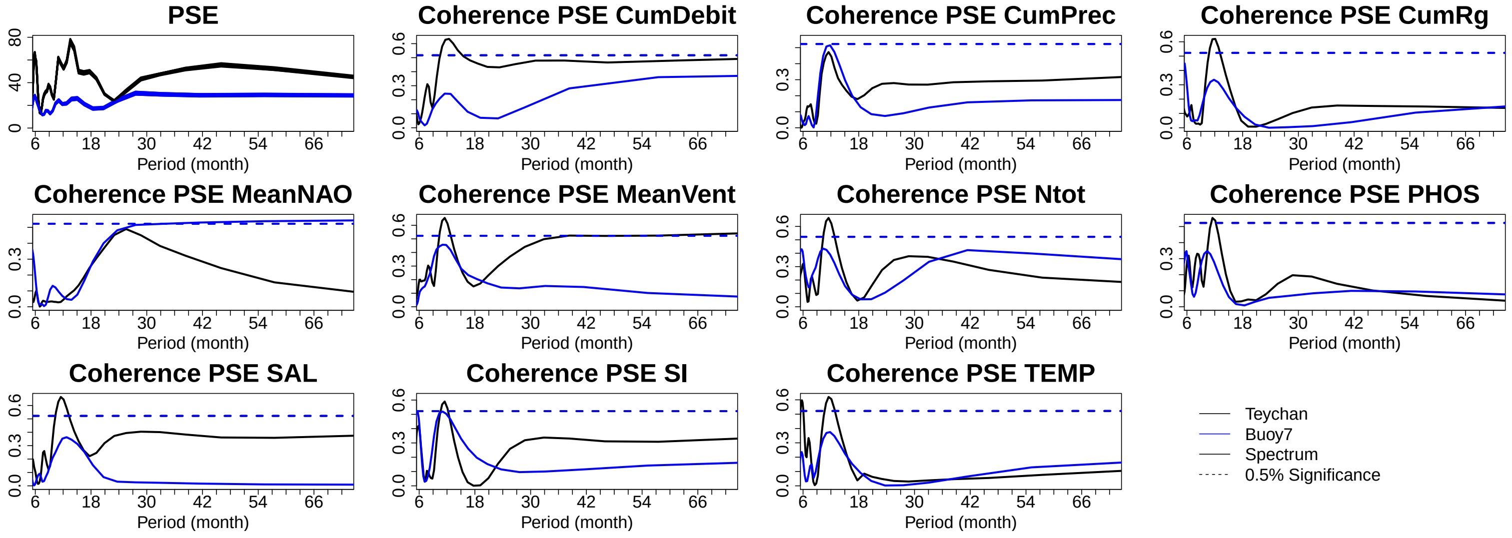
(g) LEP


NIT
Coherence NIT CumDebit
Coherence NIT CumPrec
Coherence NIT CumRg
Coherence NIT MeanNAO
Coherence NIT MeanVent
Coherence NIT Ntot
Coherence NIT PHOS
Coherence NIT SAL
Coherence NIT SI
Coherence NIT TEMP
Period (month)
6 18 30 42 54 66
Teychan
Buoy7
Spectrum
0.5% Significance

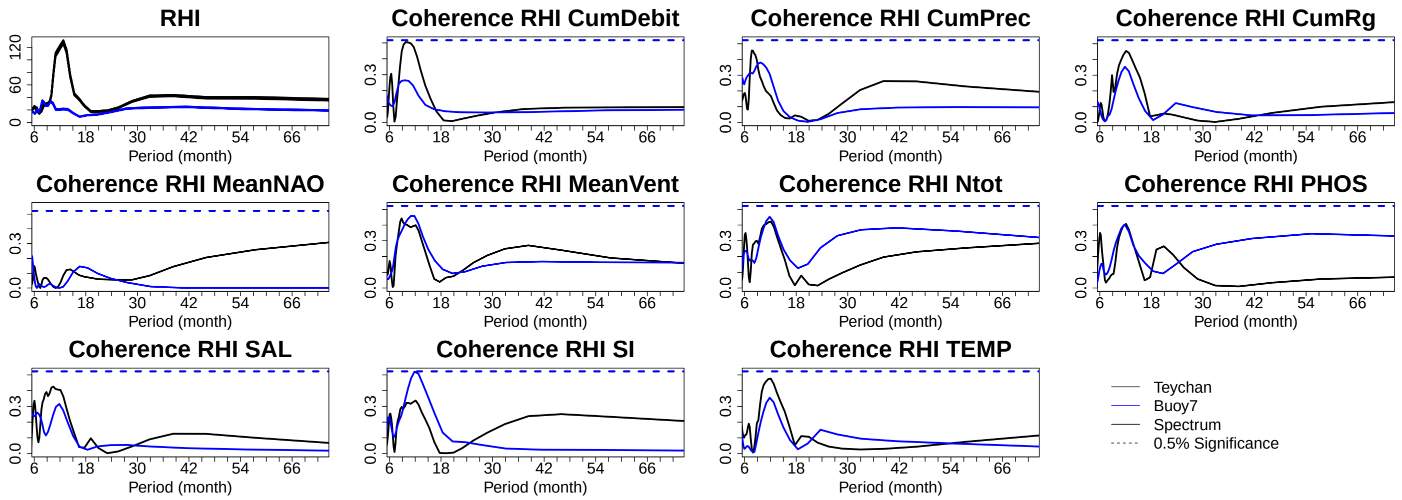
(h) NIT


PRP
Coherence PRP CumDebit
Coherence PRP CumPrec
Coherence PRP CumRg
Coherence PRP MeanNAO
Coherence PRP MeanVent
Coherence PRP Ntot
Coherence PRP PHOS
Coherence PRP SAL
Coherence PRP SI
Coherence PRP TEMP
0
20
40
0.0
0.3
0.6
0.4
0.8
6
18
30
42
54
66
Period (month)
Teychan
Buoy7
Spectrum
0.5% Significance

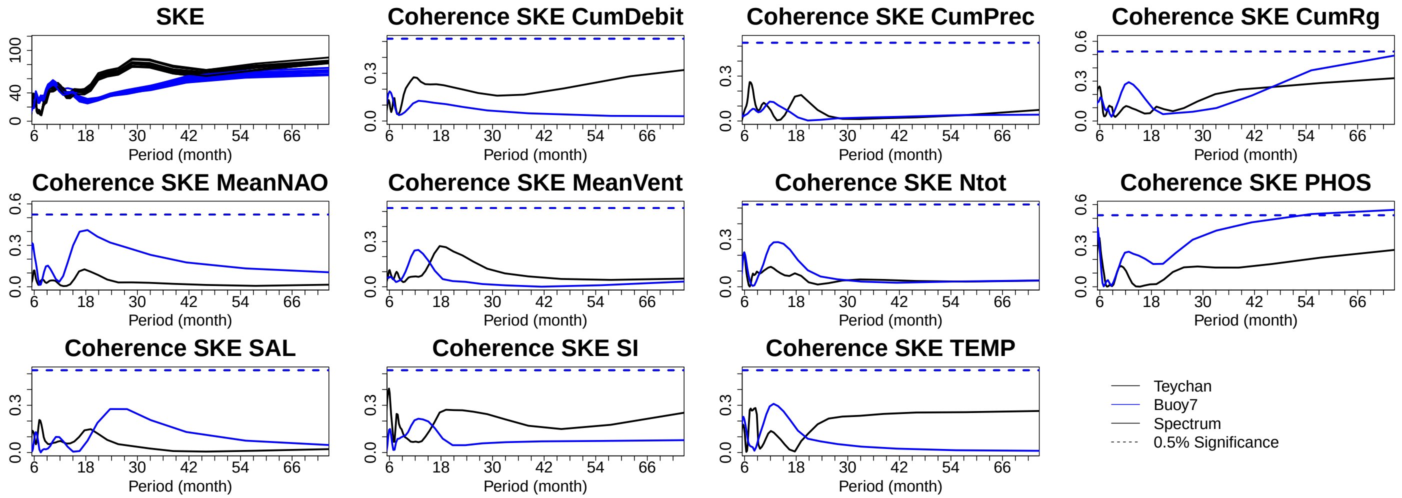
(k) PRP


PSE
Coherence PSE CumDebit
Coherence PSE CumPrec
Coherence PSE CumRg
Coherence PSE MeanNAO
Coherence PSE MeanVent
Coherence PSE Ntot
Coherence PSE PHOS
Coherence PSE SAL
Coherence PSE SI
Coherence PSE TEMP
0
40
80
0.0
0.3
0.6
6
18
30
42
54
66
Period (month)
Teychan
Buoy7
Spectrum
0.5% Significance

(l) PSE



(m) RHI



(n) SKE

Figure A1.18: Periodogram (first plot, top left) and coherence plots (remaining plots), corresponding to correlations in the spectral domain, between each planktonic groups and abiotic variables: integrated (cumulated) inflow (CumDebit), integrated (cumulated) precipitation (CumPrec), integrated (cumulated) irradiance (CumRg), mean North Atlantic Oscillation index (MeanNAO), mean wind energy (MeanVent), total nitrogen content (Ntot), phosphate concentration (PHOS), salinity (SAL), silicate concentration (SI) and water temperature (TEMP). Spectrum analyses are shown for both Teychan (black) and Buoy 7 (blue) sites. Integrated values are taken between two sampling points, i.e. every two weeks. Wind energy is averaged over 3 days. Spectrum analyses are shown for both Teychan (black) and Buoy 7 (blue) sites. Coherence is significant when plain lines are above the 0.5% threshold plotted as a dashed line. Composition of planktonic groups is described in Table 1 in the main

References

Aminot, A. & Kérouel, R. (2004). *Hydrologie des écosystèmes marins.* Quae edn.

Aminot, A. & Kérouel, R. (2007). *Dosage automatique des nutriments dans les eaux marines.* Quae edn. France.

Auger-Méthé, M., Field, C., Albertsen, C.M., Derocher, A.E., Lewis, M.A., Jonsen, I.D. & Mills Flemming, J. (2016). State-space models' dirty little secrets: even simple linear Gaussian models can have estimation problems. *Scientific Reports*, 6, 26677.

Chisholm, S. & Stross, R. (1976). Phosphate uptake kinetics in *Euglena gracilis* (Z) (Euglenophyceae) grown in light/dark cycles. II Phased PO4-limited cultures. *Journal of Phycology*, 12, 217–222.

Cloern, J.E., Foster, S.Q. & Kleckner, A.E. (2014). Phytoplankton primary production in the world's estuarine-coastal ecosystems. *Biogeosciences*, 11, 2477–2501.

David, V., Ryckaert, M., Karpytchev, M., Bacher, C., Arnaudeau, V., Vidal, N., Maurer, D. & Niquil, N. (2012). Spatial and long-term changes in the functional and structural phytoplankton communities along the French Atlantic coast. *Estuarine, Coastal and Shelf Science*, 108, 37–51.

Deborde, J., Anschutz, P., Auby, I., Glé, C., Commarieu, M.V., Maurer, D., Lecroart, P. & Abril, G. (2008). Role of tidal pumping on nutrient cycling in a temperate lagoon (Arcachon Bay, France). *Marine Chemistry*, 109, 98–114.

Feng, J., Stige, L., Durant, J., Hessen, D., Zhu, L., Hjermann, D., Llope, M. & Stenseth, N. (2014). Large-scale season-dependent effects of temperature and zooplankton on phytoplankton in the North Atlantic. *Marine Ecology Progress Series*, 502, 25–37.

Fisher, T., Harding, L., Stanley, D. & Ward, L. (1988). Phytoplankton, nutrients and turbidity in the Cheesapeake, Delaware, and Hudson Estuaries. *Estuarine, Coastal and Shelf Science*, 27, 61–93.

Glé, C. (2007). *Structure et dynamique des communautés microbiennes autotrophes et production primaire planctonique dans une lagune côtière macrotidale, le Bassin d'Arcachon. Facteurs de contrôle de type bottom-up.* Ph.D. thesis, Université de Bordeaux I, Bordeaux, France.

Glé, C., Del Amo, Y., Bec, B., Sautour, B., Froidefond, J.M., Gohin, F., Maurer, D., Plus, M., Laborde, P. & Chardy, P. (2007). Typology of environmental conditions at the onset of winter phytoplankton blooms in a shallow macrotidal coastal ecosystem, Arcachon Bay (France). *Journal of Plankton Research*, 29, 999–1014.

Glé, C., Del Amo, Y., Sautour, B., Laborde, P. & Chardy, P. (2008). Variability of nutrients and phytoplankton primary production in a shallow macrotidal coastal ecosystem (Arcachon Bay, France). *Estuarine, Coastal and Shelf Science*, 76, 642–656.

Griffiths, J.R., Hajdu, S., Downing, A.S., Hjerne, O., Larsson, U. & Winder, M. (2015). Phytoplankton community interactions and environmental sensitivity in coastal and offshore habitats. *Oikos*, 125, 1134–1143.

Gsell, A.S., Özkundakci, D., Hébert, M.P. & Adrian, R. (2016). Quantifying change in pelagic plankton network stability and topology based on empirical long-term data. *Ecological Indicators*, 65, 76–88.

Hampton, S.E., Izmest'Eva, L.R., Moore, M.V., Katz, S.L., Dennis, B. & Silow, E.A. (2008). Sixty years of environmental change in the world's largest freshwater lake - Lake Baikal, Siberia. *Global Change Biology*, 14, 1947–1958.

Hampton, S.E. & Schindler, D.E. (2006). Empirical evaluation of observation scale effects in community time series. *Oikos*, 113, 424–439.

Hood, R.R., Zhang, X., Glibert, P.M., Roman, M.R. & Stoecker, D.K. (2006). Modeling the influence of nutrients, turbulence and grazing on *Pfiesteria* population dynamics. *Harmful Algae*, 5, 459–479.

Ives, A.R., Carpenter, S.R. & Dennis, B. (1999). Community interaction webs and zooplankton responses to planktivory manipulations. *Ecology*, 80, 1405–1421.

Klug, J.L. & Cottingham, K.L. (2001). Interactions among environmental drivers: Community responses to changing nutrients and dissolved organic carbon. *Ecology*, 82, 3390–3403.

Knape, J. (2008). Estimability of density dependence in models of time series data. *Ecology*, 89, 2994–3000.

Kondrashov, D. & Ghil, M. (2006). Spatio-temporal filling of missing points in geophysical data sets. *Nonlinear Processes in Geophysics*, 13, 151–159.

Litchman, E., Klausmeier, C.A., Schofield, O.M. & Falkowski, P.G. (2007). The role of functional traits and trade-offs in structuring phytoplankton communities: scaling from cellular to ecosystem level. *Ecology Letters*, 10, 1170–1181.

Nixon, S.W. (1995). Coastal marine eutrophication: a definition, social causes, and future concerns. *Ophelia*, 41, 199–219.

Plus, M., Auby, I., Maurer, D., Trut, G., Del Amo, Y., Dumas, F. & Thouvenin, B. (2015). Phytoplankton versus macrophyte contribution to primary production and biogeochemical cycles of a coastal mesotidal system. A modelling approach. *Estuarine, Coastal and Shelf Science*, 165, 52–60.

Rigosi, A., Marcé, R., Escot, C. & Rueda, F.J. (2011). A calibration strategy for dynamic succession models including several phytoplankton groups. *Environmental Modelling & Software*, 26, 697–710.

Utermöhl, H. (1958). Zur Vervollkommnung der quantitativen Phytoplankton-Methodik. *Mitt. int. Ver. theor. angew. Limnol.*, 9.

Vasseur, D.A. & Gaedke, U. (2007). Spectral analysis unmasks synchronous and compensatory dynamics in plankton communities. *Ecology*, 88, 2058–2071.

Appendix 2. Autoregressive models

A2.1 Single-species models

In this section, we demonstrate the log-linearity of the relationships between population growth rates and population density (Fig. A2.1). We also present all residual diagnostic plots for linear autoregressive models (Fig. A2.3(a) and following). They show a relative conformity to the log-linear assumption.

A2.1.1 Log-linear, Gompertz model

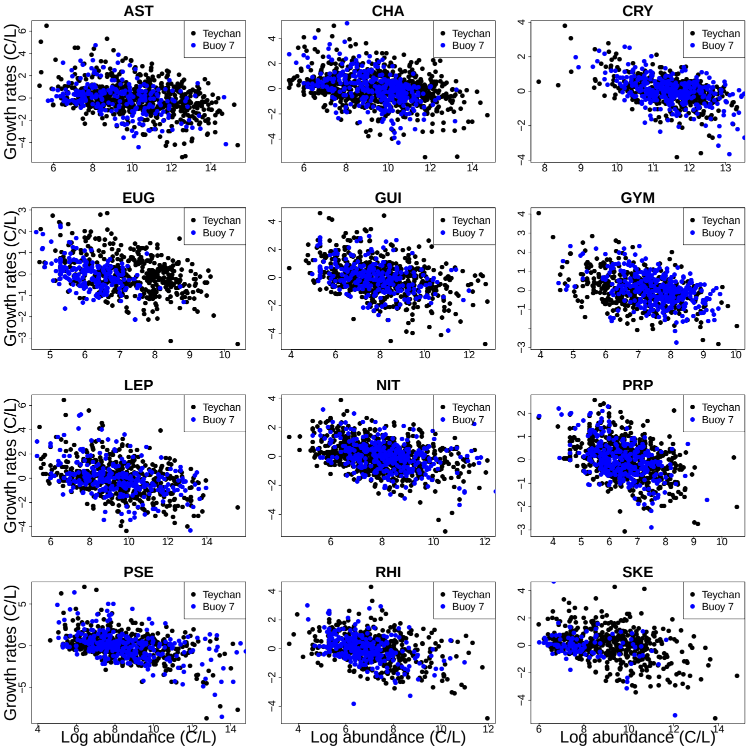


Figure A2.1: Growth rates versus log abundance (in cells per liter) for different planktonic groups, described in Table 1 in the main text.

A2.1.2 Log-linear, Ricker model

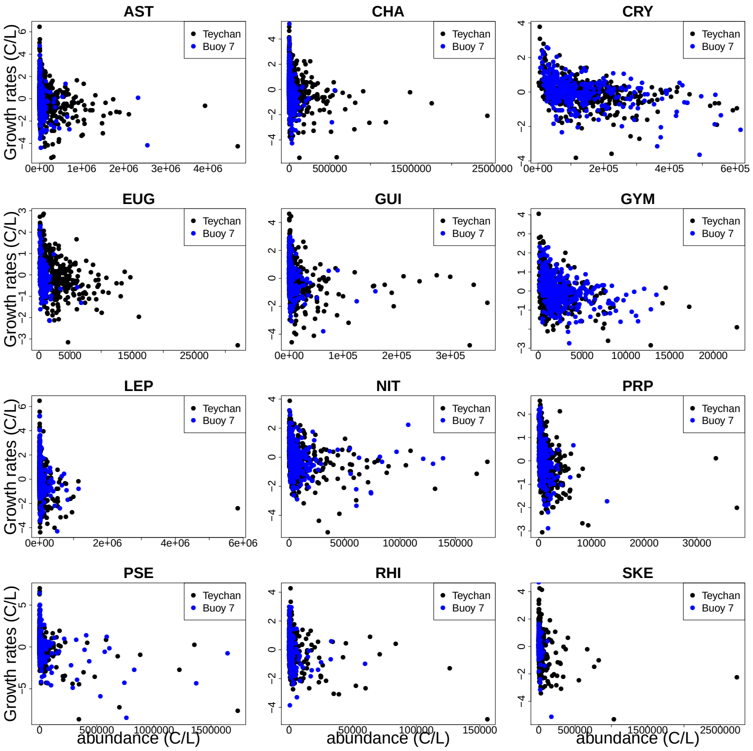


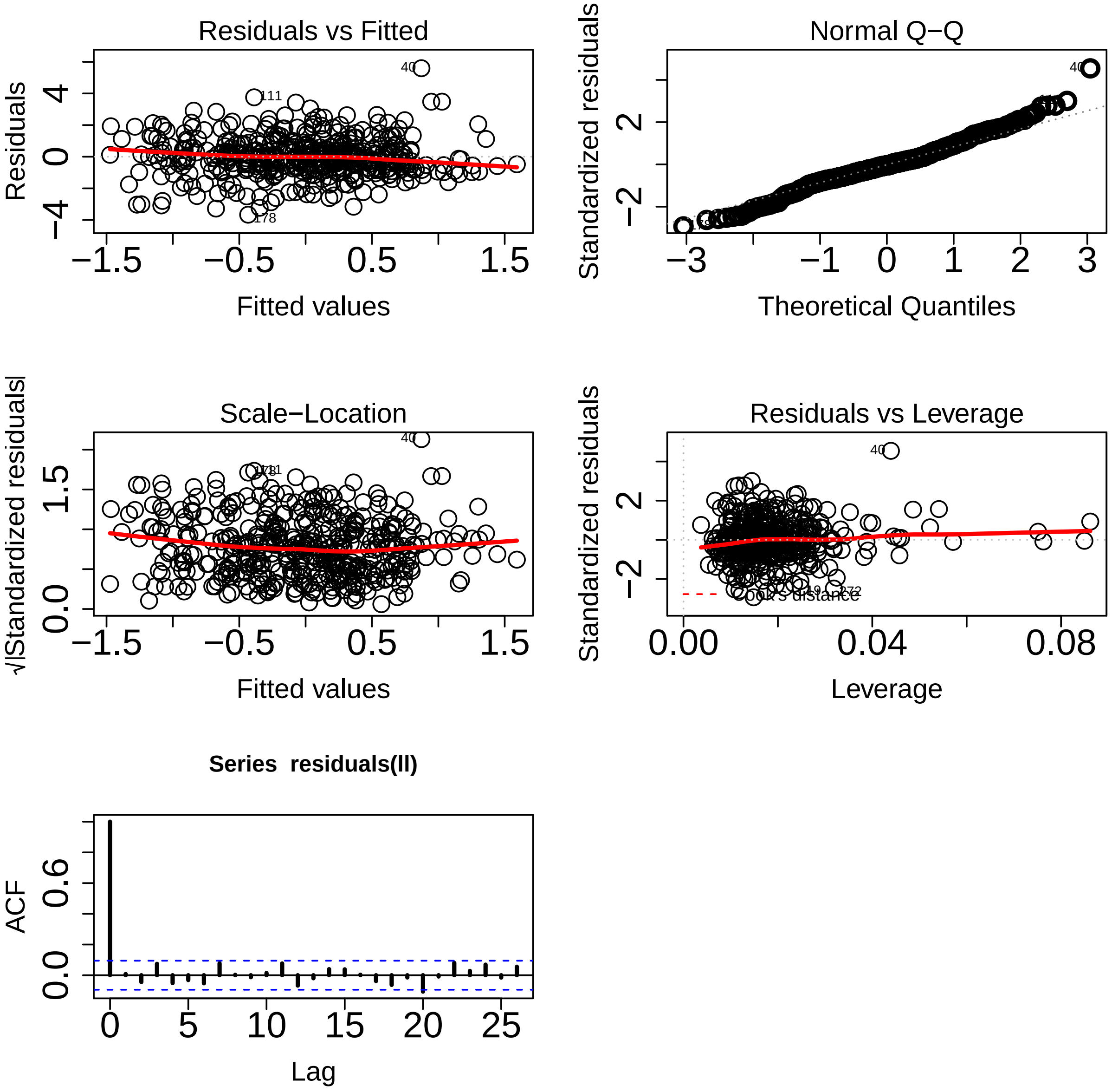
Figure A2.2: Growth rates versus raw abundance (in cells per liter) for different planktonic groups, described in Table 1 in the main text. The L-shaped plots demonstrate that the Ricker model does not fit the data.

A2.1.3 Lag order in single-species autoregressive model

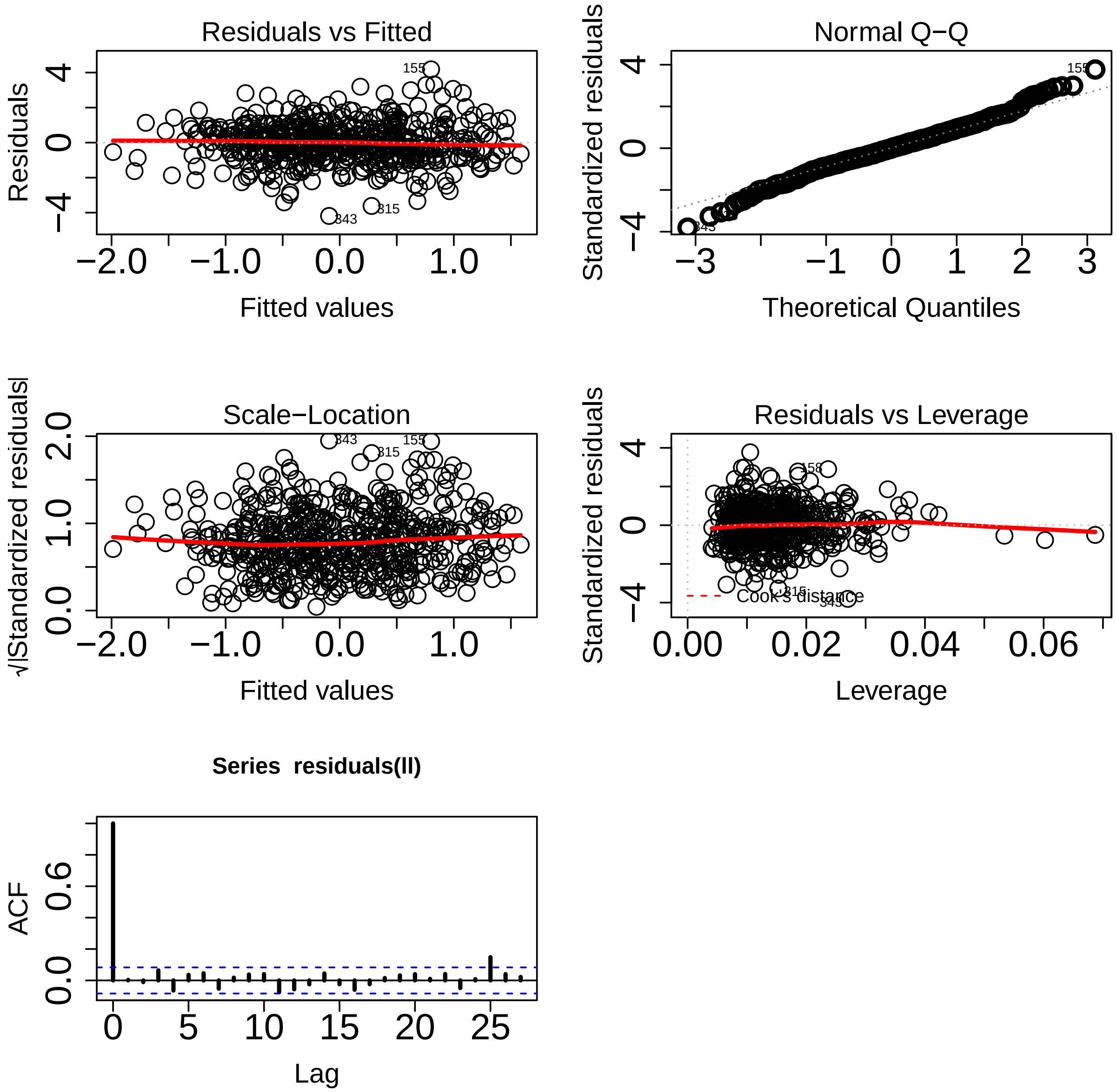
The maximum number of time lags was homogenized between species: our results showed that for AR(p), a 3^{rd} order AR model minimized $\Delta\text{AICc} = \text{AICc} - \text{AICc}_{\text{min}}$ for most species and resulted in 4 models out of 12 falling in the range $[\text{AICc}_{\text{min}}, \text{AICc}_{\text{min}} + 2]$ and 7 more within $[\text{AICc}_{\text{min}}, \text{AICc}_{\text{min}} + 4]$. Therefore, $p = 3$ was enough to capture the dynamics using single-species models. Models with $p = 1$ resulted in similar coefficients but slightly higher AICc values.

A2.1.4 Residual plots

For remaining species, see Supplementary material Appendix 6: Fig. A6.3(b)-A6.3(k).


Residuals vs Fitted
Residuals
Fitted values
−1.5
−0.5
0.5
1.5
−4
0
4
40
111
178
Normal Q−Q
Standardized residuals
Theoretical Quantiles
−3
−1
0
1
2
3
−2
2
40
Scale−Location
√|Standardized residuals|
Fitted values
0.0
1.5
40
111
Residuals vs Leverage
Standardized residuals
Leverage
0.00
0.04
0.08
−2
2
40
Cook's distance
272
Series residuals(ll)
ACF
Lag
0.0
0.6
0
5
10
15
20
25

(a) AST



(b) CHA

Figure A2.3: Residual diagnostic plots for linear AR models of planktonic growth rates explained by cumulated irradiance, salinity, wind energy and a dedicated season variable according to eq. 1 in the main text. Residuals are plotted against fitted values or leverages, showing no systematic trend. Q-Q plot show the adequation of residuals to the normal distribution. The last plot, bottom right, shows no auto-correlation in residual distributions. Composition of planktonic groups is described in Table 1 in the main text.

A2.2 MAR models: further analyses and theory

A2.2.1 MAR analyses of simulated planktonic dynamics

Model selection in autoregressive models, especially multivariate ones, is a challenging task (Ives *et al.* 2003; Holmes *et al.* 2013) and various criteria for model selection (AIC, AICc, AICb) have been developed (for the statistical philosophy behind AIC, its small-sample correction AICc and BIC, see Burnham & Anderson 2002; AICb was developed for state-space models by Cavanaugh & Shumway 1997). The main reasons for these difficulties are the autocorrelated nature of time series and the parameter richness of multivariate models. It is therefore important to make sure that our model selection procedure works in practice and not only in theory. We do this using simulation experiments.

Our approach is resolutely anchored in the model selection philosophy where a handful of scenarios corresponding to contrasted hypotheses are compared (Burnham & Anderson 2002). The high number of parameters and resulting difficulties in model selection led a number of authors to test a large number of interaction matrices, either by exhaustive search (Klug & Cottingham 2001; Beisner *et al.* 2003; Bell *et al.* 2014) or by setting parameters to 0 randomly, and relying on AIC and its derivatives to choose between models, using forward or backward selection. This method is described by Ives *et al.* (1999) and used again by Scheef *et al.* (2013); Gsell *et al.* (2016). We preferred to avoid such "automated hunt" for the best model, as we think this may result in maximum likelihood estimates with weak ecological foundations (i.e., automated stepwise selection of nonzero interaction matrix elements yields an ML model whose realism will be interpreted post-hoc). In our analyses of simulated data (below), like in our analyses of real data, we use contrasted scenarios and compare only a handful of models corresponding to these contrasted scenarios. This limits the number of models compared.

Alongside the assessment of model selection performance, another main objective was to assess the effectiveness of our seasonality variable and potential biases induced by its use.

A2.2.1.1 Design of simulation experiments

We used three baseline ecological settings, each of them with 10 repetitions (to avoid stochasticity in estimates from a single time series, while keeping the computation time reasonable). Each model run simulates the dynamics of 10 different species over 500 time steps, corresponding to the average length of the time series we observe in the REPHY data set. The different ecological settings were modeled with the same model structure (see eq. A2.1). The three ecological settings are the following:

1. No interaction between species (keeping a density-dependent growth, i.e., intragroup interactions). Species only respond to their own log-density and two environmental variables (the **B** matrix is diagonal and **C** is full)
2. No environmental effect, but interactions between species (**B** is full and **C** is null)
3. Both environmental and interaction effects, what we presume to be a plankton-like system (**B** and **C** are full)

$$\left\{\begin{array}{lcl}\mathbf{n}_{t+1} & = & \mathbf{B}\mathbf{n}_t + \mathbf{C}\mathbf{u}_{t+1} + \epsilon_t, \epsilon_t \sim \mathcal{N}_{10}(0, \mathbf{Q}) \\ \mathbf{u}_{t+1} & = & \sum_{i=1}^{5} a_i \mathbf{u}_{t-i} + 2\sin(\omega t) + \eta_t, \eta_t \sim \mathcal{N}_2(0, \mathbf{R})\end{array}\right. \text{ with } \left\{\begin{array}{c} R = \begin{bmatrix} 0.5 & 0 \\ 0 & 1 \end{bmatrix} \\ \\ \mathbf{a} = [0.1, 0.2, 0.1, 0.5, -0.1] \end{array}\right. \tag{A2.1}$$

The following questions were asked for each simulation:

- Which model is selected between a null model (no interactions) and a full-matrix (called an unconstrained matrix in MARSS)?
- How does our dedicated “season” variable affect the estimates and the model selection?

Each parameter was estimated together with its 95% confidence interval, derived from the inversion of the Hessian matrix (which we found to give similar results to more time-consuming bootstrapped intervals).

A2.2.1.2 Model selection metrics

Thereafter, the term real values (subscript r) will indicate the values used in the simulation of the data while estimated values (subscript e) are the values from the MAR(1) analyses.

We compared five different model criteria: three AIC and derivatives, BIC and cross-validation:

- $\text{AIC} = 2k - 2\ln L(\hat{\Theta}|y_r)$
- $\text{AICc} = \text{AIC} + \dfrac{2k(k+1)}{n-k-1}$
- $\text{AICb} = 2\left(\dfrac{1}{N_b}\sum_{i=1}^{N_b} -\ln\dfrac{L(\hat{\Theta}^*(i)|y)}{L(\hat{\Theta}|y_r)}\right) - 2\ln L(\hat{\Theta}|y_r)$
- $\text{BIC} = -2\ln L(\hat{\Theta}|y_r) + k\ln n$
- $R^2_{\text{pred}} = 1 - \dfrac{\sum_{t=1}^{n}(y_{e,t} - y_{r,t})^2}{\sum_{t=1}^{n}(\bar{y}_r - y_{r,t})^2}$ for cross-validation

where

- k is the number of parameters
- $L(\hat{\Theta}|y)$ is likelihood of the maximum-likelihood (ML) parameter set $\hat{\Theta}$ under data y
- n is the length of the sample y
- N_b is the number of bootstrapped datasets
- $\hat{\Theta}^*(i)$ is the ML parameter set estimated from the i-th bootstrapped data set $y^*(i)$

- $\bar{y}_r$ is the mean value of the log density along the simulated time series

Because the different criteria AIC/AICc/AICb were consistent in setting 1, the bootstrapped AIC was not added to the evaluation for settings 2 and 3. Cross-validation was performed by estimating values on two thirds of the *in silico* time series and by comparing the last third of the times series to values predicted with the fitted model through R^2_{pred} (according to Turchin 2003).

In order to assess the performance of the model selected in each setting, we used a series of indicators to evaluate the quality of the statistical inference:

- relative bias on all coefficients $\frac{1}{m}\sum_m \frac{X_r - X_e}{X_r}$ (with m the number of tested coefficients)
- proportion of simulated coefficients falling in the 95% confidence interval estimated with the Hessian matrix
- sign comparison (on significant coefficients only), $\sum_m \text{sign}(X_e) \neq \text{sign}(X_r)$
- when appropriate, depending on the ecological setting, the number of false positives and false negatives in the estimated coefficients of the interaction and environmental matrices. For instance, in the second setting, where the environment has no real effect on population dynamics, each environment coefficient estimated as significantly different from zero is a false positive. On the other hand, in this setting, an interaction coefficient deemed "not significant" is a false negative.

A2.2.1.3 Results

Model selection Tables A2.1, A2.2, A2.3 show that all AIC (AIC/AICc/AICb) always give consistent answers. AIC and BIC detect the simulated model for every ecological setting.

In the first ecological setting, the addition of a seasonal component allowed for a slightly better AIC in 2 repetitions out of 10. However, as this was not confirmed by the BIC, such a season variable was not deemed necessary to identify the right model. The last model selection criterion that we used, cross-validation, was not able to discriminate between ecological settings for any model.

Table A2.1: Comparison of different model criteria (AIC, AICc, AICb, BIC and Cross-Validation (R^2_{pred} according to Turchin 2003) for 10 repetitions of ecological setting 1 with no interaction between genera and an effect of covariates on population dynamics, modeled with a diagonal interaction matrix or an unconstrained interaction matrix, with and without a dedicated season variable.

Repetition	Model	AIC	AICc	AICbp	BIC	CV
1	diagonal, no season	-59	-58	-57	93	0.77
1	diagonal, season	-43	-41	-40	147	0.77
1	unconstrained, no season	31	41	67	525	0.93
1	unconstrained, season	42	54	80	575	0.93
2	diagonal, no season	-769	-768	-766	-617	0.84
2	diagonal, season	-756	-754	-753	-566	0.84
2	unconstrained, no season	-675	-664	-648	-180	0.94
2	unconstrained, season	-661	-649	-628	-129	0.94
3	diagonal, no season	-412	-411	-410	-260	0.92
3	diagonal, season	-415	-413	-411	-225	0.92
3	unconstrained, no season	-310	-299	-275	185	0.92
3	unconstrained, season	-319	-307	-278	214	0.92
4	diagonal, no season	-422	-421	-420	-270	0.87
4	diagonal, season	-407	-406	-404	-217	0.87
4	unconstrained, no season	-334	-324	-312	160	0.92
4	unconstrained, season	-319	-307	-291	213	0.92
5	diagonal, no season	-1432	-1431	-1429	-1279	0.92
5	diagonal, season	-1429	-1427	-1425	-1238	0.92
5	unconstrained, no season	-1356	-1345	-1330	-861	0.94
5	unconstrained, season	-1346	-1334	-1318	-813	0.94
6	diagonal, no season	794	795	796	947	0.74
6	diagonal, season	806	807	809	996	0.74
6	unconstrained, no season	893	903	918	1387	0.92
6	unconstrained, season	904	916	931	1436	0.92
7	diagonal, no season	-2292	-2291	-2290	-2140	0.94
7	diagonal, season	-2287	-2285	-2283	-2096	0.94
7	unconstrained, no season	-2189	-2179	-2167	-1695	0.95
7	unconstrained, season	-2188	-2176	-2160	-1655	0.95
8	diagonal, no season	-1565	-1564	-1563	-1412	0.87
8	diagonal, season	-1568	-1567	-1565	-1378	0.86
8	unconstrained, no season	-1456	-1446	-1427	-962	0.95
8	unconstrained, season	-1468	-1455	-1430	-935	0.95
9	diagonal, no season	-375	-374	-372	-223	0.82
9	diagonal, season	-361	-359	-357	-170	0.82
9	unconstrained, no season	-285	-275	-262	209	0.92
9	unconstrained, season	-271	-259	-245	261	0.92
10	diagonal, no season	-408	-407	-407	-256	0.87
10	diagonal, season	-401	-400	-398	-211	0.87
10	unconstrained, no season	-327	-317	-308	167	0.94
10	unconstrained, season	-334	-321	-312	199	0.94

Table A2.2: Comparison of different model criteria (AIC, AICc, AICb, BIC and Cross-Validation ($\mathrm{R}^2_{\mathrm{pred}}$ according to Turchin 2003) for 10 repetitions of ecological setting 2 with interactions between genera and without effect of covariates on population dynamics, modeled with a diagonal interaction matrix or an unconstrained interaction matrix, with and without a dedicated season variable

Repetition	Model	AIC	AICc	BIC	CV
1	diagonal, no season	9073	9074	9225	0.089
1	diagonal, season	9074	9076	9265	0.088
1	unconstrained, no season	8473	8483	8967	0.3
1	unconstrained, season	8474	8486	9006	0.3
2	diagonal, no season	8982	8983	9134	-0.015
2	diagonal, season	8993	8995	9184	-0.013
2	unconstrained, no season	8214	8225	8709	0.26
2	unconstrained, season	8224	8237	8757	0.25
3	diagonal, no season	9228	9229	9381	0.012
3	diagonal, season	9228	9229	9418	0.0067
3	unconstrained, no season	8300	8310	8794	0.29
3	unconstrained, season	8302	8315	8835	0.29
4	diagonal, no season	9230	9231	9382	0.029
4	diagonal, season	9233	9235	9423	0.027
4	unconstrained, no season	8636	8647	9131	0.18
4	unconstrained, season	8639	8651	9172	0.17
5	diagonal, no season	9421	9422	9573	0.022
5	diagonal, season	9425	9427	9615	0.017
5	unconstrained, no season	8426	8436	8920	0.24
5	unconstrained, season	8431	8443	8964	0.24
6	diagonal, no season	8974	8975	9126	0.12
6	diagonal, season	8976	8978	9166	0.11
6	unconstrained, no season	8005	8015	8499	0.35
6	unconstrained, season	8014	8027	8547	0.35
7	diagonal, no season	8967	8968	9119	0.047
7	diagonal, season	8981	8982	9171	0.051
7	unconstrained, no season	8548	8559	9043	0.23
7	unconstrained, season	8562	8575	9095	0.23
8	diagonal, no season	5338	5339	5490	0.59
8	diagonal, season	5349	5350	5539	0.58
8	unconstrained, no season	2169	2179	2663	0.93
8	unconstrained, season	2181	2193	2714	0.93
9	diagonal, no season	9203	9204	9355	0.027
9	diagonal, season	9200	9202	9391	0.019
9	unconstrained, no season	8391	8402	8886	0.23
9	unconstrained, season	8403	8415	8936	0.23
10	diagonal, no season	9355	9356	9507	-0.087
10	diagonal, season	9360	9362	9550	-0.088
10	unconstrained, no season	7961	7971	8455	0.35
10	unconstrained, season	7974	7987	8507	0.35

Table A2.3: Comparison of different model criteria (AIC, AICc, AICb, BIC and Cross-Validation (R^2_{pred} according to Turchin 2003) for 10 repetitions of ecological setting 3 with interactions between genera and an effect of covariates on population dynamics, modeled with a diagonal interaction matrix or an unconstrained interaction matrix with and without a dedicated season variable.

Repetition	Model	AIC	AICc	BIC	CV
1	diagonal, no season	5301	5302	5453	0.64
1	diagonal, season	5105	5107	5296	0.66
1	unconstrained, no season	2323	2334	2818	0.87
1	unconstrained, season	2324	2337	2857	0.87
2	diagonal, no season	4832	4833	4984	0.55
2	diagonal, season	4637	4639	4828	0.6
2	unconstrained, no season	1175	1186	1670	0.92
2	unconstrained, season	1187	1199	1720	0.92
3	diagonal, no season	4734	4735	4886	0.66
3	diagonal, season	4598	4600	4788	0.67
3	unconstrained, no season	221	231	715	0.91
3	unconstrained, season	234	247	767	0.91
4	diagonal, no season	4598	4599	4750	0.68
4	diagonal, season	4459	4461	4649	0.71
4	unconstrained, no season	1736	1747	2231	0.9
4	unconstrained, season	1744	1756	2276	0.9
5	diagonal, no season	4671	4672	4823	0.45
5	diagonal, season	4523	4525	4713	0.5
5	unconstrained, no season	-310	-300	184	0.93
5	unconstrained, season	-297	-285	236	0.93
6	diagonal, no season	6012	6013	6164	0.61
6	diagonal, season	5845	5847	6036	0.61
6	unconstrained, no season	1420	1431	1915	0.89
6	unconstrained, season	1429	1442	1962	0.89
7	diagonal, no season	3444	3445	3597	0.65
7	diagonal, season	3299	3300	3489	0.63
7	unconstrained, no season	1201	1212	1696	0.91
7	unconstrained, season	1212	1224	1744	0.91
8	diagonal, no season	-5495	-5494	-5343	0.82
8	diagonal, season	-5703	-5701	-5512	0.81
8	unconstrained, no season	-11948	-11937	-11453	1
8	unconstrained, season	-11935	-11923	-11402	1
9	diagonal, no season	4738	4739	4890	0.62
9	diagonal, season	4541	4543	4732	0.66
9	unconstrained, no season	1174	1185	1669	0.92
9	unconstrained, season	1189	1202	1722	0.92
10	diagonal, no season	4147	4148	4299	0.76
10	diagonal, season	4084	4085	4274	0.77
10	unconstrained, no season	-104	-93	391	0.96
10	unconstrained, season	-90	-77	443	0.96

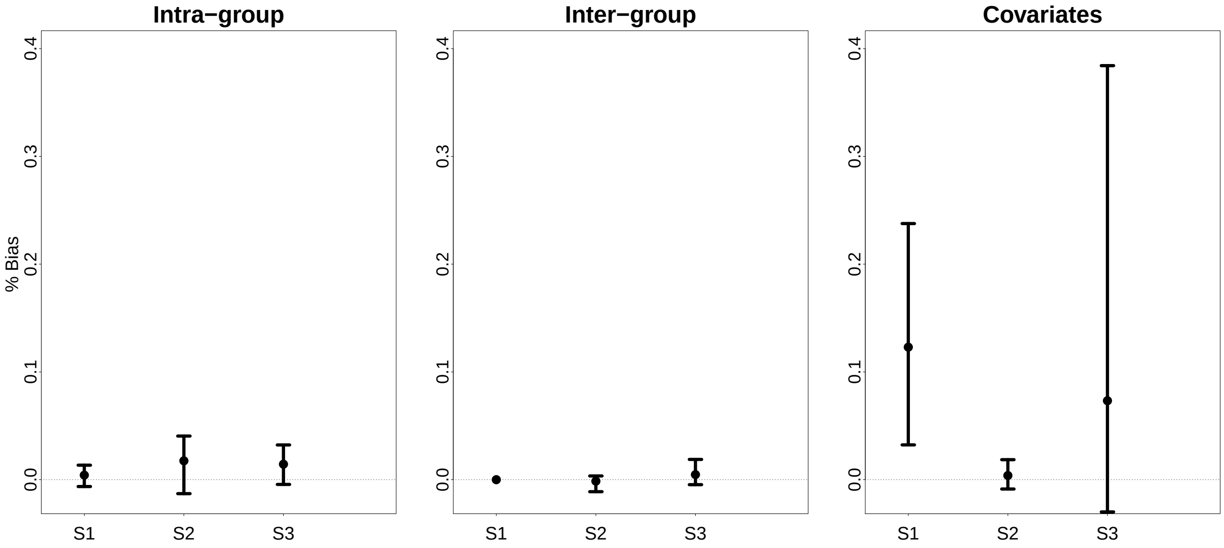


Figure A2.4: Mean bias of estimated parameters, normalized by true (simulated) values, calculated for 10 repetitions of three different ecological settings (inter-group interactions have no effect in S1; environment has no effect in S2; both play a role in S3). Difference is calculated as simulated value minus estimated value: a positive bias indicates an underestimation of matrix coefficients.

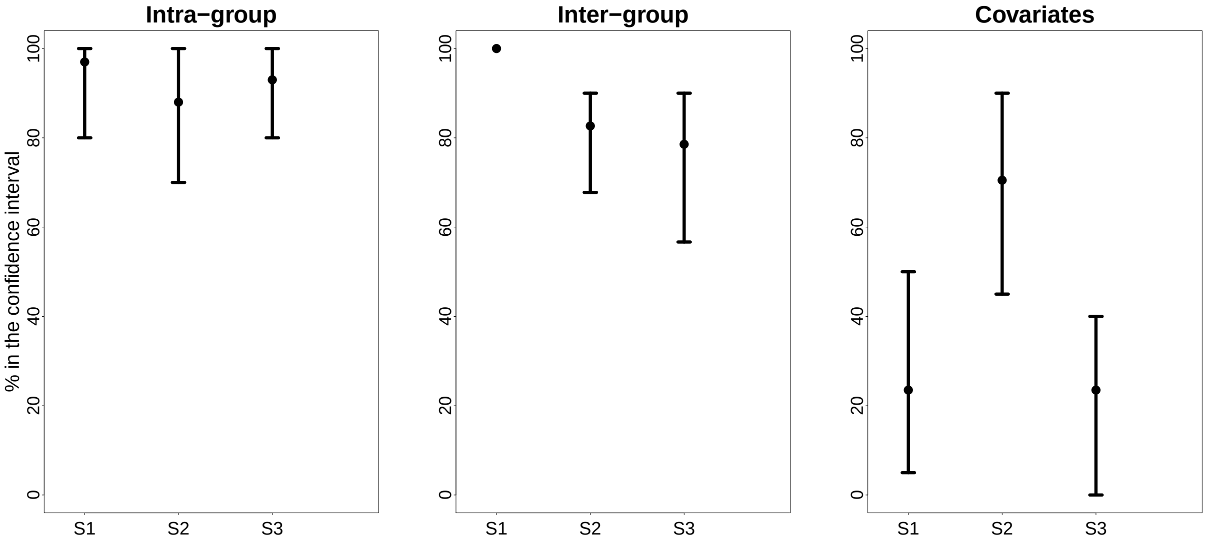


Figure A2.5: Percentage of simulated parameter value that falls in the 95% confidence interval estimated by Hessian inversion in MAR models, calculated for 10 repetitions of three different ecological settings (interactions inter-group have no effect in S1; environment has no effect in S2; both play a role in S3).

Interest of a dedicated seasonal variable In all repetitions of every ecological setting, apart from one repetition in ecological setting 1, model selection criteria tend to select simple models with no dedicated seasonal variable (small improvement in parsimony), that performed similarly to models with a dedicated seasonal variable (which we introduced in the analyses of the main text to avoid collinearity). As we wanted to compare simulated and estimated values, we focused here on models without explicit seasonal effects. Indeed, using a dedicated seasonal component would lead to adjust coefficients to covariate residuals only, which would make their interpretation more difficult in relation to simulated values. However, as the differences between both model types are small, to be consistent with the rest of the literature and avoid collinearity, we kept a seasonal component in the analyses of the main text.

MAR(1) models We compared the estimates of matrices **B** of the models discriminated by AIC and BIC to simulated coefficients. As model criteria always chose a diagonal **B** matrix in ecological setting 1, no inter-genus coefficient was considered significant: there was no false positive throughout the analyses. On the contrary, there could be false negatives, i.e. inter-genus coefficients that were not considered significant while there were different from 0 in ecological settings 2 and 3. This represented around 3% of all off-diagonal coefficients estimated in these settings. In addition, the signs of the coefficients were almost always respected: intra-genus coefficients were the same in the simulations and in the corresponding estimates, while negative inter-genus coefficients in the simulations could be estimated as positive in 10% of the estimates. Fig. A2.4 show that the relative bias remains very small for inter-genus coefficients: this indicates that such issues remain manageable. Only low values of negative coefficients are deemed positive and their values remain small, leading to small departures from simulated values. Positive inter-genus coefficients were not affected by sign change. In the most complex setting (setting 3), simulated intra-genus coefficients fell in the estimated 95% confidence interval more than 90% of the time. Off-diagonal values lied in the estimated confidence intervals 80% of the time (Fig. A2.5).

Coefficients in the environment matrix were not entirely free from false positives. In the 2nd ecological setting, in which no covariate should have an effect on population dynamics, half of the repetitions led to some estimated coefficients significantly different from 0 in matrix **C**. In 4 out of these 5 repetitions, only 2 coefficients out of 20 were deemed significant. In the last repetition, 5 coefficients out of 20 were false positives. In this case, absolute values of the coefficients were always lower than 0.2. We can also note that this repetition has the worst cross validation performance of all repetitions for this ecological setting (Table A2.2).

When matrix **C** is different from the null matrix (ecological settings 1 and 3), coefficients tend to be underestimated (Fig. A2.4); leading to only 40% of simulated covariates falling in the estimated confidence intervals in ecological setting 3 at most (Fig. A2.5). However, there was no sign error in these settings: a qualitative analysis remains possible.

A2.2.1.4 Consequence for real data analysis

Our analyses show that the interaction model is always recovered by MARSS and that significance and signs of parameters are correctly assessed for both interactions and environmental effects. On the other hand, coefficients are sometimes slightly underestimated, especially for covariates, when both environmental variables and interactions have to be taken into account. This suggests that the presence/absence (in the selected model) or sign of the coefficients should be given more attention than point estimates of coefficients.

A2.2.2 Tuning parameters in the MARSS package

We tried several values for the options offered in MARSS package. In the following, we use the same parameter names as described in Holmes *et al.* (2013) and compare our choices to the recent work of Griffiths *et al.* (2015) who also made their algorithmic choices explicit.

We performed analyses with the following tuning parameters:

- miniter=100. This parameter is the minimal number of iterations of the algorithm before accepting a local minimum. It was set as a trade-off between consistency with Griffiths *et al.* (2015), who use 200 iterations, and preliminary tests on our datasets which indicated that a smaller number could be used. In the latter case, convergence was reached in 31, 28, 25, 21 iterations for the unconstrained Teychan scenario, the intra-phylum Teychan model, the unconstrained Buoy 7 model and the intra-phylum Buoy 7 model, respectively.
- conv.test.slope.tol=0.001. This parameter is the slope of the likelihood near the maximum: we assume that the curve should be very flat, based on recommendations from Holmes *et al.* (2013). This parameter was set to 0.5 in Griffiths *et al.* (2015), thus we are much more conservative.
- The Expectation Maximization (EM) algorithm, coupled with an optimized Kalman filter (from Helske 2017), is the default in MARSS and was used here. The BFGS algorithm, which often works better with the classic Kalman filter (from Shumway & Stoffer 2010), can be used to improve the estimates according to Holmes *et al.* (2013) but is much slower. We tried BFGS and it produced similar estimates to EM, thus we chose EM.

We examined the differences made by different MARSS options on our real data. Table A2.4 shows the average difference in coefficient values.

Table A2.4: Average change in coefficient values in matrices **B** (interaction matrix, for both diagonal and off-diagonal values) and **C** (covariate effect matrix) between model fits initialized with different tuning parameters of the MARSS package. *miniter* is the minimum number of iterations for the optimization algorithm (100 in our model, 200 in Griffiths *et al.* (2015)). *conv.test.slope* is the slope of the likelihood against the number of iterations (0.001 in our model, 0.5 in Griffiths *et al.* (2015)).

	miniter			conv.test.slope		
	B diag $\times 10^{-6}$	B out $\times 10^{-5}$	C $\times 10^{-5}$	B diag	B out	C
Teychan unconstrained	-5.1	5.4	5.4	0.0	0.1	-0.2
Teychan intra-phylum	-6.7	3.3	3.4	-0.0	0.1	0.2
Buoy 7 unconstrained	-2.3	1.8	1.3	-0.0	0.5	-0.2
Buoy 7 intra-phylum	-3.4	-3.5	-7.1	-0.1	0.2	0.2

Due to computational limitations, we assessed the effect of changing the estimation algorithm for only one scenario in simulated data. The algorithm changed about 0.004% (0.09% as a maximum) of absolute diagonal values in the interaction matrix **B** and 0.0028% (maximum wa 0.09%) off-diagonal. For covariate values, the average change was around 0.0013% (maximum was 0.05%). We therefore consider the effects of change in tuning parameters on our results to be minimal.

A2.2.3 Interaction matrices definition

Table A2.5: Definition of an unconstrained interaction matrix: $0/+/-$ indicates that the coefficient can be either positive, negative or near zero (i.e., not significantly different from zero). Composition of planktonic groups is described in Table 1 in the main text.

$$B = \left[\begin{array}{cccccccccccc}
\text{AST} & \text{NIT} & \text{PSE} & \text{SKE} & \text{CHA} & \text{GUI} & \text{LEP} & \text{RHI} & \text{GYM} & \text{PRP} & \text{CRY} & \text{EUG} \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\
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\end{array}\right] \tag{A2.2}$$

Table A2.6: Definition of an interaction matrix allowing interactions only intra-phylum: 0 indicates that the coefficient is forced to be null while $0/+/-$ indicates that the coefficient can be either positive, negative or near zero. Composition of planktonic groups is described in Table 1 in the main text.

$$B = \left[\begin{array}{cccccccccccc|cc}
\text{AST} & \text{NIT} & \text{PSE} & \text{SKE} & \text{CHA} & \text{GUI} & \text{LEP} & \text{RHI} & \text{GYM} & \text{PRP} & \text{CRY} & \text{EUG} & & \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{AST} & \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{NIT} & \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{PSE} & \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{SKE} & \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{CHA} & \} \text{ Diatom} \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{GUI} & \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{LEP} & \\
0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0 & 0 & 0 & \text{RHI} & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0 & \text{GYM} & \} \text{ Dinoflagellate} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0 & \text{PRP} & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0 & \text{CRY} & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & \text{EUG} &
\end{array}\right] \tag{A2.3}$$

A2.2.4 MAR(1) results

In Table A2.8, we present the estimated coefficients for biotic and abiotic variables corresponding to the different community matrices described in section A2.2.3.

Table A2.7: Definition of an interaction matrix allowing only inter-phylum interation: 0 indicates that the coefficient is forced to be null while $0/+/-$ indicates that the coefficient can be either positive, negative or near zero. Composition of planktonic groups is described in Table 1 in the main text.

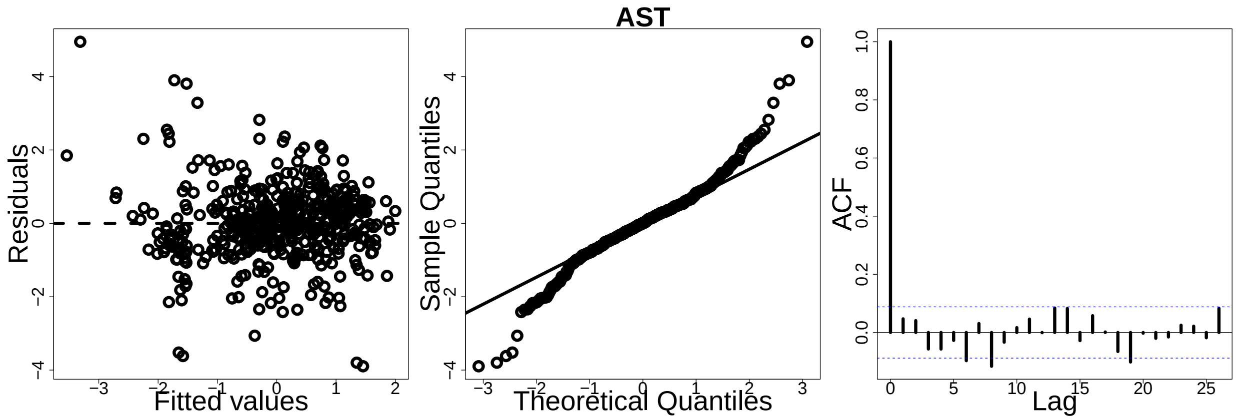
$$B = \begin{array}{c} \begin{array}{cccccccccccc} \text{AST} & \text{NIT} & \text{PSE} & \text{SKE} & \text{CHA} & \text{GUI} & \text{LEP} & \text{RHI} & \text{GYM} & \text{PRP} & \text{CRY} & \text{EUG} \end{array} \\ \left[\begin{array}{cccccccccccc} 0/+/- & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0 & 0/+/- & 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0 & 0 & 0/+/- & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0 & 0 & 0 & 0/+/- & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0 & 0 & 0 & 0 & 0/+/- & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0 & 0 & 0 & 0 & 0 & 0/+/- & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0/+/- & 0/+/- \\ 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0 & 0/+/- & 0/+/- & 0/+/- \\ 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- \\ 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- & 0/+/- \end{array}\right] \end{array} \begin{array}{l} \\ \left.\begin{array}{l} \text{AST} \\ \text{NIT} \\ \text{PSE} \\ \text{SKE} \\ \text{CHA} \\ \text{GUI} \\ \text{LEP} \\ \text{RHI} \end{array}\right\} \text{Diatom} \\ \left.\begin{array}{l} \text{GYM} \\ \text{PRP} \end{array}\right\} \text{Dinoflagellate} \\ \text{CRY} \\ \text{EUG} \end{array} \tag{A2.4}$$

Table A2.8: Model coefficients for both biotic and abiotic variables (salinity, irradiance, wind energy and a dedicated seasonal variable) at Teychan / Buoy 7. We use an unconstrained interaction matrix allowing all interactions between planktonic groups (top row), an interaction matrix allowing only intra-phylum interactions (middle row) and an interaction matrix allowing only inter-phylum interactions (bottom row). The best fitting model is given in the main text. Significant coefficients are indicated by *; statistical significance was determined by bootstrapping and $P<0.05$. The table should be read as element j having effect e_{ij} on plankton group i's growth rate. The identity matrix was subtracted to the interaction matrix, in order to make effects on growth rates comparable. Composition of planktonic groups is described in Table 1 in the main text

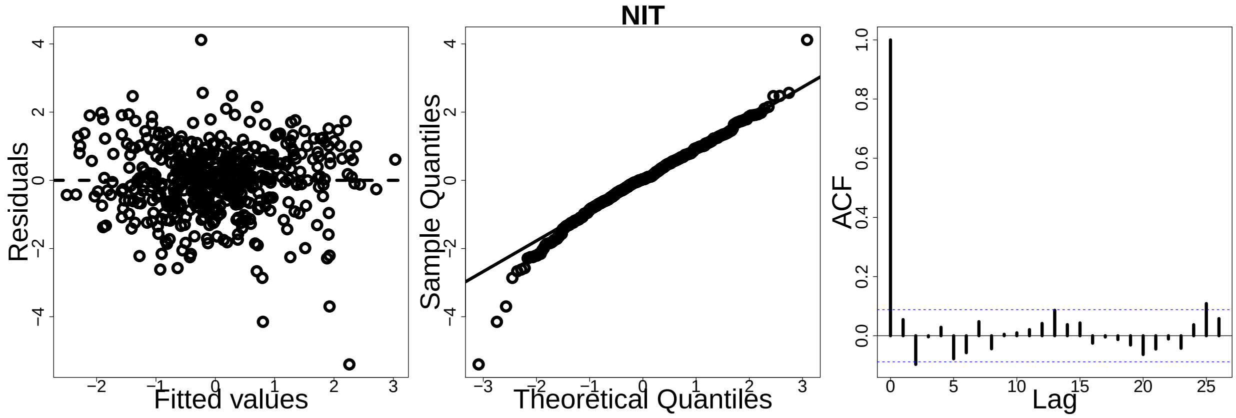
Model		AST	NIT	PSE	SKE	CHA	GUI	LEP	RHI	GYM	PRP	CRY	EUG	SAL	CumRg	Wind energy	Season
Unconstrained	AST	-0.27* / -0.38*	0.09* / 0.15*	-0.01 / 0.03	-0.01 / 0.03	-0.04 / -0.05	-0.01 / 0.02	0.02 / -0.02	0.02 / -0.03	-0.04 / -0.02	-0.02 / 0.01	0.02 / 0.08*	0.08* / 0.07	0.04 / -0.02	-0.02 / -0.07*	-0.04 / -0.03	-0.14* / -0.17*
	NIT	-0.01 / -0.05	-0.44* / -0.39*	-0.05 / -0.08*	0.03 / 0.02	0.00 / 0.00	-0.05 / 0.02	0.02 / 0.03	0.03 / -0.02	-0.06 / -0.04	0.01 / -0.01	0.06 / 0.10*	0.05 / 0.00	0.05 / -0.05	0.04 / -0.01	-0.03 / -0.03	0.20* / 0.18*
	PSE	0.06 / 0.07	-0.02 / 0.09	-0.34* / -0.39*	0.00 / -0.04	-0.01 / -0.07	0.08* / 0.00	0.03 / -0.03	-0.02 / 0.09*	0.03 / -0.06	0.05 / 0.01	0.02 / 0.05	-0.04 / -0.04	-0.02 / -0.03	0.06 / 0.06	-0.16* / -0.22*	0.02 / 0.03
	SKE	-0.05 / -0.05	0.04 / 0.04	-0.04 / 0.07	-0.26* / -0.43*	0.00 / 0.12*	0.08* / -0.03	-0.01 / -0.03	0.04 / 0.01	0.01 / -0.10*	0.01 / 0.02	-0.01 / 0.01	0.03 / 0.04	-0.01 / -0.05	0.02 / -0.07	-0.01 / -0.03	-0.04 / -0.08
	CHA	0.05* / 0.02	-0.04 / 0.00	-0.01 / -0.01	0.05 / -0.06	-0.50* / -0.60*	0.06* / 0.01	0.03 / 0.10*	0.04 / 0.12*	0.00 / 0.05	0.04 / 0.02	0.05* / -0.02	-0.05 / 0.09*	-0.09* / -0.03	0.05 / 0.03	-0.15* / -0.15*	0.31* / 0.15*
	GUI	0.03 / 0.03	0.03 / 0.02	-0.04 / -0.08	0.00 / -0.03	-0.01 / -0.15*	-0.27* / -0.27*	-0.06 / 0.04	0.00 / 0.04	-0.05 / 0.00	0.07* / 0.00	-0.04 / 0.00	-0.01 / 0.06	-0.02 / 0.02	0.06 / -0.01	-0.08* / -0.11*	0.13* / 0.03
	LEP	0.07* / 0.05	-0.09* / -0.01	0.04 / 0.06	-0.01 / -0.10*	-0.01 / -0.05	0.09* / 0.03	-0.40* / -0.41*	0.01 / 0.04	0.00 / 0.06	0.07* / 0.02	0.00 / -0.08*	-0.01 / -0.02	-0.07* / 0.00	0.13* / 0.15*	-0.06* / -0.10*	0.18* / 0.14*
	RHI	0.05 / 0.00	0.03 / 0.07	0.01 / 0.09*	0.00 / -0.10*	0.06 / -0.11*	0.09* / 0.08*	-0.08* / 0.05	-0.35* / -0.34*	0.01 / 0.00	0.04 / -0.03	-0.02 / -0.02	-0.06 / -0.05	-0.06 / 0.01	0.05 / -0.02	-0.02 / -0.13*	0.13* / 0.07
	GYM	0.01 / 0.07	-0.05 / 0.03	0.04 / 0.01	0.04 / -0.03	-0.04 / -0.03	-0.01 / 0.01	-0.04 / 0.06	0.06 / 0.06	-0.36* / -0.53*	0.03 / 0.15*	-0.01 / 0.02	0.07 / 0.04	-0.03 / -0.06	0.11* / 0.06	-0.06 / -0.14*	0.02 / -0.03
	PRP	0.10* / 0.01	0.05 / -0.04	0.00 / 0.00	0.01 / 0.01	-0.06 / 0.00	0.02 / 0.04	-0.07 / 0.08	0.00 / 0.02	-0.01 / 0.03	-0.41* / -0.43*	0.01 / 0.03	0.01 / 0.07	-0.09* / -0.07	0.16* / 0.05	-0.03 / -0.06	0.25* / 0.04
	CRY	-0.09* / -0.05	0.07 / 0.12*	-0.04 / 0.05	0.03 / -0.09	0.12* / -0.06	-0.03 / 0.01	-0.02 / 0.01	0.08 / -0.05	-0.04 / -0.03	-0.02 / 0.09	-0.50* / -0.52*	-0.01 / 0.04	-0.08 / -0.09	0.05 / 0.01	0.03 / 0.04	-0.02 / 0.08
	EUG	-0.04 / -0.10*	-0.01 / 0.08	0.00 / -0.02	0.01 / 0.05	0.11* / -0.05	0.03 / 0.09*	-0.02 / -0.04	-0.06 / -0.04	-0.02 / -0.01	0.04 / 0.01	0.06* / 0.02	-0.35* / -0.35*	-0.06 / -0.04	-0.01 / 0.05	-0.04 / 0.00	0.09* / 0.11*
Intra-phylum	AST	-0.26* / -0.26*	0.10* / 0.10*	-0.03 / -0.03	0.00 / 0.00	-0.04 / -0.04	0.01 / 0.01	0.01 / 0.01	0.00 / 0.00					0.05 / 0.05	-0.03 / -0.03	-0.04 / -0.04	-0.12* / -0.12*
	NIT	-0.01 / -0.01	-0.42* / -0.42*	-0.07 / -0.07	0.04 / 0.04	0.01 / 0.01	-0.04 / -0.04	0.01 / 0.01	0.01 / 0.01					0.05 / 0.05	0.04 / 0.04	-0.03 / -0.03	0.23* / 0.23*
	PSE	0.06 / 0.06	-0.02 / -0.02	-0.33* / -0.33*	0.00 / 0.00	0.00 / 0.00	0.08* / 0.08*	0.03 / 0.03	0.00 / 0.00					-0.03 / -0.03	0.07* / 0.07*	-0.16* / -0.16*	0.02 / 0.02
	SKE	-0.05 / -0.05	0.04 / 0.04	-0.04 / -0.04	-0.25* / -0.25*	0.00 / 0.00	0.08* / 0.08*	-0.01 / -0.01	0.04 / 0.04					-0.01 / -0.01	0.02 / 0.02	-0.01 / -0.01	-0.03 / -0.03
	CHA	0.05 / 0.05	-0.03 / -0.03	-0.01 / -0.01	0.05* / 0.05*	-0.49* / -0.49*	0.05* / 0.05*	0.03 / 0.03	0.05 / 0.05					-0.10* / -0.10*	0.06* / 0.06*	-0.15* / -0.15*	0.31* / 0.31*
	GUI	0.04 / 0.04	0.01 / 0.01	-0.04 / -0.04	0.00 / 0.00	-0.02 / -0.02	-0.26* / -0.26*	-0.06 / -0.06	0.00 / 0.00					-0.02 / -0.02	0.06 / 0.06	-0.08* / -0.08*	0.16* / 0.16*
	LEP	0.07* / 0.07*	-0.09* / -0.09*	0.05 / 0.05	-0.01 / -0.01	-0.01 / -0.01	0.09* / 0.09*	-0.40* / -0.40*	0.02 / 0.02					-0.08* / -0.08*	0.14* / 0.14*	-0.06* / -0.06*	0.21* / 0.21*
	RHI	0.05 / 0.05	0.01 / 0.01	0.02 / 0.02	-0.01 / -0.01	0.05 / 0.05	0.08* / 0.08*	-0.08 / -0.08	-0.34* / -0.34*					-0.07 / -0.07	0.05 / 0.05	-0.03 / -0.03	0.12* / 0.12*
	GYM									-0.35* / -0.35*	0.05 / 0.05	-0.02 / -0.02		-0.03 / -0.03	0.10* / 0.10*	-0.06 / -0.06	0.00 / 0.00
	PRP									-0.02 / -0.02	-0.39* / -0.39*	0.02 / 0.02		-0.06 / -0.06	0.15* / 0.15*	-0.01 / -0.01	0.15* / 0.15*
	CRY									-0.02 / -0.02	-0.01 / -0.01	-0.46* / -0.46*		-0.08* / -0.08*	0.01 / 0.01	0.00 / 0.00	0.10* / 0.10*
	EUG												-0.32* / -0.32*	-0.07* / -0.07*	-0.02 / -0.02	-0.05 / -0.05	0.17* / 0.17*
Inter-phylum	AST	-0.26* / -0.26*								-0.04 / -0.04	-0.02 / -0.02	0.04 / 0.04	0.09* / 0.09*	0.05 / 0.05	-0.04 / -0.04	-0.04 / -0.04	-0.14* / -0.14*
	NIT		-0.44* / -0.44*							-0.06 / -0.06	0.00 / 0.00	0.07 / 0.07	0.05 / 0.05	0.04 / 0.04	0.04 / 0.04	-0.03 / -0.03	0.20* / 0.20*
	PSE			-0.31* / -0.31*						0.02 / 0.02	0.06 / 0.06	0.01 / 0.01	-0.03 / -0.03	-0.01 / -0.01	0.06* / 0.06*	-0.15* / -0.15*	0.01 / 0.01
	SKE				-0.24* / -0.24*					0.01 / 0.01	0.01 / 0.01	0.01 / 0.01	0.04 / 0.04	-0.01 / -0.01	0.00 / 0.00	-0.02 / -0.02	0.01 / 0.01
	CHA					-0.44* / -0.44*				0.01 / 0.01	0.06* / 0.06*	0.04 / 0.04	-0.05 / -0.05	-0.09* / -0.09*	0.04 / 0.04	-0.15* / -0.15*	0.29* / 0.29*
	GUI						-0.28* / -0.28*			-0.07* / -0.07*	0.07* / 0.07*	-0.02 / -0.02	0.00 / 0.00	-0.01 / -0.01	0.05 / 0.05	-0.06* / -0.06*	0.07* / 0.07*
	LEP							-0.34* / -0.34*		-0.01 / -0.01	0.08* / 0.08*	-0.03 / -0.03	-0.02 / -0.02	-0.06 / -0.06	0.13* / 0.13*	-0.05 / -0.05	0.13* / 0.13*
	RHI								-0.31* / -0.31*	0.01 / 0.01	0.06 / 0.06	-0.01 / -0.01	-0.04 / -0.04	-0.04 / -0.04	0.03 / 0.03	-0.02 / -0.02	0.11* / 0.11*
	GYM	0.01 / 0.01	-0.05 / -0.05	0.04 / 0.04	0.04 / 0.04	-0.04 / -0.04	-0.01 / -0.01	-0.04 / -0.04	0.06 / 0.06	-0.35* / -0.35*		-0.01 / -0.01	0.07* / 0.07*	-0.03 / -0.03	0.11* / 0.11*	-0.06* / -0.06*	0.03 / 0.03
	PRP	0.10* / 0.10*	0.05 / 0.05	0.00 / 0.00	0.01 / 0.01	-0.07 / -0.07	0.02 / 0.02	-0.07 / -0.07	-0.01 / -0.01		-0.41* / -0.41*	0.01 / 0.01	0.01 / 0.01	-0.09* / -0.09*	0.16* / 0.16*	-0.03 / -0.03	0.25* / 0.25*
	CRY	-0.09* / -0.09*	0.07 / 0.07	-0.04 / -0.04	0.03 / 0.03	0.12* / 0.12*	-0.03 / -0.03	-0.02 / -0.02	0.08 / 0.08	-0.04 / -0.04	-0.02 / -0.02	-0.50* / -0.50*	-0.01 / -0.01	-0.08 / -0.08	0.05 / 0.05	0.03 / 0.03	-0.02 / -0.02
	EUG	-0.04 / -0.04	-0.01 / -0.01	0.00 / 0.00	0.01 / 0.01	0.11* / 0.11*	0.03 / 0.03	-0.02 / -0.02	-0.06 / -0.06	-0.02 / -0.02	0.04 / 0.04	0.06* / 0.06*	-0.35* / -0.35*	-0.06 / -0.06	-0.01 / -0.01	-0.04 / -0.04	0.09 / 0.09

A2.2.5 Diagnostics

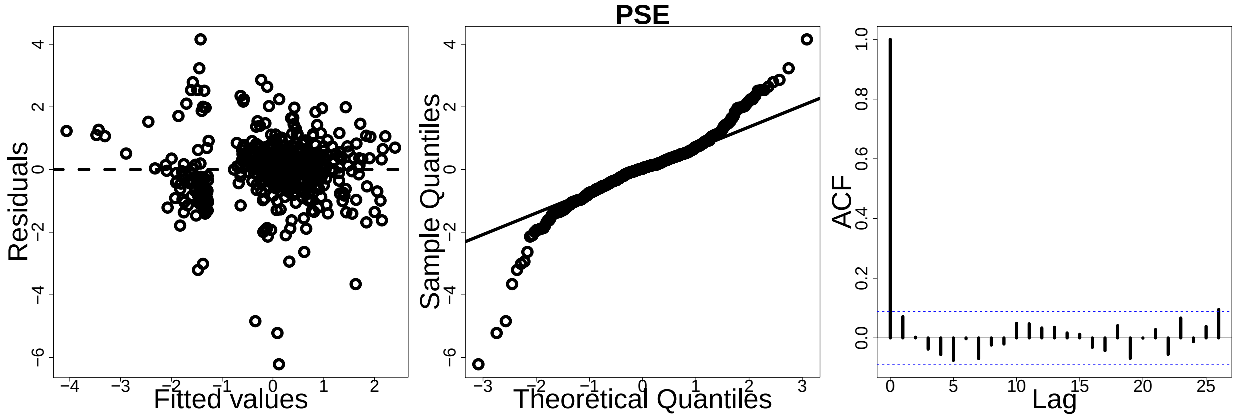
Residual diagnostic plots for MAR models



(a) AST

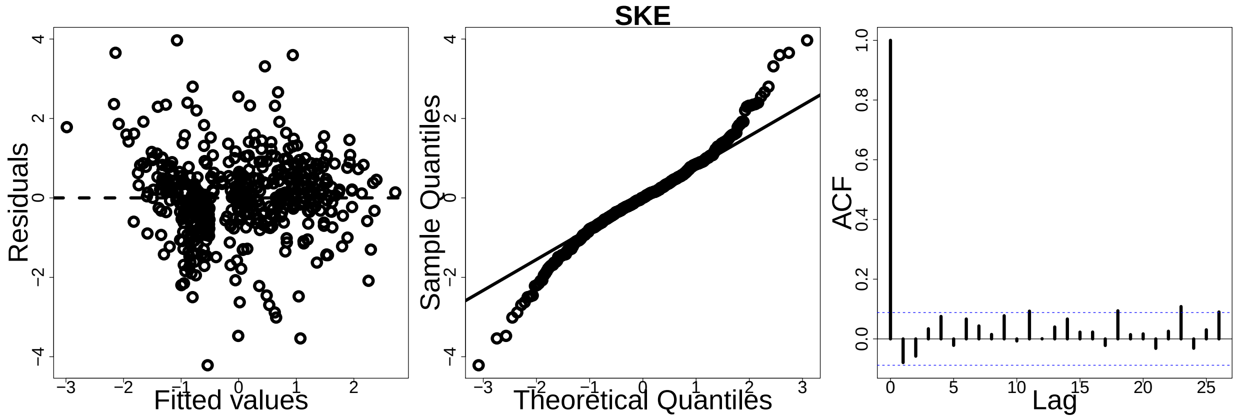


(b) NIT

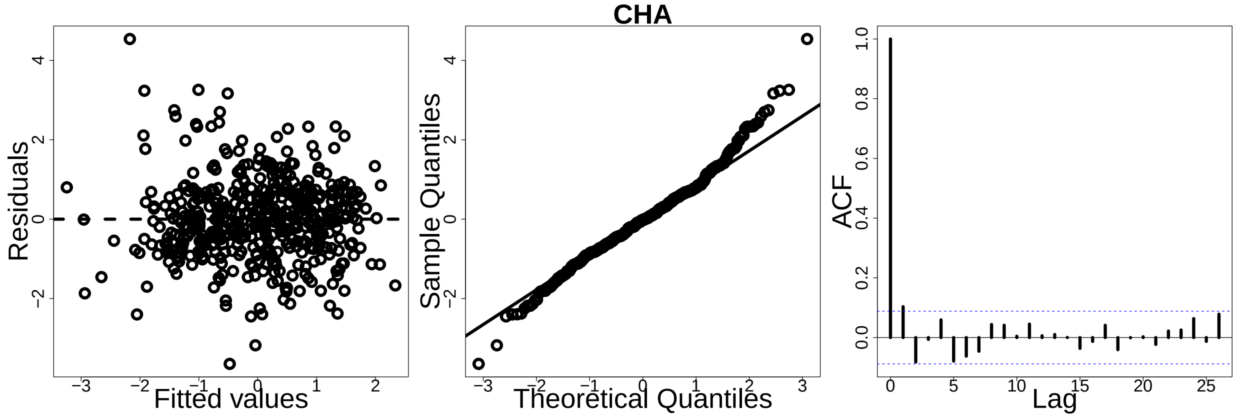


(c) PSE

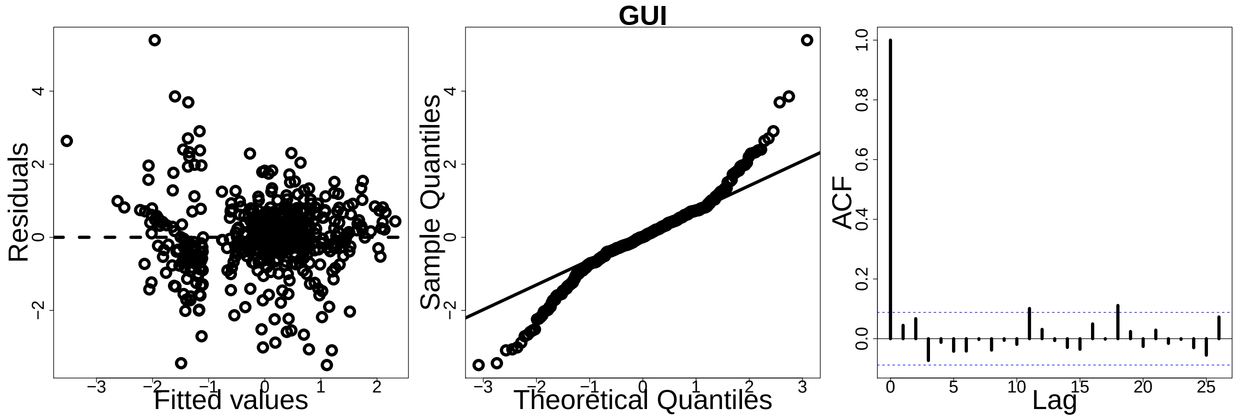
Residuals for the other MAR models are presented in Supplementary material Appendix 6: Section A6.6.



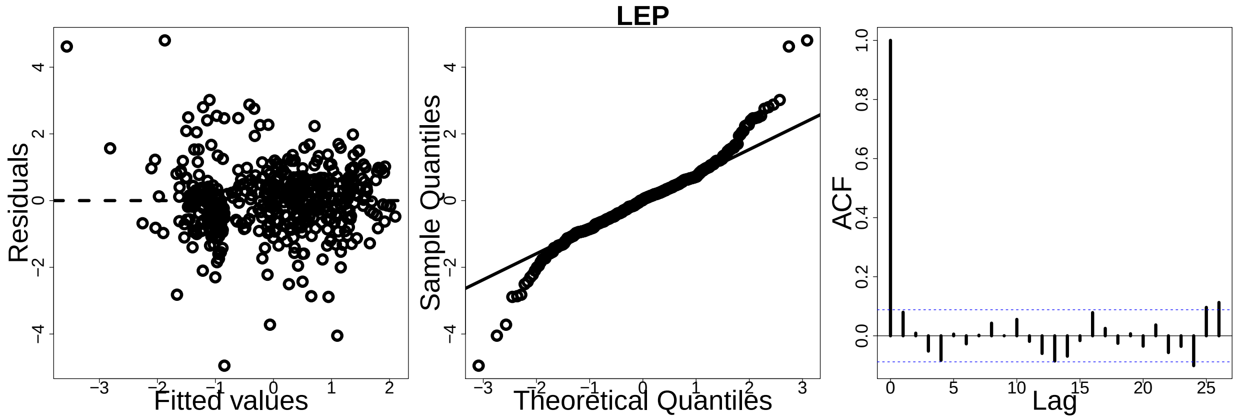
(d) SKE



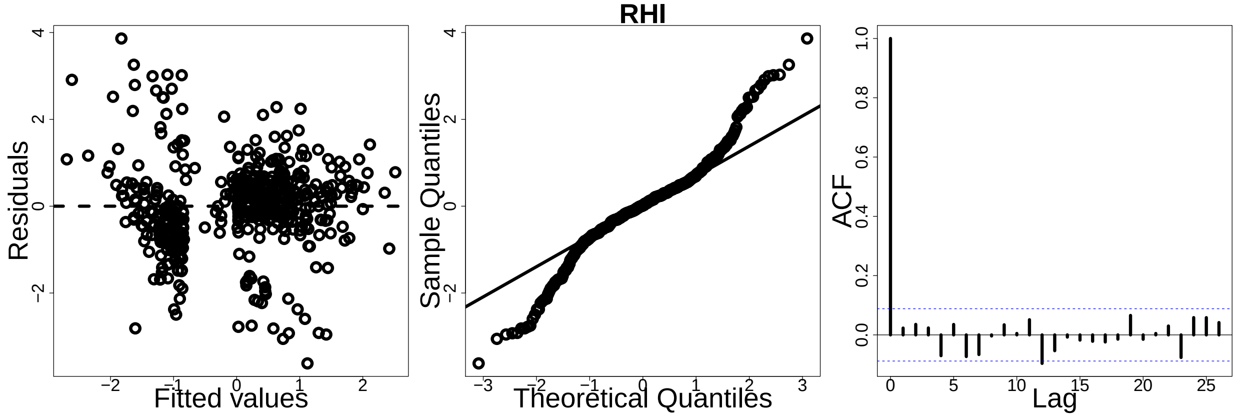
(e) CHA



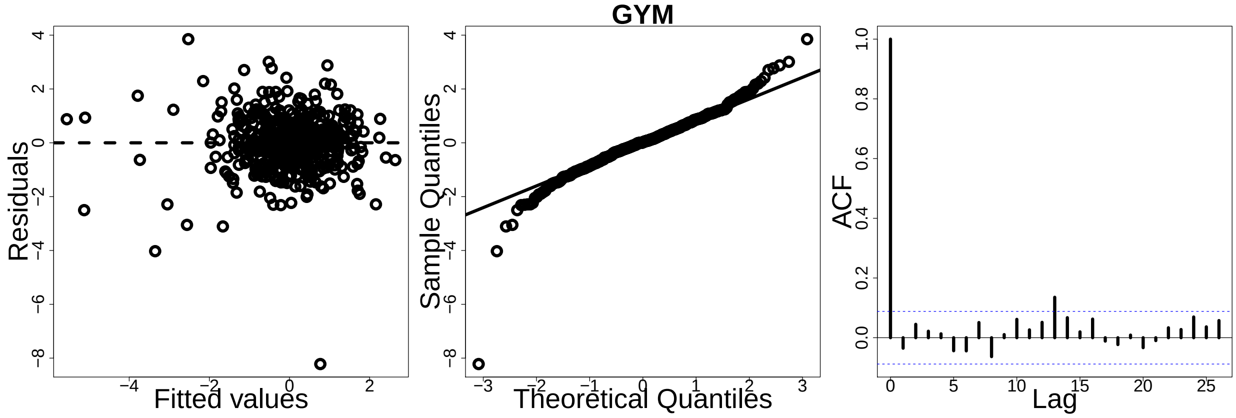
(f) GUI



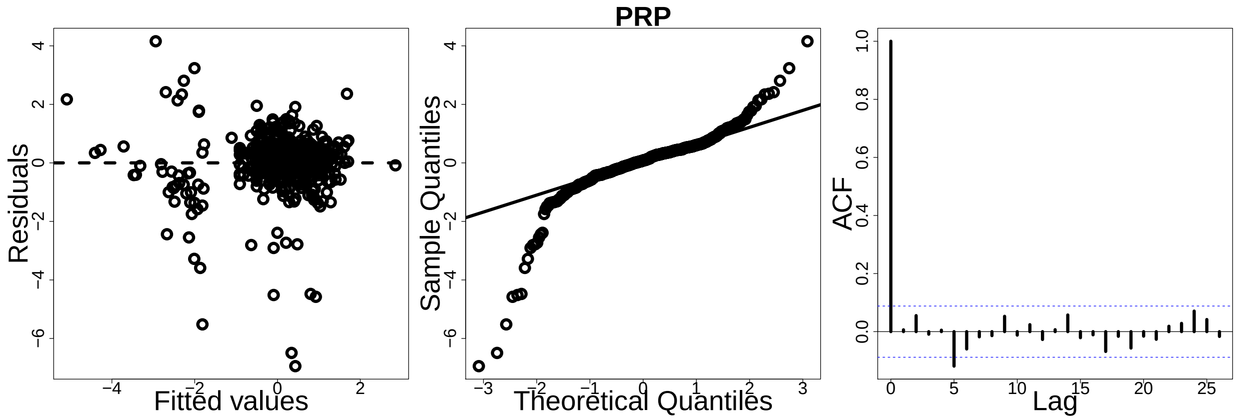
(g) LEP



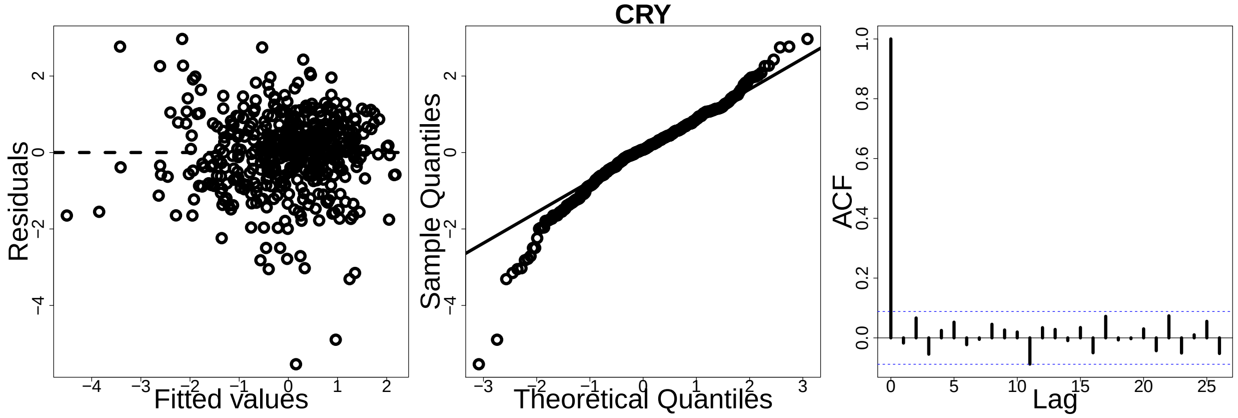
(h) RHI



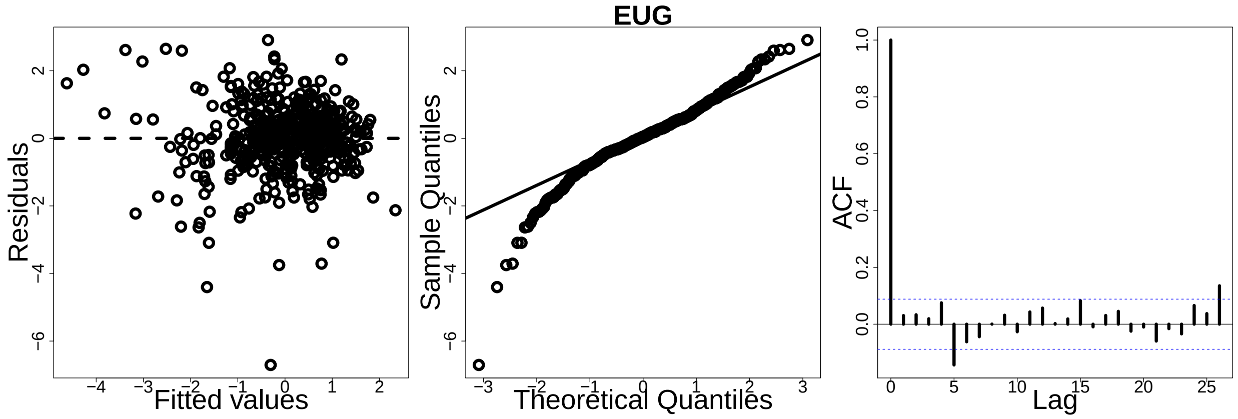
(i) GYM



(j) PRP



(k) CRY



(l) EUG

Figure A2.6: Residual examination for the MAR model using an interaction matrix only allowing intra-phylum interactions, differentiating pennate and centric diatoms, at Teychan site. From left to right, residuals plotted against fitted values, Q-Q plots, and auto-correlation of residuals. The composition of planktonic groups is described in Table 1 in the main text.

A2.2.5.1 Goodness of fit, estimated values vs observations

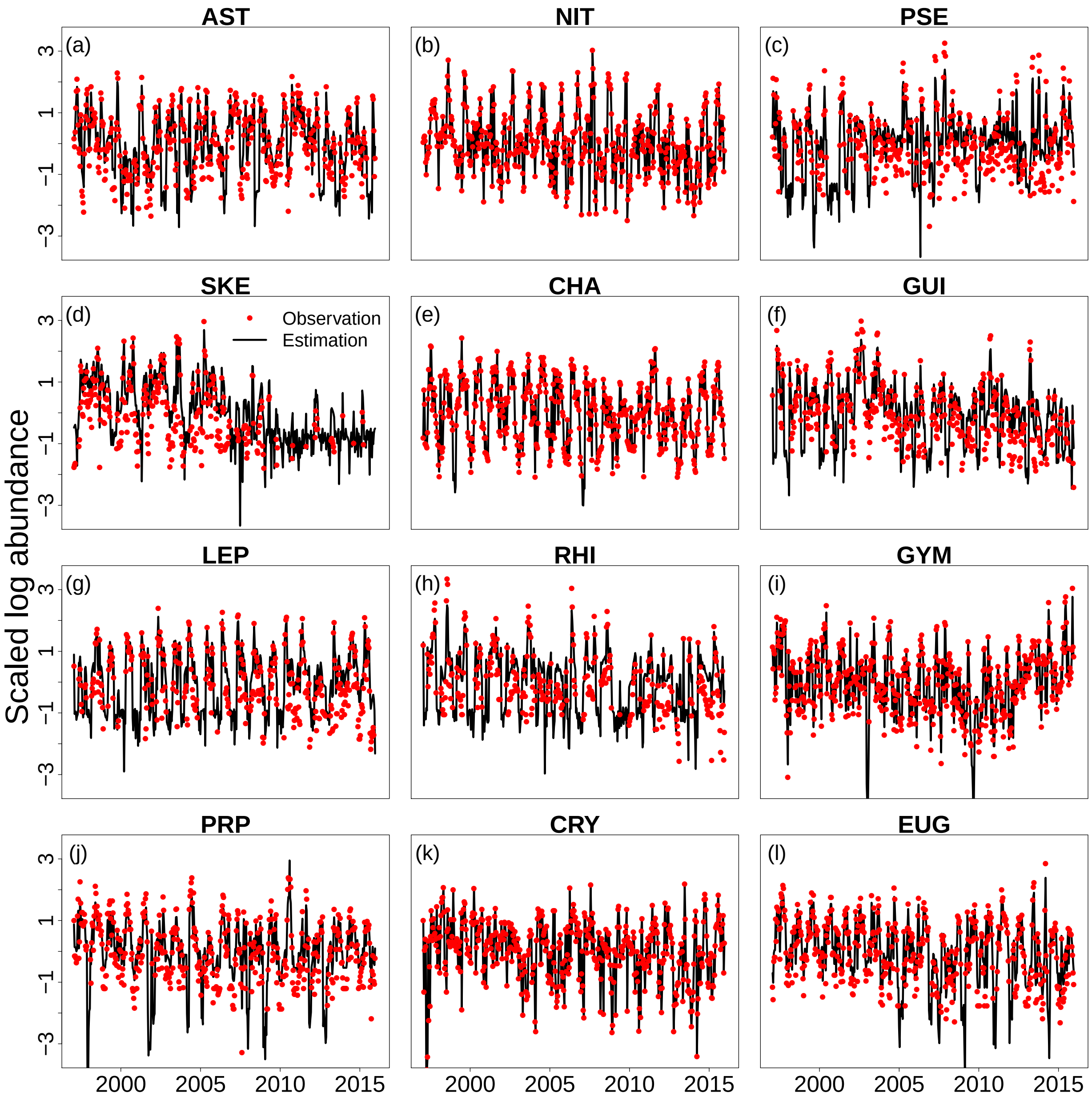


Figure A2.7: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) for Teychan site, using a diagonal interaction matrix. Composition of planktonic groups is described in Table 1 in the main text.

Estimates for the other MAR models are presented in Supplementary material Appendix 6: Section A6.7.

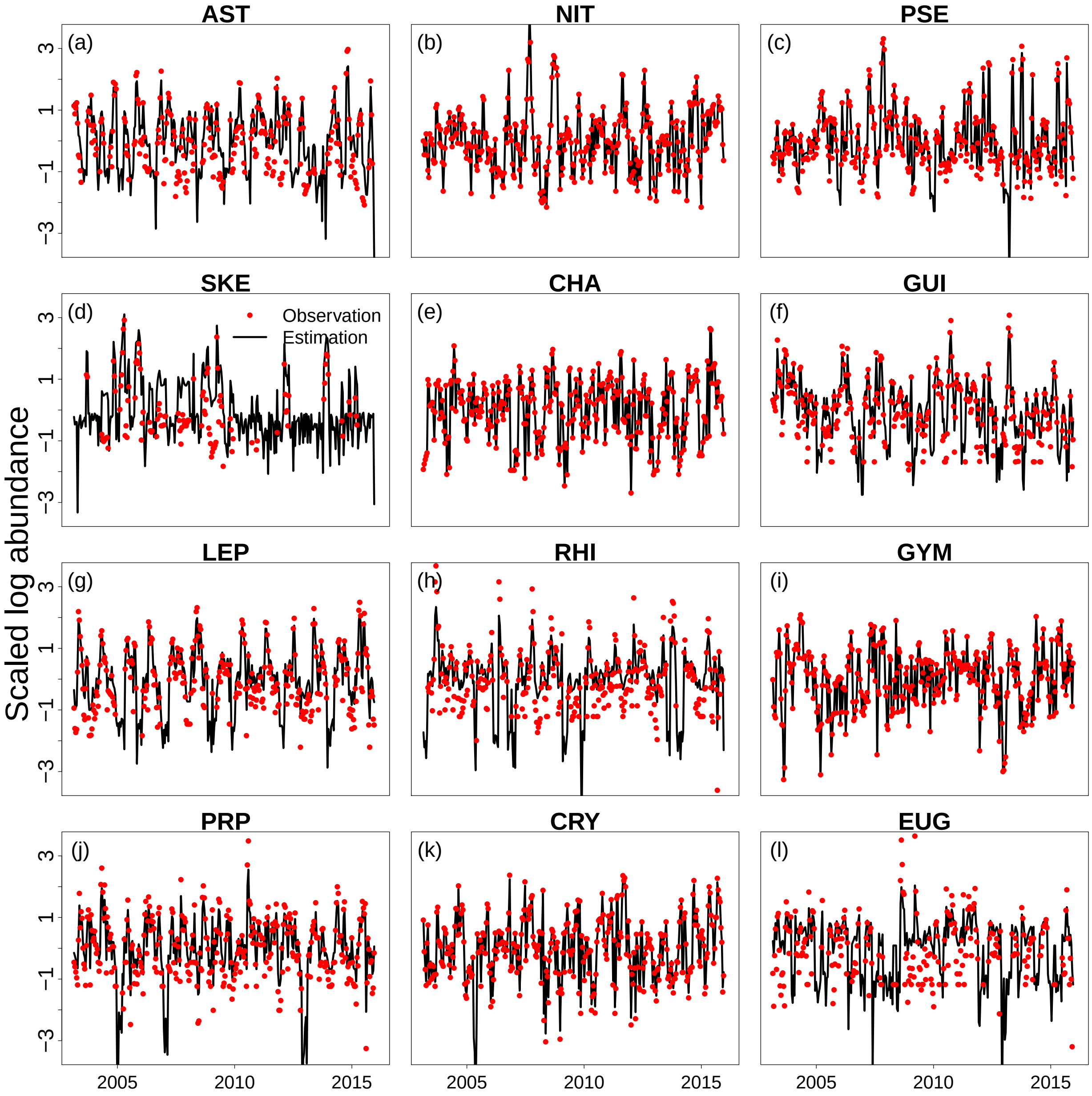
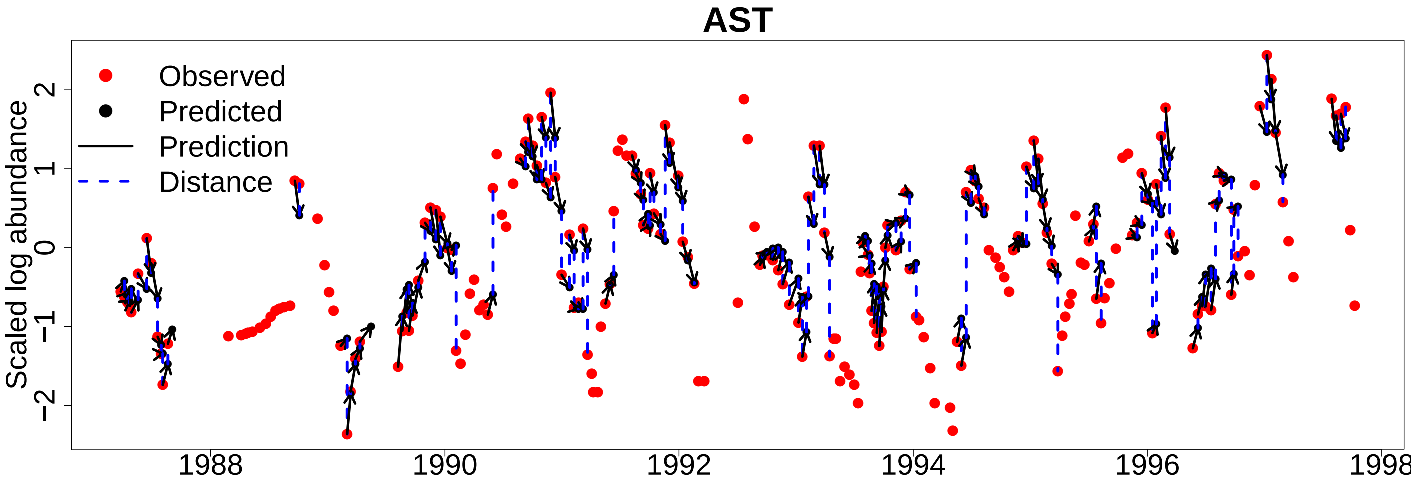


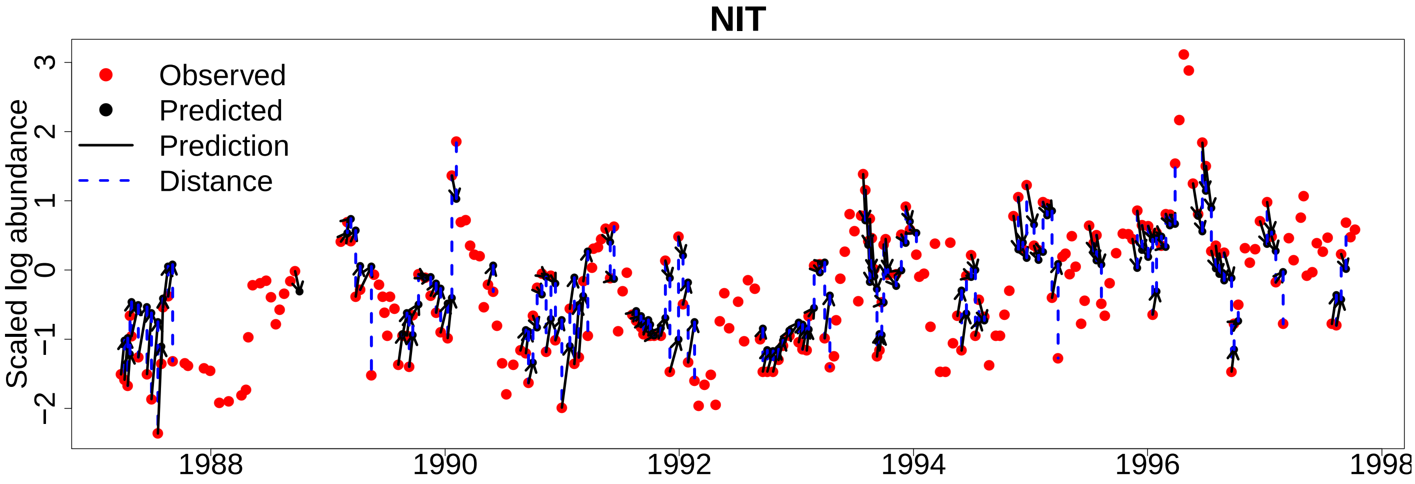
Figure A2.8: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) for Buoy 7 site, using a diagonal interaction matrix. Composition of planktonic groups is described in Table 1 in the main text.

A2.2.5.2 Quality of prediction, estimated values vs observations

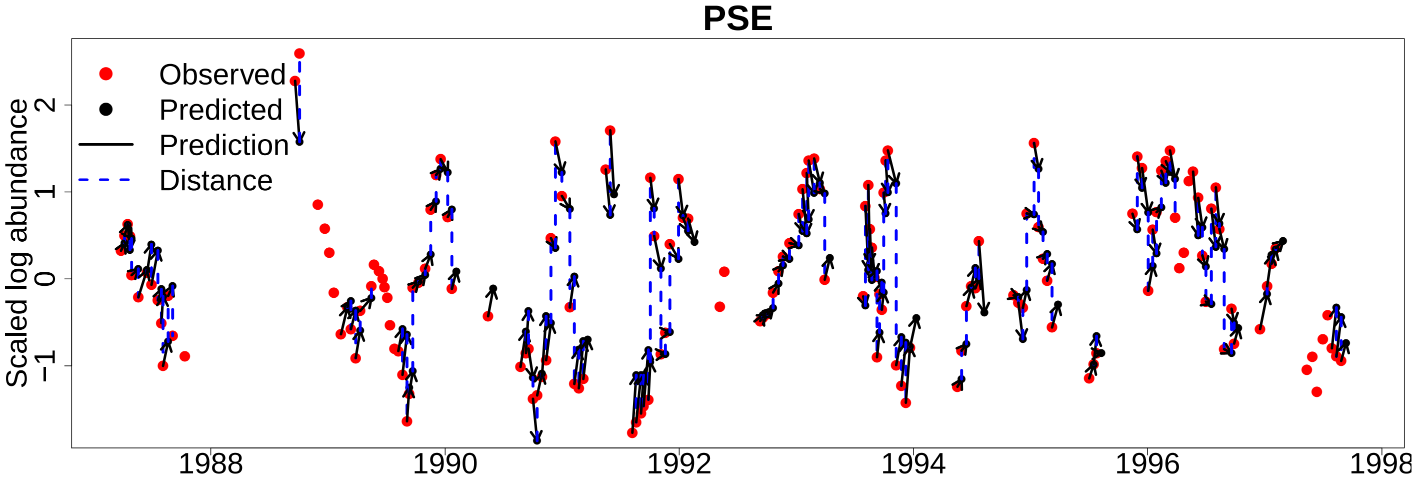
Cross-validation was performed on Teychan site by applying each model to the first 10 years (1987-1996) of the Teychan time series, that were not used for the MAR(1) model fitting. We removed the effect of cryptophytes and euglenophytes, which were not counted until 1996: their log-densities were set to zero during the prediction step.



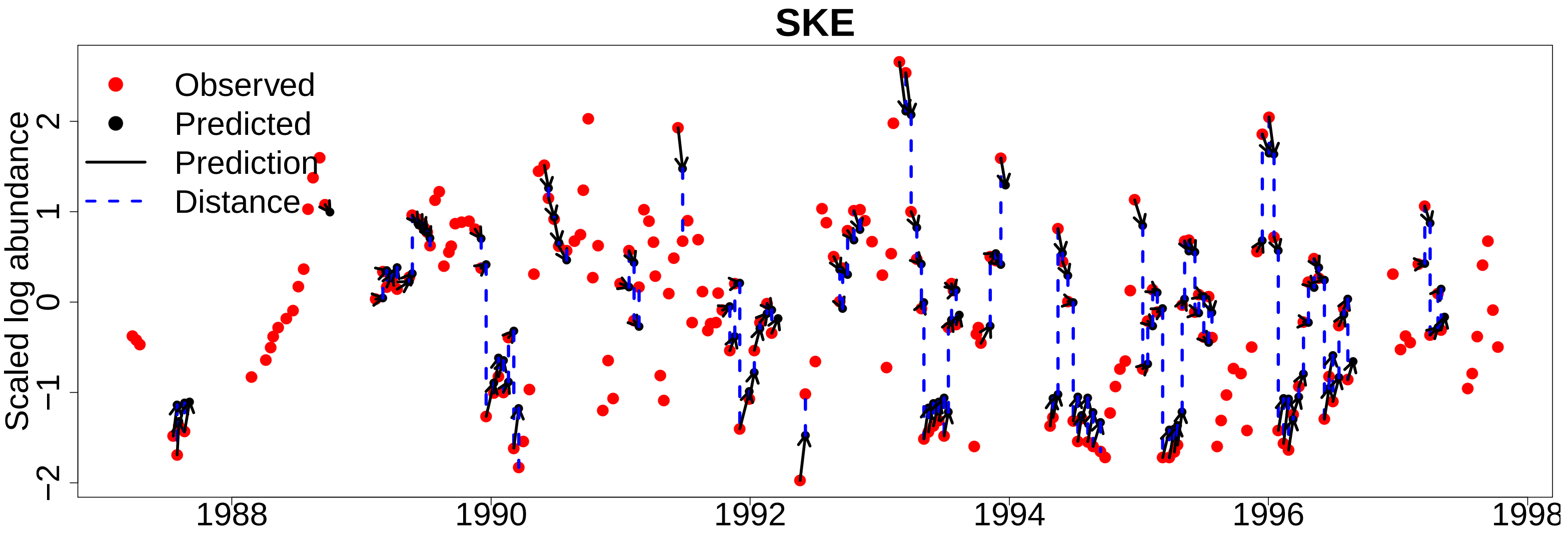
(a) AST



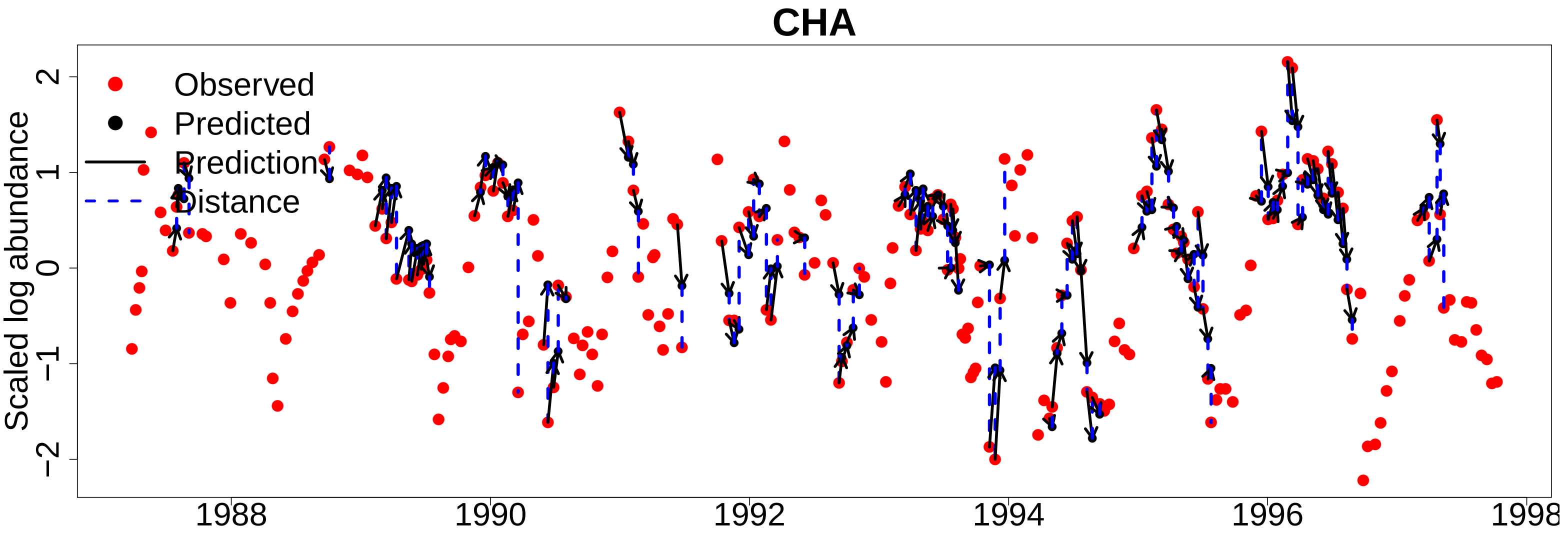
(b) NIT



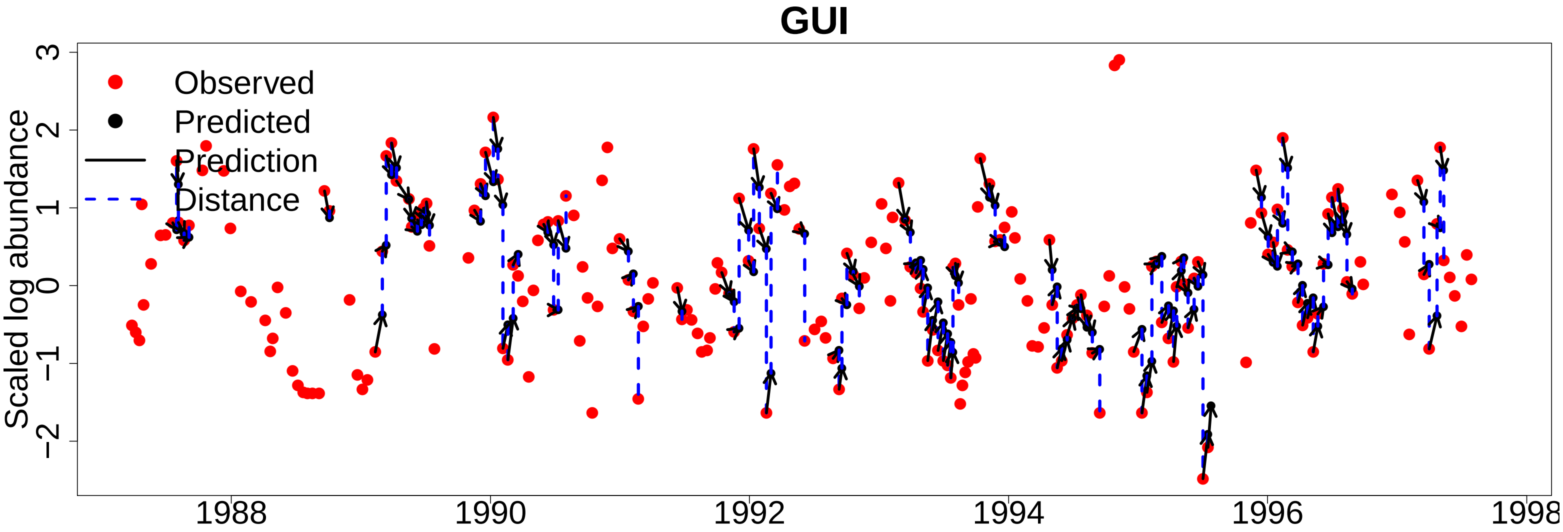
(c) PSE



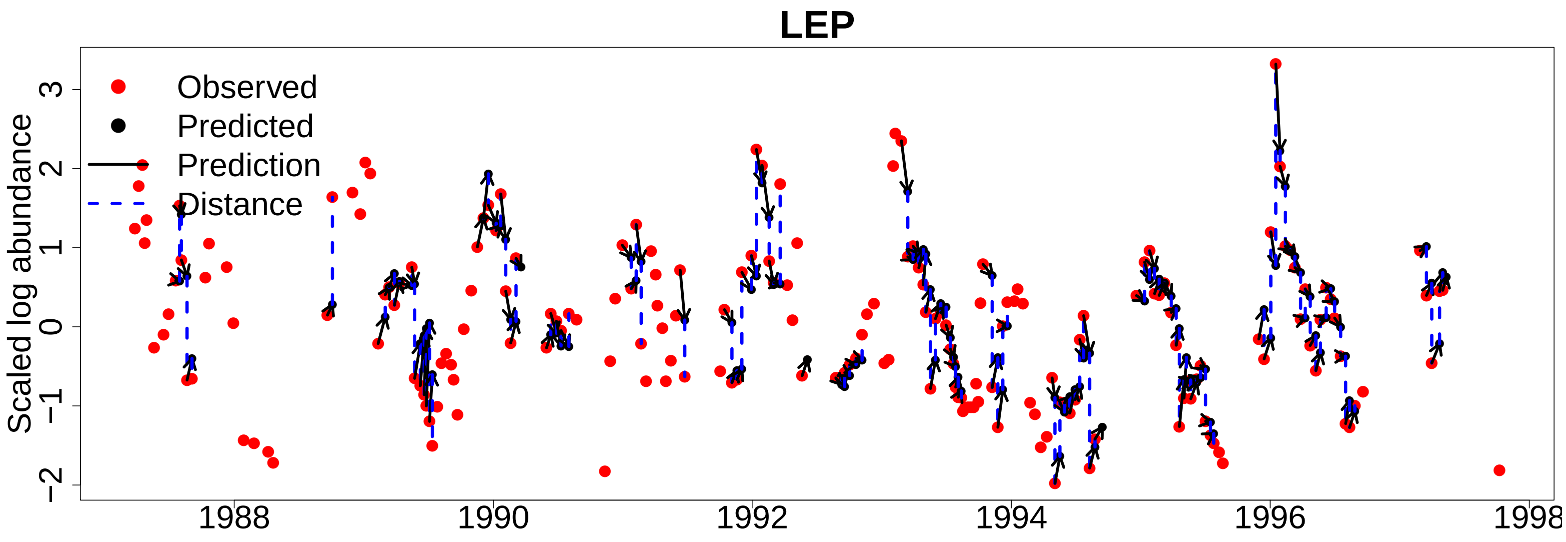
(d) SKE



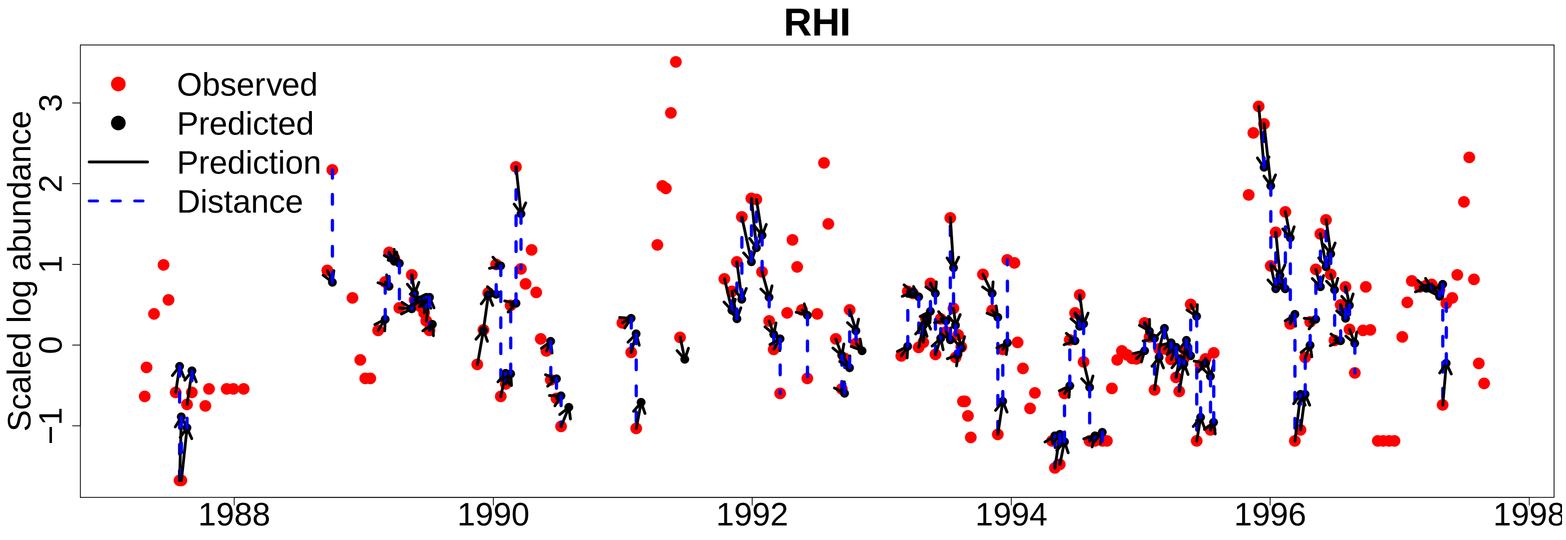
(e) CHA



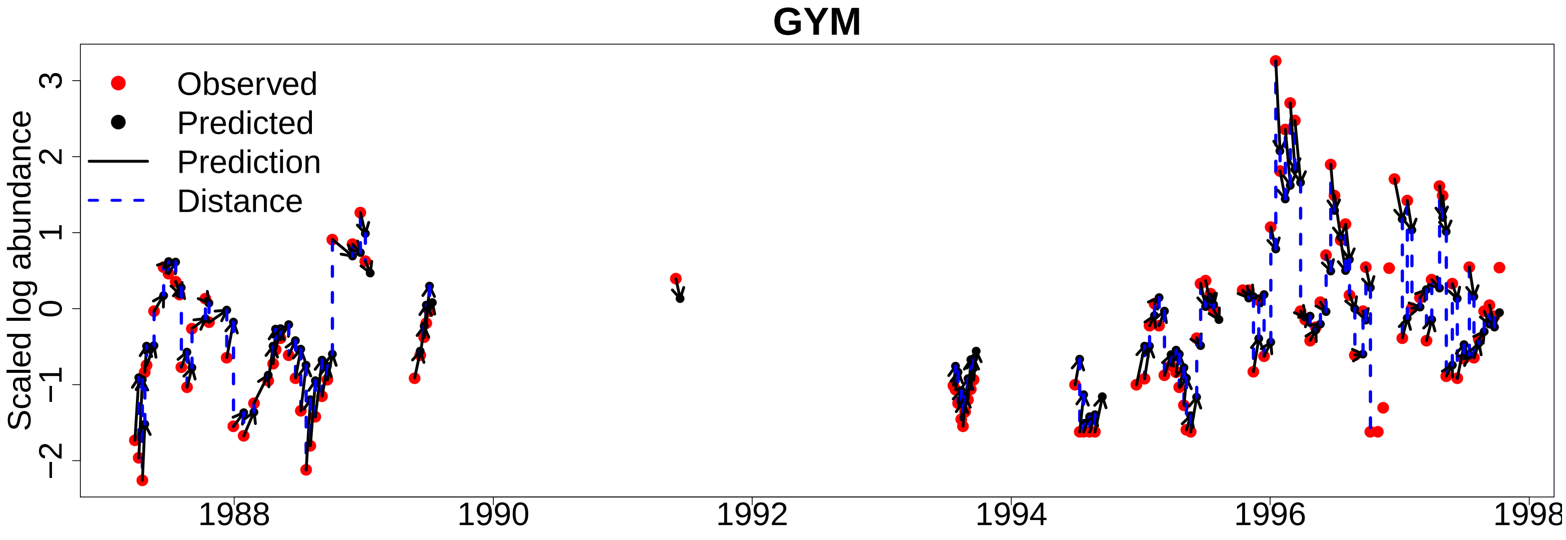
(f) GUI


LEP

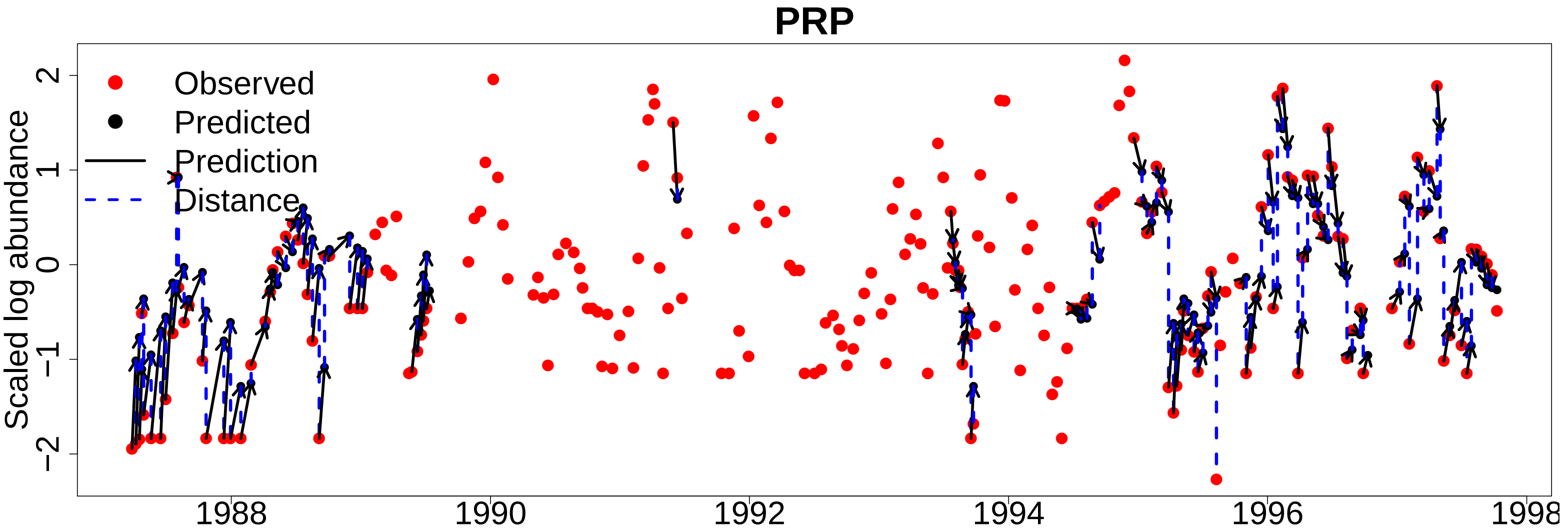
(g) LEP


RHI

(h) RHI


GYM

(i) GYM



(j) PRP

Figure A2.9: Comparison of predicted dynamics and observations for the first years of the time series (1987-1996) at Teychan site, using an interaction matrix differentiating between pennate and centric diatoms. Predicted values (black dots) are calculated with estimated parameters using the observed values (red dots) at the previous sampling date. The distance between observed and predicted value for the same sampling date is shown by blue dotted lines. EUG and CRY were not counted in the first years and their abundances were therefore not taken into account in the predictions. Estimates for the other MAR models are presented in Supplementary material Appendix 6: Section A6.8.

References

Beisner, B.E., Ives, A.R. & Carpenter, S.R. (2003). The effects of an exotic fish invasion on the prey communities of two lakes. *Journal of Animal Ecology*, 72, 331–342.

Bell, R., Fogarty, M. & Collie, J. (2014). Stability in marine fish communities. *Marine Ecology Progress Series*, 504, 221–239.

Burnham, K.P. & Anderson, D.R. (2002). *Model selection and multimodel inference: a practical information-theoretic approach*. 2nd edn. Springer, New York.

Cavanaugh, J.E. & Shumway, R.H. (1997). A bootstrap variant of AIC for state-space model selection. *Statistica Sinica*, pp. 473–496.

Griffiths, J.R., Hajdu, S., Downing, A.S., Hjerne, O., Larsson, U. & Winder, M. (2015). Phytoplankton community interactions and environmental sensitivity in coastal and offshore habitats. *Oikos*, 125, 1134–1143.

Gsell, A.S., Özkundakci, D., Hébert, M.P. & Adrian, R. (2016). Quantifying change in pelagic plankton network stability and topology based on empirical long-term data. *Ecological Indicators*, 65, 76–88.

Helske, J. (2017). KFAS: Exponential family state space models in R. *Journal of Statistical Software*, 78, 1–39.

Holmes, E., Ward, E. & Wills, K. (2013). *MARSS: Multivariate Autoregressive State-Space Modeling*. R package version 3.9.

Ives, A.R., Carpenter, S.R. & Dennis, B. (1999). Community interaction webs and zooplankton responses to planktivory manipulations. *Ecology*, 80, 1405–1421.

Ives, A.R., Dennis, B., Cottingham, K.L. & Carpenter, S.R. (2003). Estimating community stability and ecological interactions from time-series data. *Ecological monographs*, 73, 301–330.

Klug, J.L. & Cottingham, K.L. (2001). Interactions among environmental drivers: Community responses to changing nutrients and dissolved organic carbon. *Ecology*, 82, 3390–3403.

Scheef, L.P., Hampton, S.E. & Izmest'eva, L.R. (2013). Inferring plankton community structure from marine and freshwater long-term data using multivariate autoregressive models. *Limnology and Oceanography: Methods*, 11, 475–484.

Shumway, R.H. & Stoffer, D.S. (2010). *Time Series Analysis and Its Applications: With R Examples*. Springer Science & Business Media.

Turchin, P. (2003). *Complex Population Dynamics: A Theoretical/Empirical Synthesis*. Princeton University Press.

Appendix 3. Timing of covariates in MAR models

A3.1 Model selection

A3.1.1 Model selection criteria

There are two possible formulations of the MAR model when it comes to covariates: the first one, described by Ives *et al.* (2003) relates the log-abundance at time t (or $t+1$) to the values of the environmental variables at the same time t (or, $t+1$, eq. A3.1) whereas Hampton *et al.* (2013) use a lagged covariate (eq. A3.2). The latter formulation, relying on a shift in environmental data, led to a slightly different dataset. AICc and BIC in this section are therefore slightly different from those presented in the main text. All results presented here use a seasonal variable in $\mathbf{u}_t$.

$$\mathbf{n}_{t+1} = \mathbf{B}\mathbf{n}_t + \mathbf{C}\mathbf{u}_{t+1} + \mathbf{e}_t, \mathbf{e}_t \sim \mathcal{N}_p(0, \mathbf{Q}) \tag{A3.1}$$

$$\mathbf{n}_{t+1} = \mathbf{B}\mathbf{n}_t + \mathbf{C}\mathbf{u}_t + \mathbf{e}_t, \mathbf{e}_t \sim \mathcal{N}_p(0, \mathbf{Q}) \tag{A3.2}$$

Several criteria were used to compare the adequacy of these versions of the MAR(1) model.

Table A3.1: AICc and BIC for different interaction matrices at Teychan and Buoy 7 sites (see Table 4 in the main text and Appendix A2: Tables A2.5, A2.6, A2.7 for matrix definition), using the direct covariate value (eq. A3.1) or a lagged covariate (eq. A3.2)

Criteria	Model	Null	Unconstrained	Pennate vs. Centric	Diat vs. Dino	Inter-phylum
AICc	Teychan (eq. A3.1)	11921	11991	11916	11928	11976
	Teychan (eq. A3.2)	12020	12077	12010	12025	11061
	Buoy 7 (eq. A3.1)	8901	8955	8865	8895	8949
	Buoy 7 (eq. A3.2)	8969	9016	8930	8960	9013
BIC	Teychan (eq. A3.1)	12222	12834	12349	12485	12582
	Teychan (eq. A3.2)	12321	12920	12443	12582	12667
	Buoy 7 (eq. A3.1)	9173	9711	9256	9397	9494
	Buoy 7 (eq. A3.2)	9241	9772	9321	9462	9558

A3.1.2 Differences in coefficients due to timing of the covariates

Table A3.2: Model coefficients for interactions at Teychan/Buoy 7, using a matrix allowing intra-phylum interactions, differentiating between pennate and centric diatoms, and a lagged covariate (eq. A3.2). Changes resulting from adopting this model (as compared to the main text model) are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. The identity matrix was subtracted to the interaction matrix in order to make effects on growth rates comparable. Composition of planktonic groups is described in Table 1 in the main text.

	AST	NIT	PSE	SKE	CHA	GUI	LEP	RHI	GYM	PRP	CRY	EUG
AST	-0.29* (1.6%) / -0.35* (-0.7%)	0.11* (-21.1%) / 0.17* (-3.9%)	-0.03 (18.6%) / 0.00 (75.6%)									
NIT	-0.01 (51.4%) / -0.05 (-19.0%)	-0.42* (0.6%) / -0.38* (1.8%)	-0.06 (15.8%) / -0.09* (-5.6%)									
PSE	0.08* (11.2%) / 0.02 (45.4%)	-0.02 (6.8%) / 0.10 (-72.9%)	-0.33* (-1.5%) / -0.39* (0.1%)									
SKE				-0.21* (-0.2%) / -0.42* (0.6%)	-0.01 (49.0%) / 0.05 (6.9%)	0.06* (2.1%) / -0.05 (10.0%)	-0.03 (16.6%) / -0.04 (-115.2%)	0.05 (-1.4%) / 0.07 (-6.9%)				
CHA				0.05* (-5.4%) / -0.04 (-20.0%)	-0.44* (-5.6%) / -0.58* (0.8%)	0.05* (2.9%) / 0.04 (5.0%)	0.06 (-152.3%) / 0.12* (-9.7%)	0.05 (-12.9%) / 0.09* (4.5%)				
GUI				-0.01 (-41.6%) / -0.01 (26.2%)	-0.02 (41.1%) / -0.14* (2.3%)	-0.26* (-0.9%) / -0.26* (0.2%)	-0.04 (36.3%) / 0.00 (238.5%)	0.02 (-66.1%) / 0.00 (352.4%)				
LEP				-0.01 (-199.8%) / -0.13* (3.9%)	0.03 (-93.2%) / 0.01 (229.8%)	0.08* (-6.3%) / 0.05 (13.2%)	-0.34* (-5.8%) / -0.38* (-3.2%)	0.03 (-28.8%) / 0.02 (-3.7%)				
RHI				0.00 (67.3%) / -0.08 (7.9%)	0.06 (-73.4%) / -0.04 (-16.6%)	0.07* (-7.9%) / 0.07 (-3.5%)	-0.03 (51.2%) / 0.06 (17.0%)	-0.31* (-1.5%) / -0.36* (0.7%)				
GYM									-0.35* (-0.1%) / -0.50* (0.1%)	0.06 (-35.3%) / 0.23* (-16.8%)	-0.02 (-3.8%) / 0.02 (26.9%)	
PRP									-0.01 (46.4%) / 0.01 (15.8%)	-0.36* (-3.6%) / -0.36* (-2.3%)	0.05 (-8.4%) / 0.02 (16.8%)	
CRY									-0.03 (-16.2%) / -0.03 (-1.2%)	0.00 (44.6%) / 0.08 (-7.2%)	-0.44* (-2.9%) / -0.47* (-0.8%)	
EUG												-0.34* (-2.1%) / -0.39* (-0.8%)

Other results (for all interaction matrices at both sites) can be found in Supplementary material Appendix 6: section A6.4.

Table A3.3: Model coefficients for covariates at Teychan/Buoy 7, using a matrix allowing intra-phylum interactions, differentiating between pennate and centric diatoms, and a lagged covariate (eq. A3.2). Changes resulting from adopting this model (as compared to the main text model) are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. Composition of planktonic groups is described in Table 1 in the main text.

	SAL	CumRg	Wind energy	season
AST	0.03 (36.6%) / -0.01(-581.1%)	-0.04 (12.1%) / -0.09* (-14.0%)	-0.02 (46.8%) / 0.00(113.6%)	-0.15* (-4.4%) / -0.14* (13.6%)
NIT	-0.02 (153.0%) / -0.08* (-55.0%)	0.06 (-80.5%) / -0.01(41.7%)	-0.02 (42.2%) / -0.06(-185.0%)	0.23* (0.6%) / 0.19* (3.5%)
PSE	-0.05 (-40.8%) / -0.05(-120.2%)	0.05 (16.5%) / 0.06(-144.1%)	-0.08* (46.4%) / -0.07(69.2%)	0.06 (28.2%) / -0.05(-2269.7%)
SKE	0.01 (149.2%) / -0.07(5.5%)	0.02 (-118.8%) / -0.08(28.7%)	0.01 (-918.3%) / -0.02(29.8%)	0.00 (90.9%) / 0.00(88.1%)
CHA	-0.11* (-0.8%) / -0.10* (-190.7%)	0.09* (-47.1%) / 0.05(-91.1%)	-0.02 (85.0%) / -0.12* (20.6%)	0.19* (30.6%) / 0.14* (16.6%)
GUI	-0.04 (-117.9%) / -0.03(260.5%)	0.06 (-38.1%) / 0.03(-2161.4%)	-0.04 (44.1%) / -0.05(50.0%)	0.08* (43.7%) / 0.04(19.4%)
LEP	-0.10* (-91.6%) / -0.03(-123.2%)	0.13* (22.7%) / 0.19* (-10.7%)	-0.04 (-15.8%) / -0.04(63.0%)	0.03 (78.5%) / 0.01(93.6%)
RHI	-0.06 (-105.6%) / 0.01(7.6%)	0.05 (26.8%) / 0.02(154.5%)	0.03 (164.4%) / -0.09* (28.5%)	0.03 (72.3%) / 0.04(1.6%)
GYM	-0.07* (-164.6%) / -0.02(60.6%)	0.03 (67.8%) / 0.03(35.0%)	-0.07 (3.5%) / 0.00(98.9%)	-0.03 (-11193.5%) / -0.07(-141.0%)
PRP	-0.08* (-27.2%) / -0.04(44.0%)	0.13* (11.9%) / 0.12* (-70.3%)	0.03 (432.8%) / 0.01(111.4%)	0.07* (49.3%) / 0.03(60.2%)
CRY	0.00 (95.7%) / 0.05(152.5%)	0.11* (-871.7%) / 0.00(115.3%)	-0.01 (1081.4%) / -0.06(259.3%)	0.08* (26.1%) / 0.13* (-1.8%)
EUG	-0.01 (91.8%) / 0.01(110.6%)	0.13* (503.3%) / 0.07(-126.7%)	-0.03 (60.8%) / 0.07(538.4%)	0.16* (15.3%) / 0.12* (7.0%)

References

Hampton, S.E., Holmes, E.E., Scheef, L.P., Scheuerell, M.D., Katz, S.L., Pendleton, D.E. & Ward, E.J. (2013). Quantifying effects of abiotic and biotic drivers on community dynamics with multivariate autoregressive (MAR) models. *Ecology*, 94, 2663–2669.

Ives, A.R., Dennis, B., Cottingham, K.L. & Carpenter, S.R. (2003). Estimating community stability and ecological interactions from time-series data. *Ecological monographs*, 73, 301–330.

Appendix 4. Full variance-covariance matrix Q

A4.1 Model selection

A4.1.1 Model selection criteria

In our study, we chose to use a diagonal error matrix, **Q**. This Appendix shows that there are only small differences for significant coefficients in both **B** and **C** using an unconstrained Q matrix.

Table A4.1: AICc and BIC for different interaction matrices at Teychan and Buoy 7 (see Table 4 in the main text and Tables A2.5, A2.6, A2.7 in Supplementary material Appendix 2 for matrix definition), with an unconstrained variance-covariance matrix **Q**, compared to a diagonal matrix (used in the analyses in the main text)

Criterion		Null	Unconstrained	Pennate vs. Centric	Diat vs. Dino	Inter-phylum
AICc	Teychan Q diag	11970	12039	**11964**	11971	12025
	Teychan Q unconstrained	**11737**	11832	11747	11766	11802
	Buoy 7 Q diag	8924	8980	**8889**	8920	8972
	Buoy 7 Q unconstrained	8721	8786	**8698**	8728	8769
BIC	Teychan Q diag	**12271**	12882	12398	12533	12631
	Teychan Q unconstrained	**12310**	12941	12451	12592	12677
	Buoy 7 Q diag	**9196**	9736	9280	9422	9517
	Buoy 7 Q unconstrained	**9238**	9777	9331	9470	9554

A4.1.2 Differences in coefficients due to the error matrix

Table A4.2: Model coefficients for interactions at Teychan/Buoy 7 using an interaction matrix differentiating between pennate and centric diatoms, and an unconstrained variance-covariance matrix **Q** for the error term. Changes from the results obtained with a diagonal **Q** are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. The identity matrix was subtracted to the interaction matrix in order to make effects on growth rates comparable. Composition of planktonic groups is described in Table 1 in the main text.

	AST	NIT	PSE	SKE	CHA	GUI	LEP	RHI	GYM	PRP	CRY	EUG
AST	-0.30* (2.2%) / -0.35* (-0.7%)	0.11* (-12.2%) / 0.14* (11.8%)	-0.03 (2.5%) / 0.01 (-178.1%)									
NIT	-0.02 (20.5%) / -0.05 (-6.3%)	-0.42* (1.4%) / -0.38* (2.0%)	-0.07* (7.2%) / -0.09* (3.5%)									
PSE	0.06 (38.6%) / 0.01 (51.9%)	0.00 (119.0%) / 0.06 (-1.4%)	-0.35* (0.9%) / -0.40* (1.5%)									
SKE				-0.21* (0.7%) / -0.41* (0.5%)	-0.03 (-101.4%) / 0.06 (-8.3%)	0.06* (6.3%) / -0.06 (-8.6%)	-0.03 (13.4%) / -0.01 (34.2%)	0.05 (-4.1%) / 0.07 (-17.7%)				
CHA				0.04 (13.3%) / -0.02 (30.7%)	-0.46* (-1.0%) / -0.56* (-4.6%)	0.04 (28.5%) / 0.03 (30.8%)	0.02 (8.1%) / 0.12* (-10.6%)	0.04 (3.9%) / 0.07 (23.2%)				
GUI				-0.01 (-122.3%) / 0.00 (54.4%)	-0.04 (-13.6%) / -0.14* (3.8%)	-0.26* (0.1%) / -0.27* (2.0%)	-0.07 (0.9%) / 0.01 (-574.8%)	0.02 (-17.3%) / -0.01 (-1162.0%)				
LEP				-0.01 (-79.2%) / -0.12* (10.7%)	0.02 (-30.3%) / 0.00 (69.7%)	0.06* (20.5%) / 0.05 (6.7%)	-0.38* (0.4%) / -0.40* (0.0%)	0.02 (2.0%) / 0.00 (105.4%)				
RHI				0.00 (59.4%) / -0.08* (5.2%)	0.05 (-34.6%) / -0.03 (11.5%)	0.05 (16.8%) / 0.07 (2.2%)	-0.06 (5.7%) / 0.07 (1.8%)	-0.32* (0.6%) / -0.35* (0.1%)				
GYM									-0.35* (-0.6%) / -0.50* (0.4%)	0.02 (48.8%) / 0.19* (4.1%)	-0.03 (-60.5%) / 0.03 (17.0%)	
PRP									-0.02 (-18.9%) / 0.03 (-73.7%)	-0.40* (2.2%) / -0.40* (3.7%)	0.04 (10.1%) / 0.01 (60.5%)	
CRY									-0.02 (29.9%) / -0.01 (63.3%)	0.00 (49.8%) / 0.06 (24.6%)	-0.49* (4.7%) / -0.49* (4.6%)	
EUG												-0.37* (2.7%) / -0.42* (3.8%)

Remaining results (for all interaction matrices at both sites) can be found in Supplementary material Appendix 6: Section A6.5.

Table A4.3: Model coefficients for interactions at Teychan/Buoy 7 using an interaction matrix differentiating between pennate and centric diatoms, and an unconstrained variance-covariance matrix **Q** for the error term. Changes from the results obtained with a diagonal **Q** are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. Composition of planktonic groups is described in Table 1 in the main text.

	SAL	CumRg	Wind energy	season
AST	0.05 (-1.8%) / 0.00(-86.9%)	-0.04 (6.3%) / -0.09* (-5.3%)	-0.04 (5.3%) / -0.02(-13.0%)	-0.15* (-7.0%) / -0.15* (5.5%)
NIT	0.04 (1.7%) / -0.05(-0.8%)	0.03 (6.3%) / -0.02(-27.3%)	-0.04 (-0.9%) / -0.02(-8.8%)	0.23* (-1.5%) / 0.20* (-1.7%)
PSE	-0.04 (8.2%) / -0.02(4.0%)	0.07* (-11.4%) / 0.02(5.9%)	-0.15* (2.9%) / -0.22* (-0.3%)	0.07 (24.4%) / -0.01(-280.0%)
SKE	-0.02 (3.1%) / -0.08(-0.4%)	0.01 (28.9%) / -0.12* (-1.7%)	0.00 (66.9%) / -0.03(4.8%)	0.03 (-55.4%) / -0.04(-26.8%)
CHA	-0.10* (0.4%) / -0.03(2.1%)	0.06* (2.7%) / 0.03(6.5%)	-0.15* (-0.3%) / -0.15* (1.1%)	0.27* (-1.6%) / 0.16* (5.2%)
GUI	-0.02 (-0.6%) / 0.02(1.2%)	0.04 (2.7%) / 0.00(94.6%)	-0.06* (-0.5%) / -0.10* (0.0%)	0.15* (-1.7%) / 0.05(6.6%)
LEP	-0.05 (1.2%) / -0.01(6.9%)	0.16* (0.6%) / 0.17* (-1.1%)	-0.03 (-0.6%) / -0.12* (-0.2%)	0.13* (-3.1%) / 0.09* (-4.9%)
RHI	-0.03 (0.1%) / 0.01(-3.4%)	0.07* (2.3%) / -0.03(3.9%)	-0.04 (1.3%) / -0.13* (0.6%)	0.10* (5.1%) / 0.04(1.7%)
GYM	-0.03 (-12.5%) / -0.06(-0.9%)	0.10* (-1.8%) / 0.04(-1.9%)	-0.07* (-1.8%) / -0.15* (-0.4%)	0.01 (3942.3%) / -0.02(16.4%)
PRP	-0.06 (-3.9%) / -0.07(-1.5%)	0.14* (-1.5%) / 0.07(0.8%)	-0.01 (-9.3%) / -0.05(-3.1%)	0.14* (-6.7%) / 0.08* (-13.2%)
CRY	-0.09* (-2.8%) / -0.09* (-0.9%)	0.01 (19.9%) / 0.01(37.8%)	0.00 (23.1%) / 0.03(2.0%)	0.10* (-1.4%) / 0.14* (-5.8%)
EUG	-0.09* (0.8%) / -0.06(-1.0%)	-0.03 (-4.5%) / 0.03(7.3%)	-0.06* (0.5%) / -0.02(-18.1%)	0.19* (-4.4%) / 0.13* (-4.5%)

Appendix 5. Non-linear models

A5.1 Pennate and centric interactions: TAR models

Threshold multivariate autoregressive (TAR) models (see Eq. 5 in the main text) require the definition or estimation of threshold(s) between different phases, that may correspond to different dynamics.

A5.1.1 Density-based phases - nonlinear competition

We defined integrated irradiance as the main environmental driver, based on MAR(1) model results. Litchman *et al.* (2004) also showed that light conditions could impact competition for resources between plankton groups. Two log-linear MAR(1) models were fitted to the data, on both sides of the threshold: the first one corresponded to non-bloom conditions while the second one represented the dynamics during a bloom. The log-abundance threshold θ for regime switch was set to 11, which implies that blooming conditions represented about 25% of both AST and CHA time series.

A5.1.2 Definition of environment-based phases in TAR models

Defining a environmental-based TAR model when the environmental conditions are multi-dimensional requires two main choices: the choice of a unifying variable that can summarize external conditions of the system (i.e., the phase) and the definition or estimation of a threshold for such a variable. The number of different phases, and therefore thresholds, is itself open to debate. Below, we provide a detailed rationale for these choices.

Because seasonality obviously influences all variables at the annual scale, using the date as the leading environmental variable and delineating several periods throughout the year would be possible. On the other hand, D'Alelio *et al.* (2015) showed that coastal areas react below the annual scale to the movement of different water masses, which is in line with the below-annual scale temporal variation in abiotic variables that we observed in our dataset. Therefore, using an environmental indicator for defining the phase, based on a clustering of the environmental variables was also an option.

We compared different clustering methods to differentiate environmental conditions in the water masses in which plankton grow. K-means, based on Hartigan and Wong's algorithm with 5 randomly selected starting values, was compared to hierarchical clustering based on mean (Unweighted Pair Group Method with Arithmetic mean (UPGMA), following D'Alelio *et al.* (2015)) and to Ward's squared distance. This clustering used scaled salinity and chlorophyll *a* as proxies for environmental conditions in the water masses. We chose to work with 2-phase hierarchical clustering based on Ward's method. Two phases allowed to differentiate between low chlorophyll and salinity vs. high chlorophyll and salinity conditions, while making results comparable to both previous sections and other works in the literature (D'Alelio *et al.* 2015). Using this clustering method to define a phase for both Teychan and Buoy 7 datasets, a different MAR model was fitted to each phase. As before, AICc was then used to compare between diagonal and full interaction matrices.

We can see on Fig. A5.1 that using fixed dates to account for seasonal phenomena led to less differentiated groups than clustering based on environmental conditions. Within the latter approach, the Ward method built the most homogeneous and balanced clusters. Fig A5.2 shows that they correspond to bloom / non-bloom conditions. In the main text and in the following, we therefore used clustering of environmental conditions with the Ward method, rather than the dates, to define environment-based phases.

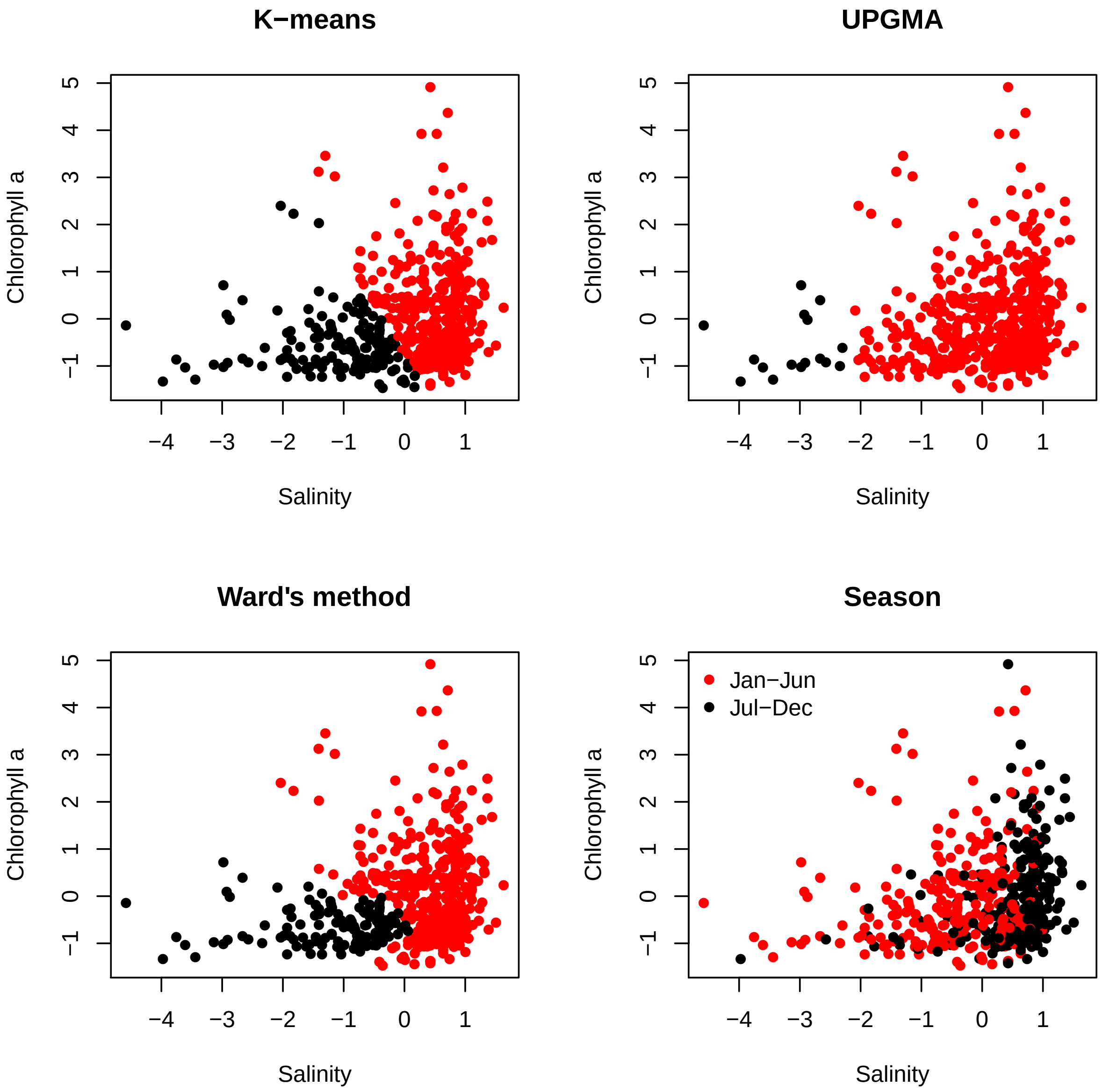


Figure A5.1: Clustering of environmental conditions in 2 phases (corresponding to red and black points), according to scaled salinity and chlorophyll *a*, based on different methods: K-means, hierarchical clustering based on arithmetic mean or on Ward's method. Bottom right corresponds to a seasonal clustering according to fixed dates.

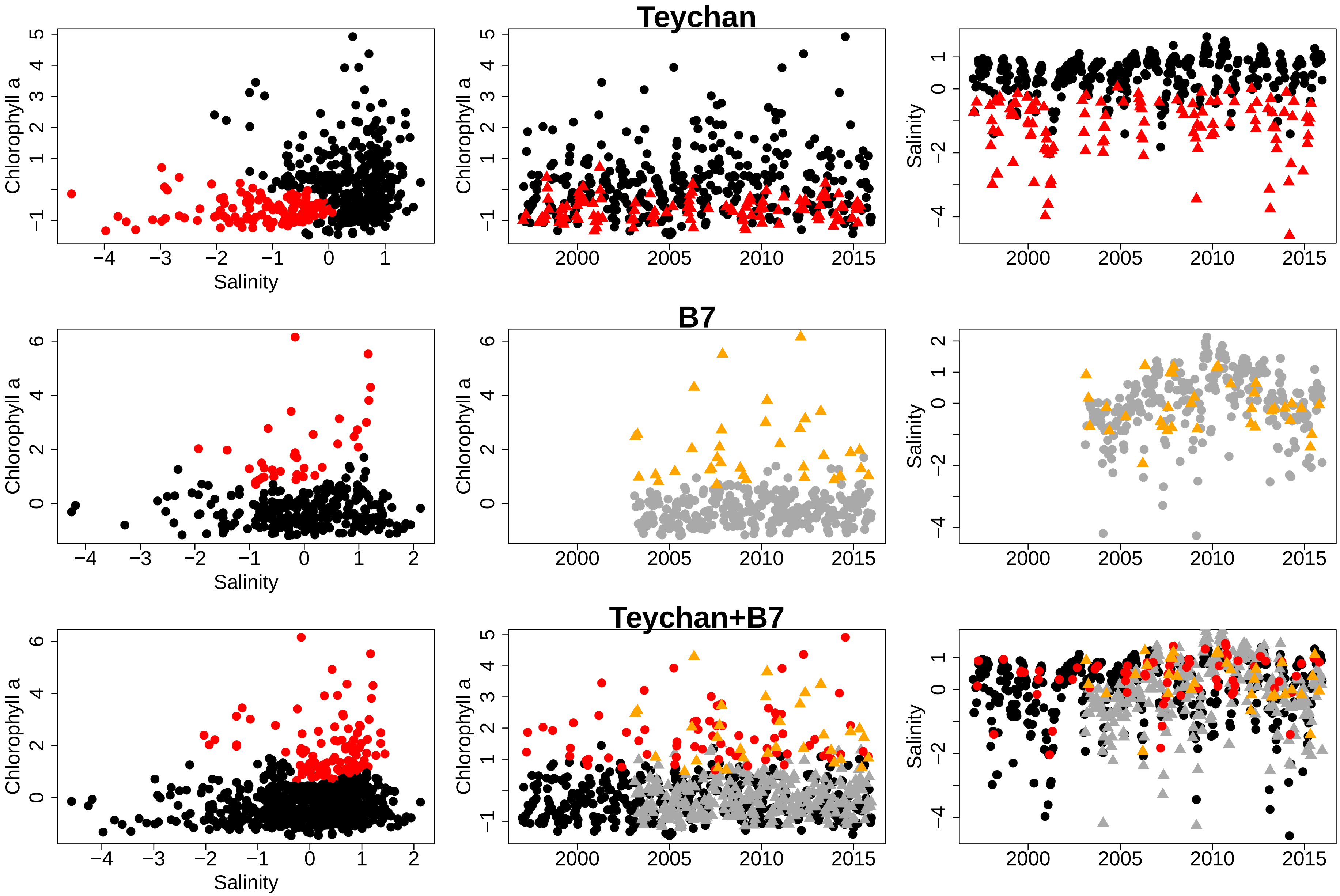


Figure A5.2: Clustering of water masses according to Ward's method using Teychan data set only (first row), Buoy 7 data set only (second row) and both (third row). Classification of each point according to its phase is indicated by different colors in the time series of chlorophyll *a* and salinity in the second and third column.

A5.1.3 Results from a threshold-MAR models

In this section, we present the results of different TAR models (described in Eq. 5). Phases in TAR models were defined for both population densities and environmental conditions. We built different sets of models two environmental drivers (temperature or integrated irradiance) for both Teychan and Buoy 7. All results are shown in Table A5.1. In line the results for Teychan shown in the main text (Table 5), intragroup coefficients are almost always significant and larger than intergroup coefficients. The only significant intergroup interaction between AST and CHA is the negative effect of CHA on AST growth rates at Buoy 7 in non-blooming conditions, and it is much lower than intragroup competition.

Table A5.1: Density- and environment-based TAR model coefficients for a linear model relating growth to log abundance of planktonic groups for *Asterionellopsis* (AST) and *Chaetoceros* (CHA) at Teychan and Buoy 7, according to Eq. 5, with integrated irradiance or temperature as the main environmental driver. Significant coefficients at the 5% threshold are indicated by *.

Site	Model	Phase		Coefficients			
				a	AST	CHA	Irradiance (x10^{-5})
Buoy 7	Density-based	Bloom	AST	12.50*	-0.94*	-0.38	2.48
			CHA	14.82*	0.25	-1.90*	11.12*
		No bloom	AST	7.05*	-0.57*	-0.21	0.67
				6.82*	-0.00	-0.83*	4.36*
	Environment-based	Bloom	AST	4.43	-0.35	-0.28	7.39
			CHA	17.13	0.36	-2.00	-4.02
		No bloom	AST	8.18*	-0.67*	-0.23*	0.84
			CHA	7.09*	0.02	-0.91*	5.21*
				a	AST	CHA	Temperature
Teychan	Density-based	Bloom	AST	6.43*	-0.57*	0.01	-0.03
			CHA	2.07	0.06	-0.49*	0.12*
		No bloom	AST	6.18*	-0.49*	-0.10	-0.02
			CHA	4.44*	-0.03	-0.54*	0.07*
Buoy 7		Bloom	AST	12.85*	-1.17*	-0.41*	0.22
			CHA	10.81	0.03	-1.26*	0.08
		No bloom	AST	6.97*	-0.55*	-0.25*	0.03
			CHA	6.65*	-0.06	-0.84*	0.09*
Teychan	Environment-based	Bloom	AST	5.76*	-0.47*	-0.17*	0.04
			CHA	2.70*	0.01	-0.46	0.09*
		No bloom	AST	6.49*	-0.51*	0.08	-0.15*
			CHA	4.51*	0.03	-0.66*	0.12*
Buoy 7		Bloom	AST	8.27	-0.54	-0.17	-0.16
			CHA	25.83	0.00	-2.06	-0.48
		No bloom	AST	7.86*	-0.67*	-0.30*	0.07
			CHA	6.69*	-0.04	-0.88*	0.11*

A5.2 Non-linear dynamics: Ricker model

Because it is sometimes difficult to judge the degree of linearity from the residuals, we fitted a Ricker model (eq. A5.1) to the growth rates of AST and CHA, similar to Loreau & de Mazancourt (2008)'s model. This model was applied to the whole Teychan time series using `lm` in R. Estimated coefficients from eq. 1 and A5.1 were used to perform simulations corresponding to the Gompertz and Ricker model, respectively. We then compared those to observed dynamics.

$$r_{1,t} = a_{1,t} + dN_{1,t} + cN_{2,t} + vu_t + \epsilon_t \tag{A5.1}$$

where $r_{1,t} = n_{1,t+1} - n_{1,t}$ is the growth rate of species 1 on a log scale, $a_{1,t}$ is the intercept, d is the density dependence of species 1 with untransformed abundance $N_{1,t}$, c is the effect of species 2 on species 1, u_t is water temperature and v is the associated effect. The growth rate of species 2 follows a symmetric equation.

Table A5.2 shows the coefficients estimated on the Ricker model, indicating significant interactions between AST and CHA. However, we note a slight decrease in R^2 when compared to first results obtained with a Gompertz model (Table 5). Simulations of both models were used as a further step in model checking: simulations for the Gompertz model (Fig. A5.3) are much more similar to observed dynamics than the simulations ran with Ricker model coefficients (Fig. A5.4). Therefore, we discard the Ricker model and confirm the apparent absence of interactions between those genera, as presented in the main text.

Table A5.2: Estimated coefficients (and standard error) using a Ricker model relating planktonic growth rates to planktonic abundance and water temperature. Significant coefficients are marked with an asterisk. Parameters are defined in the text.

Species	a	d	c	v	adj. R^2
AST	0.05 (0.40)	-1.5 10^{-6}* (2.2 10^{-7})	-1.8 10^{-6}* (8.4 10^{-7})	0.02 (0.03)	0.11
CHA	0.85* (0.35)	-2.0 10^{-6}* (4.0 10^{-7})	-7.1 10^{-7}* (2.1 10^{-7})	-0.04 (0.02)	0.09

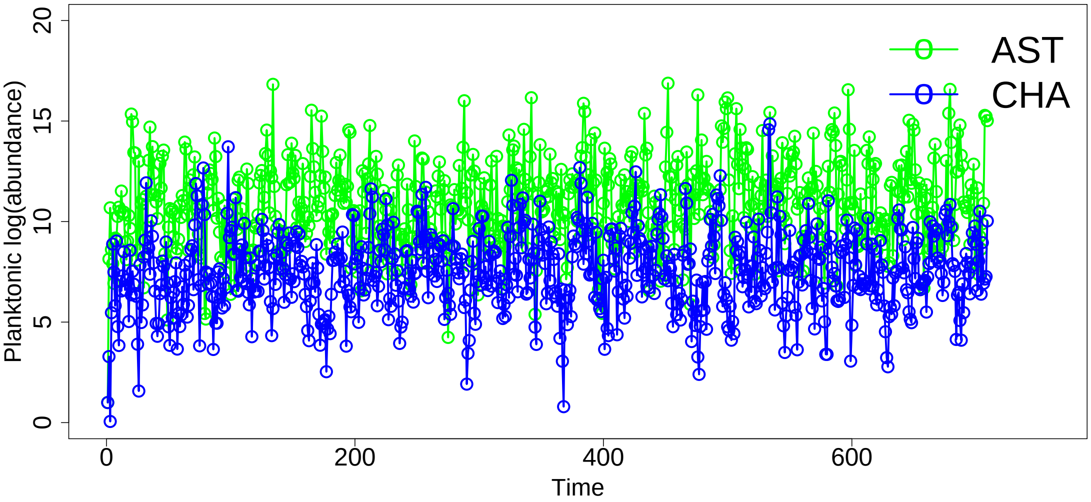


Figure A5.3: Simulation of a 2-species planktonic model using eq. 1 (Gompertz, log-linear model) with coefficients estimated on observed times series at Teychan for AST (green) and CHA (blue)

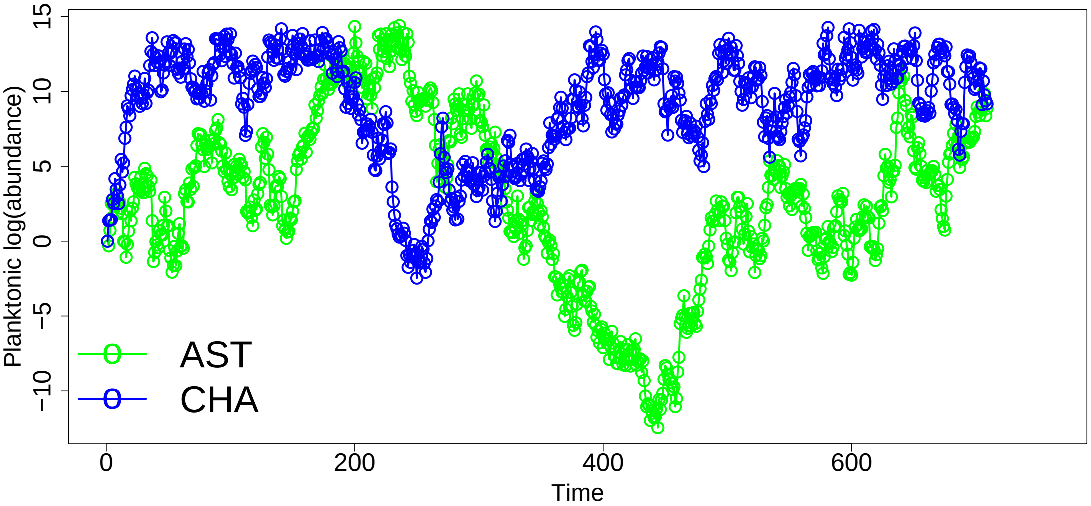


Figure A5.4: Simulation of a 2-species planktonic model using eq. A5.1 (Ricker, non-linear model) with coefficients estimated on observed times series at Teychan for AST (green) and CHA (blue)

References

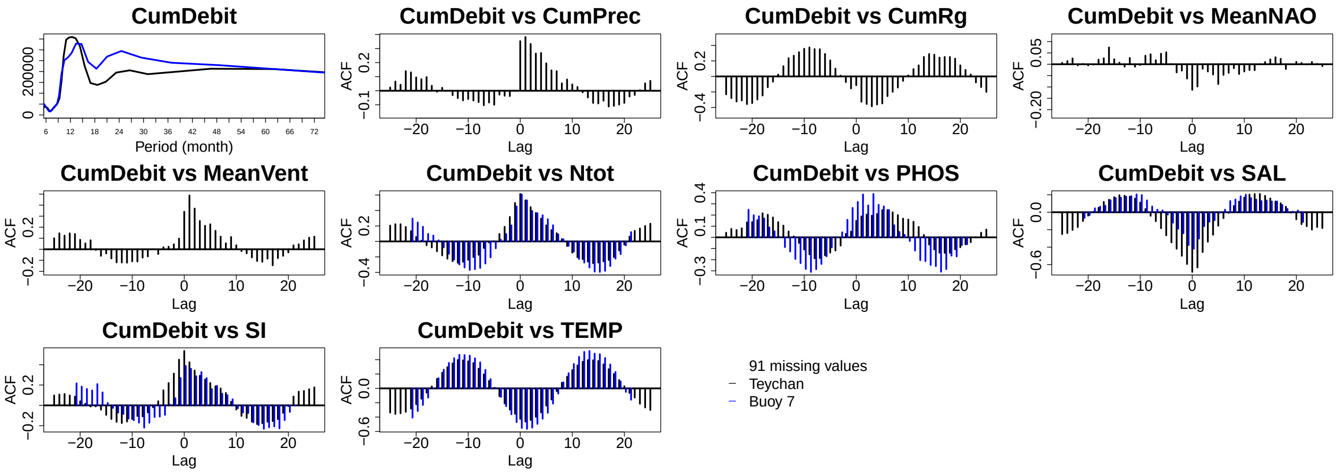
D'Alelio, D., Mazzocchi, M.G., Montresor, M., Sarno, D., Zingone, A., Di Capua, I., Franzè, G., Margiotta, F., Saggiomo, V. & Ribera d'Alcalà, M. (2015). The green-blue swing: plasticity of plankton food-webs in response to coastal oceanographic dynamics. *Marine Ecology*, 36, 1155–1170.

Litchman, E., Klausmeier, C.A. & Bossard, P. (2004). Phytoplankton nutrient competition under dynamic light regimes. *Limnology and Oceanography*, 49, 1457–1462.

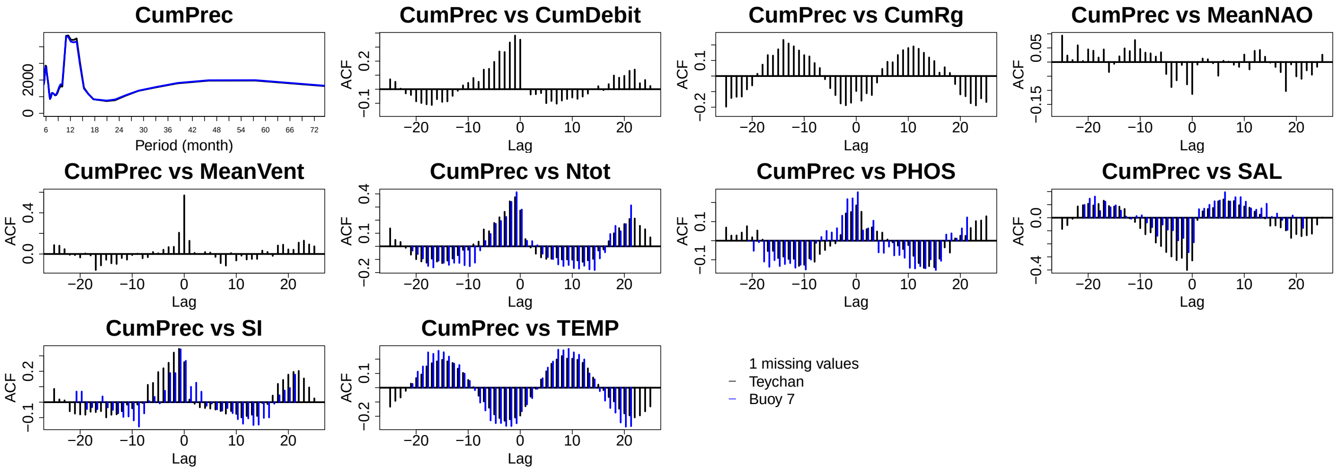
Loreau, M. & de Mazancourt, C. (2008). Species synchrony and its drivers: neutral and nonneutral community dynamics in fluctuating environments. *The American Naturalist*, 172, E48–E66.

Appendix 6. Additional graphs

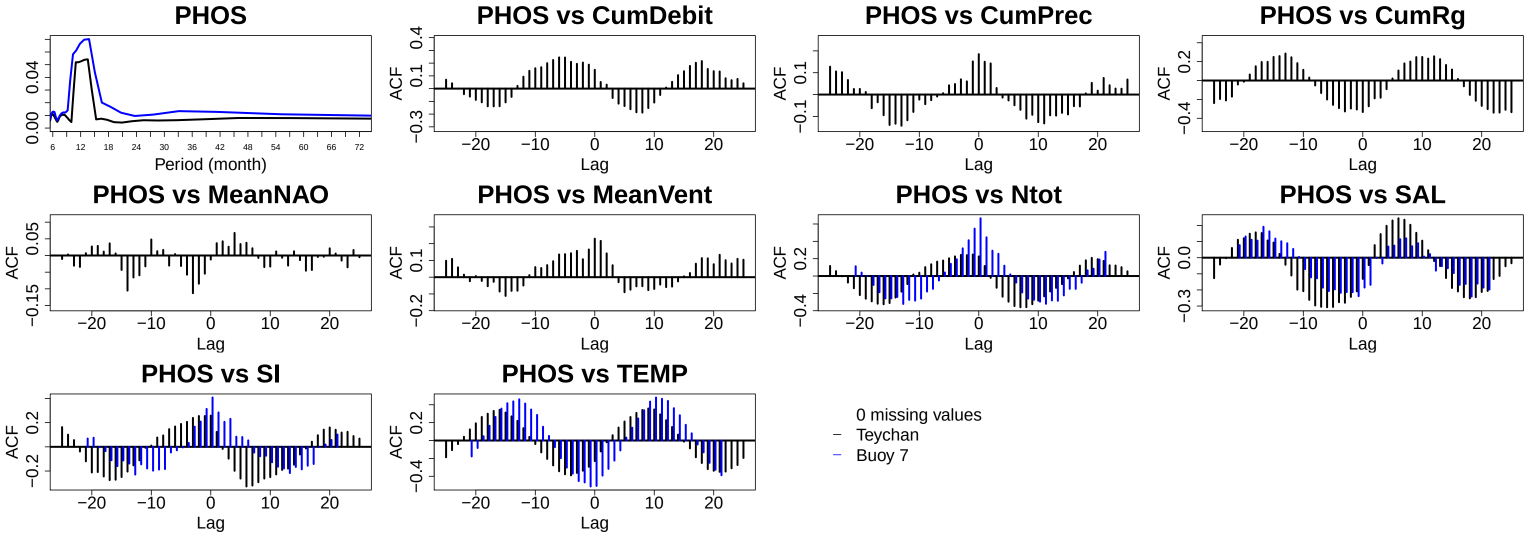
A6.1 Spectrum analysis of abiotic variables



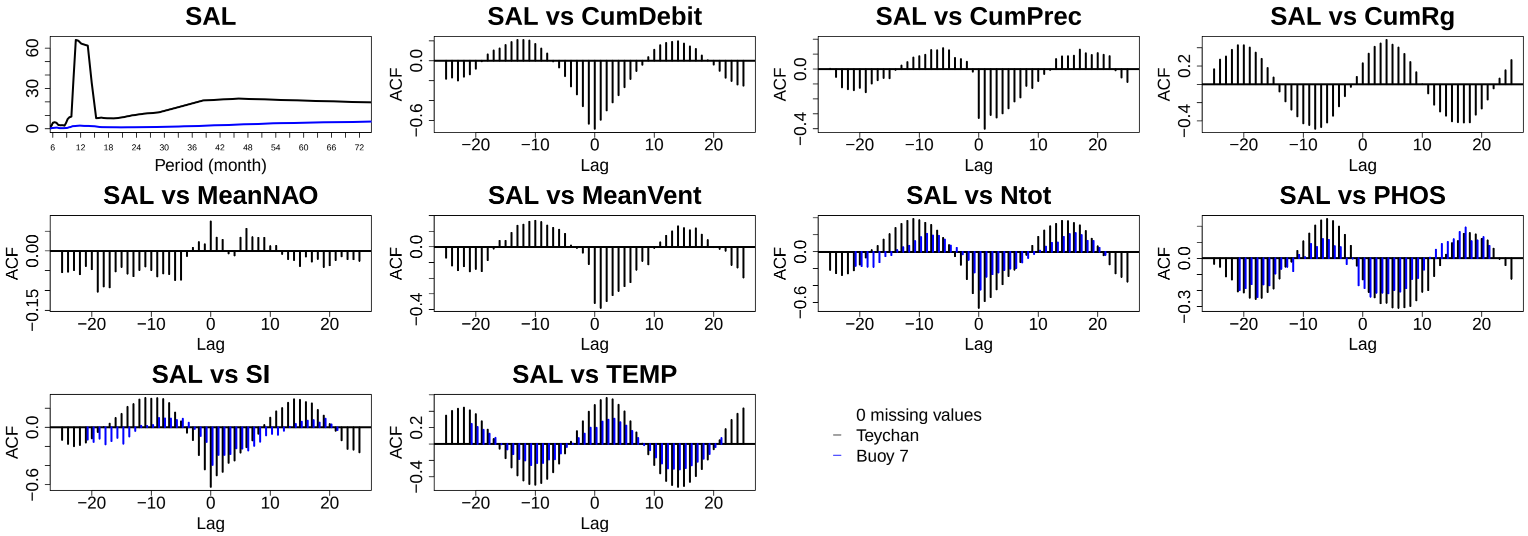
(a) Integrated inflow



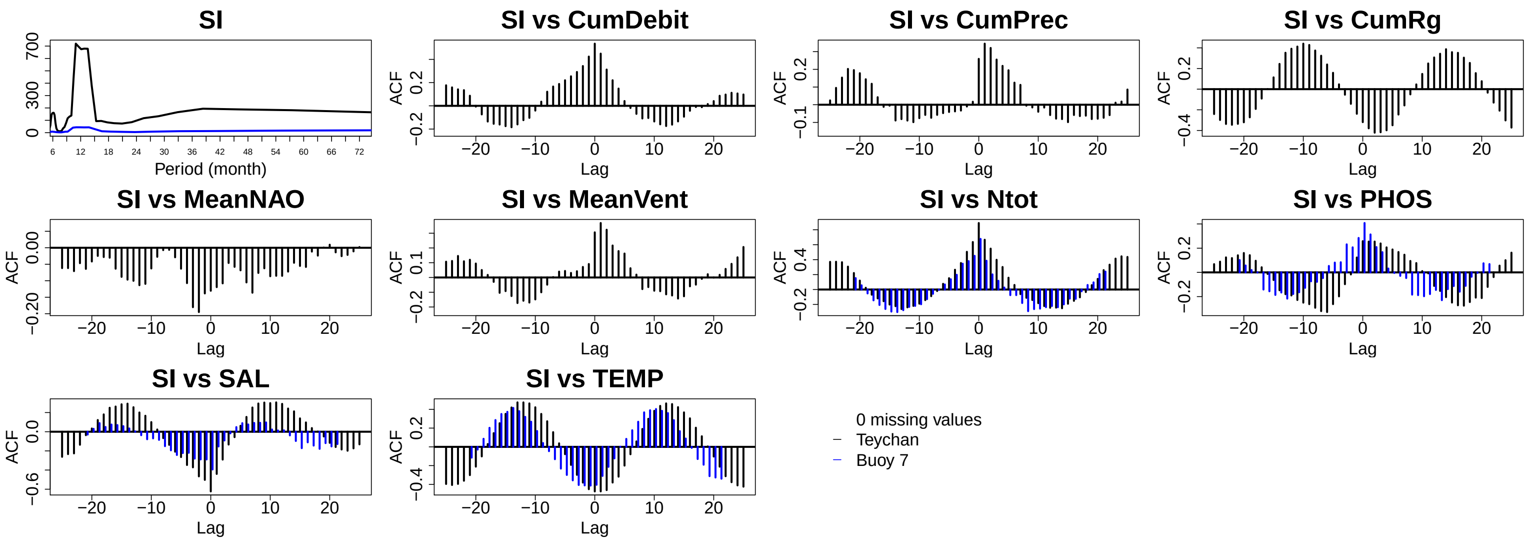
(b) Integrated precipitation



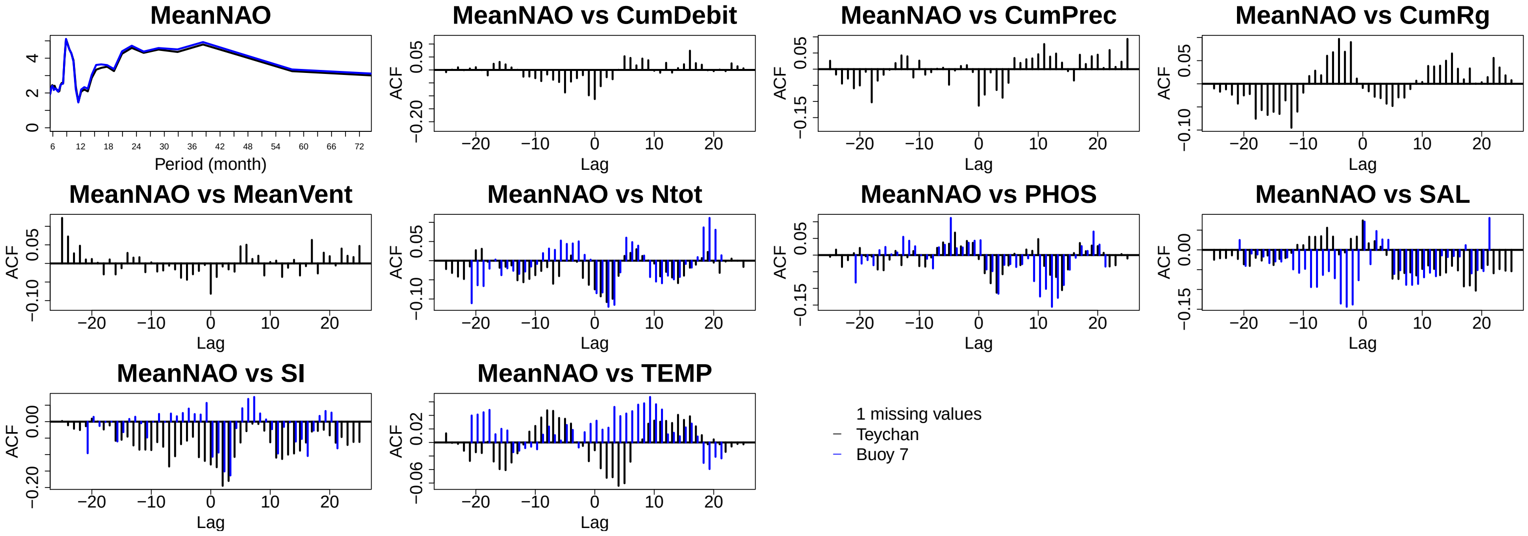
(c) PO_4^{3-}



(d) Salinity



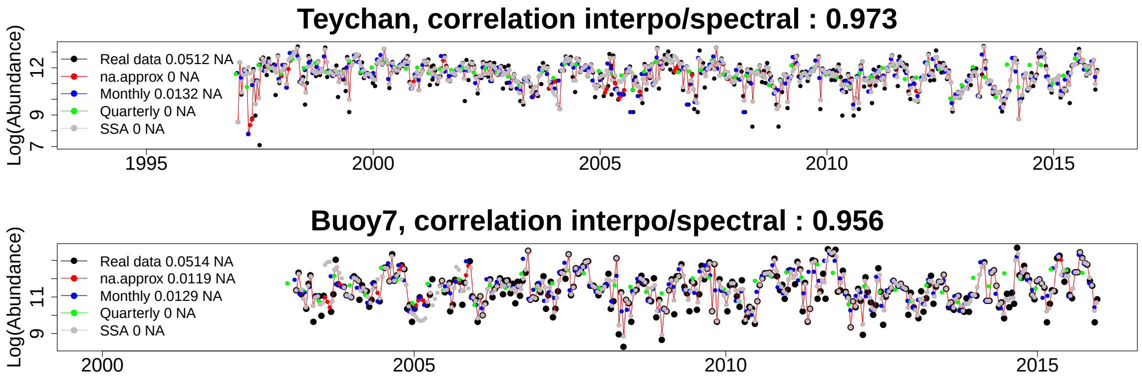
(e) Si(OH)$_4$



(f) MeanNAO

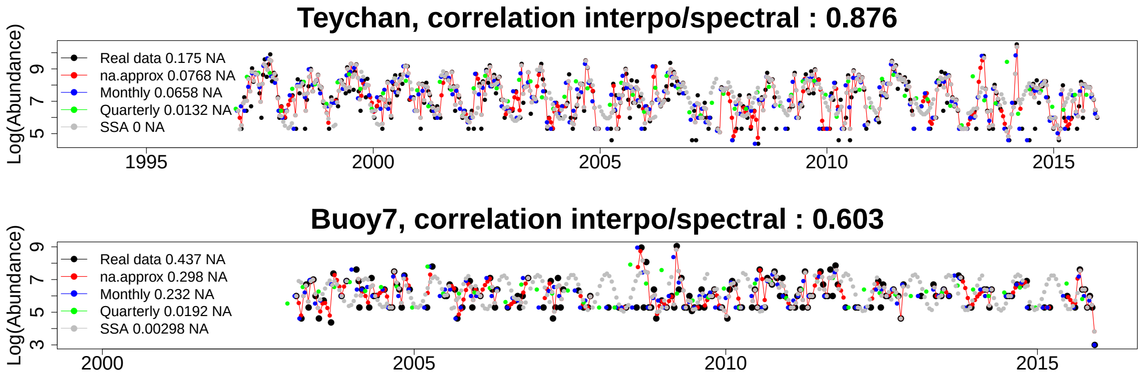
Figure A6.1: Periodogram (first plot, top left) and cross-correlation (remaining plots) between each abiotic variable: integrated inflow (CumDebit), integrated precipitation (CumPrec), phosphate concentration (PHOS), salinity (SAL), silicate concentration (SI) and mean North Atlantic Oscillation index (MeanNAO). Spectrum analyses are shown for both Teychan (black) and Buoy 7 (blue) sites. Integrated values are taken between two sampling points, i.e. every two week.

A6.2 Missing values


Teychan, correlation interpo/spectral : 0.973

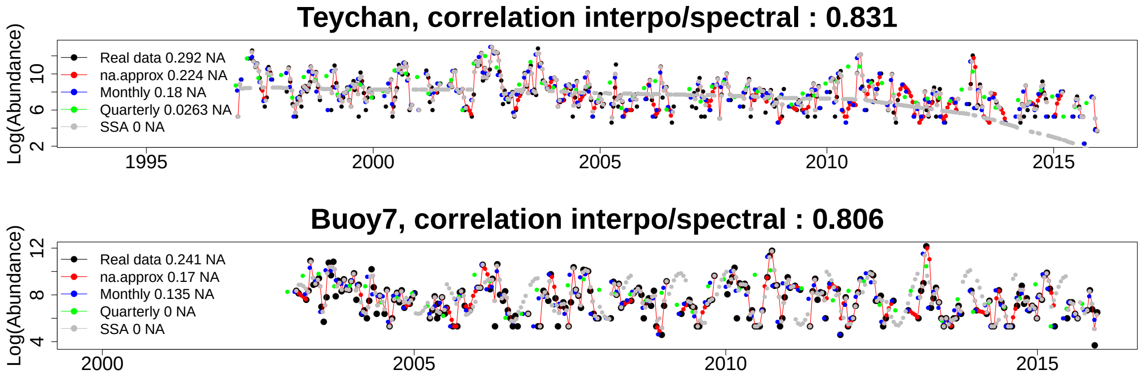
Buoy7, correlation interpo/spectral : 0.956

(a) CRY


Teychan, correlation interpo/spectral : 0.876

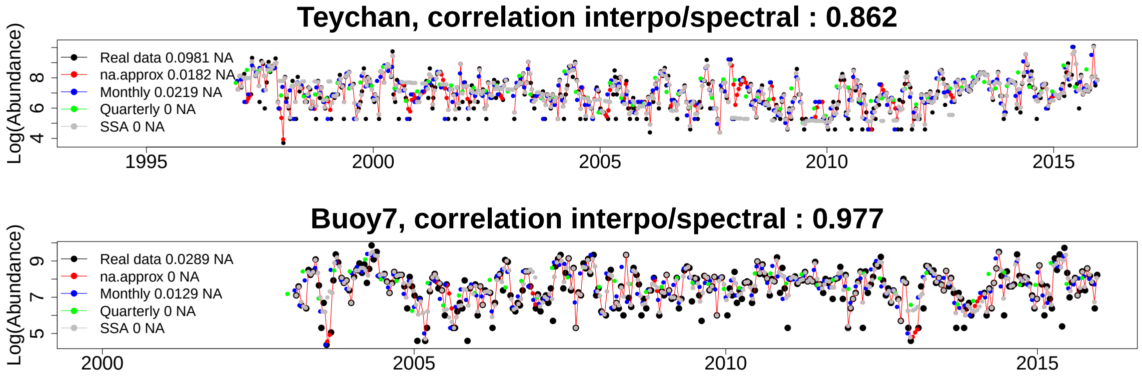
Buoy7, correlation interpo/spectral : 0.603

(b) EUG

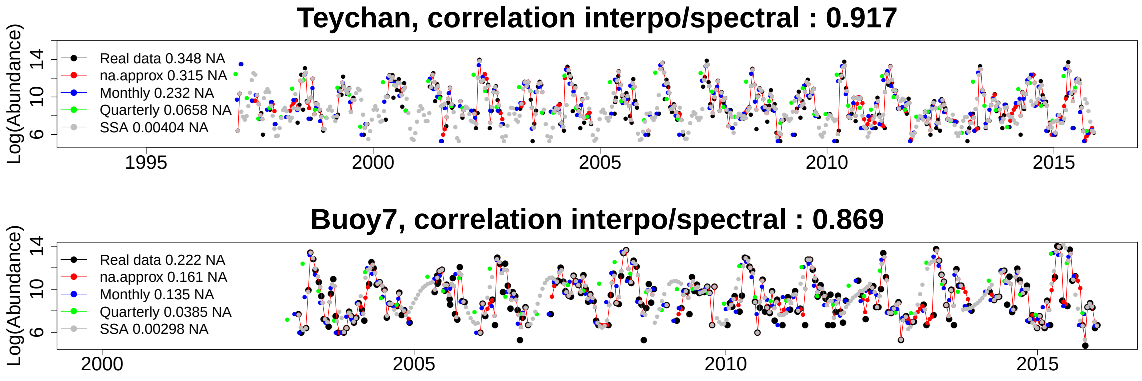

Teychan, correlation interpo/spectral : 0.831

Buoy7, correlation interpo/spectral : 0.806

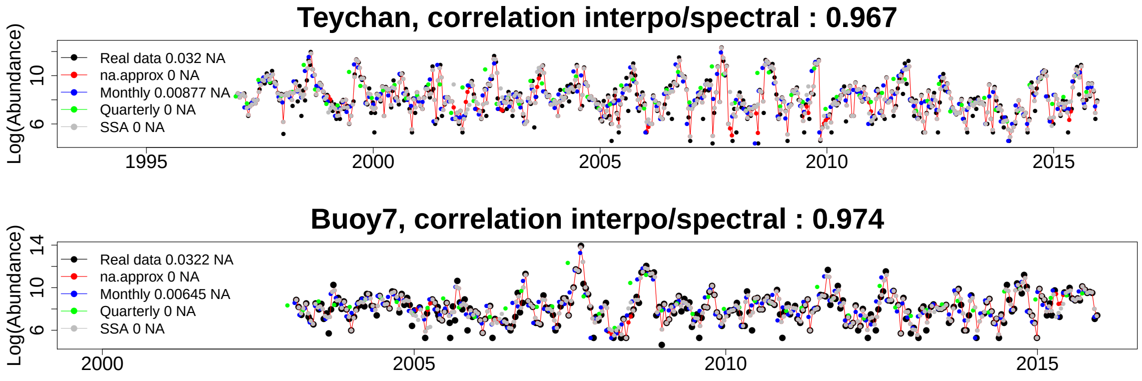
(c) GUI



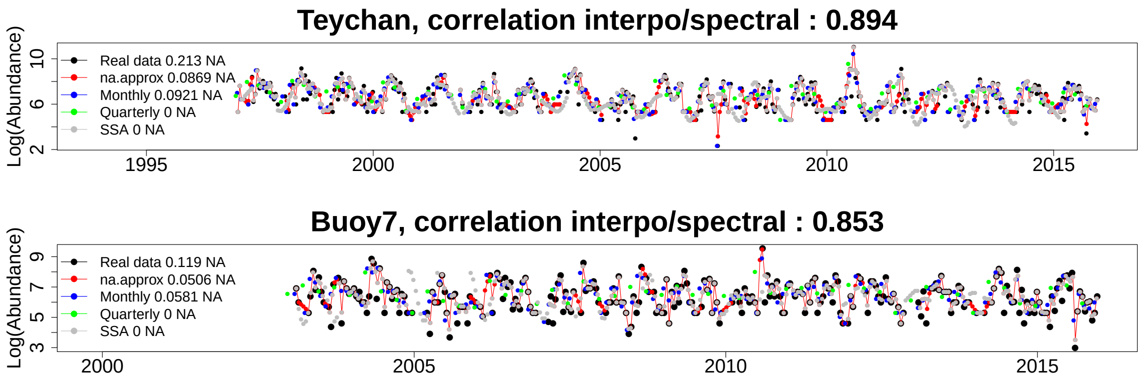
(d) GYM



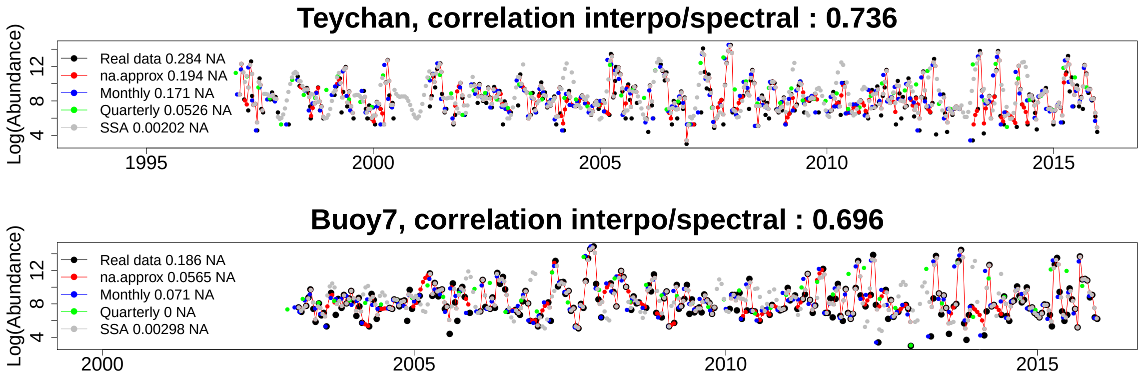
(e) LEP



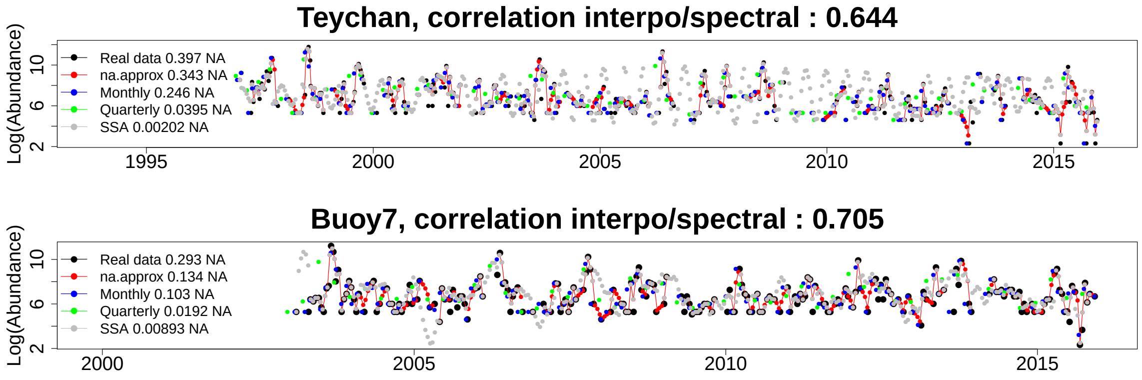
(f) NIT



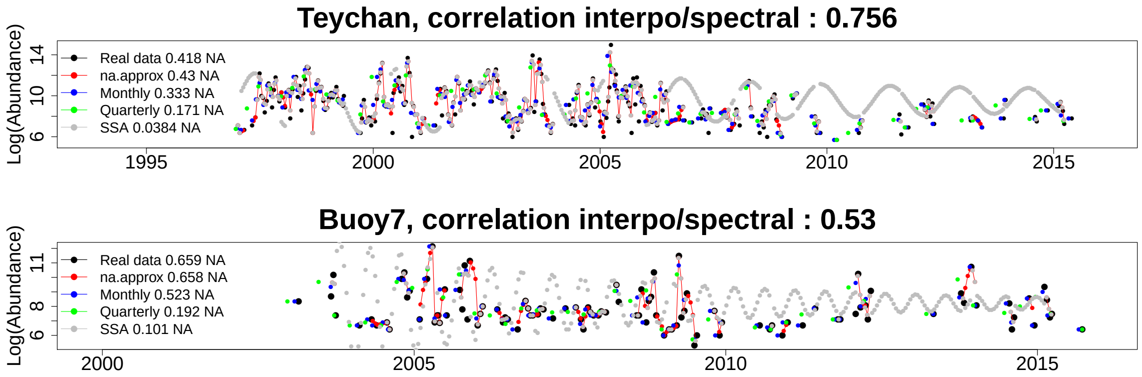
(g) PRP



(h) PSE



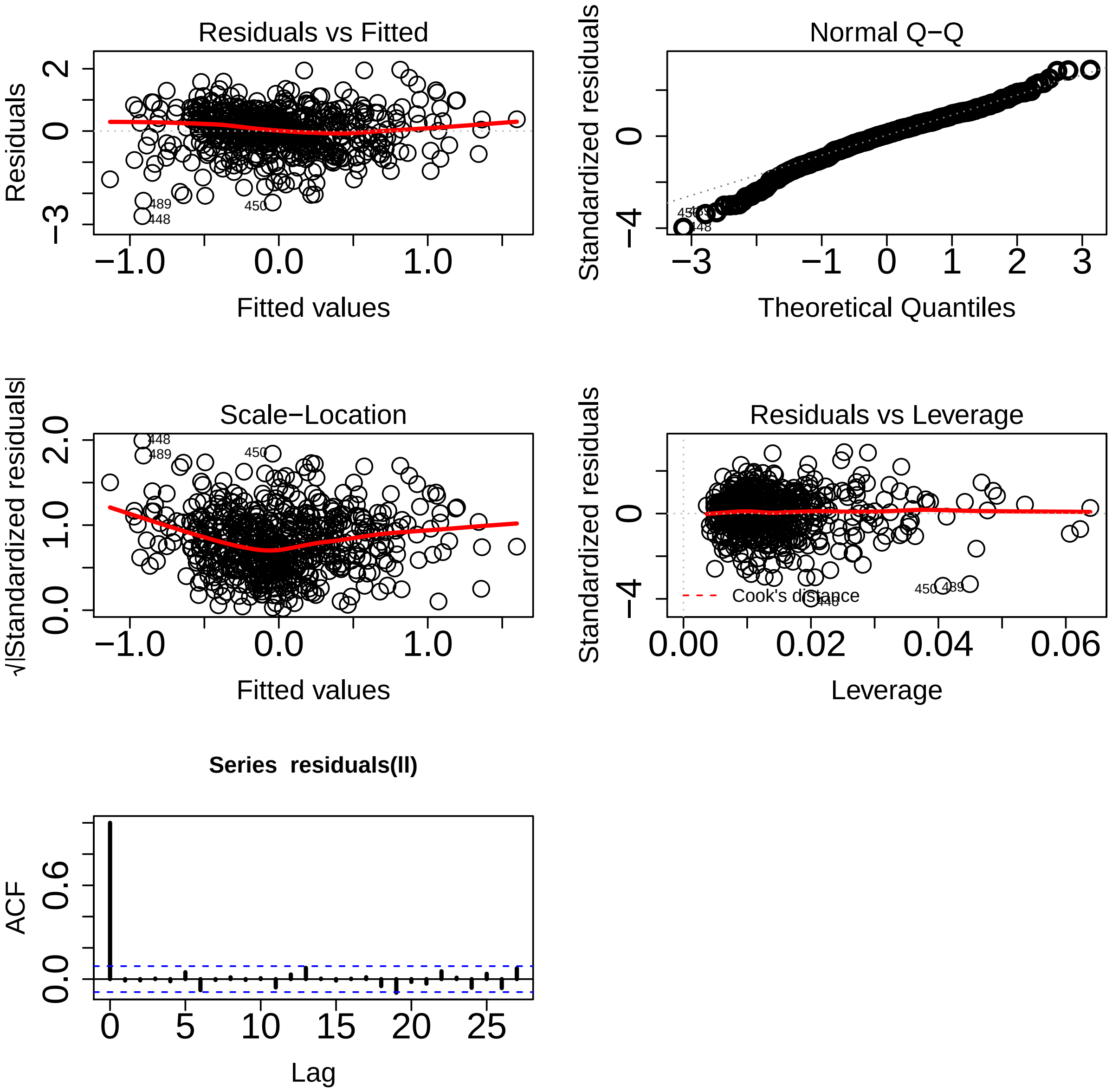
(i) RHI



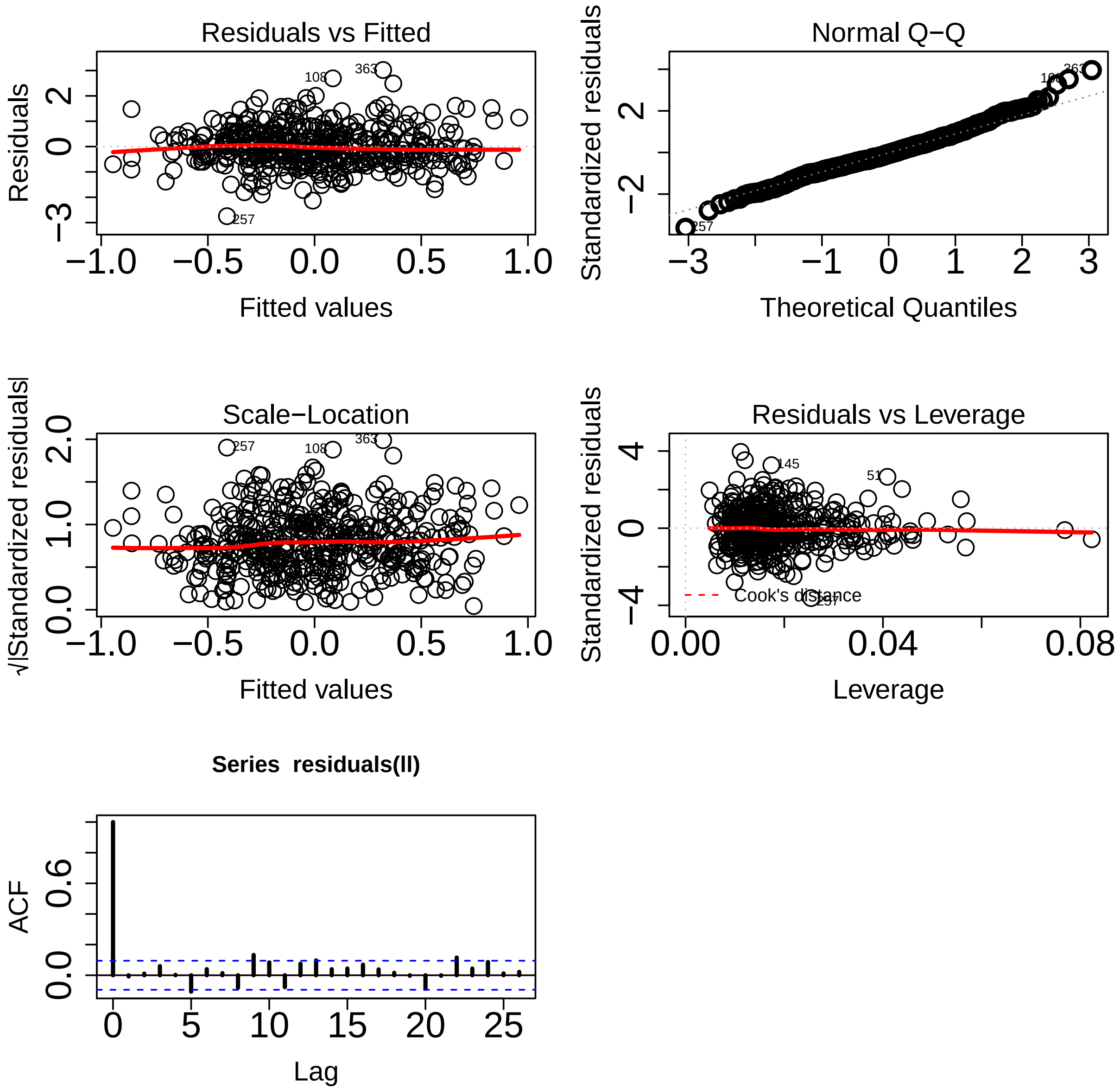
(j) SKE

Figure A6.2: Comparison between different reconstruction methods for each genus considered in our models. Red dots correspond to a linear interpolation between values separated by less than a month, which is the method we finally used in the analysis. Monthly (blue) and quarterly (green) values correspond to average values over a month or a season, respectively (described as the first method in the text above). Grey dots correspond to Singular Spectral Analysis to estimate missing values from nonparametric spectral methods. Composition of planktonic groups is described in Table 1 in the main text.

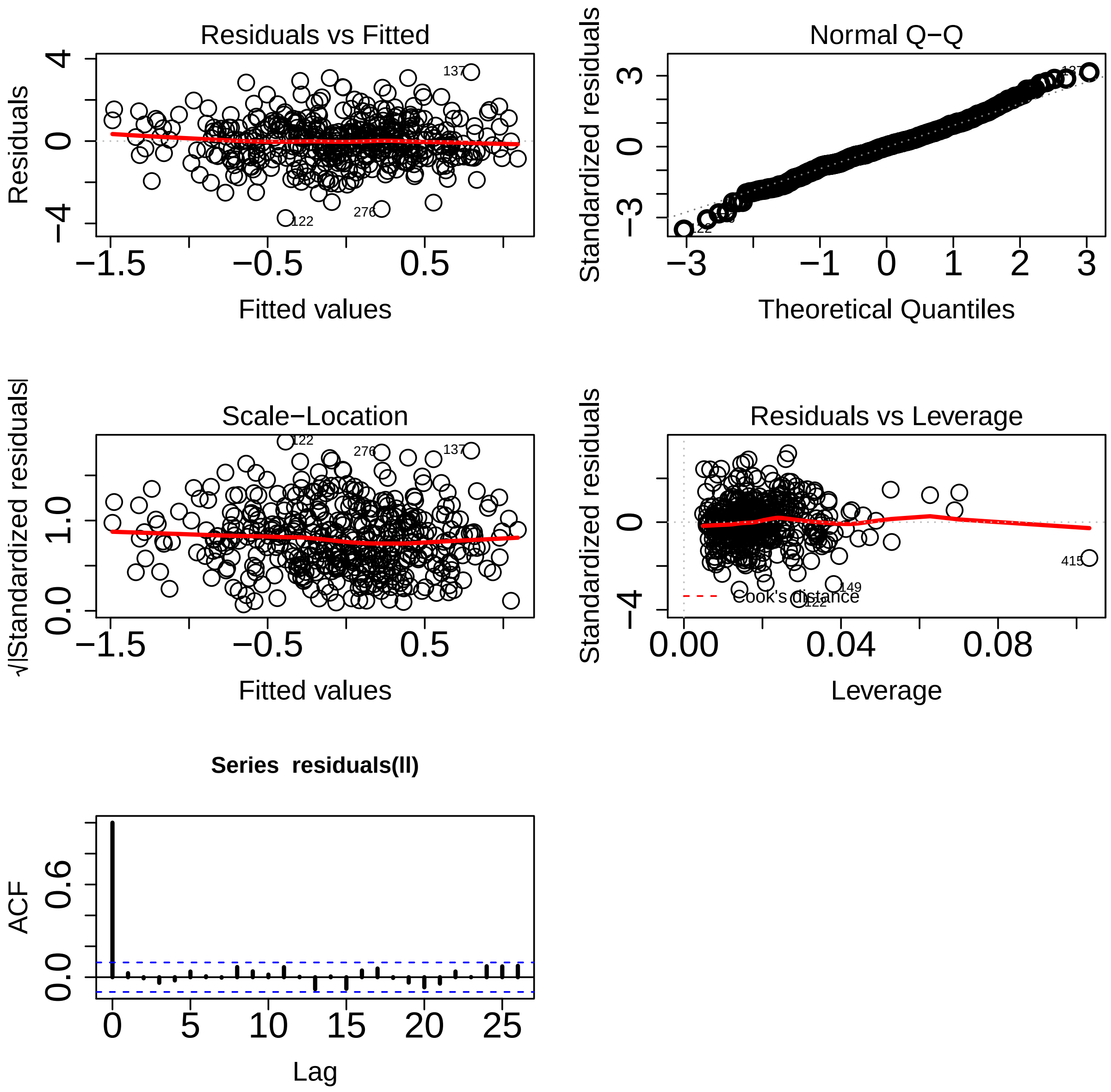
A6.3 Residual plots for single-species models



(b) CRY


Residuals vs Fitted
Residuals
Fitted values
−3
0
2
−1.0
−0.5
0.0
0.5
1.0
108
363
257
Normal Q−Q
Standardized residuals
Theoretical Quantiles
−2
2
−3
−1
0
1
2
3
257
Scale−Location
√|Standardized residuals|
Fitted values
0.0
1.0
2.0
257
108
363
Residuals vs Leverage
Standardized residuals
Leverage
−4
0
4
0.00
0.04
0.08
145
51
257
Cook's distance
Series residuals(ll)
ACF
Lag
0.0
0.6
0
5
10
15
20
25

(c) EUG


Residuals vs Fitted
Residuals
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0
−4
137
122
276
−1.5
−0.5
0.5
Fitted values
Normal Q−Q
Standardized residuals
3
0
−3
137
122
−3
−1
0
1
2
3
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
1.0
0.0
122
276
137
−1.5
−0.5
0.5
Fitted values
Residuals vs Leverage
Standardized residuals
0
−4
415
149
122
Cook's distance
0.00
0.04
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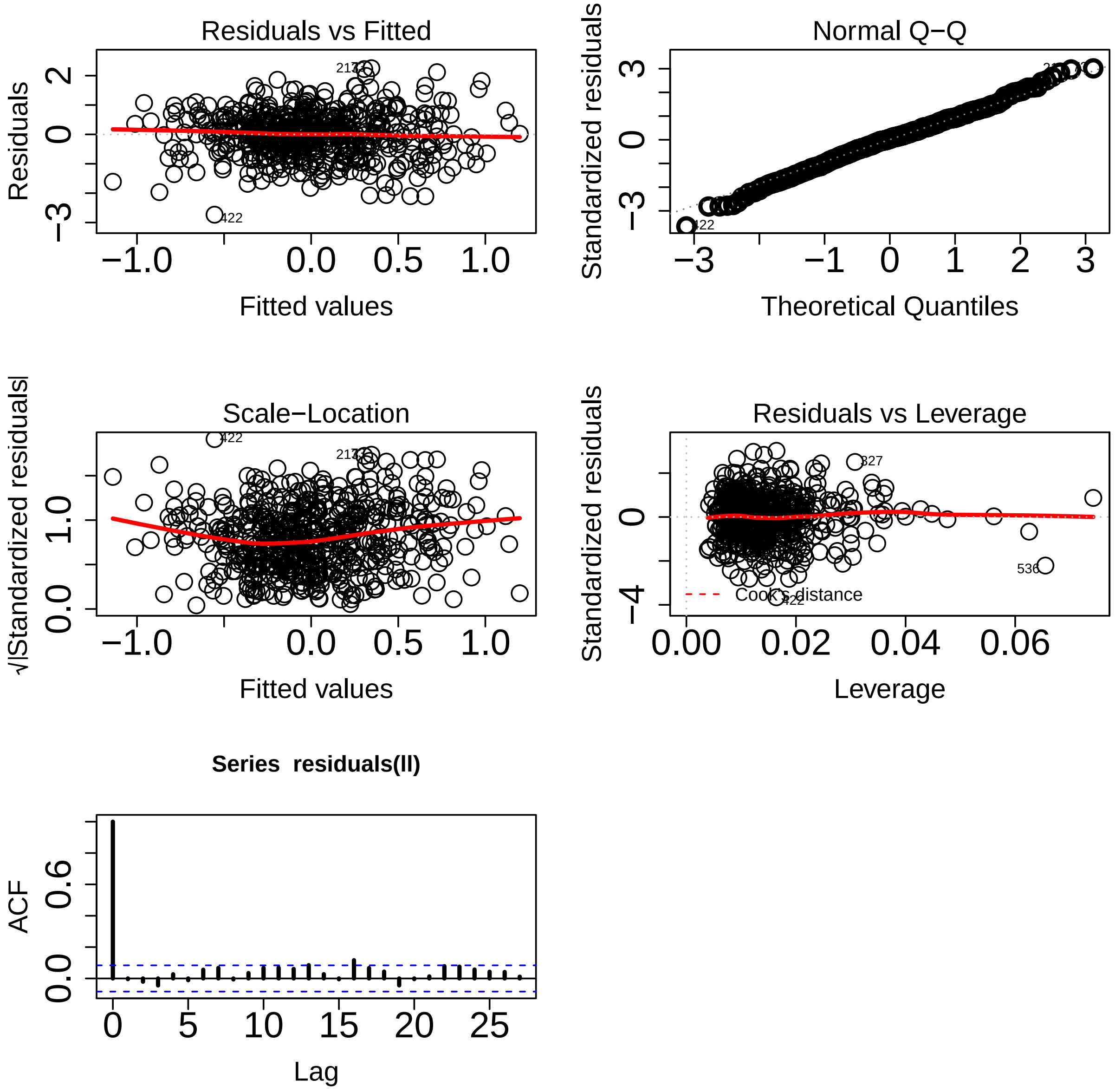
Leverage
Series residuals(ll)
ACF
0.6
0.0
0
5
10
15
20
25
Lag

(d) GUI


Residuals vs Fitted
Residuals
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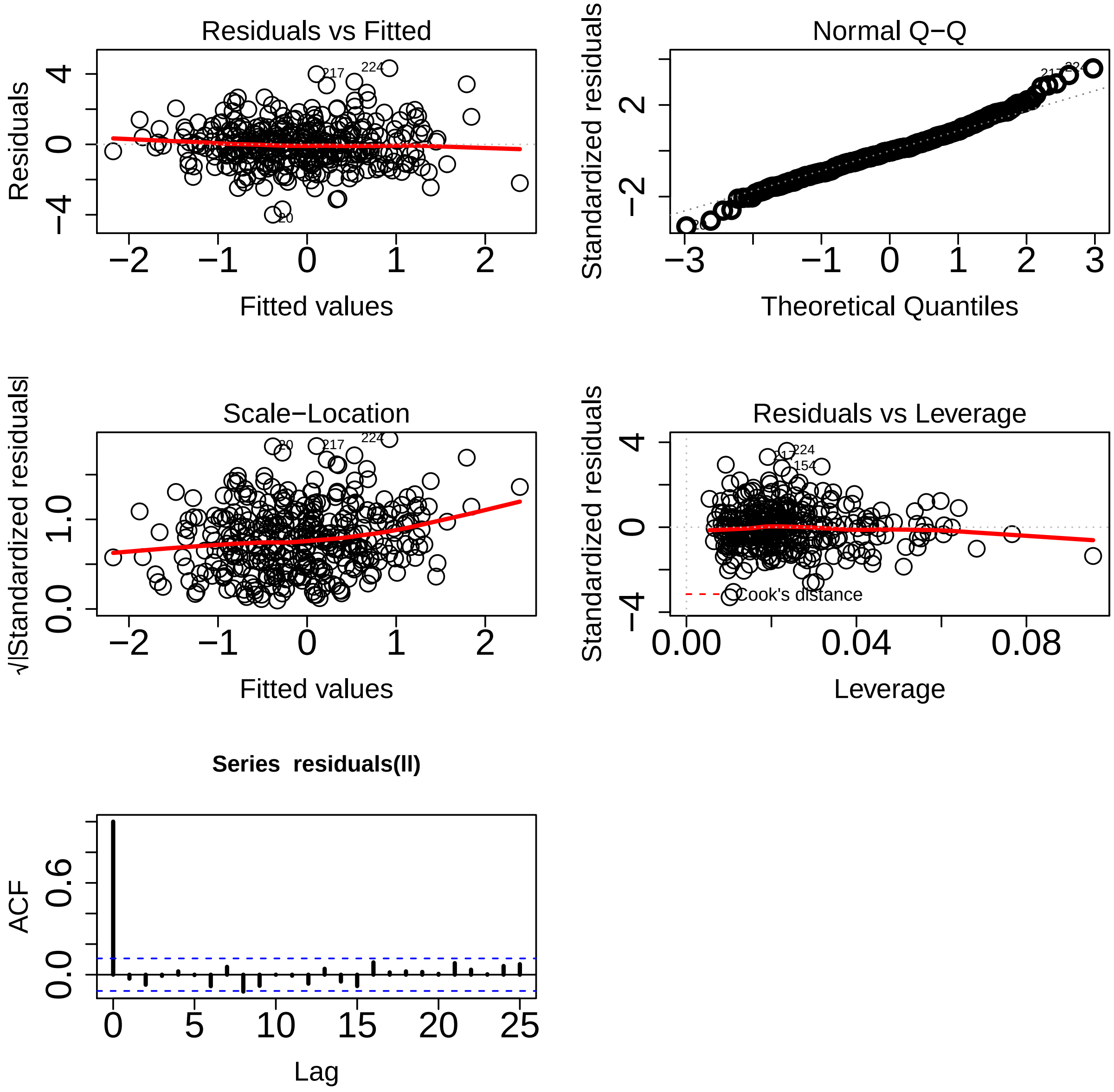
0
−3
217
422
−1.0
0.0
0.5
1.0
Fitted values
Normal Q−Q
Standardized residuals
3
0
−3
422
−3
−1
0
1
2
3
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
1.0
0.0
422
217
−1.0
0.0
0.5
1.0
Fitted values
Residuals vs Leverage
Standardized residuals
0
−4
327
536
422
Cook's distance
0.00
0.02
0.04
0.06
Leverage
Series residuals(ll)
ACF
0.6
0.0
0
5
10
15
20
25
Lag

(e) GYM


Residuals vs Fitted
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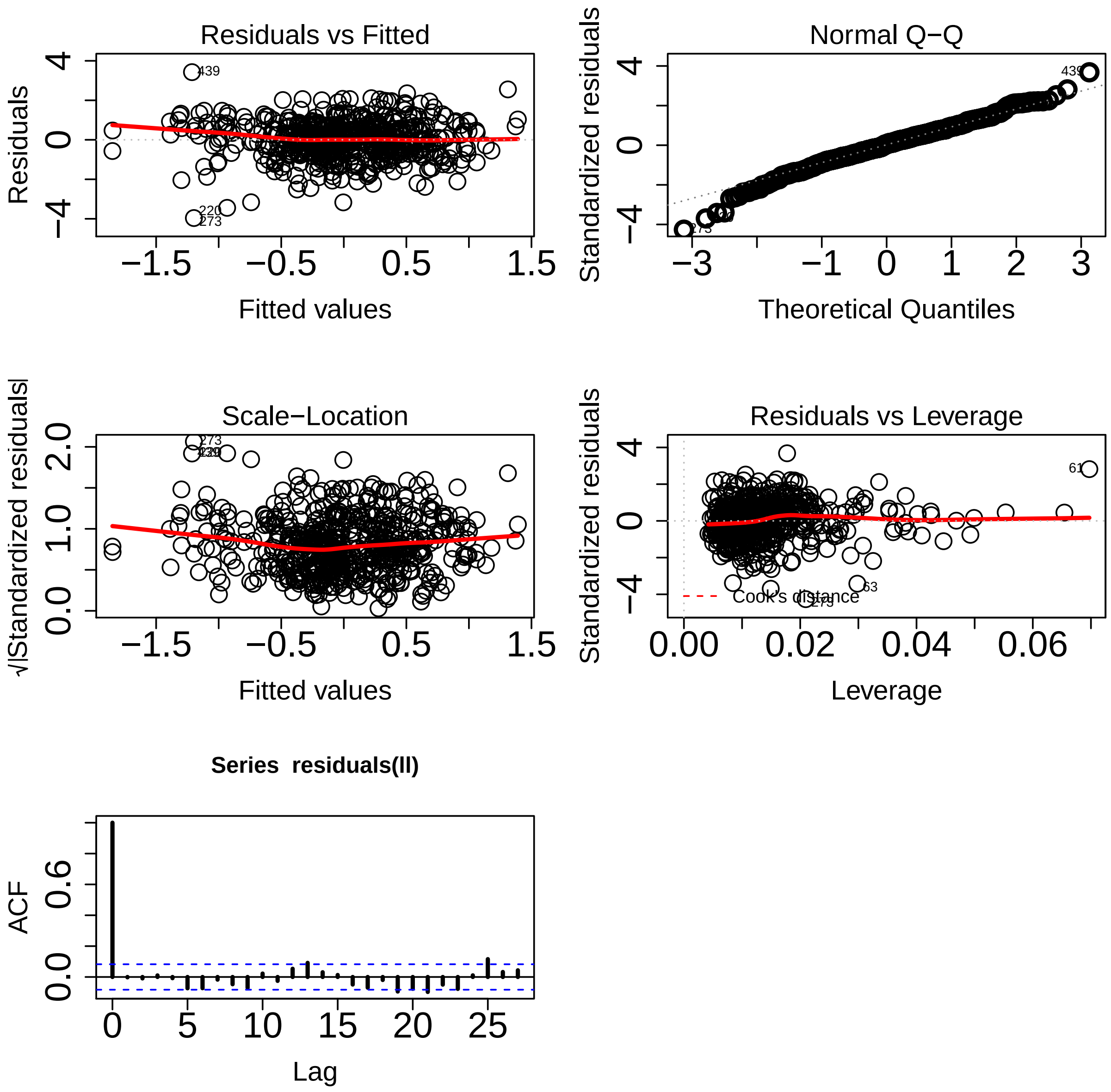
Fitted values
217
224
20
Normal Q−Q
Standardized residuals
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
Fitted values
Residuals vs Leverage
Standardized residuals
Leverage
154
Cook's distance
Series residuals(ll)
ACF
Lag

(f) LEP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Fitted values
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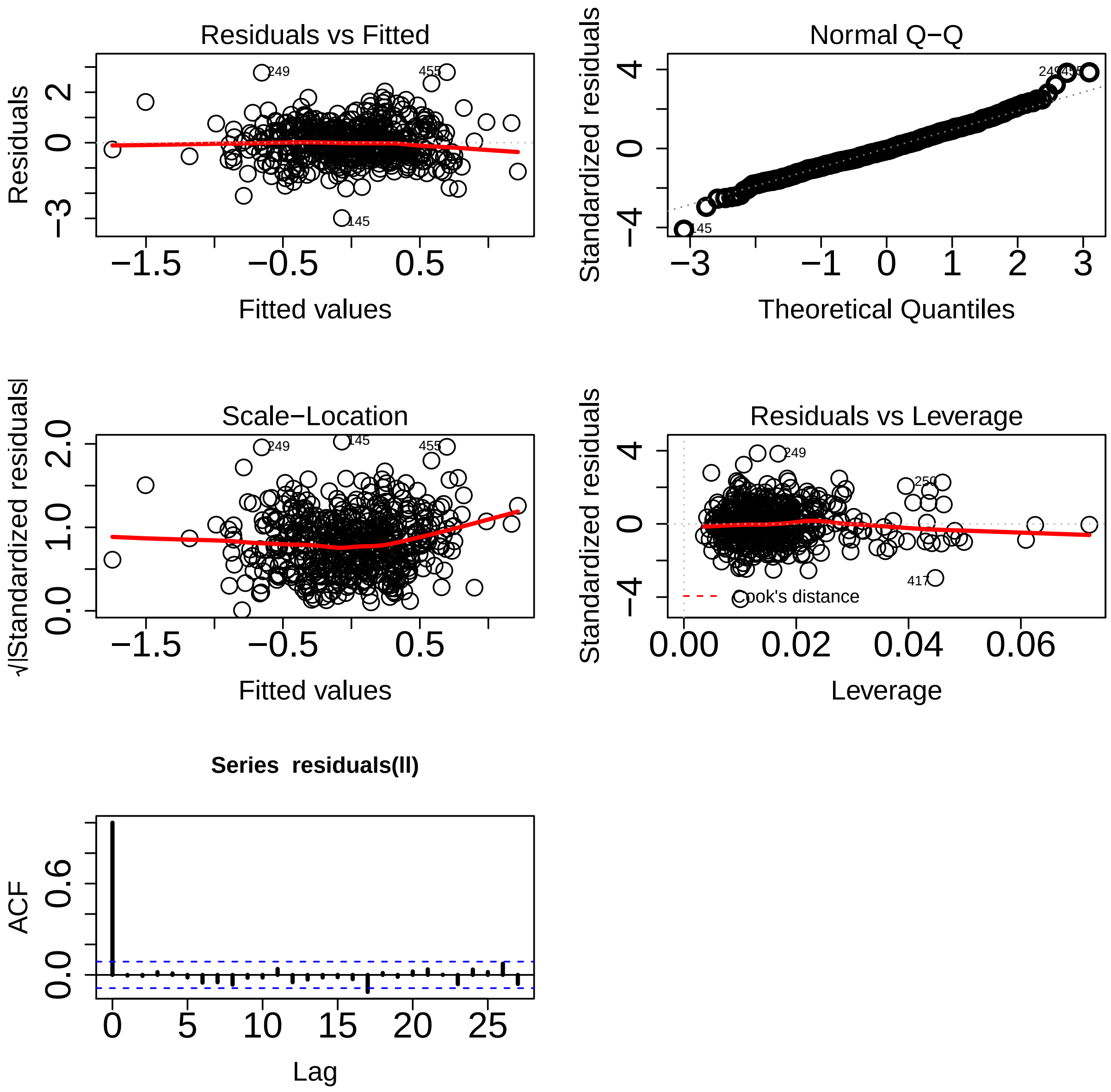
273
Normal Q−Q
Standardized residuals
Theoretical Quantiles
439
273
Scale−Location
√|Standardized residuals|
Fitted values
273
220
Residuals vs Leverage
Standardized residuals
Leverage
61
63
273
Cook's distance
Series residuals(ll)
ACF
Lag

(g) NIT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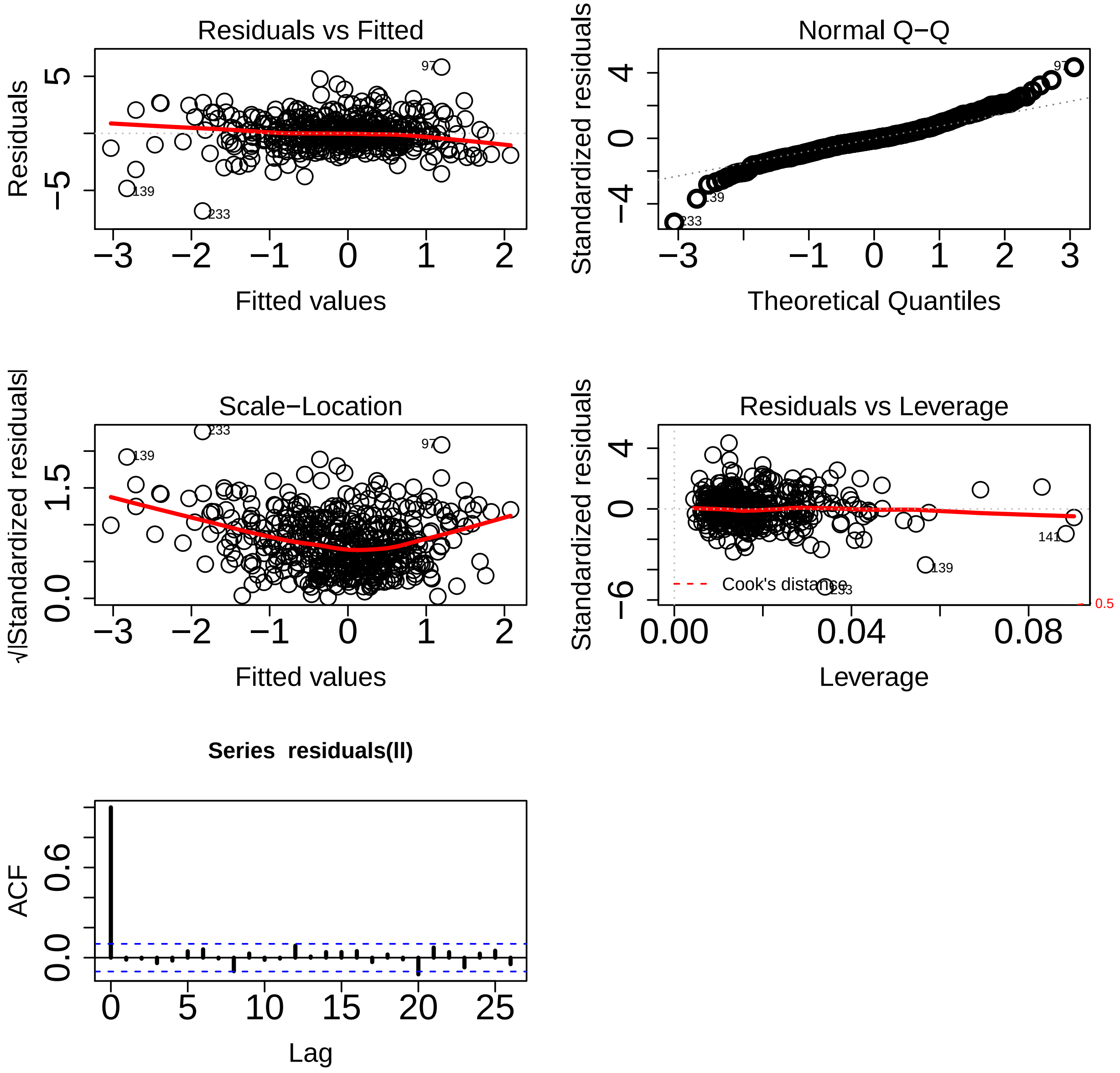
2
249
455
145
Normal Q−Q
Standardized residuals
Theoretical Quantiles
−3
−1
0
1
2
3
−4
0
4
249455
145
Scale−Location
√|Standardized residuals|
Fitted values
0.0
1.0
2.0
249
145
455
Residuals vs Leverage
Standardized residuals
Leverage
0.00
0.02
0.04
0.06
249
250
417
Cook's distance
Series residuals(ll)
ACF
Lag
0.0
0.6
0
5
10
15
20
25

(h) PRP


Residuals vs Fitted
Residuals
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−5
97
139
233
−3
−2
−1
0
1
2
Fitted values
Normal Q−Q
Standardized residuals
4
0
−4
97
139
233
−3
−1
0
1
2
3
Theoretical Quantiles
Scale−Location
√|Standardized residuals|
1.5
0.0
233
139
97
−3
−2
−1
0
1
2
Fitted values
Residuals vs Leverage
Standardized residuals
4
0
−6
Cook's distance
233
139
141
0.5
0.00
0.04
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Leverage
Series residuals(ll)
ACF
0.6
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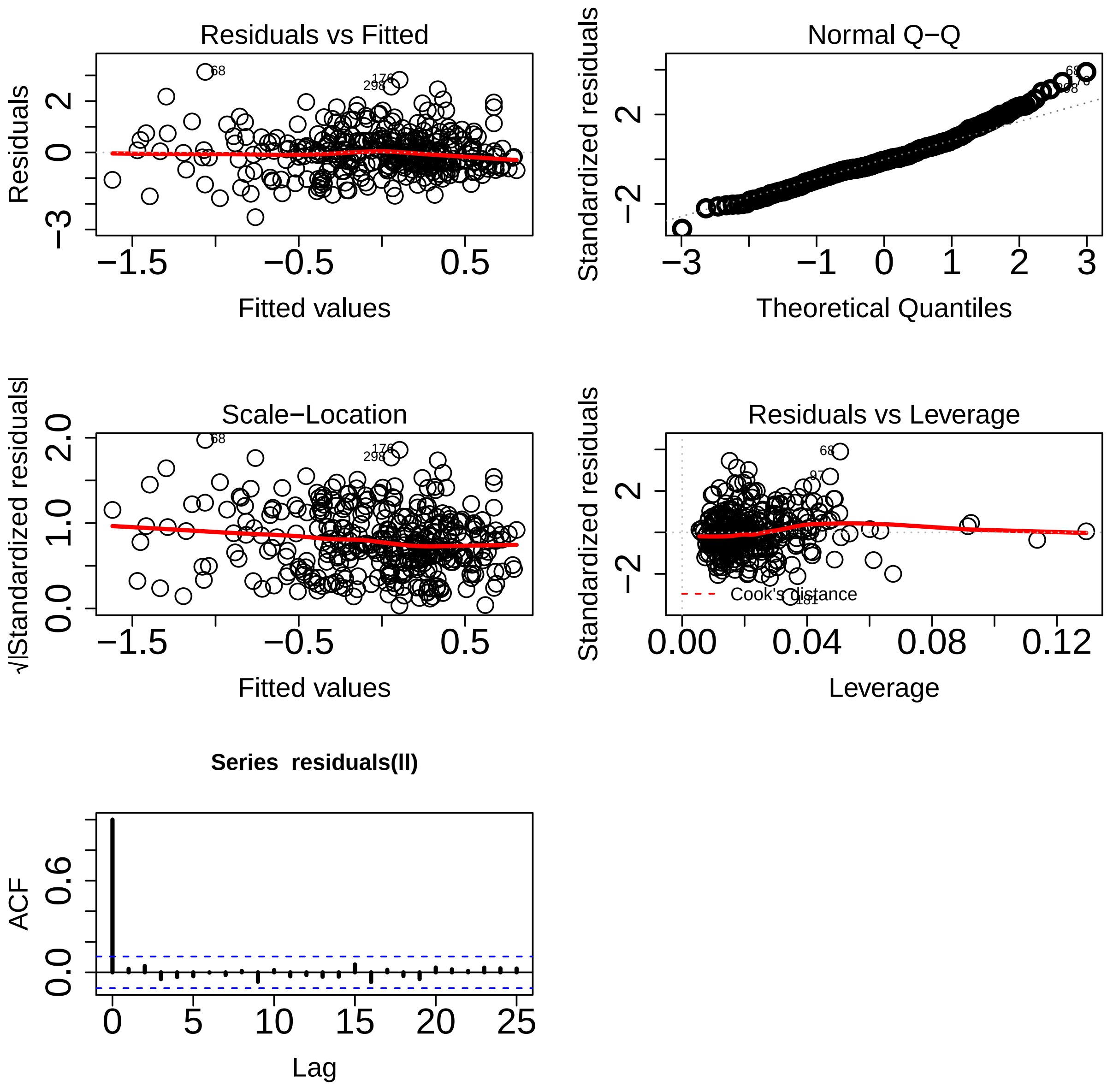
Lag

(i) PSE


Residuals vs Fitted
Residuals
Fitted values
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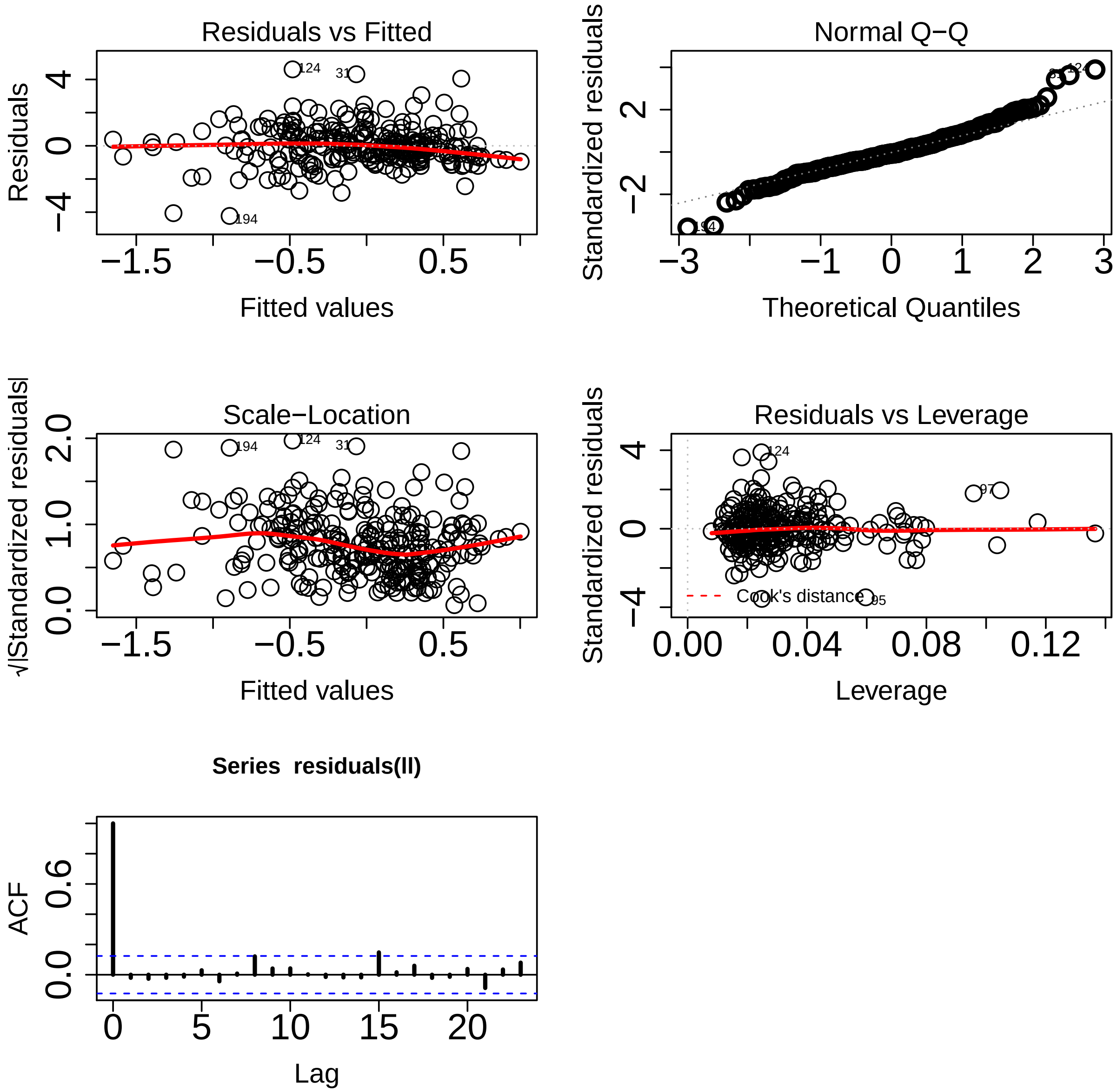
2
−1.5
−0.5
0.5
68
176
298
Normal Q−Q
Standardized residuals
Theoretical Quantiles
−2
2
−3
−1
0
1
3
Scale−Location
√|Standardized residuals|
0.0
1.0
2.0
Residuals vs Leverage
Leverage
0.00
0.04
0.08
0.12
97
181
Cook's distance
Series residuals(ll)
ACF
Lag
0.6
5
10
15
20
25

(j) RHI



(k) SKE

Figure A6.3: Residual diagnostic plots for linear models of planktonic growth rates explained by integrated irradiance, salinity, wind energy and a dedicated season variable according to eq. 1 in the main text. Residuals are plotted against fitted values or leverages, showing no systematic trend. Q-Q plots show the adequation of residuals to the normal distribution. The last plot, bottom right, shows no auto-correlation in residual distributions. Composition of planktonic groups is described in Table 1 in the main text.

A6.4 Differences in coefficients due to timing of the covariates

Table A6.1: Model coefficients for interactions at Teychan/Buoy 7, using a lagged covariate (Supplementary material Appendix 3: eq. A3.2). Changes from the results obtained with our formulation are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and P<0.05. The table should be read as element i having effect e_{ji} on plankton group j. The identity matrix was subtracted to the interaction matrix in order to make effects on growth rates comparable. Composition of planktonic groups is described in Table 1 in the main text.

Model		AST	NIT	PSE	SKE	CHA	GUI	LEP	RHI	GYM	PRP	CRY	EUG
Null	AST	-0.27* (-1.2%) / -0.30* (-2.9%)											
	NIT		-0.41* (0.3%) / -0.40* (2.2%)										
	PSE			-0.28* (-3.0%) / -0.38* (-1.4%)									
	SKE				-0.21* (2.3%) / -0.38* (3.9%)								
	CHA					-0.38* (-8.3%) / -0.52* (0.5%)							
	GUI						-0.26* (-2.6%) / -0.33* (4.6%)						
	LEP							-0.29* (-8.8%) / -0.30* (-2.1%)					
	RHI								-0.32* (1.4%) / -0.36* (6.7%)				
	GYM									-0.36* (3.3%) / -0.40* (-2.4%)			
	PRP										-0.37* (6.4%) / -0.35* (-20.1%)		
	CRY											-0.44* (-3.0%) / -0.47* (-1.8%)	
	EUG												-0.31* (-2.6%) / -0.35* (-1.4%)
Unconstrained	AST	-0.29* (3.0%) / -0.37* (-1.6%)	0.11* (-24.3%) / 0.13* (11.6%)	0.00 (105.9%) / 0.02 (24.4%)	-0.01 (-9.9%) / 0.05 (-72.0%)	-0.04 (-4.5%) / -0.03* (33.1%)	0.02 (489.2%) / 0.02 (-6.0%)	0.01 (65.8%) / -0.06 (-177.3%)	0.00 (72.6%) / -0.03 (-3.3%)	-0.06 (-25.1%) / -0.02* (23.4%)	-0.02 (28.0%) / 0.01* (-42.8%)	0.00 (110.3%) / 0.10* (-32.7%)	0.09* (-11.3%) / 0.04 (45.8%)
	NIT	0.00* (129.4%) / -0.07 (-47.7%)	-0.45* (0.7%) / -0.39* (0.2%)	-0.05 (-2.2%) / -0.08 (-1.1%)	0.04 (-19.8%) / 0.01 (26.3%)	0.01 (-131.7%) / 0.00 (-1909.3%)	-0.05 (6.3%) / 0.02 (17.5%)	0.01 (29.5%) / 0.03 (-9.3%)	0.04 (-41.4%) / -0.01* (38.8%)	-0.07* (-25.7%) / -0.04 (3.4%)	0.01 (-43.5%) / 0.00 (60.1%)	0.04 (22.7%) / 0.09* (5.5%)	0.06 (-38.1%) / -0.02* (-1549.8%)
	PSE	0.05 (5.1%) / 0.03* (51.0%)	-0.02 (25.5%) / 0.14* (-56.8%)	-0.32* (-3.3%) / -0.37* (-2.3%)	-0.02* (741.1%) / -0.06 (-41.9%)	0.02 (316.1%) / -0.06 (16.5%)	0.08* (-2.4%) / -0.01 (-237.7%)	0.04 (-26.9%) / -0.06 (-144.6%)	-0.03 (-78.8%) / 0.11* (-20.7%)	0.01 (71.8%) / -0.08 (-30.6%)	0.03 (30.4%) / 0.05 (-382.4%)	0.01 (35.9%) / 0.03 (28.9%)	-0.02 (54.2%) / -0.07 (-59.4%)
	SKE	-0.06 (-16.9%) / -0.06 (-11.4%)	0.05 (-28.4%) / 0.09 (-127.4%)	-0.05 (-9.0%) / 0.08 (-23.1%)	-0.25* (-1.4%) / -0.42* (-2.2%)	0.04 (1159.3%) / 0.03* (76.9%)	0.08 (0.2%) / -0.05 (-80.3%)	0.01 (201.2%) / -0.03 (18.6%)	0.00 (103.0%) / 0.06 (-696.7%)	0.01 (20.0%) / -0.08 (18.4%)	0.02 (-116.7%) / 0.01 (64.4%)	-0.01 (-49.6%) / -0.02 (290.3%)	0.05 (-76.4%) / 0.06 (-61.4%)
	CHA	0.04 (25.7%) / -0.01 (163.4%)	-0.03 (18.5%) / 0.03 (-995.3%)	0.00 (50.5%) / -0.01 (41.0%)	0.04 (13.7%) / -0.09* (-42.6%)	-0.45* (-9.6%) / -0.59* (-4.0%)	0.06 (0.4%) / 0.01 (7.0%)	0.06 (-133.1%) / 0.06 (36.9%)	0.02 (62.1%) / 0.12* (-1.7%)	0.01 (-103.2%) / 0.02 (47.6%)	0.04 (-14.7%) / 0.05 (-169.2%)	0.05 (11.3%) / -0.03 (-60.5%)	-0.05 (13.1%) / 0.05 (40.0%)
	GUI	0.03 (8.6%) / 0.06 (-64.2%)	0.04 (-47.4%) / 0.05 (-112.5%)	-0.08* (-89.7%) / -0.10* (-26.7%)	-0.02 (787.7%) / -0.02 (40.8%)	0.00 (77.1%) / -0.08 (49.8%)	-0.26* (-1.1%) / -0.32* (6.9%)	0.00 (92.8%) / 0.00 (88.9%)	-0.01 (714.7%) / 0.03 (11.3%)	-0.04 (14.4%) / -0.03 (-2403.8%)	0.08* (-2.7%) / 0.00 (-119.7%)	-0.04 (-7.4%) / 0.02 (983.8%)	0.00 (131.6%) / 0.02 (71.2%)
	LEP	0.06* (16.2%) / 0.01 (84.4%)	-0.09* (2.5%) / 0.02 (286.4%)	0.05 (-12.3%) / 0.05 (2.3%)	-0.02 (-95.9%) / -0.09* (11.4%)	-0.04 (-151.0%) / -0.04 (8.5%)	0.09* (-3.7%) / 0.05 (-69.6%)	-0.37* (-4.3%) / -0.39* (-4.6%)	0.03 (-85.0%) / 0.00 (91.0%)	0.01 (380.9%) / 0.05 (15.8%)	0.10* (-50.9%) / 0.06 (-158.1%)	0.01 (-8731.4%) / -0.09* (-17.1%)	0.00 (89.0%) / -0.03 (-85.6%)
	RHI	0.04 (12.3%) / -0.02 (-952.9%)	0.04 (-56.3%) / 0.09* (-30.3%)	-0.02 (331.3%) / 0.09 (4.9%)	-0.02 (-524.9%) / -0.09* (5.1%)	0.10* (-78.1%) / -0.06 (45.9%)	0.07* (12.3%) / 0.07 (7.4%)	0.01 (110.3%) / 0.05 (8.8%)	-0.38* (4.9%) / -0.40* (9.2%)	0.02 (-118.8%) / -0.02 (-3331.2%)	0.05 (-29.3%) / -0.01 (74.8%)	-0.03 (-44.0%) / 0.00 (122.0%)	-0.04 (33.4%) / -0.07 (-45.0%)
	GYM	0.00 (84.7%) / 0.04 (46.4%)	-0.04 (29.8%) / 0.07 (-115.5%)	0.02 (48.5%) / 0.01 (-13.7%)	0.02 (45.6%) / -0.03 (-20.5%)	-0.01 (77.2%) / 0.00 (112.7%)	0.00 (83.3%) / -0.01 (151.1%)	0.01 (135.0%) / 0.06 (-12.2%)	0.04 (28.9%) / 0.08 (-21.0%)	-0.38* (3.0%) / -0.53* (0.1%)	0.02 (37.0%) / 0.18* (-25.6%)	-0.03 (-115.4%) / 0.01 (38.2%)	0.08* (-17.7%) / 0.05 (-2.8%)
	PRP	0.07* (28.0%) / -0.01 (134.6%)	0.04 (11.9%) / -0.02* (45.1%)	0.03 (-691.6%) / 0.00 (-61.4%)	0.00 (73.3%) / 0.02 (-15.6%)	-0.03 (51.8%) / 0.02 (-1073.3%)	0.03 (-38.4%) / 0.04 (-9.9%)	0.02 (124.3%) / 0.05 (43.1%)	-0.02 (-459.8%) / 0.05 (-161.3%)	-0.01 (-95.8%) / 0.02 (43.9%)	-0.40* (-2.6%) / -0.41* (-3.5%)	0.03 (-168.9%) / 0.02 (12.9%)	0.06 (-481.0%) / 0.07 (-12.8%)
	CRY	-0.09 (-2.6%) / -0.06* (-21.3%)	0.07 (3.1%) / 0.08 (28.1%)	-0.07 (-102.2%) / 0.04 (21.1%)	0.05 (-59.6%) / -0.07 (19.6%)	0.15* (-24.2%) / -0.07 (-23.8%)	-0.05 (-55.9%) / 0.00 (110.6%)	0.00 (86.9%) / 0.03 (-222.1%)	0.09* (-21.6%) / -0.07 (-36.0%)	-0.06 (-47.7%) / -0.03 (-0.3%)	-0.02* (-31.4%) / 0.10 (-12.7%)	-0.50* (-1.1%) / -0.49* (-5.9%)	0.00 (136.2%) / 0.05 (-16.3%)
	EUG	-0.05 (-35.6%) / -0.06 (42.7%)	-0.01 (2.1%) / 0.10* (-26.1%)	-0.02 (-851.8%) / -0.02 (0.5%)	0.05 (-620.4%) / 0.02 (55.5%)	0.11* (-0.9%) / -0.02 (68.6%)	-0.01 (125.7%) / 0.09* (4.7%)	-0.02 (-3.6%) / -0.10 (-137.1%)	-0.02 (64.5%) / -0.02 (36.0%)	-0.05* (-123.5%) / -0.05 (-471.6%)	0.03 (27.3%) / 0.06 (-991.9%)	0.04 (29.8%) / 0.02 (-28.7%)	-0.33* (-2.7%) / -0.40* (7.4%)

Table A6.2: Model coefficients for interactions at Teychan/Buoy 7, using a lagged covariate (Supplementary material Appendix 3: eq. A3.2). Changes from the results obtained with our formulation are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. The identity matrix was subtracted to the interaction matrix in order to make effects on growth rates comparable. Composition of planktonic groups is described in Table 1 in the main text.

Model		AST	NIT	PSE	SKE	CHA	GUI	LEP	RHI	GYM	PRP	CRY	EUG
Intra-phylum	AST	-0.28* (2.4%) / -0.35* (-1.7%)	0.12* (-13.8%) / 0.16* (11.2%)	-0.01 (58.2%) / 0.02 (28.4%)	0.00 (98.5%) / 0.05 (-74.6%)	-0.05 (-32.1%) / -0.04 (25.3%)	0.03 (-503.8%) / 0.03 (-6.2%)	0.00 (102.9%) / -0.07 (-94.3%)	-0.02 (-1403.0%) / -0.03 (24.4%)				
	NIT	0.01 (167.8%) / -0.06 (-56.0%)	-0.43* (1.3%) / -0.38* (1.0%)	-0.07* (0.4%) / -0.08* (0.6%)	0.05 (-11.6%) / 0.01 (6.3%)	0.01* (19.8%) / -0.02 (-35.8%)	-0.03 (14.0%) / 0.01 (34.7%)	0.01 (38.1%) / 0.02 (-28.4%)	0.02 (-70.6%) / -0.01 (65.8%)				
	PSE	0.05 (3.8%) / 0.02 (60.0%)	-0.01 (29.0%) / 0.13* (-49.2%)	-0.31* (-2.6%) / -0.37* (-2.6%)	-0.02 (780.0%) / -0.05 (-13.8%)	0.02 (1220.1%) / -0.06 (19.4%)	0.08* (-6.4%) / -0.02 (-111.2%)	0.04 (-20.2%) / -0.05 (-77.5%)	-0.02 (-573.9%) / 0.12* (-22.5%)				
	SKE	-0.05 (-10.1%) / -0.07 (-12.0%)	0.05 (-29.4%) / 0.09 (-109.5%)	-0.05* (-12.8%) / 0.09 (-27.8%)	-0.24* (-1.9%) / -0.41* (-2.8%)	0.04 (3985.3%) / 0.02 (83.5%)	0.09* (-3.1%) / -0.05 (-64.8%)	0.01 (222.4%) / -0.05 (11.0%)	0.00 (105.7%) / 0.06 (-1449.5%)				
	CHA	0.04 (26.2%) / 0.00 (92.1%)	-0.02 (26.3%) / 0.04 (-89.6%)	-0.01 (38.5%) / -0.01 (14.2%)	0.04 (12.3%) / -0.08* (-38.4%)	-0.44* (-10.6%) / -0.57* (-3.7%)	0.05* (2.3%) / 0.03 (-16.1%)	0.06 (-134.1%) / 0.08 (27.2%)	0.03 (44.9%) / 0.11* (-6.0%)				
	GUI	0.04 (2.1%) / 0.06 (-35.8%)	0.03 (-93.1%) / 0.05 (-57.6%)	-0.08* (-94.6%) / -0.10* (-31.1%)	-0.02 (-704.8%) / -0.02 (46.5%)	-0.01 (48.1%) / -0.08* (45.4%)	-0.25* (-1.4%) / -0.32* (7.5%)	0.00 (95.4%) / 0.00 (113.4%)	-0.01 (332.4%) / 0.03* (-10.7%)				
	LEP	0.07* (9.8%) / 0.00 (92.2%)	-0.08* (8.6%) / 0.00 (108.5%)	0.05 (-11.9%) / 0.05 (6.4%)	-0.01 (-57.7%) / -0.09* (15.0%)	-0.03 (-82.9%) / -0.02* (33.5%)	0.10* (-3.6%) / 0.06 (-69.0%)	-0.37* (-5.0%) / -0.35* (-6.6%)	0.04 (-82.1%) / 0.00 (96.6%)				
	RHI	0.05 (7.0%) / -0.03 (-96.3%)	0.03 (-156.3%) / 0.08* (-42.8%)	-0.01 (142.0%) / 0.09 (4.6%)	-0.03 (-116.8%) / -0.09* (8.5%)	0.11* (-97.3%) / -0.07 (42.6%)	0.07* (11.0%) / 0.06 (16.9%)	0.01 (118.2%) / 0.05 (1.8%)	-0.37* (4.6%) / -0.39* (9.0%)				
	GYM									-0.36* (2.5%) / -0.50* (-0.3%)	0.04 (20.0%) / 0.22* (-19.8%)	-0.03 (-41.2%) / 0.03 (12.3%)	
	PRP									-0.01 (43.6%) / 0.03 (40.4%)	-0.37* (-3.4%) / -0.36* (-3.8%)	0.04 (-56.6%) / 0.03 (-10.1%)	
	CRY									-0.03 (-60.1%) / -0.03 (-3.9%)	-0.01 (-25.9%) / 0.08 (-2.6%)	-0.44* (-3.1%) / -0.47* (-2.6%)	
	EUG												-0.31* (-1.9%) / -0.35* (3.4%)
Inter-phylum	AST	-0.27* (2.3%) / -0.34* (-2.1%)								-0.06 (-26.3%) / -0.03 (-19.9%)	-0.01 (29.7%) / 0.00 (-12.9%)	0.02 (39.8%) / 0.12* (-22.7%)	0.10* (-14.1%) / 0.07 (34.3%)
	NIT		-0.44* (-0.1%) / -0.41* (1.3%)							-0.07* (-16.7%) / -0.05 (8.0%)	0.01 (-487.6%) / -0.02 (30.5%)	0.06 (17.5%) / 0.09* (11.2%)	0.07 (-35.7%) / -0.02 (-287.2%)
	PSE			-0.29* (-4.0%) / -0.37* (-1.3%)						0.00 (95.1%) / -0.07 (-41.2%)	0.05 (20.7%) / 0.04 (-150.8%)	0.00 (70.8%) / 0.07 (5.0%)	-0.01 (79.7%) / -0.06 (-55.3%)
	SKE				-0.22* (-1.6%) / -0.40* (-3.3%)					0.01 (25.5%) / -0.08 (7.2%)	0.02 (-38.4%) / 0.01 (80.1%)	0.01 (5.2%) / -0.02 (405.1%)	0.06 (-60.9%) / 0.05 (-14.6%)
	CHA					-0.40* (-8.9%) / -0.55* (-0.4%)				0.01 (-59.5%) / 0.05 (29.0%)	0.06* (-2.7%) / 0.06 (-49.2%)	0.03 (19.4%) / -0.03 (-17.2%)	-0.04 (22.1%) / 0.03 (43.1%)
	GUI						-0.27* (-1.7%) / -0.32* (5.6%)			-0.06 (12.4%) / -0.04 (-98.0%)	0.07 (2.6%) / -0.02 (32.9%)	-0.02 (7.8%) / 0.04 (-123.7%)	0.02 (-343.4%) / 0.02 (50.0%)
	LEP							-0.31* (-4.0%) / -0.34* (-1.7%)		0.01 (241.8%) / 0.07 (7.5%)	0.12* (-41.1%) / 0.05 (-149.0%)	-0.03 (11.0%) / -0.09* (-17.9%)	-0.01 (65.4%) / -0.02 (-12.0%)
	RHI								-0.34* (3.3%) / -0.37* (7.8%)	0.03 (-351.8%) / 0.01 (54.8%)	0.07* (-32.5%) / 0.00 (123.8%)	-0.02 (-68.1%) / 0.01 (315.0%)	-0.02 (43.9%) / -0.05 (-25.9%)
	GYM	0.00 (71.4%) / 0.05 (41.8%)	-0.04 (29.1%) / 0.06 (-122.6%)	0.02 (48.6%) / 0.01 (-0.5%)	0.02 (46.2%) / -0.01 (39.0%)	-0.01 (80.2%) / 0.03 (333.7%)	0.00 (88.4%) / 0.02 (32.3%)	0.01 (136.3%) / 0.10 (-29.5%)	0.04 (29.1%) / 0.07 (-16.2%)	-0.38* (3.2%) / -0.48* (-2.1%)		-0.03 (-110.2%) / 0.02 (30.8%)	0.08 (-15.0%) / 0.07 (-4.7%)
	PRP	0.08 (27.5%) / 0.00 (119.5%)	0.04 (12.7%) / -0.02 (45.2%)	0.03 (-901.8%) / 0.00 (-121.6%)	0.00 (81.4%) / 0.01 (-18.3%)	-0.03 (49.0%) / 0.02 (-355.0%)	0.03 (-41.0%) / 0.04 (-9.3%)	0.02 (122.8%) / 0.05 (43.7%)	-0.02 (-380.3%) / 0.05 (-164.9%)		-0.40* (-2.4%) / -0.40* (-2.7%)	0.03 (-171.5%) / 0.03 (18.4%)	0.06 (-500.1%) / 0.07 (-14.8%)
	CRY	-0.09* (-2.6%) / -0.06 (-21.3%)	0.07 (3.1%) / 0.08 (28.1%)	-0.07 (-102.2%) / 0.04 (21.1%)	0.05 (-59.6%) / -0.07 (19.6%)	0.15* (-24.2%) / -0.07 (-23.8%)	-0.05 (-55.9%) / 0.00 (110.6%)	0.00 (86.9%) / 0.03 (-222.1%)	0.09* (-21.6%) / -0.07 (-36.0%)	-0.06 (-47.7%) / -0.03 (-0.3%)	-0.02 (-31.4%) / 0.10 (-12.7%)	-0.50* (-1.1%) / -0.49* (-5.9%)	0.00 (136.2%) / 0.05 (-16.3%)
	EUG	-0.05 (-35.7%) / -0.06 (42.7%)	-0.01 (2.1%) / 0.10* (-26.1%)	-0.02 (-851.7%) / -0.02 (0.5%)	0.05 (-620.5%) / 0.02 (55.5%)	0.11* (-0.9%) / -0.02 (68.6%)	-0.01 (125.7%) / 0.09* (4.7%)	-0.02 (-3.6%) / -0.10 (-137.2%)	-0.02 (64.5%) / -0.02 (36.0%)	-0.05 (-123.5%) / -0.05 (-471.5%)	0.03 (27.3%) / 0.06 (-991.3%)	0.04 (29.8%) / 0.02 (-28.7%)	-0.33* (-2.7%) / -0.40* (7.4%)

Table A6.3: Model coefficients for covariates at Teychan/Buoy 7, using a lagged covariate (Supplementary material Appendix 3: eq. A3.2). Changes from the results obtained with our formulation are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and P<0.05. The table should be read as element i having effect e_{ji} on plankton group j. Composition of planktonic groups is described in Table 1 in the main text.

Model		SAL	CumRg	Wind energy	season
Null	AST	0.03 (40.4%) / -0.01(63.5%)	-0.05 (-9.7%) / -0.15* (-1.2%)	-0.03 (31.8%) / -0.02(70.3%)	-0.10* (12.8%) / -0.06(33.7%)
	NIT	-0.03 (212.6%) / -0.08(-41.9%)	0.06* (-106.5%) / 0.00(84.7%)	-0.01 (72.7%) / -0.03(-95.0%)	0.22* (0.0%) / 0.21* (0.4%)
	PSE	-0.05 (-42.7%) / -0.06(-269.0%)	0.03 (48.2%) / 0.04(-143.9%)	-0.07* (52.6%) / -0.09(60.6%)	0.01 (69.7%) / -0.02(816.4%)
	SKE	0.00 (222.8%) / -0.06(-24.2%)	0.00 (69.5%) / -0.09(6.8%)	0.00 (88.7%) / -0.01(88.3%)	0.02 (3.1%) / 0.02(-159.9%)
	CHA	-0.10* (3.5%) / -0.09(-220.4%)	0.10* (-85.3%) / 0.10* (-60.2%)	-0.03 (83.2%) / -0.14* (11.0%)	0.22* (25.5%) / 0.19* (17.3%)
	GUI	-0.04 (-184.4%) / -0.04(280.4%)	0.04 (12.1%) / 0.04(1355.3%)	-0.06 (30.5%) / -0.01(92.9%)	0.06 (41.1%) / -0.01(32.4%)
	LEP	-0.10* (-107.6%) / 0.00(42.7%)	0.12* (17.8%) / 0.17* (-8.0%)	-0.05 (2.7%) / -0.07(46.9%)	0.06 (62.0%) / -0.01(108.5%)
	RHI	-0.04 (-3.4%) / 0.05(-290.4%)	0.06 (-54.6%) / 0.06(4251.6%)	0.00 (103.7%) / -0.08(34.4%)	0.09* (23.8%) / 0.05(23.8%)
	GYM	-0.08* (-201.3%) / -0.04(36.3%)	0.05 (57.1%) / 0.05(2.6%)	-0.06 (18.6%) / -0.01(94.2%)	-0.01 (167.9%) / 0.00(111.4%)
	PRP	-0.07* (-6.2%) / -0.04(39.6%)	0.15* (-7.9%) / 0.12* (-51.6%)	0.07 (383.3%) / 0.02(152.1%)	0.08* (24.5%) / 0.03(66.3%)
	CRY	0.00 (96.0%) / 0.04(143.7%)	0.11* (-1530.4%) / 0.01(58.3%)	-0.01 (688.9%) / -0.06(309.8%)	0.07* (24.3%) / 0.15* (0.5%)
	EUG	-0.01 (86.4%) / -0.02(69.0%)	0.14* (1814.8%) / 0.06(-587.9%)	-0.02 (71.3%) / 0.05(293.7%)	0.14* (17.0%) / 0.12* (5.8%)
Unconstrained	AST	0.02 (54.2%) / 0.01(147.3%)	-0.03 (-10.4%) / -0.10* (-33.9%)	-0.03 (31.4%) / -0.01(57.7%)	-0.16* (-12.3%) / -0.13* (24.9%)
	NIT	-0.01* (126.2%) / -0.07* (-40.2%)	0.08* (-87.3%) / -0.02(-168.4%)	-0.02 (38.2%) / -0.07(-147.4%)	0.19* (4.4%) / 0.16* (11.0%)
	PSE	-0.05 (-220.9%) / -0.06(-113.2%)	0.02 (70.4%) / 0.09* (-61.5%)	-0.07* (54.9%) / -0.09* (59.1%)	-0.02 (202.0%) / -0.03(203.1%)
	SKE	0.01 (303.9%) / -0.06(-26.9%)	0.00 (71.1%) / -0.07(2.2%)	0.01 (169.9%) / 0.02(165.9%)	-0.09 (-125.9%) / -0.07(18.8%)
	CHA	-0.10* (-10.1%) / -0.09* (-188.6%)	0.08* (-61.0%) / 0.06(-96.2%)	-0.03 (78.9%) / -0.12* (21.0%)	0.23* (27.6%) / 0.12* (22.4%)
	GUI	-0.04 (-165.7%) / -0.04(294.4%)	0.05 (20.0%) / 0.07* (1201.8%)	-0.07* (3.9%) / -0.05(59.0%)	0.05 (60.2%) / 0.02(34.6%)
	LEP	-0.10* (-43.8%) / -0.01(-690.6%)	0.10 (18.6%) / 0.17* (-14.8%)	-0.05 (22.1%) / -0.06* (43.4%)	0.09* (48.8%) / 0.04(71.7%)
	RHI	-0.04 (34.9%) / 0.05(-582.3%)	0.04 (16.2%) / 0.03(271.7%)	0.02 (182.1%) / -0.07(45.2%)	0.01 (91.1%) / 0.02(70.6%)
	GYM	-0.07 (-146.9%) / -0.03(56.6%)	0.04 (58.7%) / 0.04(29.4%)	-0.05 (27.7%) / 0.02(117.2%)	-0.06 (415.2%) / -0.12* (-273.1%)
	PRP	-0.09 (-4.4%) / -0.04(43.6%)	0.16* (2.1%) / 0.12* (-131.4%)	0.07 (351.6%) / 0.04(158.6%)	0.07 (70.5%) / -0.01(122.2%)
	CRY	0.01 (116.9%) / 0.05(152.9%)	0.14* (-168.0%) / -0.03(495.8%)	0.01 (61.0%) / -0.07(246.4%)	-0.08 (-299.1%) / 0.08(-5.4%)
	EUG	0.02 (128.9%) / 0.00(98.7%)	0.15* (1622.6%) / 0.10* (-87.2%)	0.00 (89.2%) / 0.04(2582.5%)	0.07 (27.9%) / 0.10(7.1%)

Table A6.4: Model coefficients for covariates at Teychan/Buoy 7, using a lagged covariate (Supplementary material Appendix 3: eq. A3.2). Changes from the results obtained with our formulation are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and P<0.05. The table should be read as element i having effect e_{ji} on plankton group j. Composition of planktonic groups is described in Table 1 in the main text.

Model		SAL	CumRg	Wind energy	season
Intra-phylum	AST	0.02 (61.0%) / 0.00(106.1%)	-0.04 (-26.5%) / -0.10* (-15.8%)	-0.03 (19.2%) / -0.01(77.0%)	-0.12* (-0.4%) / -0.09(32.2%) /
	NIT	-0.02 (144.6%) / -0.08* (-51.8%)	0.07* (-79.0%) / -0.02(1.8%) /	-0.02 (31.9%) / -0.06(-154.2%) /	0.23* (-2.2%) / 0.18* (9.4%)
	PSE	-0.06* (-102.0%) / -0.06(-127.3%)	0.03 (62.9%) / 0.09* (-79.2%)	-0.07* (55.5%) / -0.08(64.0%)	-0.02 (174.5%) / -0.04(249.3%) /
	SKE	0.01 (216.4%) / -0.06(-13.5%)	0.01 (57.8%) / -0.08* (7.5%)	0.01 (144.4%) / 0.02(172.1%)	-0.07 (-142.7%) / -0.06(21.1%)
	CHA	-0.11* (-5.1%) / -0.09* (-171.1%)	0.09* (-57.1%) / 0.07(-84.0%)	-0.03* (80.7%) / -0.13* (17.7%)	0.22* (29.6%) / 0.14* (25.8%)
	GUI	-0.05* (-141.9%) / -0.04(307.0%)	0.06 (9.5%) / 0.07(977.4%)	-0.07* (8.1%) / -0.04(62.7%)	0.08* (46.5%) / 0.03(38.6%)
	LEP	-0.12* (-46.3%) / -0.01(-273.7%)	0.13* (6.7%) / 0.18* (-8.1%)	-0.05 (22.7%) / -0.07* (34.6%)	0.12* (39.6%) / 0.02(87.6%)
	RHI	-0.04 (36.8%) / 0.05(-422.0%)	0.05* (-2.2%) / 0.02(229.7%)	0.02 (183.0%) / -0.07* (48.4%)	0.01 (93.4%) / 0.00(104.0%)
	GYM	-0.08 (-201.9%) / -0.02(59.8%)	0.04 (61.1%) / 0.03(23.5%)	-0.05 (16.7%) / 0.00(99.1%)	-0.02 (-11296.8%) / -0.07* (-159.9%)
	PRP	-0.07* (-6.6%) / -0.04(47.0%)	0.15* (-0.7%) / 0.12* (-98.4%)	0.07 (865.3%) / 0.02(126.7%)	0.07* (48.9%) / 0.03(60.1%)
	CRY	-0.01 (90.9%) / 0.05(149.5%)	0.11* (-995.3%) / 0.00(118.2%)	-0.01 (1625.6%) / -0.05(243.6%)	0.08* (21.4%) / 0.13* (-0.7%)
	EUG	-0.01 (89.7%) / -0.02(68.0%)	0.14* (988.0%) / 0.06(-126.0%)	-0.02 (66.5%) / 0.05(1331.1%)	0.14* (16.8%) / 0.12* (2.1%)
Inter-phylum	AST	0.04 (26.9%) / 0.00(96.0%)	-0.03 (7.4%) / -0.14* (-28.1%)	-0.03 (38.2%) / -0.03(50.6%)	-0.14* (-3.3%) / -0.11* (25.2%)
	NIT	-0.02 (162.1%) / -0.07(-32.7%)	0.07* (-97.9%) / 0.01(-47.5%)	-0.01 (66.6%) / -0.05(-91.8%)	0.19* (6.2%) / 0.21* (3.3%)
	PSE	-0.04 (-374.7%) / -0.06(-173.3%)	0.02 (61.7%) / 0.05(-99.3%)	-0.07* (52.4%) / -0.10(54.1%)	-0.01 (163.3%) / -0.02(807.5%)
	SKE	0.01 (253.6%) / -0.07(-26.0%)	0.00 (506.7%) / -0.08(8.6%)	0.00 (119.8%) / -0.02(61.9%)	-0.01 (315.4%) / 0.02(645.3%)
	CHA	-0.09* (-3.4%) / -0.08(-241.1%)	0.08* (-89.4%) / 0.09(-73.6%)	-0.03 (82.0%) / -0.13* (16.2%)	0.21* (25.7%) / 0.18* (14.9%)
	GUI	-0.04 (-202.7%) / -0.04(236.8%)	0.04 (20.1%) / 0.05(-3351.5%)	-0.06 (14.6%) / -0.02(82.7%)	0.03 (60.0%) / -0.01(-26.5%)
	LEP	-0.09* (-59.6%) / 0.00(150.5%)	0.10* (26.7%) / 0.16* (-12.1%)	-0.04 (6.1%) / -0.05(39.4%)	0.03 (78.1%) / 0.02(81.0%)
	RHI	-0.03 (19.3%) / 0.06(-453.5%)	0.03 (-24.1%) / 0.05(-1905.3%)	0.00 (129.6%) / -0.08(37.4%)	0.07* (32.3%) / 0.06(25.3%)
	GYM	-0.08* (-120.3%) / -0.04(43.2%)	0.05 (56.7%) / 0.06(25.3%)	-0.05 (29.1%) / 0.03(117.8%)	-0.05 (271.8%) / -0.10(-1905.2%)
	PRP	-0.09* (-4.5%) / -0.04(43.2%)	0.16* (2.7%) / 0.12* (-122.5%)	0.07 (347.4%) / 0.03(156.7%)	0.08* (69.4%) / -0.01(125.9%)
	CRY	0.01 (116.9%) / 0.05(152.9%)	0.14* (-168.0%) / -0.03(495.8%)	0.01 (61.0%) / -0.07(246.4%)	-0.08 (-299.1%) / 0.08(-5.4%)
	EUG	0.02 (128.9%) / 0.00(98.7%)	0.15* (1622.6%) / 0.10* (-87.2%)	0.00 (89.2%) / 0.04(2586.5%)	0.07 (27.9%) / 0.10(7.1%)

A6.5 Differences in coefficients due to a full error covariance matrix

Table A6.5: Model coefficients for interactions at Teychan/Buoy 7, using a full variance/covariance error matrix. Changes from the results obtained with a diagonal error matrix are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. The identity matrix was subtracted to the interaction matrix in order to make effects on growth rates comparable. Composition of planktonic groups is described in Table 1 in the main text.

Model		AST	NIT	PSE	SKE	CHA	GUI	LEP	RHI	GYM	PRP	CRY	EUG
Null	AST	-0.28* (0.0%) / -0.32* (0.0%)											
	NIT		-0.41* (0.0%) / -0.39* (0.0%)										
	PSE			-0.30* (0.0%) / -0.39* (0.0%)									
	SKE				-0.19* (0.0%) / -0.36* (0.0%)								
	CHA					-0.43* (0.0%) / -0.51* (0.0%)							
	GUI						-0.28* (0.0%) / -0.29* (0.0%)						
	LEP							-0.35* (0.0%) / -0.31* (0.0%)					
	RHI								-0.31* (0.0%) / -0.32* (0.0%)				
	GYM									-0.34* (0.0%) / -0.42* (0.0%)			
	PRP										-0.33* (0.0%) / -0.46* (0.0%)		
	CRY											-0.46* (0.0%) / -0.48* (0.0%)	
	EUG												-0.33* (0.0%) / -0.36* (0.0%)
Unconstrained	AST	-0.27* (0.9%) / -0.39* (0.9%)	0.09* (-1.7%) / 0.13* (11.6%)	-0.01 (-10.5%) / 0.01 (53.6%)	0.01 (324.4%) / 0.03 (-10.8%)	-0.04 (-0.3%) / -0.05 (6.0%)	-0.01 (-130.1%) / 0.01 (59.4%)	0.02 (-36.5%) / -0.05 (-139.1%)	0.01 (44.7%) / -0.02 (44.5%)	-0.05 (-24.5%) / -0.01 (59.7%)	-0.01 (60.8%) / 0.04 (-419.4%)	0.01 (70.7%) / 0.05 (30.9%)	0.06 (20.3%) / 0.09* (-28.5%)
	NIT	-0.02 (-72.3%) / -0.05 (-5.0%)	-0.45* (0.2%) / -0.39* (-0.3%)	-0.06 (-11.0%) / -0.08 (1.7%)	0.05 (-42.5%) / 0.00 (122.6%)	0.00 (145.4%) / -0.01 (-2633.0%)	-0.04 (9.9%) / 0.01 (20.5%)	0.03 (-62.3%) / 0.00 (106.9%)	0.03 (-21.9%) / 0.00 (122.6%)	-0.06 (-5.6%) / -0.05 (-24.7%)	0.01 (-113.5%) / 0.02 (310.7%)	0.05 (9.4%) / 0.09* (3.4%)	0.06 (-29.3%) / 0.00 (113.0%)
	PSE	0.08* (-35.0%) / 0.02 (74.2%)	-0.02 (6.3%) / 0.09 (-0.4%)	-0.33* (-0.5%) / -0.36* (-4.4%)	0.00 (-57.7%) / -0.05 (-32.8%)	0.00 (95.9%) / -0.06 (4.6%)	0.08* (2.1%) / 0.01 (528.3%)	0.03 (3.5%) / -0.05 (-80.7%)	-0.03 (-86.3%) / 0.08 (16.8%)	0.00 (91.1%) / -0.05 (22.4%)	0.03 (25.8%) / 0.01 (-34.3%)	0.02 (-29.7%) / 0.04 (16.3%)	-0.03 (9.3%) / -0.01 (69.0%)
	SKE	-0.07* (-33.2%) / -0.02 (54.4%)	0.01 (74.9%) / 0.09 (-127.7%)	-0.04 (0.7%) / 0.09 (-39.2%)	-0.22* (-5.3%) / -0.43* (-1.2%)	0.01 (293.3%) / 0.01 (89.4%)	0.07* (18.2%) / -0.05 (-97.3%)	-0.02 (-134.2%) / -0.04 (-7.5%)	0.04 (14.5%) / 0.04 (-341.3%)	-0.01 (161.7%) / -0.08 (23.2%)	0.02 (-161.8%) / 0.06 (-193.4%)	0.00 (148.9%) / -0.02 (254.6%)	0.02 (24.2%) / 0.01 (73.8%)
	CHA	0.06 (-4.7%) / 0.00 (112.6%)	-0.04 (-2.7%) / 0.00 (245.4%)	-0.01 (-9.3%) / 0.00 (121.5%)	0.05 (-1.5%) / -0.05 (14.0%)	-0.48* (-3.7%) / -0.60* (-0.4%)	0.05 (10.3%) / 0.03 (-270.6%)	0.02 (32.1%) / 0.07 (26.4%)	0.04 (11.4%) / 0.11* (8.6%)	0.00 (102.0%) / 0.04 (2.3%)	0.03 (22.8%) / 0.03 (-38.0%)	0.05 (1.3%) / -0.01 (30.9%)	-0.04 (21.7%) / 0.08 (10.4%)
	GUI	0.05 (-84.1%) / 0.02 (30.7%)	0.00 (85.4%) / 0.02 (29.4%)	-0.09* (-110.1%) / -0.09* (-11.6%)	0.01 (-275.0%) / 0.00 (113.9%)	0.01 (226.8%) / -0.14* (9.2%)	-0.29* (2.9%) / -0.26* (-1.5%)	-0.03 (50.8%) / 0.01 (66.2%)	-0.01 (759.4%) / 0.04 (1.3%)	-0.06 (-19.6%) / 0.00 (-262.0%)	0.08* (-10.1%) / 0.00 (-72.3%)	-0.04 (-4.4%) / 0.01 (770.2%)	-0.01 (36.0%) / 0.02 (71.9%)
	LEP	0.06 (18.4%) / 0.04 (20.3%)	-0.08* (8.4%) / -0.02 (-21.1%)	0.04 (7.2%) / 0.05 (9.5%)	0.01 (190.3%) / -0.10* (7.9%)	-0.01 (19.0%) / -0.09 (-78.8%)	0.08* (12.8%) / 0.04 (-21.0%)	-0.39* (-1.6%) / -0.38* (-4.9%)	0.01 (39.2%) / 0.01 (76.3%)	-0.01 (-78.6%) / 0.05 (19.7%)	0.06 (7.3%) / 0.07 (-185.2%)	-0.01 (10057.7%) / -0.10* (-23.9%)	-0.02 (-53.6%) / -0.04 (-89.5%)
	RHI	0.05 (-16.6%) / 0.02 (1193.6%)	0.05 (-65.4%) / 0.04 (40.4%)	0.00 (95.1%) / 0.08 (16.7%)	0.02 (843.8%) / -0.08 (24.5%)	0.06 (-6.3%) / - 0.08 (23.4%)	0.08* (5.4%) / 0.09* (-13.5%)	-0.05 (37.0%) / 0.02 (68.4%)	-0.36* (1.1%) / -0.34* (-1.2%)	0.01 (22.4%) / 0.00 (418.7%)	0.05 (-21.5%) / -0.05 (-48.7%)	-0.05 (-106.8%) / -0.02 (11.8%)	-0.05 (22.6%) / -0.06 (-18.1%)
	GYM	0.02 (-74.2%) / 0.03 (51.8%)	-0.06 (-10.9%) / 0.04 (-14.0%)	0.02 (42.6%) / 0.02 (-108.0%)	0.03 (4.7%) / -0.03 (0.1%)	-0.04 (5.0%) / -0.02 (37.1%)	0.00 (52.9%) / -0.02 (266.6%)	-0.02 (51.8%) / 0.04 (33.2%)	0.05 (8.2%) / 0.05 (16.7%)	-0.36* (-0.2%) / -0.53* (1.2%)	0.01 (57.7%) / 0.20* (-39.1%)	-0.02 (-44.5%) / 0.02 (25.5%)	0.09* (-28.0%) / 0.04 (12.1%)
	PRP	0.07* (37.1%) / 0.00 (120.9%)	0.04 (5.1%) / -0.05 (-15.5%)	0.03 (-559.6%) / -0.01 (-242.7%)	0.02 (-50.6%) / 0.01 (61.1%)	-0.06 (3.1%) / -0.02 (1098.3%)	0.02 (-17.4%) / 0.02 (42.0%)	-0.03 (57.1%) / 0.06 (33.0%)	-0.01 (-261.2%) / 0.05 (-163.5%)	0.00 (79.3%) / 0.02 (25.5%)	-0.38* (-6.2%) / -0.40* (-4.8%)	0.00 (99.7%) / 0.01 (60.8%)	0.03 (-147.8%) / 0.12* (-81.4%)
	CRY	-0.09 (0.2%) / -0.08 (-69.9%)	0.08 (-6.3%) / 0.10 (12.6%)	-0.05 (-27.0%) / 0.05 (4.9%)	0.03 (2.3%) / -0.07 (24.0%)	0.11 (5.9%) / -0.05 (20.1%)	-0.02 (27.1%) / -0.02 (264.0%)	0.04 (275.9%) / 0.03 (-159.6%)	0.06 (23.0%) / -0.03 (37.4%)	-0.05 (-9.5%) / -0.03 (-6.0%)	-0.03 (-76.2%) / 0.10 (-8.2%)	-0.51* (0.2%) / -0.50* (-4.7%)	0.01 (192.9%) / 0.06 (-50.9%)
	EUG	-0.04 (-6.9%) / -0.08 (13.4%)	-0.02 (-73.1%) / 0.08 (8.8%)	0.00 (-0.7%) / -0.03 (-41.5%)	0.02 (-234.2%) / 0.03 (47.2%)	0.11* (-2.3%) / -0.01 (86.9%)	0.02 (28.7%) / 0.07 (20.2%)	0.00 (73.0%) / -0.12* (-201.4%)	-0.07* (-10.7%) / 0.03 (188.9%)	-0.03 (-31.0%) / -0.03 (-220.0%)	0.04 (13.1%) / 0.04 (-762.4%)	0.05 (17.2%) / 0.04 (-136.0%)	-0.36* (1.6%) / -0.38* (4.4%)

Table A6.6: Model coefficients for interactions at Teychan/Buoy 7, full variance/covariance error matrix. Changes from the results obtained with a diagonal error matrix are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. The identity matrix was subtracted to the interaction matrix in order to make effects on growth rates comparable. Composition of planktonic groups is described in Table 1 in the main text.

Model		AST	NIT	PSE	SKE	CHA	GUI	LEP	RHI	GYM	PRP	CRY	EUG
Intra-phylum	AST	-0.27* (0.9%) / -0.35* (-1.6%)	0.10* (3.8%) / 0.15* (17.8%)	-0.03 (-5.3%) / 0.01 (66.3%)	0.01 (-288.2%) / 0.04 (-56.3%)	-0.05 (-18.8%) / -0.03 (37.1%)	0.00 (186.3%) / 0.02 (23.1%)	0.02 (-131.7%) / -0.06 (-74.9%)	0.00 (-157.3%) / -0.03 (15.7%)				
	NIT	0.00 (69.3%) / -0.03 (31.6%)	-0.42* (0.6%) / -0.39* (2.0%)	-0.07* (0.4%) / -0.08 (0.1%)	0.04 (2.0%) / 0.00 (148.6%)	-0.02 (425.2%) / -0.01 (16.7%)	-0.03 (13.0%) / 0.01 (68.4%)	0.02 (-97.7%) / 0.00 (98.6%)	0.01 (-8.7%) / -0.01 (75.2%)				
	PSE	0.06 (0.0%) / 0.02 (71.9%)	-0.01 (73.5%) / 0.09 (-9.9%)	-0.34* (1.7%) / -0.35* (-5.8%)	0.00 (3.1%) / -0.06 (-47.2%)	0.03 (1564.8%) / -0.07 (8.9%)	0.07* (5.8%) / -0.01 (39.6%)	0.04 (-21.3%) / -0.04 (-40.8%)	-0.02 (-521.6%) / 0.06 (34.4%)				
	SKE	-0.06* (-28.7%) / -0.02 (61.1%)	0.01 (68.3%) / 0.09 (-116.9%)	-0.04 (-7.9%) / 0.10 (-43.7%)	-0.22* (-4.5%) / -0.42* (-1.6%)	0.00 (189.3%) / 0.01 (93.0%)	0.07* (18.4%) / -0.05 (-85.0%)	-0.02 (-140.4%) / -0.04 (28.1%)	0.04 (11.2%) / 0.04 (-930.7%)				
	CHA	0.04 (16.0%) / 0.01 (59.4%)	-0.03 (3.5%) / 0.01 (45.4%)	-0.02 (-78.4%) / 0.01 (246.6%)	0.04 (10.5%) / -0.05 (11.8%)	-0.46* (-6.1%) / -0.58* (-1.1%)	0.04 (19.4%) / 0.05 (-87.4%)	0.02 (6.3%) / 0.08 (26.6%)	0.04 (14.5%) / 0.08 (22.0%)				
	GUI	0.07* (-68.8%) / 0.03 (37.0%)	-0.01 (146.6%) / 0.02 (40.8%)	-0.09* (-124.0%) / -0.09* (-16.5%)	0.00 (51.6%) / 0.01 (116.0%)	-0.01 (56.3%) / -0.13* (10.5%)	-0.29* (3.2%) / -0.27* (0.5%)	-0.03 (52.8%) / 0.01 (83.4%)	0.00 (128.0%) / 0.02 (33.4%)				
	LEP	0.05 (28.9%) / 0.04 (20.8%)	-0.08* (9.5%) / -0.04 (-29.2%)	0.04 (14.1%) / 0.05 (11.6%)	0.00 (154.7%) / -0.09* (14.6%)	0.00 (79.3%) / -0.07 (-95.6%)	0.08* (17.2%) / 0.04 (-12.8%)	-0.38* (-2.7%) / -0.35* (-5.7%)	0.02 (19.4%) / 0.00 (103.8%)				
	RHI	0.05 (6.1%) / 0.00 (125.6%)	0.02 (-98.2%) / 0.03 (44.3%)	0.01 (48.7%) / 0.07 (19.6%)	0.01 (199.4%) / -0.08* (24.3%)	0.07 (-27.4%) / -0.09 (21.7%)	0.07* (9.9%) / 0.08 (-8.1%)	-0.04 (49.9%) / 0.01 (85.7%)	-0.34* (1.1%) / -0.32* (-2.1%)				
	GYM									-0.34* (-1.7%) / -0.53* (5.5%)	0.01 (78.5%) / 0.21* (-17.0%)	-0.03 (-69.2%) / 0.03 (20.2%)	
	PRP									0.00 (90.9%) / 0.02 (51.9%)	-0.37* (-3.3%) / -0.39* (0.2%)	0.01 (73.1%) / 0.02 (22.5%)	
	CRY									-0.01 (46.9%) / -0.03 (-3.6%)	-0.02 (-98.3%) / 0.07 (9.7%)	-0.48* (3.8%) / -0.49* (0.4%)	
	EUG												-0.36* (5.4%) / -0.36* (3.9%)
Inter-phylum	AST	-0.28* (3.6%) / -0.35* (0.2%)								-0.05 (-21.2%) / -0.02 (21.6%)	0.00 (82.2%) / 0.01 (-275.9%)	0.03 (29.1%) / 0.07 (25.4%)	0.08* (12.3%) / 0.12* (-19.9%)
	NIT		-0.46* (3.6%) / -0.40* (0.1%)							-0.06 (-0.8%) / -0.06 (-12.5%)	0.01 (-442.1%) / -0.01 (49.7%)	0.07* (-3.4%) / 0.10* (1.3%)	0.06 (-33.0%) / 0.00 (98.7%)
	PSE			-0.32* (0.9%) / -0.38* (-0.7%)						0.00 (109.4%) / -0.04 (22.4%)	0.05 (19.0%) / -0.01 (139.3%)	0.01 (-13.5%) / 0.06 (12.5%)	-0.02 (29.0%) / -0.01 (86.1%)
	SKE				-0.21* (-3.7%) / -0.42* (0.0%)					-0.01 (227.7%) / -0.08 (7.8%)	0.02 (-38.9%) / 0.07 (-116.4%)	0.02 (-81.2%) / -0.01 (318.6%)	0.03 (30.5%) / 0.01 (66.8%)
	CHA					-0.44* (-0.7%) / -0.51* (-9.8%)				0.00 (42.0%) / 0.06 (12.3%)	0.05 (19.0%) / 0.02 (47.7%)	0.04 (-0.2%) / -0.01 (48.9%)	-0.03 (26.0%) / 0.05 (6.9%)
	GUI						-0.33* (7.3%) / -0.29* (2.1%)			-0.08* (-23.9%) / -0.03 (-39.0%)	0.08* (-14.1%) / -0.04 (-55.3%)	-0.02 (-11.0%) / 0.03 (-83.1%)	0.02 (-284.0%) / 0.01 (74.4%)
	LEP							-0.34* (1.0%) / -0.35* (-0.9%)		-0.01 (-15.8%) / 0.06 (21.9%)	0.07* (9.9%) / 0.04 (-92.1%)	-0.03 (-8.7%) / -0.09* (-20.2%)	-0.02 (-12.5%) / -0.03 (-71.1%)
	RHI								-0.32* (1.0%) / -0.32* (0.7%)	0.01 (-34.7%) / 0.03 (2.4%)	0.07 (-21.7%) / -0.02 (-17.8%)	-0.03 (-172.6%) / -0.01 (-0.7%)	-0.02 (61.5%) / -0.05 (-12.2%)
	GYM	0.00 (130.7%) / 0.06 (37.3%)	-0.05 (1.2%) / 0.04 (-34.9%)	0.03 (24.5%) / 0.05 (-369.8%)	0.02 (55.4%) / 0.00 (94.8%)	-0.03 (8.3%) / 0.03 (389.7%)	-0.03 (-296.5%) / 0.00 (111.0%)	-0.02 (56.2%) / 0.08 (5.4%)	0.05 (20.4%) / 0.04 (42.1%)	-0.35* (-0.1%) / -0.49* (0.9%)		-0.02 (-43.4%) / 0.03 (1.0%)	0.10* (-34.0%) / 0.06 (-2.3%)
	PRP	0.05 (47.9%) / 0.00 (107.6%)	0.04 (15.8%) / -0.07 (-62.4%)	0.03 (-791.6%) / 0.00 (163.0%)	0.01 (23.6%) / 0.03 (-99.5%)	-0.06 (2.5%) / 0.04 (-647.6%)	0.00 (87.1%) / 0.02 (60.3%)	-0.02 (66.0%) / 0.08 (12.0%)	-0.02 (-229.6%) / 0.03 (-76.0%)		-0.38* (-6.7%) / -0.44* (4.1%)	0.00 (79.8%) / 0.03 (23.1%)	0.03 (-228.7%) / 0.12* (-92.7%)
	CRY	-0.06 (30.3%) / -0.07 (-38.1%)	0.07 (7.4%) / 0.08 (33.3%)	-0.03 (10.4%) / 0.06 (-4.4%)	0.02 (33.8%) / -0.07 (19.1%)	0.11* (5.0%) / -0.03 (48.5%)	0.00 (110.1%) / -0.02 (281.2%)	0.04 (263.4%) / 0.05 (-356.6%)	0.04 (44.9%) / -0.02 (65.1%)	-0.04 (-4.9%) / -0.03 (11.5%)	-0.03 (-115.8%) / 0.04 (50.3%)	-0.50* (-1.4%) / -0.49* (-6.1%)	0.00 (168.8%) / 0.08 (-83.4%)
	EUG	-0.03 (14.7%) / -0.08 (16.9%)	-0.03 (-185.5%) / 0.07 (17.4%)	0.02 (824.2%) / -0.01 (55.8%)	0.02 (-161.0%) / 0.02 (52.7%)	0.11* (-3.8%) / 0.00 (101.0%)	0.02 (11.4%) / 0.07 (18.1%)	0.00 (77.3%) / -0.12* (-189.3%)	-0.08* (-23.4%) / 0.02 (166.9%)	-0.03 (-38.5%) / -0.04 (-313.0%)	0.04 (18.9%) / 0.04 (-772.2%)	0.06 (3.7%) / 0.04 (-151.2%)	-0.35* (1.1%) / -0.38* (4.5%)

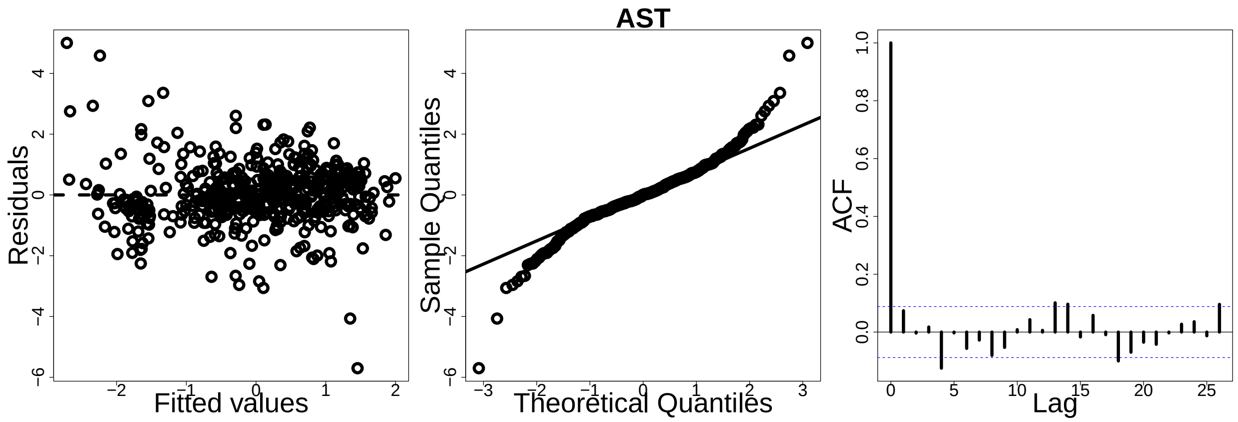
Table A6.7: Model coefficients for covariates at Teychan/Buoy 7, full variance/covariance error matrix. Changes from the results obtained with a diagonal error matrix are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. Composition of planktonic groups is described in Table 1 in the main text.

Model		SAL	CumRg	Wind energy	season
Null	AST	0.06 (0.0%) / -0.04(0.0%)	-0.05 (0.0%) / -0.14* (0.0%)	-0.04 (0.0%) / -0.05(0.0%)	-0.11* (0.0%) / -0.08* (0.0%)
	NIT	0.03 (0.0%) / -0.05(0.0%)	0.03 (0.0%) / -0.01(0.0%)	-0.03 (0.0%) / -0.01(0.0%)	0.22* (0.0%) / 0.21* (0.0%)
	PSE	-0.04 (0.0%) / -0.02(0.0%)	0.07* (0.0%) / 0.02(0.0%)	-0.15* (0.0%) / -0.23* (0.0%)	0.03 (0.0%) / 0.00(0.0%)
	SKE	0.00 (0.0%) / -0.05(0.0%)	0.02 (0.0%) / -0.09* (0.0%)	-0.01 (0.0%) / -0.08(0.0%)	0.03 (0.0%) / 0.01(0.0%)
	CHA	-0.11* (0.0%) / -0.03(0.0%)	0.05* (0.0%) / 0.06(0.0%)	-0.15* (0.0%) / -0.16* (0.0%)	0.30* (0.0%) / 0.23* (0.0%)
	GUI	-0.02 (0.0%) / 0.02(0.0%)	0.05 (0.0%) / 0.00(0.0%)	-0.08* (0.0%) / -0.10* (0.0%)	0.09* (0.0%) / -0.01(0.0%)
	LEP	-0.05 (0.0%) / 0.00(0.0%)	0.15* (0.0%) / 0.16* (0.0%)	-0.05 (0.0%) / -0.13* (0.0%)	0.16* (0.0%) / 0.06* (0.0%)
	RHI	-0.04 (0.0%) / 0.01(0.0%)	0.04 (0.0%) / 0.00(0.0%)	-0.03 (0.0%) / -0.12* (0.0%)	0.12* (0.0%) / 0.07(0.0%)
	GYM	-0.03 (0.0%) / -0.06(0.0%)	0.11* (0.0%) / 0.06(0.0%)	-0.07 (0.0%) / -0.17* (0.0%)	0.02 (0.0%) / 0.03(0.0%)
	PRP	-0.07* (0.0%) / -0.07(0.0%)	0.14* (0.0%) / 0.08(0.0%)	-0.02 (0.0%) / -0.03(0.0%)	0.11* (0.0%) / 0.10* (0.0%)
	CRY	-0.08 (0.0%) / -0.10* (0.0%)	0.01 (0.0%) / 0.02(0.0%)	0.00 (0.0%) / 0.03(0.0%)	0.09* (0.0%) / 0.15* (0.0%)
	EUG	-0.05 (0.0%) / -0.05(0.0%)	-0.01 (0.0%) / 0.01(0.0%)	-0.06 (0.0%) / -0.03(0.0%)	0.17* (0.0%) / 0.13* (0.0%)
Unconstrained	AST	0.05 (-18.6%) / -0.02(11.9%)	-0.02 (0.3%) / -0.08* (-1.1%)	-0.05 (-29.1%) / -0.03(3.0%)	-0.14* (3.1%) / -0.16* (5.2%)
	NIT	0.06 (-8.4%) / -0.05(2.8%)	0.05 (-9.6%) / 0.00(42.3%)	-0.03 (10.5%) / -0.03(4.8%)	0.18* (8.8%) / 0.18* (-0.5%)
	PSE	-0.04 (-174.0%) / -0.02(33.5%)	0.06 (5.5%) / 0.05(6.2%)	-0.16* (-3.3%) / -0.21* (3.3%)	0.03 (-84.5%) / 0.01(71.5%)
	SKE	0.01 (228.9%) / -0.06(-23.6%)	0.03 (-67.9%) / -0.08(-4.5%)	0.01 (157.9%) / -0.03(-7.6%)	-0.04 (7.0%) / -0.08(7.6%)
	CHA	-0.10* (-9.4%) / -0.03(4.1%)	0.05 (-8.3%) / 0.04(-7.5%)	-0.16* (-3.4%) / -0.15* (-0.4%)	0.31* (-0.1%) / 0.17* (-8.3%)
	GUI	0.01 (134.9%) / 0.03(-57.8%)	0.07* (-9.7%) / 0.01(308.5%)	-0.08* (-6.8%) / -0.09* (17.0%)	0.13* (-3.2%) / 0.05(-51.0%)
	LEP	-0.07* (9.7%) / -0.01(-765.6%)	0.14* (-10.8%) / 0.13* (12.2%)	-0.07* (-14.5%) / -0.11* (-9.2%)	0.17* (4.5%) / 0.14* (2.5%)
	RHI	-0.04 (34.8%) / 0.01(-30.7%)	0.07* (-39.5%) / -0.02(-10.7%)	-0.01 (78.1%) / -0.14* (-5.0%)	0.10 (22.9%) / 0.09(-32.2%) /
	GYM	-0.03 (-1.5%) / -0.06(3.3%)	0.11* (-2.9%) / 0.05(9.9%)	-0.07* (-12.5%) / -0.14* (3.1%)	0.01 (21.0%) / -0.06(-78.0%)
	PRP	-0.10* (-10.3%) / -0.07(1.6%)	0.16* (3.4%) / 0.05(0.6%)	-0.03 (-3.0%) / -0.05(19.7%)	0.19* (26.3%) / 0.04(1.6%)
	CRY	-0.08 (4.4%) / -0.09(5.3%)	0.05 (5.1%) / 0.01(25.3%)	0.03 (-5.0%) / 0.05(-3.9%)	-0.05 (-145.6%) / 0.04(52.0%)
	EUG	-0.07* (-26.9%) / 0.00(94.5%)	-0.02 (-78.4%) / 0.06(-23.7%)	-0.06 (-34.8%) / 0.01(450.2%)	0.10* (-8.2%) / 0.12* (-6.6%)

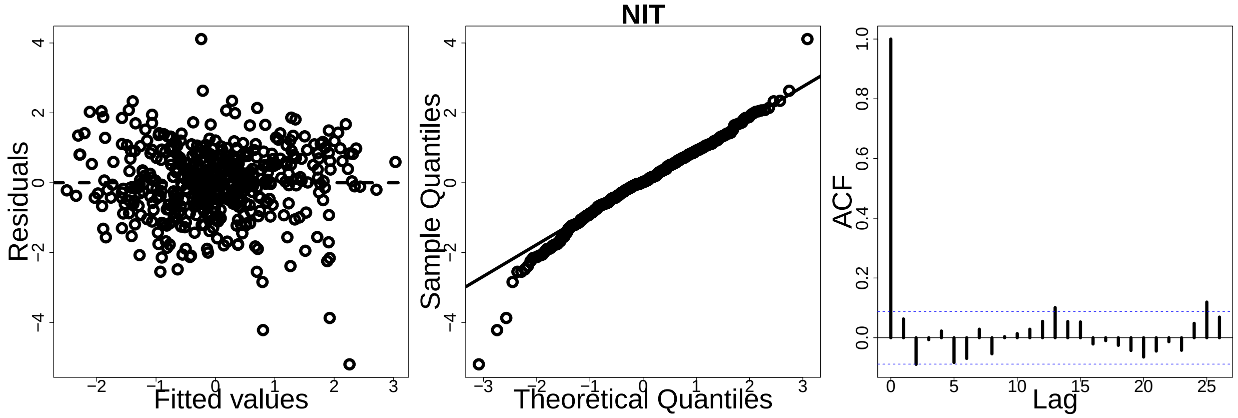
Table A6.8: Model coefficients for covariates at Teychan/Buoy 7, full variance/covariance error matrix. Changes from the results obtained with a diagonal error matrix are indicated between parentheses. Significance of coefficients (*) was determined by bootstrapping and $P<0.05$. The table should be read as element i having effect e_{ji} on plankton group j. Composition of planktonic groups is described in Table 1 in the main text.

Model		SAL	CumRg	Wind energy	season
Intra-phylum	AST	0.06 (-17.7%) / -0.03(3.9%)	-0.04 (-7.6%) / -0.08* (6.2%)	-0.05 (-31.9%) / -0.03(-13.6%)	-0.12* (3.3%) / -0.10* (21.4%)
	NIT	0.05 (-4.4%) / -0.05(-2.2%)	0.04 (7.6%) / -0.02(12.9%)	-0.03 (-9.2%) / -0.02(-11.6%)	0.24* (-8.7%) / 0.21* (-7.0%)
	PSE	-0.05 (-72.0%) / -0.02(28.9%)	0.07* (4.5%) / 0.05(10.6%)	-0.16* (-0.6%) / -0.21* (2.8%)	0.00 (105.3%) / 0.01(59.6%)
	SKE	0.01 (192.0%) / -0.06(-25.5%)	0.03 (-47.3%) / -0.08(10.0%)	0.01 (144.2%) / -0.04(-8.8%)	-0.02 (44.7%) / -0.07(2.7%)
	CHA	-0.11* (-3.0%) / -0.03(3.6%)	0.06* (-2.8%) / 0.04(-1.1%)	-0.16* (-2.1%) / -0.16* (-1.8%)	0.30* (4.0%) / 0.20* (-6.6%)
	GUI	0.00 (123.9%) / 0.03(-65.8%)	0.07* (-7.7%) / 0.01(254.3%)	-0.09* (-8.7%) / -0.09* (16.7%)	0.17* (-9.4%) / 0.06(-21.0%)
	LEP	-0.07* (14.7%) / -0.01(-457.2%)	0.15* (-10.2%) / 0.15* (8.8%)	-0.07* (-10.7%) / -0.12* (-13.5%)	0.18* (13.0%) / 0.13* (-1.9%)
	RHI	-0.04 (40.8%) / 0.01(-33.4%)	0.07* (-32.2%) / -0.01(15.9%)	0.00 (80.7%) / -0.13* (-3.1%)	0.08 (29.3%) / 0.06(-46.5%)
	GYM	-0.03 (-20.5%) / -0.06(-2.3%)	0.10* (-3.4%) / 0.05(-5.0%)	-0.07* (-11.9%) / -0.15* (1.3%)	0.02 (9881.6%) / -0.03(-10.4%)
	PRP	-0.08* (-21.0%) / -0.07(-1.3%)	0.15* (1.1%) / 0.06(3.6%)	-0.02 (-103.0%) / -0.05(16.7%)	0.14* (7.0%) / 0.08* (-8.6%)
	CRY	-0.09* (-3.2%) / -0.09* (5.9%)	0.01 (5.6%) / 0.01(17.2%)	0.00 (92.4%) / 0.04(5.3%)	0.11* (-6.6%) / 0.13* (-1.8%)
	EUG	-0.09* (-20.5%) / -0.02(65.0%)	-0.02 (-56.8%) / 0.01(45.8%)	-0.06* (-30.1%) / -0.01(-52.0%)	0.19* (-10.1%) / 0.13* (-5.0%)
Inter-phylum	AST	0.06 (-17.2%) / -0.03(4.2%)	-0.04 (-4.7%) / -0.11* (-2.7%)	-0.05 (-22.1%) / -0.05(4.2%)	-0.14* (-4.3%) / -0.15* (0.2%)
	NIT	0.04 (-4.7%) / -0.05(1.1%)	0.03 (7.9%) / 0.00(32.6%)	-0.03 (-1.8%) / -0.02(2.9%)	0.20* (2.0%) / 0.21* (1.5%)
	PSE	-0.03 (-225.9%) / -0.02(16.6%)	0.06 (3.3%) / 0.03(-21.5%)	-0.15* (-0.6%) / -0.22* (2.3%)	0.02 (-49.9%) / 0.00(7.9%)
	SKE	0.00 (144.1%) / -0.06(-11.7%)	0.01 (1890.5%) / -0.11* (-25.1%)	0.00 (111.1%) / -0.05(-1.9%)	0.01 (-1.2%) / -0.04(-1197.4%)
	CHA	-0.09* (-7.2%) / -0.02(3.0%)	0.05 (-2.8%) / 0.06(-12.0%)	-0.15* (-2.8%) / -0.15* (2.6%)	0.29* (0.4%) / 0.20* (6.2%)
	GUI	0.00 (132.9%) / 0.04(-30.2%)	0.06 (-9.8%) / 0.01(-843.0%)	-0.06* (2.5%) / -0.08* (16.2%)	0.09* (-23.2%) / 0.00(94.2%)
	LEP	-0.05 (9.7%) / 0.00(159.9%)	0.15* (-8.4%) / 0.14* (4.5%)	-0.06 (-22.7%) / -0.10* (-7.4%)	0.13* (-3.6%) / 0.08* (2.4%)
	RHI	-0.01 (60.4%) / 0.02(-51.9%)	0.04 (-45.6%) / -0.01(600.3%)	0.00 (110.2%) / -0.13* (-3.4%)	0.10* (10.6%) / 0.07(9.2%)
	GYM	-0.03 (15.5%) / -0.07(2.6%)	0.11* (3.4%) / 0.07(4.0%)	-0.07* (-7.3%) / -0.14* (5.6%)	0.02 (45.0%) / -0.04(-620.7%)
	PRP	-0.09* (-6.0%) / -0.07(0.8%)	0.15* (6.1%) / 0.05(0.9%)	-0.03 (1.3%) / -0.05(23.2%)	0.19* (26.4%) / 0.03(27.8%)
	CRY	-0.08* (-6.6%) / -0.09(1.7%)	0.04 (14.0%) / 0.00(42.7%)	0.02 (14.3%) / 0.04(4.8%)	-0.04 (-94.3%) / 0.04(43.9%)
	EUG	-0.08* (-33.4%) / 0.00(92.5%)	-0.02 (-132.2%) / 0.06(-17.7%)	-0.06 (-36.3%) / 0.01(492.6%)	0.10* (-10.1%) / 0.12* (-5.2%)

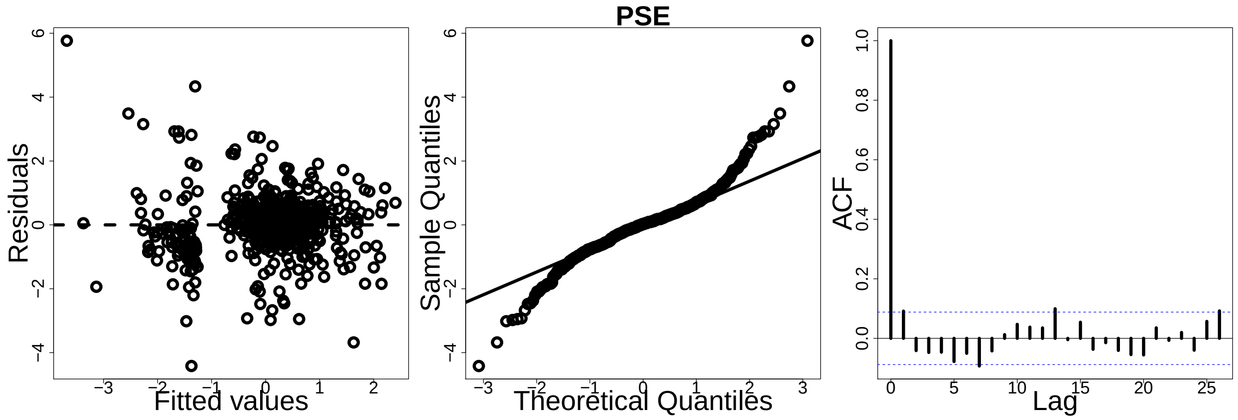
A6.6 Residual diagnostic plots for MAR models



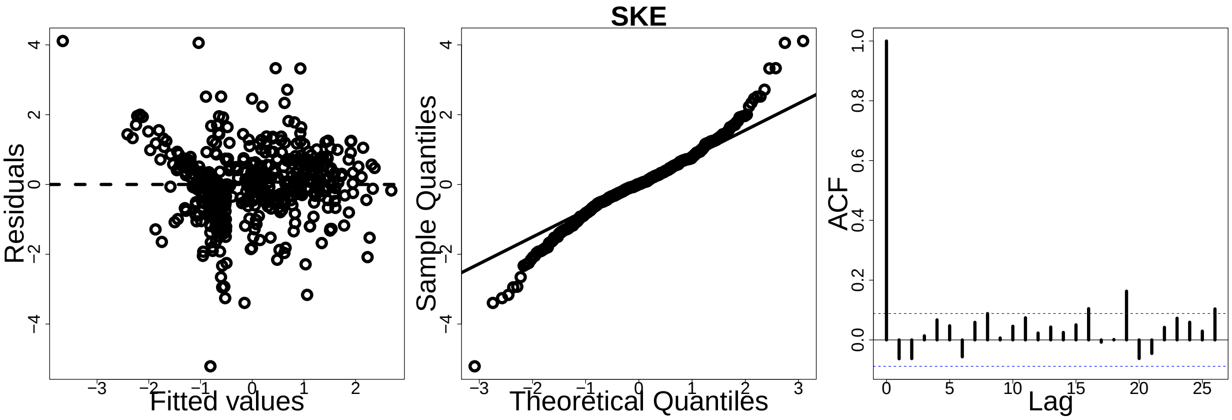
(a) AST



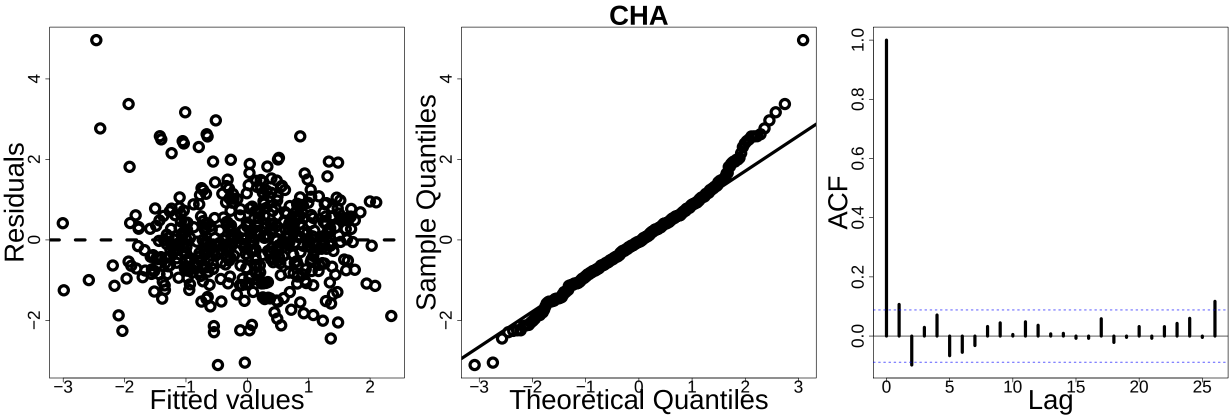
(b) NIT



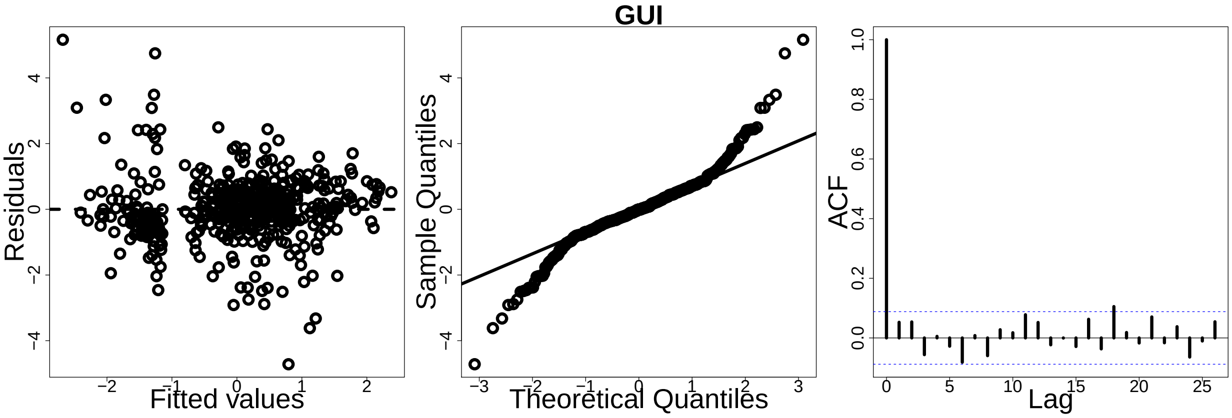
(c) PSE


SKE

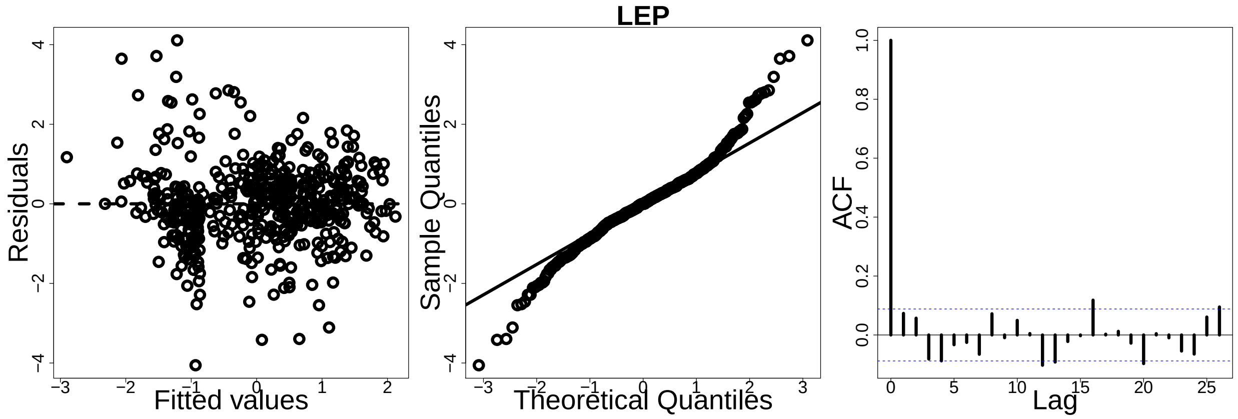
(d) SKE


CHA

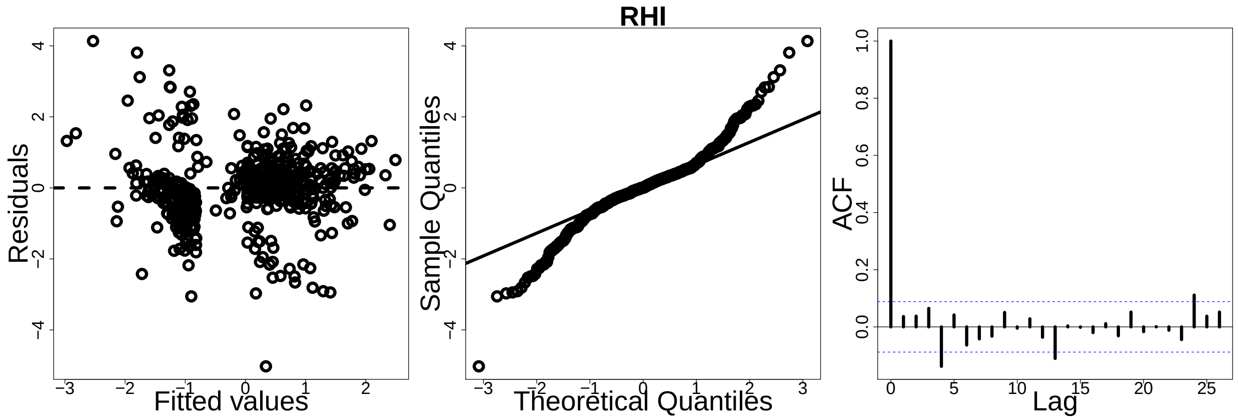
(e) CHA


GUI

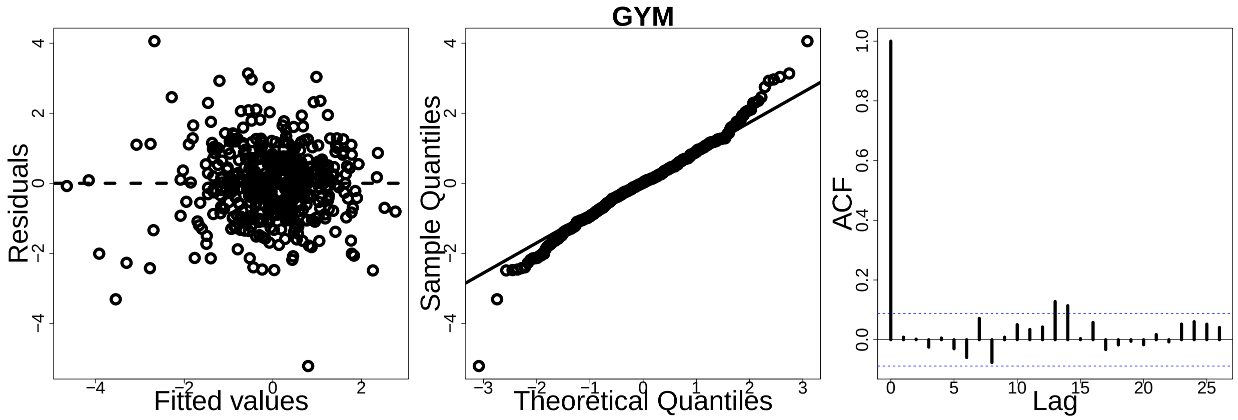
(f) GUI



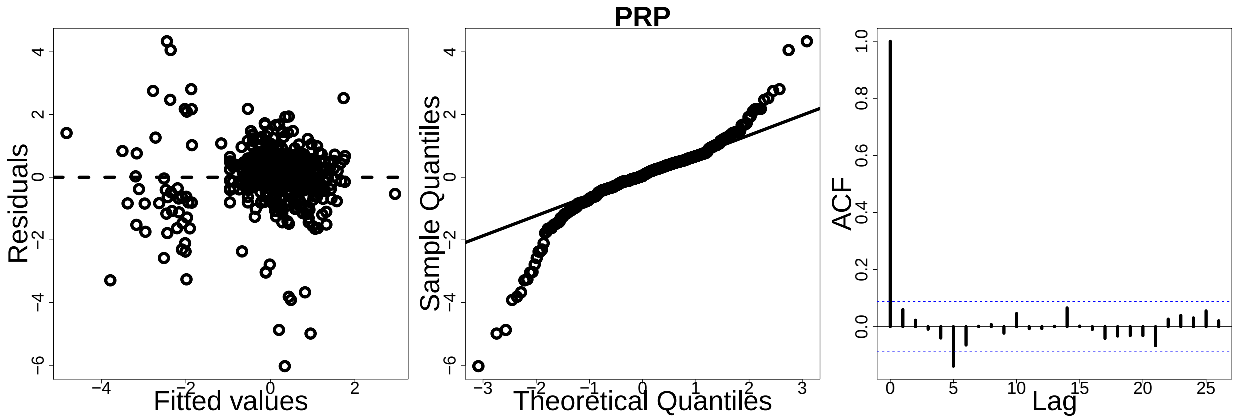
(g) LEP



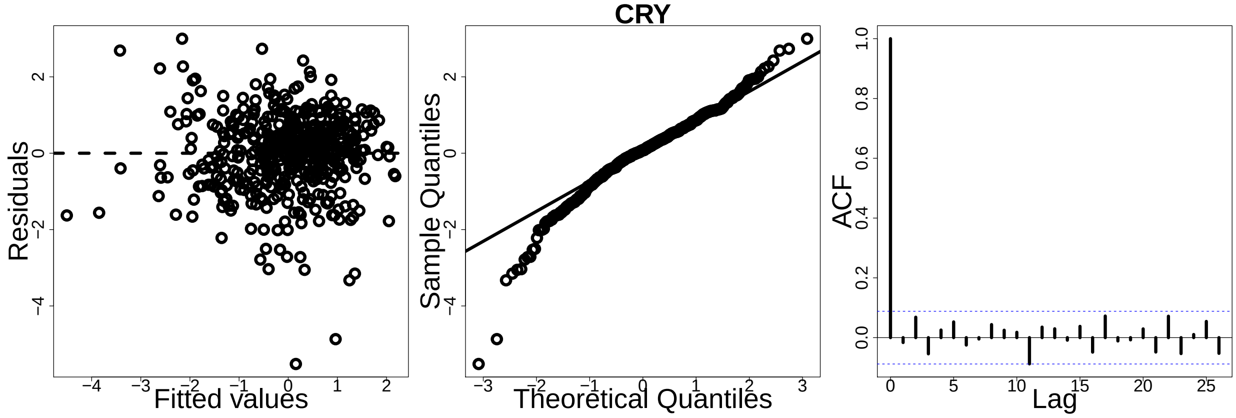
(h) RHI



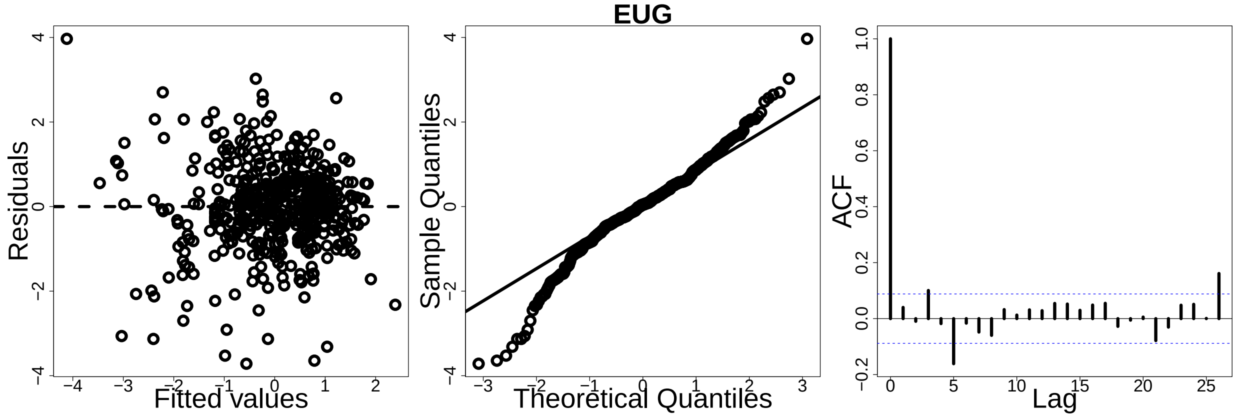
(i) GYM



(j) PRP

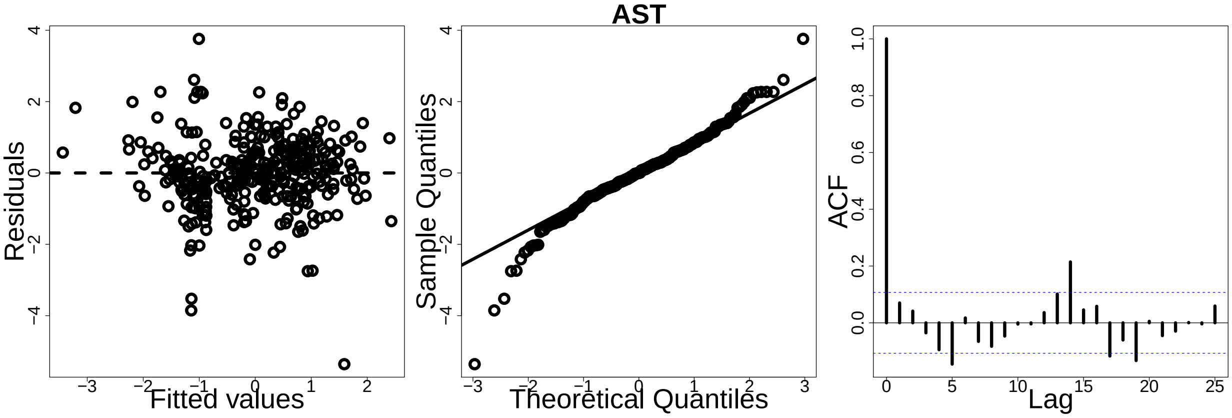


(k) CRY

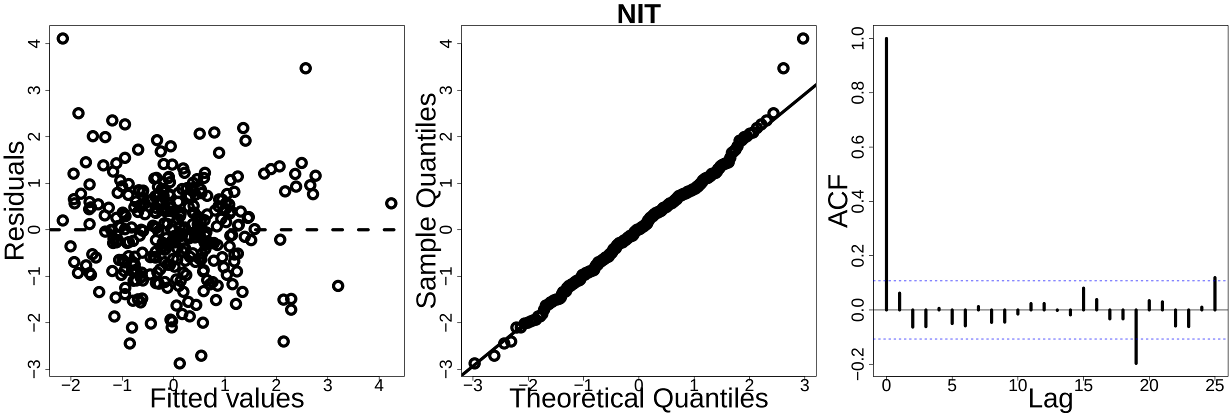


(l) EUG

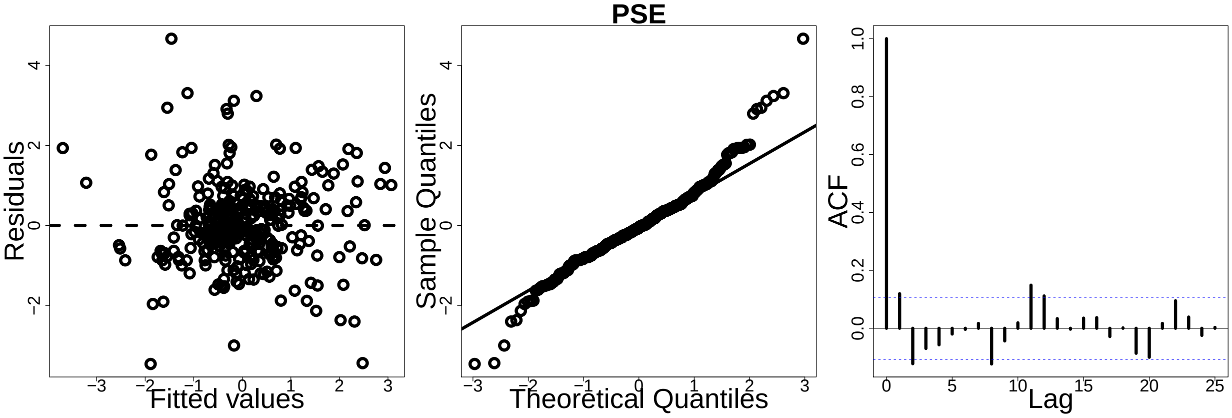
Figure A6.4: Residual examination for a MAR model using a diagonal interaction matrix at Teychan site. From left to right, residuals plotted against fitted values, Q-Q plots, and auto-correlation of residuals. The composition of planktonic groups is described in Table 1 in the main text.



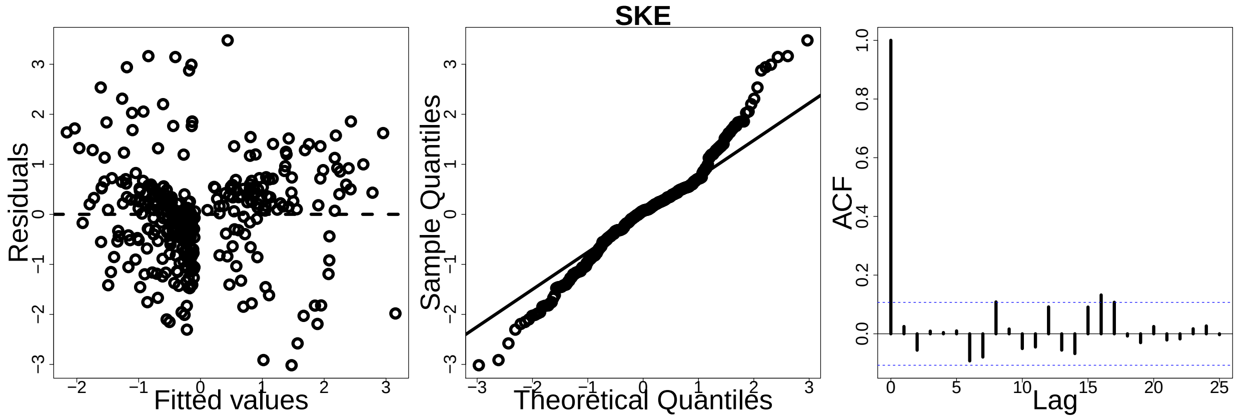
(a) AST



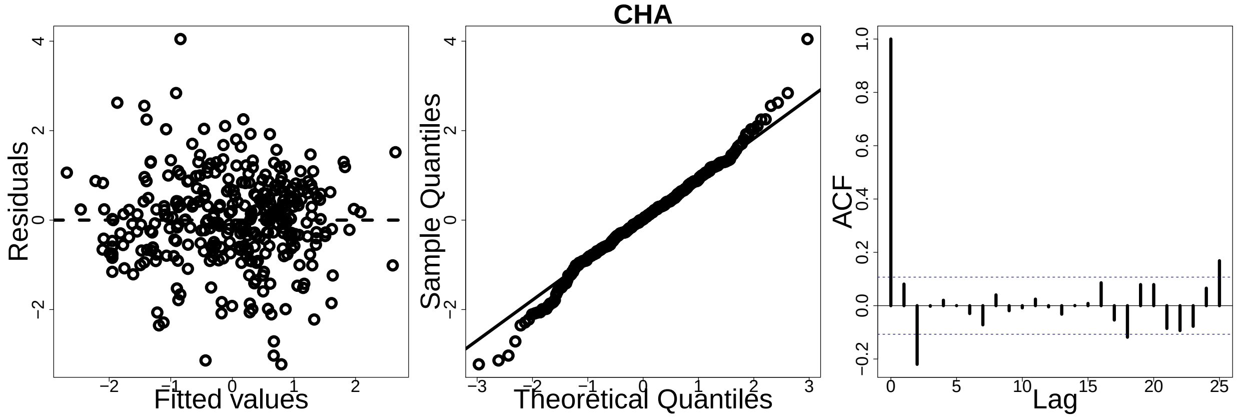
(b) NIT



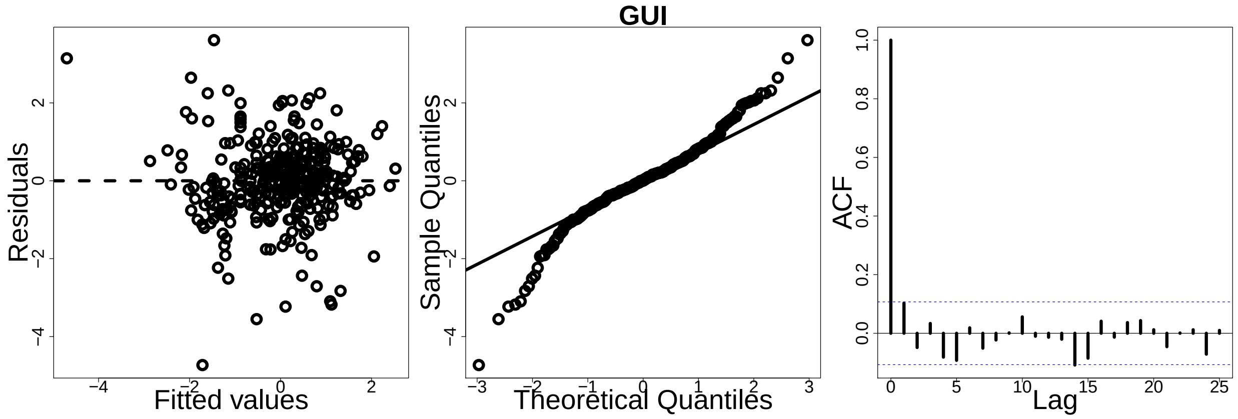
(c) PSE



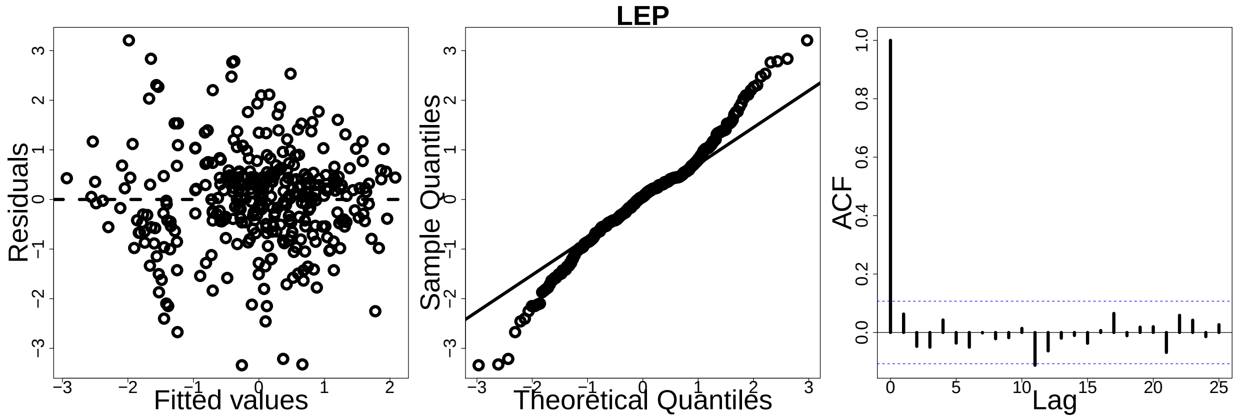
(d) SKE



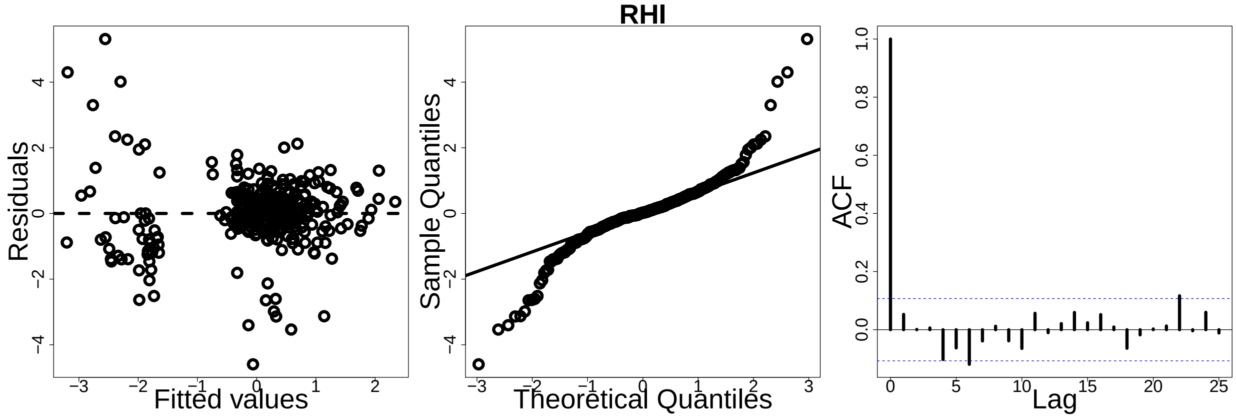
(e) CHA



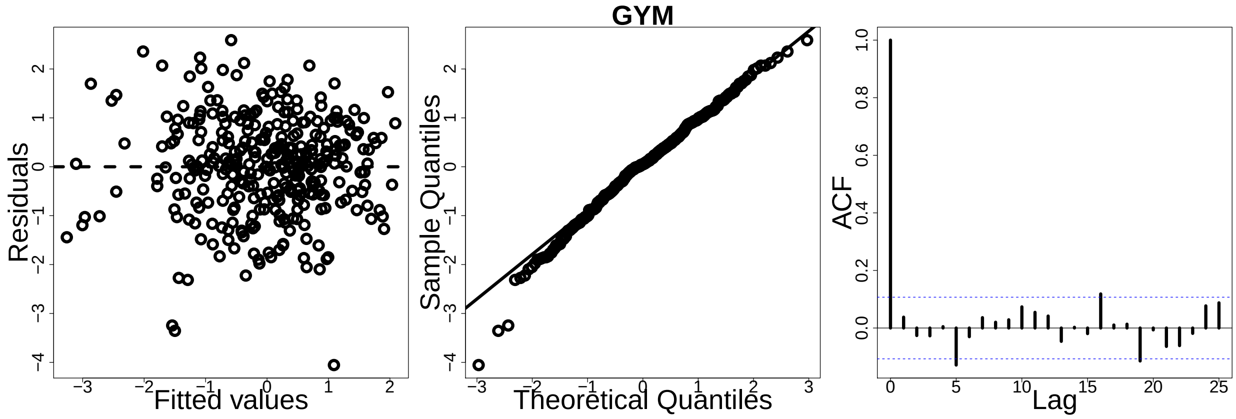
(f) GUI



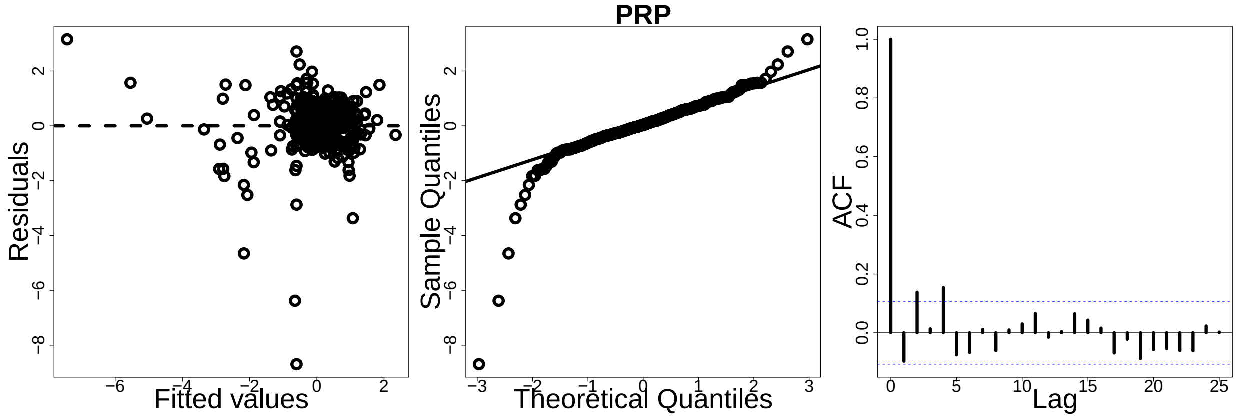
(g) LEP



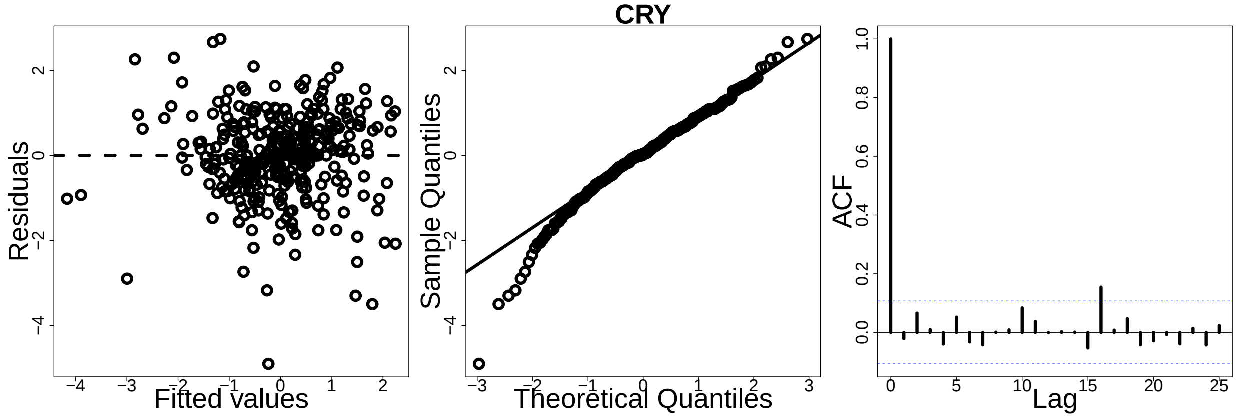
(h) RHI



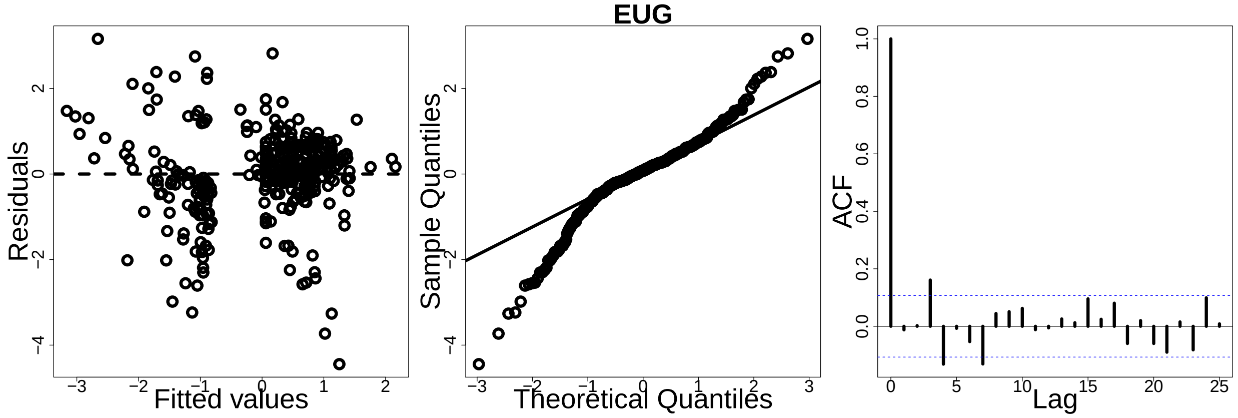
(i) GYM



(j) PRP

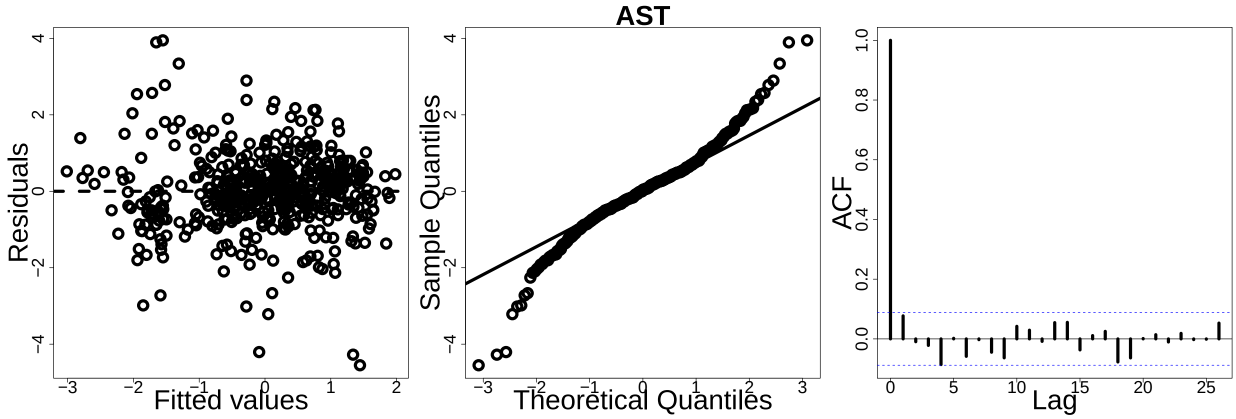


(k) CRY

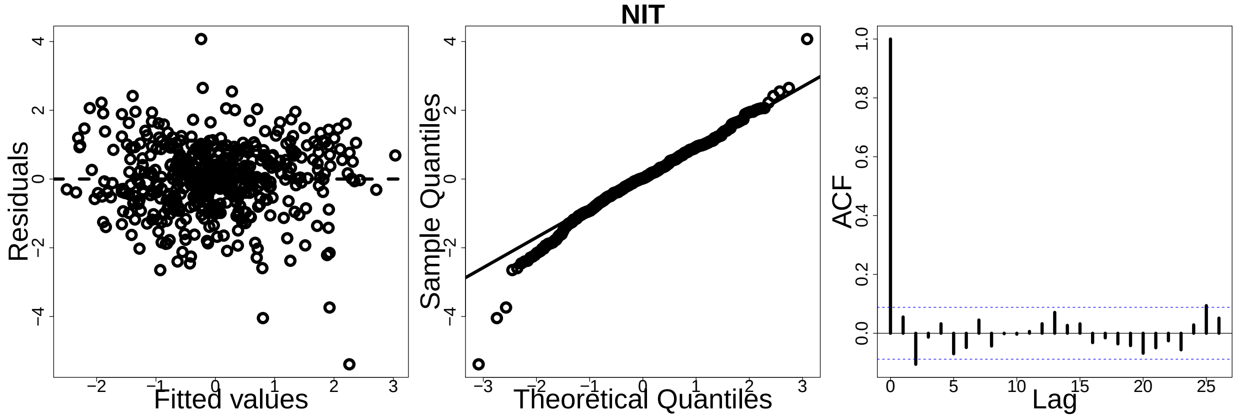


(l) EUG

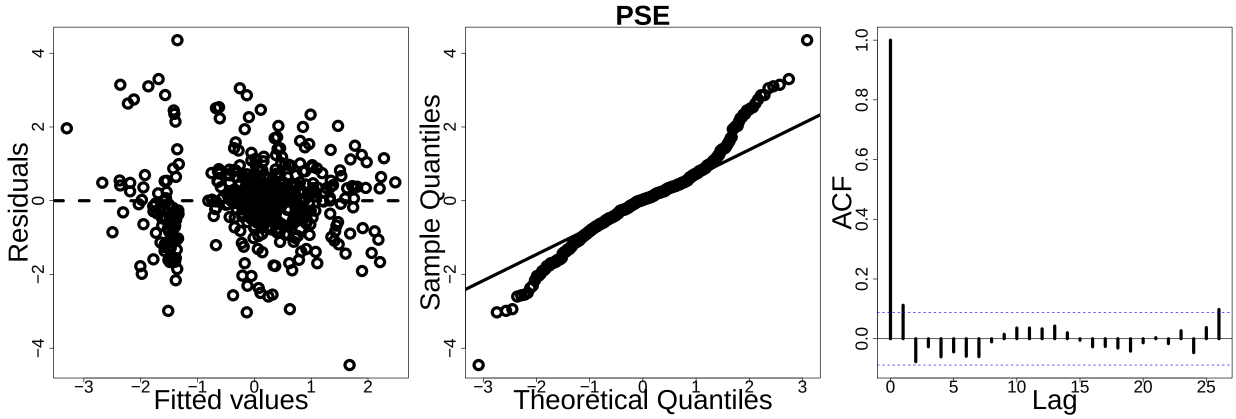
Figure A6.5: Residual examination for a MAR model using a diagonal interaction matrix at Buoy 7 site. From left to right, residuals plotted against fitted values, Q-Q plots, and auto-correlation of residuals. The composition of planktonic groups is described in Table 1 in the main text.



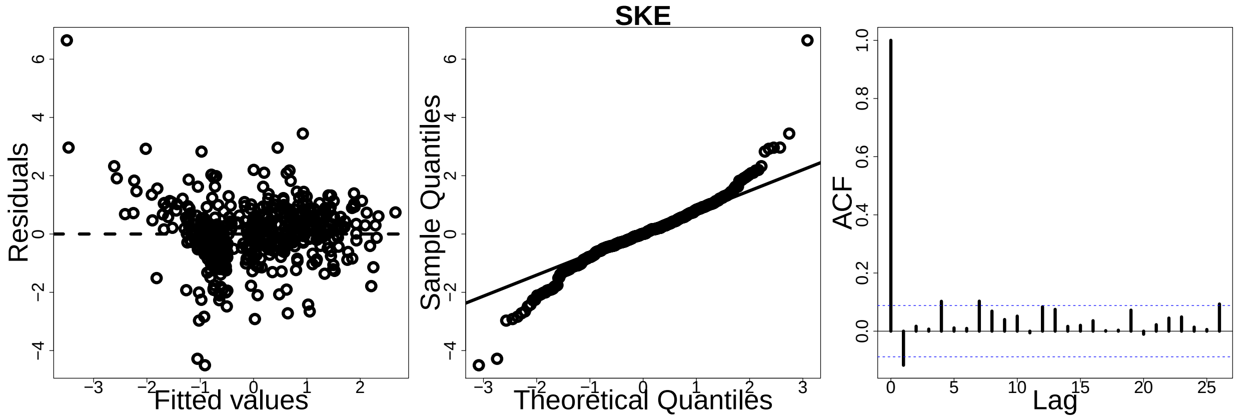
(a) AST



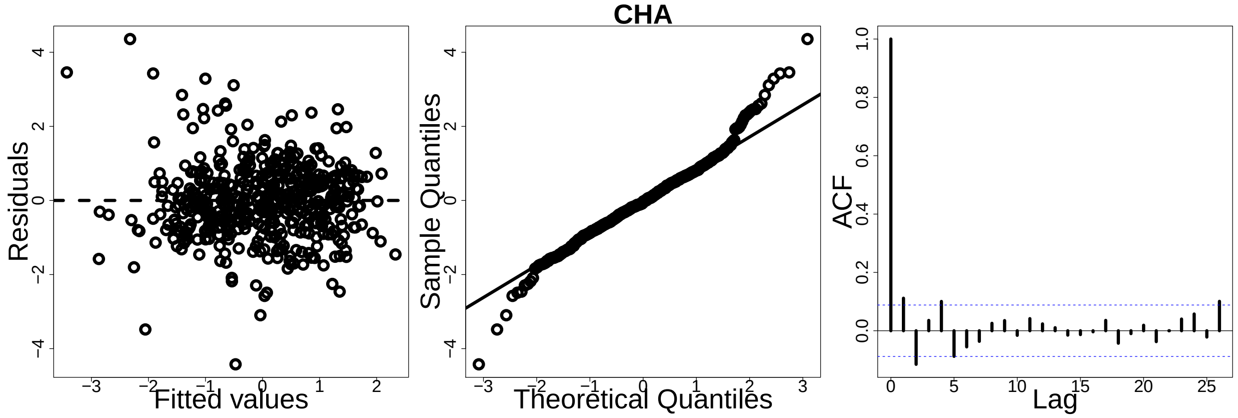
(b) NIT



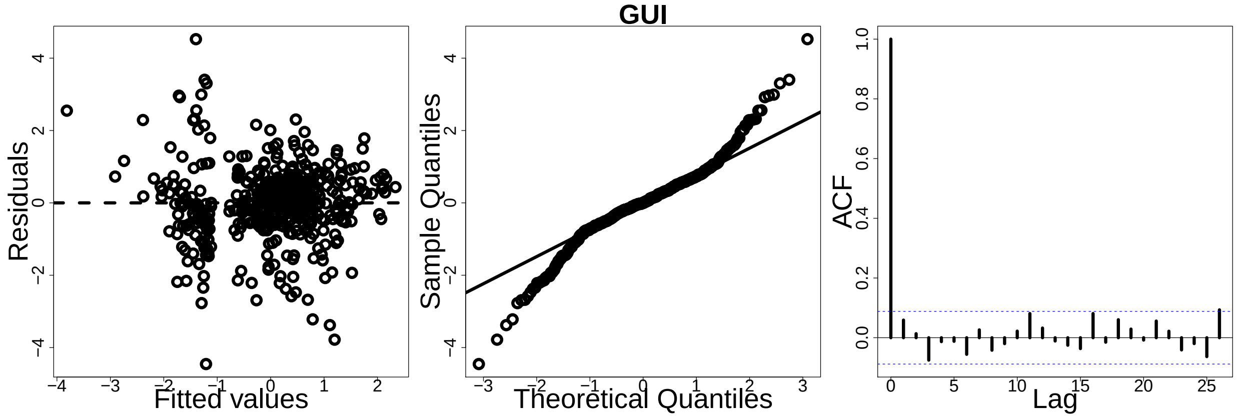
(c) PSE



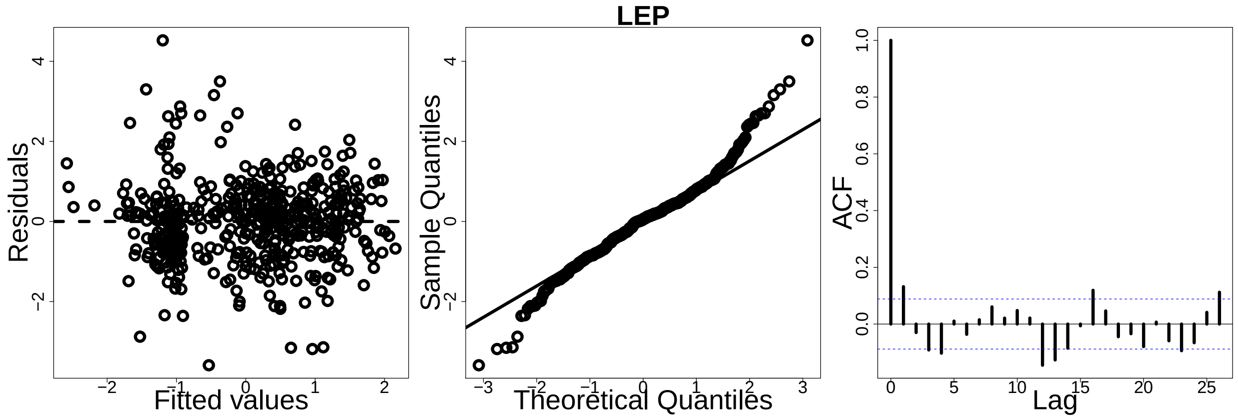
(d) SKE



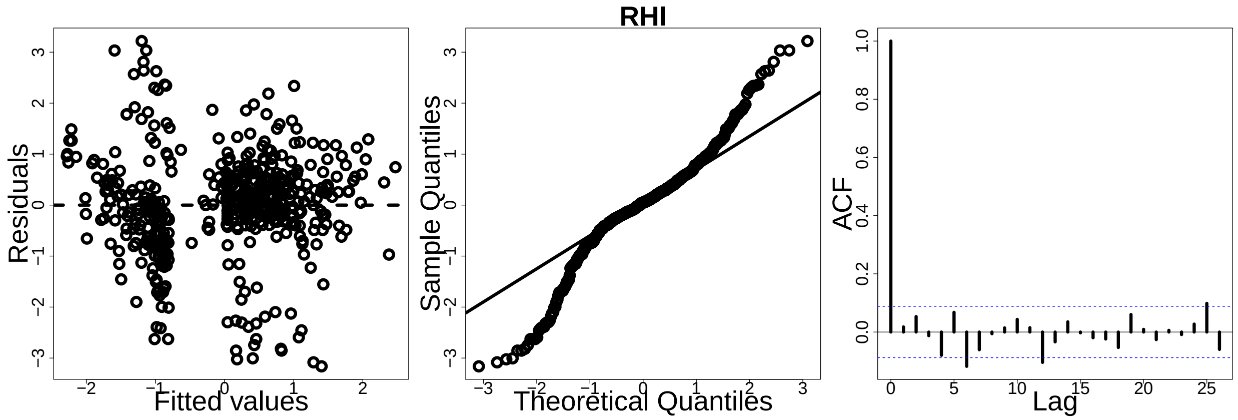
(e) CHA



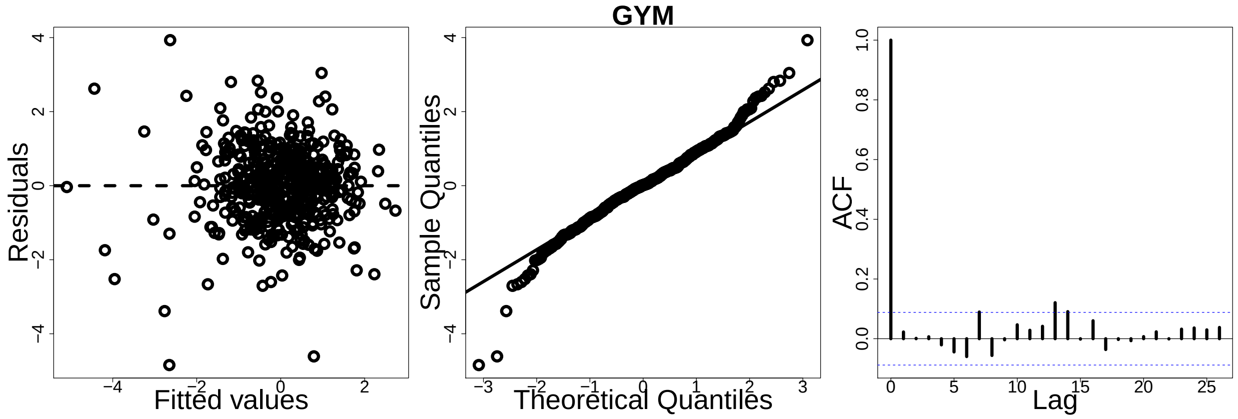
(f) GUI



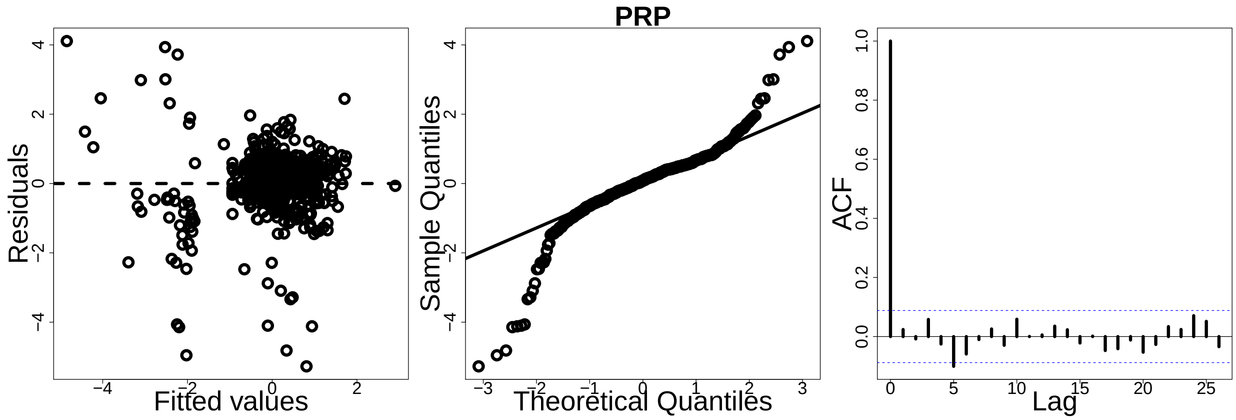
(g) LEP



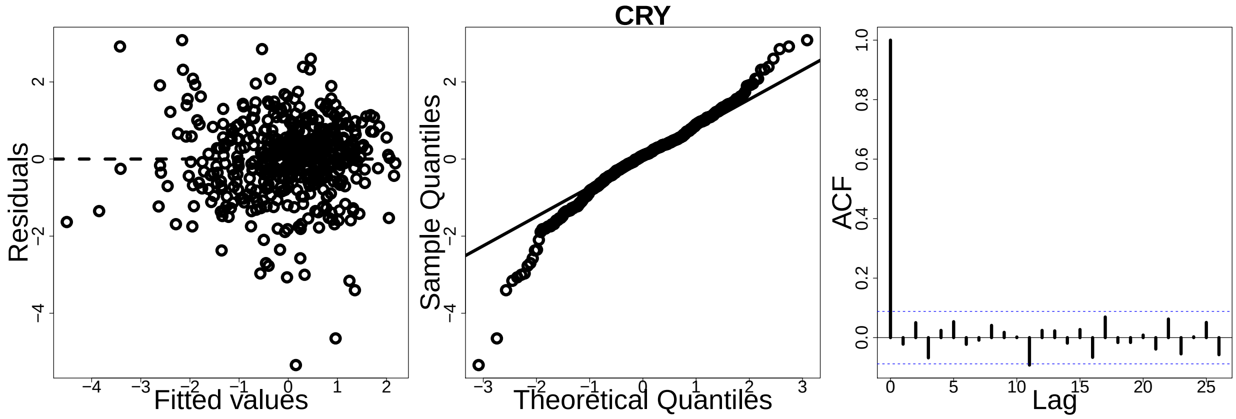
(h) RHI



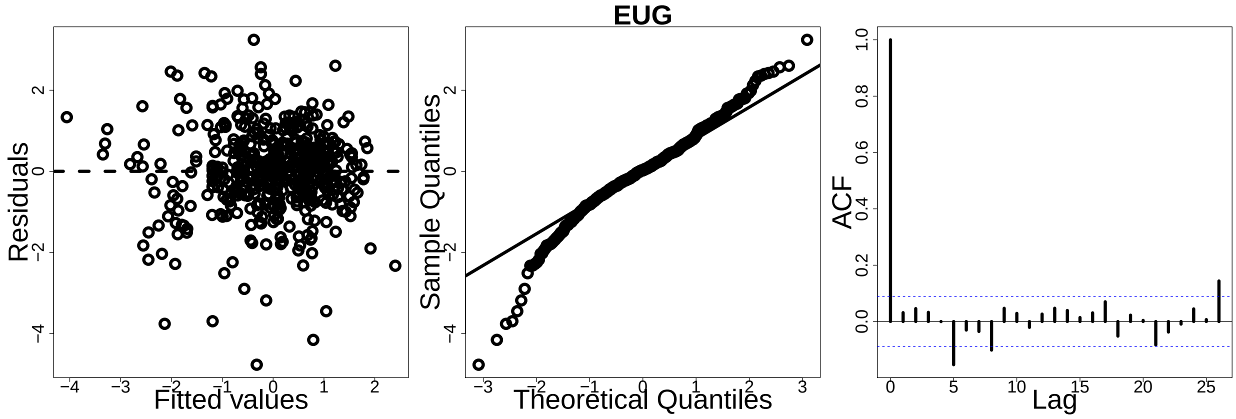
(i) GYM



(j) PRP

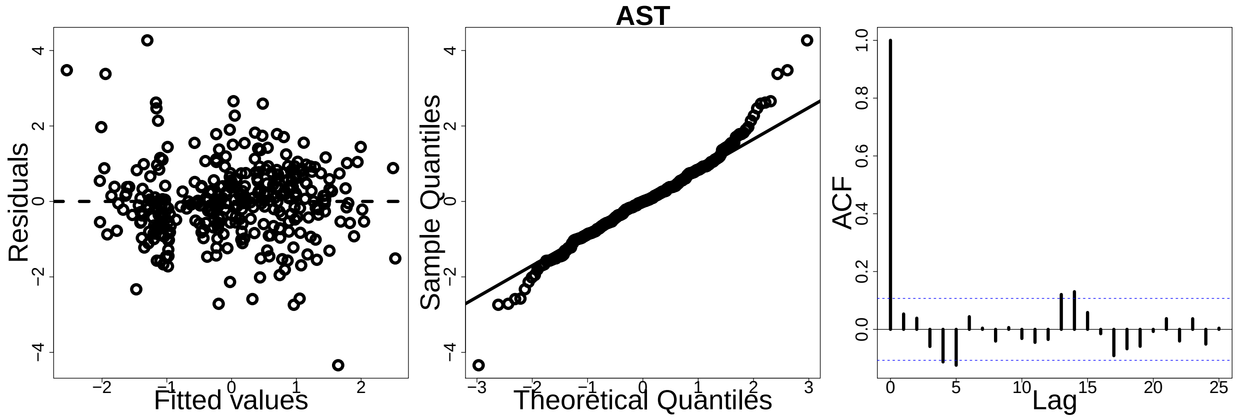


(k) CRY

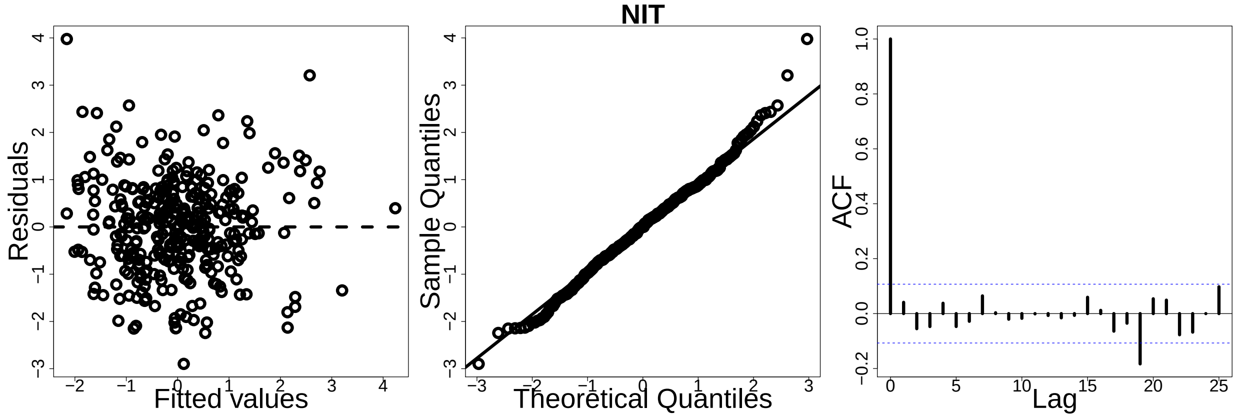


(l) EUG

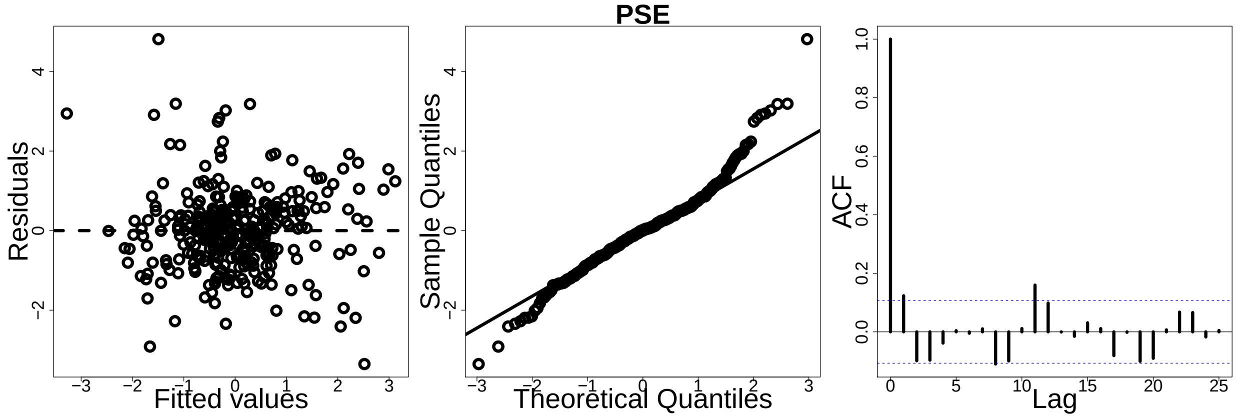
Figure A6.6: Residual examination for a MAR model using an unconstrained interaction matrix at Teychan site. From left to right, residuals plotted against fitted values, Q-Q plots, and auto-correlation of residuals. The composition of planktonic groups is described in Table 1 in the main text.



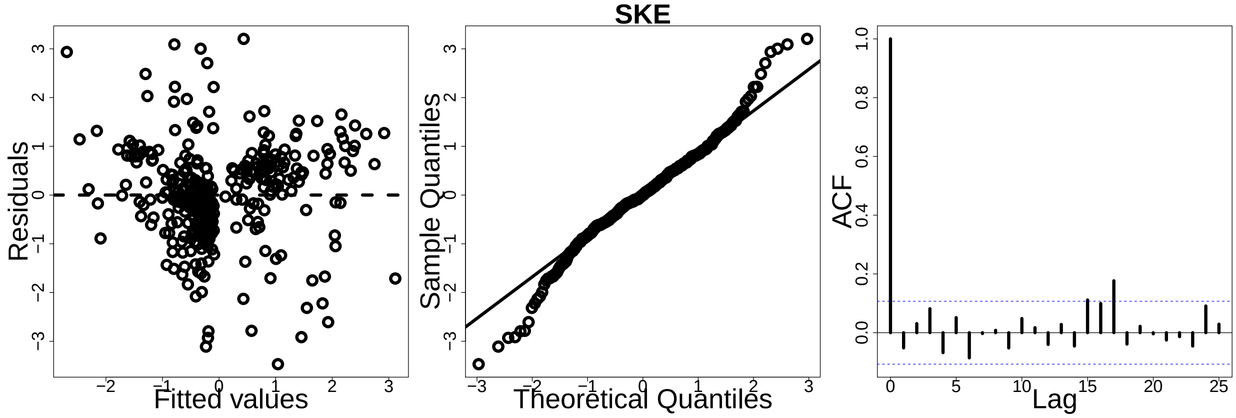
(a) AST



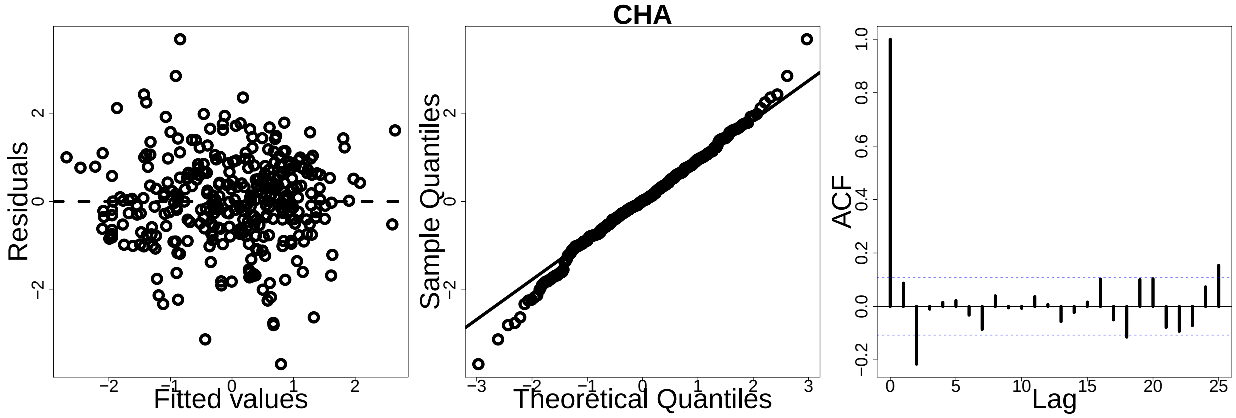
(b) NIT



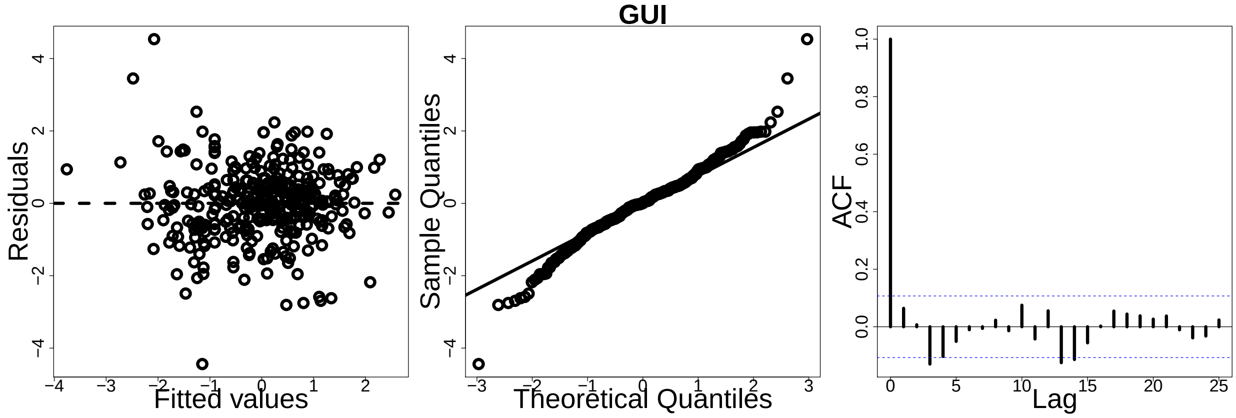
(c) PSE



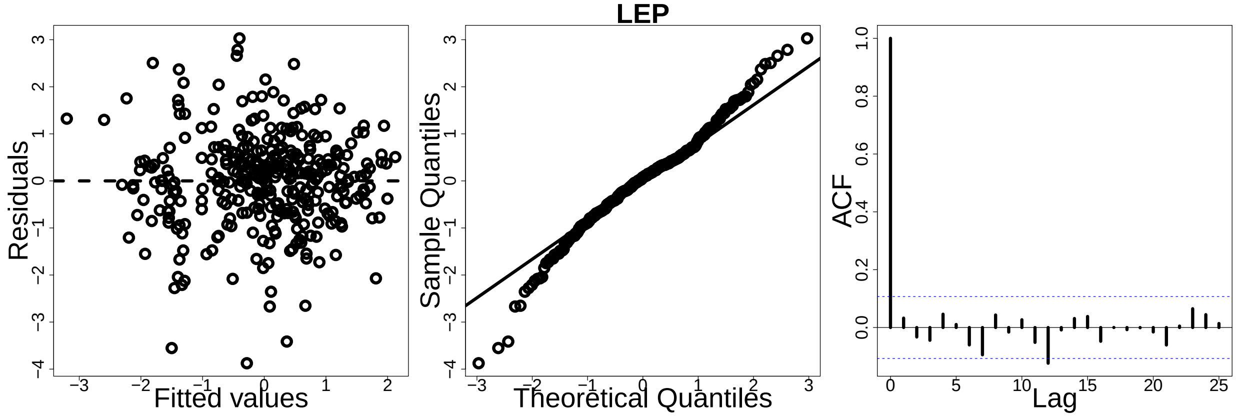
(d) SKE



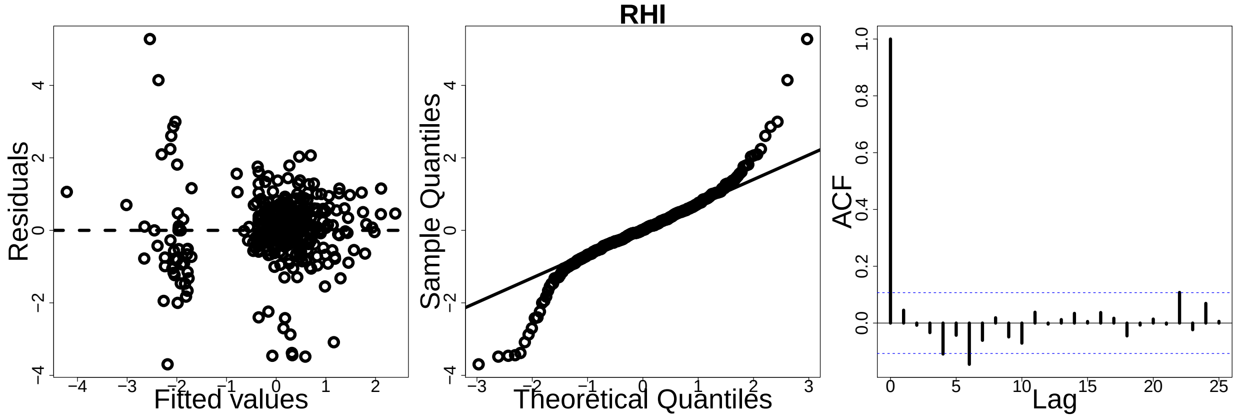
(e) CHA



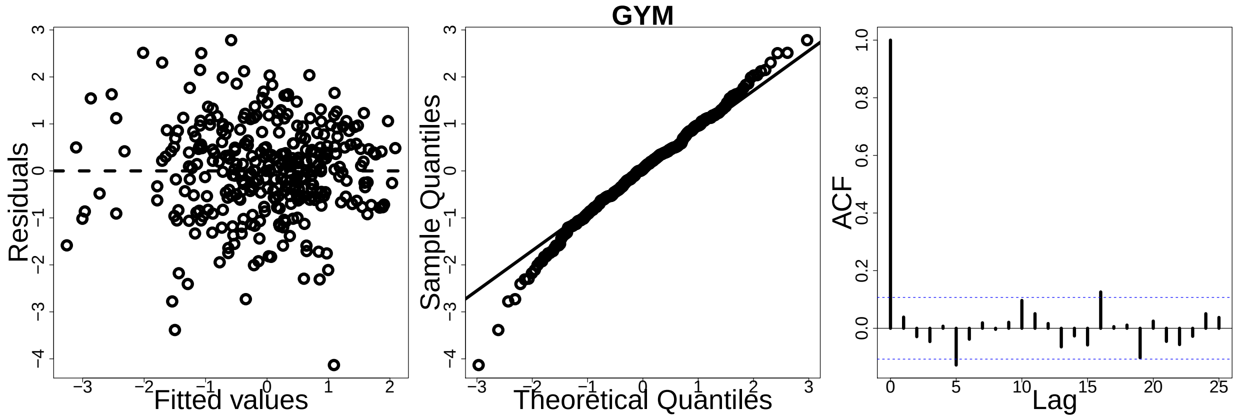
(f) GUI



(g) LEP



(h) RHI



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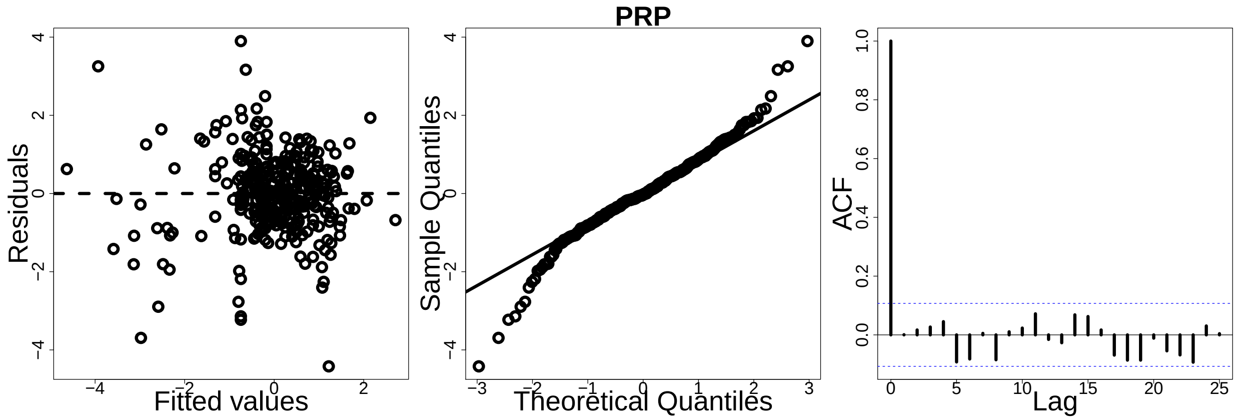
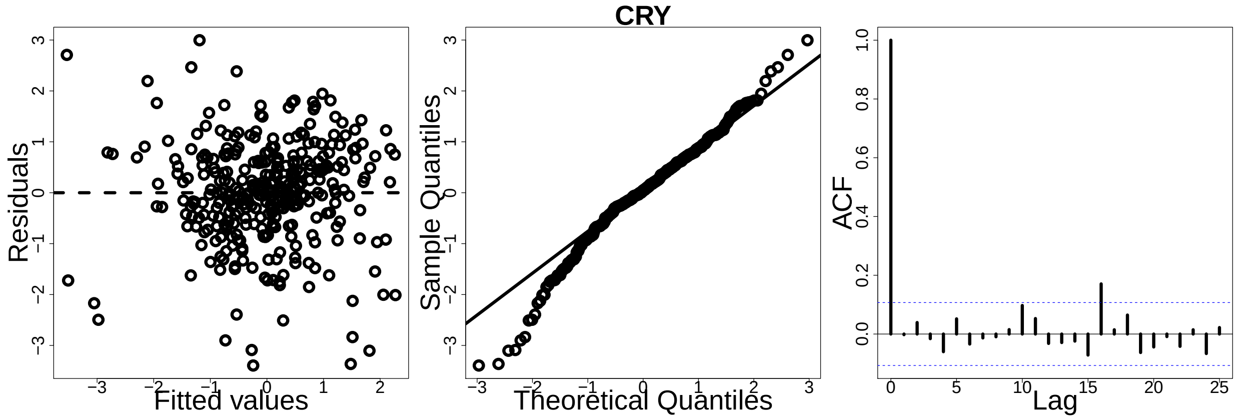
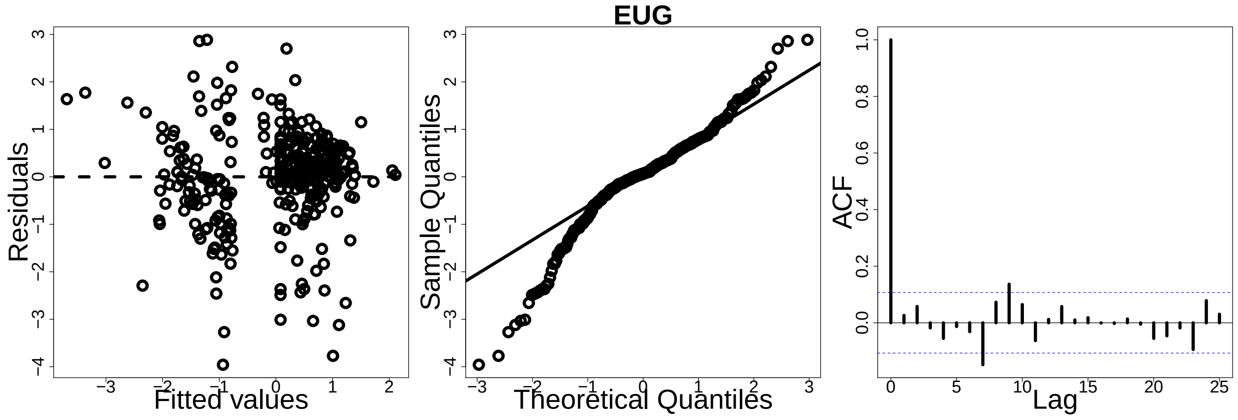


(j) PRP

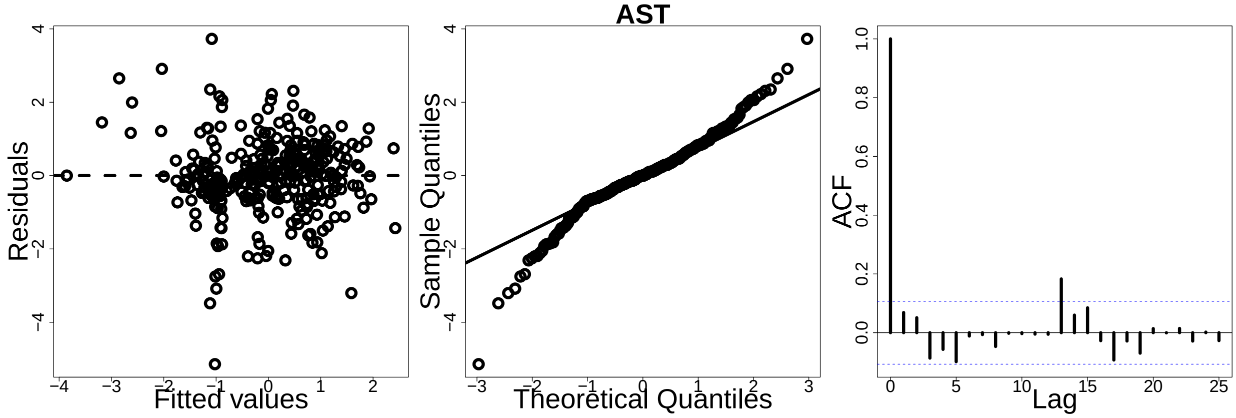


(k) CRY

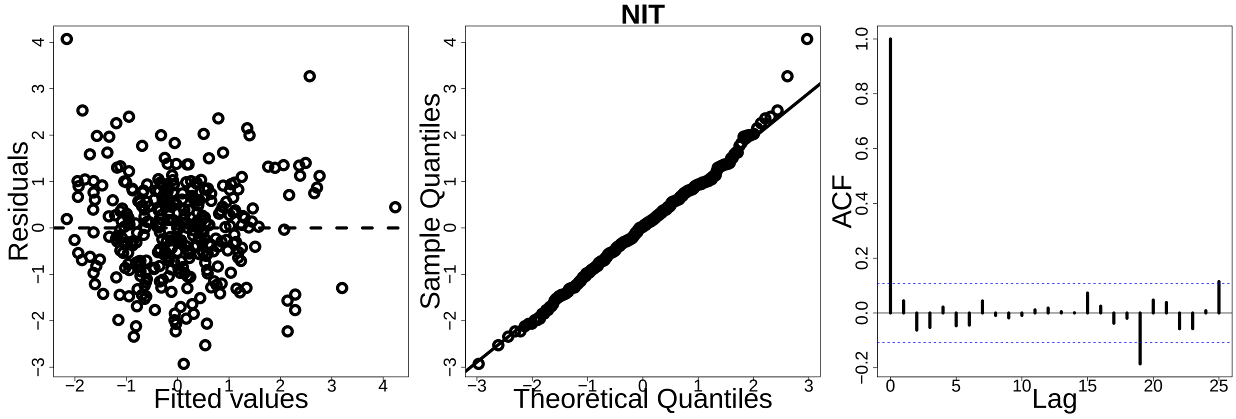


(l) EUG

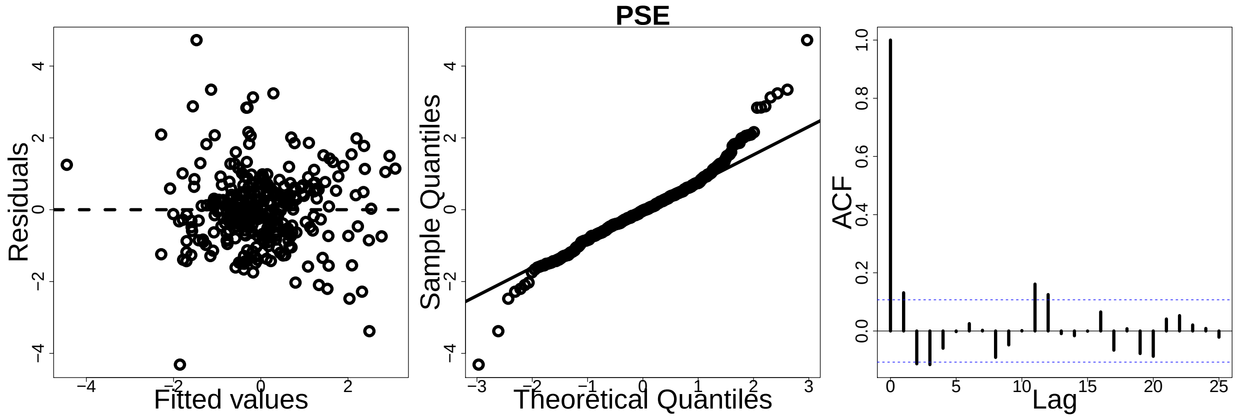
Figure A6.7: Residual examination for a MAR model using an unconstrained interaction matrix at Buoy 7 site. From left to right, residuals plotted against fitted values, Q-Q plots, and auto-correlation of residuals. The composition of planktonic groups is described in Table 1 in the main text.



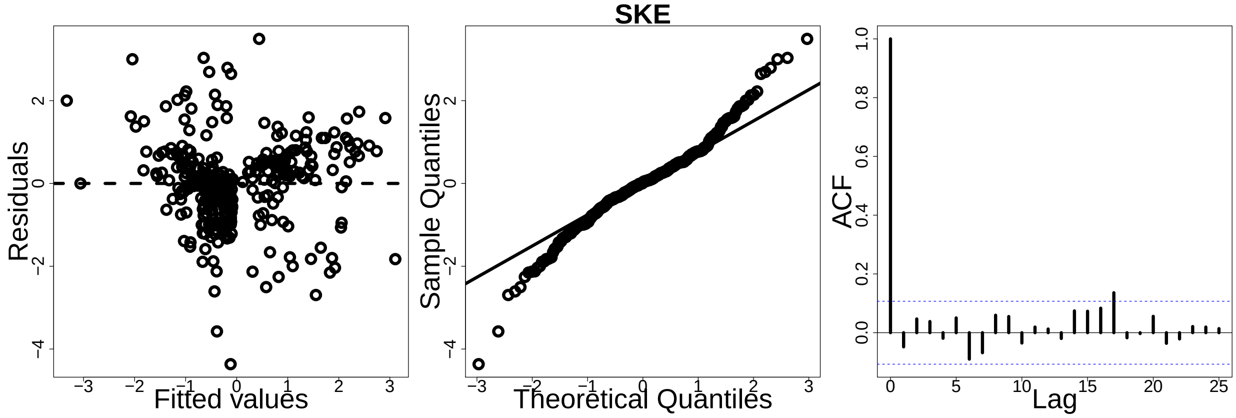
(a) AST



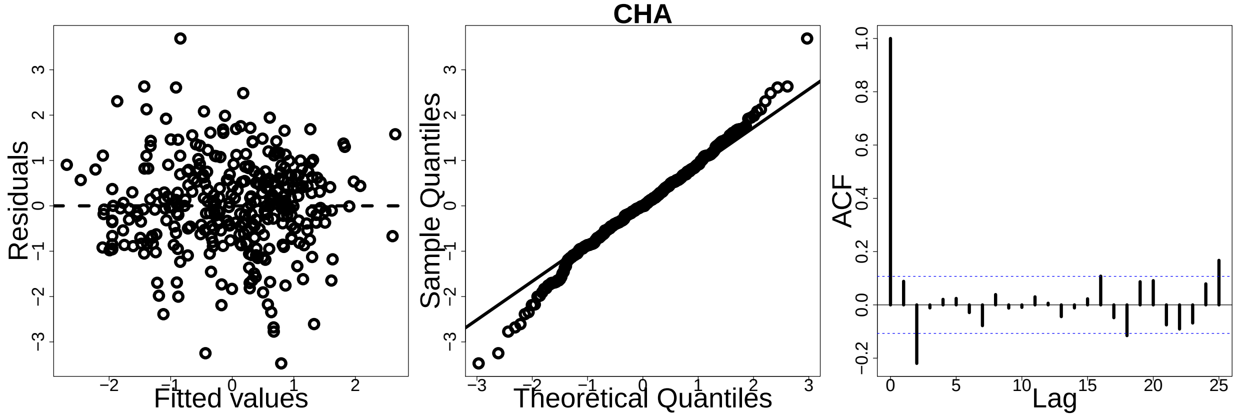
(b) NIT



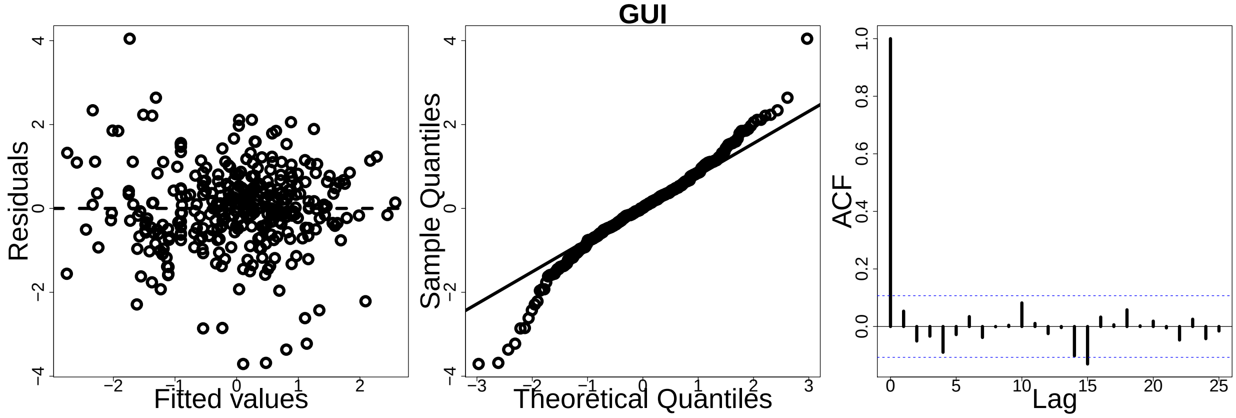
(c) PSE



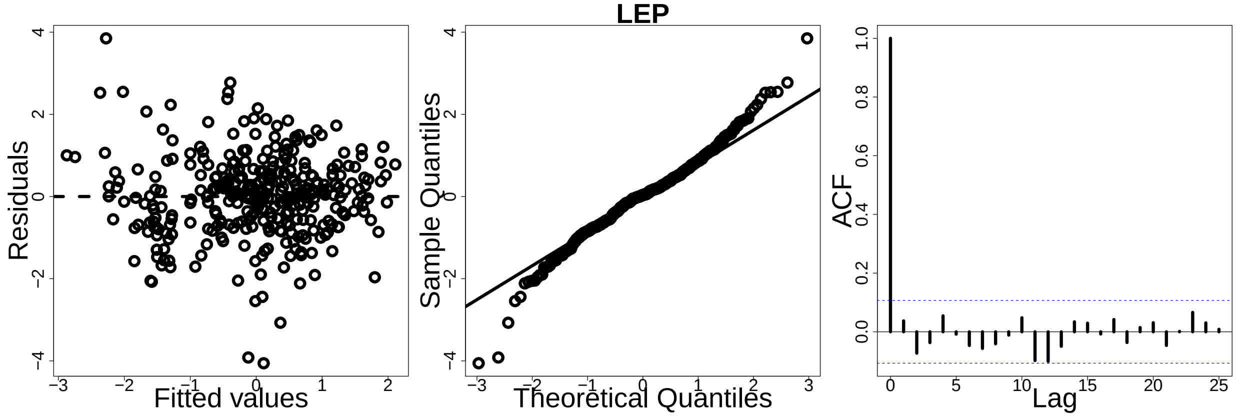
(d) SKE



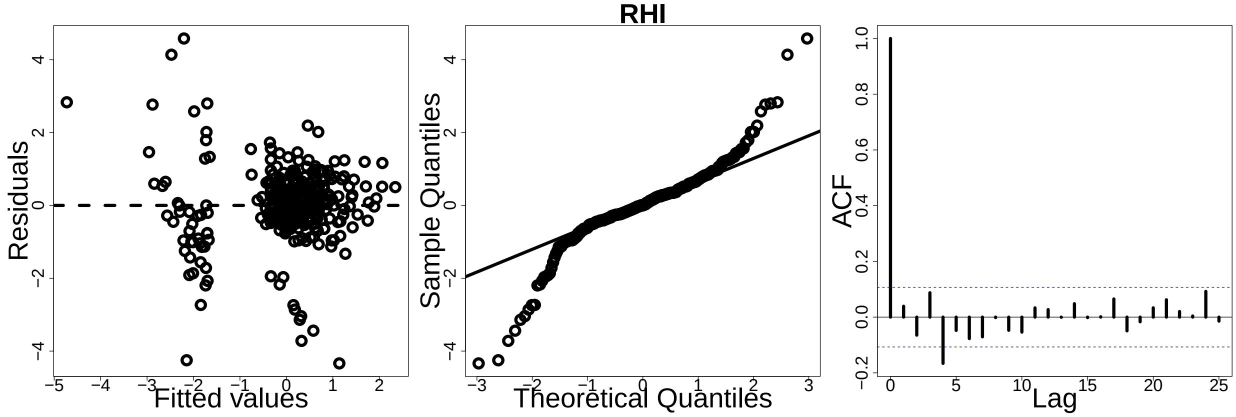
(e) CHA



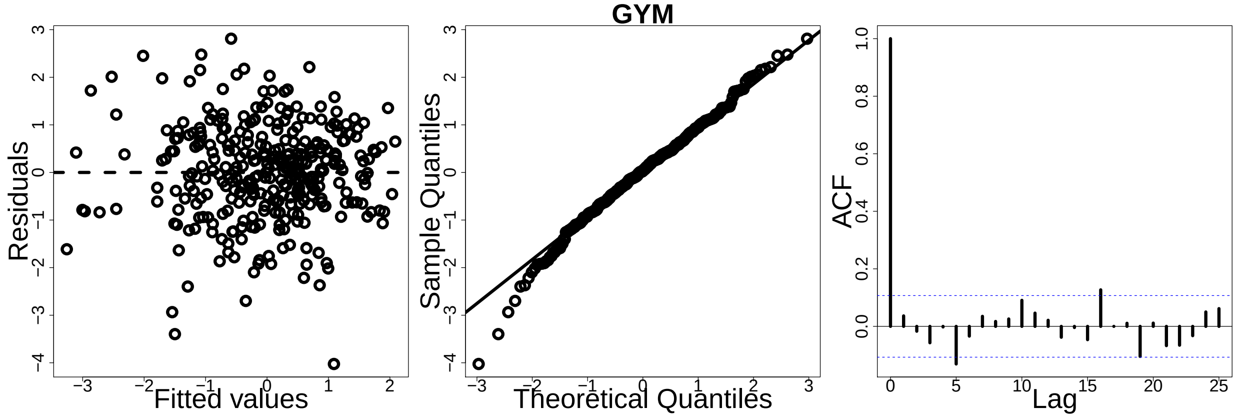
(f) GUI



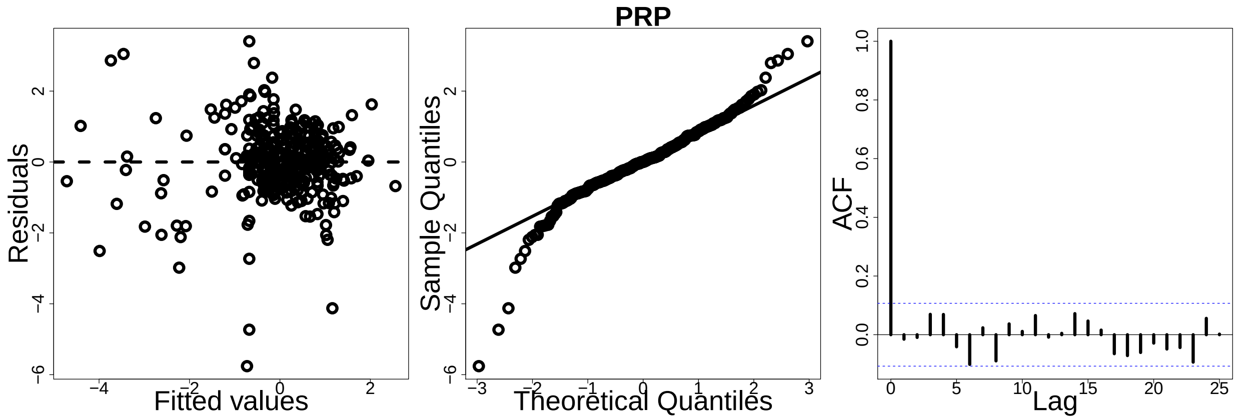
(g) LEP



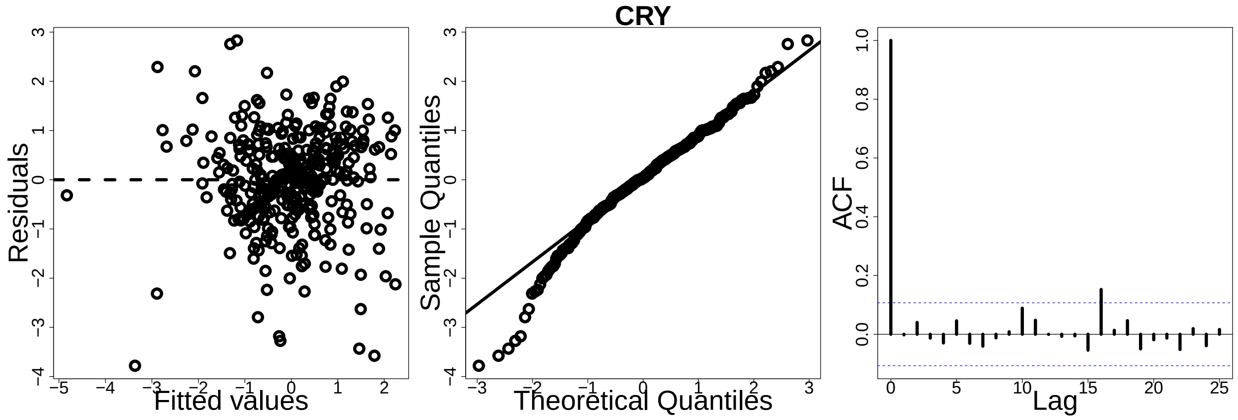
(h) RHI



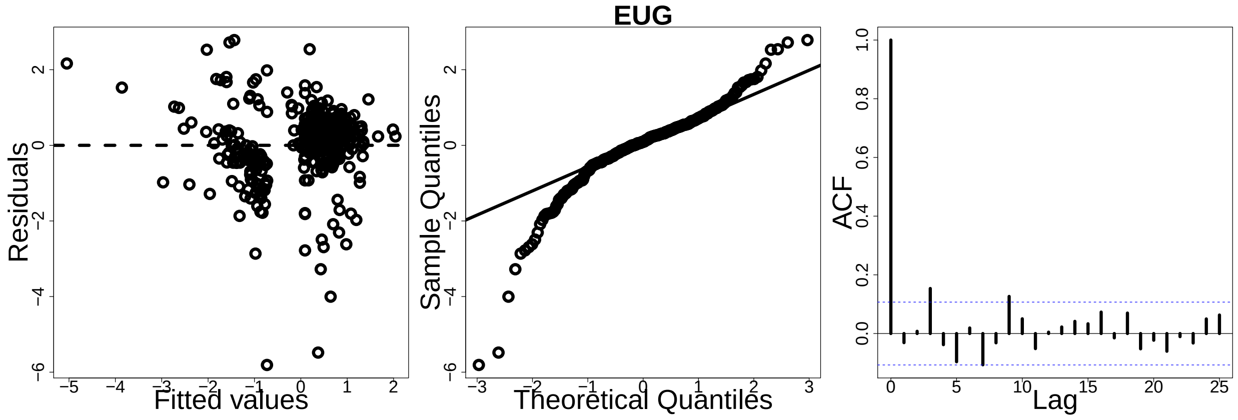
(i) GYM



(j) PRP



(k) CRY



(l) EUG

Figure A6.8: Residual examination for a MAR model using an interaction matrix only allowing intra-phylum interactions, differentiating pennate and centric diatoms, at Buoy 7 site. From left to right, residuals plotted against fitted values, Q-Q plots, and auto-correlation of residuals. The composition of planktonic groups is described in Table 1 in the main text.

A6.7 Goodness of fit, estimated values vs observations

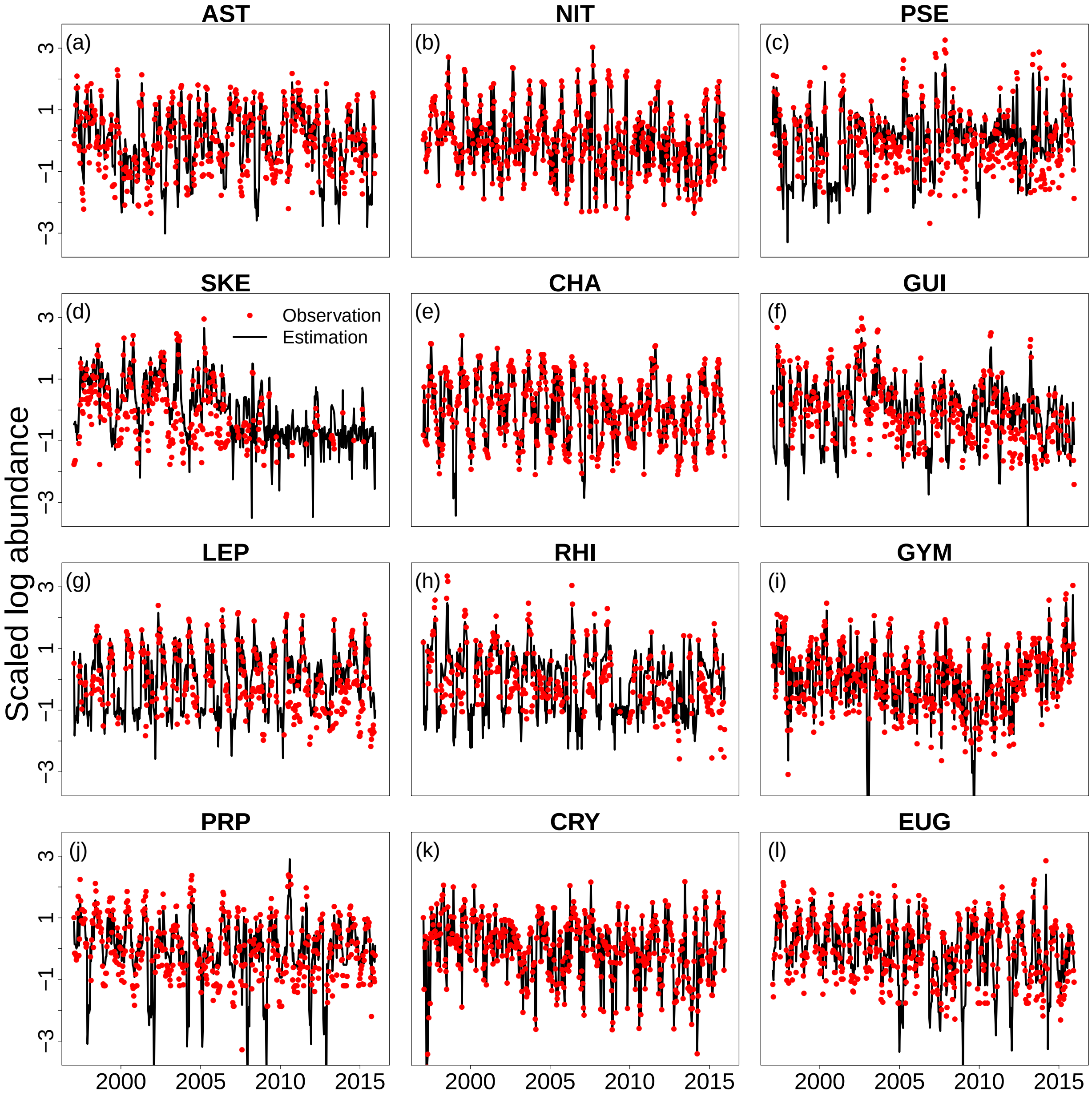


Figure A6.9: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) at Teychan, using an unconstrained interaction matrix. Composition of planktonic groups is described in Table 1 in the main text.

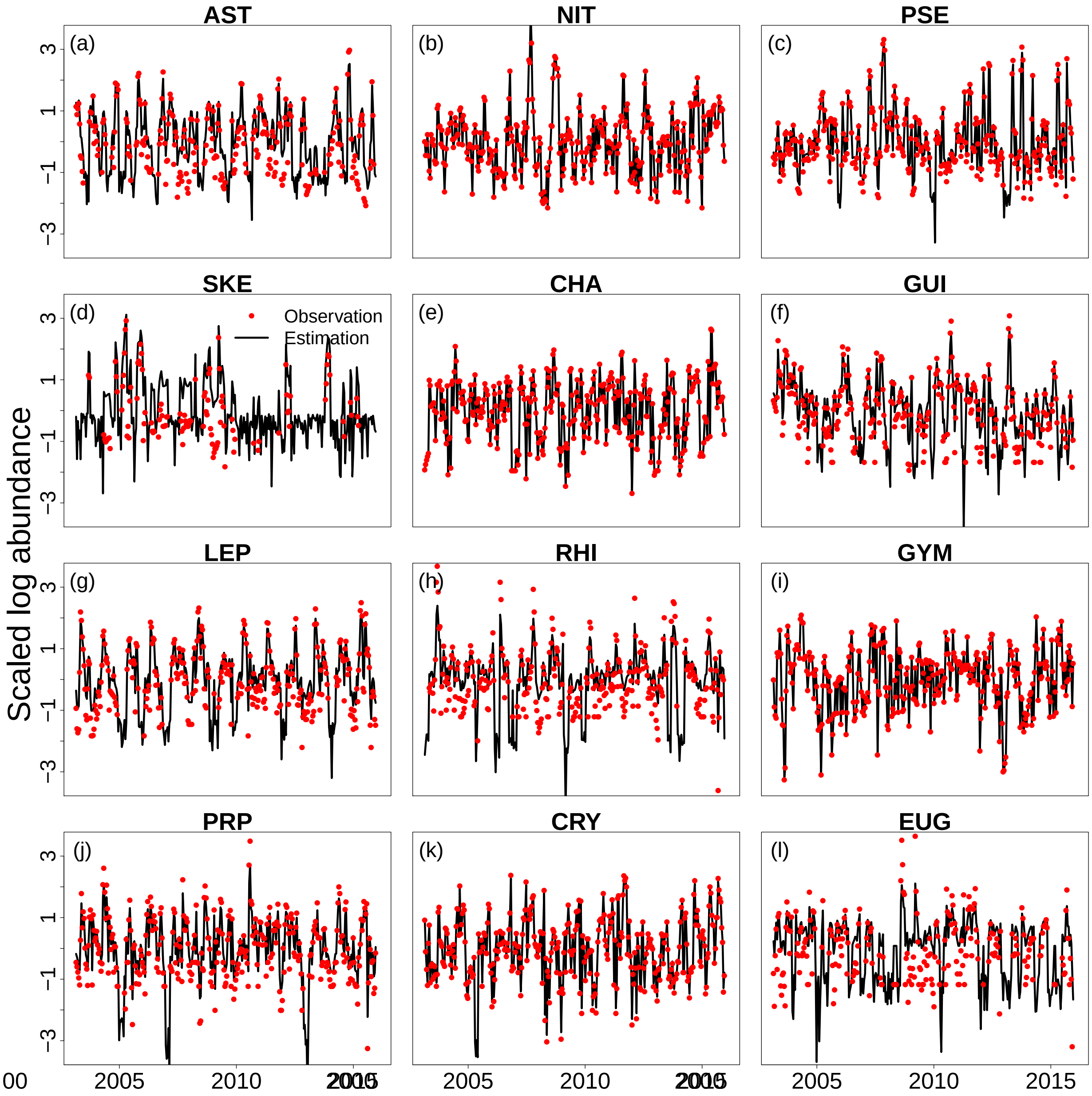


Figure A6.10: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) at Buoy 7, using an unconstrained interaction matrix. Composition of planktonic groups is described in Table 1 in the main text.

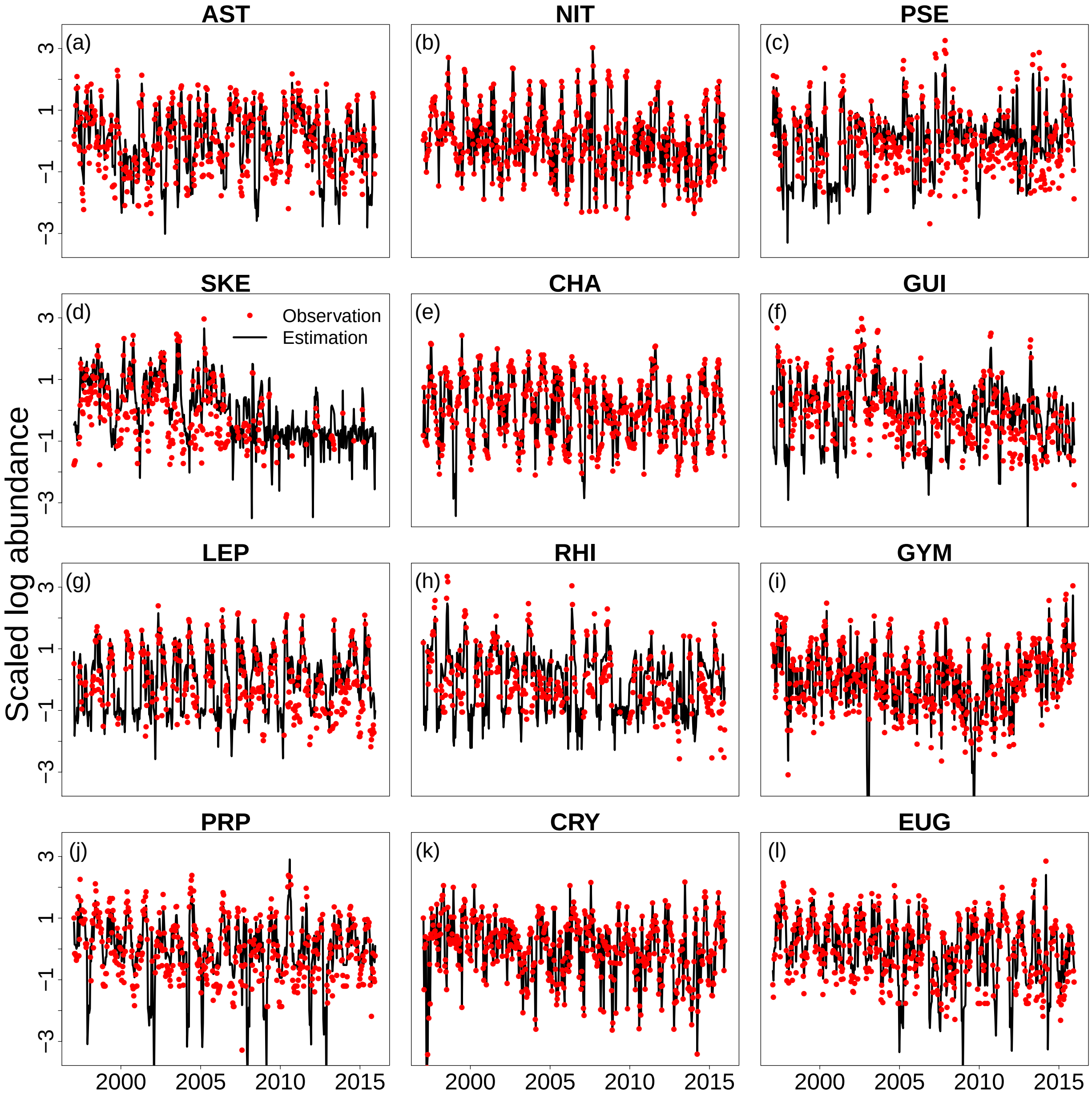


Figure A6.11: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) at Teychan, using an interaction matrix allowing only intra-phylum interactions. Composition of planktonic groups is described in Table 1 in the main text.

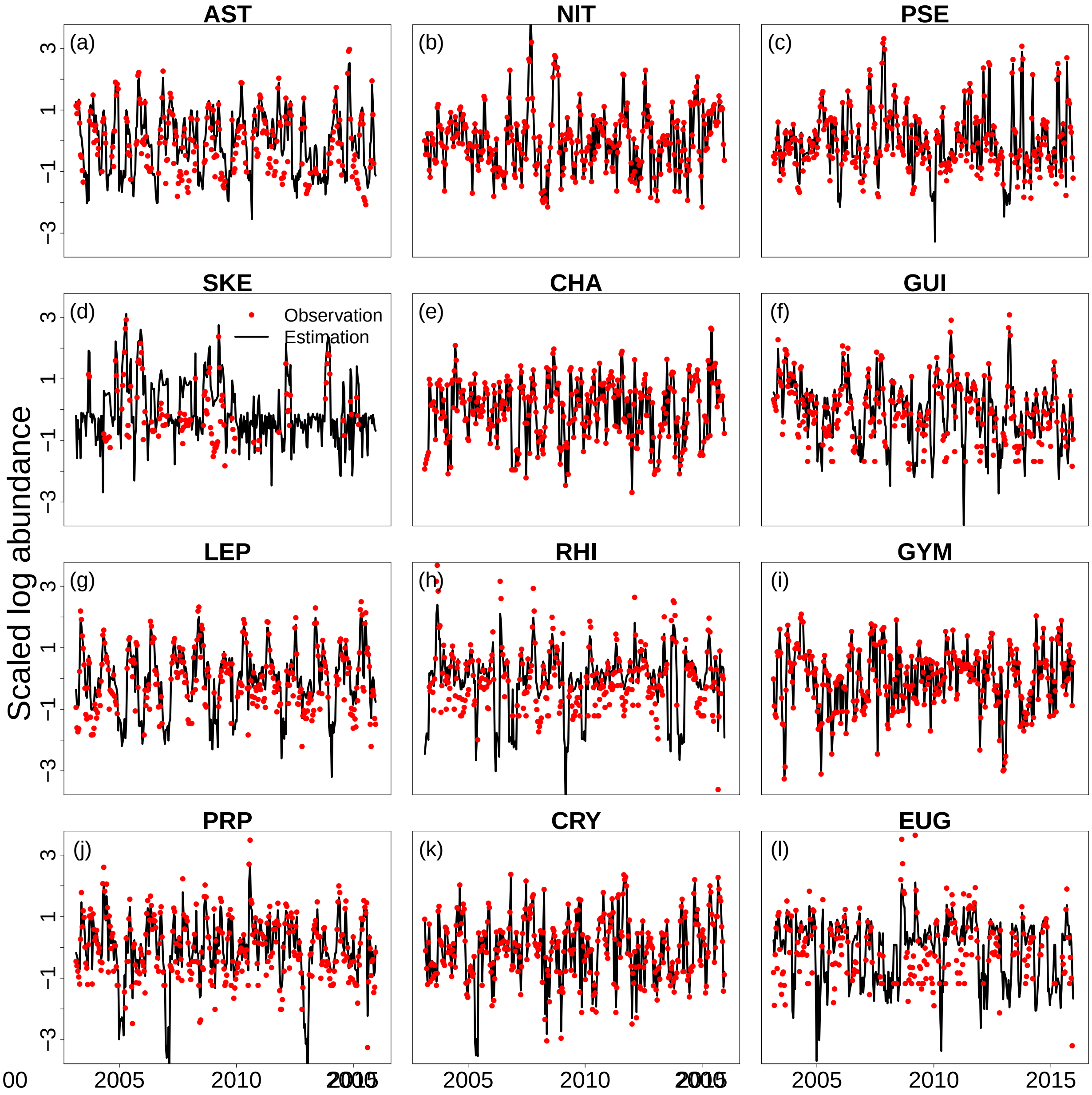


Figure A6.12: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) at Buoy 7, using an interaction matrix allowing only intra-phylum interactions. Composition of planktonic groups is described in Table 1 in the main text.

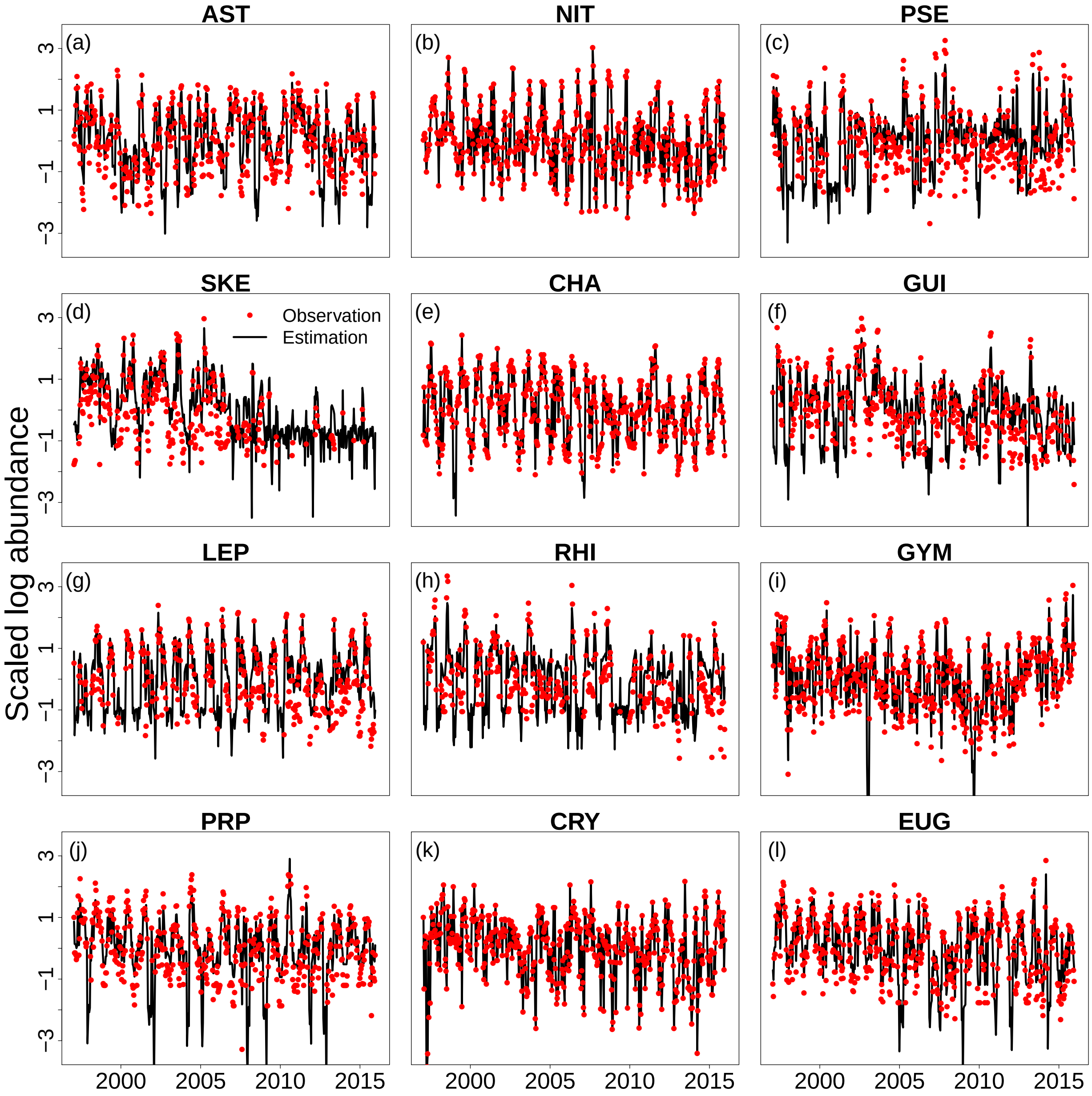


Figure A6.13: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) at Teychan, using an interaction matrix allowing only inter-phylum interactions. Composition of planktonic groups is described in Table 1 in the main text.

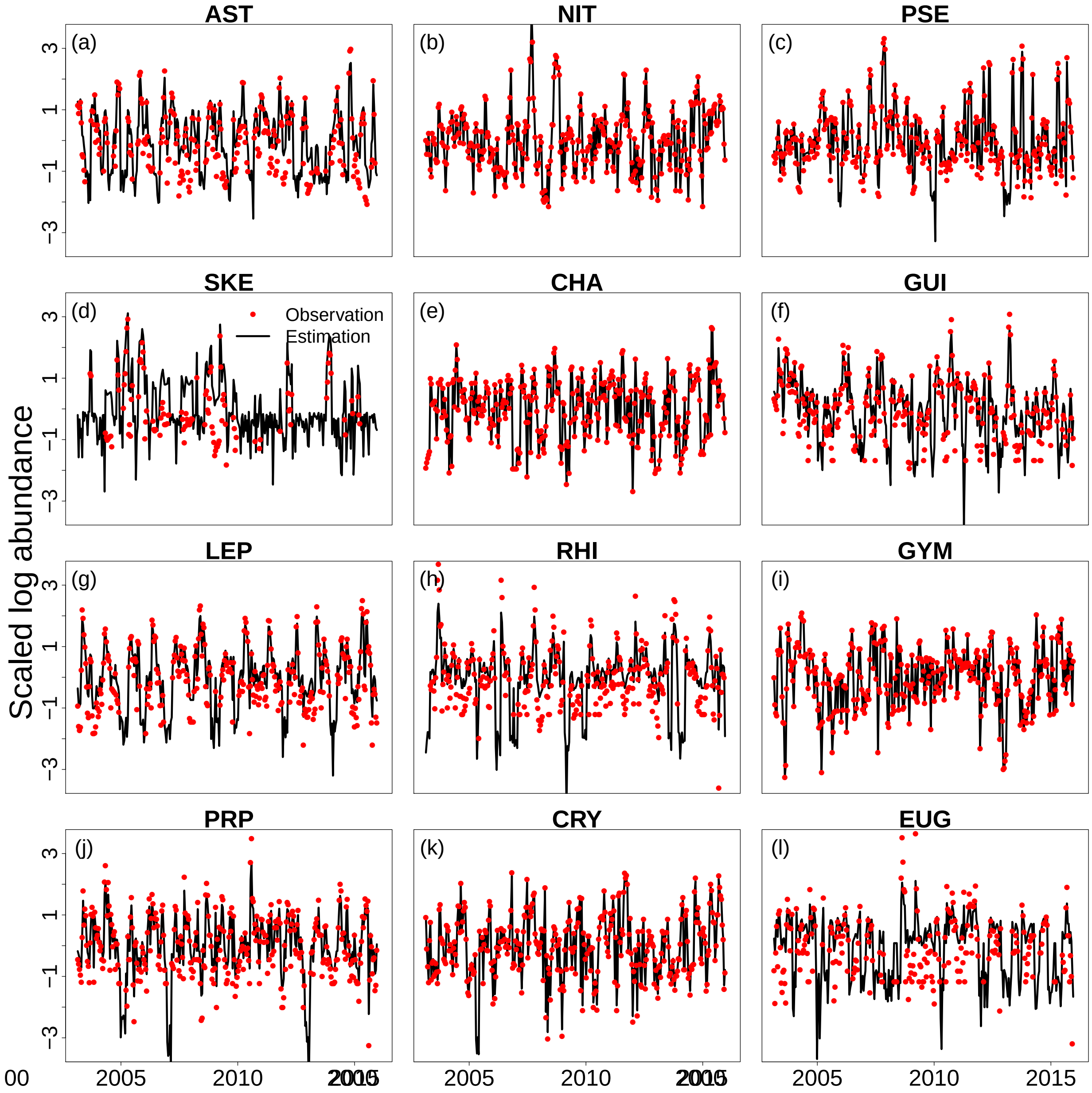
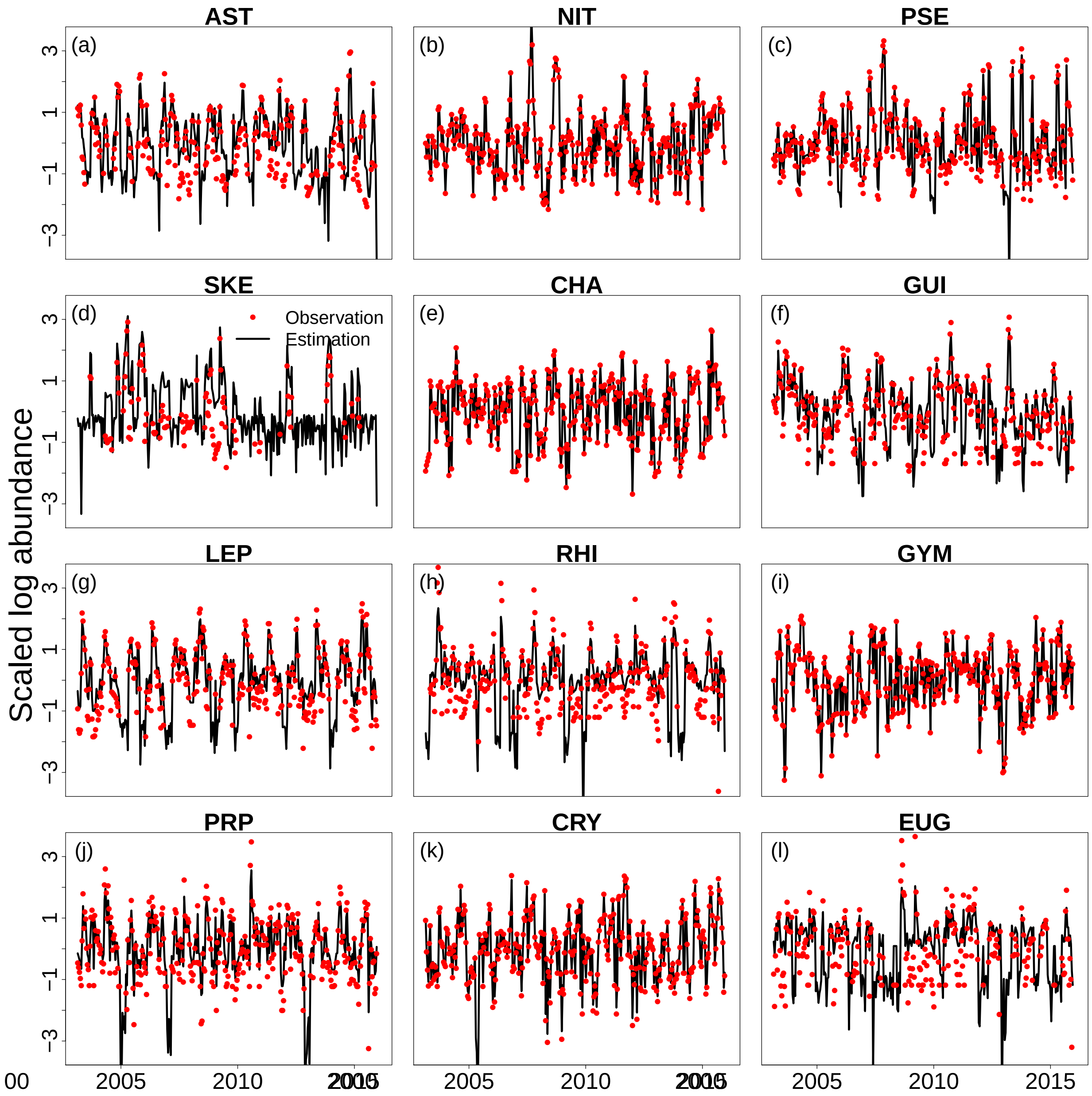


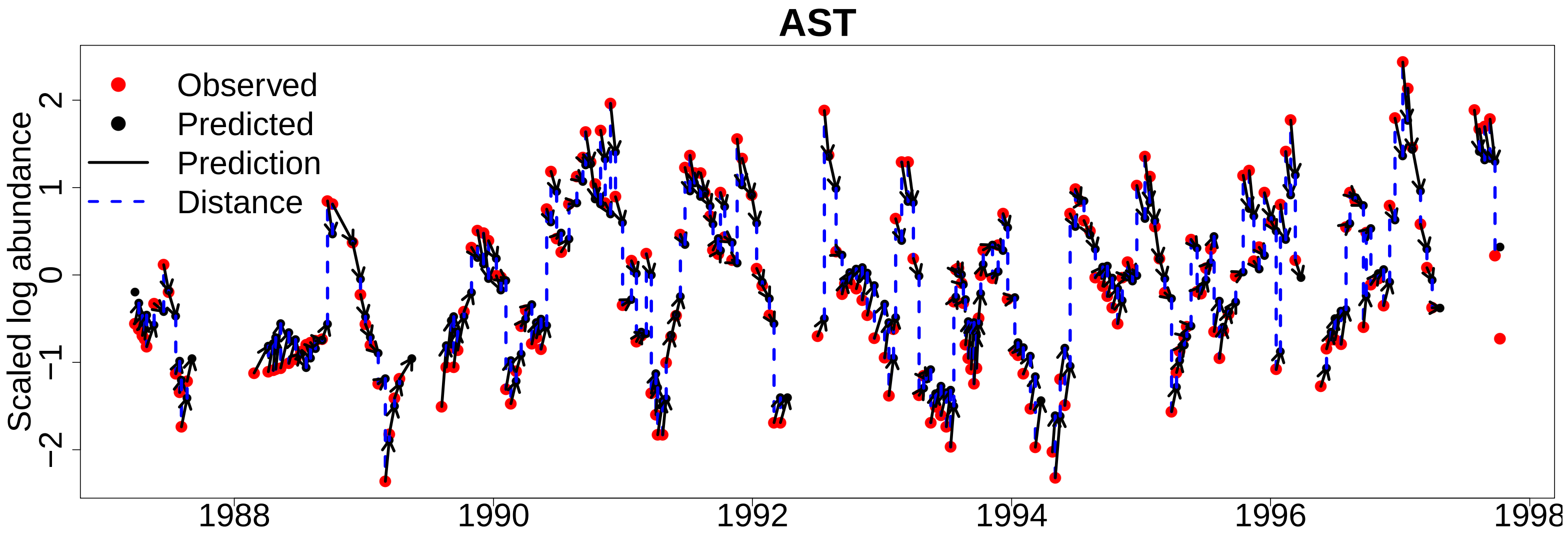
Figure A6.14: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) at Buoy 7, using an interaction matrix allowing only inter-phylum interactions. Composition of planktonic groups is described in Table 1 in the main text.



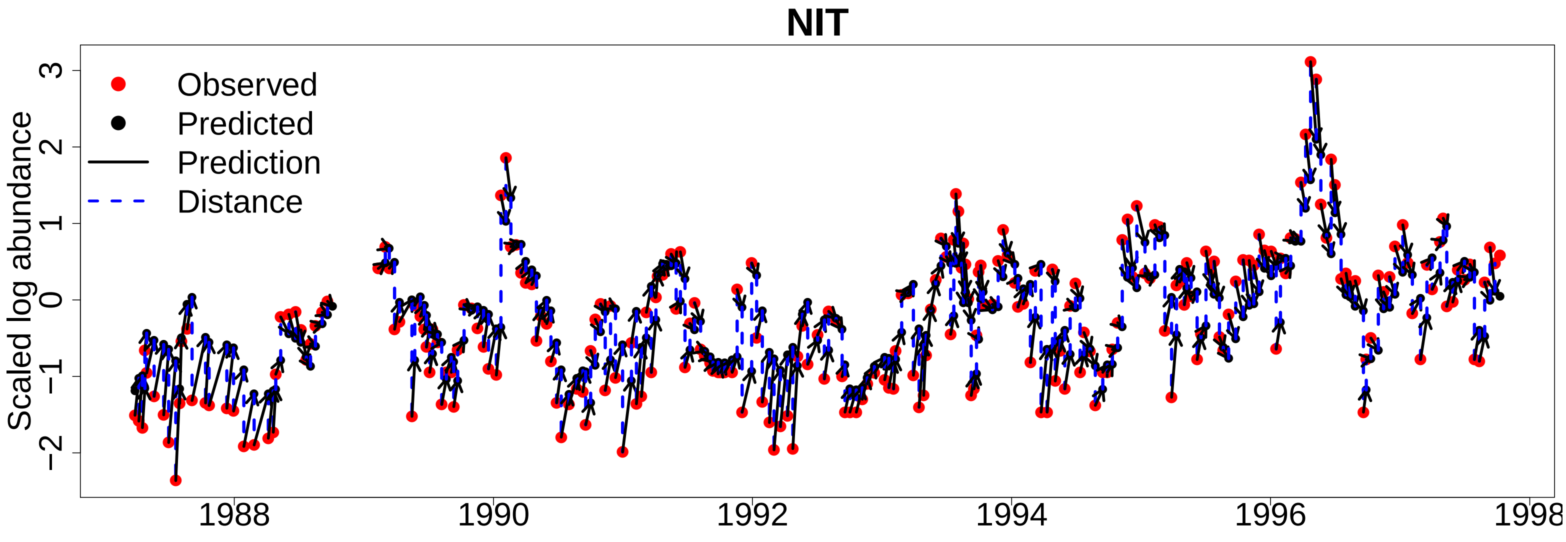
(b)

Figure A6.15: Smoothed states obtained with the Kalman filter used in MARSS package (black line) compared to observations (red dots) for Buoy 7 site, using an interaction matrix allowing only intra-phylum interactions, differentiating between pennate and centric diatoms. Composition of planktonic groups is described in Table 1 in the main text.

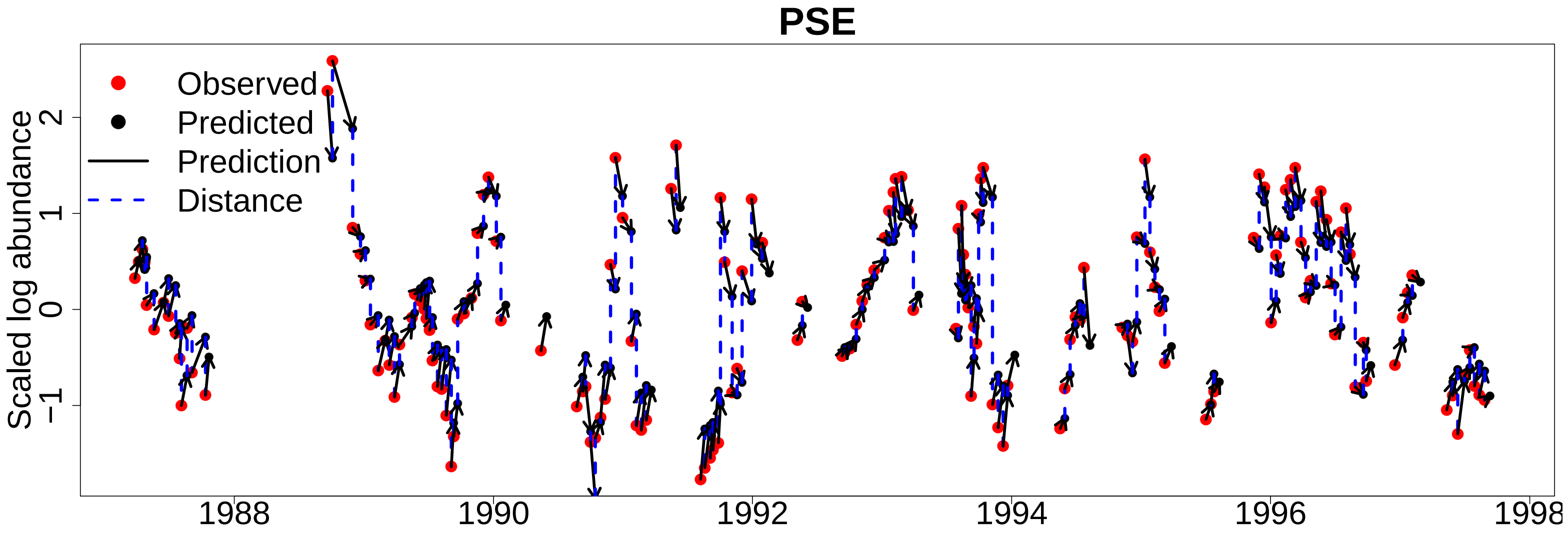
A6.8 Quality of prediction, estimated values vs observations



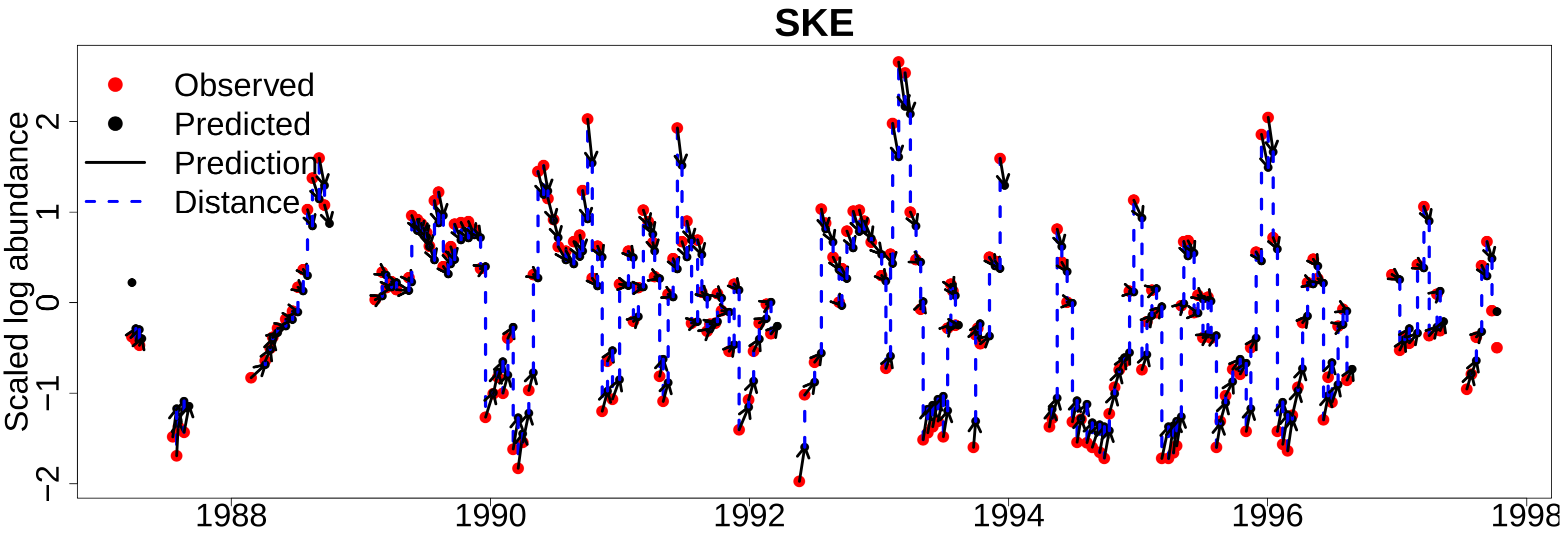
(a) AST



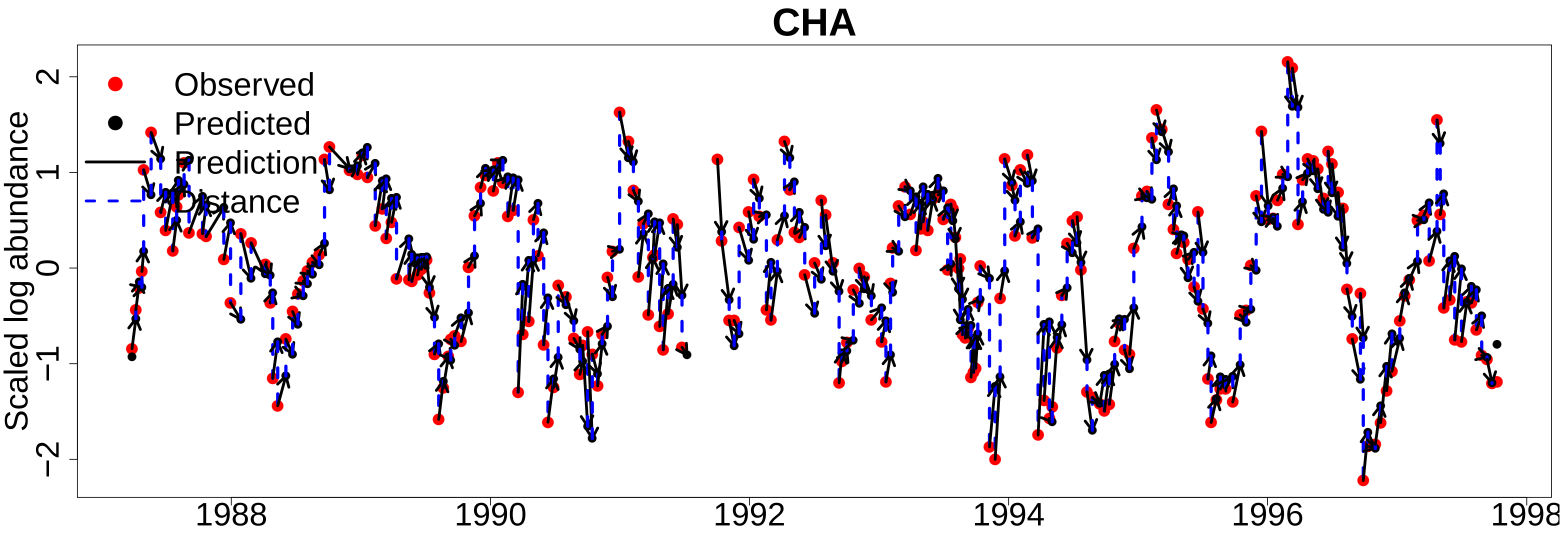
(b) NIT



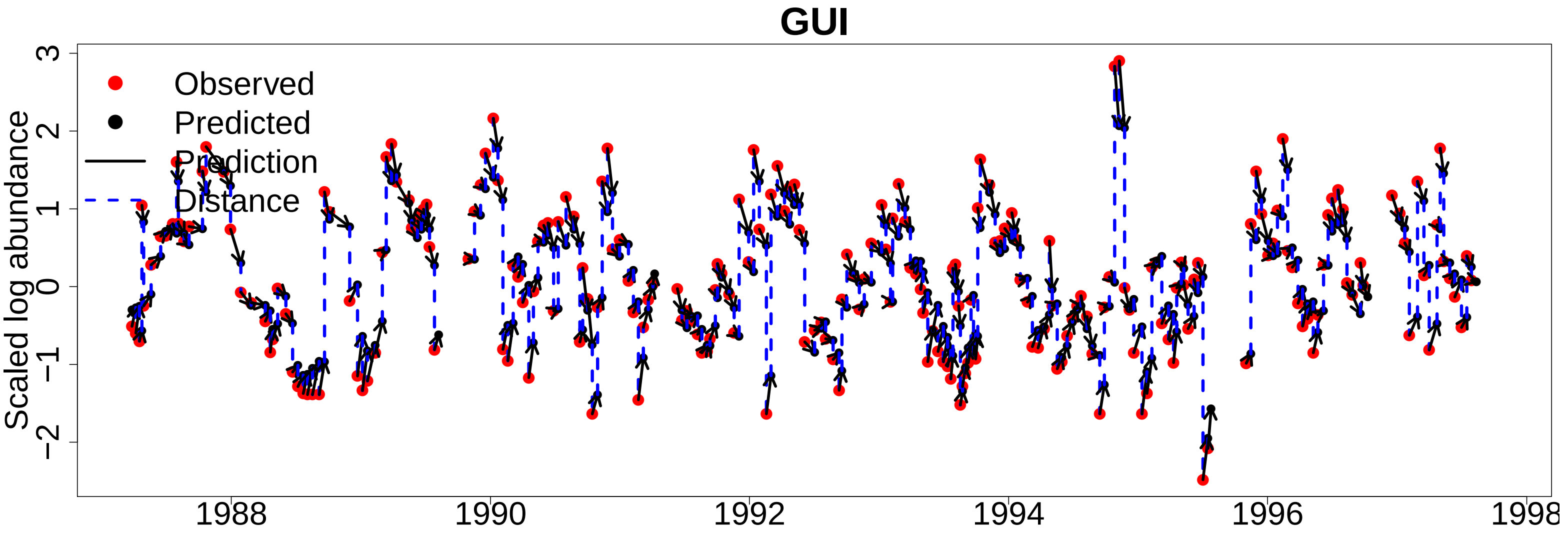
(c) PSE



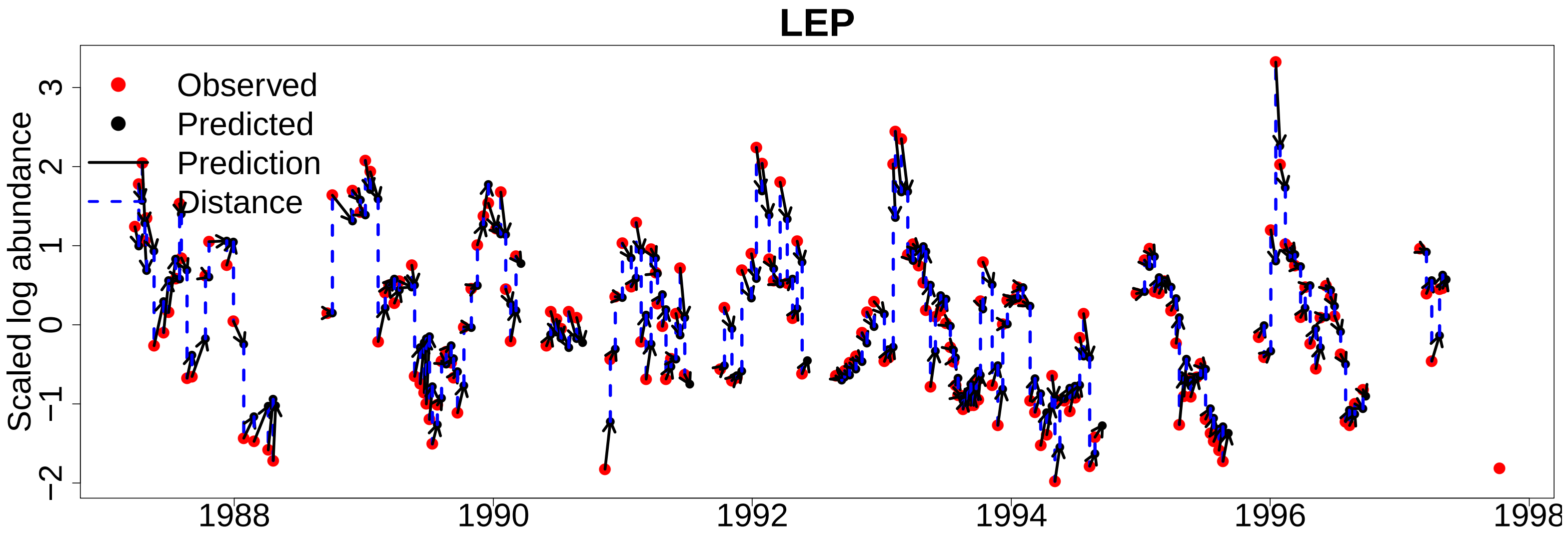
(d) SKE



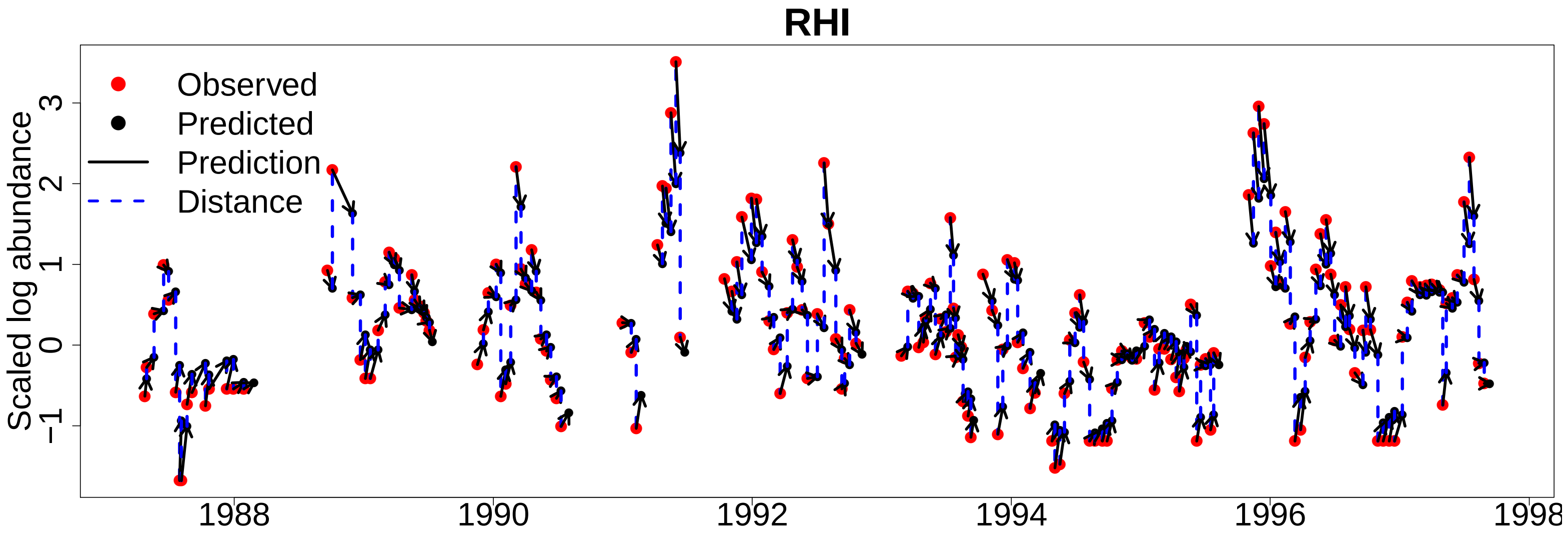
(e) CHA



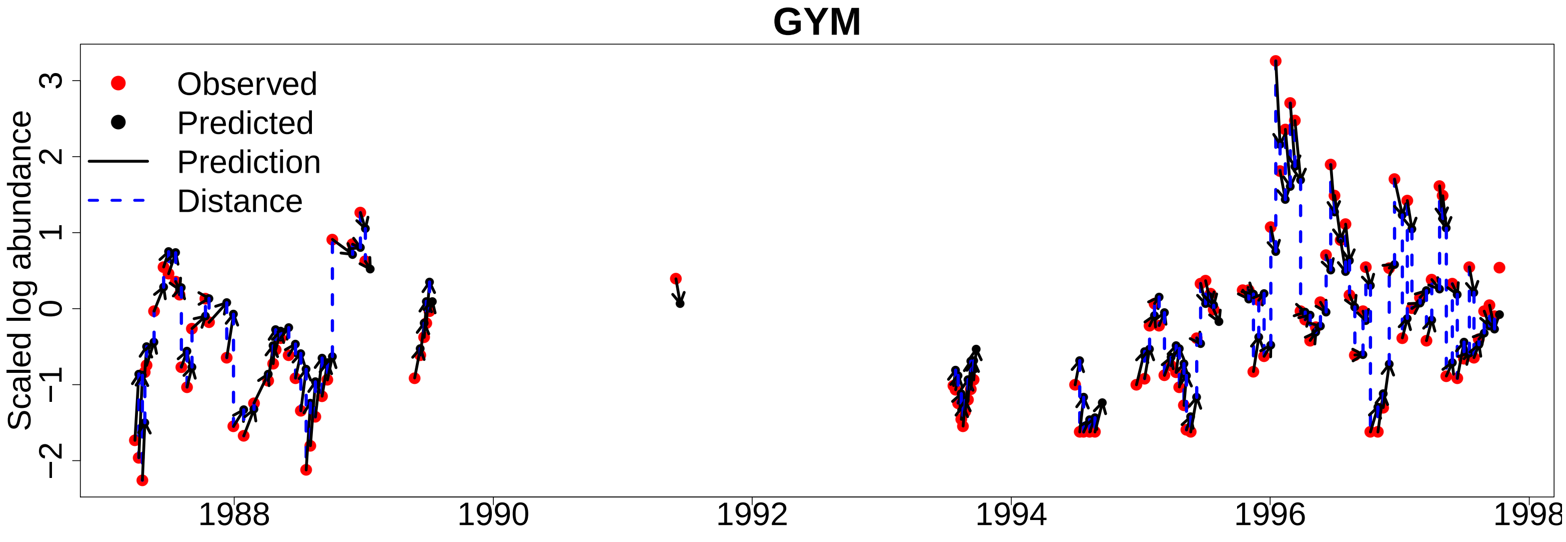
(f) GUI



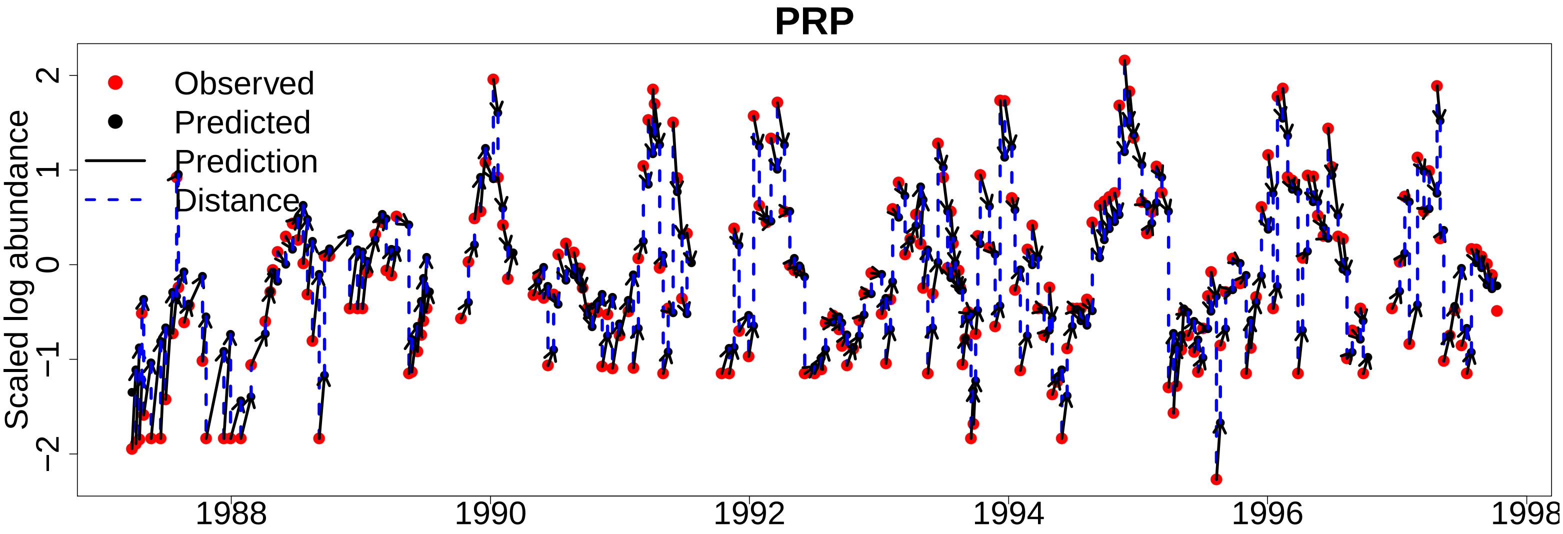
(g) LEP



(h) RHI

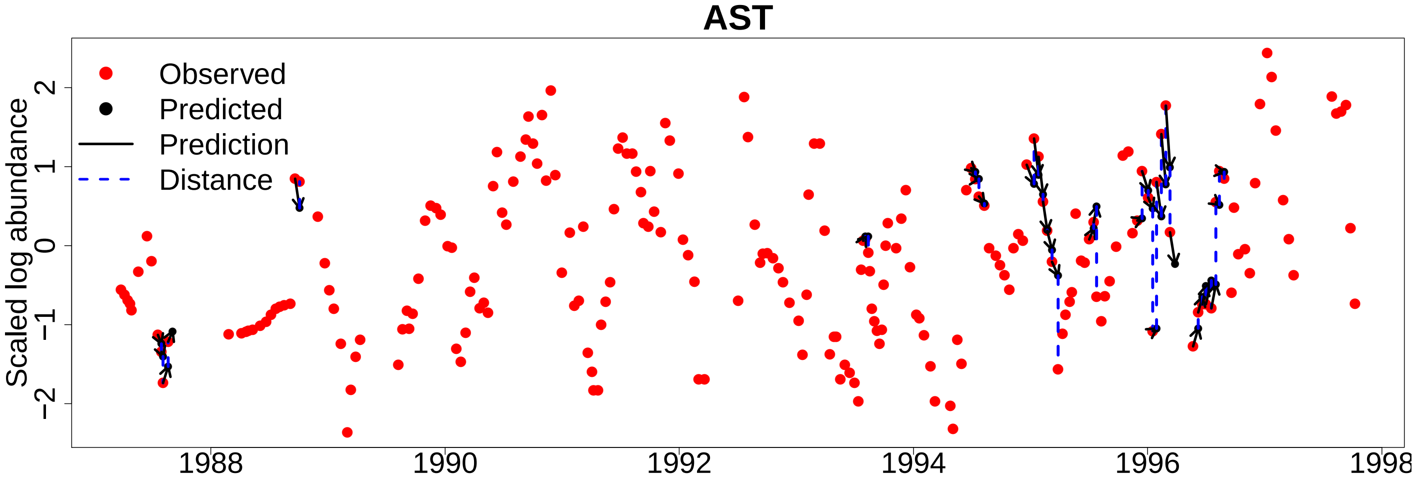


(i) GYM

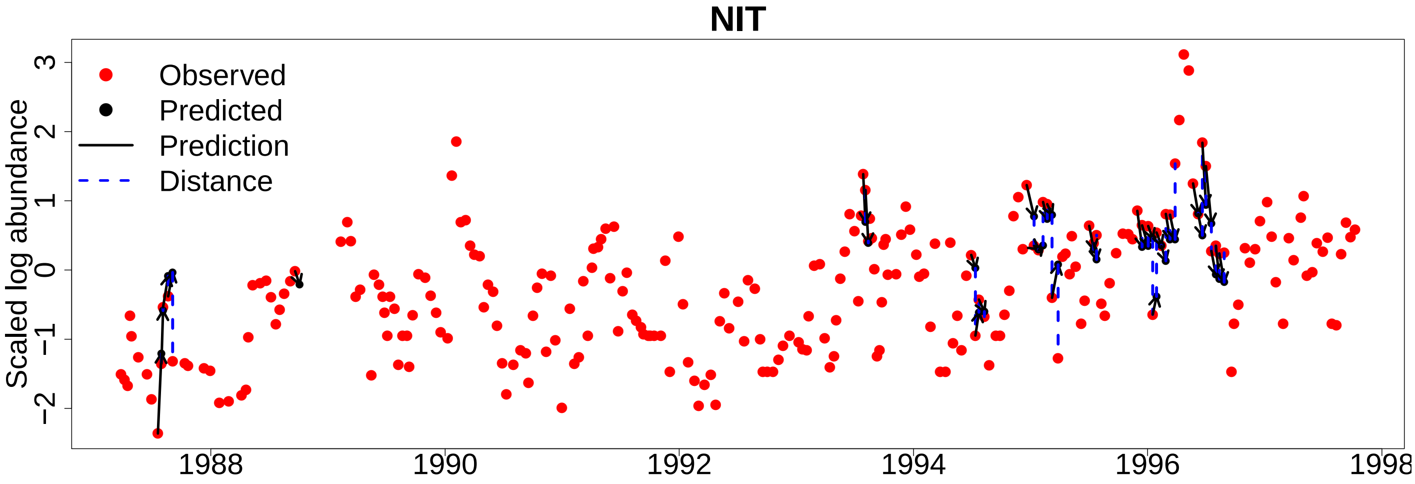


(j) PRP

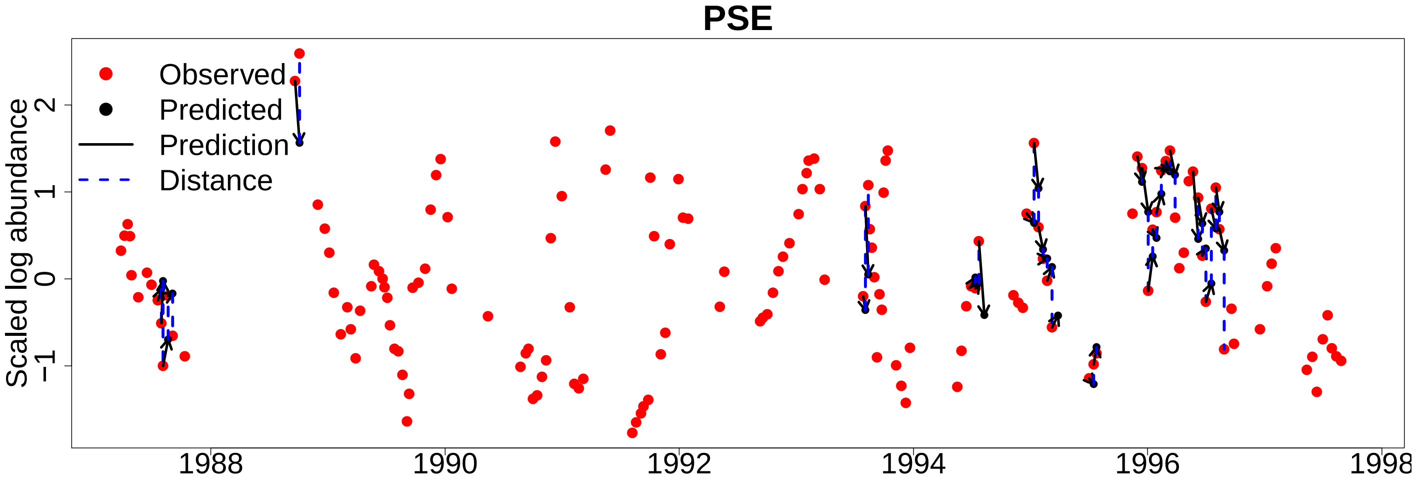
Figure A6.16: Comparison of predicted dynamics and observations for the first years of the time series (1987-1996) at Teychan site, using an interaction matrix only allowing intra-group interactions. Predicted values (black dots) are calculated with estimated parameters using the observed value (red dots) at the previous sampling date. The distance between observed and predicted value for the same sampling date is shown by blue arrows. EUG and CRY were not counted in the first years and their abundance was therefore set to 0 in the predictions. Large gaps can be introduced when there are missing values for certain groups, as one missing value can reverberate across the entire network.



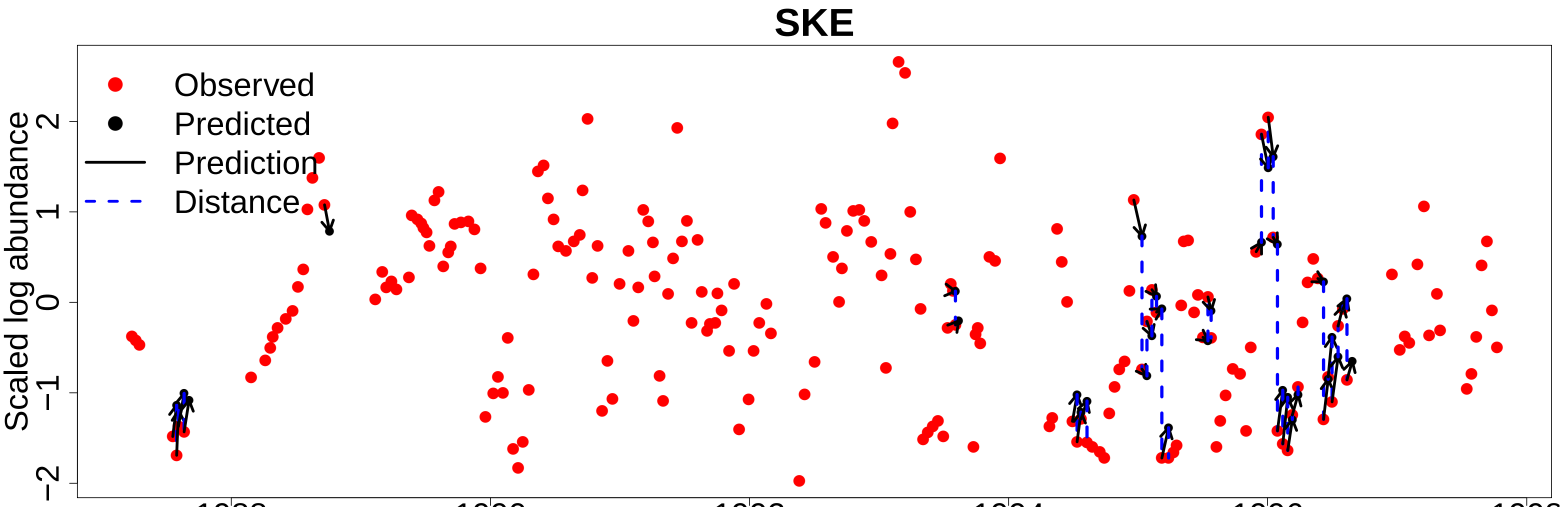
(a) AST



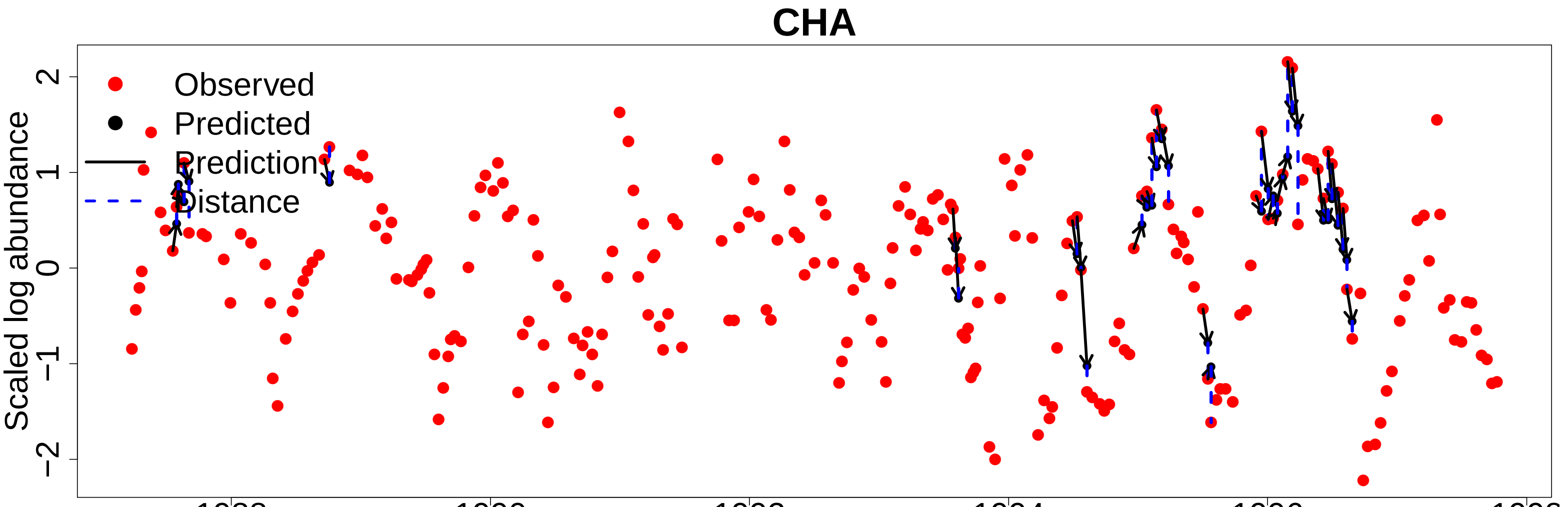
(b) NIT



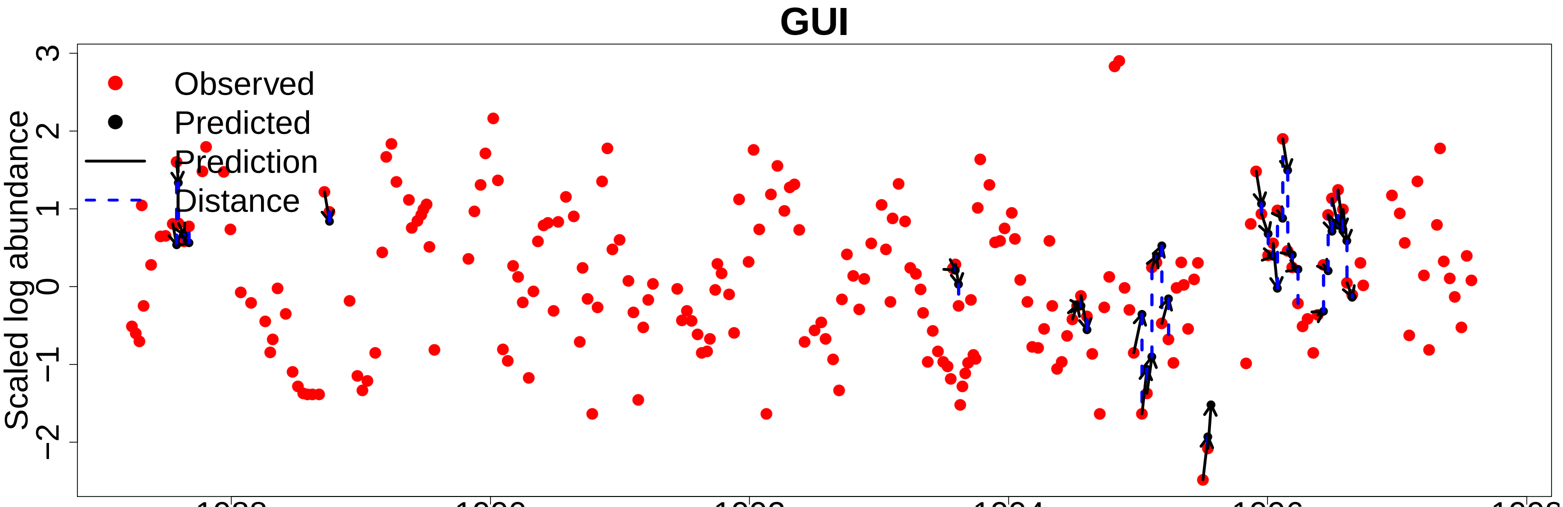
(c) PSE



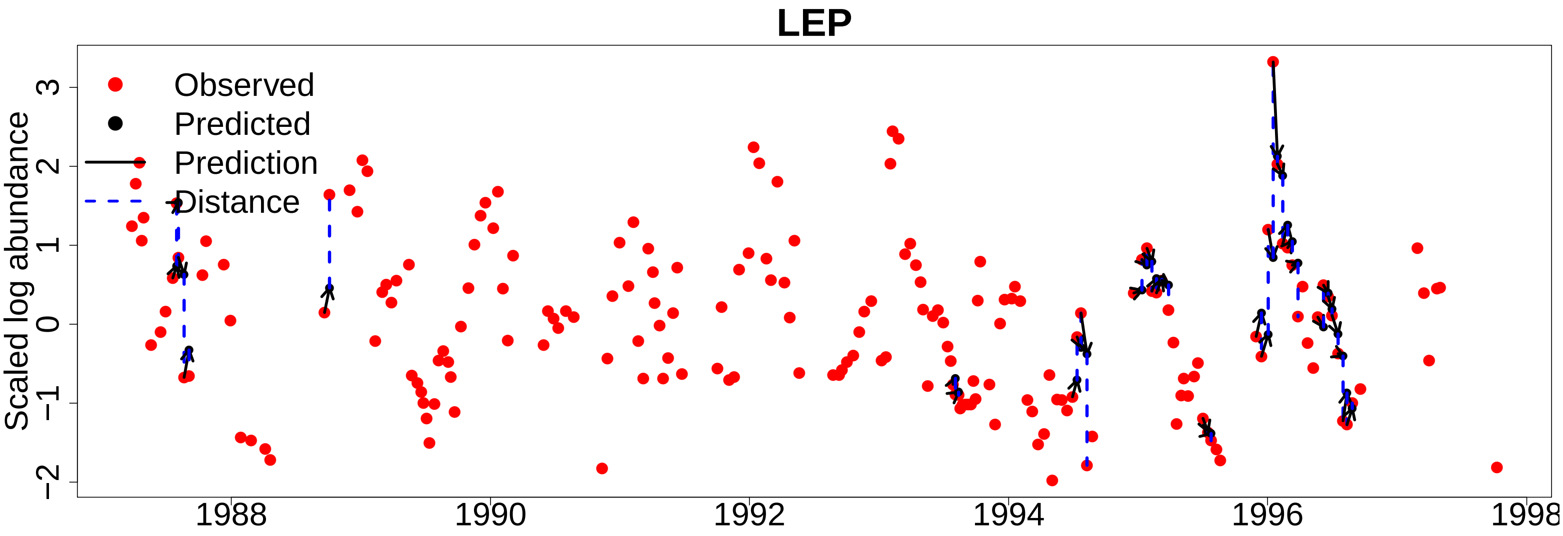
(d) SKE



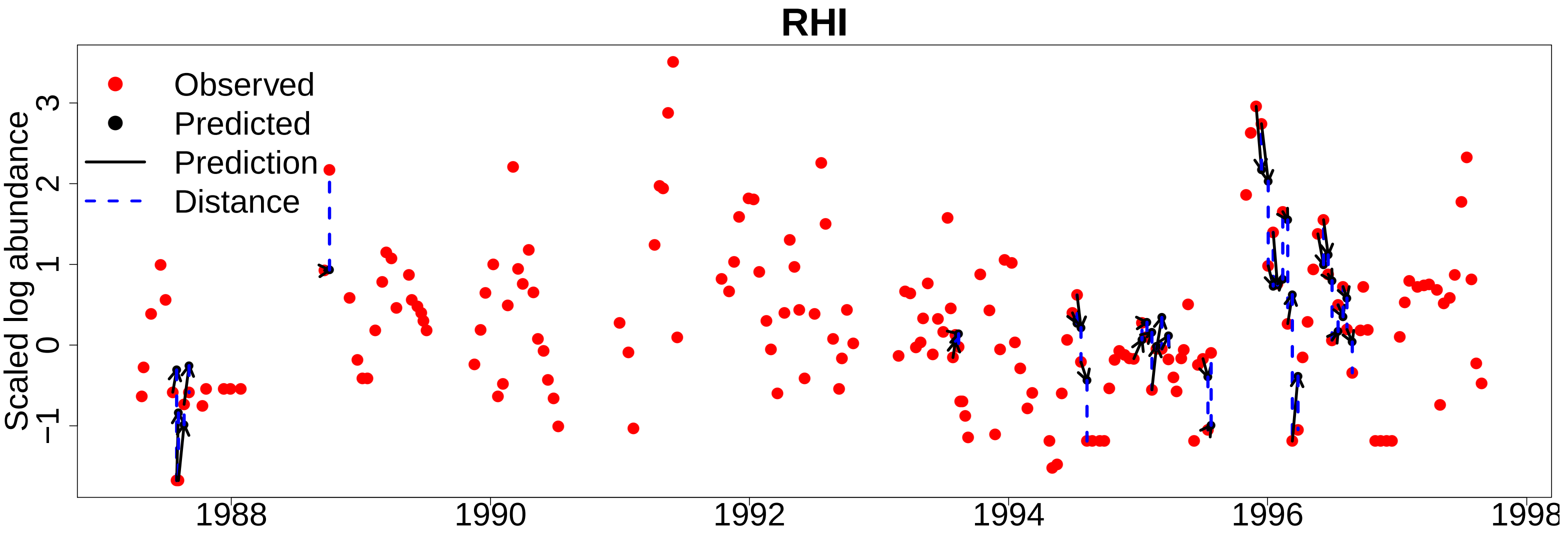
(e) CHA



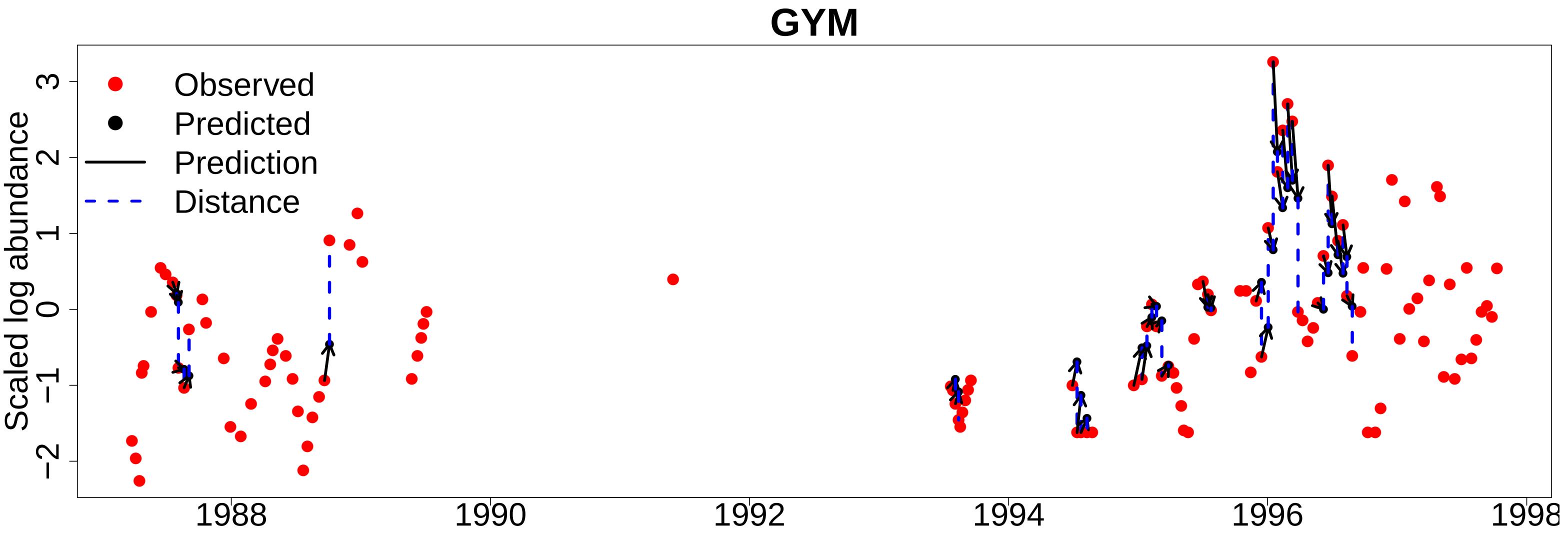
(f) GUI



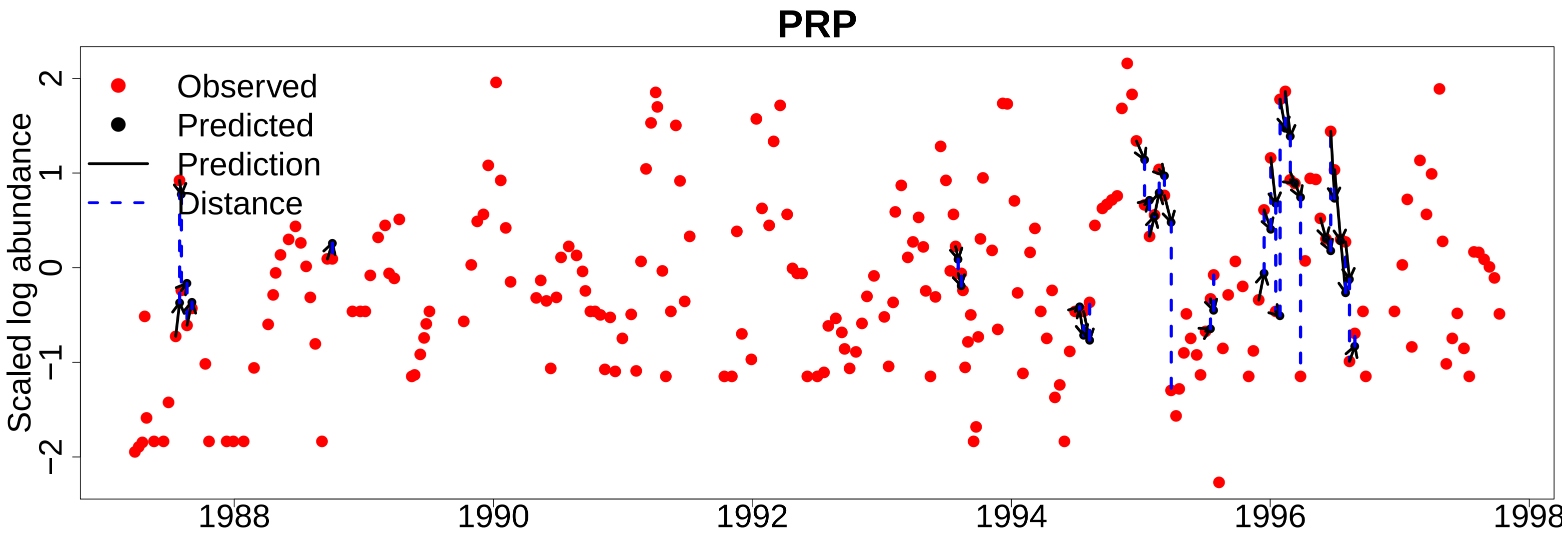
(g) LEP



(h) RHI



(i) GYM



(j) PRP

Figure A6.17: Comparison of predicted dynamics and observations for the first years of the time series (1987-1996) at Teychan site, using an unconstrained interaction matrix. Predicted values (black dots) are calculated with estimated parameters using the observed value (red dots) at the previous sampling date. The distance between observed and predicted value for the same sampling date is shown by blue arrows. EUG and CRY were not counted in the first years and their abundance was therefore set to 0 in the predictions. Large gaps can be introduced when there are missing values for certain groups, as they all impact each other and one missing value can reverberate across the entire network.