Qu, Y., Wu, N., Guse, B., Fohrer, N. (2022): Distinct indicators of land use and hydrology characterize different aspects of riverine phytoplankton communities. - Science of the Total Environment, 851, Part 2, 158209.

https://doi.org/10.1016/j.scitotenv.2022.158209

Distinct indicators of land use and hydrology characterize different aspects of riverine phytoplankton communities

Yueming Qu[1,2,*], Naicheng Wu[1,3,*], Björn Guse[1,4], Nicola Fohrer[1]

[1] Department of Hydrology and Water Resources Management, Institute for Natural Resource Conservation, Kiel University, Kiel, Germany

[2] UK Centre for Ecology and Hydrology, Wallingford, United Kingdom

[3] Department of Geography and Spatial Information Techniques, Ningbo University, Ningbo, China

[4] Section Hydrology, GFZ German Research Centre for Geosciences, Potsdam, Germany

[*] Corresponding authors: yqu@hydrology.uni-kiel.de (Y. Qu), nwu@hydrology.uni-kiel.de (N. Wu)

ABSTRACT

Given the many threats to freshwater biodiversity, we need to be able to resolve which of the multiple stressors present in rivers are most important in driving change. Phytoplankton are a key component of the aquatic ecosystem, their abundance, species richness and functional richness are important indicators of ecosystem health. In this study, spatial variables, physiochemical conditions, water flow alterations and land use patterns were considered as the joint stressors from a lowland rural catchment. A modelling approach combining an ecohydrological model with machine learning

was applied. The results implied that land use and flow regime, rather than nutrients, were most important in explaining differences in the phytoplankton community. In particular, the percentage of water body area and medium level residential urban area were key to driving the rising phytoplankton abundance in this rural catchment. The proportion of forest and pasture area were the leading factors controlling the variations of species richness. In this case deciduous forest cover affected the species richness in a positive way, whilst, pasture share had a negative effect. Indicators of hydrological alteration were found to be the best predictors for the differences in functional richness. This integrated model framework was found to be suitable for analysis of complex environmental conditions in river basin management. A key message would be the significance of forest area preservation and ecohydrological restoration in maintaining both phytoplankton richness and their functional role in river ecosystems.

Keywords: riverine phytoplankton community, multiple stressors, integrated models, river basin management

1. Introduction

Environmental change accelerates the loss of biodiversity and threatens vulnerable freshwater ecosystems (Alahuhta et al., 2019, Kakouei et al., 2021). Freshwater ecosystems are among the most imperiled on earth, with rivers being particularly susceptible to global change due to several factors, for example, simplification of the habitat, altered water residence times, changes in nutrient loads and increasing arrival of new chemicals (Ormerod et al., 2010; Jackson et al., 2016). Compared with marine, land and even lake ecosystems, studies on river ecosystems are still relatively scarce. However, rivers are important linkage among all other different ecosystems, and are closely related to human activities in the watershed (Tang et al., 2017). The maintenance and protection of river ecosystem health is thus critical to human health and social development.

River ecosystems are synergistically influenced by multiple stressors including natural factors (i.e., dispersal, slope, altitude etc.) and anthropogenic factors (i.e., climate change, land-cover change, eutrophication etc.). First of all, the river network structure plays an important role in structuring the aquatic biotic community which is passively diffuse with water flow (Heino et al., 2015). For example, the single directionality of rivers can give a disproportionate effect on biological spread, which in turn potentially changes the viability and intermediate coexistence of populations (Heino et al., 2010). Next, flow regime alteration is significantly correlated with aquatic ecological processes (Rolls et al., 2018). Intensified episodes of flood and drought occurrences caused by extreme climate events simplify aquatic biodiversity (Tonkin, 2018), and more likely allow invasive exotic species find their niche space in modified habitat (Bunn & Arthington, 2002). The unstable flow conditions caused watershed management to become more challenging. For instance, in

55 northern Germany, a rising annual flow rate and higher chance of flooding during peak flow
56 (Asadieh & Krakauer, 2017) with a reduction in flow during low flow seasons were anticipated
57 subsequently destabilizing the ecosystem structure (Kakouei et al., 2018). Droughts and low flow
58 events might trigger eutrophication, even cyanobacteria and algae blooms worldwide (Qu et al.,
59 2019, Pathak et al., 2021, Ye et al., 2021). Flow sensitive algal species was displaced by tolerant
60 species during the high flow disturbance (Wu et al., 2019).

61 Last but far from the least, land use also acts as a crucial factor for biodiversity (Allan 2004; Kremen
62 & Merenlender 2018). It was reported that land use change from wetland to rangeland generally
63 resulted in incremental change of peak discharge volume (Davis et al., 2015), while catchment with
64 higher forest land cover related to better water quality and higher biodiversity (Oeding et al., 2018;
65 Wilkinson et al., 2018). Agricultural intensification imposes a variety of stressors on streams,
66 including temperature extremes, nutrient peaks, augmented fine sediment inputs, increased
67 frequency and magnitude of peak flows and lowered base flow patterns (Paul & Meyer, 2001;
68 Lange et al., 2016; Wagner & Waske 2016; dos Reis Oliveira et al., 2018). These risks may be
69 magnified for small streams in farming areas (Walsh et al., 2005). The pattern of riverine
70 phytoplankton communities are ultimately subjected to shifts in their richness, abundance and
71 composition under changes of multiple stressors (Rietkerk et al., 2021). However, the extent of
72 impacts from modified land cover pattern on riverine phytoplankton is still largely unclear and
73 hindered by landscape mosaic.

74 To mitigate the impact of multiple stressors requires targeted case studies that focus on key
75 compartments within river networks to develop a general framework for implementing river basin

management in human-impacted landscapes. Therefore, we propose a framework (Fig. 1) that aim to (1) determine the most influencing factors from spatial parameters, land use pattern, indices of hydrological alteration and local physiochemical variables when observing multidimensional biological descriptors, and (2) simulate the response of phytoplankton to combined key determinants, of phytoplankton as manifested in term of changes in community biological characterization, including abundance, species richness (SR) and functional richness (FR). In this study, we focused on phytoplankton community because it is pronounced primary producer to support the aquatic ecosystem (Wu et al., 2011, Jackson et al., 2016), and they are highly sensitive responder to environmental changes (Wu et al., 2017, Shoener et al., 2019; Charles et al., 2021). The riverine phytoplankton has been discussed their critical contributions in promoting the river ecosystem have been addressed from food web and metabolism aspects from recent studies (Kim et al., 2021; Pathak et al., 2022). The three bioindicators were chosen because they are showing different aspects of the community characterization, not only reflecting the biological resources from both quantity and quality point of view, but also useful features illustrating the complex relationship between biology and environment (Cardinale et al., 2006; Soliveres et al., 2016). Abundance has been widely used as the bioindicator to value the population of primary production (Read et al., 2014; Moorhouse et al., 2018). SR is a fundamental biodiversity indicator and a convenient tool for applied ecologist, as the irreplaceable metric to measure and further interpret. FR groups the species with similar functioning in the ecosystem by the species' morphological, physiological, and phenological traits which affect their growth, reproduction and survival abilities can best present the response of phytoplankton community to environment changes (Wu et al., 2017; Wijewardene et al., 2021). All of them are valuable and comparable tools for broader

stakeholders and environmental managers to receive intelligible and straightforward information to support further diagnosis based on the primary producer phytoplankton in the streams. In this paper, we posed two questions: (1) are the key determinants for the abundance and richness of phytoplankton community the same? (2) can one management strategy best benefit both the taxonomic and functional richness at the same time? Thus, we hypothesized that:

H1: Agricultural land use and nutrients are the most influential factors for the phytoplankton community in the rural streams. Management of fertilizer application in arable land is the most important aspect;

H2: By regulation land use and nutrients input might be helpful for controlling algal abundance but hydrological condition are more important determinants for composition structure, and their relative importance differs from taxonomic to functional richness.

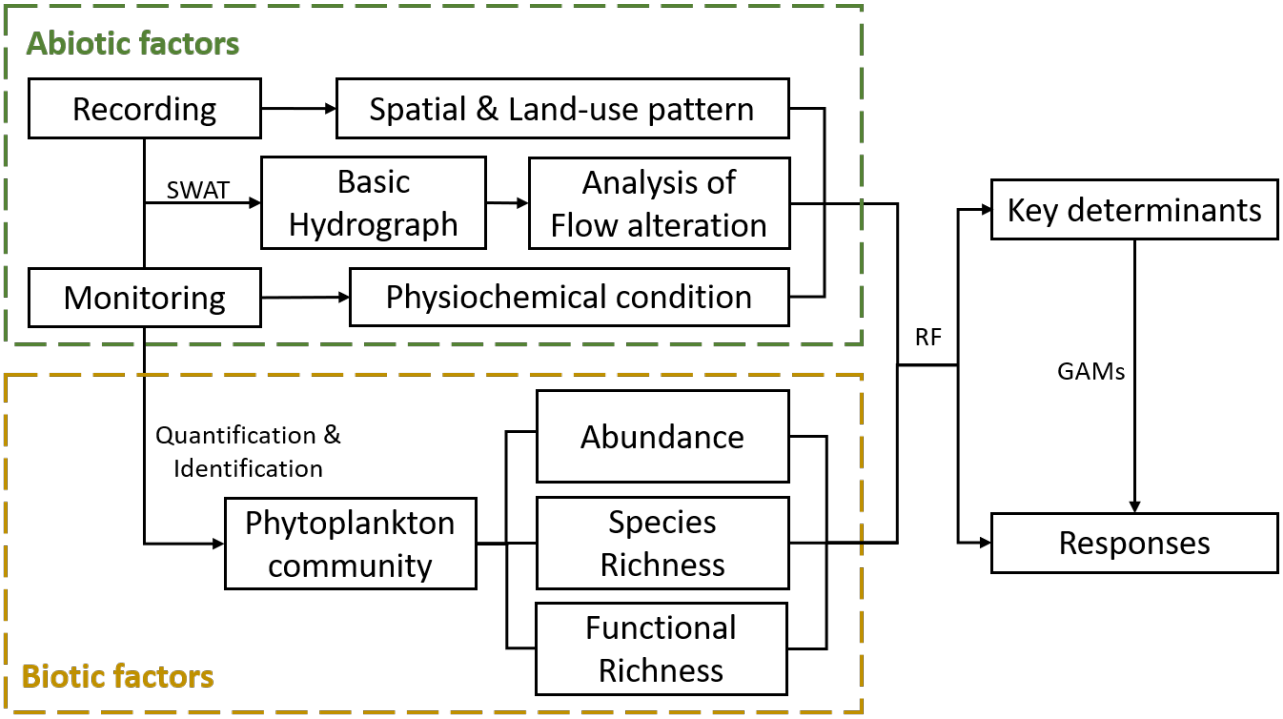


Fig. 1 Working framework of the study. The abbreviation SWAT represent the Soil and Water Assessment Tool. RF represent Random Forest. GAMs represent Generalized Additive Models.

112 ## 2. Materials and methods

113 ### 2.1. Study area

114 Our study river, Treene, is located in the Schleswig-Holstein state of Germany, belonging to the
115 northern lowland region of Europe (Fig. 2). It is the largest tributary of the Eider River in a
116 temperate climate zone influenced by marine climate, with mild temperature and high precipitation
117 in winter. The catchment area is 481 km^2 at catchment outlet Treia. The annual average discharge
118 at the gauging station Treia is 6.23 m^3/s (Guse et al., 2015b). River substrate is mainly composed by
119 sand and gravel. The land cover is dominated by agriculture and pasture (Marquardt, 2008). The
120 northeast highland in the upstream part of the Treene catchment is characterized by gentle slopes
121 and more fertile soils, allowing a cultivation of high value crops, such as wheat, barley and rape
122 seed (Eastern Hillands). The southwestern part of the watershed is characterized by poorer sandy
123 soils and low fertility with a higher percentage of pasture (Geest landscape). Only a small part of the
124 catchment is covered by forests (8%) and urban areas (8%). There are two major tributaries called
125 Jerrisbek and Bollingstedter Au (LAND S-H, 2006). The data for this study area were taken from field
126 investigations and a modeled data base from a long-time monitoring study (see description in Guse
127 et al., 2015a).

128 Field surveys carried out included representative samples from all 4 seasons (Winter - December of
129 2014, Spring - March of 2015, Summer - June of 2015 and Autumn - September of 2015,
130 respectively) on 53 sampling sites which covered the mainstream and major tributaries of the
131 catchment (Fig. 2), resulting in a total of 212 samples. Among the 53 sampling sites, we have 16
132 sites in the main stream named as Tr01- Tr16 (Tr for the mainstream of Treene), and 37 sites in 5

different tributaries named as the sub-basin where they are located abbreviated as: Bo for Bollingstedter Au, Je for Jerrisbek, Ju for Juebek, Ki for Kielstau, Sa for Sankermark See). At each sampling site, we conducted investigations in five parts: spatial factors, land cover pattern, hydrological indicators, water physicochemical condition and phytoplankton community (Fig. 1).

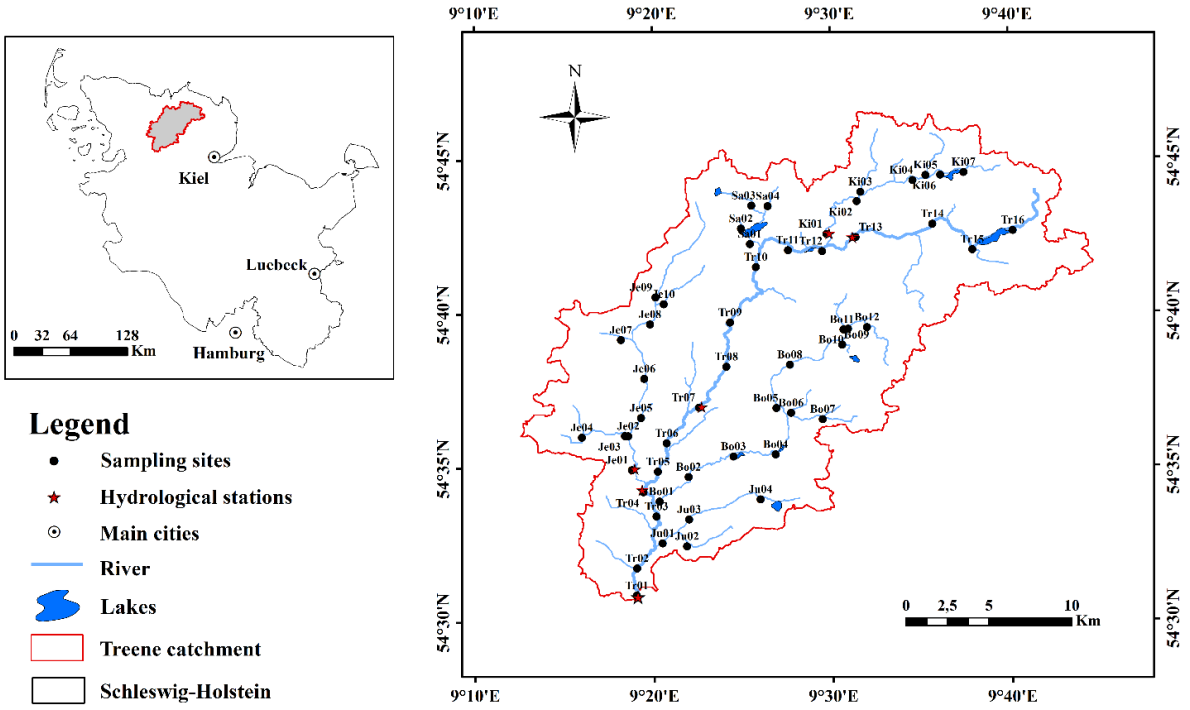


Fig. 2 The location of the Treene catchment, 53 sampling points and 6 hydrological stations in Schleswig - Holstein state of Germany. The abbreviated sites named according to each sub-basin where they are located: Bo for Bollingstedter Au, Je for Jerrisbek, Ju for Juebek, Ki for Kielstau, Sa for Sankermark See, and Tr for the mainstream of Treene. The numbers count along the longitudinal axis of rivers from the outlet to upstream. The sampling points in close distance of lakes are not located in the lake but situated systematically downstream following the lakes.

2.2. Phytoplankton community

At each sampling site, phytoplankton samples were quantitatively collected from the surface (0-

145 0.5m depth) of the river by a volume sampler (Sigee, 2019). The 10 L collecting device concentrated
146 10 L water sample through a 20 μm mesh size plankton net into a collecting vessel, and then
147 transferred the into a 50 mL bottle for further sedimentation and identification. We apply the
148 traditional method for the algal quantification in this study. Before counting and identifying,
149 samples had been settled down and concentrated with the Utermöhl methodology (Utermöhl,
150 1958). All samples were received two times for checking classification under an upright optical
151 microscope (Nikon Eclipse E200-LED, Germany) by two different magnifications: first at ×400
152 magnification for classification of the soft algae, second at ×1000 under oil immersion for
153 determination of the diatom species. Permanent diatom slides were prepared after acid digestion
154 for the second step. Phytoplankton were counted, identified to species level and measured the
155 biovolume for calculating the abundance, species richness and further functional richness. The
156 counting unit was individual (unicell) and at least 300 units were counted for each sample. More
157 detailed procedures have been described in previous articles (Qu et al., 2018; Wu et al., 2018).
158 Phytoplankton species were assigned into 19 categories from five types of functional traits
159 according to the information from literature: (1) biovolume [pico: <5 μm^3, nano: 5–100 μm^3, micro:
160 100–300 μm^3, meso: 300–600 μm^3, macro: 600–1500 μm^3 and large: > 1500 μm^3] (Abonyi et al.,
161 2018, Kruk et al., 2017), (2) ecological guild [low profile, high profile, motile, planktonic] (Rimet &
162 Bouchez, 2012; Guiry, 2010), (3) life form [colonial, filamentous, flagellates, unicellular] (Kruk et al.,
163 2017, Abonyi et al., 2018), (4) nitrogen fixation [yes or no] (Stancheva et al. 2013), (5) spore
164 information [no spore formation, zoospores, akinetes, oospore and zygospores] (Agrawal, 2009;
165 Lange et al., 2016). More details on studies traits can be found in Table A 1 in the Appendix and in
166 previous articles (Wu et al., 2018). In this study, although carefully collected and counted, there is an

undeniable underestimation of the small sized (pico and/or nano biovolume) phytoplankton since the limitation of the 20 µm plankton net.

2.3. Spatial factors

Spatial variables were described by Principal Coordinates of Neighbour Matrices (PCNM) based on a Moran's Eigenvector Map (Borcard et al., 1992). The PCNM variables effectively model spatial structures among sites, they can illustrate spatial relations among sites at multiple scales, which is commonly used to describe species dispersal processes (Curry & Baird, 2015). The spatial variables with small code (e.g., PCNM1) indicate broad-scale spatial pattern, while fine-scale pattern with larger code (e.g., up to PCNM32 in our study). The spatial variables were computed using the function 'pcnm' of the R package vegan (version 2.6-2, Oksanen et al. 2022). There are 32 eigenvalues of PCNM component which were included as the spatial variables in the study area (details can be found in previous paper Wu et al., 2018).

2.4. Water physicochemical condition

The physicochemical condition is characterized by thirteen parameters (details see Appendix Table A. 1). Water temperature (WT, ° Celsius), pH, electric conductivity (EC, us/cm), and dissolved oxygen (DO, mg/L) of the surface water were measured in situ with Portable Meter (WTM Multi 340i and WTW Cond 330i, Germany), while water depth (m) was measured with a measuring tape and flow velocity (m/s) using a digital water velocity meter (FlowSens Single Axis Electromagnetic Flow Meter, Hydrometrie, Germany). Simultaneously, two water samples (500 ml each) were collected at the same place and time for analyzing the nutrients. Part of them were filtered immediately through

187 GF/F glass microfiber filter (Whatmann 1825-047) when reaching the lab. Both filtered and
188 unfiltered samples were kept frozen at -20 °C until measurement. The concentration of total
189 phosphorus (TP, mg/L) was measured in unfiltered water samples, and the remaining parameters
190 including orthophosphate-phosphorus (PO_4-P, mg/L), ammonium-nitrogen (NH_4-N, mg/L), nitrate-
191 nitrogen (NO_3-N, mg/L), nitrite-nitrogen (NO_2-N, mg/L), chloride (Cl, mg/L) and sulphate (SO_4, mg/L)
192 were measured in filtered samples according to the standard methods of DEV (Deutsche
193 Einheitsverfahren zur Wasser, Abwasser- und Schlammuntersuchung). Dissolved inorganic nitrogen
194 (DIN, mg/L) is the sum of NH_4-N, NO_3-N and NO_2-N. Total suspended solids (TSS, mg/L) were
195 measured according to Standard Operating Procedure for Total Suspended Solid Analysis (Connor et
196 al., 1998).

197 **2.5. Hydrologic indicators**

198 As a widely used ecohydrologic model, the Soil and Water Assessment Tool (SWAT, Arnold & Allan,
199 1999) was implemented for the study catchment to model site-specific hydrological stressors of the
200 phytoplankton community. In the SWAT model, the water balance is resolved and the most relevant
201 hydrological processes are calculated. The spatially distributed SWAT model provides model results
202 for each of the hydrologic response unit that possess unique water related attributes in this sub-
203 basin. Thus, spatial patterns of different hydrological variables can be derived in a daily resolution.
204 The SWAT model was already applied worldwide and has been well established in our study area in
205 long-term daily resolution (Schmalz & Fohrer, 2009; Guse et al., 2015a; Haas et al., 2016). Our
206 modeling period was sub-divided into a calibration period (2001 to 2005) and a validation period
207 (2006 to 2016) based on the hydrological stations in the Treene catchment (Fig. 2), The model

performance has been evaluated by Nash-Sutcliffe Efficiency, Percent Bias and RSR (root mean square error divided by standard deviation) (see further description in Guse et al., 2015a and Guse et al., 2015b). The SWAT model version used in the study was SWAT 2009 9.3.7 with revision 488. From the outputs of the SWAT model, Indictors of Hydrological Alteration (IHA metrics, Richter et al., 1996), which provide ecologically relevant information on the duration, magnitude, frequency, timing, and rate of flow events (Olden & Poff, 2003, Kiesel et al., 2017 & 2020; Hutchins et al., 2021), were calculated for the sampling sites. Together with the *in-situ* measurement (flow velocity and water depth), they comprised as the hydrologic indicators (details see Appendix Fig. A. 2 and Table A. 4).

2.6. Land cover pattern

Land cover data of our study area was downloaded from the Schleswig-Holstein State Bureau of Surveying and Geo-information (LVERMGEO-SH, 2012). Land cover types were classified into eleven categories for analysis: agricultural land-generic (AGRL), deciduous forest (FRSD), evergreen forest (FRSE), forest mixed (FRST), total forest (TOFR, the summary of deciduous forest, evergreen forest and mixed forest), rangeland (RNGE), industrial (UIDU), residential-low density (URLD), residential-medium density (URMD), water (WATR), wetland (WETL) and winter pasture (WPAS). ArcGIS (Version 10.0, ESRI, US) was used to process the area of each sampling site by land cover category. The land cover area is accumulative along the longitudinal river continuum. The upstream watershed was determined for each site, and the land cover areas were converted to proportions for following analyses (details can be found in the previous paper Qu et al., 2018b; 2019; Wu et al., 2018 and also see Appendix Table A. 3). We assume that under the current land use policy the land

use pattern was unchanged during the investigation one-year period.

2.7. Statistical methods

To explore the relationships between abiotic predictors (water physicochemical parameters, hydrological indicators, land use variables and spatial factors) and phytoplankton biotic conditions, we conducted analysis as follows (Fig. 1): firstly, abiotic environmental factors were pre-selected excluding the ones with significant multi-collinearity (with variance inflation factor >10 (O'Brien, 2007) and Spearman's rank correlation coefficient |r| >= 0.75). All abiotic variables were tested for collinearity by function '*cor*' in R package of *stats* (version 4.1.0, R Development Core Team, 2021). Secondly, a machine learning algorithm random forest (RF) model was applied to rank multiple stressors hierarchy, and identify the key determinants for our target bio-indicators. RF generates a combination of decision trees and can be used to evaluate which predictor variables are the most important ones. The performance criteria were tested by the random forest out-of-bag (OOB) procedure with cross-validation. Variable importance is assessed based on changes in the mean square error (MSE) of the model compared with a model based on permuted data, where a higher percentage increase of MSE (%IncMSE) indicates a higher importance of that variable. To gain an overview of how the environmental variables might affect the conditions of phytoplankton community, RF was performed on the whole year dataset of the investigation, as well as for each season individually. In this study, RF was developed by function 'randomForest' from the R package *randomForest* (Liaw, 2022). To rank the variables importance, function 'importance' was followed from the same package. In addition, a first impression of the responses from the combined top two stressors were estimated by the partial dependence plots (function: gg_variable, package:

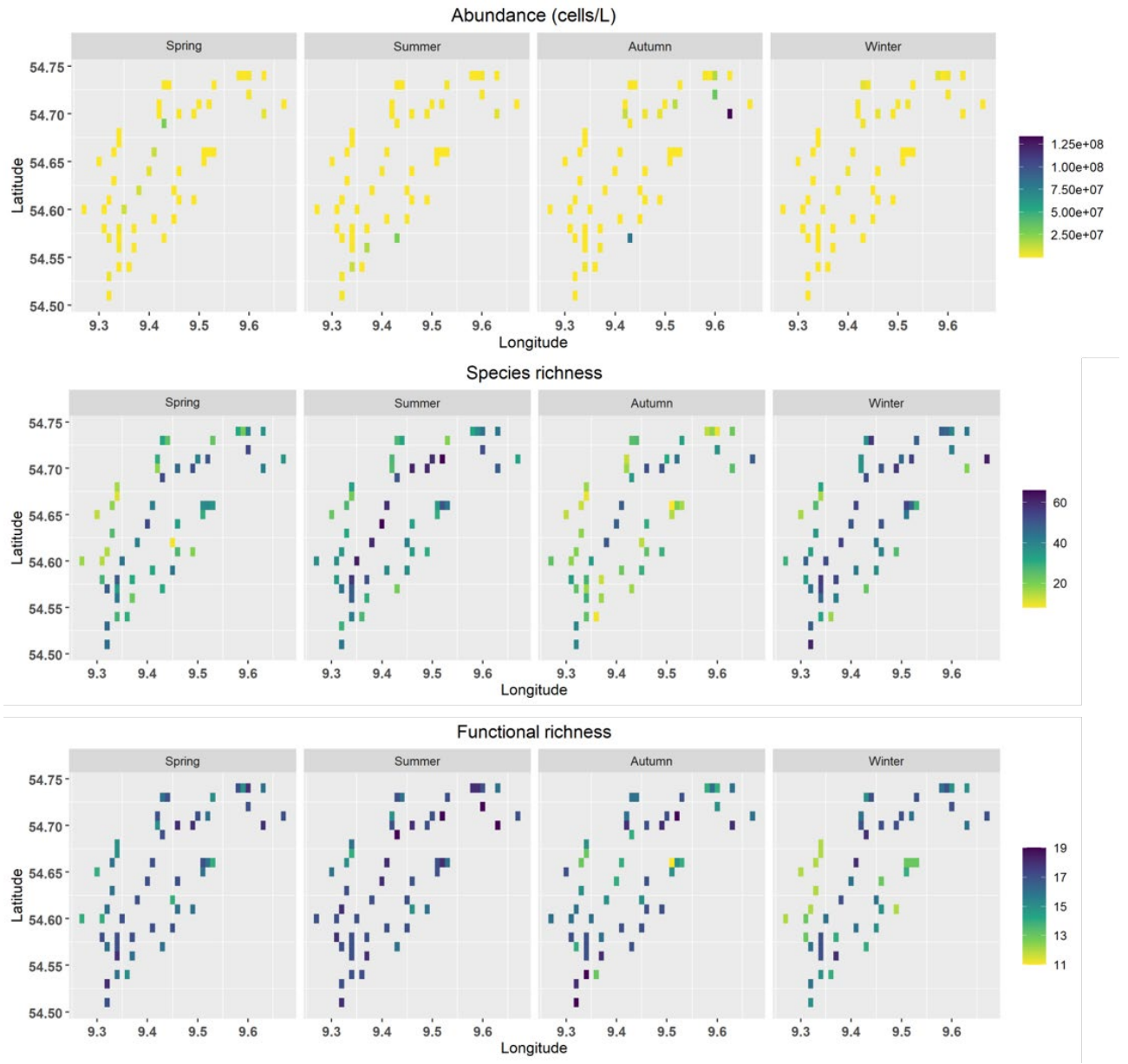
ggRandomForest, Ehrlinger, 2016). Thirdly, based on the screening results from RF, Generalized Additive Models (GAMs) were utilized to setup an integrated understanding between stressors and responses at the regional scale, and disentangle the potential changing trend of the biotic resources. GAMs are a powerful method to test the potential effects of the combined stressors across the temporal and spatially varying conditions, by using highly interpretable splines to model non-linear relationships between covariates and response that are learned from the data. It was deemed suitable due to the non-linear trends during our data exploration step and the partial dependence plots from the RF results. The model was implemented by the R package *mgcv* for fitting the GAMs (Wood, 2022). Month, latitude and longitude have considered as the random effect for their autocorrelation effects. Interactions between coordinates and the main effects have also been considered to achieve a better simulation for the three bioindicators models, respectively. In specific, interactions between coordinates and the urban land cover included for the abundance simulation, forest land cover for species richness model, and for functional richness, including the spatial autocorrelation of the key hydrological indicators improved the model performance. To help the model selection, Shrinkage smoothers were added as a tenser product smooth and AIC scores have been considered to compare the models with different fixed effects structures. All statistical analyses were performed with the R software (version 4.1.0, R Development Core Team 2021).

3. Results

3.1 Phytoplankton dynamics and environment variations

Although there is a missed detection rate on the unicellular algae whose diameter less than 20 μm,

we observed dissimilarity for different seasons and subbasins. The observed phytoplankton abundance, species richness and functional richness in the mainstream of the river was higher than in the tributaries among the four seasons (Fig. 3). a total number of 396 algae and cyanobacteria taxa were observed during this one-year seasonal study, with 260 taxa from Bacillariophyta, 62 Chlorophyta, 9 Charophyta, 35 Cyanobacteria, 17 Euglenozoa, 8 Miozoa, 4 Cryptophyta and 1 Chrysophyta. Seasonal variations can also be distinguished from the graph where the highest abundance and the lowest number of SR appeared in September, whilst relatively high SR is in June and low FR in December. The higher amount of SR in December was mainly attributed to more diverse diatom being detected with similar functional traits. The highest SR was in summer season, attributed to high taxonomic diversity of Chlorophyta in the community; while lowest during autumn season, influenced by a Cyanobacteria bloom. We also observed *Stephanodiscus hantzschii Grunow* bloom during the spring time in the tributary of Sankermarker See. The eastern tributaries Jerrisbek, Bollingstedter Au were similar in their species composition and mainly dominated by benthic diatoms which has been resuspended in the water column. In particular, the tributary Jerrisbek has high share of winter pasture land cover area in its sub-basin and hold lower abundance than the rest of the streams, with relatively low species composition. The observed Euglenozoa and Miozoa species were mainly detected from the tributary of Kielstau with a relatively high nutrients concentration and share of agricultural land cover area in the sub-basin (Table A. 3 and Fig. A. 1).



289

290 Fig. 3 Observed phytoplankton community abundance, species richness and functional richness spatiotemporal

291 distribution variations in the Treene river network

292 **3.2. Determine the environmental factors importance**

293 To identify the main factors that influence the phytoplankton variations, RF models were calibrated

294 based on the 212 samples considering the entire one-year variation and each individual seasonal

295 split (Table 1). The model showed best performance for simulating the abundance variations
296 (explaining 67.61%), followed by the species richness models (explaining 52.66%). The values of
297 abundance have been log transferred before computing the random forest regressions. The model
298 simulation for functional richness is slightly lower than the others, but still explained 42.13% of the
299 variances. The importance of features was defined based on mean decrease in the accuracy from
300 the model output (Fig. A. 3). The most important predictors for abundance were the land cover
301 percentages of water body and medium-density urban area. The water cover was also detected as
302 the best explanatory variable for the abundance distribution variations during summer and autumn
303 season. The share of deciduous forest and winter pasture land cover were the top predicting factors
304 for variations of species richness for the overall one-year observation, as well as in the autumn and
305 winter time. Two hydrological alteration indices were selected as the best predictors for the
306 differentiations of functional richness. Most of the dissimilarity of the bioindicators within a season
307 were better explained by flow regime: rate of change (Hv54 and Hv57) and the skewness of flow
308 (Hv28). The concentration of orthophosphate showed special importance for the abundance
309 dynamics in the winter time (Table 1).

310 Table 1. Model results from random forest including the explanation percentage and the most importance
311 influencing variables. The top two variables are indicated for the one-year models, and the top one for each
312 season. WATR represents for water land cover, URMD for medium density urban land cover, FRSD for deciduous
313 forest, WPAS for winter pasture, Hv21 for skewness of 7 days before, Hv28 for skewness of 14 days flow, Hv40 for
314 low flood pulse count 14 days, Hv54 for rate of change 3 days, Hv57 for rate of change 30 days, PO_4-P for
315 Orthophosphate-phosphorus.

	Model output	One-year	Spring	Summer	Autumn	Winter
Abundance	Variances explained (%)	67.61	63.08	41.76	54.02	62.51
(log_transferred)	Key determinants	WATR, URMD	Hv57	WATR	WATR	PO_4-P
Species richness	Variances explained (%)	52.66	53.72	53.61	41.96	38.13
	Key determinants	FRSD, WPAS	Hv57	Hv54	FRSD	FRSD
Functional richness *	Variances explained (%)	42.13	NA	NA	NA	63.06
	Key determinants	Hv21, Hv40	NA	NA	NA	Hv28

316 * Functional richness reflects seasonal succession but limited variation within one season (i.e., spring, summer and
317 autumn have limited unique value for establishing reliable regression model, which have written as NA, not
318 applicable).

319 **3.3. Responses of phytoplankton community to multiple stressors**

320 Based on the outcome from the random forest, the joint effect by the top two most influencing
321 factors were presented. Both partial dependency plots, as well as generalized additive models were
322 fitted for simulating the responses of the phytoplankton community variations from the three
323 aspects of phytoplankton characterization. The abundance enlarged with the increasing water and
324 urban land cover percentage. Forest cover affected the species richness in a positive way, while,
325 pasture share gave a negative effect (Fig. 4). A continuously rise in phytoplankton species richness
326 has been observed in relation to the share of the deciduous forest land cover. For winter pasture
327 land cover share beneath 20%, SR was unrelated, whereas the SR presented a substantial decrease
328 above 20% share and less sensitivity once again above 40 % (Appendix Fig. A. 3). Both skewness of 7
329 days and Hv40 for low flood pulse count 14 days presented a negative trend with FR (Fig. 4). In

particular, the FR were shown visibly decreasing as the skewness of 7 days (Hv21) greater than value of 2 (Appendix Fig. A. 3).

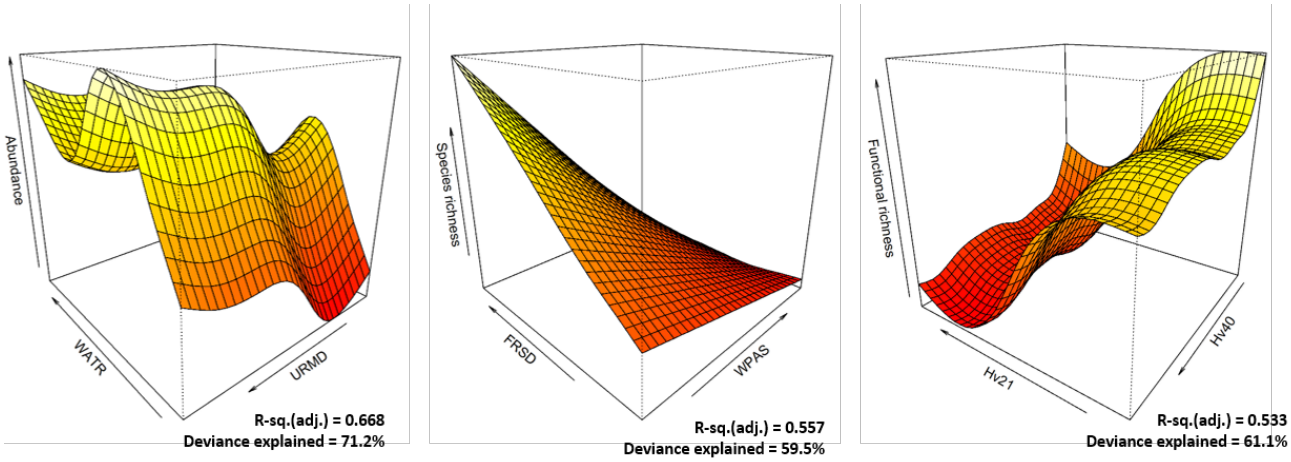


Fig. 4 Phytoplankton community abundance (presented by log transferred abundance value), species richness and functional richness response simulation by generalized addictive models (GAMs), each shown under their key determinants. WATR refers to water land cover, URMD for medium density urban land cover, FRSD for deciduous forest, WPAS for winter pasture, Hv21 for skewness of 7 days before, Hv40 for low flood pulse count 14 days.

4. Discussion

4.1 Impacts from land use modification

In this one-year seasonal observational study, we disentangled the relationship between the four groups of abiotic variables (i.e., spatial factors, water physiochemical condition, land cover pattern and hydrological indicators) and the multiple aspects of phytoplankton community bioindicators (i.e., abundance, species richness and functional richness). Our first hypothesis has misapprehended the important variables. In our study area, land cover by waterbody and urban area have been detected as the key determinants for the abundance variations across one-year. This result is

consistent to our previous finding in the study area as well as findings of others. Higher abundance attributed to higher waterbody area in the catchment (Qu et al., 2018). Tributaries connected to lentic waterbody, which have slower flow and higher residence time, resulting in more favorable condition for phytoplankton growth (Bussi et al., 2016). Higher phytoplankton abundance may be due to increases in urban land use and decreases in forest habitat (Kakouei et al., 2021). On one hand, river in urban area needs special concern on phosphorus control (Hutchins and Hitt, 2019). Additionally, urban area percentage was detected indirectly impact on phytoplankton functional groups through the influence of phosphate and total phosphorus concentration in the river Treene (Qu et al. 2019). In this study, land cover by deciduous forest emerged as the most significant key predictor of phytoplankton species richness. This is conceivable due to the combined and interactive effects derived from the land cover patterns (Fuß et al., 2017), and a series of related processes that amplify changes imposed on the biotic recipient. For example, rivers passing through the forest land cover largely retain in a relative pristine state with meanders and provide wood debris, and leaf litter to the linking waterbodies (Allen et al., 2021). The leaky woody structure in the area helped to create and enhance more complex aquatic habitats which potentially benefit the biodiversity conservation (Turunen et al., 2017; Wohl, 2017). Moreover, the riparian woodland as part of the land cover pattern in the catchment potentially impact greater resistance to flooding and erosion and improve aquatic water quality (Baker et al., 2021). Similarly, Smucker et al. (2013) detected that riparian buffer with above 65% forest and wetland coverage greatly reduced effects of pasture land use on motile and high-P diatoms. Mutinova et al. (2020) observed a reduction in pollution tolerant diatoms to represent the tangible benefits of forested riparian buffers for stream biodiversity. In general, land cover pattern act as an integrated indicator sum-up the impacts from

various aspects, Besides nutrients, land cover link with other pollutions (Kelso and Baker, 2022), hydrology (Guse et al., 2015b; Baker et al., 2021), river geo-physical characteristics and riparian habitat conditions. Moreover, biological integrity metric is sensitive to land cover alteration (Gerhel et al., 2002). Apart from phytoplankton community, other aquatic biota, for example microbial community (Fasching et al., 2020), zooplankton (Sługocki et al., 2019) and fish (da Silva Almeida et al., 2022) are influenced by land cover all closely linking with phytoplankton community pattern.

4.2 Impacts of flow regime alteration

Although landcover appears to be the primary driver for phytoplankton abundance and species richness, differences in seasonality have a secondary impact on contributions of hydrological alteration impacts. Besides, the abundance and species richness, we observed a significant effect on riverine phytoplankton community functional richness from hydrological alteration indices rather than forest land cover. The finding agreed with our second hypothesis. The key determinants for the phytoplankton community multiple aspects of bioindicators depended greatly on the specific changes. However, it showed inconsistency from the previous study (Kakouei et al., 2022), which saw the importance of environmental factors for taxonomic and functional bioindicators stayed in a same pattern. Consistently, others have found light, nutrients, water temperature, and seasonality are the key determinant for both taxonomic and functional bioindicators of lake phytoplankton. Nevertheless, unlike the lake, biomes in the river ecosystem are sensitive to response to the flow regime significantly, so as are the riverine phytoplankton.

Hydrological indicators derived from model simulations were used to describe the flow regime and contributed to several important stressors which affected the phytoplankton community patterns

(Table 1). We observed that the distribution variation of abundance in the spring time, species richness during spring and summer, and functional richness in the winter period were all best predicted by the flow alteration indices. It has been found in previous studies both in the river Treene and elsewhere that flow regime potentially affects the abundance (Qu et al., 2018a; Schneider et al., 2018; Atazadeh et al., 2021), species composition (Qu et al., 2018b) and has implications for their ecosystem functioning (Marazzi et al., 2017; Wu et al., 2019; Guo et al., 2020; Wu et al., 2022). Flow alteration indices have also been detected as indirect factors that affect the ecological processes in rivers by regulating water quality, such as nutrients and sediment input, and then enhance their influence on phytoplankton community (Kim et al., 2019; Qu et al., 2019). Usually, hydrological indices integrated over long period of time, such as seasonal or annual, lead to a better understanding and prediction for the hydrological process (Olden & Poff, 2003, Kiesel et al., 2017). Hydrological variables measured over weekly and biweekly period of time are overlooked. However, our results emphasized that the critical impact of short-term hydrological indices (e.g., skewness of 7 days, 14 days flow and low flow pulse count for 14 days) outperformed other indicators in shaping the magnitude of riverine phytoplankton dynamics (Table 1 & Fig. A. 3). This consistency in identification strengthens our confidence in the underlying model establishment (Wu et al., 2016; Wu et al., 2018, Qu et al., 2018a, Wu et al., 2022). On the other hand, we assume that this can be explained by the short life cycle of phytoplankton (Lehtinen *et al.* 2017). It highlighted the importance of time lags for the phytoplankton community resilience functioning (Guo et al., 2020; 2021). Nevertheless, we found it is an interesting finding and worth further analysis in the future studies.

4.3 Implications for river basin management

The ecological modeling methods for environmental management are improving. Integrated hydrological and ecological modeling improves our understanding of the status of aquatic biodiversity and opens new opportunities to apply methods such as diagnostic tools for river ecosystem management (Bussi et al., 2018; Schuwirth et al., 2019). Various statistical approaches in combination with different spatial scale can be applied to develop better relationship between land use and bioindicator for better river basin management (Schäfer & Piggott, 2018; Escala et al., 2019). However, it is more difficult to achieve higher diversity at regional scale, although an inclusion of multiple stressors did appear to be essential and crucial for managing at the catchment level (Piggott et al., 2015). Species benefits are often scale-dependent via thresholds or non-linear relationship (Gergel et al., 2002; Huggett et al., 2005). Considering watershed aspect would help us to better understand the interaction between anthropogenic and natural impacts. As shown in this study, land use change and flow alteration may have different level of effects on riverine phytoplankton, hence while the critical stressors may change during time and space. In the agriculture dominant area, coverting arable land to pasture would potentially reduce nutrients loading (Haas et al., 2017; Teshager et al., 2017). However, the compensatory conversion that arises from the additional forest replacement to cropland would offset the benefits. Additionally, the optimal location and amount of woodland in facing forest fragmentation need greater concern (Ammer et al., 2018). The function of the left woodland inside and outside of the rural and urban dominant catchment is worthy of further and deeper understanding (Vergnes et al., 2012; Kong et al., 2021).

In addition, we are aware of a general issue of unbalance in the relationships between taxonomic and functional richness provision (Fleming et al., 2021). Hence, a qualitative increase in species richness could partially not increase ecosystem functioning because of redundancy. Similarly, functionality could be increased by enhancing the abundance of key species, without changes in species richness (Soliveres et al., 2016, Duffy et al., 2017). Also, management to increase a single indicator or function is likely to decrease another indicator or multifunctionality (Meyer et al., 2018). There is an demand to improve understanding of how multi-functionality respond to multiple stressors and to optimise management at different spatial patterns of implementation.

Last but not the least, there is a valid criticism of the study on the phytoplankton collection approach. The observed species were subjected to the limitation of the mesh size (20 μm) of the plankton net. Although plankton net is efficient for the waterbodies with low-density population, and is beneficial for obtaining a more comprehensive species composition by filtrating a relative greater volume of water sample, this collection approach may lead the individuals smaller than 20 μm to be overlooked (Sigee, 2019). Moreover, observed nano/picoplankton (e.g., species in genus of *Merismopedia* and *Phormidium*) in this study might attribute to the species colony or filament life-form strategy. Potential unicellular species (e.g., species from genus *Raphidocelis* or *Synechococcus*) may largely be underestimated due to escaping. Thus, further work would be needed to accurately determine the actual phytoplankton standing stocks, and the key drivers of the nano/picoplankton which were commonly underestimated but might compose a significant proportion of the community under certain circumstances. In addition, introducing other detection approach, such as advanced full sample flow cytometry assay to the long-term river ecosystem

monitoring, would be helpful to ensure a more sensitive and accurate estimation of phytoplankton community (Read et al., 2014).

5. Conclusion

In summary, we observed how the response of phytoplankton species richness changed under the identified key stressors from spatial factors, physiochemical conditions, flow disturbances and land-use patterns over the year. Our results (1) implied a high contribution of phytoplankton abundance came from the connected lentic waterbodies, (2) highlighted that forest areas were potentially beneficial in maintaining algal species richness, and (3) emphasized the importance of flow regime influence on functional richness. Our findings suggest that preserving forest areas and ecohydrological restoration is key to protecting the richness and functional role of phytoplankton in river ecosystems. Considering and simulating the changes of phytoplankton community from multiple dimensional aspects is important in river basin management. Human impacts on lowland rivers are ubiquitous, and resultant land-use related stressors and altered flow regime could interact with changing biotic responses. Therefore, aquatic biological monitoring programs require expansion to integrate characterization of local environmental surroundings and landscape mosaic of the river basin. The integrated modeling method is highly recommended for better understanding the implications of riverine phytoplankton community dynamics under multiple stressors.

Acknowledgments

This study has been funded by German Research Foundation (Deutsche Forschungsgemeinschaft DFG, Germany) grants (FO 301/15-1, FO 301/15-2, WU 749/1-1, WU 749/1-2, and the project GU 1466/1-1 Hydrological Consistency in Modelling, Germany). There are financial supports by China

Scholarship Council (CSC, China) (Yueming Qu). We thank the laboratory crew of the Institute of Natural Resources Conservation of the Christian-Albrechts-University of Kiel for carrying out the water quality analysis. Thank Dr. Fuqiang Li, Zhao Pan and other friends for their supports during the field campaigns. We also thank Dr. Michael Hutchins for helping in revising the language. We appreciate the helpful comments of the anonymous reviewers who helped us improve this article.

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Appendix

Distinct indicators of land use and hydrology characterize different aspects of riverine phytoplankton communities

Yueming Qu[1,2*], Naicheng Wu [1,3*], Björn Guse[1,4], Nicola Fohrer[1]

[1] Department of Hydrology and Water Resources Management, Institute for Natural Resource Conservation, Kiel University, Kiel, Germany

[2] UK Centre for Ecology and Hydrology, Wallingford, United Kingdom

[3] Department of Geography and Spatial Information Techniques, Ningbo University, Ningbo, China

[4] Section Hydrology, GFZ German Research Centre for Geosciences, Potsdam, Germany

Table A. 1 Phytoplankton functional traits and categories of each trait in this study

Traits	Categories	Code
1. Cell size	Pico (< 5 µm3)	BioVol_C0
	Nano (5-100 µm3)	BioVol_C1
	Micro (100-300 µm3)	BioVol_C2
	Meso (300-600 µm3)	BioVol_C3
	Macro (600-1500 µm3)	BioVol_C4
	Large (> 1500 µm3)	BioVol_C5
2. Ecological guild	Low profile	LowPro
	High profile	HigPro
	Motile taxa	MotTax
	Planktonic taxa	PlaTax
3. Life form	Colonial	LifFor_col
	Filamentous	LifFor_fil
	Flagellate	LifFor_fla
	Unicellular	LifFor_uni
4. Nitrogen fixation	Yes (1) or No (0)	Nitfix
5. Spore formation	No spore formation	SpoFor_non
	Zoospores	SpoFor_zoo.auto
	Akinetes	SpoFro_aki.cyst
	Oospores and zygospores	SpoFro_oos.zyg

Table A. 2 Identified phytoplankton species in the study and their functional traits. The presence of the traits is represented as "1" and the absence of the traits is represented as "0". Descriptions of the codes use for traits can be found in Table A. 1.

Taxon	BioVol_C0	BioVol_C1	BioVol_C2	BioVol_C3	BioVol_C4	BioVol_C5	Low Pro	Hig Pro	Mot Tax	Pla Tax	LifFor_col	LifFor_fil	LifFor_fla	LifFor_uni	Nitfix	SpoFor_non	SpoFor_zoo.auto	SpoFro_aki.cyst	SpoFro_oos.zyg
Achnanthes delicatula	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Achnanthes exigua	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0

Achnanthidium pyrenaicum	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Achnanthidium minutissimum	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Achnanthes petersenii	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Achnanthes minutissima	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Achnanthes oblongella	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Actinocyclus normanii	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Amphora copulata	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Amphora eximia	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Amphora indistincta	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Amphora ovalis	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Amphora pediculus	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Amphora polonica	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0

Anomoeoneis sphaerophora	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Asterionella formosa	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Aulacoseira ambigua	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	1	0
Aulacoseira granulata	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	1	0	1	0
Actinocyclus normanii	0	0	0	0	0	1	1	0	0	1	0	0	0	1	0	1	0	0	0
Brachysira brebissonii	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Caloneis amphisbaena	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Caloneis silicula	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Cavinula scuteloides	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Cyclostephanos invistatus	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	1	0
Cyclostephanos dubius	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	1	0

Cyclotella (Puncticulata) balatonis	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	1	0
Cyclotella costei	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	1	0
Cyclotella meneghiniana	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	1	0
Cyclotella temperei	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	1	0
Cymatopleura elliptica	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Cymatopleura solea	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Cymbela aspera	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Cymbela cymbiformis	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Cymbela excisa	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Cymbela neocistula	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Cymbela turgidula	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Cymbopleura naviculiformis	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Cocconeis neodiminuta	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	0	0

Cocconeis pediculus	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
Cocconeis placentula	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Cocconeis pseudolineata	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Craticula accomoda	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Craticula ambigua	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Craticula cuspidata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Diatoma anceps	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Diatoma ehrenbergii	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0
Diatoma tenuis	0	0	0	1	0	0	0	1	1	1	1	0	0	0	0	1	0	0	0
Diatoma vulgaris	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0
Discotella pseudostelligera	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0
Diploneis krammeri	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Diploneis separanda	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Ellerbeckia arenaria	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0	1	0	0	0

Encyonema ventriocosum	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0
Encyonema lange-bertalotti	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0
Encyonema silesiacum	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0
Encyonopsis microcephala	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Epithemia adnata	0	0	0	0	1	0	0	0	1	0	0	0	0	1	1	1	0	0	0
Eucocconeis laevis	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Eunotia bilunaris	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	0
Eunotia diodon	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	0
Eunotia incisa	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Eunotia minor	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Eunotia nymanniana	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Eunotia soleirolii	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	0
Eunotia subarcuatoides	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0

Eunotia tenella	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Fragilaria austriaca	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Fragilaria capucina	0	1	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Fragilaria crotonensis	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Fragilaria famelica	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Fragilaria gracilis	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Fragilaria mesolepta	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilaria parasitica var.subconstricta	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilaria parasitica	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilaria recapitellata	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilaria rumpens	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0

Fragilaria tenera	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Fragilaria vaucheriae	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilariforma bicapitata	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilariforma constricta	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilariforma nitzschioides	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Fragilariforma virescens	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Frustulia crassinervia	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0
Frustulia saxonica	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	0	0
Frustulia weinholdii	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	0	0
Frustulia vulgaris	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	0	0
Gyrosigma acumminatum	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0

Gyrosigma attenuatum	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Gyrosigma obtusatum	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Geissleria decussis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Gomphonema acidoclinatum	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema angustum	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema auguri	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema auritum	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema capitatum	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema elegantissimum	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema exilissimum	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema hebridense	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0

Gomphonema innocens	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema micropus	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema minusculum	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema minutum	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema olivaceum	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema parvulum	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema pumilum	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema pseudoaugur	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema sarcophagus	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema subclavian	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema truncatum	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0

Gomphonema variostigmatum	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
Gomphonema vibrio	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0
Hantzschia amphioxys	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
Hantzschia abundans	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0
Hippodonta capitata	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Karayevia clevei	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Karayevia colbei	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Kolbayasiella subtilissima	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Lemnicola hungarica	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	1	0	0	0
Luticola mutica	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Melosira varians	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	1	0	0	0
Meridion circulare	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	1	0	0	0

Meridion circulare var.constrictum	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Navicula angusta	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula antoonii	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula cari	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula capitatoradiata	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula cryptocephala	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula cryptotenella	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula germanii	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula gotlandica	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula gregaria	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula lanceolata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula lundi	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula menisculus	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula notha	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0

Navicula oblonga	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula oppugnata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula radiosa	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula recens	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula reichardtii	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula reichardtiana	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula rhynchocephala	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula rhynchotella	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula sancti-naumii	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula slevicensis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula tenelloides	0	1	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula tripunctata	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula trivialis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0

Navicula trophicatrix	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula viridula	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Navicula wildii	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Neidium affine	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Neidium ampliatum	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Neidium binodis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Neidium dubium	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia acicularis	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia adamata	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia amphibia	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia capitellata	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia commutata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia constricta	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia dubia	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia fonticola	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0

Nitzschia sociabilis	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia gracilis	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia graciliformis	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia hantzchiana	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia heufleriana	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia hungarica	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia intermedia	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia linearis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia palea	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia paleacea	0	1	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia sigmoidea	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia tenuis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia recta	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia umbonata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Nitzschia wuellerstorffii	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0

Paribellus protracta	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Paribellus protractoides	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia appendiculata	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia biceps	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia borealis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia frequentis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia gibba	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia grunowii	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia isselana	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia lundi	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia microstauron	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia nobilis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia nodosa	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0

Pinnularia schoefelderi	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia subcommutata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia subgibba var. Undulata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia viridiformis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pinnularia viridis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Placoneis clementis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Placoneis ignorata	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Placoneis paraelginesis	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Placoneis placentula	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Planothidium delicatulum	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Planothidium dubium	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0

Planothidium frequentissimum	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Planothidium joursacense	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Planothidium lanceolatum	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Planothidium rostratum	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Platessa conspicua	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Prestauroneis integra	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Pseudostaurosira binodis	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Pseudostaurosira brevistriata	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Punticulata balatonis	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Punticulata radiosa	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Reimeria sinuata	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0

Rhoicosphenia abbreviata	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	0	0
Sellaphora bacillum	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Sellaphora laevissima	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Sellaphora pseudopupula	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Sellaphora pupula	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroforma exiguiformis	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Stauroneis acidoclinata	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis acuta	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis amphicephala	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis anceps	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis gracilis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0

Stauroneis kriegeri	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis leguminosis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis separanda	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis smithii	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis phoenicenteron	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Stauroneis thermicola	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Staurosira binodis	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Staurosira brevistriata	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Staurosira construens	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Staurosira venter	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Staurosirella leptostauron	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0

Staurosirella martyi	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Staurosirella pinnata	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Stephanodiscus hantzschii	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	1	0
Stephanodiscus hantzschii f.tenuis	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	1	0
Stephanodiscus minutulus	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	1	0
Stephanodiscus neoastrea	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	1	0
Stephanodiscus parvus	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	1	0
Surirella angusta	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella brebissonii var. kuetzingii	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella brebissonii	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella crumena	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella elegans	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella lacrimula	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0

Surirella minuta	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella ovalis	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella roba	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Surirella visurgis	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0
Tabellaria flocculosa	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Tabellaria ventricosa	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
Tabularia fasciculata	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Ulnaria acus	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	0
Ulnaria danica	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	0
Ulnaria delicatissima var.angustissima	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0
Ulnaria ulna	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	0
Navicula spp	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0
Microcystis aeruginosa	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Microcystis flos-aquae	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0

Microcystis viridis	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Microcystis wesenbergii	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Microcystis botrys	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Aphanothece minutissima	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Synechocystis spp	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Synechococcus elongates	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Rhabdoderma lineare	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Chroococcus minus	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Woronichinia naegeliana	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Gomphosphaeria aponina	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Aphanothece clathrata	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Aphanothece nidulans	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0

Aphanocapsa incerta	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Aphanocapsa holsatica	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Merismopedia tenuissima	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Lyngbya majuscula	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Planktolyngbya linmetica	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Planktothrix agardhii	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
limnothrix lauterbornii	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
limnothrix redekei	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
limnothrix spp.	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Phormidium ambiguum	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Phormidium autumnale	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Oscillatoria limosa	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0

Oscillatoria subcontorta	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Pseudanabaena limnetica	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Pseudanabaena catenata	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Spirulina major	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Spirulina spp.	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Jaaginema subtilissimum	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0
Anabaena flos-aquae	0	1	0	0	0	0	0	0	0	1	0	1	0	0	1	1	0	1	0
Aphanizomenon flos-aquae	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	1	0
Aphanizomenon issatschenkoi	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	1	0
Chroomonas acuta	0	1	0	0	0	0	0	0	1	0	0	0	1	1	0	1	0	0	0
Cryptomonas rostrata	0	0	0	1	0	0	0	0	1	0	0	0	1	1	0	1	0	0	0
Cryptomonas ovata	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	0	0

Cryptomonas erosa	0	0	0	0	1	0	0	0	1	0	0	0	1	1	0	1	0	0	0
Ceratium hirundinella	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	1	0
Peridiniopsis cunningtonii	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	1	0
Peridiniopsis kevei	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	1	0
Peridiniopsis polonicum	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	1	0
Peridinium bipes	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	1	0
Peridinium cinctum	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	1	0
Peridinium gatunense	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	1	0
Peridinium spp.	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	1	0	0	0
Dinobryon divergens	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	1	0	1	0
Euglena agilis	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Euglena viridis	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Euglena geniculata	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Eutreptia viridis	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0

Phacus alatus	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Phacus caudatus	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Phacus curvicauda	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Phacus longicauda	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Phacus orbicularis	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Lepocinclis acus	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Lepocinclis ovum	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Monomorphina pyrum	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Trachelomonas volvocina	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Trachelomonas volvocinopsis	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Trachelomonas intermedia	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Trachelomonas hispida	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0

Trachelomonas planctonica	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	1	0
Pteromonas cordiformis	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	0	1	0	0
Characium limneticum	0	0	1	0	0	0	0	0	0	1	0	0	1	1	0	0	1	0	0
Carteria klebsii	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	0	1	0	0
Chlamydomonas globosa	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	0	1	0	1
Chlamydomonas ehrenbergii	0	0	0	0	0	1	0	0	0	1	0	0	1	1	0	0	1	0	1
Chlorella vulgaris	0	0	0	0	0	1	0	0	1	0	1	0	1	1	0	0	1	0	0
Phacotus lenticularis	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0	1	0	0
Planctoccus sphaerocystiformis	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0
Planktosphaeria gelatinosa	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0
Eudorina elegans	0	1	0	0	0	0	0	0	0	1	1	0	1	0	0	1	0	0	1

Pandorina morum	0	0	0	0	1	0	0	0	0	1	1	0	1	0	0	1	0	0	1
Sphaerocystis schroeteri	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Dictyosphaerium pulchellum	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Tetraëdron caudatum	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Tetraëdron minimum	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Tetraëdron trigonum	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Treubaria planctonica	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Ankyra lanceolata	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0
Schroederia setigera	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0
Kirchneriella contorta	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Kirchneriella obesa	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Selenastrum bibraianum	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0

Selenastrum minutum	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Ankistrodesmus falcatus	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Ankistrodesmus falcatus var. Mirabilis	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Ankistrodesmus spiralis	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Monoraphidium contortum	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0
Oocystis lacustris	0	0	1	0	0	0	0	0	0	1	1	0	0	1	0	0	1	0	0
Nephrocytium aghardianum	0	0	1	0	0	0	0	0	0	1	1	0	0	1	0	0	1	0	0
Pediastrum boryanum	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	1	0	0
Pediastrum boryanum var. longicorne	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Pediastrum duplex	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Pediastrum simplex	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0

Pediastrum tetras	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Scenedesmus acuminatus	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Scenedesmus arcuatus	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Scenedesmus denticulatus	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Scenedesmus ecornis	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Scenedesmus dimorphus	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Desmodesmus communis	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Desmodesmus armatus	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Desmodesmus invermedius	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Desmodesmus opoliensis	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Desmodesmus abundans	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0

Desmodesmus denticulatus	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Crucigeniella apiculata	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Crucigeniella quadrata	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Crucigenia tetrapedia	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Coelastrum astroideum	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Coelastrum microprum	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Coelastrum reticulatum	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Actinastrum hantzschii	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Lagerheimia ciliata	0	0	0	0	1	0	0	0	0	1	0	0	1	1	0	0	1	0	0
Lagerheimia genevensis	0	1	0	0	0	0	0	0	0	1	0	0	1	1	0	0	1	0	0

Lagerheimia wratislaviensis	0	0	1	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0
Ulothrix sp1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	1	0	1
Ulothrix sptenerrima	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	1
Staurastrum chaetoceras	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1
Eutetramorus fotti	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Tetrastrum glabrum	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Tetrastrum komarekii	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Tetrastrum staurogeniaeforme	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
Actinotaenium cruciferum	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1
Closterium kuetzingii	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1
Closterium venus	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1

Closterium acerosum	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1
Closterium gracile	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1
Closterium nematodes	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1
Cosmarium granatum	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1
Cosmarium reniforme	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1
Staurastrum tetracerum	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	1

Fig A. 1 Nutrients spatiotemporal distribution variations in the Treene river network (abbreviations Tr represent the main stream of Treene, Ki represent the tributary Kielstau, Sa represent the tributary Sankelmark See, Bo represent the tributary Bollingstedter Au, Je represent the tributary Jerrisbek, Ju represent Juebek)

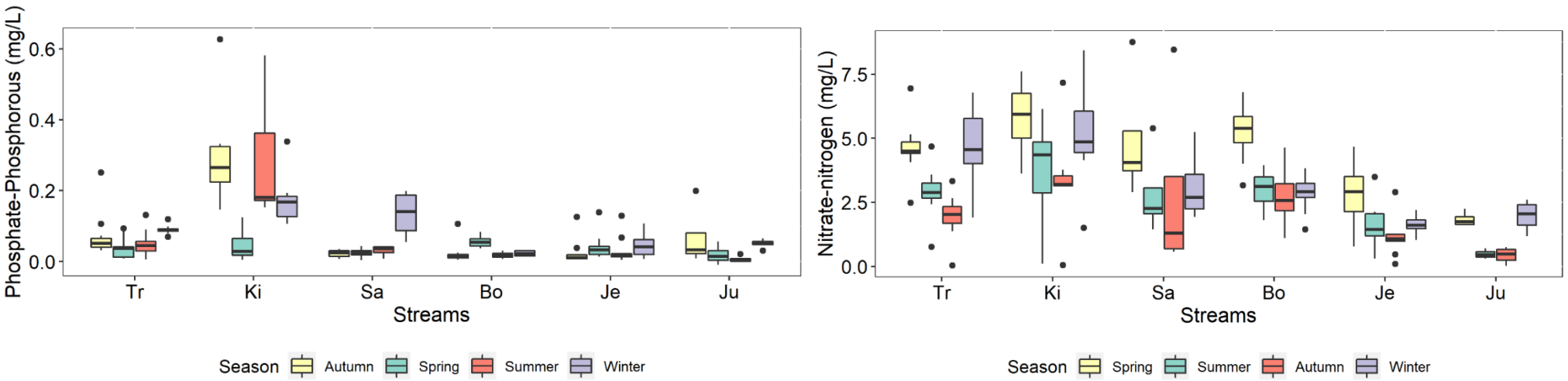


Table A 3 Summary of water physicochemical parameters used in this study

Code	Units	Description	Average	Max	Min
WT	°C	Water temperature	10.57	0.20	19.20
pH	-	Acidic or basic of water	7.83	6.73	9.73
EC	µs/cm	Electrical conductivity	506.80	344.00	740.00
DO	mg/L	Dissolved oxygen	9.39	2.93	19.00
TP	mg/L	Total phosphate	0.22	0.03	1.10
PO4-P	mg/L	Orthophosphate-phosphorus	0.07	0.00	0.63
NH4-N	mg/L	Ammonium-nitrogen	0.27	0.00	2.27
NO3-N	mg/L	Nitrate-nitrogen	3.15	0.02	8.76
NO2-N	mg/L	Nitrite-nitrogen	0.02	0.00	0.22
DIN	mg/L	Dissolved inorganic nitrogen	3.43	0.05	9.33
CL	mg/L	Chloride	27.37	13.56	41.71
SO4	mg/L	Sulfate	39.06	10.32	107.64
TSP	mg/L	Total suspended solids	12.15	0	87.88

Fig A. 2 Water flow (intraday flow on the sampling day) spatiotemporal variations in the Treene river network

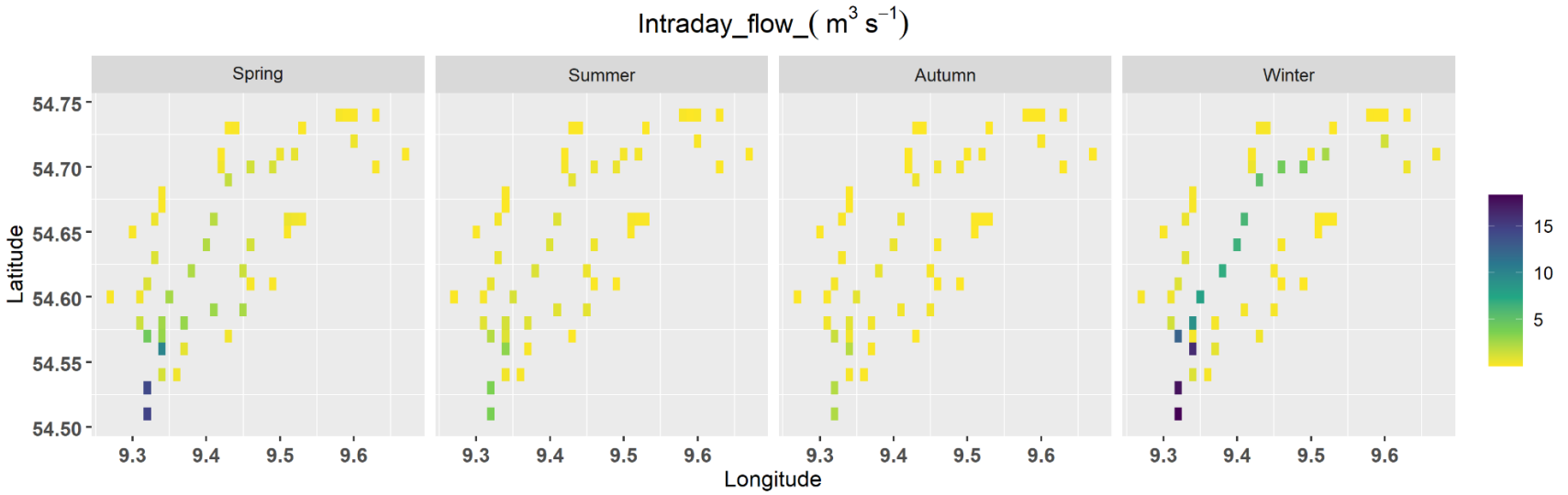


Table A. 4 Description of the hydrological indices used in this study

Code	Hydrologic index	Definition
	Magnitude of flow events	
H01	Intraday flows (m^3/s)	Intraday flows
H02	the first day before (m^3/s)	Flows from the first day before the sampling day
H03	the second day before (m^3/s)	Flows from the second day before the sampling day
H04	The third day before (m^3/s)	Flows from the third day before the sampling day
H05	The fourth day before (m^3/s)	Flows from the fourth day before the sampling day
H06	Mean flows in 3 days (m^3/s)	Mean flow in 3 days (including the sampling day)
H07	Mean flows of 3 days before (m^3/s)	Mean flows of 3 days before (not including the sampling day)
H08	Median flows in 3 days (m^3/s)	Median flows in 3 days (including the sampling day)
H09	Median flows of 3 days before (m^3/s)	Median flows of 3 days before (not including the sampling day)
H10	Variability in 3 days flows	Coefficient of variation in 3 days flows (including the sampling day)
H11	Variability flows of 3 days before	Coefficient of variation flows of 3 days before (not including the sampling day)
H12	Skewness in 3 days flows	(Mean flow in 3 days-median flow in 3 days)/median flow in 3 days
H13	Skewness of 3 days before	(Mean flow of 3 days before-median flow of 3 days before)/median flow of 3 days before
H14	Mean in 7 days flows (m^3/s)	Mean flows in 7 days (including the sampling day)
H15	Mean flows of 7 days before (m^3/s)	Mean flows of 7 days before (not including the sampling day)
H16	Median in 7 days flows (m^3/s)	Median flows in 7 days (including the sampling day)
H17	Median flows of 7 days before (m^3/s)	Median flows of 7 days before (not including the sampling day)
H18	Variability in 7 days flows	Coefficient of variation in 7 days flows (including the sampling day)
H19	Variability flows of 7 days before	Coefficient of variation of 7 days before (not including the sampling day)
H20	Skewness in 7 days flows	(Mean flow in 7 days-median flow in 7 days)/median flow in 7 days
H21	Skewness of 7 days before	(Mean flow of 7 days before-median flow of 7 days before)/median flow of 7 days before
H22	Mean in 14 days flows (m^3/s)	Mean flows in 14 days (including the sampling day)
H23	Mean flows of 14 days before (m^3/s)	Mean flows of 14 days before (not including the sampling day)
H24	Median in 14 days flows (m^3/s)	Median flows in 14 days (including the sampling day)
H25	Median flows of 14 days before (m^3/s)	Median flows of 14 days before (not including the sampling day)
H26	Variability in 14 days flows	Coefficient of variation in 14 days flows (including the sampling day)
H27	Variability flows of 14 days before	Coefficient of variation of 14 days before (not including the sampling day)

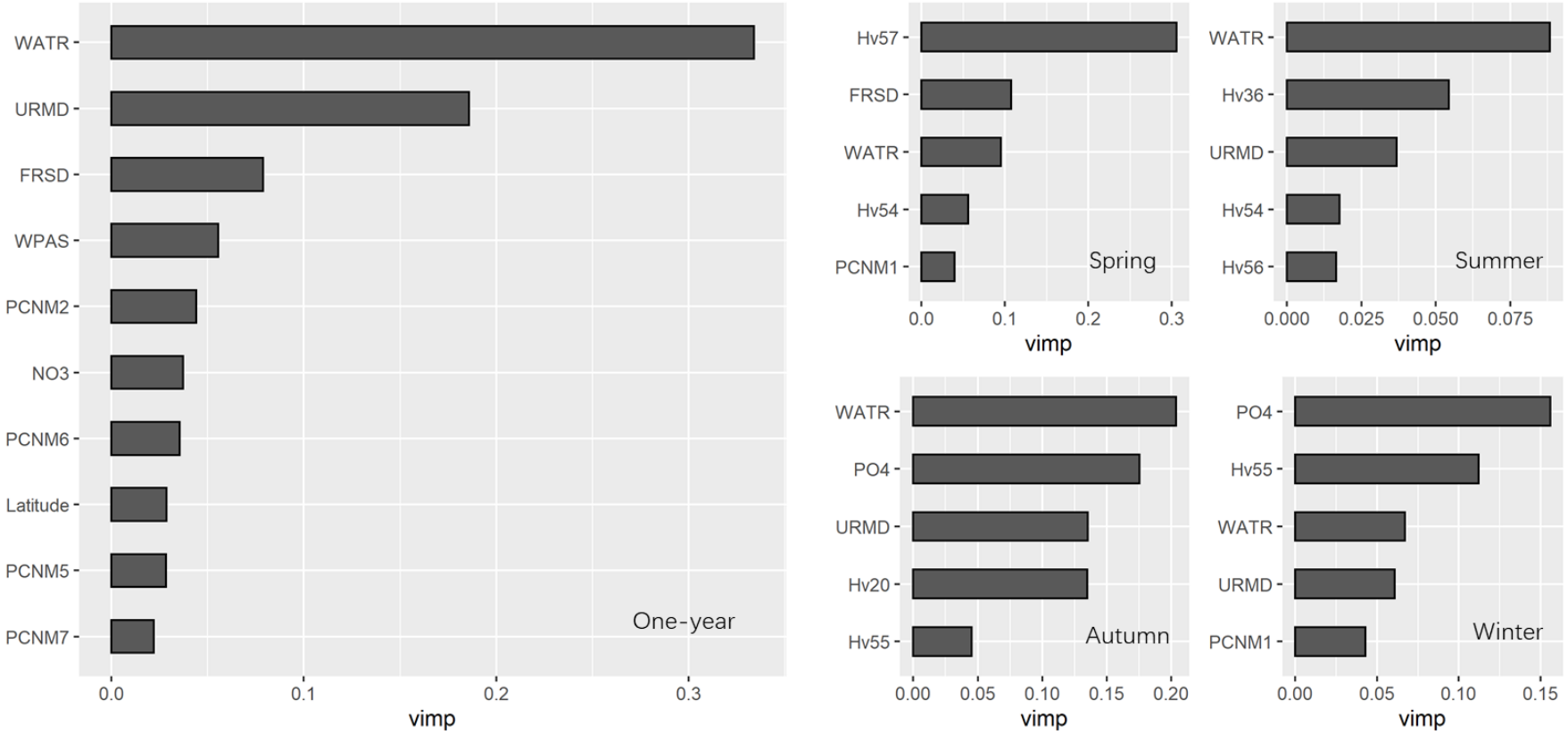
H28	Skewness in 14 days flows	(Mean flow in 14 days-median flow in 14 days)/median flow in 14 days
H29	Skewness of 14 days before	(Mean flow of 14 days before-median flow of 14 days before)/median flow of 14 days before
H30	Mean flows in 30 days (m^3/s)	Mean flows in 30 days (including the sampling day)
H31	Mean flows of 30 days before (m^3/s)	Mean flows of 30 days before (not including the sampling day)
H32	Median flows in 30 days (m^3/s)	Median flows in 30 days (including the sampling day)
H33	Median flows of 30 days before (m^3/s)	Median flows of 30 days before (not including the sampling day)
H34	Variability in 30 days flows	Coefficient of variation in 30 days flows (including the sampling day)
H35	Variability flows of 30 days before	Coefficient of variation of 30 days before (not including the sampling day)
H36	Skewness in 30 days flows	(Mean flow in 30 days-median flow in 30 days)/median flow in 30 days
H37	Skewness of 30 days before	(Mean flow of 30 days before-median flow of 30 days before)/median flow of 30 days before
	Frequency of flow events	
H38	Low flood pulse count 3 days (d)	Number of occurrences during 3 days which the magnitude of flow remains below a lower threshold. Low flow pulses are defined as the number of days in which the flow drops below the 25^{th} percentile (low pulse) of all daily values for the time period (2010-2016).
H39	Low flood pulse count 7 days (d)	Number of occurrences during 7 days which the magnitude of flow remains below a lower threshold.
H40	Low flood pulse count 14 days (d)	Number of occurrences during 14 days which the magnitude of flow remains below a lower threshold.
H41	Low flood pulse count 30 days (d)	Number of occurrences during 30 days which the magnitude of flow remains below a lower threshold.
H42	High flood pulse count 3 days (d)	Number of occurrences during 3 days which the magnitude of flow remains above a higher threshold. High flood pulses are defined as the number of days in which the flow rises above the 75th percentile (high pulse) of all daily values for the time period (2010-2016).
H43	High flood pulse count 7 days (d)	Number of occurrences during 7 days which the magnitude of flow remains above a higher threshold.
H44	High flood pulse count 14 days (d)	Number of occurrences during 14 days which the magnitude of flow remains above a higher threshold.
H45	High flood pulse count 30 days (d)	Number of occurrences during 30 days which the magnitude of flow remains above a higher threshold.
H46	Low flood pulse count 3 days (%)	The percentage of low flood pulse count in 3 days, which means H38 divide 3.
H47	Low flood pulse count 7 days (%)	The percentage of low flood pulse count in 7 days, which means H39 Divide 7.

H48	Low flood pulse count 14 days (%)	The percentage of low flood pulse count in 14 days, which means H40 Divide 14.
H49	Low flood pulse count 30 days (%)	The percentage of low flood pulse count in 30 days, which means H41 Divide 30.
H50	High flood pulse count 3 days (%)	The percentage of high flood pulse count in 3 days, which means H42 divide 3.
H51	High flood pulse count 7 days (%)	The percentage of high flood pulse count in 7 days, which means H43 divide 7.
H52	High flood pulse count 14 days (%)	The percentage of high flood pulse count in 14 days, which means H44 divide 14.
H53	High flood pulse count 30 days (%)	The percentage of high flood pulse count in 30 days, which means H45 divide 30.
	Rate of change in flow events	
H54	Rate of change 3 days	Mean rate of changes in flow from 1st day to the 3rd day
H55	Rate of change 7 days	Mean rate of changes in flow from 1st day to the 7th day
H56	Rate of change 14 days	Mean rate of changes in flow from 1st day to the 14th day
H57	Rate of change 30 days	Mean rate of changes in flow from 1st day to the 30th day
	In situ measurement	
WIDTH	River width (m)	River width measured *in situ* at the sampling point
DEPTH	River depth (m)	River depth measured *in situ* at the sampling point
VELOCITY	Flow velocity (m/s)	Flow velocity measured *in situ* at the sampling point

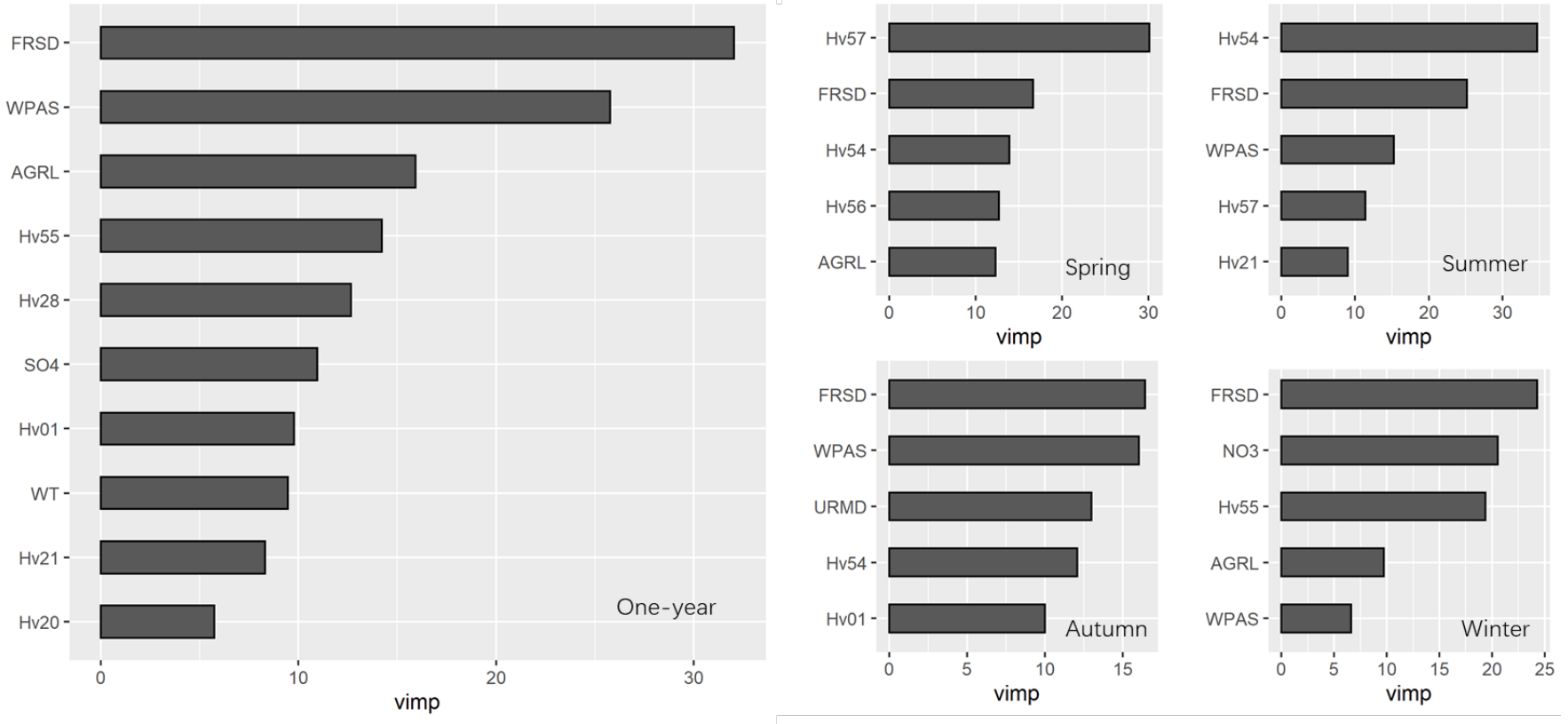
Table A. 5 Summary of land use variables used in this study

Code	Units	Description	Average	Min	Max
AGRL	%	Agricultural land - generic	52.68	15.04	79.65
FRSD	%	Deciduous forest	2.05	0.01	6.68
FRSE	%	Evergreen forest	0.86	0.04	4.16
FRST	%	Forest mixed	2.48	0.02	13.4
TOFR	%	Total forest	5.38	0.86	14.95
RNGE	%	Rangeland	0.75	0.00	4.33
UIDU	%	Industrial	4.27	2.98	8.41
URLD	%	Residential - low density	0.39	0.00	1.76
URMD	%	Residential – medium density	5.27	2.65	9.79
WATR	%	Water	1.80	0.66	5.42
WETL	%	Wetlands	0.98	0.00	7.19
WPAS	%	Winter pasture	28.48	7.22	70.97

Abundance (log-transferred)



Species richness



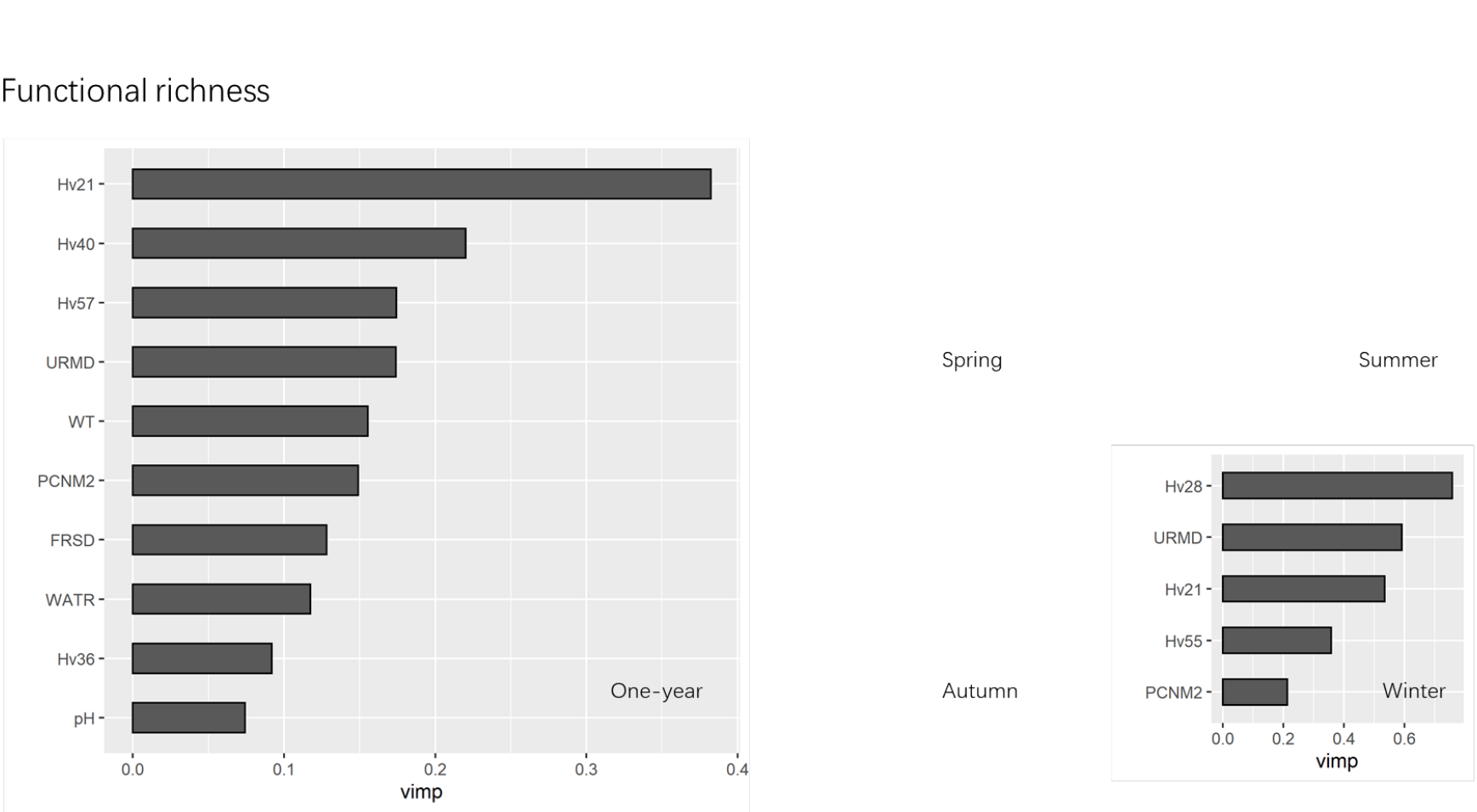
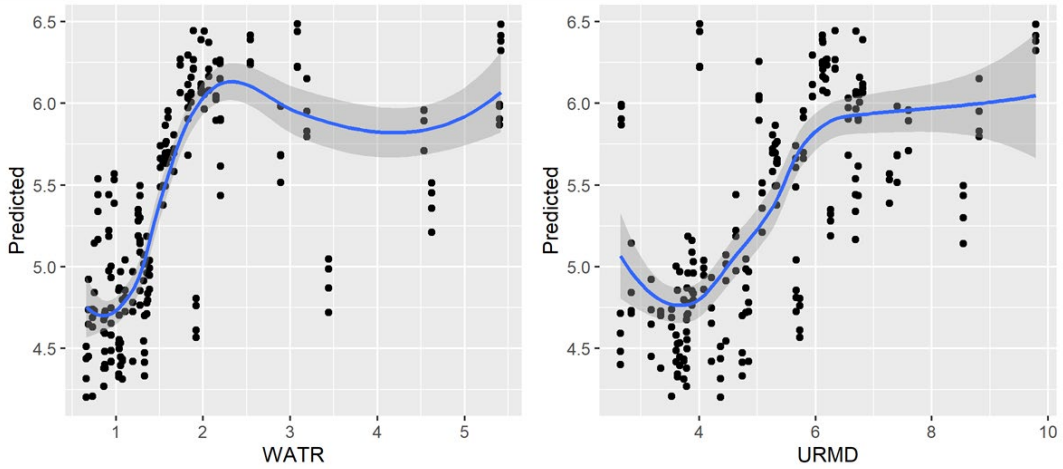
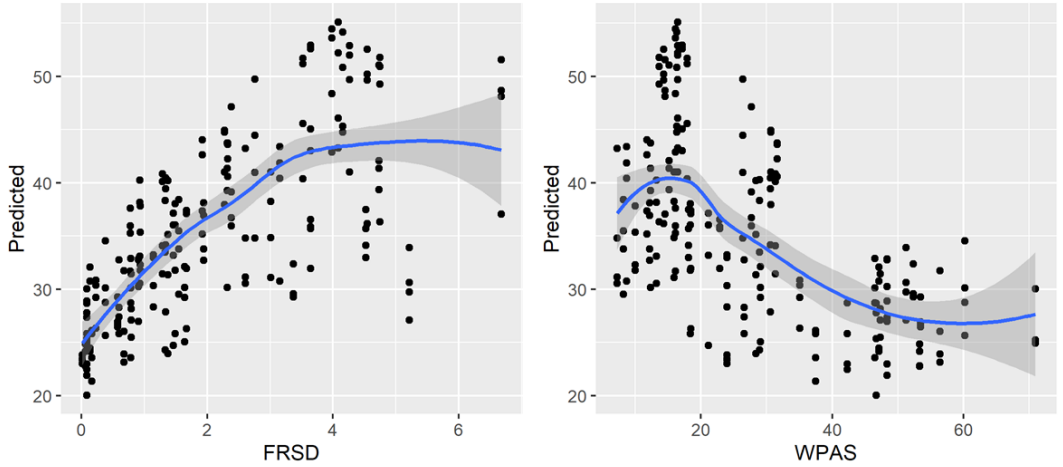


Fig. A. 3 Bar chart ordered by parameters' importance for log-transferred abundance, species richness and functional richness Random Forest model. Large numbers of the variable importance indicate a high predictive capacity of a variable, the top 10 predictors for the one-year model, and top 5 predictors for the seasonal models. The response of functional richness in spring, summer and autumn models have limited unique value for establishing reliable regression model. Abbreviations showing in the figure can be found at Appendix_2 in Table A. 3, Table A. 4 and Table A. 5.

Abundance (log-transferred)



Species richness



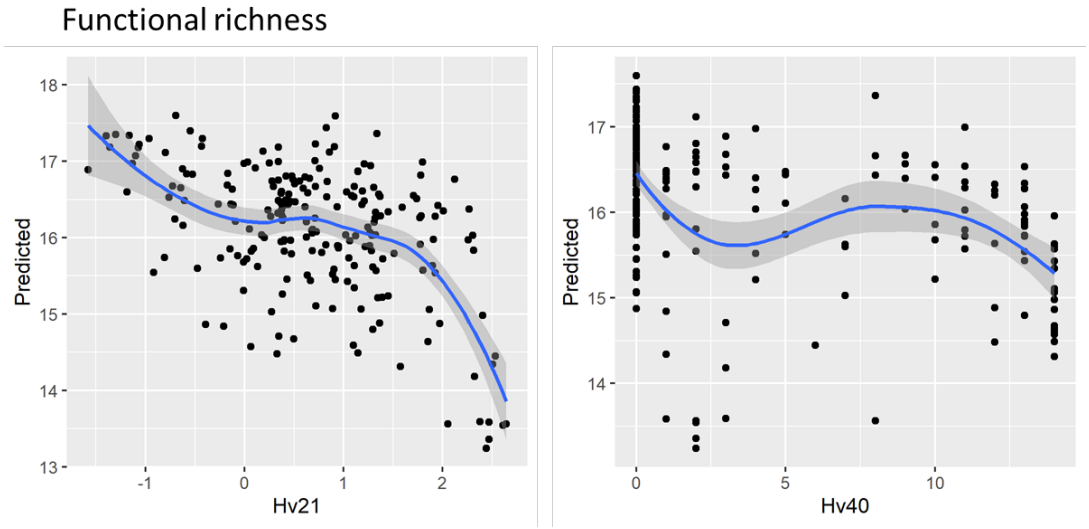


Fig A. 4 Partial dependence plots bason on the one-year random forest models showing the response of log-transferred abundance, species richness and functional richness against their top two predictors, individually. WATR represent for water land cover, URMD for medium density urban land cover, FRSD for deciduous forest, WPAS for winter pasture, Hv21 for skewness of 7 days before, Hv40 for low flood pulse count 14 days.