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## Unravelling the effect of flow regime on macroinvertebrates and benthic algae in regulated versus unregulated streams

Short title: Effects of flow regime on macroinvertebrates and benthic algae

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## Supplementary information

A more detailed description of the methodology, including fully documented code for the statistical analysis, is available online here.

## Keywords

River; hydrology; periphyton; macrozoobenthos; flow variability; cyanobacteria; Indicators of Hydrological Alteration;


#### Abstract

Variability in riverine flow regimes is important for aquatic biodiversity. However, across the globe, management of water resources has altered natural flow dynamics. We explored relationships between flow regime (calculated from three years' daily averaged discharge), and water chemistry, benthic algae, as well as macroinvertebrate datasets from 64 sites across Germany and Norway. To deal with multicollinearity while maintaining interpretability, we performed principal component (PC) analyses for each dataset in each country, and selected the metric with the highest absolute loading on each PC to represent that PC. We then used L1regularised (lasso) regression to link differences in water chemistry and hydrology to differences in ecology, and compared this approach to the more popular best-subsets ordinary least squares (OLS) regression. The results obtained using lasso regression were broadly comparable to those produced by bestsubsets OLS, but the lasso approach "rejected" more models than the best-subsets approach. When lasso identified a plausible model, it was the same or similar to the best model found by best-subsets OLS. The lasso method was more "discerning", i.e. it identified a smaller number of potentially interesting models, while best-subsets regression seemed to find "too many" relationships. We identified two response variables that were potentially affected by regulation: (i) river regulation may lead to higher cyanobacterial abundance, possibly via a less variable flow regime; (ii) reduced flow variability may lead to a reduced proportion of grazers and scrapers, possibly indicating a shift towards an increased importance of heterotrophic energy sources in ecosystems with less variable flows.


## 1. Introduction

Natural variability in riverine flow regimes maintains ecological gradients, impacting aquatic biodiversity (Poff et al., 2007; Richter et al., 1997; Schneider and Petrin, 2017). However, exploitation of freshwater resources such as industrial abstractions, hydropower generation and drinking water supply has significantly altered natural flow dynamics across the globe (Poff et al., 2007). $37 \%$ of European rivers are affected by flow regulation (www.ecologic.eu/11663) and, in Norway, where hydropower provides $>95 \%$ of the total electricity generated, more than two-thirds of river basins are affected by hydromorphological alteration (www.nve.no). Understanding the effects of flow alteration on aquatic ecology is crucial for the sustainable management of regulated river systems, but linking indicators of hydrological change to ecology is not straightforward because (1) properly replicated and controlled experiments are rarely possible in practice in fluvial ecosystems (Richter et al., 1997), (2) species assemblages in experimental flumes often differ from the assemblages in adjacent watercourses, raising questions on the relevance of flume experiments (Bækkelie et al., 2017), and (3) field data may reflect the effects of correlated variables rather than the effects of the variables of interest.

The "natural flow paradigm" (Poff et al., 1997) provides a rationale for linking hydrological indicators (HIs) to ecological responses, and a range of HIs have been proposed for assessing the extent of ecohydrological change. Olden \& Poff (2003) conducted a comparison of more than 170 flow-derived metrics and concluded that the suite of indices commonly referred to as the "Indicators of Hydrological Alteration" (IHA; Richter et al., 1996) typically provide an adequate summary of the overall flow regime. The IHA methodology defines 33 statistics in five broad classes, and the approach has been widely applied to characterise compensation flows that mimic the natural regime. However, in the context of linking HIs to ecological datasets, multicollinearity between the IHA variables usually necessitates dimensionality reduction (Olden and Poff, 2003; Yang et al., 2008). A simpler approach is the "ecochange" concept proposed by Vogel et al. (2007), in which hydrological alteration is estimated from the difference between "before" and "after" flow duration curves. Gao et al. (2009) demonstrated that this method provides an effective summary of the IHA output without multicollinearity issues, but it is only applicable to study designs where flow data are available both before and after some well-defined intervention (such as building a dam).

Although many studies focus on developing indicators of hydrological change, comparatively few establish convincing links between these metrics and measures of ecological health/resilience. In the presence of strong multicollinearity, common pre-processing approaches for linking hydrological and ecological variables include using PCA or (Non-)Metric (Multi-)Dimensional Scaling (NMDS) to identify relevant subsets of explanatory variables from an initial broader suite, followed by regression analysis to identify potentially interesting relationships: Monk et al. (2007) used PCA followed by stepwise linear regression to investigate relationships between around 200 HIs and macroinvertebrate metrics at 83 locations in England and Wales; Yang et al. (2008) used a genetic programming approach to perform variable selection and identify significant relationships between time series of fish species diversity and the IHA parameters calculated for a catchment in Illinois, USA; and Schneider and Petrin (2017) used NMDS and stepwise regression to link hydrology and water chemistry variables to benthic algae and macroinvertebrate assemblages at 40 sites in Norway.

Here, we explored relationships between hydrology, water chemistry, benthic algae and macroinvertebrate datasets collated for 64 sites across Germany and Norway. We use two independent datasets collected in two countries to identify potentially causal relationships between regulation/hydrology and aquatic biota. We used the approach of Richter et al. (1996) to develop an initial set of HIs, which were then distilled to a more informative subset following the recommendations of Olden and Poff (2003) and Gao et al. (2009). We expected (1) ecological and (2) hydrochemical \& hydrological differences between regulated and unregulated streams, and we hypothesized (3) that the hydrochemical and hydrological differences may plausibly explain the ecological differences.

When testing hypothesis 3 , we avoided using stepwise or "best-subsets" regression techniques - despite their popularity in the literature - because in cases where significance testing is of interest these methods have been criticised for "overfitting" the data, leading to inflated estimates of significance (Harrell, 2001). Instead, we present an alternative approach using L1regularised (lasso) regression with qualitative analysis of the "lasso path", which we believe is both more robust and more informative than iterative variable selection procedures. Results obtained using "best-subsets" regression are included for comparison.

## 2. Methodology

### 2.1 Site locations

Data were collected from 64 sites (Fig. 1), half of which were classified as "regulated" i.e. they had an anthropogenically modified flow regime. 24 sites ( 12 regulated) were in Western Germany and the remaining 40 ( 20 regulated) in Southern Norway. The study sites were selected to be located close to flow gauging stations, such that daily average flow measurements were available. River regulation is a multifaceted term, and our dataset comprises "minimum discharge" sites (those from which freshwater is abstracted and bypasses the river), sites downstream from outlets of hydropower plants, and sites downstream from dams and weirs.

The German sites were small and medium sized siliceous mountain streams in the state of North Rhine-Westphalia. Elevations ranged from 50 to 350 m a.s.l. and the median drainage area was $147 \mathrm{~km}^{2}$ (range: 11 to $800 \mathrm{~km}^{2}$ ). Land cover comprised mostly deciduous forest dominating the hillslopes with settlements and agricultural areas at lower elevations and along valley floors. The geology was siliceous, with precipitation ranging from 800 to $1600 \mathrm{~mm} / \mathrm{yr}$.

The median drainage area of the Norwegian sites was $375 \mathrm{~km}^{2}$ (range: 7 to $2335 \mathrm{~km}^{2}$ ). Elevations ranged from 15 to 990 m a.s.l. and land cover from alpine mats to largely coniferous forest, as well as settlements and agricultural areas along valley floors. The geology was siliceous and average precipitation ranged from 600 to $3500 \mathrm{~mm} / \mathrm{yr}$.

### 2.2 Ecological data

Benthic algae and macroinvertebrate surveys were conducted at all 64 sites. The German data originated from national monitoring surveys during late summers and autumns between 2006
and 2012. In Norway, fieldwork took place during September 2013, and samples were taken as close as possible to the respective hydrological gauging stations. The distance between sampling points and gauging stations was $<5 \mathrm{~km}$ in Germany and $<1 \mathrm{~km}$ in Norway, and the differences in drainage area between sampling sites and gauging stations was $<10 \%$.

## Benthic algae

Samples of soft-bodied benthic algae (defined as algae, attached to the river bottom or in close contact on or within patches of attached aquatic plants, including cyanobacteria but excluding diatoms) were taken according to European standard procedures (EN 15708:2009) along an approximately 10 m length of river bottom using an "aquascope" (a bucket with a transparent bottom). Diatoms were not included due to the great differences in methodology for sample preparation and enumeration between diatom and non-diatom benthic algae. In Germany, a 5level scale was used to record abundance of benthic algae at each site: 1 , microscopically rare; 2 , microscopically abundant; 3 , maximum $5 \%$ cover; $4,5 \%$ to $33 \%$ cover; 5 , more than $33 \%$ cover. In Norway, percentage cover of each form of macroscopically visible benthic algae was recorded, and the abundance of each microscopic taxon was estimated in the laboratory as "rare", "common" or "abundant". To enable comparative data analysis, we translated the cover data recorded in Norway into the 5 -level scale used in Germany. All samples were examined under a microscope and all non-diatom algae identified to species, wherever possible. For some genera of filamentous green algae, whose vegetative forms cannot be determined to species level (e.g. Spirogyra Link or Mougeotia C. Agardh), categories based mainly on filament width were used.

Prior to analysis, the taxonomic levels were harmonized between German and Norwegian datasets. From the harmonised dataset, we calculated overall taxon richness, as well as richness of the most abundant algal groups, i.e. red algae, green algae, and cyanobacteria (Table 1). We approximated total benthic algal abundance at each site by summarising the cubed 5-level values for each taxon. This was done because the 5 -level scale used for abundance estimation of benthic algae in Germany is non-linear. Using cubed 5-level values for total abundance is a method commonly used for submerged macrophytes (Melzer, 1999) and is regarded as the "best possible" approximation for comparing abundances among algal groups and among sites. Other response variables were calculated (e.g. cover of Phormidium sp., cover of cyanobacteria with heterocysts, eutrophication indices used for ecological status assessment, etc.), but omitted from further analysis since they either showed little variation, co-varied with other response variables, or were inapplicable in one of the countries.

## Macroinvertebrates

In Germany, the multi-habitat sampling procedure was applied. Benthic invertebrates were collected from a total of 20 sample units from representative substrates (i.e. those covering more than $5 \%$ of the sample reach). Each sampling unit had a size of $25 \times 25 \mathrm{~cm}$ (resulting in $1.25 \mathrm{~m}^{2}$ of stream bottom being sampled), and was sampled by means of kick sampling. At each site in Norway, macroinvertebrates were collected in ten replicates using a Surber net (sampling area $0.1 \mathrm{~m}^{2}$; mesh size $500 \mu \mathrm{~m}$ ). The substrate mainly consisted of gravel, pebbles,
cobbles or small boulders, that were agitated to a depth of $\sim 10 \mathrm{~cm}$ for one minute during sampling. All samples were immediately preserved in 70\% ethanol for later analysis.

In the laboratory, samples were sorted using a $500 \mu \mathrm{~m}$ sieve and the macroinvertebrates classified to the lowest possible taxonomic level, usually species. In Germany, macroinvertebrate identification was performed to the level of the Operational Taxalist (http://www.fliessgewaesserbewertung.de/en/download/bestimmung/), which means most taxa were identified to species, but with genus level for certain Plecoptera and Trichoptera, family level for Oligochaeta, and from genus to subfamily level for Diptera. In Norway, some dipteran taxa and microcaddisflies (Hydroptilidae) could only be identified to genus. In addition, bryozoans, nematodes, oligochaetes, water mites, cladocerans, ostracods, non-biting midges and blackflies were not identified any further. Prior to data analysis, taxonomic levels were harmonized between the German and Norwegian datasets.

We calculated common bioassessment indices and abundance ratios of functional feeding groups (FFG) of macroinvertebrates using ASTERICS (www.fliessgewaesserbewertung.de/; Table 1). FFGs are used to characterize ecosystem attributes such as the relative importance of autotrophic and heterotrophic organic carbon as the basis of the food web (Doledec et al., 2015).

### 2.3. Water chemistry

In Germany, water samples were taken within one month of biological sampling, while in Norway, water samples were taken together with the biological samples. At four German sites, there was a considerable time gap between the dates of macroinvertebrate surveys and the collection of hydrochemical samples. The corresponding sites were therefore removed from the macroinvertebrate dataset, leaving 64 sites for benthic algae and 60 for macroinvertebrates. Water chemistry was analysed at accredited laboratories using the following national standard procedures (Norway/Germany): total organic carbon (TOC; NS/DIN EN 1484), Total phosphorus (TP; NS/DIN EN ISO 15681-2), and Total nitrogen (TN; NS 4743/ DIN 38409 H 28 ). In addition, pH and conductivity were measured in both countries using handheld instruments.

### 2.4. Hydrological indices

Near-complete time series of average daily flow were available for all locations for a period of three years prior to sampling. Beyond three years, some of the discharge records had substantial data gaps, so the three-year period prior to sampling was chosen to represent medium-term hydrological conditions at each watercourse. Three years seem an appropriate time frame for our analysis because macroinvertebrates and benthic algae may rapidly recolonize a stream site after an extreme event (Power et al., 2013). Consequently, older records of river flow are increasingly unlikely to have persistent effects on present day macroinvertebrate and benthic algal composition.

Small data gaps in each series, up to a maximum of 7 days in length, were filled using linear interpolation (because we had no indications of extreme events during these short periods), and
a suite of 62 HIs were calculated from the daily flow values at each location (Table 2). Selection of HIs was initially based on the 33 IHA metrics defined by Richter et al. (1996), but modified to produce a single statistic for each variable for the entire three-year period. For example, rather than using the Julian date of each annual maximum to represent the timing of extreme events (as per Richter et al.), we calculated the number of days prior to sampling to the maximum flow in the series (and also to the last point when flows exceeded the $95^{\text {th }}$ percentile).

Exploratory analysis of the modified set of IHA metrics revealed that some variables exhibited very little variation in our dataset. In addition, previous analysis of the Norwegian data found that important predictors included metrics representing flow ranges, as well as indices of monthly maxima and minima (Schneider and Petrin, 2017). This finding was broadly consistent with the work of Olden and Poff (2003), who noted that the IHA methodology often fails to adequately quantify the magnitude of extreme flow conditions. We therefore expanded the set of HIs in our analysis to include monthly minimum and maximum discharges, together with a number of overall indices of flow variability, such as the coefficient of variation (CV), the interquartile range (IQR) and the 90 -percentile-range (Table 2).

### 2.5. Analysis procedure

The workflow for the analysis is summarised below and described in detail in Appendices A1A4. Data processing was performed using Python 2.7 (Python Software Foundation, 2016) and all code is available in the Supplementary Information.

1. Define hydrological regimes and stratify the dataset
2. Use dimensionality reduction to ameliorate collinearity among variables, separately for each dataset (benthic algae, macroinvertebrates, water chemistry, hydrology) and each country (Norway, Germany); identify subsets of variables that broadly represent overall variability in each dataset
3. Test hypotheses 1 and 2 by comparing the metrics selected in step 2 at regulated versus unregulated sites
4. Use regression techniques on the variables showing substantial differences in step 3 to quantify relationships between hydrology, water chemistry and biota (hypothesis 3 ), and interpret their ecological significance

Germany and Norway have different climates and hydrological regimes (Appendix A1). German sites are characterised by high autumn and winter flows generally declining throughout the summer. In contrast, Norwegian sites are heavily influenced by snow accumulation and melting processes, typified by low flows during the winter and peak discharges during May and June. A number of previous studies (Monk et al., 2007; Olden and Poff, 2003) found that the most representative hydrological metrics vary according to stream type. For this reason, we began by performing separate analyses on the German and Norwegian datasets before analysing the pooled data (to create an analysis with greater statistical power). We regard the occurrence of similar relationships in the Norwegian, German and pooled datasets as particularly interesting, as they increase the weight of evidence.

## Dimensionality reduction

The set of calculated metrics comprised two binary categorical variables (Germany/Norway; regulated/unregulated) and almost 100 continuous variables ( 62 HIs , 23 macroinvertebrate metrics, 8 benthic algae metrics and 5 water chemistry variables), many of which are similar in nature (e.g. maxima, minima, and percentiles of flow). Exploratory data analysis using pairwise correlation matrices revealed substantial multicollinearity, which was reduced using the PCA algorithm in Scikit-Learn (v0.18.1; Pedregosa et al., 2011) to identify a smaller set of near-orthogonal variables capable of explaining most of the variance. Olden and Poff (2003) suggested PCA as a pragmatic method for variable selection in the context of eco-hydrological data analyses. One disadvantage, however, is that linear combinations of the input variables can become difficult to interpret in a meaningful way. We therefore followed the approach of Gao et al. (2009) by choosing the metric with the highest absolute loading on each principal component (PC) to represent that PC. In cases where several metrics had approximately the same maximum loading, all candidate variables were carried forward for further analysis (such variables are marked in brackets in Table 3). This method has the advantage of retaining meaningful variables and facilitating interpretation, while also reducing multicollinearity. Note, however, that collinearity is not eliminated completely, because the selected variables for each PC are no longer orthogonal.

We use the Kaiser-Guttman criterion (KGC; Gao et al., 2009) to decide how many PCs to keep. The KGC recommends keeping all components with eigenvalues greater than 1, which in the analysis presented here typically selects between 3 and 10 PCs , explaining around $80-90 \%$ of the overall variance. Variables were first standardized by subtracting the mean and dividing by the standard deviation, and separate PCAs were applied to each of the four datasets (benthic algae, macroinvertebrates, water chemistry, hydrology) in each country. Further details are provided in Appendix A2.

## Tests for differences

The metrics selected by PCA were tested to explore statistical differences between regulated and unregulated sites using a robust Bayesian approach (Kruschke, 2012) implemented using the PyMC3 package (v3.0; Salvatier et al., 2016). A detailed explanation is provided in Appendix A3. Within a Bayesian framework, probabilities are interpreted as "degrees of belief", so our approach permits statements such as (for example), "given our data, there is $85 \%$ probability that regulated sites in Norway have a higher macroinvertebrate abundance than unregulated sites".

## Regularised multiple linear regression

The 64 sites comprising our dataset encompassed a range of regulation and also a variety of natural flow regimes, so there may be no clear-cut distinction between regimes at "regulated" and "unregulated" sites. As well as analysing differences between regulated and unregulated sites, we therefore also analysed the dataset as a continuous spectrum of hydrological regimes, rather than making a binary classification, in order to better understand the relationships between variables.

The regression analysis considered the same set of response and explanatory variables for both countries, as this makes it possible to directly compare models between countries, and to estimate combined models based on the "pooled" data from both countries. The set of response and explanatory variables included all those showing substantial differences between regulated and unregulated sites in either country (i.e. the union of the variables for Norway and Germany shown in Table 4).

Despite dimensionality reduction using PCA, the number of combinations of response and explanatory variables under consideration was still large. Previous studies (e.g. Monk et al., 2007; Schneider and Petrin, 2017) applied stepwise or best-subsets regression in this situation, but these techniques are problematic when significance testing is of interest (Harrell, 2001). We therefore used the more robust approach of lasso regression (Hastie et al., 2009), using standardized data to identify the most important relationships between ecological (response) and explanatory variables. A detailed explanation of this method is given in Appendix A4. The lasso can easily be used to assess which predictors are important in the model, but estimating the strength of the relationships (i.e. the model coefficients) is more difficult. One pragmatic solution is to use the lasso to identify the best model (or a small number of candidate models), and then use OLS regression with the unstandardized data to estimate the coefficients directly in the original data units (Hastie et al., 2009). This is the approach adopted here.

Finally, for purposes of comparison, we also applied "best-subsets" regression to identify the best OLS model out of all possible combinations of explanatory variables (judged according to the Bayesian Information Criterion; BIC). This method is computationally intensive and prone to "overfitting", but it is nevertheless widely used and therefore offers an interesting contrast to the lasso.

All regression analyses were carried out separately for each country. In addition, datasets were "pooled" and additional analyses of the combined Norwegian and German data carried out. Individually, the ecological, chemical, and hydrological gradients in each country may be small, whereas in the combined dataset they were larger. The combined analyses therefore made it easier to constrain regression relationships, albeit with the caveat that additional complications were introduced by combining measurements from two different hydrological regimes, and by introducing a possible "country effect". However, if similar relationships occurred in the Norwegian, German and combined dataset, that strengthened the significance of the findings.

## 3. Results

### 3.1. Differences between regulated and unregulated sites

Table 3 summarizes the variables with the strongest gradients in each dataset and each country. See Appendix A2 and the online code repository for further details of the PCA procedure.

Each of the variables listed in Table 3 was tested for differences between regulated and unregulated sites using a Bayesian approach (Table 4; see Appendix A3 and the online code
repository for further details). Table 4 only includes metrics with a posterior probability of a difference between regulated and unregulated sites assessed to be worthy of further investigation: cases where posterior probabilities of differences were small ( $<75 \%$ ), or the model diagnostics indicated problems with the assumptions (based on the posterior predictive check - see Appendix A3) were disregarded.

Consistent differences between regulated and unregulated sites in both countries included (1) the higher abundance of cyanobacteria, (2) the slightly higher German saprobic index, (3) the higher mean flow, (4) the lower coefficient of variation in flow regime and (5) the slightly higher total nitrogen concentration at regulated than unregulated sites.

The observed differences in biota between regulated and unregulated sites (Table 4) may reflect coincidence, river regulation, or a causal relationship with a co-variate. Our data cannot differentiate among these. To gain a more detailed understanding of the relationships between response and explanatory variables, we used lasso regression.

### 3.2. Regression analysis

We summarised the results of the OLS analysis obtained for the best lasso model and compared them with results from a "best-subsets" approach, separately for the Norwegian, German and combined datasets (Table 5; see Appendix A4 and the online code repository for further details). The same sets of response and explanatory variables were used in both countries (i.e. all variables in Table 3) to facilitate model comparison.

The positive relationship between the coefficient of variation of flows (CV) and the proportion of grazers and scrapers consistently occurred in the Norwegian, German and combined datasets. In both, Germany and Norway, a $10 \%$ decrease in flow variability was associated with a $1.3 \%$ to $2 \%$ decrease in the proportion of grazers and scrapers (Fig. 2, Table 5). A similar result was also achieved with OLS "best-subset" regression, although in the Norwegian dataset the best model was achieved using December maximum flow and the number of flow reversals per year, instead of CV (Table 5).

Using the best-subset approach, three more relationships consistently occurred in the German, Norwegian and combined datasets: the German saprobic index, Shannon-Wiener diversity, and the proportion of swimmers and divers were significantly related to flow variables (Table 5). However, for the German saprobic index, explanatory variables differed between Norway and Germany (Table 5), rendering the relationship unreliable. For the proportion of swimmers and divers, the number of high pulses consistently occurred in all three datasets, but with different signs (positive in Germany and negative in Norway), also rendering the relationship unreliable. However, a high October maximum flow was consistently associated with a higher macroinvertebrate diversity in the German, Norwegian and combined datasets (Table 5).

All other relationships were either unexplained in one country (no model performed significantly better than the null model), weakly explained, or inconsistent between countries. Since we did not want to overinterpret our data, we only show the results (Table 5), but do not discuss them further, so that other researchers may compare our results with their own data.

## 4. Discussion

We used two independent datasets that were collected in two countries to identify potentially interesting relationships between hydrological regulation and aquatic biota, supposing that the occurrence of similar relationships in Germany and Norway reduces the likelihood that the relationships occurred by chance. We found systematic differences in water chemistry and hydrology between regulated and unregulated streams, regardless of differences in general flow patterns between Norway and Germany (Appendix A1). In both countries, regulated rivers were characterised by a lower coefficient of variation in flow (Table 4), consistent with the expectation that regulated rivers have a more stable flow regime (Poff et al., 2007). Also, regulated rivers were characterized by higher TN concentrations. The reason for this, however, remains unclear, given that river regulation may have ambivalent effects on water chemistry. Hydropower plants usually withdraw hypolimnetic water, where nutrient concentrations are typically higher than at the surface (Kunz et al., 2013), leading to higher nutrient concentrations downstream from the outlets. On the other hand, reservoirs may act as nutrient traps, reducing nutrient concentrations downstream (Kunz et al., 2011). As regulated rivers also had a higher mean flow (Table 4), we suspect that the enhanced TN concentrations may simply reflect river size. We lack data on land use in the catchments, but a larger proportion of agricultural and urban land use further downstream is likely to be associated with higher nitrogen levels in aquatic ecosystems (Schindler, 2006). The higher mean flow at regulated sites is simply related to the fact that many large rivers are regulated today (Poff et al., 2007), so rivers with an unregulated flow regime will mostly be found upstream, where mean flow is low.

Only two biological variables consistently differed between regulated and unregulated sites in both Germany and Norway. The abundance of cyanobacteria and the German saprobic index were higher at regulated sites (Table 4). However, the increase in the German saprobic index was very small, and likely is only indirectly related to regulation through the generally larger size of the regulated rivers: macroinvertebrate assemblages will often shift towards species tolerating higher organic pollution levels along the river continuum (Rosenberg and Resh, 1993). An effect of stream flow on the abundance of cyanobacteria has been shown before (Schneider, 2015) suggesting that the reduced flow variation in regulated rivers (Table 4) may indeed lead to an increase in cyanobacterial abundance. This may be due to reduced scouring in regulated rivers (prolonged periods of high discharge may decrease Phormidium cover, probably due to substrate movement; Schneider, 2015), or indirectly related to higher fine sediment deposition in regulated rivers (Phormidium is able to trap sediment (Aristi et al., 2017), and use phosphorus released from the entrapped sediment (Wood et al., 2015)).

When relating the observed differences in ecology to differences in hydrology and water chemistry, we found that the results obtained using lasso regression were broadly comparable to those produced by the more commonly used best-subsets OLS. However, the lasso approach seems more conservative, presumably because the cross-validation procedure employed by lasso provides a more rigorous test for actual predictive power. When lasso does suggest a plausible model, it is usually the same or similar to the best model found by best-subsets OLS. In the context of significance testing, the lasso is statistically more robust and, in addition, consideration of the lasso path (Appendix A4) provides valuable additional insights concerning
the relationships between variables and trade-offs between model complexity and goodness-of-fit. We believe the combined methodology presented here offers a pragmatic approach to variable selection and significance testing that will also perform well using larger datasets (unlike best-subsets or stepwise approaches).

The key pattern in our models was that the proportion of grazers and scrapers increased with a more variable flow regime (Table 5). These results agree with results from flume experiments (Ceola et al. 2013) suggesting that a stochastic flow regime increases grazing rates compared to stable flow conditions, probably due to a larger number of microhabitats with reduced shear stress and hence better foraging conditions for grazers than under constant flow conditions. Doledec et al. (2015) found an increased proportion of grazers following an increase in the daily minimum flow in regulated rivers. Grazers and scrapers feed on periphyton, and a higher proportion of grazers and scrapers therefore suggests a shift towards a more autotrophic basis of the food web (Doledec et al., 2015). Although the relationship between the coefficient of variation in flow and the proportion of grazers and scrapers was not very strong (Table 5), it nevertheless indicated that reduced flow variability may coincide with a shift from an autotrophic towards a more heterotrophic basis of the food web. A reduced proportion of grazers and scrapers in rivers with a less variable flow regime may also contribute to the increased cover of cyanobacteria observed in regulated rivers (because they are less grazed upon).

The best-subset approach also indicated that high October maximum flows were associated with higher macroinvertebrate diversity (Table 5). However, Poff and Zimmermann (2010) reported that both increasing and decreasing macroinvertebrate diversity may occur in response to elevated flows. Consequently, this relationship should not be over-interpreted; since it only occurred in the best-subset approach and was not picked up by the lasso, it perhaps illustrates the argument that best-subset regression is prone to finding "too many" significant relationships.

In conclusion, we identified two biological response variables that were potentially affected by regulation/flow regime: (i) river regulation may lead to higher cyanobacterial abundance, possibly via a less variable flow regime, and (ii) reduced flow variability may lead to a reduced proportion of grazers and scrapers, possibly indicating a shift towards an increased importance of heterotrophic energy sources in the ecosystem. We cannot exclude that other response variables also were affected by regulation/flow regime, but these were not picked up in our analyses (e.g. because the gradient in our data was too short). The high number of potentially interesting variables, combined with strong multicollinearity, complicates the interpretation of our results. Nevertheless, we believe the changes in community composition indicated by our analyses are strong enough to warrant further investigation.

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Table 1: Ecological indices calculated at each site.

| Benthic algae metrics | Macroinvertebrate metrics |
| :---: | :---: |
| Species richness metrics <br> - Overall taxon richness <br> - Red algae richness <br> - Green algae richness <br> - Cyanobacteria richness <br> Abundance metrics <br> - Overall abundance <br> - Red algae abundance <br> - Green algae abundance <br> - Cyanobacteria abundance | Overall metrics <br> - Abundance (ind $/ m^{2}$ ) <br> - Taxon richness <br> - Number of Genera <br> - Average score per Taxon <br> - German Saprobic Index <br> - Diversity (Shannon-Wiener-Index) <br> - Life Index <br> - Evenness <br> - EPT-Taxa (\%) <br> Feeding behaviour metrics <br> - Grazers and scrapers (\%) <br> - Miners (\%) <br> - Xylophagous Taxa (\%) <br> - Shredders (\%) <br> - Gatherers/Collectors (\%) <br> - Active filter feeders (\%) <br> - Passive filter feeders (\%) <br> - Predators (\%) <br> - Parasites (\%) <br> Locomotion metrics <br> - Swimming/skating (\%) <br> - Swimming/diving (\%) <br> - Burrowing/boring (\%) <br> - Sprawling/walking (\%) <br> - (Semi-) sessile (\%) |


| Group | Variable(s) | Number of metrics | Description |
| :---: | :---: | :---: | :---: |
| Magnitude of overall water conditions | Mean discharge | 1 | The mean daily flow over the entire 3-year period |
|  | Min, P05, P25, P50, P75, P95, max, range, IQR, 90-percentilerange | 10 | Flow percentiles. The range is calculated as (max-min); the IQR as (P75-P25); the 90-percentile-range as (P95-P05) |
|  | Coefficient of variation of flows | 1 | A dimensionless measure of variability: $c v=\frac{\sigma}{\mu}$ |
| Magnitude of monthly water conditions | Monthly minimum, mean and maximum discharge | 36 | The minimum, mean and maximum of all daily flow values in each month over the period of interest |
| Timing of extremes | Days to the last extreme event | 4 | The number of days from the sampling date to the minimum and maximum flows in the record. <br> The numbers of days to the last point in the record where flows either exceeded the P95 value or fell below the P05 value |
| Magnitude, frequency and duration of extremes | Moving averages | 6 | The minimum and maximum of 7-, 30- and 90day centred moving averages over the period of interest |
|  | Average number of reversals per year | 1 | The average number of times per year where the flow record switches from rising to falling or vice-versa |
|  | Number of high pulses | 1 | The average number of "events" each year where the flow is greater than P90 |
| Rates of change | The average daily rise and fall rate | 2 | The average rate of change (m3/s/day) from all periods when flows are increasing and all periods when flows are decreasing. (Periods where flows are constant are not included) |

Table 2: 62 hydrological indicators (HI) calculated from daily flow data. IQR, interquartile range; $c v$, coefficient of variation; $\sigma$, standard deviation of flows; $\mu$, mean flow.

Table 3: Variables selected for further analysis using PCA. The selected variables represented the strongest gradients in each dataset and country. Metrics in brackets had loadings very close to the maximum, and were therefore also included - see text for details.

| Variable type | Variable category | Germany | Norway |
| :---: | :---: | :---: | :---: |
| Response | Benthic algae | Overall PB richness | Overall PB richness |
|  |  | Cyanobacteria abundance | Cyanobacteria abundance |
|  |  | Green algae richness | Red algae abundance |
|  |  |  | (Overall PB abundance) |
|  | Macroinvertebrates | Number of taxa or genera | Overall abundance |
|  |  | German saprobic index | German saprobic index |
|  |  | Evenness | Shannon-Wiener diversity |
|  |  | LIFE index | Shredders |
|  |  | Passive filter feeders | Sprawlers and walkers |
|  |  | Predators | Swimmers and divers |
|  |  | Sprawlers and walkers |  |
|  |  | Burrowers and borers |  |
|  |  | (Active filter feeders) |  |
|  |  | (Grazers and scrapers) |  |
| Explanatory | Water chemistry | Conductivity | Conductivity |
|  |  | TP | TP |
|  |  | (TN) | TN |
|  |  | (TOC) | (TOC) |
|  | Hydrology | Mean | Mean |
|  |  | Coefficient of variation | October maximum |
|  |  | Number of high pulses | December maximum |
|  |  | Days to p05 | Days to p95 |
|  |  | Days to maximum | Days to maximum |
|  |  | Days to minimum | Number of reversals |
|  |  |  | Range |
|  |  |  | (Coefficient of variation) |

Table 4: Metrics with a $\geq 75 \%$ posterior probability of differences between regulated and unregulated sites. Negative differences imply a metric is lower at regulated sites than at unregulated ones. Brackets as in Table 3. HPD, Highest Posterior Density. Metrics marked in bold denote consistent differences 629 between regulated and unregulated sites in Germany and Norway.

| Country | Category | Metric | Mean difference | 95\% HPD <br> interval | Probability of difference |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | benthic algae | Overall PB richness [-] | 1.2 | -1.5 to +3.8 | 83 \% |
|  |  | Cyanobacteria abundance [-] | 22.7 | +3 to +45 | $99 \%$ |
|  |  | Green algae richness [-] | 0.5 | -0.9 to +1.8 | 78 \% |
|  | macroinvertebrates | Number of taxa [-] | -4.4 | -16 to +8 | 77 \% |
|  |  | Number of genera [-] | -3.6 | -13 to +6 | 78 \% |
|  |  | German saprobic index [-] | 0.05 | -0.1 to +0.2 | 76 \% |
|  |  | Evenness [-] | -0.05 | -0.14 to +0.04 | 89 \% |
|  |  | Sprawlers and walkers [\%] | 6.2 | -3 to +15 | 92 \% |
|  |  | (Active filter feeders) [\%] | -0.8 | -2.6 to +1.1 | 83 \% |
|  |  | (Grazers and scrapers) [\%] | -5.9 | -18 to +6 | 85 \% |
|  | hydrology | Mean flow [ ${ }^{3}$. ${ }^{-1}$ ] | 1.4 | -2.4 to +5.6 | 77 \% |
|  |  | Coefficient of variation [-] | -0.33 | -0.51 to -0.13 | 100 \% |
|  |  | Number of high pulses [-] | -2 | -4 to -1 | 100 \% |
|  | water chemistry | Conductivity [ $\mu \mathrm{S} . \mathrm{cm}^{-1}$ ] | 66.9 | -40.0 to +176.0 | 90 \% |
|  |  | (Total nitrogen) [mgN. ${ }^{-1}$ ] | 0.5 | -0.7 to +1.7 | 82 \% |
|  |  | (Total organic carbon) [mgC. ${ }^{-1}$ ] | -0.9 | -2.7 to +0.9 | 87 \% |
| $\begin{aligned} & \text { त } \\ & \substack{0 \\ \mathbf{3} \\ \mathbf{2}} \end{aligned}$ | benthic algae | Cyanobacteria abundance [-] | 37 | -9 to +85 | 94 \% |
|  |  | (Overall PB abundance) [-] | 61 | -57 to +185 | 84 \% |
|  | macroinvertebrates | Overall MZB abundance [-] | 305 | -304 to +873 | 85 \% |
|  |  | German saprobic index [-] | 0.04 | -0.06 to +0.13 | 78 \% |
|  |  | Shannon-Wiener diversity [-] | 0.17 | -0.1 to + 0.5 | 86 \% |
|  |  | Shredders [\%] | -1.9 | -4.7 to +0.9 | 92 \% |
|  |  | Swimmers and divers [\%] | -9 | -19 to 0 | 97 \% |
|  | hydrology | Mean flow [ $\mathrm{m}^{3} . \mathrm{s}^{-1}$ ] | 5.7 | -3.9 to +16.0 | 88 \% |
|  |  | October maximum flow [ $\mathrm{m}^{3} . \mathrm{s}^{-1}$ ] | 19.6 | -18.3 to +58.6 | 84 \% |
|  |  | December maximum flow [ $\left.\mathrm{m}^{3} . \mathrm{s}^{-1}\right]$ | 14.2 | +4.1 to +24.1 | $100 \%$ |
|  |  | Number of reversals per year [-] | 25 | +13 to +36 | 100 \% |
|  |  | Range of flows [m ${ }^{3} . \mathrm{s}^{-1}$ ] | 51 | -48 to +151 | 85 \% |
|  |  | (Coefficient of variation) [-] | -0.23 | -0.43 to -0.02 | 98 \% |
|  | water chemistry | Total nitrogen [mgN. ${ }^{-1}$ ] | 0.08 | +0.02 to +0.13 | 99 \% |
|  |  | (Total Organic Carbon) [mgC. ${ }^{-1}$ ] | 1 | 0 to +2 | 98 \% |

Table 5: Summary of fitted regression models. PB, Benthic algae (phytobenthos); MZB, macroinvertebrates (macrozoobenthos); F-prob, F-statistic for overall model significance; BIC, Bayesian Information Criterion. "country" is a binary variable ( 1 for Norway; 0 for Germany); colour code: red, there are obvious problems with the model (e.g. overfitting, residuals not normally distributed); yellow, the best identified model is no better than the null model; green, the model is worthy of further consideration. Bold letters: all variables in the model were significant at $p=0.05$.

|  |  | Response | Best lasso model OLS results |  |  |  | Best subsets OLS results |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | $\left\|\begin{array}{c} \text { Varaiable } \\ \text { type } \end{array}\right\|$ |  | Model | Adj. $\mathrm{R}^{2}$ | F-prob | BIC | Model | Adj. $\mathrm{R}^{2}$ | F-prob | BIC |
|  | PB |  | $-0.005^{*}$ cond $+0.069^{*}$ max10-0.61*n_hi_pulse_yr-0.03*revs_per_yr-0.25*toc +17 Null model <br> $-0.0044^{*}$ cond-0.37*n_hi_pulse_yr-0.031*revs_per_yr+11 $-21^{*}$ n_hi_pulse_yr-14*toc $+3.6 \mathrm{e}+02$ | $\begin{array}{\|c\|} \hline 0.43 \\ 0.53 \\ 0.24 \\ \hline \end{array}$ | $\begin{gathered} \hline 0.008 \\ - \\ 0.000 \\ 0.021 \\ \hline \end{gathered}$ | $\begin{gathered} 116.5 \\ \hline- \\ 75.2 \\ 285.0 \end{gathered}$ |  $-20^{*}$ n_hi_pulse_yr $+3.1 \mathrm{e}+02$ | $\begin{array}{\|l\|} \hline 0.51 \\ 0.60 \\ 0.53 \\ 0.18 \\ \hline \end{array}$ | $\begin{aligned} & 0.001 \\ & \hline 0.002 \\ & 0.000 \\ & 0.022 \\ & \hline 0.0 \\ & \hline \end{aligned}$ | $\begin{aligned} & \hline 111.3 \\ & 232.1 \\ & 75.2 \\ & 284.9 \\ & \hline \end{aligned}$ |
|  | mzB | Overall MZB abundance | Null model |  |  |  |  | 0.52 | 0.004 | 309.0 |
|  |  | Number of taxa | Null model |  |  |  | $-28 *{ }^{*}$ cv+0.87* ${ }^{\text {max } 10-0.69 * * e v s \_p e r \_y r+1.5 e+02 ~}$ | 0.38 | 0.012 | 157.9 |
|  |  | German saprobic index | Null model |  |  | - | $-0.01^{*}$ max $10+0.039^{*}$ mean $+0.036^{*}$ tn+1.6 | 0.37 | 0.016 | -23.4 |
|  |  | Evenness Shanno-Weiner diversivi | Null model |  |  |  | Null model |  | - | - |
|  |  | Shannon-Weiner diversity |  | - |  | - | ${ }^{+0.0188^{*} \text { max } 10-0.013^{*} \text { revs_per_yr }+4}$ | 0.26 | 0.030 | 19.6 |
|  |  | Sprawlers and walkers Shredders | Null model |  |  | - | Null model Null model |  | $\square$ |  |
|  |  | Swimmers and divers | +2**_hi_pulse_yr+0.32**evs_per_yr-1.2**n-0.99**toc-27 | 0.38 | 0.022 | 140.7 | +2**_hi_pulse_yr+0.29*revs_per_yr-32 | 0.36 | 0.000 | 138.1 |
|  |  | (Active filter feeders) | Null model |  |  |  | Null model |  |  |  |
|  |  | (Grazers and scrapers) | $20^{*} \mathrm{cv}+13$ | 0.18 | 0.038 | 157.7 | $20^{*} \mathrm{c}+13$ | 0.18 | 0.038 | 157.7 |
|  | PB | Overall PB richness | Null model |  |  |  | Null model |  |  |  |
|  |  | Cyanobacteria abundance | -0.69*cond-55*cv+0.51**max12+4.9*n_hi_pulse__r-0.067*range $+2.9 \mathrm{e}+02^{*}$ tn+1.3e+02 | 0.25 | 0.015 | 476.4 | $-86 *$ cv+8.4*n_hi_pulse_yr+1.7e+02 | 0.20 | 0.006 | 468.6 |
|  |  | Green algae richness | Null model |  |  | - | Null model |  |  |  |
|  | MzB | Overall MzB abundance |  |  |  |  | -1.6e+03 ${ }^{\text {moctadel }}$.2e+03 |  |  |  |
|  |  | Number of taxa | +42*tn+19 | 0.16 | 0.007 | 291.4 | $+0.13^{*}$ cond $-9.3{ }^{*}$ cv $+1.88^{+t o c}+31$ | 0.26 | 0.003 | 291.2 |
|  |  | German saprobic index | -0.014**_hi_pulse_yr +1.7 | 0.10 | 0.024 | -37.1 | -0.014*n_hi__pulse_yr +1.7 | 0.10 | 0.024 | -37.1 |
|  |  | Evenness | $+0.0011^{*}$ max $10+0.00025^{*}$ max12+0.0051*n_hi_pulse_rr-0.00038**range $+0.4 *$ tn-0.0024*tocto.46 | 0.33 | 0.003 | -49.9 | $+0.0011^{*}$ max $10-0.00042^{*}$ range $+0.41^{*}$ tn +0.51 | 0.35 | 0.000 | -59.0 |
|  |  | Shannon-Weiner diversity | $+1.9{ }^{*} \mathrm{tn}+0.063^{*}$ toc +1.4 | 0.27 | 0.001 | 49.9 | $+0.0034^{*}$ max $10-0.0014^{*}$ range $+2.5{ }^{*} \mathrm{tn}+1.5$ | 0.44 | 0.000 | 42.3 |
|  |  | Sprawlers and walkers | Null model |  |  | - | Null model |  |  |  |
|  |  | Shredders | Null model |  |  |  | Null model |  | - | - |
|  |  | Swimmers and divers |  | 0.43 | 0.000 | 326.5 | + $15^{*} \mathrm{cc}$ - $1.33^{*}$ __hi_pulse_yr-3.7**oc+20 | 0.41 | 0.000 | 318.2 |
|  |  | (Active filter feeders) | $-4.4{ }^{*}$ cr-0.0068* ${ }^{\text {range }+11}$ | 0.21 | 0.005 | 215.6 | $-6.7{ }^{*} \mathrm{cv}-0.078^{*}$ mean +14 | 0.26 | 0.002 | 213.2 |
|  |  | (Grazers and scrapers) | $13.2{ }^{*} \mathrm{cv}+13.2$ | 0.09 | 0.034 | 318.5 | -0.16* ${ }^{\text {max }} 12-0.17^{*}$ revs_per_yr 53 | 0.16 | 0.015 | 317.9 |
| $\frac{\stackrel{3}{5}}{\frac{5}{4}}$ | PB | Overall PB richness | -0.013* ${ }^{*}$ cond $+11^{*}$ country +11 | 0.61 | 0.000 | 422.8 | +16**country +6.5 | 0.61 | 0.000 | 420.4 |
|  |  | Cyanobacteria abundance | $+1.2 e+022^{*}$ country $63^{3}$ cv+0.49**max12+6.3*n_hi_pulse_yr +37 | 0.50 | 0.000 | 731.7 | +1.1e+02**country-71**v+6.9*n_hi_pulse_yr+55 | 0.49 | 0.000 | 730.0 |
|  |  | Green algae richness | $-0.0099{ }^{*}$ cond $+7.6^{*}$ country 6.3 | 0.63 | 0.000 | 369.6 | +11** country +2.7 | 0.63 | 0.000 | 367.6 |
|  |  | (Overall PB abundance) | -0.26*cond $+2.9 \mathrm{e}+02^{*}$ country $-1.1 \mathrm{e}+02^{*}$ cr $+0.366^{*}$ max10+3.6e+02 | 0.60 | 0.000 | 843.8 | $+3.9 \mathrm{e}+02^{*}$ country+1.5e+02 | 0.59 | 0.000 | 836.6 |
|  | mzB | Overall MZB abundance | $-1.4{ }^{\text {e }}+03^{*}$ cv+11**ean-14**evs_per_yr-1.4e+02**tn+4.6e+03 | 0.18 | 0.005 | 1023.0 | $-1.6 e+03^{*}$ cr-1-15*revs_per_yr-1.7e+02**n+5.1e+03 | 0.18 | 0.003 | 1020.0 |
|  |  | Number of taxa | $-13^{*}$ country+1.1*toc 37 | 0.29 | 0.000 | 464.0 | $-14 * *$ country 42 | 0.28 | 0.000 | 462.1 |
|  |  | German saprobic index | +0.00029**ond- $0.044^{*}$ country $-0.014^{*}$ __hi_pulse_yr+0.027** n+1.7 | 0.45 | 0.000 | -51.8 | $+0.00066^{*}$ cond-0.014*n_hi_pulse_yr+1.7 | 0.45 | 0.000 | -58.7 |
|  |  | Evenness | ountry+0.001**max10+0.00032*max12+0.0063*n_hi_pulse_rr-0.00034*range-0.00045**evs_per_ry+0.014*t | 0.44 | 0.000 | -88.7 | -0.13* country $+0.0011^{*}$ max10-0.00038* ${ }^{\text {range }}+0.015^{*}$ toc +0.68 | 0.44 | 0.000 | -97.1 |
|  |  | Shannon-Weiner diversity | $-0.54 *$ country $+0.0039 * *$ max $12-0.00078{ }^{*}$ range $+0.082^{*}$ toc +2.3 | 0.49 | 0.000 | 78.5 | $-0.67 *$ country $+0.0034 *$ max $10-0.0012 *$ range $+0.084^{*}$ toc +2.4 | 0.52 | 0.000 | 74.3 |
|  |  | Sprawlers and walkers Shredders | Null model $\quad \begin{aligned} & \text { Nutr } \\ & +0.011^{*} \text { cond }-3 * \text { country } 7.7\end{aligned}$ | 0.21 | 0.000 | 389.6 | ${ }_{\text {Null model }}^{+0.0188^{*} \text { cond }+4.7}$ |  |  |  |
|  |  | Swimmers and divers |  | 0.37 | 0.000 | 473.4 | +0.02*cond-0.31* ${ }^{\text {mean- }-0.97 * \text { n_hi_pulse_yr+0.046**ange }-2.7 * \text { toc }+30}$ | 0.36 | 0.000 | 467.8 |
|  |  | (Active filter feeders) |  | 0.20 | 0.002 | 318.1 | $+3.4{ }^{*}$ country $-4^{*}$ cvo $+0.035^{*}$ max12-0.085**mean +6.3 | 0.25 | 0.001 | 314.7 |
|  |  | (Grazers and scrapers) | $-7.6{ }^{*}$ country $+15^{*} \mathrm{cv}+19$ | 0.18 | 0.002 | 475.8 | $-7.6^{*}$ country $+15^{*} \mathrm{cv}+19$ | 0.18 | 0.002 | 475.8 |

Figures


Fig. 1: Map of sampling locations.


Fig. 2. Proportion of grazers and scrapers in relation to the coefficient of variation (CV) in the flow regime; regression lines are drawn from the combined regulated and unregulated sites in each country

## Appendices

## Appendix A1: Hydrological regimes



Fig. A1: Monthly flows relative to the mean in (a) Germany ( $n=24$ ) and (b) Norway ( $n=40$ ). Cl, confidence interval.

## Appendix A2: PCA

Fig. A2 shows the results of the PCA for benthic algae in Germany. The KGC implies keeping the first three PCs, which together explain $83 \%$ of the total variance. The PC loadings (see online code repository) indicate that PC1 is dominated by an inverse correlation with overall benthic algae richness and abundance, so sites with high scores on PC1 tend to have lower richness and abundance. PC2 is dominated by an inverse relationship with green algae richness and abundance, and PC3 is dominated by a similar relationship for cyanobacteria abundance.

Fig. A2b suggests it may be possible to use PC1 to distinguish between regulated and unregulated locations: a straight line drawn at approximately $P C 1=0$ broadly divides the data into "regulated" and "unregulated" subsets, with only a small number of misclassification errors. The implication is that unregulated sites in Germany tend to have lower overall benthic algae richness and abundance than regulated sites - an observation that is tested more rigorously in subsequent phases of the analysis.


Fig. A2: PCA results for German benthic algae data. (a) Eigenvalues for each PC. (b) Projection of the data onto the first 2 PC axes

## Appendix A3: Bayesian test for differences

For testing for differences between regulated and unregulated sites, we adopted a robust Bayesian approach (Kruschke, 2012), in which the variables of interest are assumed to be t-distributed, rather than Normally distributed (as in a standard t-test). Compared to a Normal distribution, the t-distribution has an additional degrees-of-freedom parameter, $v$. As $v \rightarrow \infty$, the t-distribution becomes a Normal distribution, while values of $v$ close to 0 give the distribution heavier tails. These heavy tails mean the t-distribution penalises extreme values less severely than a Normal distribution, making the test more robust to outliers.

In each test we have two groups of data, from the regulated and unregulated sites. Following Kruschke (2012), we assume that each group is drawn from a t-distribution with the same number of degrees-of-freedom, and the aim is to estimate whether the other distribution parameters are different.

$$
\begin{align*}
& \text { reg }_{i} \sim T\left(v, \mu_{1}, \sigma_{1}^{2}\right)  \tag{1}\\
& \text { unreg }_{i} \sim T\left(v, \mu_{2}, \sigma_{2}^{2}\right) \tag{2}
\end{align*}
$$

Where reg $_{i}$ and $u n r e g_{i}$ are the observed values for regulated and unregulated sites, respectively; $v$ is the number of degrees-of-freedom (assumed the same for both groups); $\mu_{1}$ and $\mu_{2}$ are the (possibly different) means for each group; and $\sigma_{1}$ and $\sigma_{2}$ are the (possibly different) standard deviations.

We set broad, uninformative priors on these quantities: the priors for the $\mu_{j}$ are Gaussian with the means equal to the overall mean of the pooled data, $\bar{y}$, and a variance that is twice the variance of the pooled data, $\bar{\sigma}$; the priors for the $\sigma_{j}$ are assumed to be Uniform on the interval between 0 and $\sigma_{\max }$, where $\sigma_{\max }$ is large relative to the variance in the pooled data; and the prior for $v$ is an exponential distribution with mean 30 , chosen because it allocates credibility evenly over the range between "nearly normal" and "heavy tailed" (Kruschke, 2012). This arrangement is illustrated in Fig. A3_1.


Fig. A3_1: Hierarchical diagram illustrating a robust Bayesian test for differences between two groups. After Kruschke (2012)

The posterior distribution $P\left(\mu_{1}, \mu_{2}, \sigma_{1}, \sigma_{2}, v \mid D\right)$, where $D$ are the observed data, was explored via Markov chain Monte Carlo (MCMC) sampling using the PyMC3 package (Salvatier et al., 2016) for the Python programming language (Python Software Foundation, 2016). The goodness-of-fit of the model was assessed using "posterior predictive checks" (Gelman et al., 2004) and, when the fit was deemed acceptable, marginal posterior distributions were constructed for the differences between means, ( $\mu_{1}-\mu_{2}$ ), and standard deviations, ( $\sigma_{1}-$ $\sigma_{2}$ ). The Highest Posterior Density (HPD) intervals and the proportions of each distribution greater than or less than zero were then used to estimate the (Bayesian) probability that differences between regulated and unregulated sites were statistically significant.


Fig. A3_2: Differences in the coefficient of variation of flows between regulated and unregulated sites in Norway. (a) Posterior distribution for the difference between group means, $\left(\mu_{1}-\mu_{2}\right)$. (b) Posterior for the difference between group standard deviations, $\left(\sigma_{1}-\sigma_{2}\right)$. (c) PPC for unregulated sites. (d) PPC for regulated sites.

Fig. A3_2 shows an example of the output for differences in the coefficient of variation of flows between regulated and unregulated sites in Norway. Fig. A3_2a shows the posterior distribution for the difference between group means, $\left(\mu_{1}-\mu_{2}\right)$, while Fig. A3_2b shows the difference between group standard deviations, $\left(\sigma_{1}-\sigma_{2}\right)$. The mean difference in the coefficient of variation between the two groups is -0.23 (Fig. A3_2a), implying that flows at regulated sites are, on average, $23 \%$ less dispersed than under natural flow regimes. The $95 \%$ HPD extends from $-2 \%$ to $-43 \%$, and more than $98 \%$ of the posterior distribution is less than zero. There is therefore high probability that, given the data and the prior assumptions, flows at regulated sites are less variable than at unregulated sites. Similarly, there is strong evidence that regulated sites exhibit a greater range of coefficients of variation than unregulated ones (Fig. A3_2b).

The lower row of plots on Fig. A3_2 shows the Posterior Predictive Checks (PPCs) for unregulated (Fig. A3_2c) and regulated (Fig. A3_2d) sites. Black vertical lines show the means of the observed data in each group, while the smoothed histograms show distributions for synthetic means, generated by simulating from the fitted model. Substantial differences between simulated and observed values indicate a poorly fitting model and should be investigated further, but in this example the fit seems adequate. Additional details regarding model checking are provided in the online code repository.

## Appendix A4: L1-regularised ("lasso") regression

The commonly used stepwise and best-subsets regression approaches have a number of well-documented limitations in the context of variable selection and significance testing (Harrell, 2001). A more robust approach is to use regularized regression, such as ridge or lasso, both of which accept a degree of bias in the model predictions in return for parameter estimates that have lower variance and are therefore more stable (Hastie et al., 2009).

Ridge regression has advantages when there are lots of collinear predictors, whereas the lasso incorporates "feature selection" and can be useful when the aim is to produce a parsimonious model, which may be easier to interpret. Since multicollinearity had already been addressed to some extent using PCA, lasso regression was chosen to identify the most important relationships between ecological (response) and explanatory variables.

The "loss function" minimised by lasso regression is:

$$
\begin{equation*}
\min _{\theta}\left[\frac{1}{2 n}\|X \theta-y\|_{2}^{2}+\alpha\|\theta\|_{1}\right] \tag{3}
\end{equation*}
$$

Where $\theta$ is the vector of model parameters; $n$ is the number of samples; $X$ is the design matrix; $y$ is the vector of observations; and $\alpha$ is a parameter controlling the amount of regularisation. The first term in this expression is proportional to the usual loss function for Ordinary Least Squares (OLS) regression, whereas the second is proportional to the L1-norm of the parameter vector. Large values of $\alpha$ therefore impose a heavy penalty on large parameter values, producing "sparse" models where most parameters are set to zero. In contrast, $\alpha=0$ corresponds to the OLS solution.

Lasso regression must be performed on standardized predictors, as otherwise the regularization penalty is applied unevenly across the variables. Regularization also means the lasso coefficient estimates are not consistent (i.e. they do not necessarily converge as the sample size grows) and they are biased towards zero. The lasso can therefore be easily used to assess which predictors are important in the model, but estimating the strength of the relationships (i.e. the model coefficients) is more difficult. One pragmatic solution is to use the lasso to identify the best model (or a small number of candidate models), and then use OLS regression with the unstandardized data to estimate the coefficients directly in the original data units (Hastie et al., 2009).

In the approach adopted here, the best fitting lasso model was chosen as the one with the lowest mean squared test error under k-fold cross-validation across a range of values for $\alpha$. In addition, plots of the "lasso path" (Fig. 6) were assessed in order to better understand relationships between variables - in particular to identify and remove strong collinearity between predictors. The analysis was performed using scikit-learn (Pedregosa et al., 2011).

For small to medium sized datasets, the choice of $k$ in $k$-fold cross-validation can substantially affect the validation curve. For each model, a range of k-values (usually 3, 5, 7 and, sometimes, 9) was explored to see whether the location of the test-error minimum was robust. Models where the minimum was strongly dependent on $k$ were categorised as unreliable (highlighted in red on Table 5).

Fig. A4_1 shows the lasso path for a model where the response variable is "proportion of macroinvertebrate swimmers and divers (\%) in Germany". The plot illustrates how the standardised model coefficients of the best model (selected through cross-validation) vary with the penalty weight, $\alpha$ (equation 3 ). Small values of $-\log (\alpha)$ correspond to strong regularisation, such that all model coefficients are forced to zero (the "null" model). Larger values of $-\log (\alpha)$ mean less regularisation, so models towards the right-hand margin of the plot approximate the OLS solution.

Fig. A4_1: Lasso path for "proportion of macroinvertebrate swimmers and divers (\%) in Germany". Range, range of flows (maximum - minimum); Mean, average long-term flow; Revs Per Yr, average number of flow reversals per year; Cond, conductivity; CV, coefficient of variation; High Pulses, Number of high pulses ( $>90^{\text {th }}$ percentile) per year; TOC, total organic carbon; TN, total nitrogen; Dec Max, December maximum flow; Oct Max, October maximum flow.


Fig. A4_2: Average cross-validation score as a function of the regularisation parameter, $\alpha$.

As the amount of regularisation is reduced (reading from left to right along the $x$-axis), parameters that come into the model first can be interpreted as having a stronger relationship to the response. In addition, the shape of the lasso path for each variable provides information regarding any remaining collinearity between predictors. The plot can be interpreted as follows:

- The first variable to enter the model is "Revs Per Yr ". The coefficient value is positive and increases rapidly, implying a strong positive correlation between the proportion of swimmers and divers and the average number of flow reversals per year.
- The next variable to enter is "TOC". This relationship is negative and the magnitude increases steadily throughout the path, implying that high TOC concentrations are associated with fewer swimmers and divers.
- The third variable to enter the model is the number of high flow pulses. The coefficient is positive and increases steadily until around $-\log (\alpha)=1.3$, at which point both "Oct Max" and "CV" enter the model. These two new variables are collinear with "High Pulses" and "Revs Per Yr", as shown by the distinct kinks in the paths for these variables: the trace for "Revs Per Yr" appears to be increasing to offset the negative influence of "Oct Max", while the coefficient for "High Pulses" slowly decreases, implying that once "CV" and "Oct Max" are included in the model, the importance of "High Pulses" is reduced. This provides evidence that, by around $-\log (\alpha)=1.3$, the model is already beginning to "overfit" the data. By the time the variables "Mean" and "Dec Max" enter the model, at around $-\log (\alpha)=2.2$, there is very clear evidence of overfitting, with obvious collinearity between "Mean", "Oct Max", "Dec Max", "Range" and "Revs Per Yr".

Consideration of the lasso path provides useful qualitative insights into relationships between explanatory variables and the response, and also between the explanatory variables themselves. For the example shown in Fig. A4_1, a relatively parsimonious model with little obvious collinearity can be constructed for values of $-\log (\alpha)$ less than around 1.3. The best overall lasso model can be identified quantitatively by calculating the mean squared test error for a range of values of the regularisation parameter, $\alpha$ (Fig. A4_2). The minimum mean squared cross-validation error occurs at $-\log (\alpha) \approx 1.1$, which is in agreement with the qualitative assessment of the lasso path. By comparison to Fig. A4_1, it is clear that this model includes four explanatory variables with non-zero coefficients: "Revs Per Yr", "TOC", "High Pulses" and "TN". According to the lasso approach, these variables are "significantly" associated with the response. Further details of this model, including plots of residuals and fitted versus observed values, can be found in the online code repository.

