

Arranz, I., Hsieh, C., Mehner, T. and Brucet, S. 2018. Systematic deviations from linear size spectra of lake fish communities are correlated with predator–prey interactions and lake-use intensity. – *Oikos* doi: 10.1111/oik.05355

## Appendix 1

Table A1-1. Minimum, maximum, and arithmetic mean (in parentheses) of the environmental and morphometric information for the German lakes.

| Environmental information              |                   |
|--|-------------------|
| Max. temp. (°C)                        | 16.6–18.6 (17.44) |
| Total phosphorus (mg m <sup>-3</sup> ) | 10–402 (69.13)    |
| pH                                     | 7.5–9.3 (8.4)     |
| Morphometric information               |                   |
| Depth (m)                              | 1.2–72.3 (18.57)  |
| Area (km <sup>2</sup> )                | 0.5–113 (4.70)    |
| Elevation (m)                          | 1–98 (46.62)      |

Table A1-2. Results of the Spearman's rank correlations between the size-class specific logPPR, and the size-class specific residuals deviating from linearity across the 74 lakes. We only included those size classes where both predator and prey are present at least in two lakes.

| No. of size class | Correlation of logPPR with residuals in each size class |
|-------------------|---|
| 10                | 0.028   |
| 11                | -0.101  |
| 12                | -0.085  |
| 13                | -0.190  |
| 14                | -0.020  |
| 15                | -0.404  |
| 16                | -0.316  |
| 17                | -0.324  |
| 18                | 0.244   |
| 19                | -0.058  |
| 20                | 0.131   |

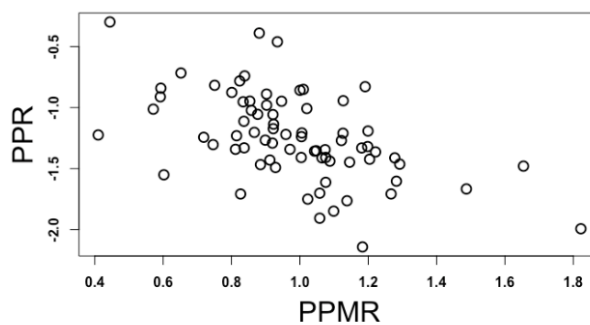


Figure A1-1. Correlation between the predator-prey size ratio (logPPMR) and the predator-prey abundance ratio (logPPR) across the 74 German lakes (Spearman's correlation  $r_s = -0.54$ , p-value < 0.05).

## Appendix 2

### Comparison of the slopes based on the MLE and OLS calculations

The correlation between MLE and OLS slopes is high (Pearson's rank correlation  $r_p = 0.72$ ), and the regression coefficient of a linear model between OLS and MLE slopes did not differ from one (slope  $0.93 \pm 0.11$ , t-test p-value = 0.55).

We used the ordinary least squares (OLS) method because it directly provides (and is based on) the residuals from linearity per size class. MLE approaches would not allow calculating size-specific residuals (Edwards et al. 2017). Furthermore, these MLE approaches are often very sensitive with respect to the distribution of fish in the smallest size classes, and result in extremely biased slopes for the entire spectrum if the size distribution of very small or large fish is somewhat irregular (T. Mehner unpubl.).

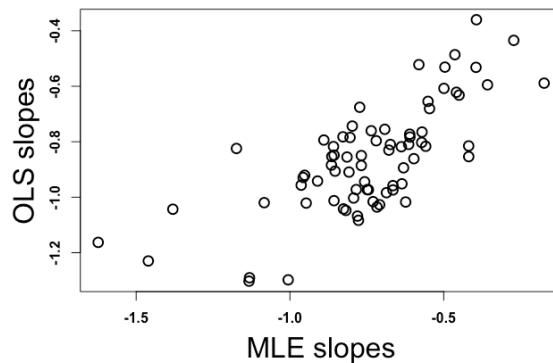


Figure A2-1. Comparison between the two different slopes based on the maximum likelihood (MLE) and ordinary least squares (OLS) approaches. MLE slopes were calculated from binning the data but using a bounded method to fit the observations. OLS slopes were calculated from linear regressions.

## Appendix 3

To detect whether significant differences exist in species composition among the clusters found by K-means, we used discriminant analysis (DA) (Legendre and Legendre 1998). DA classified the samples into pre-defined groups, which in our case were the clusters defined according to the similarity in residual variation. We limited the DA to fish species that occurred in at least 50% of the lakes, because many rare fish species were present in only few lakes, which may lead to statistical problems due to a zero-inflated species  $\times$  lakes presence/absence matrix. The omission of rare species did not have a significant effect on the nonlinear structures because their numerical contribution is very low across lakes (total proportion about 3%). Thus, the DA was done using log CPUE of bleak (*Alburnus alburnus*), common bream, predator ( $> 32$  g) perch, prey ( $< 32$  g) perch, predator pike (*Esox lucius*), roach, rudd (*Scardinius erythrophthalmus*), ruffe, tench (*Tinca tinca*), and white bream. The percentage of correctly classified cases reflects the degree to which the samples yield consistent information. A 10-fold cross-validation was used to test the predictive accuracy (Miller and Miller 2010).

Table A3-1. Results of discriminant analysis (DA) of dominant fish species in the communities of 74 German lakes between three lake groups according to the K-means clustering based on similarity of residual patterns.

|            | Eigenvalue | % of variance | Wilk's Lambda | $\chi^2$ | df | p-value    |
|------------|------------|---------------|---------------|----------|----|------------|
| Function 1 | 0.88       | 78.2          | 0.43          | 56.50    | 20 | $< 0.0001$ |
| Function 2 | 0.24       | 21.8          | 0.80          | 14.56    | 9  | 0.104      |

Table A3-2. Relative contribution of the most representative species to the first discriminant function of the DA. Perch and pike were separated into prey and predators according to the 32 g size threshold.

|                | Function 1 |
|----------------|------------|
| Bleak          | 0.17       |
| Common bream   | -0.03      |
| Predator perch | 0.26       |
| Predator pike  | 0.02       |
| Prey perch     | 0.07       |
| Roach          | -0.35      |
| Rudd           | 0.17       |
| Ruffe          | 0.21       |
| Tench          | 0.22       |
| White bream    | 0.00       |

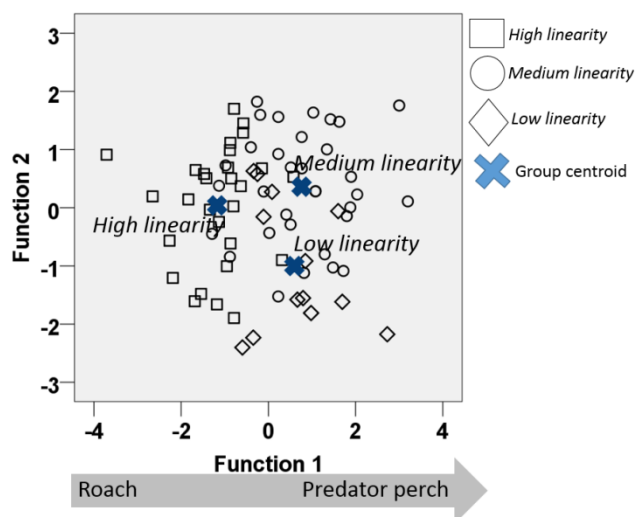


Figure A3-1. Results of discriminant analysis (DA) for the CPUE of the most common fish species in 74 German lakes. Symbols indicate the three cluster groups determined by K-means clustering, based on the similarity of the residual patterns. For the significant function 1, the dominant species are indicated in Supplementary material Appendix 3 Table A3-2. Predator perch = perch >32 g.

## Appendix 4

### Sensitivity analyses of the size spectra with respect to the size class width

Table A4-1. PLS results when a smaller size class width (i.e. a numerical series of size bins based on  $\log_2/2.5$ ) was applied for all fish in the size range of 6 g to 1024 g. Anthropogenic pressures and trophic interactions were treated as predictors (first column).  $R^2X$  (respectively  $R^2Y$ ): percentage of predictor variance explained by the full model.  $Q^2Y$ : predictive performance of the model estimated by cross validation. Significant predictors are in bold (p-value < 0.05). Shoreline bank modification and fish exploitation were categorical variables. Ind. net<sup>-1</sup> night<sup>-1</sup>: total individuals of fish caught per net and night.

|  | $R^2X$<br>(cum) | $R^2Y$<br>(cum) | $Q^2Y$<br>(cum) | p-value<br>$R^2Y$ | p-value<br>$Q^2Y$ |
|--|-----------------|-----------------|-----------------|-------------------|-------------------|
| <u>Anthropogenic pressures</u>                               |                 |                 |                 |                   |                   |
| Shoreline bank modification                                  | 0.155           | 0.0616          | -0.298          | 0.938             | 0.953             |
| Fish exploitation  | 0.24            | 0.155           | 0.0635          | 0.276             | <b>0.029</b>      |
| Total phosphorus (mg m <sup>-3</sup> )                       | 0.198           | 0.355           | 0.139           | <b>0.001</b>      | <b>0.002</b>      |
| <u>Trophic interactions</u>                                  |                 |                 |                 |                   |                   |
| CPUE prey (ind. net <sup>-1</sup> night <sup>-1</sup> )      | 0.158           | 0.162           | -0.0437         | 0.182             | 0.221             |
| CPUE predators (ind. net <sup>-1</sup> night <sup>-1</sup> ) | 0.213           | 0.239           | 0.102           | <b>0.029</b>      | <b>0.004</b>      |
| Mean body size prey (g)                                      | 0.189           | 0.263           | 0.0292          | <b>0.013</b>      | <b>0.025</b>      |
| Mean body size predator (g)                                  | 0.192           | 0.179           | -0.0323         | 0.141             | 0.132             |
| Predator-prey mass ratio (logPPMR)                           | 0.185           | 0.253           | 0.063           | <b>0.026</b>      | <b>0.006</b>      |
| Predator-prey ratio (logPPR)                                 | 0.186           | 0.307           | 0.0941          | <b>0.006</b>      | <b>0.002</b>      |

## Appendix 5

### Sensitivity analyses of the size spectra with respect to predator size thresholds

Table A5-1. PLS results when piscivorous species were considered predators at a threshold of > 23 g, representing the 7th size class. Predator–prey interactions were treated as predictors (first column).  $R^2X$  (respectively  $R^2Y$ ): percentage of predictor variance explained by the full model.  $Q^2Y$ : predictive performance of the model estimated by cross validation. Significant predictors are in bold (p-value < 0.05).

|  | $R^2X$<br>(cum) | $R^2Y$<br>(cum) | $Q^2Y$<br>(cum) | p-value<br>$R^2Y$ | p-value<br>$Q^2Y$ |
|--|-----------------|-----------------|-----------------|-------------------|-------------------|
| <u>Trophic interactions</u>                                  |                 |                 |                 |                   |                   |
| CPUE prey (ind. net <sup>-1</sup> night <sup>-1</sup> )      | 0.233           | 0.159           | -0.0259         | 0.203             | 0.115             |
| CPUE predators (ind. net <sup>-1</sup> night <sup>-1</sup> ) | 0.241           | 0.35            | 0.204           | <b>0.001</b>      | <b>0.001</b>      |
| Mean body size prey (g)                                      | 0.195           | 0.276           | 0.0538          | <b>0.013</b>      | <b>0.01</b>       |
| Mean body size predator (g)                                  | 0.167           | 0.212           | -0.0887         | 0.068             | 0.43              |
| Predator–prey mass ratio (logPPMR)                           | 0.166           | 0.207           | 0.0132          | 0.059             | <b>0.024</b>      |
| Predator–prey ratio (logPPR)                                 | 0.198           | 0.332           | 0.0538          | <b>0.003</b>      | <b>0.011</b>      |

Table A5-2. PLS results when piscivorous species were considered predators at a threshold > 45 g, representing the 9th size class. Predator–prey interactions were treated as predictors (first column). R<sup>2</sup>X (respectively R<sup>2</sup>Y): percentage of predictor variance explained by the full model. Q<sup>2</sup>Y: predictive performance of the model estimated by cross validation. Significant predictors are in bold (p-value < 0.05).

|  | R <sup>2</sup> X<br>(cum) | R <sup>2</sup> Y<br>(cum) | Q <sup>2</sup> Y<br>(cum) | p-value<br>R <sup>2</sup> Y | p-value<br>Q <sup>2</sup> Y |
|--|---------------------------|---------------------------|---------------------------|-----------------------------|-----------------------------|
| <u>Trophic interactions</u>                                  |                           |                           |                           |                             |                             |
| CPUE prey (ind. net <sup>-1</sup> night <sup>-1</sup> )      | 0.235                     | 0.167                     | -0.016                    | 0.188                       | 0.071                       |
| CPUE predators (ind. net <sup>-1</sup> night <sup>-1</sup> ) | 0.25                      | 0.328                     | 0.201                     | <b>0.001</b>                | <b>0.001</b>                |
| Mean body size prey (g)                                      | 0.198                     | 0.297                     | 0.0926                    | <b>0.001</b>                | <b>0.003</b>                |
| Mean body size predator (g)                                  | 0.224                     | 0.204                     | 0.0494                    | 0.065                       | <b>0.019</b>                |
| Predator–prey mass ratio (logPPMR)                           | 0.198                     | 0.191                     | 0.0743                    | 0.082                       | <b>0.007</b>                |
| Predator–prey ratio (logPPR)                                 | 0.217                     | 0.297                     | 0.0839                    | <b>0.006</b>                | <b>0.008</b>                |