

This is an Open Access document downloaded from ORCA, Cardiff University's institutional repository: <https://orca.cardiff.ac.uk/id/eprint/145133/>

This is the author's version of a work that was submitted to / accepted for publication.

Citation for final published version:

Perkins, Daniel M., Durance, Isabelle , Jackson, Michelle, Jones, J. Iwan, Lauridsen, Rasmus B., Layer-Dobra, Katrin, Reiss, Julia, Thompson, Murray S. A. and Woodward, Guy 2021. Systematic variation in food web body-size structure linked to external subsidies. *Biology Letters* 17 (3) , 20200798. 10.1098/rsbl.2020.0798

Publishers page: <http://dx.doi.org/10.1098/rsbl.2020.0798>

Please note:

Changes made as a result of publishing processes such as copy-editing, formatting and page numbers may not be reflected in this version. For the definitive version of this publication, please refer to the published source. You are advised to consult the publisher's version if you wish to cite this paper.

This version is being made available in accordance with publisher policies. See <http://orca.cf.ac.uk/policies.html> for usage policies. Copyright and moral rights for publications made available in ORCA are retained by the copyright holders.



1 **Title: Systematic variation in food web body-size structure linked to external subsidies**

2  
3 **Authors:** Daniel M. Perkins<sup>1\*</sup>, Isabelle Durance<sup>2</sup>, Michelle Jackson<sup>3</sup>, J. Iwan Jones<sup>4,5</sup>,  
4 Rasmus B. Lauridsen<sup>4,6</sup>, Katrin Layer-Dobra<sup>7</sup>, Julia Reiss<sup>1</sup>, Murray S. A. Thompson<sup>8</sup> & Guy  
5 Woodward<sup>7</sup>

6  
7 **Mail corresponding author:** \* daniel.perkins@roehampton.ac.uk

8  
9 **Affiliations:** <sup>1</sup>*Department of Life Sciences, Whitelands College, University of Roehampton,*  
10 *London SW15 4JD, UK;* <sup>2</sup>*Cardiff Water Research Institute, Cardiff School of Biosciences,*  
11 *Cardiff University, PO Box 915, Cardiff CF10 3TL, UK;* <sup>3</sup> *Department of Zoology, University*  
12 *of Oxford, Oxford, OX1 3SZ;* <sup>4</sup>*School of Biological and Chemical Sciences, Queen Mary*  
13 *University of London, London E1 4NS, UK;* <sup>5</sup>*Centre for Ecology and Hydrology,*  
14 *Wallingford, OX10 8BB, UK;* <sup>6</sup>*Game & Wildlife Conservation Trust, Salmon & Trout*  
15 *Research Centre, Wareham, Dorset BH20 6BB;* <sup>7</sup>*Grand Challenges in Ecosystems and the*  
16 *Environment, Department of Life Sciences, Imperial College London, Silwood Park Campus,*  
17 *SL5 7PY, UK;* <sup>8</sup>*Centre for Environment, Fisheries and Aquaculture Science, Lowestoft*  
18 *Laboratory, Pakefield Road, Lowestoft, Suffolk, NR33 0HT, UK*

19  
20  
21 **Key words:** allometric scaling, body size, food webs, metabolic theory, stable isotopes,  
22 streams, secondary structure.

1 **Abstract**

2 The relationship between body mass (M) and size class abundance (N) depicts patterns of  
3 community structure and energy flow through food webs. While the general assumption is  
4 that M and N scale linearly (on log-log scales), non-linearity is regularly observed in natural  
5 systems, and is theorised to be driven by non-linear scaling of trophic level (TL) with M  
6 resulting in the rapid transfer of energy to consumers in certain size classes. We tested this  
7 hypothesis with data from 31 stream food webs. We predicted that allochthonous subsidies  
8 higher in the web results in non-linear M-TL relationships and systematic abundance peaks in  
9 macroinvertebrate- and fish size classes (latter containing salmonids), that exploit terrestrial  
10 plant material and terrestrial invertebrates, respectively. Indeed, both M-N and M-TL  
11 significantly deviated from linear relationships and the observed curvature in M-TL scaling  
12 was inversely related to that observed in M-N relationships. Systemic peaks in M-N, and  
13 troughs in M-TL occurred in size classes dominated by generalist invertebrates, and brown  
14 trout. Our study reveals how allochthonous resources entering high in the web systematically  
15 shape community size structure and demonstrates the relevance of a generalized metabolic  
16 scaling model for understanding patterns of energy transfer in energetically ‘open’ food webs.

17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34

## 1 **1. Introduction**

2  
3 The scaling of organism abundance with body mass is recognised as one of the few ‘laws’ in  
4 ecology [1,2]. When plotted on double logarithmic axes, total abundance (N) typically  
5 declines linearly with body mass (M) classes (M-N relationship *henceforth*) and reflects the  
6 efficiency of energy transfer from prey (of smaller size) to predators (of larger size) [1].  
7 Consequently, M-N relationships have been used for many decades as an integrated proxy for  
8 food web structure [3], particularly in strongly size-structured aquatic ecosystems [4].  
9 According to metabolic scaling theory [5,6], the slope of the M-N relationship can be  
10 predicted by the general model:  $-\frac{3}{4} + \log(\text{TE}) / \log(\text{PPMR})$ , where PPMR is the community-  
11 wide mean predator–prey mass ratio (the mean size of predators relative to prey) and TE is  
12 the trophic transfer efficiency. Thus, metabolic theory predicts a negative, linear M-N slope  
13 on log-log axes, and this has been reported widely in the literature [1,2].

14 However, these patterns are by no means universal and pronounced deviations from a  
15 linear M-N slope (and thus power-law relationship) are regularly observed [11]. This is  
16 commonly referred to as ‘secondary structure’ [11] and is characterised by dome-shaped  
17 patterns in the log-log M-N space [10–14], signifying that some size classes are over-  
18 represented relative to others. Although typically ignored, such deviations might provide an  
19 important signal of additional factors structuring natural food webs that can significantly  
20 improve predictions of energy flow over ‘simpler’ metabolic models [5,6].

21 A generalized metabolic scaling model of Chang et al. [13] proposes that the  
22 secondary structure of M-N relationships can arise under equilibrium conditions when the  
23 monotonic positive relationship between (log) body mass and trophic level (TL) is violated;  
24 that is, the M–TL relationship is nonlinear and PPMR varies with body mass. For example,  
25 large omnivorous zooplankton in lakes can occupy a lower trophic level than smaller, more  
26 carnivorous zooplankton but can exhibit similar abundances, resulting in points of local  
27 minima and maxima clearly visible in the residuals from linear M-N and M-TL fitting [13].

28 Allochthonous subsidies entering food webs in more ‘energetically open’ systems  
29 could conceivably lead to similar non-linearity in M-N and M-TL, if this additional energy is  
30 not uniformly accessible throughout the food web. For instance, energy flow in streams is  
31 supported by allochthonous resources received from the catchment [15], with terrestrial plant  
32 material and terrestrial invertebrates supporting a significant proportion of the production of  
33 detritivorous invertebrates [16] and drift-feeding fish, such as salmonids [17–19],  
34 respectively. Large invertebrates and fish that exploit these terrestrial subsidies should (in

1 theory) therefore have especially high abundances and occupy similar or lower trophic levels  
2 than other smaller, less abundant, organisms not exploiting the subsidy. Stable isotope  
3 analysis is a useful tool to test the latter and estimate the trophic position of consumers [7–9]  
4 and can be used to test this idea: nitrogen isotope values ( $\delta^{15}\text{N}$ ) increase predictably with  
5 trophic level [7–9] and if consumers of terrestrial plant material and terrestrial invertebrates -  
6 which exhibit lower  $\delta^{15}\text{N}$  values than autochthonous counterparts (e.g. [20,21]) - manifest  
7 lower  $\delta^{15}\text{N}$  than expected based on their body size, it is indicative of more generalist feeding  
8 via the exploitation of subsidies from beyond the aquatic food web.

9 Here, we build upon an extensive analysis of M-N scaling in 31 streams across the  
10 UK [19] by constructing M-TL relationships from size-based  $\delta^{15}\text{N}$  analysis to test these ideas  
11 about size structure and energy flow in these energetically open ecosystems. Specifically, we  
12 hypothesised that (i) stream food webs show nonlinear M-N and M- $\delta^{15}\text{N}$  relationships; (ii) the  
13 extent of non-linearity in M- $\delta^{15}\text{N}$  relationships can be predicted from M-N scaling (and *vice*  
14 *versa* [17]) and (iii) non-linearity of M-N and M- $\delta^{15}\text{N}$  relationships is linked to greater  
15 allochthonous resource use by certain consumer size classes.

## 16 17 **2. Methods**

### 18 19 **(a) Data acquisition**

20 We analysed data from Perkins et al. [19] comprising the body mass, numerical abundance  
21 and stable isotopic ratios of invertebrates and fish ( $10^{-3}$  to  $10^6$  mg dry mass) from 31 streams,  
22 spanning a broad environmental gradient (Table S1). Quantitative depletion electrofishing  
23 and invertebrate benthic sampling was performed over 25 - 100 m reaches at each stream,  
24 once in spring between 2005-2012 [19], to derive body mass and abundance per unit area  
25 data. Linear dimensions (e.g. head capsule width or body length) of each individual were  
26 measured to estimate body mass and individuals were identified to a high taxonomic level  
27 (usually species).

28 Fish fin clips and whole invertebrates (as well as basal and terrestrial resources) were  
29 analysed for carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ) stable isotopes, selecting a range of different  
30 sized individuals for each taxon (see Appendix S1 for detailed methods). Taxa sampled for  
31 isotope analysis represented the majority of macroinvertebrate and fish biomass (on average  
32 64 % and 94 %, respectively; Table S2).

### 33 34 **(b) Body mass-abundance and body mass-trophic level scaling**

1 M-N relationships were constructed with these data in Perkins et al. [19] using the  
2 logarithmic binning method, with individuals from a food web assigned to six ( $\log_{10}$ ) body  
3 mass bins, determined based upon the body mass range of each web [22]. Here we use the  
4 same binning approach and bin positions to estimate M-TL relationships using the isotope  
5 dataset [23]. We constructed M- $\delta^{15}\text{N}$  relationships [7–9], where  $\delta^{15}\text{N}$  represents the relative  
6 trophic level of consumers. We did this rather than converting  $\delta^{15}\text{N}$  to TL using a known  
7 baseline [13,24] because allochthonous (e.g. terrestrial detritus) and autochthonous (e.g.  
8 biofilm) basal resources in stream food webs can have very different  $\delta^{15}\text{N}$  values [20,21] but  
9 effectively have the same trophic level (TL = 1). Therefore changes in nitrogen isotope values  
10 of consumers do not necessarily reflect changes in trophic level. Instead, M- $\delta^{15}\text{N}$   
11 relationships allow us to identify the ‘apparent’ trophic level of each consumer size class and  
12 their primary resource (i.e. allochthonous or autochthonous). We account for potential  
13 variation in  $\delta^{15}\text{N}$  baselines between streams using cluster analysis and our statistical modeling  
14 approach (described below).  $\delta^{15}\text{N}$  values were biomass-weighted to reflect the proportional  
15 biomass of each taxon within each size bin [8,9], by calculating the contribution to total bin  
16 biomass for each taxon (Appendix S1).

17

### 18 **(c) Statistical analysis**

19 We followed the approach of Chang et al. [13] and grouped communities (streams) together  
20 using *K*-means cluster analysis (Fig. S1) because this yields a more robust estimate of the M-  
21  $\delta^{15}\text{N}$  relationship compared to doing this for individual food webs when sample sizes are  
22 small (Table S2). This was performed on the basis of similarity in mean  $\delta^{15}\text{N}$  and  $\delta^{13}\text{C}$  of  
23 invertebrates and fish (trophic structure), and the taxonomic richness (node diversity) of these  
24 groups (six variables  $\times$  31 streams matrix). *K*-means clustering was performed in R v 3.4.0  
25 [25] and the optimal number of clusters was determined from the lowest AIC score [12]. Two  
26 distinct clusters emerged with 8 (lowland, eutrophic) streams in cluster  $k_1$  and 23 (upland,  
27 oligotrophic) streams in cluster  $k_2$  (Fig. S1).

28 We tested for curvature in M-N and M- $\delta^{15}\text{N}$  relationships (hypothesis i) for each  
29 cluster using a two-step fitting procedure (after [13]). First, linear mixed effects analysis was  
30 performed using the lme4 package in R to determine M-N or M- $\delta^{15}\text{N}$  relationships for each  
31 cluster separately, with stream fitted as a random effect on the intercept [13] (Table S3).  
32 Second, the within-group residuals of the models were extracted and tested for polynomial  
33 relationships with body mass [13]. We fitted cubic, quadratic and linear models and assessed

1 model fit through AIC scores, and performed backwards model selection on these nested  
2 models using *F*-tests [26].

3 To test the generalized metabolic scaling model (hypothesis ii) we used the  
4 polynomial M-N relationship for each cluster to derive the predicted polynomial coefficients  
5 of the M- $\delta^{15}\text{N}$  relationships (after [13]). We adopted this approach rather than *vice versa*,  
6 since we expect the M-N dataset to be sampled with less error than the M-TL dataset where  
7 not all representatives within a size class were sampled (Table S2). To evaluate the model  
8 performance, a prediction on the second- or third-order coefficient was considered  
9 statistically consistent with the empirical observation if its 95% confidence interval overlaps  
10 with that of the observed coefficients [13].

11 Finally, to test whether non-linearity of M-N and M-TL relationships is linked to  
12 greater allochthonous resource use by certain consumer size classes (hypothesis iii), we  
13 inspected the taxonomic composition and allochthonous feeding by taxa within the size  
14 classes that overlapped with points of local minima and maxima of M-N and M- $\delta^{15}\text{N}$   
15 relationships. We further assessed whether allochthonous food resources for invertebrates and  
16 salmonids had distinct isotopic signatures compared to their autochthonous counterparts.  
17 Traditionally  $\delta^{13}\text{C}$  is used to distinguish between such sources ([24]), but in our data  
18 differences between autochthonous and allochthonous sources were weak (Fig. S2),  
19 compared to differences in  $\delta^{15}\text{N}$  [20,21]. Therefore, analysis of variance (ANOVA) was used  
20 to test for differences in  $\delta^{15}\text{N}$  between allochthonous detritus and biofilm, two ubiquitous  
21 resources for primary consumers [16]. In addition, we used detailed data from Tadnoll Brook  
22 where both terrestrial and stream invertebrates had been sampled more intensively [19], and  
23 compared using ANOVA  $\delta^{15}\text{N}$  values of these resources, as key components of salmonid diet  
24 [17–19].

### 28 **3. Results**

29  
30 Both M-N and M- $\delta^{15}\text{N}$  were reasonably approximated by linear relationships for both stream  
31 clusters (Fig. 1a,c). As hypothesized, however, significant curvature in M-N and M- $\delta^{15}\text{N}$   
32 residuals were evident for each cluster (Fig. 1b,d) and within individual sites (Fig. S3). AIC  
33 scores and backwards model selection revealed that these non-linear patterns were best  
34 characterised by 3<sup>rd</sup> order (cubic) polynomial models (Table 1), thus consistent with our

1 prediction of two distinct entry points for energy from allochthonous resources along the  
2 body mass continuum. Indeed, the cubic model provided a significantly better fit than the  
3 simpler quadratic or linear model (Table 1 & Table S3), with one marginal exception (Table  
4 1). Estimates of N and  $\delta^{15}\text{N}$  from linear models deviated considerably from those estimated  
5 from polynomial relationships for large invertebrate and fish size classes, indicated by large  
6 residual values ( $> 1$ ; Fig. 1b,d & Fig. 2).

7 As hypothesized, the generalized metabolic scaling model [13] successfully predicted  
8 the link between the non-linear M-N and M- $\delta^{15}\text{N}$  relationships. Model predictions based upon  
9 polynomial fit to M-N residuals were statistically consistent with the observed residuals of  
10 M- $\delta^{15}\text{N}$  relationships in three of the four cases (Table 2).

11 Two clear local maxima were evident in residuals of M-N relationships (Fig. 1b),  
12 occurring at approximately zero and five on the log<sub>10</sub> body mass scale (c. 1 mg and 100g dry  
13 weight, respectively), the same size classes where local minima in M- $\delta^{15}\text{N}$  residuals occurred  
14 (Fig. 1d; Fig. 2a). In line with our expectations, the relatively lower  $\delta^{15}\text{N}$  of these invertebrate  
15 and fish size classes (Fig. 2b,c) matched the consistently more depleted  $\delta^{15}\text{N}$  of allochthonous  
16 resources than their autochthonous counterparts: detritus had significantly lower  $\delta^{15}\text{N}$   
17 compared to biofilms ( $k_1$  ANOVA:  $F_{1,14} = 7.36, P = 0.0169$  &  $k_2$  ANOVA:  $F_{1,44} = 8.79, P =$   
18  $0.0049$ ; Fig. 2d) and  $\delta^{15}\text{N}$  of terrestrial prey taxa was significantly lower than comparable  
19 stream invertebrates (ANOVA:  $F_{1,46} = 41.21, P < 0.0001$ ; Fig. 2e). Thus, non-linearity in M-  
20 N and M- $\delta^{15}\text{N}$  scaling (Fig. 2a) was associated with more depleted  $\delta^{15}\text{N}$  (and relatively higher  
21 abundances) of large invertebrate and fish size classes (Fig. 2b,c), matching the lower  $\delta^{15}\text{N}$   
22 values of allochthonous resources (Fig. 2d,e).

#### 25 4. Discussion

26  
27 Our results reveal systematic variation in the scaling of trophic level and abundance with  
28 body mass among a large-scale stream food web dataset. Whilst as a first approximation N  
29 scales with M as predicted by general metabolic theory [5,6], the significant deviation from  
30 linear M-N relationships we observed signifies that some body mass classes are clearly over  
31 represented in terms of ‘expected’ abundance in an energetically closed system [10–14]. This  
32 was evident within individual sites (Fig. S3) and clusters of sites (Fig. 1). The generalised  
33 metabolic model [13] generally predicted the non-linearity in M- $\delta^{15}\text{N}$  relationships (and  
34 hence variation in PPMR) based upon the observed variation in M-N scaling. Our study



1 therefore supports the notion that M-N and M-TL relationships are quantitatively linked [13],  
2 and demonstrates that a more nuanced approach for characterising food web size structure  
3 can provide significantly better estimates of how abundance and trophic level changes with  
4 consumer body mass.

5 The extent of non-linearity in M-N and M- $\delta^{15}\text{N}$  relationships was similar for both  
6 stream clusters despite marked variation in trophic structure, diversity and composition (Fig.  
7 S1). This is somewhat surprising, especially as there was considerable background  
8 environmental variation between streams (lowland, eutrophic streams in  $k_1$  and upland,  
9 oligotrophic streams in  $k_2$ , Table S1) and given that pelagic systems have been shown to have  
10 stronger secondary structure when they are eutrophic [14]. The consistent non-linear M-N  
11 and M- $\delta^{15}\text{N}$  scaling we observed therefore suggests that running waters may be controlled by  
12 different mechanisms from those found in pelagic communities [14].

13 We suggest that allochthonous inputs (re)shape the size structure of stream food webs  
14 and give rise to the consistent non-linear relationships. Plotting residuals, we show that  
15 systemic peaks in M-N, and troughs in M- $\delta^{15}\text{N}$ , residuals occurred in size classes dominated  
16 by large generalist invertebrates [16] such as the crustacean *Gammarus pulex* (Fig. 2b), and  
17 the salmonid, *Salmo trutta* (Fig. 2c), which feed extensively on terrestrial prey items [18,19].  
18 The relatively lower  $\delta^{15}\text{N}$  (and higher abundance) of these classes, which had more depleted  
19 nitrogen isotope ratios than autochthonous counterparts [20,21], signifies that their utilisation  
20 of allochthonous resources subsidises their numerical abundance. Omnivory and complex  
21 microbial interactions have been proposed to give rise to non-linear M-TL relationships and  
22 secondary structure in aquatic food webs [13]; our results suggest that dominance of  
23 generalist consumers fuelled by allochthonous inputs high in stream food webs can result in  
24 similar patterns, reinforcing the notion that curvature in these relationships can be used as a  
25 measure of trophic complexity [13] or indeed the ‘openness’ of food webs. Further research is  
26 now required to understand how widespread this phenomenon might be within and across  
27 different ecosystems. The analytical framework used here could provide an instructive  
28 approach, especially where external subsidies have distinct  $\delta^{15}\text{N}$  values. For instance, the  
29 transportation of marine derived nitrogen via anadromous salmon carcasses is widely  
30 recognised to subsidise terrestrial food webs. In this case we might expect peaks (rather than  
31 troughs) in M- $\delta^{15}\text{N}$  relationships for size classes of terrestrial invertebrates that utilise this  
32 resource [27], but the extent of non-linearity in the M- $\delta^{15}\text{N}$  relationships should be  
33 quantitatively linked to that observed in M-N relationships [28]. Intriguingly, species such as  
34 brown trout and *G. pulex* are often seen as keystone species in many UK rivers and their

1 disproportionately influential roles might in fact be driven by their ability to partially  
2 decouple from the stream food web.

3 Here we show that non-linearity in M-N and M-TL relationships are related and  
4 linked to allochthonous inputs entering these food webs, and greater energy flow to large  
5 consumers so they appear “superabundant” as a result. Assessing non-linearity in body size  
6 structure could therefore provide a general, and yet powerful, approach for defining the  
7 complexity and dynamics of ecological communities, potentially paving the way for better  
8 assessments of energy flow in natural ecosystems.

9

10

### 11 **Funding**

12 The data underpinning this study were collected through Natural Environment Research  
13 Council grants NE/J015288/1 (awarded to G.W & I.D which also supported D.M.P. & K.L-  
14 D.) and NE/C511905/1 (awarded to J.I.J and which also supported R.B.L.), as well as  
15 research grants from the John Spedan Lewis Foundation (which supported M.S.A.T.), and  
16 British Ecological Society (awarded to D.M.P).

17

### 18 **Acknowledgements**

19 We thank two anonymous reviews who provided helpful comments that improved the  
20 manuscript.

21

22

23

### 24 **References**

25

- 26 1. White, E. P., Ernest, S. K. M., Kerkhoff, A. J. & Enquist, B. J. 2007 Relationships  
27 between body size and abundance in ecology. *Trends Ecol. Evol.* **22**, 323–30.  
28 (doi:10.1016/j.tree.2007.03.007)
- 29 2. Marquet, P. a, Quiñones, R. a, Abades, S., Labra, F., Tognelli, M., Arim, M. &  
30 Rivadeneira, M. 2005 Scaling and power-laws in ecological systems. *J. Exp. Biol.*  
31 **208**, 1749–69. (doi:10.1242/jeb.01588)
- 32 3. Yvon-Durocher, G., Reiss, J., Blanchard, J., Ebenman, B., Perkins, D. M.,  
33 Reuman, D. C., Thierry, A., Woodward, G. & Petchey, O. L. 2011 Across  
34 ecosystem comparisons of size structure: methods, approaches and prospects.

- 1 *Oikos* **120**, 550–563. (doi:10.1111/j.1600-0706.2010.18863.x)
- 2 4. Kerr, S. R. & Dickie, L. M. 2001 *The biomass spectrum: a predator-prey theory*  
3 *of aquatic production*. Columbia University Press.
- 4 5. Brown, J. H. & Gillooly, J. F. 2003 Ecological food webs: high-quality data  
5 facilitate theoretical unification. *Proc. Natl. Acad. Sci. U. S. A.* **100**, 1467–1468.  
6 (doi:10.1073/pnas.0630310100)
- 7 6. Brown, J., Gillooly, J., Allen, A., Savage, V. & West, G. 2004 Toward a  
8 metabolic theory of ecology. *Ecology* **85**, 1771–1789.
- 9 7. Jennings, S., Warr, K. & Mackinson, S. 2002 Use of size-based production and  
10 stable isotope analyses to predict trophic transfer efficiencies and predator-prey  
11 body mass ratios in food webs. *Mar. Ecol. Prog. Ser.* **240**, 11–20.  
12 (doi:10.3354/meps240011)
- 13 8. Trebilco, R., Dulvy, N. K., Anderson, S. C. & Salomon, A. K. 2016 The paradox  
14 of inverted biomass pyramids in kelp forest fish communities. *Proc. R. Soc. B*  
15 **283**, 20160816.
- 16 9. Trueman, C. N., Johnston, G., O’Hea, B. & MacKenzie, K. M. 2014 Trophic  
17 interactions of fish communities at midwater depths enhance long-term carbon  
18 storage and benthic production on continental slopes. *Proc. R. Soc. B Biol. Sci.*  
19 **281**, 20140669.
- 20 10. Sprules, W. G. & Goyke, A. P. 1994 Size-based structure and production in the  
21 pelagia of Lakes Ontario and Michigan. *Can. J. Fish. Aquat. Sci.* **51**, 2603–2611.
- 22 11. Gasol, J. M., Guerrero, R. & Pedros-Alio, C. 1991 Seasonal variations in size  
23 structure and procaryotic dominance in sulfurous Lake Ciso. *Limnol. Oceanogr.*  
24 **36**, 860–872.
- 25 12. Arranz, I., Hsieh, C. hao, Mehner, T. & Brucet, S. 2019 Systematic deviations  
26 from linear size spectra of lake fish communities are correlated with predator–  
27 prey interactions and lake-use intensity. *Oikos* **128**, 33–44.  
28 (doi:10.1111/oik.05355)
- 29 13. Chang, C.-W., Miki, T., Shiah, F.-K., Kao, S., Wu, J.-T., Sastri, A. R. & Hsieh, C.  
30 2014 Linking secondary structure of individual size distribution with nonlinear  
31 size-trophic level relationship in food webs. *Ecology* **95**, 897–909.
- 32 14. Rossberg, A. G., Gaedke, U. & Kratina, P. 2019 Dome patterns in pelagic size  
33 spectra reveal strong trophic cascades. *Nat. Commun.* **10**, 1–11.
- 34 15. Baxter, C. V, Fausch, K. D. & Carl Saunders, W. 2005 Tangled webs: reciprocal

- 1 flows of invertebrate prey link streams and riparian zones. *Freshw. Biol.* **50**, 201–  
2 220.
- 3 16. Cummins, K. W., Petersen, R. C., Howard, F. O., Wuycheck, J. C. & Holt, V. I.  
4 1973 The utilization of leaf litter by stream detritivores. *Ecology* **54**, 336–345.
- 5 17. Nakano, S., Miyasaka, H. & Kuhara, N. 1999 Terrestrial-aquatic linkages:  
6 riparian arthropod inputs alter trophic cascades in a stream food web. *Ecology* **80**,  
7 2435–2441.
- 8 18. Dineen, G., Harrison, S. S. C. & Giller, P. S. 2007 Diet partitioning in sympatric  
9 Atlantic salmon and brown trout in streams with contrasting riparian vegetation.  
10 *J. Fish Biol.* **71**, 17–38.
- 11 19. Perkins, D. M. et al. 2018 Bending the rules: exploitation of allochthonous  
12 resources by a top-predator modifies size-abundance scaling in stream food webs.  
13 *Ecol. Lett.* **21**, 1771–1780.
- 14 20. Twining, C. W., Brenna, J. T., Lawrence, P., Winkler, D. W., Flecker, A. S. &  
15 Hairston Jr, N. G. 2019 Aquatic and terrestrial resources are not nutritionally  
16 reciprocal for consumers. *Funct. Ecol.* **33**, 2042–2052.
- 17 21. Layer, K., Hildrew, A. G., Jenkins, G. B., Riede, J. O., Rossiter, S. J., Townsend,  
18 C. R. & Woodward, G. 2011 Long-term dynamics of a well-characterised food  
19 web: four decades of acidification and recovery in the Broadstone Stream model  
20 system. *Adv. Ecol. Res.* **44**, 69–117.
- 21 22. Perkins, D. M. et al. 2018 Data from: Bending the rules: exploitation of  
22 allochthonous resources by a top-predator modifies size-abundance scaling in  
23 stream food webs. (doi:doi.org/10.6084/m9.figshare.6882311)
- 24 23. Perkins, D. M., Durance, I., Jackson, M., Jones, J. I., Lauridsen, R. B., Layer-  
25 Dobra, K., Reiss, J., Thompson, M. S. A. & Woodward, G. 2021 Data from:  
26 Systematic variation in food web body-size structure linked to external subsidies.  
27 (doi:doi.org/10.6084/m9.figshare.9610112)
- 28 24. Post, D. M. 2002 Using stable isotopes to estimate trophic position: models,  
29 methods, and assumptions. *Ecology* **83**, 703–718.
- 30 25. R Development Core Team 2017 A language and environment for statistical  
31 computing.
- 32 26. Crawley, M. 2012 *The R book*.
- 33 27. Hocking, M. D., Ring, R. A. & Reimchen, T. E. 2009 The ecology of terrestrial

- 1           invertebrates on Pacific salmon carcasses. *Ecol. Res.* **24**, 1091–1100.
- 2   28.   Hocking, M. D., Dulvy, N. K., Reynolds, J. D., Ring, R. A. & Reimchen, T. E.
- 3           2013 Salmon subsidize an escape from a size spectrum. *Proc. R. Soc. London B*
- 4           *Biol. Sci.* **280**, 20122433.
- 5

**Table 1** Output from the analysis of body mass – abundance (M-N) and body mass – trophic level (M- $\delta^{15}\text{N}$ ) residuals for both stream clusters ( $k_1$  &  $k_2$ ). The 3rd order polynomial model is ranked best based upon AIC and results from  $F$ -tests highlight a significant decrease in model fit going from this most complex model to simpler (2<sup>nd</sup> order or linear) models, with one marginal exception.

<b>M-N</b>	<b>Model</b>	<b>AIC</b>	<b>Df</b>	<b>Res.Df</b>	<b>F-value</b>	<b>P-value</b>
$k_1$	log M + I(log M <sup>2</sup> ) + I(log M <sup>3</sup> )	84.33	5	44		
	log M + I(log M <sup>2</sup> )	110.12	4	45	34.49	<0.0001
	log M	113.17	3	46	21.61	<0.0001
$k_2$	log M + I(log M <sup>2</sup> ) + I(log M <sup>3</sup> )	161.46	5	112		
	log M + I(log M <sup>2</sup> )	212.76	4	113	65.32	<0.0001
	log M	228.55	3	114	47.35	<0.0001

  

<b>M-<math>\delta^{15}\text{N}</math></b>	<b>Model</b>	<b>AIC</b>	<b>Df</b>	<b>Res.Df</b>	<b>F-value</b>	<b>P-value</b>
$k_1$	log M + I(log M <sup>2</sup> ) + I(log M <sup>3</sup> )	121.28	5	34		
	log M + I(log M <sup>2</sup> )	123.95	4	35	4.44	0.0425
	log M	122.60	3	36	2.55	0.0926
$k_2$	log M + I(log M <sup>2</sup> ) + I(log M <sup>3</sup> )	311.95	5	104		
	log M + I(log M <sup>2</sup> )	324.47	4	105	14.97	0.0002
	log M	323.88	3	106	8.26	0.0005

**Table 2** Testing the generalized metabolic scaling model. The observations of the second- and third-order polynomial coefficients fitted to M- $\delta^{15}\text{N}$  residuals are generally consistent with predictions derived from the M-N secondary structure.

Cluster	Coefficient	Predicted			Observed		
		Estimate	Lower 95% CI	Upper 95% CI	Estimate	Lower 95% CI	Upper 95% CI
$k_1$	2nd order	0.27	0.19	0.36	0.33	0.03	0.63
	3rd order	-0.05	-0.07	-0.03	-0.04	-0.09	0.00
$k_2$	2nd order	0.26	0.21	0.31	0.37	0.19	0.56
	3rd order	-0.06	-0.08	-0.05	-0.06	-0.09	-0.03

**Figure 1** Body mass – abundance (a & b) and body mass – trophic level (c & d) relationships across 31 UK streams. Each data point (up to six per stream) denotes the abundance or biomass-weighted  $\delta^{15}\text{N}$  of a given size class. Linear fits (a & c) are estimated from mixed-effects modeling for each stream cluster ( $k_1$  &  $k_2$ ) and cubic polynomial relationships (b & d) are fitted to the residuals of these models. The dashed lines in (a) & (c) represent the significant polynomial fits to the raw data (Appendix S2).

**Figure 2** Systematic curvature in size structure linked to allochthonous inputs to stream food webs. (a) Curvature in the residuals of M-N (black curve) and M-  $\delta^{15}\text{N}$  (grey curve) relationships for both stream clusters ( $k_1$  &  $k_2$ ). (b & c) Wordle charts (based upon species abundance) for size classes overlapping with local maxima / minima of polynomial relationships (grey rectangles shown in (a)). (d & e) Comparison of  $\delta^{15}\text{N}$  between allochthonous and autochthonous resources. Significance codes: \*  $p < 0.05$ , \*\*  $p < 0.01$  & \*\*\*  $p < 0.001$ .