

1 **Biological traits and the transfer of persistent organic pollutants through river**  
2 **food webs**

3 Fredric M. Windsor<sup>1,2,†</sup>, M. Glória Pereira<sup>3</sup>, Charles R. Tyler<sup>2</sup>, Stephen J. Ormerod<sup>1</sup>

4 <sup>1</sup> School of Biosciences, Cardiff University, Cardiff, South Glamorgan, CF10 3AX, UK.

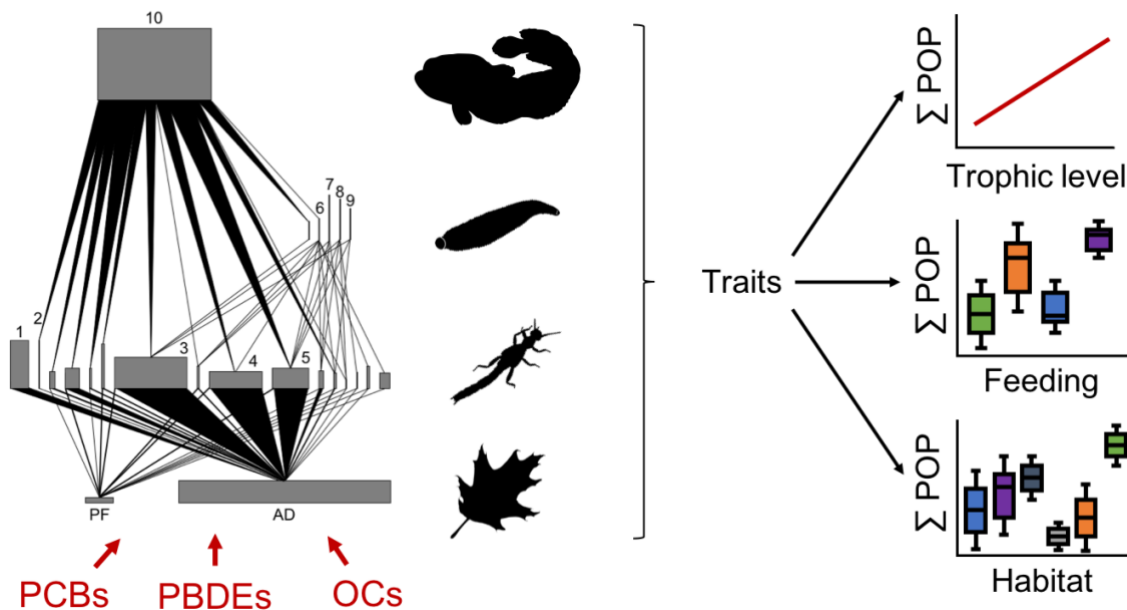
5 <sup>2</sup> Biosciences, University of Exeter, Exeter, Devon, EX4 4QD, UK.

6 <sup>3</sup> Centre for Ecology and Hydrology, Lancaster, Lancashire, LA1 4AP, UK.

7 \*Email: [fredric.windsor@newcastle.ac.uk](mailto:fredric.windsor@newcastle.ac.uk)

8 †Current address: School of Natural and Environmental Sciences, Newcastle  
9 University, Newcastle upon Tyne, Tyne and Wear, NE1 7RU, UK.

10 **Table of contents graphic**



11 **Abstract**

12 Freshwater organisms remain at risk from bioaccumulation and biomagnification of  
13 persistent organic pollutants (POPs), but factors affecting their transfer through food  
14 webs are poorly understood. Here we investigate transfer pathways of polychlorinated  
15 biphenyls (PCBs), polybrominated diphenyl ethers (PBDEs) and organochlorine (OCs)  
16 through a river food web, assessing the distribution and flux between basal resources  
17 (n=3), macroinvertebrates (n=22) and fish (n=1). We investigate the effects of  
18 biological traits on observed patterns and use trait-based models to predict POP  
19 bioaccumulation. Transfer pathways differed among POPs and traits such as habitat  
20 affinity, feeding behaviour and body size explained some variation in POP burdens  
21 between organisms. Trait-based models indicated that relationships between POPs,  
22 trophic transfers and traits were relatively well conserved across a wider array of river  
23 food webs. Although providing more consistent predictions of POP bioaccumulation  
24 than steady-state models, variability in bioaccumulation across food webs limited the  
25 accuracy of trait-model predictions. As some of the first data to illustrate how  
26 ecological processes alter the flux of pollutants through river food webs, these results  
27 reveal important links between POPs and contrasting energetic pathways. These data  
28 also show the utility of trait-based methods in the assessment of persistent  
29 contaminants, but further field validations are required.

30 **Key words:** bioaccumulation, biomagnification, ecological networks, organochlorines,  
31 PBDEs, PCBs, pesticides, legacy pollution, xenobiotics.

## 32 **1. Introduction**

33 Xenobiotic pollutants – chemicals which do not occur naturally in the environment –  
34 are distributed widely across the Earth’s freshwater ecosystems<sup>1</sup>. These pollutants are  
35 particularly hazardous to individual organisms and have impacts through a diverse  
36 array of pathways, including endocrine disruption<sup>2</sup>. Multiple taxonomic groups are at  
37 risk, including microbes<sup>3</sup>, benthic invertebrates<sup>4</sup>, fish<sup>5</sup> and aquatic birds<sup>6</sup>. In natural  
38 systems, these negative effects can transcend levels of biological organisation to  
39 affect populations, communities and ecosystems with consequences for ecosystem  
40 services and the functioning of the socio-biological system<sup>2,7</sup>.

41 Legacy organic chemicals are a group of xenobiotic pollutants that have largely been  
42 withdrawn from legal use, but remain widespread across freshwater ecosystems either  
43 because of their persistence, or low-level recirculation from discarded materials, land-  
44 fill or local illicit use<sup>8</sup>. Generally referred to as persistent organic pollutants (POPs),  
45 across Europe these chemicals often occur at relatively low environmental  
46 concentrations<sup>9</sup>, but their hydrophobic and lipophilic nature enables accumulation in  
47 freshwater organisms (invertebrates, fish, mammals) as well as significant  
48 magnification across the trophic levels of aquatic food webs<sup>10–15</sup>. Although the  
49 environmental concentrations of these chemicals might suggest a relatively low  
50 potential for ecological risks, long-term exposure, assimilation and subsequent  
51 accumulation and/or magnification of persistent contaminants could represent a  
52 continued threat to individual organisms, population and communities across the wider  
53 freshwater ecosystem<sup>2</sup>.

54 Although the bioaccumulation and biomagnification of POPs are key to understanding  
55 ecological risks from persistent and hydrophobic chemicals, factors affecting transfer  
56 processes and cascading ecological effects across trophic levels are poorly

57 understood<sup>16,17</sup>. Existing research suggests that chemical characteristics, organism  
58 biology and environmental characteristics might interact to influence the distribution  
59 and concentrations of POPs in aquatic and terrestrial food webs<sup>12,13,18</sup>, with chemical  
60 structure and concentration particularly important<sup>15,19</sup>. Food web structure might also  
61 affect POP behaviour, but much of the existing work has involved relatively simple  
62 ecosystems with restricted taxonomic or functional diversity and limited trophic  
63 interactions. Thus, although the general principle of bioaccumulation and trophic  
64 magnification of persistent pollutants is well established<sup>13</sup>, there is limited knowledge  
65 of how complex, multi-layer trophic interactions affect POP transfers. This includes  
66 significant gaps in understanding how persistent organic contaminants might enter  
67 and pervade river food webs linked to basal resources arising from autochthony (i.e.  
68 in-river primary production) or allochthony (i.e. matter such as leaf-litter originating  
69 from the riparian zone or catchment). These two resources contribute significantly to  
70 carbon and energy fluxes throughout freshwater ecosystems and are fundamental to  
71 their functioning<sup>20</sup>. Any change in the transfer of energy from basal resources has the  
72 potential to affect organism exposure to contaminants across trophic levels.

73 As well as insights from food-webs, biological trait analysis might also improve  
74 understanding of POP fluxes through ecosystems. Trait analysis has expanded  
75 generally in freshwater ecology, and has been applied to an increasing array of  
76 problems<sup>21</sup>. Although experimental studies have assessed the influence of biological  
77 traits on the accumulation of xenobiotic pollutants within the tissues of aquatic  
78 organisms<sup>22–25</sup>, the primary focus has been on physiological traits (e.g. size, growth)  
79 in just a small number of organisms from individual taxonomic groups. In natural  
80 systems, however, trait diversity is large<sup>26</sup> and influences several processes through  
81 variations in: (i) morphological and physiological traits, including biomass, mouthpart

82 morphology and life-cycle duration; (ii) ecological traits, regulating events or  
83 processes, including factors such as time of emergence, growth rate and dispersal  
84 mechanisms; and (iii) behavioural traits, relating to the specific activities of the  
85 organism, for example feeding and habitat preferences. All might affect the transfer  
86 and effects of POPs in freshwater communities<sup>2</sup>.

87 In this study, we aimed to assess transfer pathways of persistent pollutants  
88 (polychlorinated biphenyls [PCBs], polybrominated diphenyl ethers [PBDEs] and  
89 organochlorines [OCs]) through river food webs while also investigating the influence  
90 of biological traits on POP bioaccumulation across different aquatic taxa. Our focus  
91 on these legacy pollutants reflects their value as model substances whose distribution  
92 and behaviour are sufficiently well understood to aid in the development of methods  
93 for understanding the flux of compounds through food webs. We quantified POP body  
94 burdens and trophic interactions across a river food web in South Wales (United  
95 Kingdom), and used relationships among trophic transfers, biological traits and  
96 contaminant data to develop novel, trait-based models to estimate POP  
97 bioaccumulation across eight further UK river food webs. By comparing predictions  
98 from trait-based models and steady-state equations with direct measurements of  
99 bioaccumulation for invertebrate taxa, we tested the applicability of trait-based  
100 methods for field assessments of environmental pollution. We hypothesised that:

- 101 1. The transfer of POPs through food webs occurs alongside the flux of energy  
102 associated with different aquatic resources
- 103 2. Variation in bioaccumulation and biomagnification of POPs in food webs are  
104 related to biological traits
- 105 3. Trait-based models suitably predict the bioaccumulation of persistent organic  
106 pollutants across multiple food webs

## 107 **2. Methods and Materials**

### 108 **2.1. Sample site and the T1 food web**

109 The analysis of bioaccumulation, biomagnification trophic transfer of persistent  
110 pollutants through a river food web focussed on a 20 m stretch downstream of the  
111 Cynon Valley Wastewater Treatment Works (WwTWs) discharge into the River Taff,  
112 South Wales (51°37'41.8" N, 3°19'45.4" W) (T1; Fig. 1). This facility receives  
113 wastewater from the Rhondda-Cynon Valleys (approx. 63,000 people), and involves  
114 primary and secondary treatment, consisting of settlement, mechanical filtering and  
115 biological processing using percolating filter-beds. The surrounding catchment is  
116 highly urbanised (~20%), and contains a range of pollution sources, including  
117 combined sewer overflows, storm drains and road runoff drains, all of which have  
118 previously been shown to contribute to anthropogenic pollution loads in the Taff river  
119 system<sup>27</sup>. The diversity of discharges and presence of legacy pollutants in benthic  
120 sediments and biota at this location make it suitable to assess pollutant transfer  
121 through the food web – which consist of a range of invertebrates, and fish taxa that  
122 are representative of other hill streams recovering from past insanitary pollution<sup>28,29</sup>.

123 Samples were collected from 26 components of the river food web at T1 (May–August  
124 2017) including: basal resources (n = 3; microbial biofilm, macrophytes and sediment-  
125 bound allochthonous detritus), invertebrate taxa (n = 21), benthic fish (n = 1). All  
126 samples were collected under consultation and licence from Natural Resources Wales  
127 (see Table 1 for taxonomic detail). Methods varied with sample type. For basal  
128 resources, we amalgamated sediment grab samples (2 g) and biofilm scrapes (4 cm<sup>2</sup>).  
129 Composite samples of whole organisms were used for invertebrate taxa (5–200  
130 individuals per taxon) and composite samples of livers for fish (n = 5 individuals). We  
131 used fish livers as this organ provides a short-term store of dietary lipids<sup>30</sup>, thus

132 allowing evaluation of the trophic transfers of POPs from prey items<sup>31</sup>. Although POP  
133 concentrations in liver tissue are generally higher than in other fish tissues, they reflect  
134 variation in POP concentrations in other tissues and among individuals<sup>32,33</sup>.  
135 Approximately 1–2 g of each sample was collected and stored at -80°C rinsed glass  
136 vials (hexane/acetone; 1:1, v/v) until analysis (see Appendix S2 for detailed methods).

### 137 **3. Chemical analyses**

138 Environmental samples were analysed at the Centre for Ecology and Hydrology (CEH,  
139 Lancaster) for a range of contaminants (OCs: *p,p'*-DDT, *p,p'*-DDE and *p,p'*-DDD  
140 [TDE], dieldrin [HEOD],  $\alpha$ - and  $\gamma$ -hexachlorocyclohexane [HCH], hexachlorobenzene  
141 [HCB]; 36 PCB congeners and 23 PBDE congeners). Samples (0.5–2 g) were thawed,  
142 weighed accurately, ground with sand, dried with anhydrous sodium sulphate, spiked  
143 with internal recovery standards (<sup>13</sup>C OCs, <sup>13</sup>C PCBs and <sup>13</sup>C PBDEs), and Soxhlet-  
144 extracted with dichloromethane for 16 hours. A small proportion of the extract was  
145 subsampled and evaporated to zero volume under N, the lipid content was then  
146 determined gravimetrically. The remaining extract was subsequently cleaned using  
147 automated size exclusion chromatography followed by solid phase extraction through  
148 an alumina glass column packed with pre-treated alumina (12 hours at 550 °C) that  
149 was deactivated using deionised water 5% (w/w). The extract was divided into two:  
150 one fraction was spiked with internal standards (<sup>13</sup>C OCs and <sup>13</sup>C PCBs) for OCs and  
151 PCBs, and <sup>13</sup>C PBDEs for the PBDEs analyses. An aliquot of extract was injected into  
152 the gas chromatograph – mass spectrometer (Agilent, Wokingham, UK) using a 50 m  
153 (OCs and PCBs) or 25 m (PBDEs) HT8 column (0.22 mm internal diameter and 0.25  
154  $\mu$ m film thickness; SGE, Milton Keynes, UK), and programmable temperature  
155 vaporization inlet using different methods for OC/PCBs and PBDEs. Injector  
156 temperature was 250 °C and helium was used as the gas carrier (2.0 mL min<sup>-1</sup>). An

157 isothermal temperature regime was programmed at 50 °C for 2 min, then ramped at  
158 45 °C min<sup>-1</sup> to 200 °C, 1.5 °C min<sup>-1</sup> to 240 °C, 2 °C min<sup>-1</sup> to 285 °C, 50 °C min<sup>-1</sup> to 325  
159 °C and 350 °C for 10 minutes. Compounds were in electron ionisation mode. The  
160 internal standard method was used to quantify residues as well as calibration curves  
161 of commercially available standards for PCBs and OCs (Greyhound Ltd, Birkenhead,  
162 UK), and PBDEs (LGC Ltd., Teddington, UK). A series of procedural blanks were  
163 concurrently run, and samples were corrected based on recovery spikes. Recovery  
164 values were relatively consistent across all sample media and all compounds (85.8–  
165 103.9%). The detection limits for analyses averaged 0.04–0.11 ng g<sup>-1</sup> wet weight for  
166 all PBDE and PCB congeners, and OC compounds (Appendix S2).

167 Our metrics and concentrations are reported using wet weights (ww) for several  
168 reasons. First, for samples with low lipid contents, normalisation produces unreliable  
169 results, with unfeasible concentrations (e.g. >6000 ng g<sup>-1</sup> lipid weight for invertebrate  
170 taxa). This reflects poor performance of gravimetric lipid calculations for samples with  
171 <1% lipid concentrations<sup>34</sup>. Second, there are arguments against lipid normalisation  
172 under certain circumstances, such as here, where there is marked variation in the  
173 relationship between lipid content, trophic level and chemical concentrations<sup>35</sup>. Third,  
174 it is erroneous to presume that chemicals partition only to tissue lipids in organisms<sup>36</sup>,  
175 and although hydrophobic contaminants bind to lipids, not all contaminants will be  
176 solely associated with these compounds Fourth, wet weight concentrations are used  
177 in both bioaccumulation models and environmental risk assessments<sup>37–39</sup>. We also  
178 use wet weight for sediments due to the relatively low variation in particulate organic  
179 matter content across samples (0.04–0.06%).



### 180 **3.1. Quantitative food web construction**

181 To construct a quantitative network for the food web at T1, and to act as a basis for  
182 understanding pollutant flux, we used the trophic basis of production<sup>40</sup>. In outline, this  
183 uses of secondary production estimates while food web links are expressed as the  
184 flow of biomass from resources to consumers based on dietary information and  
185 estimates of secondary production that form the basis for energy flux (see Appendix  
186 S1). For macroinvertebrates, taxon-level secondary production ( $\text{mg m}^{-2} \text{ yr}^{-1}$ ) estimates  
187 were derived from monthly samples over 2016–2017 ( $n = 36$ ) in which individuals were  
188 identified to the lowest practical taxonomic unit (usually species or genus), counted  
189 and biomass derived from head width or body length measurement to the nearest  
190 0.1 mm ( $n = 9921$ ) using a Nikon SMZ800N stereomicroscope (Nikon, Tokyo, Japan),  
191 with a Lumenera Infinity 1-1M camera (Lumenera, Ontario, Canada) and visual  
192 analysis software (Infinity Analyse, version 6.5.4). Individual biomass (mg dry weight)  
193 was then calculated following published length-mass relationships<sup>41,42</sup>, and secondary  
194 production was calculated using the size-frequency method<sup>43</sup>. For rare taxa ( $n < 5$ )  
195 production was estimated using the Production/Biomass (P/B) value for the most  
196 closely related taxa. Fish secondary production could not be directly estimated, and  
197 instead we used a P/B ratio (2.00) derived from existing literature<sup>44</sup> coupled with an  
198 estimate of biomass ( $\text{g m}^{-2}$ ) generated from an electrofishing survey during July 2017,  
199 under licence from Natural Resources Wales.

200 Trophic links between organisms were derived from gut dissection of individual  
201 macroinvertebrates ( $n = 545$ ) and fish ( $n = 15$ ) in which the digestive tract of each  
202 individual was removed, and relative proportions of prey items enumerated using a  
203 gridded graticule. Where possible, organic material was identified as either plant  
204 fragments (and other allochthonous detritus) or microbial biofilms (polysaccharide

205 chains, diatoms, algae and other aquatic primary producers). We calculated a mean  
206 value of the proportion of resources utilised for each taxon, including both basal  
207 resources and other invertebrates. These proportions were then used in conjunction  
208 with the trophic basis of production method, to quantify food webs<sup>40</sup>. Based on data,  
209 the total flux of biomass to consumers (consumption) for each taxon could be  
210 separated among resources from (i) microbial biofilms (autochthonous) or (ii) detritus,  
211 organic matter and plant fragments (allochthonous).

212 The trophic level of each component of the quantitative food web ( $n = 26$ ), was  
213 calculated based on invertebrate community data, and modelled links across the wider  
214 food web, which comprised of 71 taxa (see Windsor et al.<sup>29</sup>). Trophic levels were  
215 chain-averaged (1 plus the weighted average of chain length of paths from the  
216 organism to the basal resources), where weights are the flux of energy and materials<sup>45</sup>  
217 to allow for extrapolation across river food webs. We also report a more common  
218 metric, prey-averaged trophic level (1 plus the mean trophic level of the consumer's  
219 resources), throughout the results section.

### 220 **3.2. Statistical analyses**

221 Data analysis used 'R' statistical software (version 3.4.0)<sup>46</sup>. Values for PCBs, PBDEs  
222 and OCs below the detection limits were noted throughout as not detected (ND), and  
223 for statistical analyses a value equal to the minimum detection limit (0.04 ng g<sup>-1</sup> ww)  
224 was applied. Prior to further analyses a series of exploratory steps, following Zuur et  
225 al.<sup>47</sup>, were completed to understand the structure of POP concentration data  
226 (heteroscedasticity, normality, outliers) and to inform the selection of further statistical  
227 tests and models.

228 To address the first hypothesis we analysed covariation in POP and transfer pathway  
229 data directly using Generalised Linear Models (GLMs)<sup>48</sup> with contaminant body burden  
230 data and data regarding the proportion of secondary production associated with the  
231 two types of basal resources (allochthonous and autochthonous). Further to this, these  
232 data were also used to calculate metrics describing the accumulation, magnification  
233 and transfer of POPs between organisms sampled from the T1 food web. Sediment  
234 bioaccumulation factors (BSAFs) for each taxon sampled were calculated using tissue  
235 concentration data in conjunction with the concentrations measured in sediment  
236 samples, following Equation 1:

$$(1) \quad \text{BSAF} = \frac{C_B}{C_{\text{STO}}}$$

237 where  $C_B$  is the concentration of POP groups (PBDEs, PCBs and OCs) measured in  
238 the tissues of the target organism ( $\text{ng g}^{-1}$  ww) and  $C_{\text{STO}}$  is the concentration measured  
239 in organic matter and sediments ( $\text{ng g}^{-1}$  ww). Biomagnification factors (BMFs) were  
240 also calculated for taxa across the food web to assess the organism-specific levels of  
241 biomagnification, following Equation 2:

$$(2) \quad \text{BMF} = \frac{C_B}{\sum(P_i C_{D_i})}$$

242 where  $C_B$  is the concentration of xenobiotic pollutants measured in the tissues of the  
243 target organism ( $\text{ng g}^{-1}$  ww),  $P_i$  is the proportion of prey organism or basal resource  
244 (sediments, detritus, plant material or microbial biofilm) observed in the diet of the  
245 target organism  $i$  (0–1) and  $C_{D_i}$  is the concentration of persistent pollutants measured  
246 in the tissues of the prey organism  $i$  ( $\text{ng g}^{-1}$  ww).

247 For the second hypothesis, we used trait data for the macroinvertebrates sampled at  
248 the T1 food web, collated from a European fuzzy-coded trait database<sup>49</sup>, to investigate  
249 inter-taxon variation within communities<sup>50,51</sup> and understand the consequences of

250 such structure for the transfer of pollutants. These trait data were supplemented by  
251 non-fuzzy, categorised feeding guild data for macroinvertebrate taxa of South Wales  
252 (Durance I & Ormerod S J, Unpublished data). Traits included those expected to be  
253 directly related to the accumulation of pollutants (e.g. feeding behaviour, trophic level  
254 and habitat affinity), as well as those that may indirectly alter accumulation, e.g. factors  
255 that determine the distribution of organisms in river systems and the pollution tolerance  
256 of taxa. In the following analyses, disaggregated trait data were utilised to assess the  
257 relationships between biological traits, bioaccumulation and biomagnification of POPs.  
258 Prior to trait-based modelling, trait affinity data were standardised across grouping  
259 features (overarching trait groups, for example feeding preference) to allow for  
260 improved comparisons between different traits and organisms. The exact methods  
261 used in the preparation and standardisation of fuzzy-coded trait data are described in  
262 more detail by Gutiérrez-Cánovas et al.<sup>52</sup>. Traits were selected initially based on their  
263 correlation with the BSAFs for each chemical group PBDEs, PCBs and OCs; Appendix  
264 S3) across the sampled taxa in the T1 river food web. We use BSAF values in models  
265 to minimise the effect of concentration-dependence which influences bioaccumulation  
266 of POPs and restricts the applicability of these models to other food webs where  
267 environmental concentrations may differ to those observed at the T1 food web. This  
268 allows for predictions across multiple sites, used to test the third hypothesis. Traits  
269 with an average coefficient of  $R \geq |0.40|$  were selected for further analysis. For this  
270 subset of traits the relationships between trait affinity and the BSAF values for PBDEs,  
271 PCBs and OCs, were assessed using GLMs. Global models were constructed for each  
272 chemical using the corrected Akaike Information Criterion (AICc) and the *dredge*  
273 function in 'MuMin'<sup>53</sup>. GLMs were then validated following procedures detailed in Zuur  
274 et al.<sup>54</sup> and Thomas et al.<sup>55</sup>. Residual normality was assessed using QQ plots,

275 homogeneity of variance was determined by plotting residuals against fitted values  
276 and influential observations were investigated using Cook's leverage distances.

277 The third hypothesis was tested using the BSAF GLMs (detailed above), a steady-  
278 state equation for estimating chemical bioaccumulation (AQUAWEB 1.2; Arnot and  
279 Gobas<sup>38</sup>), and a wider dataset of BSAFs calculated for invertebrate taxa from eight  
280 other river food webs sampled across South Wales, UK (Windsor<sup>56</sup>; Fig. 1).  
281 AQUAWEB models the bioaccumulation of non-ionic hydrophobic pollutants in  
282 organisms from concentrations in sediments and water by calculating the uptake and  
283 dietary transfer of chemicals. The model uses a series of toxicokinetic and  
284 toxicodynamic equations to predict the steady-state concentrations of compounds in  
285 compartments of the environment<sup>38</sup>. Through comparisons between the predictions  
286 from these two models and measured BSAFs, we assess the relative accuracy of both  
287 trophic- and trait-based models. Here we use Mean Absolute Error (MAE; Willmott and  
288 Matsuura<sup>57</sup>) calculated for relationships between the observed and predicted BSAFs  
289 to assess the performance and accuracy of models.

## 290 **4. Results**

### 291 **4.1. Concentrations of PCBs, PBDEs and OCs in the T1 food web**

292 POP concentrations varied widely in organisms at T1 (Table 1) and over 55% of  
293 compounds analysed were detected in <10% of samples. This was particularly true  
294 for some of the scarcer congeners, and for example PCBs 31, 126 and 157 were only  
295 observed in sediments and microbial biofilms. Conversely, PBDE congeners 28, 49,  
296 99, 100, 153 and 154, PCB 52 and *p,p'*-DDT were only observed in tissue samples  
297 from invertebrates and fish. Rather than treatment at congener level, therefore,

298 concentration data were aggregated for different chemical groups (PCBs, PBDEs and  
299 OCs) in further assessments of bioaccumulation and trophic magnification.

300 Total concentrations of PBDEs (Coefficient of variation [CV] = 0.61), PCBs (CV = 0.51)  
301 and OCs (CV = 0.64) remained highly variable across the T1 food web even after  
302 aggregation (Table 1). This, in part, reflected the magnification of POPs across trophic  
303 levels (Table 2), with predators such as *C. gobio*, *E. octoculata* and *Polycelis* spp.  
304 having the highest total concentrations of PBDEs, PCBs and OCs. Trophic level did  
305 not explain all variation, however (Table 3), and even some organisms feeding on the  
306 same resources and occupying the same trophic level had significantly differing  
307 pollutant concentrations at the same sample site (Table 1).

#### 308 **4.2. Transfer pathways of POPs through the T1 food web**

309 Trophic transfer pathways at T1 appeared to differ among PBDEs, PCBs and OCs  
310 (Table 2). Chlorinated compounds, particularly PCBs, were associated with the flux of  
311 allochthonous carbon from benthic detritus and organic matter (plant fragments) in  
312 samples from sediments, with higher concentrations observed in taxa making use of  
313 a greater proportion of these resources (Table 2 and Fig. 2). Taxa consuming a greater  
314 mass of allochthonous resources, as well as those consuming secondary production  
315 derived from allochthonous resources, appeared to have higher PCB concentrations  
316 ( $R_2 = 0.22$ ,  $F_{1,20} = 5.68$ ,  $p = 0.027$ ). In comparison, higher concentrations of PBDEs  
317 were associated with the flux of autochthonous carbon, increasing in taxa consuming  
318 primary and secondary production derived from microbial biofilms ( $R_2 = 0.48$ ,  
319  $F_{1,20} = 10.79$ ,  $p < 0.001$ ). Despite these significant relationships, the low  $R_2$  values in  
320 these for models indicate unexplained variation in POP concentrations, and there was  
321 no relationship with either autochthonous or allochthonous carbon consumption and  
322 the concentrations or flux of OCs ( $R_2 = 0.02$ ,  $F_{1,20} = 0.33$ ,  $p = 0.574$ ). The majority of

323 residual variation instead reflected the biological traits of different invertebrates, and  
324 this is considered below (Table 3).

#### 325 **4.3. Influence of biological traits on bioaccumulation**

326 Concentrations of POPs across the invertebrate food web were variable and related  
327 to biological traits, e.g. habitat affinity, substrate use, body size and voltinism (Table  
328 3). While there was some variation across chemical groups, biological traits explained  
329 a significant amount of the variation in PBDEs, PCBs and OCs across the food web  
330 (Table 3). Models constructed from biological traits in the T1 food web were able to  
331 predict BSAFs for PBDEs and OCs ( $R_2 = 0.92$ ,  $F_{1,61} = 712.60$ ,  $p < 0.001$ ; Fig. 3A) with  
332 a relatively low error (MAE = 0.14). For PCBs, the prediction of BSAF values was  
333 hindered by the low detection frequency (Table 1), which resulted in a relatively poor  
334  $R_2$  in the model. As such, BSAFs for PCBs were not predicted for validation sites.

#### 335 **4.4. Multi-model comparisons**

336 In trait-based models used to predict BSAFs for invertebrates more widely across  
337 South Wales, the PCB model was weakest ( $R_2 = 0.47$ ; Fig. 3B). In contrast, for both  
338 OCs and PBDEs, trait-based models were outperformed the AQUAWEB model for  
339 predicting BSAFs across the catchments (Fig. 3), with trait-based models having  
340 stronger linear relationships between observed and predicted values ( $R_2 = 0.22$ ,  
341  $F_{1,82} = 28.55$ ,  $p < 0.001$ ), as well as lower MAE for PBDEs and OCs, in comparison to  
342 AQUAWEB ( $R_2 = 0.03$ ,  $F_{1,82} = 2.51$ ,  $p = 0.117$ ). The inclusion of biological traits  
343 describing habitat affinities, physiological characteristics and trophic factors thus  
344 improved the accuracy and precision of predictions, although significant unexplained  
345 variation remained ( $R_2 = 0.22$ ). In general, predictions from the AQUAWEB model for  
346 PBDEs and PCBs were hindered by the infrequent detection of POPs in sediments

347 (coarse sand and gravel substrate), which often had concentrations below the mean  
348 limits of detection ( $\sim 0.04$  ng g<sup>-1</sup> ww). As trait-based models were not reliant on  
349 environmental concentration data they were less affected by this problem.

## 350 **5. Discussion**

351 The flux of POPs through the T1 river food web occurred through pathways linked to  
352 primary and secondary production arising from both allochthonous and autochthonous  
353 resources. These trophic transfers did not explain all variation in the POP  
354 concentrations measured in organisms, and POP bioaccumulation was related to the  
355 physiological, ecological and behavioural biological traits of organisms. Trait-based  
356 models constructed from twenty invertebrate taxa captured significant variation in the  
357 BSAFs for POP compounds across a wider suite of river food webs across South  
358 Wales. Despite performing better than steady-state equations, however, trait-based  
359 models were only able to estimate BSAFs to within one order of magnitude. Both these  
360 prediction methods were hindered by the low detection frequencies of POPs across  
361 environmental matrices (sediments and biofilms), as well as the significant variation in  
362 bioaccumulation not related to the combination of trophic interactions, biological traits  
363 or environmental concentrations of POPs. In total, these findings show how  
364 physiological, phenological and behavioural traits, as well as trophic characteristics of  
365 organisms (e.g. feeding habits), affect the flux and accumulation of POPs, but also  
366 highlight the variable nature of pollutant transfers across aquatic food webs.

367 There are several caveats over field-based assessments of pollutant transfers through  
368 food webs that should be considered when interpreting our findings. Firstly, although  
369 trait diversity was relatively high within the T1 food web, only a single food web was  
370 analysed in depth. Focusing on a single food web increased the potential influence of  
371 site-specific characteristics but limited the potentially confounding variation associated



372 with the structure of food webs and environmental conditions while capturing greater  
373 taxonomic and functional diversity than previous assessments. This, in turn, allowed  
374 for the construction of trait-based models and enabled predictions across sites.  
375 Secondly, there remain challenges associated with the use of fuzzy-coded trait data<sup>21</sup>:  
376 despite representing noisy data (e.g. size, feeding behaviour and substrate  
377 preferences), the multivariate nature of fuzzy coding makes the statistical assessment  
378 of relationships between groups of traits (e.g. feeding behaviour), trait affinities and  
379 other variables difficult. Our study assessed relationships between trait affinities and  
380 BSAF values, yet a more parsimonious approach would be to summarise the  
381 multivariate trait characteristics of individual taxa prior to modelling. Nevertheless,  
382 although trait-space methods exist for summarising and understanding the diversity of  
383 traits across taxa or communities (e.g. Gutiérrez-Cánovas et al.<sup>52</sup>), there are few  
384 suitable methods for consolidating fuzzy-coded trait data regarding individual taxa for  
385 predictive modelling purposes. Notwithstanding these caveats, our findings provide  
386 novel information about transfer pathways and the influence of biological traits on  
387 pollutant dynamics in natural systems.

388 Contaminant data coupled with information on the flux of energy and material across  
389 trophic interactions indicated multiple transfer pathways of PBDEs, PCBs and OCs  
390 through the T1 food web. Although widely detected, groups of POPs (PBDEs, PCBs  
391 and OCs) appeared to be differentially distributed across food web compartments, with  
392 initial partitioning occurring in the basal resources and a subsequent proliferation  
393 through the network alongside the transfer of different resources. Such partitioning  
394 and differential distribution of POPs across the basal resources, as well as across the  
395 wider food web may result from several factors. Firstly, the chemical properties of  
396 pollutants (e.g. partitioning coefficients) might alter the accumulation of POPs and

397 generate differential accumulation across food webs. Characteristics such as polarity,  
398 hydrophobicity and lipophilicity ( $\log K_{ow}$ ), as well as half-life (degradability), all  
399 influence the potential distribution of pollutants in the aquatic environment. For  
400 example, it has been previously shown that OCs have a high affinity for fine  
401 sediments<sup>58</sup> and plant detritus<sup>59</sup>, whilst PBDEs have been observed in high  
402 concentrations in microbial biofilms<sup>60</sup>. Thus, it may be that the affinity of different  
403 pollutant groups varies across these resources, and the interaction between the  
404 chemical properties of the pollutants and basal resources (e.g. organic matter content,  
405 polarity, hydrophobicity) could explain variable distributions across compartments. A  
406 second potential explanation is that pollutants may be partitioned as a result of their  
407 sources across the environment. For example, OCs and PCBs are often more  
408 prevalent in sediment and benthic organic matter as a result of their remobilisation  
409 across catchments (e.g. de Perre et al.<sup>61</sup>). In comparison, PBDEs may be present in  
410 microbial biofilms as a result of their more contemporary emissions, greater aqueous  
411 concentrations and thus greater potential for storage in surficial biofilms (e.g. Bartons  
412 et al.<sup>62</sup>). Certainly, the presence of highly brominated congeners across the food web  
413 indicates the potential for recent or active emissions, as these congeners are liable to  
414 degrade into less brominated congeners in the environment<sup>63</sup>. Although all plausible  
415 explanations, the exact mechanism responsible for the observed partitioning of  
416 different chemical groups across the food web remains uncertain. Further research,  
417 across multiple food webs, is also required to understand whether these patterns are  
418 present across multiple systems, or whether this is an artefact of environmental  
419 conditions present in our study.

420 Concentrations and the levels of bioaccumulation of all POPs in the T1 food web were  
421 related to variation in the biological traits of organisms. Some traits appeared to

422 consistently influence the concentrations of POP compounds, for example, affinity of  
423 organisms with different habitats in river systems (e.g. side pools, slow flowing regions  
424 of the channel and lowland systems), feeding behaviour (e.g. predator, filterer and  
425 grazer) and organism trophic level. Such patterns, in particular associations with  
426 feeding habitat, have been observed widely across aquatic food webs<sup>19,22,64–66</sup>. The  
427 other statistical relationships between ecological and behavioural traits further point  
428 towards the potential for the differential distribution of persistent compounds across  
429 the longitudinal and transversal profile of river systems. As a specific example, in the  
430 T1 food web organisms associated with side pools, twigs and detritus, as well as  
431 lowland stream systems exhibited higher OC, PCB and PBDE body burdens. Similar  
432 observations in tropical food webs for OCs reveal that slow flowing stream regions  
433 support greater volumes of fine sediment and detritus, facilitating an enhanced  
434 bioavailability and bioaccumulation of chemicals<sup>67</sup>. Yet, in general relationships such  
435 as this remain poorly understood. Other trait-pollutant relationships were specific to  
436 individual compounds. For example, OC bioaccumulation was greater in smaller  
437 organisms, potentially as a result of the biotransformation of compounds within larger  
438 invertebrates at higher trophic levels in the food web, as is shown for other organic  
439 pollutants<sup>68</sup>. The absence of this allometric relationship for PCBs and PBDEs may  
440 result from the fact that these chemicals are not rapidly transformed, e.g. the absence  
441 of PCB congener biotransformation in the tissues of mysids<sup>69</sup>. Here again, there is  
442 uncertainty about the basis for these relationships, especially as many processes  
443 related to the transformation of persistent chemicals are difficult to assess in natural  
444 systems without further information on chiral congeners<sup>69</sup>.

445 The enhanced accuracy of predictions from trait-based models, in comparison to  
446 steady-state equations, complements previous research that suggests that the

447 biological and ecological characteristics of food webs strongly influences the levels of  
448 accumulation and magnification<sup>15</sup>. Furthermore, this supports previous studies which  
449 have also shown the relatively limited effectiveness of steady-state models (traditional  
450 first-order, single compartment models) for predicting field-based BSAFs for  
451 organisms within river food webs due to the fact these models do not encapsulate  
452 dynamic processes<sup>70</sup>. Trait-models, however, were only able to predict BSAFs with  
453 approximately an order of magnitude accuracy, and large variation in BSAFs were  
454 observed across the wider suite of river food webs. This points towards exogenous  
455 drivers of variation in the bioaccumulation of POPs across these food webs. The  
456 unexplained variation likely results from differences in the bioavailability of POPs  
457 across sites or significant differences in the structure of the food webs. We thus  
458 suggest that the trait-based models presented here explained existing variation in  
459 bioaccumulation associated with biological traits, yet environmental variation and  
460 remaining broad-scale biological variation, relating to food web structure, perturbed  
461 accurate predictions.

462 Although only marginally better than existing methods in this study, the development  
463 of trait-based analyses is important, with several potential benefits. Firstly, modelling  
464 with invertebrate traits, that are conserved across continental scales<sup>71</sup>, provides a  
465 potential technique for large scale monitoring of the ecological risk from contaminants.  
466 Based on the assumption that taxa with similar biological traits respond similarly to  
467 pollutant exposure, the problems associated with highly variable regional taxonomy,  
468 and thus challenges in estimating risk for individual species, could be avoided.  
469 Secondly, such methods present an opportunity for early-warning tools to indicate the  
470 potential risk of bioaccumulation or ecological effects for organisms with specific  
471 combinations of biological traits. The development of such tools may contribute to

472 important next steps in improving assessments of risk relating to chemicals in advance  
473 of their introduction to the environment (see Godfray et al.<sup>72</sup>). More research is  
474 required to understand just how widely applicable trait-based methods are for  
475 predicting accumulation and ecological risk in different systems.

476 In summary, findings from this study demonstrate the importance of transfer pathways  
477 and biological traits in influencing the bioaccumulation and trophic magnification of  
478 pollutants across a riverine food web. Specific groups of chemicals were shown to  
479 accumulate differentially, in response to a variety of resources and transfer pathways  
480 within the food web. Magnification occurred for all compounds, yet biological traits  
481 influenced the relationship between trophic level and observed bioaccumulation –  
482 indicating that organisms occupying the same trophic level may be differential  
483 exposed to POPs. Trait-based models relatively predicted the bioaccumulation of  
484 POPs across multiple samples sites in South Wales relatively accurately. The trait-  
485 based model required less prior knowledge compared to other bioaccumulation  
486 models, such as AQUAWEB, and was based on publicly available trait data for  
487 freshwater invertebrates. This study demonstrates the importance of biological traits  
488 for the trophic transfer of pollutants and indicates the potential power of trait-based  
489 analyses for the prediction of food web scale ecotoxicological processes.

Table 1. Concentrations of POPs in the T1 river food web.

Sample	Trophic level*	Group	Lipid (%)	Concentration (ng g <sup>-1</sup> ww)**		
				∑PBDEs	∑PCBs	∑OCs
Sediment***	1.00	Resource	0.00	0.27	2.73	7.53
<i>Fontinalis</i> spp.	1.00	Resource	0.02	ND	18.30	1.95
Microbial biofilm	1.00	Resource	0.02	1.97	2.66	0.96
<i>Asellus</i> spp.	2.00	Gatherer	0.06	0.54	ND	1.56
<i>Leuctra</i> spp.	2.00	Shredder	0.09	1.10	12.24	7.68
<i>Rhithrogena semicolorata</i>	2.00	Grazer	0.15	2.03	ND	6.70
<i>Caenis</i> spp.	2.00	Gatherer	0.06	1.22	ND	6.92
Naididae	2.00	Gatherer	0.11	1.34	ND	2.87
<i>Ecdyonurus</i> spp.	2.00	Grazer	0.15	1.19	1.70	2.54
<i>Baetis</i> spp.	2.00	Grazer	0.15	3.64	0.56	4.86
<i>Radix</i> spp.	2.00	Grazer	0.05	1.35	4.40	6.30
<i>Heptagenia</i> spp.	2.00	Grazer	0.03	1.65	3.81	2.40
<i>Eiseniella tetraedra</i>	2.00	Gatherer	0.09	2.00	11.87	6.09
<i>Lepidostoma hirtum</i>	2.00	Gatherer	0.15	1.36	ND	24.28
Simuliidae	5.20	Filterer	0.08	1.12	0.66	0.36
<i>Serratella ignita</i>	5.24	Grazer	0.18	1.78	1.18	7.09
<i>Sericostoma personatum</i>	7.60	Gatherer	0.32	9.82	1.30	90.98
<i>Gammarus pulex</i>	8.06	Shredder	0.04	1.60	0.36	5.36
<i>Hydropsyche</i> spp.	8.69	Filterer	0.11	7.60	1.39	55.93
<i>Polycelis</i> spp.	8.77	Predator	0.39	8.29	1.65	127.94
<i>Platambus maculatus</i>	9.44	Predator	0.05	6.18	11.24	11.58
<i>Rhyacophila dorsalis</i>	9.98	Predator	0.14	1.67	ND	22.09
<i>Polycentropus</i> spp.	10.14	Predator	0.19	1.89	ND	27.19
<i>Erpobdella octoculata</i>	10.80	Predator	0.03	3.68	8.15	5.90
<i>Cottus gobio</i>	11.09	Predator	0.50	32.70	78.60	45.84

\*Chain-averaged trophic level (see Table 2 for prey-averaged values), \*\*ND = Not detected (below the limits of detection), \*\*\*Organic matter content was 0.04%

**Table 2. BSAFs and BMFs for PCBs, PBDEs and OCs across organisms in the T1 river food web.**

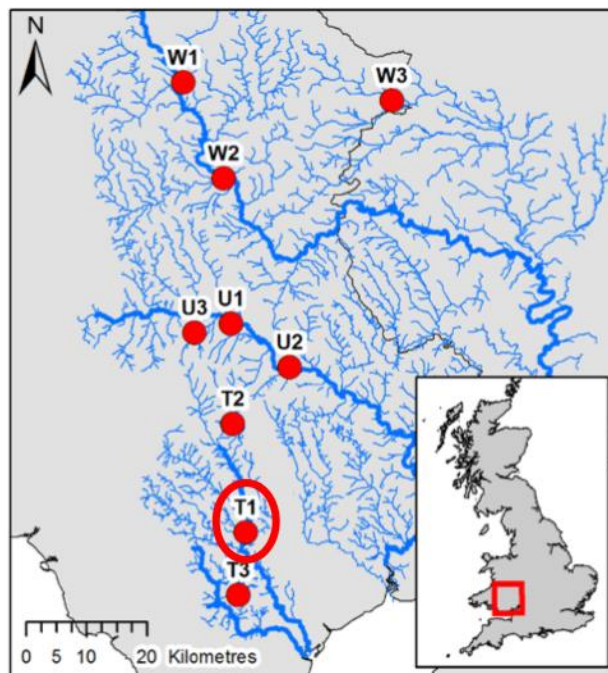
Sample	Trophic level (averaged)		Carbon ratio (Auto:Allo)	BSAF			BMF		
	Chain	Prey		∑PBDEs	∑PCBs	∑OCs	∑PBDEs	∑PCBs	∑OCs
<i>Asellus aquaticus</i>	2.00	2.00	0.49	2.04	-	0.21	0.49	-	0.37
<i>Leuctra</i> spp.	2.00	2.00	0.09	4.15	4.48	1.02	0.99	4.55	2.73
<i>Rhithrogena semicolorata</i>	2.00	2.00	4.98	7.64	-	0.89	1.03	-	7.99
<i>Caenis</i> spp.	2.00	2.00	0.50	4.59	-	0.92	1.09	-	1.58
Naididae	2.00	2.00	0.49	5.06	-	0.38	1.20	-	1.63
<i>Ecdyonurus</i> spp.	2.00	2.00	5.01	4.48	0.62	0.34	0.61	0.64	0.37
<i>Baetis</i> spp.	2.00	2.00	2.00	13.68	0.20	0.65	3.25	0.21	0.68
<i>Radix</i> spp.	2.00	2.00	0.49	5.07	1.61	0.84	1.21	1.64	0.60
<i>Heptagenia</i> spp.	2.00	2.00	2.01	6.21	1.40	0.32	1.48	1.42	1.15
<i>Eiseniella tetraedra</i>	2.00	2.00	0.11	7.51	4.35	0.81	1.79	4.41	1.67
<i>Lepidostoma hirtum</i>	2.00	2.00	0.49	5.12	-	3.22	1.22	-	1.26
Simuliidae	5.20	3.49	0.49	4.19	0.24	0.05	1.00	0.33	1.28
<i>Serratella ignita</i>	5.24	3.26	4.99	6.69	0.43	0.94	0.90	0.44	2.49
<i>Sericostoma personatum</i>	7.60	3.29	0.51	36.95	0.47	12.08	7.13	0.72	0.51
<i>Gammarus pulex</i>	8.06	3.44	0.02	6.02	0.13	0.71	0.99	0.09	1.01
<i>Hydropsyche</i> spp.	8.69	3.31	0.37	28.60	0.51	7.42	5.64	0.43	3.77
<i>Polycelis</i> spp.	8.77	3.61	0.39	31.19	0.60	16.98	7.55	0.50	26.63
<i>Platambus maculatus</i>	9.44	3.58	0.17	23.24	4.12	1.54	23.24	5.42	6.65
<i>Rhyacophila dorsalis</i>	9.98	3.29	0.62	6.28	-	2.93	0.85	-	6.41
<i>Polycentropus</i> spp.	10.14	3.29	0.57	7.13	-	3.61	0.94	-	1.97
<i>Erpobdella octoculata</i>	10.80	3.55	0.52	13.84	2.99	0.78	96.91	20.90	51.96
<i>Cottus gobio</i>	11.09	4.23	0.56	123.03	28.79	6.08	9.62	22.73	2.89

**Table 3. Results of predictive trait-based models relating biological traits to POP BSAFs in the T1 food web.** Relationships are presented as trait affinities within grouping features (see *Methods and materials*). Data were derived from both fuzzy-coded trait databases and food web data.

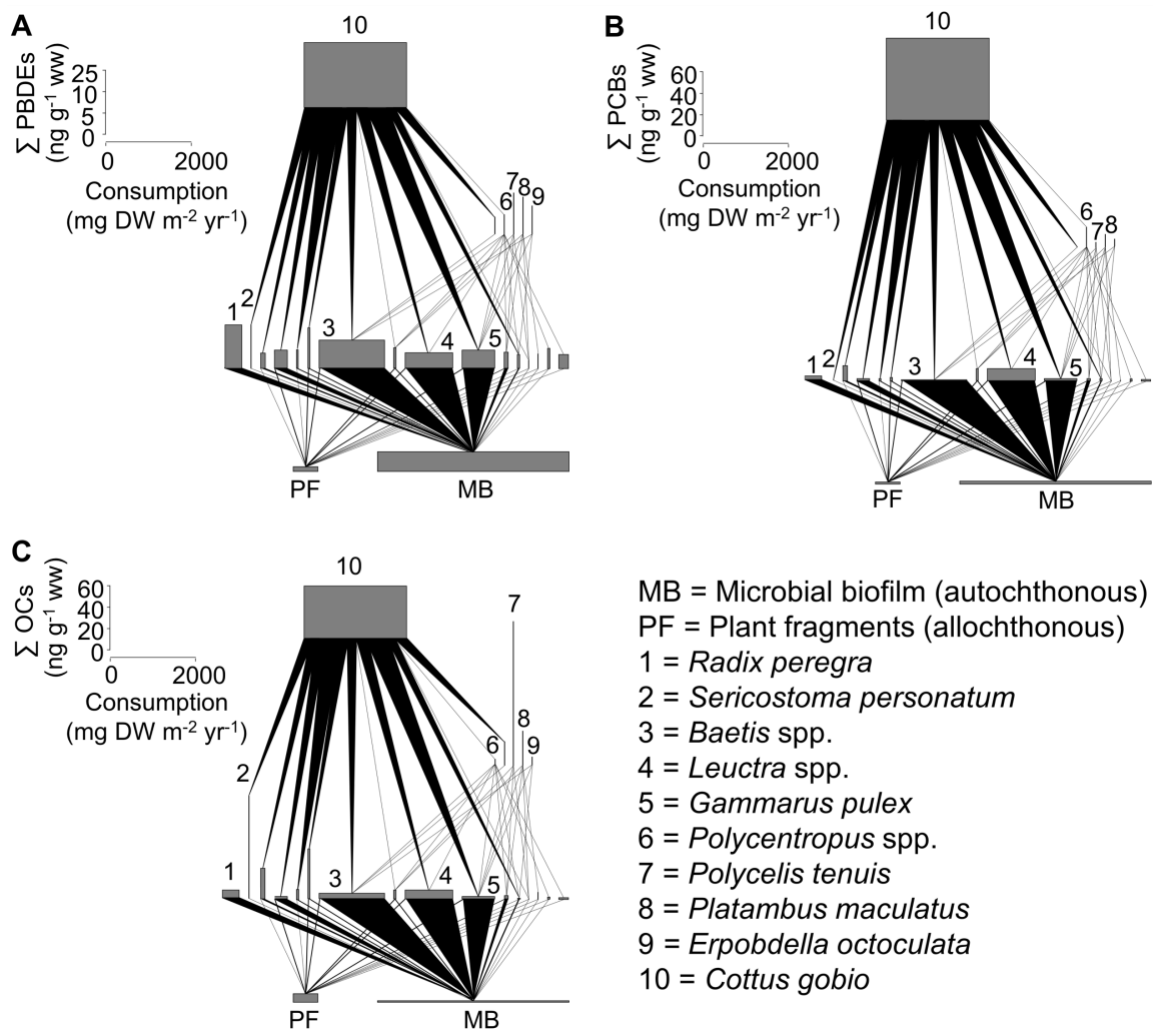
Pollutant	AICc	R <sub>2</sub>	Grouping feature (trait)	Effect ( $\pm$ SE)	t	p
$\Sigma$ PBDEs	38.40	0.69	Trophic level (Chain averaged)	0.11 (0.03)	3.46	0.003
			Feeding behaviour (Functional feeding guild)	1.93 (0.71)	2.78	0.081
			Longitudinal distribution (Estuary)	-3.27 (1.23)	-2.65	0.017
			Substrate (Microphytes)	-2.36 (3.01)	-0.79	0.445
			Reproduction (Isolated cemented eggs)	0.64 (0.25)	2.56	0.021
$\Sigma$ PCBs	76.81	0.47	Trophic level (Chain averaged)	0.17 (0.19)	0.87	0.235
			Feeding behaviour (Functional feeding guild)	1.71 (1.36)	1.25	0.027
			Longitudinal distribution (Estuary)	-5.30 (4.27)	-1.81	0.201
			Transversal distribution (Banks and side pools)	2.57 (2.73)	0.95	0.113
			Respiration (Gills)	-1.91 (1.23)	-1.55	0.042
$\Sigma$ OCs	54.10	0.84	Trophic level (Chain averaged)	0.14 (0.06)	2.77	0.019
			Feeding behaviour (Functional feeding guild)	1.77 (0.55)	3.23	0.009
			Dispersal mode (Active aquatic)	3.21 (0.82)	3.91	0.003
			Reproduction (Clutch cemented eggs)	0.40 (0.22)	1.83	0.098
			Substrate (Twigs and detritus)	-0.55 (1.51)	-0.55	0.593
			Saprobity (Oligosaprobic)	4.57 (0.83)	5.49	<0.001

AICc = Corrected Akaike Information Criterion; Effect = Effect size from GLM; SE = standard error; t = t-statistic from a Wald test.

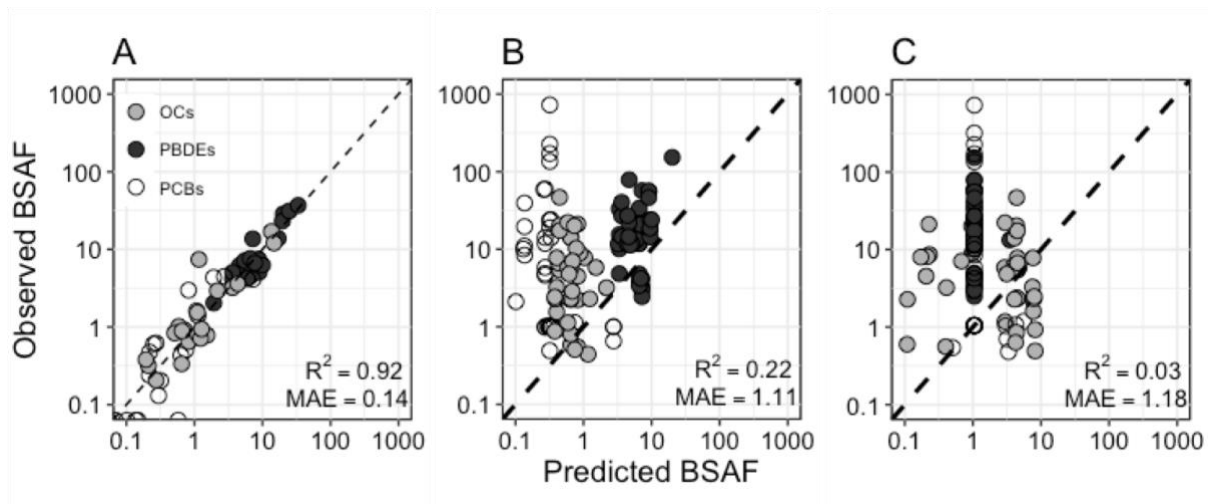




**Fig 1. Location of the T1 sample site.** T1 is part of a wider network of sites across South Wales which are used here for the validation of trait-models.



**Fig. 2. Quantitative food webs representing the flux of organic matter through the T1 river food web.** Data used to construct food webs were collected from monthly samples over an annual cycle (2016–2017). Food webs were summarised into four approximate trophic levels: the lowest bars are basal resources, the middle bars are primary and secondary macroinvertebrate consumers respectively, and the top bar is a predatory fish taxon (*Cottus gobio*). The relative height and width of bars correspond to the concentration of POP groups (PBDEs, PCBs and OCs) and the total consumption (total biomass flux from resources to consumers) for each taxon, respectively (see inset scales). The width of bars for basal resources relates to the total consumption of the resource by macroinvertebrate consumers (total flux from each resource to consumers). Black triangles linking the trophic levels are the contributions of resource fluxes to production in each consumer, aggregating to total inflow. The concentrations of each group of POPs measured in the tissues of organisms are reported on a wet weight basis (ng g<sup>-1</sup> ww).



**Fig. 3. Predicted versus observed POP BSAFs for trait-based and steady-state models data across river food webs in South Wales (UK). (A)** Data from the T1 food web. **(B)** Trait-based model predictions for validation data. **(C)** AQUAWEB 2.0 predictions for validation data. Validation data from Windsor (2019). Individual data points represent BSAFs calculated for individual organisms. Solid black lines indicate a 1:1 relationship between observed and predicted BSAF values. PCBs were excluded from statistical analyses due to the low detection frequency in chemical analyses, and thus the restricted proportion of explained variance in models which reduced the predictive ability of the trait-based model (presented here as hollow points).

492 **Supporting information**

493 **pdf.** Equations for trophic basis of production, taxa list for the T1 food web, trait data  
494 for sampled taxa, limits of detection for Gas Chromatography – Mass Spectrometry  
495 and relationships between traits and contaminant bioaccumulation.  
496 **txt.** Raw persistent organic compound concentration data for samples.

497 **Acknowledgements**

498 This work was supported by a studentship through the GW4+ Doctoral Training  
499 Partnership from the Natural Environment Research Council [NE/L002434/] (FMW).

500 Thanks go to the Environment Agency and Natural Resources Wales for providing  
501 secondary data. FMW would like to thank Heather Carter and Alex Hunter at CEH for  
502 assistance with chemical analyses of POPs. Finally, thanks to the many research  
503 assistants for help with data collection and sample processing.

504 **References**

- 505 (1) Malaj, E.; von der Ohe, P. C.; Grote, M.; Kühne, R.; Mondy, C. P.; Usseglio-  
506 Polatera, P.; Brack, W.; Schäfer, R. B. Organic Chemicals Jeopardize the  
507 Health of Freshwater Ecosystems on the Continental Scale. *Proc. Natl. Acad.*  
508 *Sci.* **2014**, *111* (26), 9549–9554. <https://doi.org/10.1073/pnas.1321082111>.
- 509 (2) Windsor, F. M.; Ormerod, S. J.; Tyler, C. R. Endocrine Disruption in Aquatic  
510 Systems: Up-Scaling Research to Address Ecological Consequences. *Biol.*  
511 *Rev.* **2018**, *93* (1), 626–641. <https://doi.org/10.1111/brv.12360>.
- 512 (3) López-Doval, J. C.; Ricart, M.; Guasch, H.; Romaní, A. M.; Sabater, S.;  
513 Muñoz, I. Does Grazing Pressure Modify Diuron Toxicity in a Biofilm  
514 Community? *Arch. Environ. Contam. Toxicol.* **2010**, *58* (4), 955–962.  
515 <https://doi.org/10.1007/s00244-009-9441-5>.
- 516 (4) Soin, T.; Smagghe, G. Endocrine Disruption in Aquatic Insects: A Review.  
517 *Ecotoxicology* **2007**, *16* (1), 83–93. [https://doi.org/10.1007/s10646-006-0118-](https://doi.org/10.1007/s10646-006-0118-9)  
518 [9](https://doi.org/10.1007/s10646-006-0118-9).
- 519 (5) Kloas, W.; Urbatzka, R.; Opitz, R.; Würtz, S.; Behrends, T.; Hermelink, B.;  
520 Hofmann, F.; Jagnytsch, O.; Kroupova, H.; Lorenz, C.; et al. Endocrine  
521 Disruption in Aquatic Vertebrates. *Ann. N. Y. Acad. Sci.* **2009**, *1163*, 187–200.  
522 <https://doi.org/10.1111/j.1749-6632.2009.04453.x>.
- 523 (6) Morrissey, C. A.; Stanton, D. W. G.; Tyler, C. R.; Pereira, M. G.; Newton, J.;  
524 Durance, I.; Ormerod, S. J. Developmental Impairment in Eurasian Dipper  
525 Nestlings Exposed to Urban Stream Pollutants. *Environ. Toxicol. Chem.* **2014**,  
526 *33* (6), 1315–1323. <https://doi.org/10.1002/etc.2555>.
- 527 (7) Chagnon, M.; Kreuzweiser, D.; Mitchell, E. A. D.; Morrissey, C. A.; Noome, D.  
528 A.; Van der Sluijs, J. P. Risks of Large-Scale Use of Systemic Insecticides to  
529 Ecosystem Functioning and Services. *Environ. Sci. Pollut. Res.* **2015**, *22* (1),  
530 119–134. <https://doi.org/10.1007/s11356-014-3277-x>.
- 531 (8) McKnight, U. S.; Rasmussen, J. J.; Kronvang, B.; Binning, P. J.; Berg, P. L.  
532 Sources, Occurrence and Predicted Aquatic Impact of Legacy and  
533 Contemporary Pesticides in Streams. *Environ. Pollut.* **2015**, *200*, 64–76.  
534 <https://doi.org/10.1016/J.ENVPOL.2015.02.015>.

- 535 (9) Rasmussen, J. J.; Wiberg-Larsen, P.; Baattrup-Pedersen, A.; Cedergreen, N.;  
536 McKnight, U. S.; Kreuger, J.; Jacobsen, D.; Kristensen, E. A.; Friberg, N. The  
537 Legacy of Pesticide Pollution: An Overlooked Factor in Current Risk  
538 Assessments of Freshwater Systems. *Water Res.* **2015**, *49*, 25–32.  
539 <https://doi.org/10.1016/j.watres.2015.07.021>.
- 540 (10) Streets, S. S.; Henderson, S. A.; Stoner, A. D.; Carlson, D. L.; Simcik, M. F.;  
541 Swackhamer, D. L. Partitioning and Bioaccumulation of PBDEs and PCBs in  
542 Lake Michigan. *Environ. Sci. Technol.* **2006**, *40* (23), 7263–7269.  
543 <https://doi.org/10.1021/es061337p>.
- 544 (11) Wu, J.-P.; Luo, X.-J.; Zhang, Y.; Yu, M.; Chen, S.-J.; Mai, B.-X.; Yang, Z.-Y.  
545 Biomagnification of Polybrominated Diphenyl Ethers (PBDEs) and  
546 Polychlorinated Biphenyls in a Highly Contaminated Freshwater Food Web  
547 from South China. *Environ. Pollut.* **2009**, *157* (3), 904–909.  
548 <https://doi.org/10.1016/j.envpol.2008.11.001>.
- 549 (12) Kelly, B. C.; Ikonomou, M. G.; Blair, J. D.; Morin, A. E.; Gobas, F. A. P. C.  
550 Food Web-Specific Biomagnification of Persistent Organic Pollutants. *Science*  
551 *(80-. )*. **2007**, *317* (5835), 236–239. <https://doi.org/10.1126/science.1138275>.
- 552 (13) Walters, D. M.; Jardine, T. D.; Cade, B. S.; Kidd, K. A.; Muir, D. C. G.; Leipzig-  
553 Scott, P. Trophic Magnification of Organic Chemicals: A Global Synthesis.  
554 *Environ. Sci. Technol.* **2016**, *50* (9), 4650–4658.  
555 <https://doi.org/10.1021/acs.est.6b00201>.
- 556 (14) Walters, D. M.; Mills, M. A.; Cade, B. S.; Burkard, L. P. Trophic Magnification  
557 of PCBs and Its Relationship to the Octanol–water Partition Coefficient.  
558 *Environ. Sci. Technol.* **2011**, *45* (9), 3917–3924.  
559 <https://doi.org/10.1021/es103158s>.
- 560 (15) Walters, D. M.; Fritz, K. M.; Johnson, B. R.; Lazorchak, J. M.; McCormick, F.  
561 H. Influence of Trophic Position and Spatial Location on Polychlorinated  
562 Biphenyl (PCB) Bioaccumulation in a Stream Food Web. *Environ. Sci.*  
563 *Technol.* **2008**, *42* (7), 2316–2322. <https://doi.org/10.1021/es0715849>.
- 564 (16) Meador, J. P.; Adams, W. J.; Escher, B. I.; McCarty, L. S.; McElroy, A. E.;  
565 Sappington, K. G. The Tissue Residue Approach for Toxicity Assessment:  
566 Findings and Critical Reviews from a Society of Environmental Toxicology and

- 567 Chemistry Pellston Workshop. *Integr. Environ. Assess. Manag.* **2011**, 7 (1), 2–  
568 6. <https://doi.org/10.1002/ieam.133>.
- 569 (17) Escher, B. I.; Ashauer, R.; Dyer, S.; Hermens, J. L.; Lee, J.-H.; Leslie, H. A.;  
570 Mayer, P.; Meador, J. P.; Warne, M. S. Crucial Role of Mechanisms and  
571 Modes of Toxic Action for Understanding Tissue Residue Toxicity and Internal  
572 Effect Concentrations of Organic Chemicals. *Integr. Environ. Assess. Manag.*  
573 **2011**, 7 (1), 28–49. <https://doi.org/10.1002/ieam.100>.
- 574 (18) Kelly, B. C.; Ikononou, M. G.; Blair, J. D.; Gobas, F. A. P. C. Bioaccumulation  
575 Behaviour of Polybrominated Diphenyl Ethers (PBDEs) in a Canadian Arctic  
576 Marine Food Web. *Sci. Total Environ.* **2008**, 401 (1–3), 60–72.  
577 <https://doi.org/10.1016/j.scitotenv.2008.03.045>.
- 578 (19) Fisk, A. T.; Hobson, K. A.; Norstrom, R. J. Influence of Chemical and Biological  
579 Factors on Trophic Transfer of Persistent Organic Pollutants in the Northwater  
580 Polynya Marine Food Web. *Environ. Sci. Technol.* **2001**, 35 (4), 732–738.  
581 <https://doi.org/10.1021/ES001459W>.
- 582 (20) Brett, M. T.; Bunn, S. E.; Chandra, S.; Galloway, A. W. E.; Guo, F.; Kainz, M.  
583 J.; Kankaala, P.; Lau, D. C. P.; Moulton, T. P.; Power, M. E.; et al. How  
584 Important Are Terrestrial Organic Carbon Inputs for Secondary Production in  
585 Freshwater Ecosystems? *Freshw. Biol.* **2017**, 62 (5), 833–853.  
586 <https://doi.org/10.1111/fwb.12909>.
- 587 (21) Menezes, S.; Baird, D. J.; Soares, A. M. V. M. Beyond Taxonomy: A Review of  
588 Macroinvertebrate Trait-Based Community Descriptors as Tools for  
589 Freshwater Biomonitoring. *J. Appl. Ecol.* **2010**, 47 (4), 711–719.  
590 <https://doi.org/10.1111/j.1365-2664.2010.01819.x>.
- 591 (22) Sidney, L. A.; Diepens, N. J.; Guo, X.; Koelmans, A. A. Trait-Based Modelling  
592 of Bioaccumulation by Freshwater Benthic Invertebrates. *Aquat. Toxicol.* **2016**,  
593 176, 88–96. <https://doi.org/10.1016/j.aquatox.2016.04.017>.
- 594 (23) Rubach, M. N.; Ashauer, R.; Buchwalter, D. B.; De Lange, H.; Hamer, M.;  
595 Preuss, T. G.; Töpke, K.; Maund, S. J. Framework for Traits-Based  
596 Assessment in Ecotoxicology. *Integr. Environ. Assess. Manag.* **2011**, 7 (2),  
597 172–186. <https://doi.org/10.1002/ieam.105>.



- 598 (24) Diepens, N. J.; Van den Heuvel-Greve, M. J.; Koelmans, A. A. Modeling of  
599 Bioaccumulation in Marine Benthic Invertebrates Using a Multispecies  
600 Experimental Approach. *Environ. Sci. Technol.* **2015**, *49* (22), 13575–13585.  
601 <https://doi.org/10.1021/acs.est.5b02500>.
- 602 (25) Gaskell, P. N.; Brooks, A. C.; Maltby, L. Variation in the Bioaccumulation of a  
603 Sediment-Sorbed Hydrophobic Compound by Benthic Macroinvertebrates:  
604 Patterns and Mechanisms. *Environ. Sci. Technol.* **2007**, *41* (5), 1783–1789.  
605 <https://doi.org/10.1021/es061934b>.
- 606 (26) Schmera, D.; Podani, J.; Heino, J.; Erős, T.; Poff, N. L. A Proposed Unified  
607 Terminology of Species Traits in Stream Ecology. *Freshw. Sci.* **2015**, *34* (3),  
608 823–830. <https://doi.org/10.1086/681623>.
- 609 (27) Williams, A. T.; Simmons, S. L. Sources of Riverine Litter: The River Taff,  
610 South Wales, UK. *Water, Air, Soil Pollut.* **1999**, *112* (1/2), 197–216.  
611 <https://doi.org/10.1023/A:1005000724803>.
- 612 (28) Vaughan, I. P.; Ormerod, S. J. Large-Scale, Long-Term Trends in British River  
613 Macroinvertebrates. *Glob. Chang. Biol.* **2012**, *18* (7), 2184–2194.  
614 <https://doi.org/10.1111/j.1365-2486.2012.02662.x>.
- 615 (29) Windsor, F. M.; Pereira, M. G.; Tyler, C. R.; Ormerod, S. J. Persistent  
616 Contaminants as Potential Constraints on the Recovery of Urban River Food  
617 Webs from Gross Pollution. *Water Res.* **2019**, *163*, 114858.  
618 <https://doi.org/10.1016/j.watres.2019.114858>.
- 619 (30) Tocher, D. R. Metabolism and Functions of Lipids and Fatty Acids in Teleost  
620 Fish. *Rev. Fish. Sci.* **2003**, *11* (2), 107–184.  
621 <https://doi.org/10.1080/713610925>.
- 622 (31) Monosson, E.; Ashley, J. T. F.; McElroy, A. E.; Woltering, D.; Elskus, A. A.  
623 PCB Congener Distributions in Muscle, Liver and Gonad of *Fundulus*  
624 *Heteroclitus* from the Lower Hudson River Estuary and Newark Bay.  
625 *Chemosphere* **2003**, *52* (4), 777–787. [https://doi.org/10.1016/S0045-](https://doi.org/10.1016/S0045-6535(03)00228-5)  
626 [6535\(03\)00228-5](https://doi.org/10.1016/S0045-6535(03)00228-5).
- 627 (32) Borghesi, N.; Corsolini, S.; Focardi, S. Levels of Polybrominated Diphenyl  
628 Ethers (PBDEs) and Organochlorine Pollutants in Two Species of Antarctic

- 629 Fish (*Chionodraco Hamatus* and *Trematomus Bernacchii*). *Chemosphere*  
630 **2008**, 73 (2), 155–160. <https://doi.org/10.1016/j.chemosphere.2008.06.031>.
- 631 (33) Teil, M. J.; Tlili, K.; Blanchard, M.; Chevreuil, M.; Alliot, F.; Labadie, P.  
632 Occurrence of Polybrominated Diphenyl Ethers, Polychlorinated Biphenyls,  
633 and Phthalates in Freshwater Fish from the Orge River (Ile-de France). *Arch.*  
634 *Environ. Contam. Toxicol.* **2012**, 63 (1), 101–113.  
635 <https://doi.org/10.1007/s00244-011-9746-z>.
- 636 (34) Muir, D.; Sverko, E. Analytical Methods for PCBs and Organochlorine  
637 Pesticides in Environmental Monitoring and Surveillance: A Critical Appraisal.  
638 *Anal. Bioanal. Chem.* **2006**, 386 (4), 769–789. [https://doi.org/10.1007/s00216-](https://doi.org/10.1007/s00216-006-0765-y)  
639 [006-0765-y](https://doi.org/10.1007/s00216-006-0765-y).
- 640 (35) Hebert, C. E.; Keenleyside, K. A. To Normalize or Not to Normalize? Fat Is the  
641 Question. *Environ. Toxicol. Chem.* **1995**, 14 (5), 801–807.  
642 <https://doi.org/10.1002/etc.5620140509>.
- 643 (36) Powell, D. E.; Schøyen, M.; Øxnevad, S.; Gerhards, R.; Böhmer, T.; Koerner,  
644 M.; Durham, J.; Huff, D. W. Bioaccumulation and Trophic Transfer of Cyclic  
645 Volatile Methylsiloxanes (CVMS) in the Aquatic Marine Food Webs of the  
646 Oslofjord, Norway. *Sci. Total Environ.* **2018**, 622–623, 127–139.  
647 <https://doi.org/10.1016/J.SCITOTENV.2017.11.237>.
- 648 (37) Thomann, R. V. Bioaccumulation Model of Organic Chemical Distribution in  
649 Aquatic Food Chains. *Environ. Sci. Technol.* **1989**, 23 (6), 699–707.  
650 <https://doi.org/10.1021/es00064a008>.
- 651 (38) Arnot, J. A.; Gobas, F. A. P. C. A Food Web Bioaccumulation Model for  
652 Organic Chemicals in Aquatic Ecosystems. *Environ. Toxicol. Chem.* **2004**, 23  
653 (10), 2343–2355. <https://doi.org/10.1897/03-438>.
- 654 (39) Ross, P. S.; Birnbaum, L. S. Integrated Human and Ecological Risk  
655 Assessment: A Case Study of Persistent Organic Pollutants (POPs) in  
656 Humans and Wildlife. *Hum. Ecol. Risk Assess. An Int. J.* **2003**, 9 (1), 303–324.  
657 <https://doi.org/10.1080/727073292>.
- 658 (40) Benke, A. C.; Wallace, J. B. Trophic Basis of Production among Riverine  
659 Caddisflies: Implication for Food Web Analysis. *Ecology* **1997**, 78 (4), 1132–

- 660 1145. [https://doi.org/10.1890/0012-9658\(1997\)078\[1132:TBOPAR\]2.0.CO;2](https://doi.org/10.1890/0012-9658(1997)078[1132:TBOPAR]2.0.CO;2).
- 661 (41) Baumgärtner, D.; Rothhaupt, K.-O. Predictive Length–Dry Mass Regressions  
662 for Freshwater Invertebrates in a Pre-Alpine Lake Littoral. *Int. Rev. Hydrobiol.*  
663 **2003**, *88* (5), 453–463. <https://doi.org/10.1002/iroh.200310632>.
- 664 (42) Benke, A. C.; Hury, A. D.; Smock, L. A.; Wallace, J. B. Length-Mass  
665 Relationships for Freshwater Macroinvertebrates in North America with  
666 Particular Reference to the Southeastern United States. *J. North Am. Benthol.*  
667 *Soc.* **1999**, *18* (3), 308–343. <https://doi.org/10.2307/1468447>.
- 668 (43) Waters, T. F. Secondary Production in Inland Waters. *Adv. Ecol. Res.* **1977**,  
669 *10*, 91–164. [https://doi.org/10.1016/S0065-2504\(08\)60235-4](https://doi.org/10.1016/S0065-2504(08)60235-4).
- 670 (44) Mills, C. A.; Mann, R. H. K. The Bullhead Cottus Gobio, a Versatile and  
671 Successful Fish. In *51st Annual Report of the Freshwater Biological*  
672 *Association*; Freshwater Biological Association: Ambleside, UK, 1983; pp 76–  
673 88.
- 674 (45) Martinez, N. D. Artifacts or Attributes? Effects of Resolution on the Little Rock  
675 Lake Food Web. *Ecol. Monogr.* **1991**, *61* (4), 367–392.  
676 <https://doi.org/10.2307/2937047>.
- 677 (46) R Core Team. *R: A Languages and Environment for Statistical Computing*; R  
678 Foundation for Statistical Computing: Vienna, Austria, 2015.
- 679 (47) Zuur, A. F.; Ieno, E. N.; Elphick, C. S. A Protocol for Data Exploration to Avoid  
680 Common Statistical Problems. *Methods Ecol. Evol.* **2010**, *1* (1), 3–14.  
681 <https://doi.org/10.1111/j.2041-210X.2009.00001.x>.
- 682 (48) Nelder, J. A.; Baker, R. J. Generalized Linear Models. In *Encyclopedia of*  
683 *Statistical Sciences*; Kotz, S., Read, C. B., Balakrishnan, N., Vidakovic, B.,  
684 Johnson, N. L., Eds.; John Wiley & Sons, Inc.: New York, NY, USA, 2006; p 4.  
685 <https://doi.org/10.1002/0471667196.ess0866.pub2>.
- 686 (49) Tachet, H.; Bournaud, P.; Usseglio-Polatera, P. *Invertébrés d'Eau Douce*,  
687 Second cor.; CNRS éditions: Paris, 2002.
- 688 (50) Chevenet, F.; Dolédec, S.; Chessel, D. A Fuzzy Coding Approach for the  
689 Analysis of Long-Term Ecological Data. *Freshw. Biol.* **1994**, *31* (3), 295–309.  
690 <https://doi.org/10.1111/j.1365-2427.1994.tb01742.x>.

- 691 (51) Statzner, B.; Resh, V. H.; Roux, A. L. The Synthesis of Long-Term Ecological  
692 Research in the Context of Concurrently Developed Ecological Theory: Design  
693 of a Research Strategy for the Upper Rhône River and Its Floodplain. *Freshw.*  
694 *Biol.* **1994**, *31* (3), 253–263. [https://doi.org/10.1111/j.1365-](https://doi.org/10.1111/j.1365-2427.1994.tb01739.x)  
695 [2427.1994.tb01739.x](https://doi.org/10.1111/j.1365-2427.1994.tb01739.x).
- 696 (52) Gutiérrez-Cánovas, C.; Sánchez-Fernández, D.; Velasco, J.; Millán, A.;  
697 Bonada, N. Similarity in the Difference: Changes in Community Functional  
698 Features along Natural and Anthropogenic Stress Gradients. *Ecology* **2015**, *96*  
699 (9), 2458–2466. <https://doi.org/10.1890/14-1447.1>.
- 700 (53) Bartoń, K. MuMIn: multi-model inference, R package. version 1.42.1  
701 <https://cran.r-project.org/web/packages/MuMIn> (accessed Jul 21, 2018).
- 702 (54) Zuur, A. F.; Ieno, E. N.; Smith, G. M. *Analysing Ecological Data*; Springer:  
703 New York, USA, 2007.
- 704 (55) Thomas, R.; Lello, J.; Medeiros, R.; Pollard, A.; Seward, A.; Smith, J.; Vafidis,  
705 J.; Vaughan, I. *Data Analysis with R Statistical Software: A Guidebook for*  
706 *Scientists*; Eco-Explore: Newport, UK, 2015.
- 707 (56) Windsor, F. M. The Transfer and Effects of Xenobiotic Pollutants in Freshwater  
708 Ecosystems, PhD Thesis. Cardiff University, 2019.
- 709 (57) Willmott, C.; Matsuura, K. Advantages of the Mean Absolute Error (MAE) over  
710 the Root Mean Square Error (RMSE) in Assessing Average Model  
711 Performance. *Clim. Res.* **2005**, *30* (1), 79–82.  
712 <https://doi.org/10.3354/cr030079>.
- 713 (58) Sarkar, S. K.; Binelli, A.; Riva, C.; Parolini, M.; Chatterjee, M.; Bhattacharya, A.  
714 K.; Bhattacharya, B. D.; Satpathy, K. K. Organochlorine Pesticide Residues in  
715 Sediment Cores of Sunderban Wetland, Northeastern Part of Bay of Bengal,  
716 India, and Their Ecotoxicological Significance. *Arch. Environ. Contam. Toxicol.*  
717 **2008**, *55* (3), 358–371. <https://doi.org/10.1007/s00244-008-9133-6>.
- 718 (59) Odum, W. E.; Drifmeyer, J. E. Sorption of Pollutants by Plant Detritus: A  
719 Review. *Environ. Health Perspect.* **1978**, *27*, 133–137.  
720 <https://doi.org/10.1289/ehp.7827133>.
- 721 (60) Wang, J.; Bi, Y.; Henkelmann, B.; Wang, Z.; Pfister, G.; Schramm, K.-W.

- 722 Levels and Distribution of Polybrominated Diphenyl Ethers in Three Gorges  
723 Reservoir, China. *Emerg. Contam.* **2017**, 3 (1), 40–45.  
724 <https://doi.org/10.1016/J.EMCON.2017.01.003>.
- 725 (61) de Perre, C.; Trimble, A. J.; Maul, J. D.; Lydy, M. J. Ecological Bioavailability of  
726 Permethrin and p,P'-DDT: Toxicity Depends on Type of Organic Matter  
727 Resource. *Chemosphere* **2014**, 96, 67–73.  
728 <https://doi.org/10.1016/J.CHEMOSPHERE.2013.07.030>.
- 729 (62) Bartrons, M.; Catalan, J.; Penuelas, J. Spatial and Temporal Trends of Organic  
730 Pollutants in Vegetation from Remote and Rural Areas. *Sci. Rep.* **2016**, 6 (1),  
731 25446. <https://doi.org/10.1038/srep25446>.
- 732 (63) Siddiqi, M. A.; Laessig, R. H.; Reed, K. D. Polybrominated Diphenyl Ethers  
733 (PBDEs): New Pollutants-Old Diseases. *Clin. Med. Res.* **2003**, 1 (4), 281–290.
- 734 (64) Liu, Y.; Luo, X.-J.; Huang, L.-Q.; Yu, L.-H.; Mai, B.-X. Bioaccumulation of  
735 Persistent Halogenated Organic Pollutants in Insects: Common Alterations to  
736 the Pollutant Pattern for Different Insects during Metamorphosis. *Environ. Sci.*  
737 *Technol.* **2018**, 52 (9), 5145–5153. <https://doi.org/10.1021/acs.est.8b00616>.
- 738 (65) Zhang, Y.; Luo, X.-J.; Wu, J.-P.; Liu, J.; Wang, J.; Chen, S.-J.; Mai, B.-X.  
739 Contaminant Pattern and Bioaccumulation of Legacy and Emerging  
740 Organohalogen Pollutants in the Aquatic Biota from an E-Waste Recycling  
741 Region in South China. *Environ. Toxicol. Chem.* **2010**, 29 (4), 852–859.  
742 <https://doi.org/10.1002/etc.122>.
- 743 (66) Yu, M.; Luo, X.-J.; Wu, J.-P.; Chen, S.-J.; Mai, B.-X. Bioaccumulation and  
744 Trophic Transfer of Polybrominated Diphenyl Ethers (PBDEs) in Biota from the  
745 Pearl River Estuary, South China. *Environ. Int.* **2009**, 35 (7), 1090–1095.  
746 <https://doi.org/10.1016/j.envint.2009.06.007>.
- 747 (67) Coat, S.; Monti, D.; Legendre, P.; Bouchon, C.; Massat, F.; Lepoint, G.  
748 Organochlorine Pollution in Tropical Rivers (Guadeloupe): Role of Ecological  
749 Factors in Food Web Bioaccumulation. *Environ. Pollut.* **2011**, 159 (6), 1692–  
750 1701. <https://doi.org/10.1016/J.ENVPOL.2011.02.036>.
- 751 (68) Verrengia Guerrero, N. R.; Taylor, M. G.; Davies, N. A.; Lawrence, M. A. M.;  
752 Edwards, P. A.; Simkiss, K.; Wider, E. A. Evidence of Differences in the

- 753 Biotransformation of Organic Contaminants in Three Species of Freshwater  
754 Invertebrates. *Environ. Pollut.* **2002**, *117* (3), 523–530.  
755 [https://doi.org/10.1016/S0269-7491\(01\)00132-4](https://doi.org/10.1016/S0269-7491(01)00132-4).
- 756 (69) Wong, C. S.; Mabury, S. A.; Whittle, D. M.; Backus, S. M.; Teixeira, C.;  
757 DeVault, D. S.; Bronte, C. R.; Muir, D. C. G. Organochlorine Compounds in  
758 Lake Superior: Chiral Polychlorinated Biphenyls and Biotransformation in the  
759 Aquatic Food Web. *Environ. Sci. Technol.* **2004**, *38* (1), 84–92.  
760 <https://doi.org/10.1021/ES0346983>.
- 761 (70) van Beusekom, O. C.; Eljarrat, E.; Barceló, D.; Koelmans, A. A. Dynamic  
762 Modeling of Food-Chain Accumulation of Brominated Flame Retardants in Fish  
763 from the Ebro River Basin, Spain. *Environ. Toxicol. Chem.* **2006**, *25* (10),  
764 2553. <https://doi.org/10.1897/05-409R.1>.
- 765 (71) Statzner, B.; Bêche, L. A. Can Biological Invertebrate Traits Resolve Effects of  
766 Multiple Stressors on Running Water Ecosystems? *Freshw. Biol.* **2010**, *55*,  
767 80–119. <https://doi.org/10.1111/j.1365-2427.2009.02369.x>.
- 768 (72) Godfray, H. C. J.; Stephens, A. E. A.; Jepson, P. D.; Jobling, S.; Johnson, A.  
769 C.; Matthiessen, P.; Sumpter, J. P.; Tyler, C. R.; McLean, A. R. A Restatement  
770 of the Natural Science Evidence Base on the Effects of Endocrine Disrupting  
771 Chemicals on Wildlife. *Proc. R. Soc. B Biol. Sci.* **2019**, *286* (1897), 20182416.  
772 <https://doi.org/10.1098/rspb.2018.2416>.
- 773