

1 **KF-metaweb: A trophic metaweb of freshwater ecosystems of South Korea**

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9 **Abstract**

10 **Motivation:** The metaweb is a dictionary of nodes and their potential interactions developed for a
11 particular region, focusing on a particular type of ecosystem. Based on the local biodiversity
12 information at different spatial and temporal scales, the regional metaweb can be easily decomposed
13 into local webs. The generated local webs are useful for understanding spatiotemporal variations in
14 ecological interactions in a particular region. In this study, an attempt was made to develop a trophic
15 metaweb for freshwater ecosystems in South Korea, called the KF-metaweb. The metaweb contains
16 23074 interactions between 446 taxa collected from 730 studies. This metaweb can be used to
17 understand the spatiotemporal variability of different local food webs and the effects of the
18 environment on food web properties. Furthermore, this is the first metaweb developed for any Asian
19 ecosystem that contains information about many interactions that are unavailable in any other existing
20 database. In addition, this metaweb study enriches our global understanding of ecological interactions.

21 **Main types of variables contained:** The data contained trophic interactions between resources (prey)
22 and consumers (predators).

23 **Spatial location and grain:** The mainland of South Korea and Jeju Island.

24 **Time period and grain:** 2008–2021

25 **Major taxa:** Microalgae (belonging to the phyla Cyanobacteria, Bygrae, Cryophyta, Myozoa,
26 Ochrophyta, Charophyta, Chlorophyta, Euglenozoa, and Mycetozoa), zooplankton (belonging to the
27 phyla Arthropoda and Rotifera), benthic macroinvertebrates (Platyhelminthes, Annelida, Arthropoda,
28 and Mollusca), and fish.

29 **Level of measurement:** Minimum taxonomic resolution was at the genus level for fish and benthic
30 macroinvertebrates and order level for zooplankton and microalgae.

31 **Software format:** Excel (*.xlsx)

32

33 **KEYWORDS:** species interaction; aquatic community; river; streams; reservoirs; prey-predator
34 interaction; food web

35 **Introduction**

36 Understanding ecological interactions is crucial for effective conservation planning and for gaining a
37 comprehensive understanding of ecology (Stork, 2010). Unfortunately, the scarcity of ecological
38 interaction data, often referred to as the “Eltonian shortfall,” has hindered research in this field due to
39 the demand for greater effort and expertise (Delmas *et al.*, 2019). Fortunately, as larger databases
40 containing information on interactions, biodiversity, traits, and other essential parameters have
41 gradually emerged (Delmas *et al.*, 2019), the situation is improving. There is growing interest in
42 understanding the spatiotemporal variability of ecological networks (Pilosof *et al.*, 2017; Strydom *et*
43 *al.*, 2021). The main challenge to the spatiotemporal understanding of ecological networks is their
44 static nature (McCann & Rooney, 2009). To resolve this issue, differential equations that demand
45 more parameters, that is, more data, are sometimes used (Christensen & Walters, 2004; Park *et al.*,
46 2008). The use of metawebs can be a good solution for mitigating this issue, with comparatively fewer
47 data requirements.

48 Metaweb is a dictionary of nodes and their potential interactions developed for a particular region,
49 focusing on particular types of ecosystems (Dunne, 2006). Based on local biodiversity information, the
50 metaweb can be easily decomposed into local webs to understand local-level ecological interactions.
51 Thus, it is possible to generate a large number of local webs for different localities and time periods,
52 facilitating an understanding of spatiotemporal variations in the network (Kortsch *et al.*, 2019; Olivier
53 *et al.*, 2019). Additionally, it is possible to relate network properties to environmental variables to
54 understand the influence of climatic factors and habitat properties on network structure and functions
55 (Albouy *et al.*, 2019; Kortsch *et al.*, 2019). Although this concept seems promising and easy to
56 implement, its development in this field is very recent, especially since 2019.

57 In this study, a metaweb was developed for aquatic organisms in freshwater ecosystems of South
58 Korea. Taxa in the database were gathered from the literature and monitoring datasets. The metaweb
59 was developed through an intensive literature survey of the potential interactions between these taxa.
60 Subsequently, the metaweb was analyzed for its structural properties and the importance of different
61 taxa. This metaweb can be used to understand the spatiotemporal variability of different local food
62 webs and the effects of the environment on food web properties. Furthermore, this is the first metaweb
63 developed for any Asian ecosystem that contains information about many interactions that are

64 unavailable in any other existing database. This highlights the importance of the metaweb in a global
65 context to better understand ecological interactions, which will ultimately help improve conservation
66 planning and environmental management.

67

68 **Methods**

69 *Taxonomic and geographical coverage*

70 This database, named KF-metaweb, covers the interactions among different taxa (nodes) sampled from
71 different streams, rivers, and freshwater lakes in South Korea (Figure 1). A list of taxa was compiled
72 from biomonitoring data from the Aquatic Ecosystem Survey and Health Assessment Method:
73 Stream/River (<https://water.nier.go.kr>), which was collected from 2008 to 2021, covering 3032
74 sampling locations (National Institute of Environmental Research, 2019), and the Survey on the
75 Environment and Ecosystem of Lakes (Wonju Regional Environmental Office, 2019, 2020, 2021).
76 Additionally, a list of taxa was obtained from the National Ecosystem Survey (<https://nie-ecobank.kr>),
77 and unpublished data were collected from reservoirs following national data collection guidelines
78 (MoE, 2017).

79 *Taxonomy and systematics*

80 Owing to the unavailability of interaction data at higher taxonomic resolutions, the maximum
81 taxonomic resolution of the metaweb was set to the genus level for benthic macroinvertebrates and
82 fish, and in the case of zooplankton and microalgae, it was set to the order level. In some instances, the
83 specimens were identified only up to the subfamily level (e.g., Acentropinae), family level (e.g.,
84 Saldidae), or class level (e.g., Collembola) in the original datasets. All the nodes were classified into
85 five taxonomic hierarchies according to the Global Biodiversity Information Facility (GBIF;
86 <https://www.gbif.org/>) backbone taxonomy: family, order, class, phylum, and kingdom. Some names
87 were updated to match those used in GBIF and checked for other inconsistencies, such as the presence
88 of synonyms and spelling mistakes.

89 *Development of the metaweb*

90 To develop the metaweb (KF-metaweb), geographical and ecological boundaries should be defined
91 first. In this case, the geographical boundary was South Korea, whereas the ecological boundary was a
92 freshwater ecosystem, including streams, rivers, and reservoirs (Step 1 in Figure 2). Thereafter, the list
93 of nodes for which the metaweb was to be developed was compiled from the biomonitoring data, as
94 stated earlier. Interactions for the nodes were then searched in 730 different scientific studies, gray
95 literature, and online databases. In this case, interactions documented in the regional literature were

96 prioritized. Thereafter, the knowledge gap was filled with further data collection from the international
97 literature (Step 2 in Figure 2). Subsequently, the similarity in interactions in the same taxonomic
98 categories was checked because, in many cases, interactions are documented at higher taxonomic
99 levels, resulting in the same set of interactions for all members belonging to that taxonomic category.
100 In this case, these nodes are merged at a higher taxonomic level (Step 3 in Figure 2). To complete the
101 trophic metaweb, additional nodes were added, including macrophytes, detritus, and Spongillidae.
102 Some nodes with no trophic interactions in the metaweb were removed, for example, (1) parasitic
103 species (*Torix*, *Theromyzon*, *Hirudo*, and other species) were removed for not having any trophic
104 interactions, and (2) Nematomorpha were removed to avoid any documented trophic interactions in
105 the metaweb. This resulted in a total of 446 final nodes in our metaweb, consisting of 49 nodes of
106 microalgae, six nodes of zooplankton, 281 nodes of macroinvertebrates, and 107 nodes of fish,
107 macrophytes, Spongillidae, and detritus. Following this, the list format of the initial metaweb was
108 transformed into a wide matrix format to check for inconsistencies in interactions. As depicted in
109 Figure 2 in Step 4, the rows and columns of the matrix represent resources and consumers,
110 respectively. If the sum of a column is zero, the consumer has no resources, which indicates that it is a
111 basal node (D in the matrix of Figure 2). Similarly, if the sum of a row is zero, this indicates that the
112 resource has no consumers, which means that it is a top node (or apex predator) (F in the matrix shown
113 in Figure 2). If the sum over both the rows and columns is zero for a particular node, it represents a
114 node that does not have any interactions (A in the matrix of Figure 2). Here, inconsistencies result if
115 (i) any node does not have any interactions or (ii) any intermediate or top nodes are represented as
116 basal nodes. In these cases, the first intensive search for additional trophic interactions was conducted.
117 If no interaction is found, then the node is merged with a taxonomically similar node; for example, in
118 Step 5 of Figure 2, nodes A and C are merged so as not to have any interactions with node A. Finally,
119 the matrix is transformed into a list format to represent the final version of the metaweb as a list.

120 *Analysis of metaweb*

121 The metaweb was analyzed at two levels: metaweb and node. The metaweb-level analysis focuses on
122 understanding the structural properties of the metaweb. In this case, size, connectance, link density,
123 proportion of top nodes, proportion of basal nodes, proportion of intermediate nodes, proportion of
124 cannibals, omnivory, generality, vulnerability, and clustering coefficient are calculated with
125 ‘multiweb’ package (Saravia *et al.*, 2022) in R (R Core Team, 2023). Modularity is calculated with
126 ‘igraph’ package (Csardi & Nepusz, 2006) in R with an edge-betweenness algorithm to detect the
127 modules in the metaweb as it is a binary network (Leger *et al.*, 2015). Nestedness was calculated with
128 ‘unodf’ package (Cantor *et al.*, 2017) in R. At the node level, the importance of each node in the
129 metaweb was assessed based on centrality, measured with ‘igraph’ package (Csardi & Nepusz, 2006)
130 in R. Further, prey-averaged trophic levels (Levine, 1980) of different nodes were calculated with the

131 package ‘cheddar’ (Hudson *et al.*, 2013) in R to understand their relative trophic position in this
132 trophic metaweb.

133

134 **Results**

135 *Metaseb database*

136 This database is available in the latest Excel Workbook (*.xlsx) format and includes four sheets:
137 ‘Metaweb,’ ‘Node taxonomy,’ ‘Reference’ and ‘Trophic level.’ The first sheet contains the
138 interactions among different nodes. It has three columns, i.e., ‘resource,’ ‘consumer’ and ‘reference.’
139 The first and second columns contain the names of the resource and consumer nodes, respectively, and
140 the third column contains the source-to-source interaction as a reference number. The second sheet
141 contains the names of all the nodes, along with their taxonomy. It has eight columns: ‘Node,’ ‘Genus,’
142 ‘Family,’ ‘Order,’ ‘Class,’ ‘Phylum,’ ‘Kingdom,’ and ‘Category.’ In the last column, the nodes are
143 categorized into broad groups: macroinvertebrates, fish, microalgae, sponges, zooplankton, detritus,
144 and macrophytes. The third sheet contains two columns: a reference number and a reference. The
145 references used in the first sheet can be found in the third sheet using reference numbers. The last
146 sheet, ‘Trophic Level’ contains the prey-averaged trophic level of each node. It contains two columns:
147 ‘Node’ and ‘Trophic level.’

148 *Structural analysis of the metaweb*

149 This metaweb has 446 nodes and 23,074 interactions, with a link density and connectance of 51.74
150 and 0.116, respectively. The average path length within our metaweb is 2.36, accompanied by mean
151 and maximum trophic levels of 2.67 and 4.62, respectively. The proportions of the top, basal,
152 intermediate, and cannibalistic nodes are 0, 0.11, 0.89, and 0.23, respectively. Notably, the degree of
153 omnivory in metawebs is 0.58. The value of the clustering coefficient is 0.38, which indicates that the
154 nodes in this metaweb have, on average, well-connected neighbors. The generality and vulnerability of
155 our metaweb are 58.42 ± 1.44 (mean \pm standard deviation) and 51.73 ± 0.64 , respectively. The
156 modularity of our metaweb was 0.034, which is a lower modularity value. Nestedness for consumers is
157 0.37 and for resources is 0.46. This indicates a slightly nested structure of the metaweb with generalist
158 resources that share their consumers with specialist resource nodes.

159 *Nodes*

160 Most of the nodes are represented by macroinvertebrates (63%), followed by fish (24%), and
161 microalgae (11%) (Figure 3). Figure 4 shows the detailed composition of the nodes belonging to
162 different groups. Among the macroinvertebrates, most nodes belonged to the phylum Arthropoda

163 (80%), followed by Mollusca (12.1%). In Arthropoda, most nodes belonged to class Insecta (85.8%),
164 followed by Malacostraca (12%). Most nodes belonging to the class Insecta fell in the order of
165 Trichoptera (26%), Diptera (18%), Plecoptera (13%), Hemiptera (12%), and Coleoptera (12%). Most
166 fish belonged to the orders Cypriniformes (35%) and Perciformes (32%). Classes Bacillariophyceae
167 (42%) and Chlorophyceae (11%) constituted a major portion of microalgal nodes. Microalgae,
168 macrophytes, and detritus are the basal nodes of this metaweb.

169 *Interactions*

170 Most of the interactions in this metaweb originated from macroinvertebrates (81.48%), that is, where
171 macroinvertebrates are resources (Figure 3), whereas microalgae and fish contribute 10.03% and
172 5.03% of the total interactions, respectively. Most of the flows originating from macroinvertebrates go
173 to fish (52.01%), whereas the remaining portion (39.08%) is consumed by macroinvertebrates. The
174 majority of the fish resources are consumed by fish (86.83%), followed by macroinvertebrates
175 (13.07%). In the microalga, 73.42% of the flow ended in macroinvertebrates, followed by fish
176 (23.21%) and zooplankton (4.21%). 78.12% and 19.53% of the detrital flows end up in
177 macroinvertebrates and fishes, respectively. Macrophytes act as resources mostly for the
178 macroinvertebrates (60.58%) followed by fishes (38.46%). Flows originating from zooplankton
179 mostly end up in fish (51.17%), followed by macroinvertebrates (44.63%) and zooplankton (4.2%). It
180 is important to note that the importance of detritus and macrophytes is largely underrepresented
181 because their communities are not detailed.

182 *Node importance*

183 Four measures of centrality are used to identify the important nodes in the metaweb: degree centrality,
184 closeness centrality, betweenness centrality, and eigenvector centrality. Degree centrality (Freeman,
185 1977), a local measure of the number of interactions between a species. This can be further divided
186 into in-degree and out-degree in the case of a directed network, which indicate the number of flows a
187 node receives and contributes, respectively. The in-degree value was highest in fish nodes, with
188 *Anguilla* (348), *Opsariichthys* (294), and *Oreochromis* (286) having the highest values. This indicates
189 a relatively high position of fish at this trophic level. Among macroinvertebrates, Tabanidae (277),
190 Dytiscidae (272), and Anotogaster (268) have the highest in-degree values, although their overall
191 rankings were sixth, ninth, and twelfth, respectively. Regarding the out-degree, detritus (257),
192 Chironomidae (170), and Naviculales (140) have the highest values, indicating their importance as
193 resources in the metaweb.

194 Closeness centrality (Freeman, 1978; Freeman *et al.*, 1979) is a global measure that indicates the
195 proximity of a species to all other species in a network in terms of the shortest distance between nodes.

196 A directed web can be further divided into in- and out-, where the former and latter indicate the paths
197 to and from a node, respectively. Approximately 63 nodes have the maximum values of in-closeness
198 centrality, indicating their relative importance as consumers in the metaweb. Among these, one node is
199 fish (*Acanthorhodeus*), one node is Spongillidae, and all other nodes are macroinvertebrates
200 (dominated by Trichoptera, Gastropoda, and Plecoptera). In contrast, Chironomidae, Copepoda,
201 Diplostraca, Gammaridae, and Baetidae have the highest out-closeness centrality, indicating their
202 relative importance as resources.

203 Betweenness centrality (Freeman, 1977) describes the number of times a species is between a pair of
204 other species; that is, how many paths pass through it. All the top ten nodes with higher betweenness
205 centrality values belong to invertebrates, with *Diplonychus*, Chironomidae, *Barbronia*, *Acetes* and
206 *Macrostemum* having the highest values. This indicates the importance of these nodes as intermediate
207 nodes.

208 In the case of eigenvector centrality (Bonacich, 1987), the node that simultaneously influence all its
209 partners obtains the highest score. In this case, *Opsariichthys* is the most central node, followed by
210 *Anguilla* and *Pseudorasbora*. Except *Diplonychus*, all other nodes in the top ten nodes having highest
211 eigenvector centrality are fish.

212 The relative role of each node in the meta-food web is indicated by the trophic level in the fourth sheet
213 of the attached dataset. *Dineutus* (4.62) has the highest trophic position, followed by *Diplonychus*
214 (4.48), *Ilyocoris* (4.45), *Misgurnus* (4.34), and *Lethocerus* (4.27).

215

216 **Usage notes**

217 This database contains information not available in other existing databases, including global
218 databases such as GloBI (Poelen *et al.*, 2014). Furthermore, this is the first metaweb from Asia that
219 indicates its potential to fill critical gaps in understanding ecological interactions. Data are provided in
220 Excel workbook format (*.xlsx), which can be easily converted into other formats such as *.csv and
221 used with any software or programming language. This metaweb can be used to infer local webs for
222 the region in which it is developed, such as the global marine metaweb (Albouy *et al.*, 2019), the
223 German Blight metaweb(Olivier *et al.*, 2019), European Tetrapod metaweb (Braga *et al.*, 2019), and
224 the Swiss Blue and Green metaweb (Ho *et al.*, 2022). From the inferred local webs, it is possible to
225 understand how the network properties vary spatiotemporally. Furthermore, variations in
226 spatiotemporal properties with environmental variables can be used to understand the influence of the
227 environment on the structure of ecological networks. Further, it is important to note that many taxa are

228 at the high taxonomic level like order or family in the database. Therefore, more focus will be to
229 increase taxonomic resolution of the database in the later versions.

230 **Data availability statement**

231 The database (KF-metaweb) is accessible from Figshare (Adhurya *et al.*, 2023).

232

233

234 **References**

235 Adhurya, S., Park, Y.-S. & Lee, D.-Y. (2023) KF-metaweb: A trophic metaweb of freshwater
236 ecosystems of South Korea. <https://doi.org/10.6084/m9.figshare.24037764.v1>.

237 Albouy, C., Archambault, P., Appeltans, W., Araújo, M.B., Beauchesne, D., Cazelles, K., Cirtwill, A.R.,
238 Fortin, M.-J., Galiana, N., Leroux, S.J., Pellissier, L., Poisot, T., Stouffer, D.B., Wood, S.A. &
239 Gravel, D. (2019) The marine fish food web is globally connected. *Nature Ecology & Evolution*,
240 **3**, 1153–1161. <https://doi.org/10.1038/s41559-019-0950-y>.

241 Bonacich, P. (1987) Power and Centrality: A Family of Measures. *American Journal of Sociology*, **92**,
242 1170–1182. <https://doi.org/10.1086/228631>.

243 Braga, J., Pollock, L.J., Barros, C., Galiana, N., Montoya, J.M., Gravel, D., Maiorano, L.,
244 Montemaggiore, A., Ficetola, G.F., Dray, S. & Thuiller, W. (2019) Spatial analyses of multi-
245 trophic terrestrial vertebrate assemblages in Europe. *Global Ecology and Biogeography*, **28**, 1636–
246 1648. <https://doi.org/10.1111/geb.12981>.

247 Cantor, M., Pires, M.M., Marquitti, F.M.D., Raimundo, R.L.G., Sebastián-González, E., Coltri, P.P.,
248 Perez, S.I., Barneche, D.R., Brandt, D.Y.C., Nunes, K., Daura-Jorge, F.G., Floeter, S.R. &
249 Guimarães, P.R. (2017) Nestedness across biological scales. *PLOS ONE*, **12**, e0171691.
250 <https://doi.org/10.1371/journal.pone.0171691>.

251 Christensen, V. & Walters, C.J. (2004) Ecopath with Ecosim: methods, capabilities and limitations.
252 *Ecological Modelling*, **172**, 109–139. <https://doi.org/10.1016/j.ecolmodel.2003.09.003>.

253 Csardi, G. & Nepusz, T. (2006) The igraph software package for complex network research.
254 *InterJournal, Complex Sy*, 1695.

255 Delmas, E., Besson, M., Brice, M.-H., Burkle, L.A., Dalla Riva, G. V., Fortin, M.-J., Gravel, D.,
256 Guimarães, P.R., Hembry, D.H., Newman, E.A., Olesen, J.M., Pires, M.M., Yeakel, J.D. & Poisot,

- 257 T. (2019) Analysing ecological networks of species interactions. *Biological Reviews*, **94**, 16–36.
258 <https://doi.org/10.1111/brv.12433>.
- 259 Dunne, J.A. (2006) *The Network Structure of Food Webs*. *Ecological Networks: Linking Structure to*
260 *Dynamics in Food Webs* (ed. by M. Pascual and J.A. Dunne) , pp. 27–86. Oxford University Press.
- 261 Freeman, L.C. (1977) A Set of Measures of Centrality Based on Betweenness. *Sociometry*, **40**, 35.
262 <https://doi.org/10.2307/3033543>.
- 263 Freeman, L.C. (1978) Centrality in social networks conceptual clarification. *Social Networks*, **1**, 215–
264 239. [https://doi.org/10.1016/0378-8733\(78\)90021-7](https://doi.org/10.1016/0378-8733(78)90021-7).
- 265 Freeman, L.C., Roeder, D. & Mulholland, R.R. (1979) Centrality in social networks: ii. experimental
266 results. *Social Networks*, **2**, 119–141. [https://doi.org/10.1016/0378-8733\(79\)90002-9](https://doi.org/10.1016/0378-8733(79)90002-9).
- 267 Ho, H.-C., Brodersen, J., Gossner, M.M., Graham, C.H., Kaeser, S., Reji Chacko, M., Seehausen, O.,
268 Zimmermann, N.E., Pellissier, L. & Altermatt, F. (2022) Blue and green food webs respond
269 differently to elevation and land use. *Nature Communications*, **13**, 6415.
270 <https://doi.org/10.1038/s41467-022-34132-9>.
- 271 Hudson, L.N., Emerson, R., Jenkins, G.B., Layer, K., Ledger, M.E., Pichler, D.E., Thompson, M.S.A.,
272 O’Gorman, E.J., Woodward, G. & Reuman, D.C. (2013) Cheddar: analysis and visualisation of
273 ecological communities in R. *Methods in Ecology and Evolution*, **4**, 99–104.
274 <https://doi.org/10.1111/2041-210X.12005>.
- 275 Kortsch, S., Primicerio, R., Aschan, M., Lind, S., Dolgov, A. V. & Planque, B. (2019) Food-web
276 structure varies along environmental gradients in a high-latitude marine ecosystem. *Ecography*,
277 **42**, 295–308. <https://doi.org/10.1111/ecog.03443>.
- 278 Leger, J., Daudin, J. & Vacher, C. (2015) Clustering methods differ in their ability to detect patterns in
279 ecological networks. *Methods in Ecology and Evolution*, **6**, 474–481.
280 <https://doi.org/10.1111/2041-210X.12334>.
- 281 Levine, S. (1980) Several measures of trophic structure applicable to complex food webs. *Journal of*
282 *Theoretical Biology*, **83**, 195–207. [https://doi.org/10.1016/0022-5193\(80\)90288-X](https://doi.org/10.1016/0022-5193(80)90288-X).
- 283 McCann, K.S. & Rooney, N. (2009) The more food webs change, the more they stay the same.
284 *Philosophical Transactions of the Royal Society B: Biological Sciences*, **364**, 1789–1801.
285 <https://doi.org/10.1098/rstb.2008.0273>.
- 286 MoE (2017) *Environmental survey guidelines for lakes and reservoirs (호소환경 조사지침)*, Ministry

- 287 of Environment, Sejong, Korea 94p.
- 288 National Institute of Environmental Research (2019) *수생태계 현황 조사 및 건강성 평가 방법 등에*
 289 *관한 지침: 하천편 (Guidelines for aquatic ecosystem survey and health assessment methods:*
 290 *stream/river) [In Korean language], 127p.*
 291 <https://dl.nanet.go.kr/file/fileDownload.do?linkSystemId=NADL&controlNo=MONO120205428>
 292 7.
- 293 Olivier, P., Frelat, R., Bonsdorff, E., Kortsch, S., Kröncke, I., Möllmann, C., Neumann, H., Sell, A.F.
 294 & Nordström, M.C. (2019) Exploring the temporal variability of a food web using long-term
 295 biomonitoring data. *Ecography*, **42**, 2107–2121. <https://doi.org/10.1111/ecog.04461>.
- 296 Park, R.A., Clough, J.S. & Wellman, M.C. (2008) AQUATOX: Modeling environmental fate and
 297 ecological effects in aquatic ecosystems. *Ecological Modelling*, **213**, 1–15.
 298 <https://doi.org/10.1016/j.ecolmodel.2008.01.015>.
- 299 Pilosof, S., Porter, M.A., Pascual, M. & Kéfi, S. (2017) The multilayer nature of ecological networks.
 300 *Nature Ecology & Evolution*, **1**, 0101. <https://doi.org/10.1038/s41559-017-0101>.
- 301 Poelen, J.H., Simons, J.D. & Mungall, C.J. (2014) Global biotic interactions: An open infrastructure to
 302 share and analyze species-interaction datasets. *Ecological Informatics*, **24**, 148–159.
 303 <https://doi.org/10.1016/j.ecoinf.2014.08.005>.
- 304 R Core Team (2023) R: A Language and Environment for Statistical Computing.
- 305 Saravia, L.A., Marina, T.I., Kristensen, N.P., De Troch, M. & Momo, F.R. (2022) Ecological network
 306 assembly: How the regional metaweb influences local food webs. *Journal of Animal Ecology*, **91**,
 307 630–642. <https://doi.org/10.1111/1365-2656.13652>.
- 308 Stork, N.E. (2010) Re-assessing current extinction rates. *Biodiversity and Conservation*, **19**, 357–371.
 309 <https://doi.org/10.1007/s10531-009-9761-9>.
- 310 Strydom, T., Catchen, M.D., Banville, F., Caron, D., Dansereau, G., Desjardins-Proulx, P., Forero-
 311 Muñoz, N.R., Higinio, G., Mercier, B., Gonzalez, A., Gravel, D., Pollock, L. & Poisot, T. (2021)
 312 A roadmap towards predicting species interaction networks (across space and time). *Philosophical*
 313 *Transactions of the Royal Society B: Biological Sciences*, **376**, 20210063.
 314 <https://doi.org/10.1098/rstb.2021.0063>.
- 315 Wonju Regional Environmental Office (2020) *Survey on the environment and ecosystem of lakes*,
 316 Wonju Regional Environmental Office, Wonju, Korea 712p.

317 Wonju Regional Environmental Office (2021) *Survey on the environment and ecosystem of lakes*,
318 Wonju Regional Environmental Office, Wonju, Korea 616p.

319 Wonju Regional Environmental Office (2019) *Survey on the Environment and Ecosystem of Lakes*,
320 Wonju Regional Environmental Office, Wonju, Korea 674p.

321

322

323 **Data availability statement**

324 The database (KF-metaweb) is accessible from Figshare (Adhurya *et al.*, 2023).

325 **Figure legend**

326 Figure 1: Location of the biomonitoring survey sites across South Korea for different reservoirs (indigo)
327 and streams/rivers (red) [at right].

328 Figure 2: Conceptual diagram for the development of the metaweb. The figure is elaborated in the
329 subsection 'Development of the metaweb'.

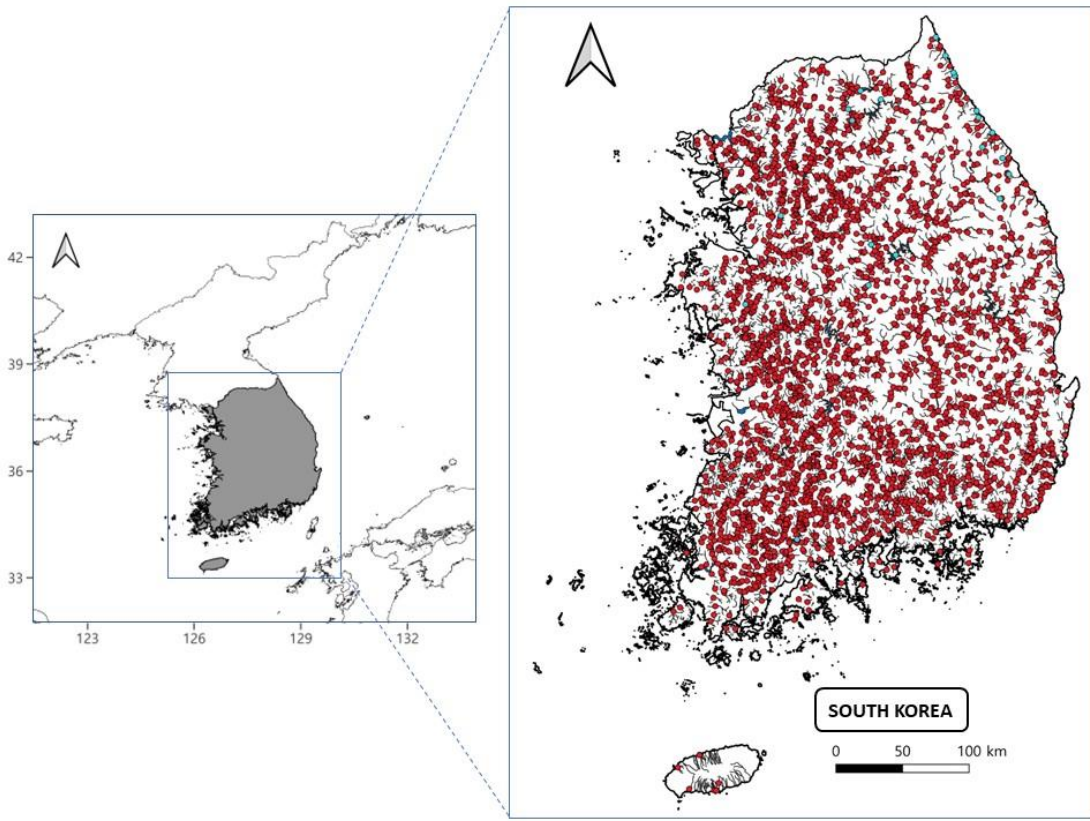
330 Figure 3: Summary of the metaweb representing flows between different categories of organisms. The
331 percentage value outside the circle indicates the total flow contributed by the nodes belonging to a
332 particular category, whereas the percentage value inside the circle represents amount of flow going from
333 a particular category to other categories. Here, only the values greater than 1% are shown.

334 Figure 4: Composition of different node groups. From top-left, phylum level composition of
335 macroinvertebrates; order level composition of insects (top-right); order level composition of fishes
336 (bottom-left); and class level composition of microalgae.

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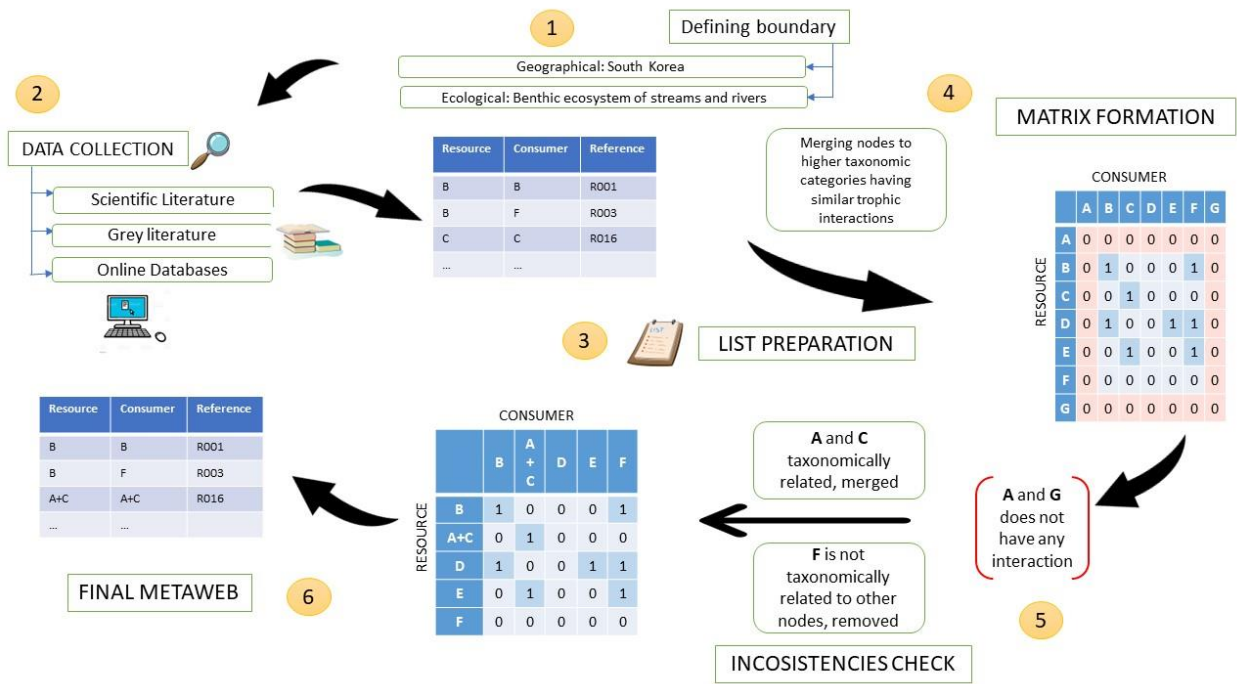
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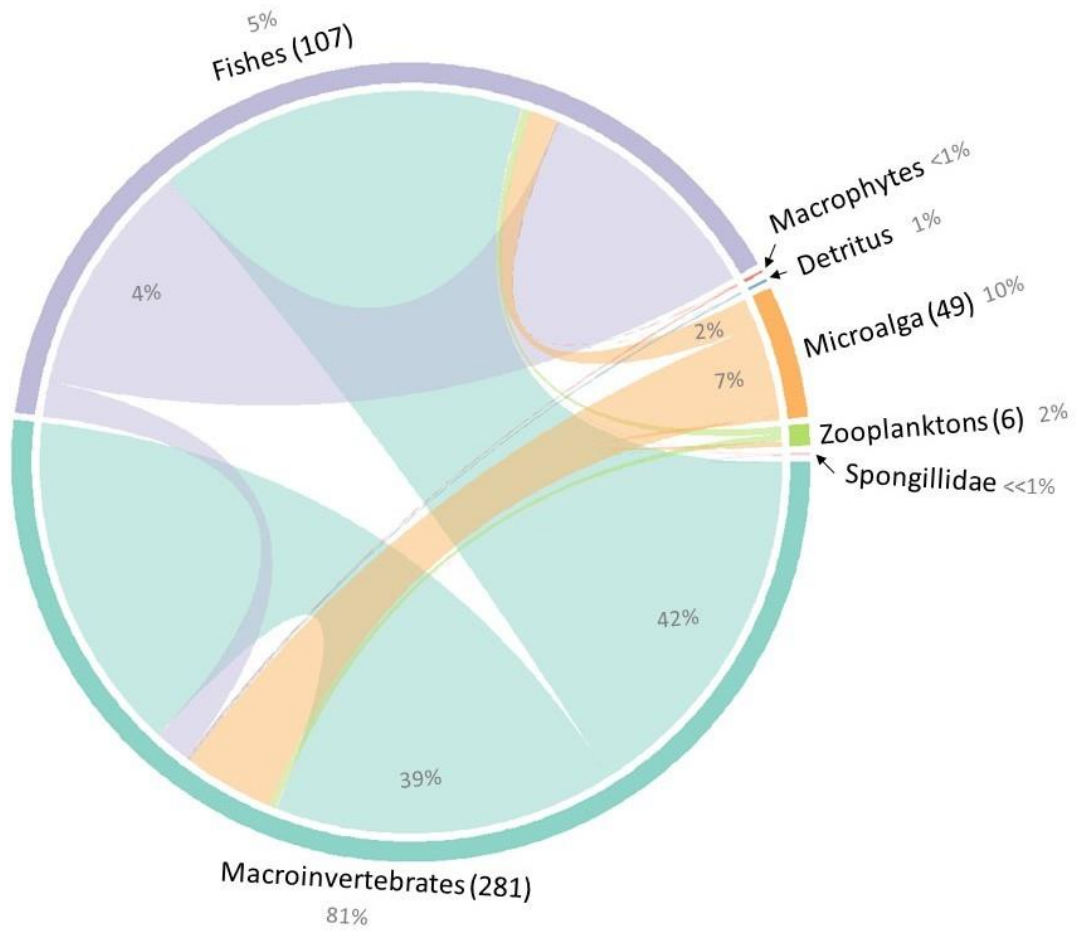
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341 **Figure 1**

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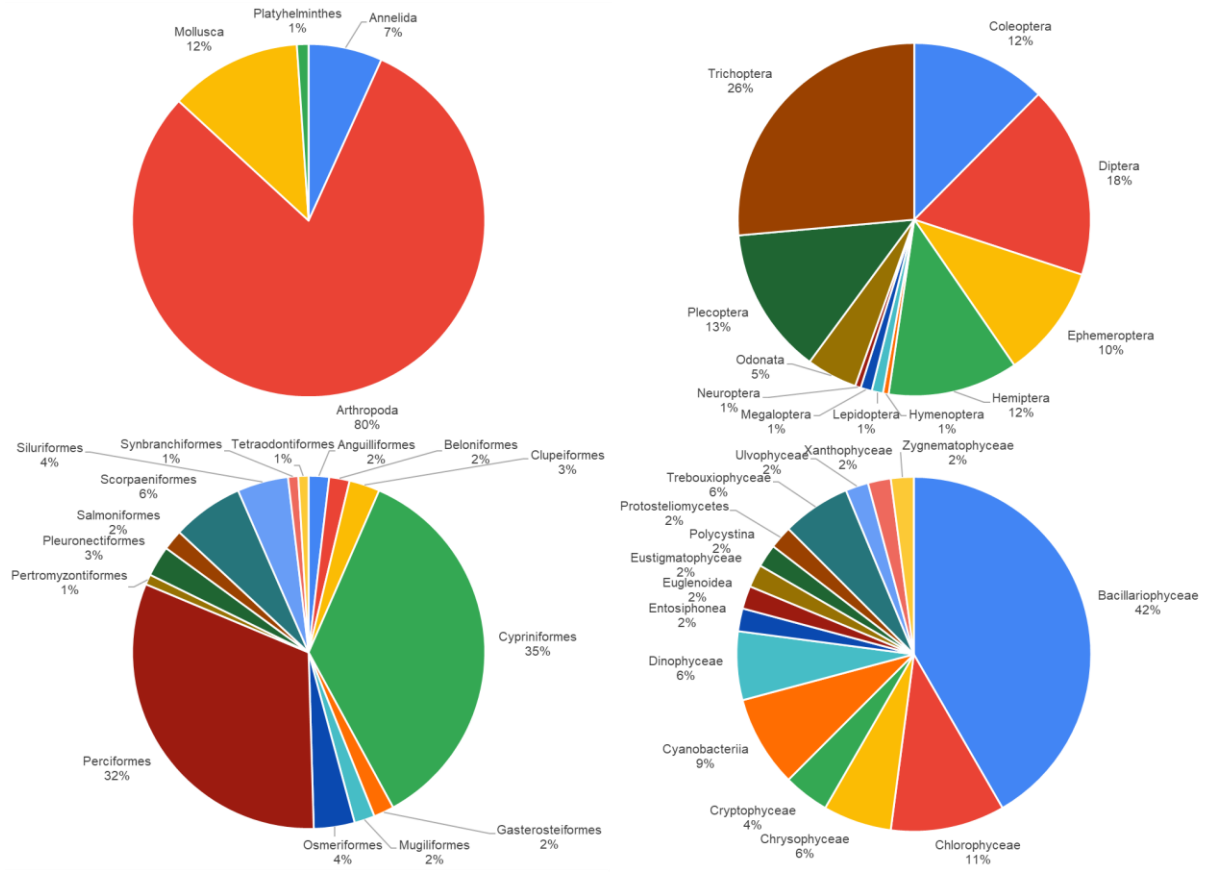


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348 **Figure 3**



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351 **Figure 4**

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