OVERVIEW RESULTS: Harmonized invertebrate grouping feature databases

Results harmonized grouping feature databases

We used information on invertebrate traits for the regions Europe, North America, Australia, and New Zealand to establish harmonized grouping feature databases. Trait information for Europe was obtained by the Freshwaterecology database (Schmidt-Kloiber and Hering 2015) and complemented by Tachet (Usseglio-Polatera et al. 2000) when information was missing (e.g. for the grouping feature size). Trait information for North America was obtained from Laura Twardochleb and complemented by Vieira et al. 2006 (Vieira et al. 2006). Philippe Usseglio-Polatera provided information on body form for European and North American taxa. For Australia and New Zealand, we used trait databases from Kefford et al. (Kefford et al. 2020) and Philips and Smith respectively (Philips and Smith 2018).

We selected seven grouping features that we harmonized into 26 traits. The grouping features were chosen based on the availability of trait information across databases and so that they describe different parts of the biology of an organism: life history (Voltinism), morphology (Respiration, Body form, Size), ecology (Locomotion, Feeding mode) and reproduction (Oviposition). We used fuzzy coded traits for establishing our harmonized databases unless data quality prohibited and then we used binary traits, i.e categorical and continuous traits were converted into binary traits. Data processing prior harmonization also involved amalgamation of duplicate taxa on species, genus or family-level and conversion of trait affinities to percentages per trait. We omitted taxa with a lower taxonomic resolution than family-level. The following results relate to the harmonized grouping feature databases.

1 Taxonomic coverage of the trait databases

Regarding the taxonomical coverage, the New Zealand database has, as expected, the smallest taxon pool (478 taxa, Table 1). By contrast, the largest taxon pool is spanned by the European trait database with 4110 taxa followed by the North American trait database that contained trait information on 3753 taxa. The Australian database contains 1402 taxa. The European, New Zealand, and North American databases have most taxa on the highest taxonomical resolution while the Australian database has a similar number of taxa on species and genus-level.

Table 1: Number of taxa per harmonized database and per taxonomic level. Numbers in parenthesis show relative frequencies in percentage.

Database	Nr. of taxa	Species	Genus	Family	Nr. aquatic taxa
Europe	4110	3848 (93.63)	237 (5.77)	25 (0.61)	3579 (87.08)
North America	3753	2414 (64.32)	1163 (30.99)	176 (4.69)	3305 (88.06)
Australia	1402	564 (40.23)	578 (41.23)	260 (18.54)	1016 (72.47)
New Zealand	478	404 (84.52)	47 (9.83)	27 (5.65)	443 (92.68)

2 Completeness of trait information

The amount of entries with available information for the individual grouping features varied strongly for the European, North American, and Australian databases (Table 2). By contrast, the New Zealand database contained complete trait information for most of the investigated grouping features (between 94 % and 100 %).

Table 2: Displayed is the percentage of entries that have information for the individual grouping features per database.

Database	Body form	Oviposition	Voltinism	Locomotion	Size	Respiration	Feeding mode
EU	7	16	24	33	11	56	65
NOA	28	13	47	52	73	44	63
AUS	5	48	51	42	78	70	99
NZ	100	94	100	99	100	100	99

3 Description of trait aggregation methods

Traits of the harmonized grouping feature databases were aggregated to family-level using three approaches. I) we directly aggregated taxa to family-level giving equal weight to every species. We denote this aggregation as *direct_agg*. For the *direct_agg* we tested aggregating with the median and the mean. We added *median* or *mean* to *direct_agg* to indicate when we used which method. II) taxa were aggregated stepwise, i.e first to the genus-level and subsequently to the family-level. By using this approach, we give equal weights to each genus. Hereafter, we abbreviate this aggregation type as *stepwise_agg*. We tested the *stepwise_agg* using the mean and the median, using the same naming as for the *direct_agg*. III) taxa were aggregated using a weighted mean approach, denoted as *weighted_agg*. This method weights the genera according to the number of their species present in the databases.

Trait affinities ranged between 0 and 1. Hence, the maximum differences possible is 1 or -1 (corresponds to 100 %). For convenience, we report absolute trait differences.

4 Differences in trait affinities obtained by trait aggregation methods compared to traits assigned at family-level

Aggregated trait affinities using five trait aggregation methods (*direct_agg (median)*, *direct_agg (mean)*, *stepwise_agg (median)*, *stepwise_agg (mean)*, and *weighted_agg*) were compared to trait affinities assigned at family-level by experts, which were available for the Australian and North American database for a limited subset of grouping features and taxa. For the Australian database, we compared aggregated trait affinities with assigned trait affinities resolved at family-level for the grouping features feeding mode and size by using data from Chessman 2018 (Chessman 2018). We could carry out the comparison to all taxa available in Chessman 2018, which contained trait information for 220 families. Considering each factor combination of family and investigated trait this amounts to 1760 cases. For the North American database, we compared aggregated trait affinities with assigned trait affinities on family-level for the grouping features feeding mode, respiration, size, voltinism, and locomotion from Pyne et al. Trait information in the Pyne et al. database was available on the categorical scale and was converted to binary traits prior to the comparison with aggregated trait affinities. Trait information on family-level in the Pyne et al. database was available for 94 families of which all were present in the aggregated North American database (total number of cases 1598).

The percentage of differing cases of trait affinities obtained by the trait aggregation methods compared to trait affinities assigned at family-level varied between 16.18 % and 22.9 % for the Australian database. For the North American database, comparison of the trait aggregation methods to trait affinities assigned at family-level yielded between 15.3 % and 47 % differing cases (Table 3).

For both databases maximum differences of 1 occurred for all investigated grouping features (Figure 1 and Figure 2). In general, trait aggregation methods using the median yielded fewer cases with differences compared to approaches using the mean. However, using the median produced greater differences for both databases.

Table 3: Amount of differing cases, the minimum and maximum, and means and standard deviations of absolute differences between trait affinities assigned at family-level and aggregated trait affinities.

| Database	Comparison to traits at fam.-lvl.	Differing cases [%]	Min. differences	Max. differences	Mean abs. differences	SD abs. differences
Australia (Chessman)	direct_agg (median)	16.53	0.01	1.00	0.45	0.27
	direct_agg (mean)	23.24	< 0.01	0.99	0.34	0.23
	stepwise_agg (median)	17.90	0.01	1.00	0.42	0.26
	stepwise_agg (mean)	23.24	< 0.01	0.99	0.33	0.22
	weighted_agg	23.24	< 0.01	1.00	0.34	0.24
North America (Pyne)	direct_agg (median)	15.33	0.17	1.00	0.70	0.26
	direct_agg (mean)	47.00	< 0.01	1.00	0.30	0.26
	stepwise_agg (median)	18.00	0.08	1.00	0.63	0.28
	stepwise_agg (mean)	47.00	< 0.01	1.00	0.30	0.27
	weighted_agg	47.00	< 0.01	1.00	0.31	0.28
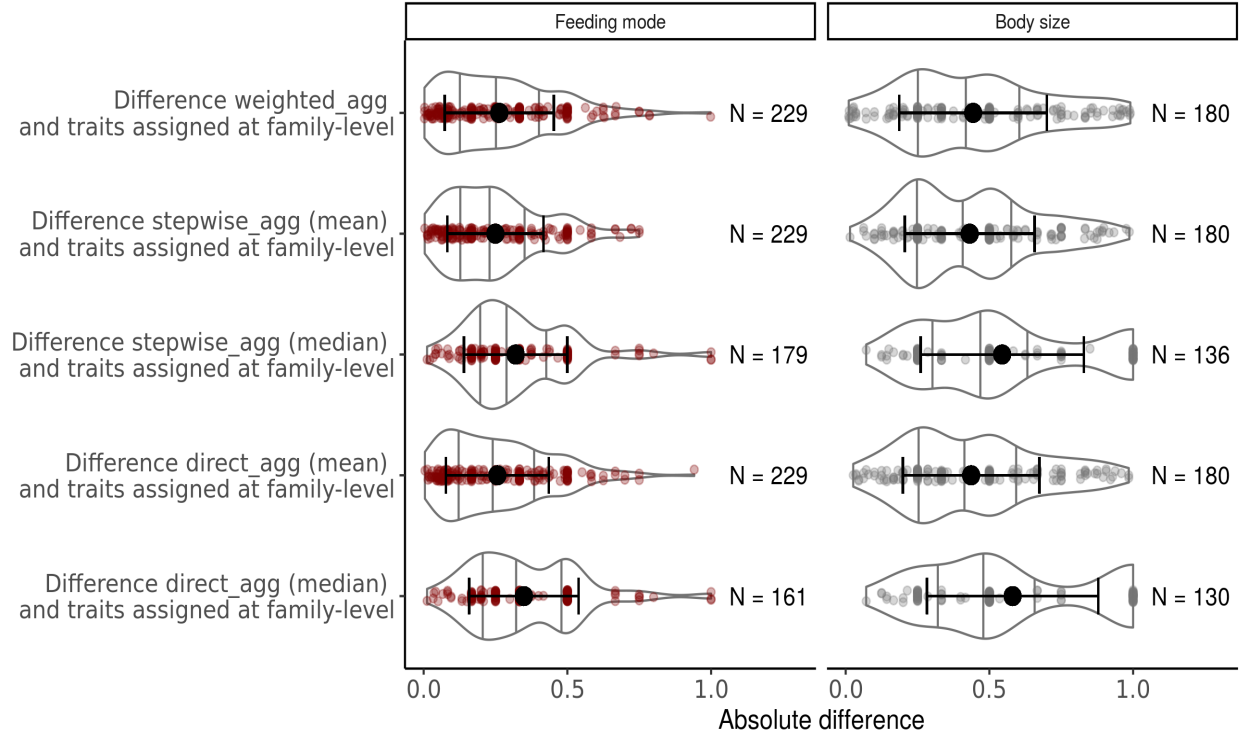
Figure 1: Absolute differences in trait affinities between aggregated traits and traits assigned at family-level by Chessman 2018 for the grouping features feeding mode and body size. N denotes the number of cases for each comparison. The black dot indicates the mean absolute difference, the error bars the standard deviation. The gray horizontal lines show the 25th, 50th and 75th quantile of the density estimate.
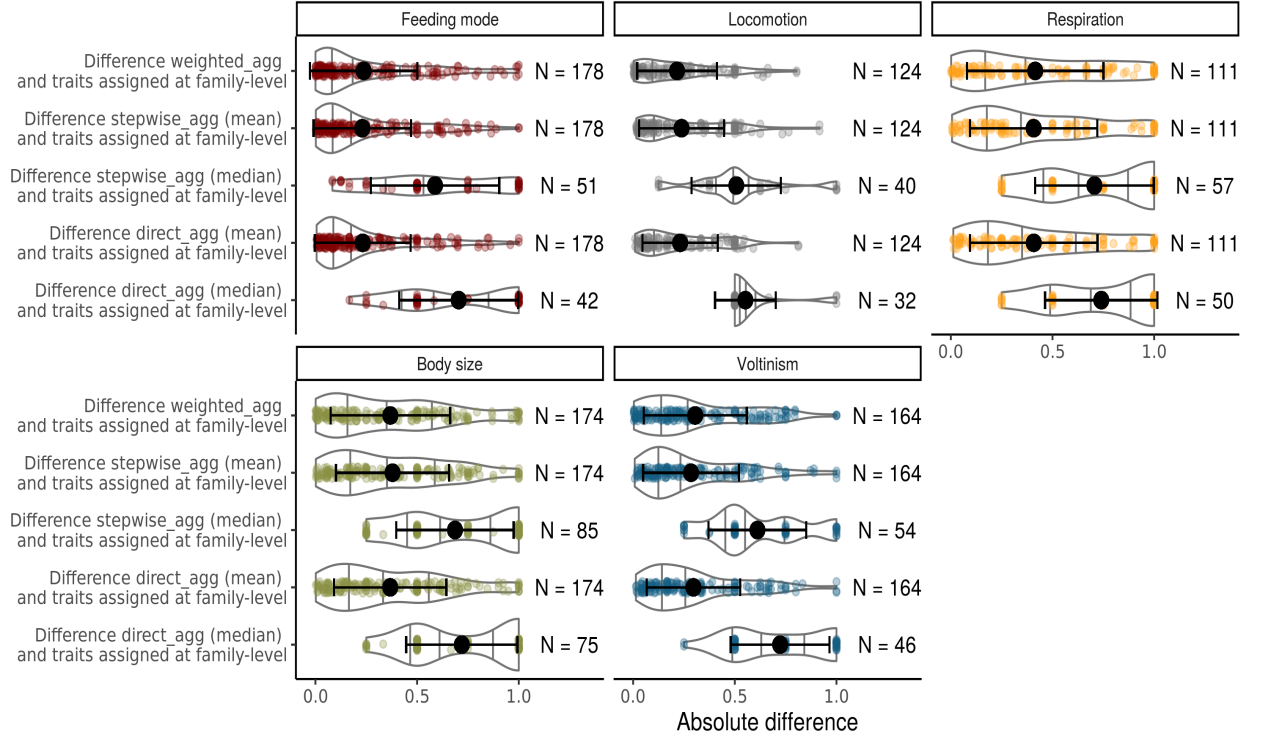
Figure 2: Absolute differences in trait affinities between aggregated traits and traits assigned at family-level by Pyne et al. for the grouping features feeding mode, locomotion, respiration, body size and voltinism. N denotes the number of cases for each comparison. The black dot indicates the mean absolute difference, the error bars the standard deviation. The gray horizontal lines show the 25th, 50th and 75th quantile of the density estimate.

5 Re-analysis of Szöcs et al. 2014 using harmonized and aggregated grouping features

To investigate how harmonizing grouping features and aggregating invertebrate traits might change the results in the analysis of trait-environment relationships we replicated the data analysis of Szöcs et al. 2014 (Szöcs et al. 2014) using the harmonized grouping features *Body size, Feeding mode, Locomotion, Reproduction/Oviposition, Respiration* and *Voltinism* (21 grouping features have been used in total) and aggregated traits using the aforementioned aggregation methods. The harmonized grouping features used are those that responded strongly to salinity in the study of Szöcs et. al. 2014, except for life cycle duration. For testing the effect of aggregated traits we assigned to each taxon in Szöcs et al. 2014 the aggregated trait value from the established harmonized European grouping feature database for its corresponding family.

Here, we limit our analysis to the RDA of traits constrained by electric conductivity of the original publication (see appendix for a more in-depth comparison to the original results). Overall, using the harmonized grouping features lead only to slightly different results in comparison to the original analysis. Sites with high salinity were characterized by multivoltine, oviparous, gill-respirating, and shredder species. Only species with the trait life cycle duration > 1 year fail to characterize sites with high salinization. Also, life cycle duration $<= 1$ year is not anymore characterizing sites not impacted by salinity. Like in the original analysis, transition and upstream sites from the point source are characterized by univoltine species and species that lay their eggs in an aquatic environment. The usage of aggregated traits yielded similar species scores for every aggregation method. Also, for every aggregation method compared, using at family-level aggregated traits did only slightly change the RDA species scores compared to not aggregated traits (Figure 3). Hence, the interpretation of the trait composition is the same as when only using harmonized grouping features. An overview of the harmonization for the European trait databases can be found in the supporting information in section .
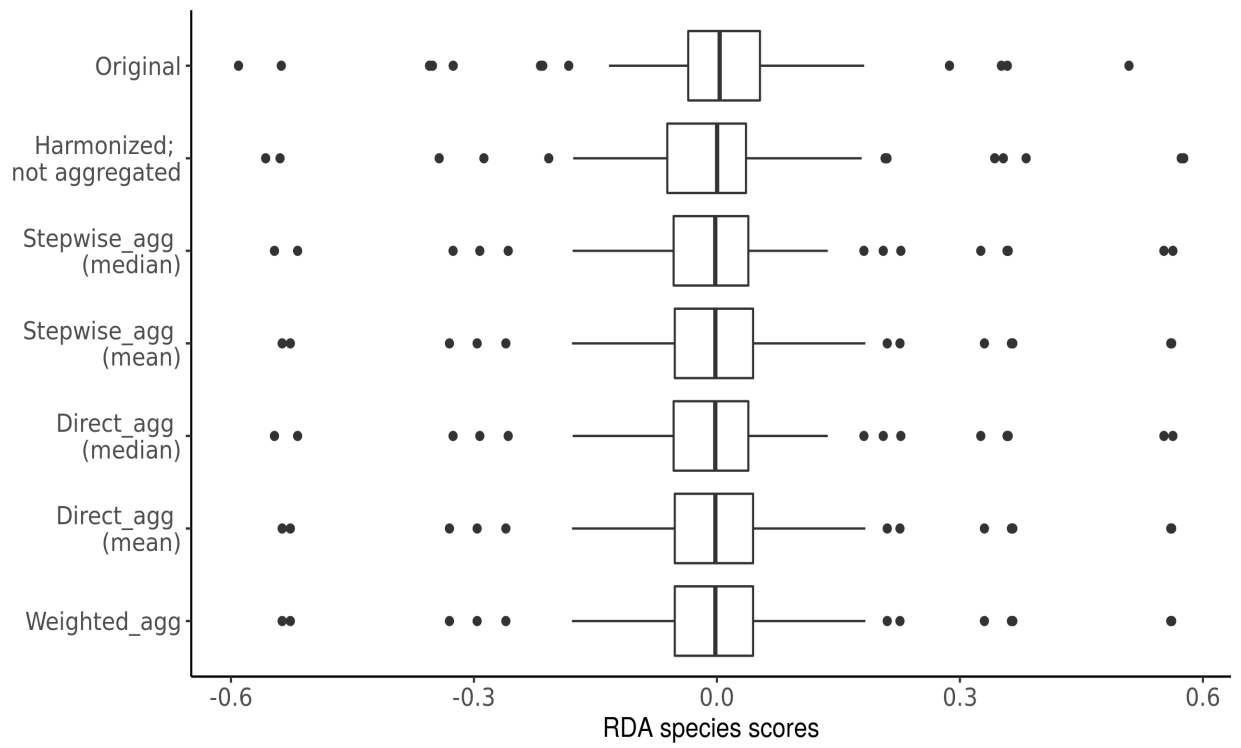
Figure 3: Species scores obtained by RDA from the original analysis (Szöcs et al. 2014), using harmonized grouping features, and using harmonized grouping features with assigned trait affinities from traits aggregated to family-level.

6   Discrepancies of invertebrate trait definitions

Definitions of grouping features and traits varied in their level of detail. The Tachet, Freshwaterecology, and North American (Twardochleb) trait databases provided more detailed descriptions of their trait information compared to the North American (Vieira) and New Zealand databases. An exception is the Australian trait database which is a collection of seven trait datasets (Kefford et al. 2020). Thus, grouping features occur multiple times with varying differentiation into traits. Depending on the dataset trait information is described with more or less detail.

The definition of grouping features varied across databases mainly concerning their differentiation into traits but also in their scope. We provide a summary of discrepancies in trait definitions in the appendix (Table S8). Both, differences in differentiation and scope can lead to discrepancies in trait definitions. For example, for the grouping feature feeding mode discrepancies arise because traits are assigned in different ways. Tachet defines predators as carvers, engulfers and swallowers. By contrast, in the North American (Twardochleb) database predators are defined as engulfers and carnivorous piercers. In turn, in the Tachet database, piercers are defined as a separate trait encompassing herbivorous and carnivorous piercers. Furthermore, the scope in the Freshwaterecology database for feeding mode is primarily on the food source of a species (except for filterers), while the other databases focus on the strategies of food acquisition. Therefore, the Freshwaterecology database defines e.g. predator as "eating from prey", while the other databases use the mouthpart morphology in their definition. The Tachet database captures the food source in an additional grouping feature. Varying levels of differentiation are also present in all other investigated grouping features between the trait databases (see for details Table 4 and Table S8). Locomotion definitions differ also in scope between databases. Freshwaterecology and New Zealand databases describe locomotion as the way of movement of an organism, Tachet as substrate relation, the North American (Vieira) as how organisms deal with flow, Australia as attachment, and the North American (Twardochleb) database includes among the way of movement also the location of movement. Similarly, regarding reproduction trait databases differ in their scope. Reproduction is captured in one grouping feature and defined as location of oviposit clutches and mode of reproduction in the Freshwaterecology and Tachet databases. North America (Vieira) provides information on the oviposition location but not on reproductive behavior. The Australian database report traits for reproductive behavior but also on oviposition site. The New Zealand database distinguishes three grouping features related to reproduction: reproductive technique, oviposition site (e.g. water surface, terrestrial), and egg/egg mass (e.g. free, cemented).

Various codings of traits are used throughout the databases (e.g. binary, fuzzy, continuous). The freshwaterecology and Australian use different codings in their databases. Tachet and the New Zealand database use exclusively fuzzy coding. Both North American trait databases contain categorical grouping features that can be converted into traits using a binary coding (Table 4). Binary coding represents a simple approach in which a taxon either expresses a trait or not. Fuzzy coding characterizes the affinity of an organism to exert a certain trait. It is used to account for plasticity in traits, e.g. taking into account that traits can change over the development time of an organism. Usually, fuzzy coded affinities are converted into proportional values. Continuous coding is used for traits like body size.

Table 4: Number of traits per grouping feature and type of coding of the traits for the respective grouping feature per database.

Database	Feeding Mode	Voltinism	Locomotion	Respiration	Reproduction	Size	Body Form
Freshwater-ecology	10 10 point assignment system	6 single category assignment system	6 10 point assignment system	7 presence/absence assignment system	9	-	-
Tachet	7 fuzzy [0 − 3]	3	8 fuzzy [0 − 5]	5	8 fuzzy [0 − 3]	7	-
North America (Twardochleb)	6	3	10	3 binary	10	3	-
North America (Vieira)	8	3	9	8 binary	10	3	5
Australia	16 [a] binary; proportional [0 − 1]; fuzzy [0 − 3]	7	9 binary; fuzzy [0 − 3]	10 binary; proportional scale [0 − 1]; fuzzy [0 − 3]	13 [b] categorical	9 binary; continuous; fuzzy [0 − 3]	4 fuzzy codes [0 − 3]
New Zealand	6	3	4	4 fuzzy [0 − 3]	4	5	4

a Some of the traits were similar (e.g. trait *Shredder*, *Shredder*, *Detrivore*, and *Collector*, *Shredder*).
b Many traits were rather comments than traits in the original database and were not considered.

References

Chessman, B. C. (Mar. 1, 2018). "Dissolved-oxygen, current and temperature preferences of stream invertebrates estimated from field distributions: application to assemblage responses to drought". In: *Hydrobiologia* 809.1, pp. 141–153. ISSN: 1573-5117. DOI: 10.1007/s10750-017-3455-1. URL: https://doi.org/10.1007/s10750-017-3455-1 (visited on 09/08/2019).

Kefford, Ben J. et al. (July 2020). "An integrated database of stream macroinvertebrate traits for Australia: concept and application". In: *Ecological Indicators* 114, p. 106280. ISSN: 1470160X. DOI: 10.1016/j.ecolind.2020.106280. URL: https://linkinghub.elsevier.com/retrieve/pii/S1470160X2030217X (visited on 05/05/2020).

Philips, Ngaire and Brian Smith (2018). "New Zealand Freshwater Macroinvertebrate Trait Database". In: *NIWA*.

Schmidt-Kloiber, Astrid and Daniel Hering (June 1, 2015). "www.freshwaterecology.info – An online tool that unifies, standardises and codifies more than 20,000 European freshwater organisms and their ecological preferences". In: *Ecological Indicators* 53, pp. 271–282. ISSN: 1470-160X. DOI: 10.1016/j.ecolind.2015.02.007. URL: http://www.sciencedirect.com/science/article/pii/S1470160X15000758 (visited on 06/21/2019).

Szöcs, Eduard et al. (Jan. 2014). "Effects of anthropogenic salinization on biological traits and community composition of stream macroinvertebrates". In: *Science of The Total Environment* 468-469, pp. 943–949. ISSN: 00489697. DOI: 10.1016/j.scitotenv.2013.08.058. URL: https://linkinghub.elsevier.com/retrieve/pii/S0048969713009728 (visited on 03/26/2020).

Usseglio-Polatera, Philippe et al. (Apr. 1, 2000). "Biomonitoring through biological traits of benthic macroinvertebrates: how to use species trait databases?" In: *Hydrobiologia* 422.0, pp. 153–162. ISSN: 1573-5117. DOI: 10.1023/A:1017042921298. URL: https://doi.org/10.1023/A:1017042921298 (visited on 06/21/2019).

Vieira, Nicole K M et al. (2006). "A Database of Lotic Invertebrate Traits for North America". In: p. 19.

Supporting Information

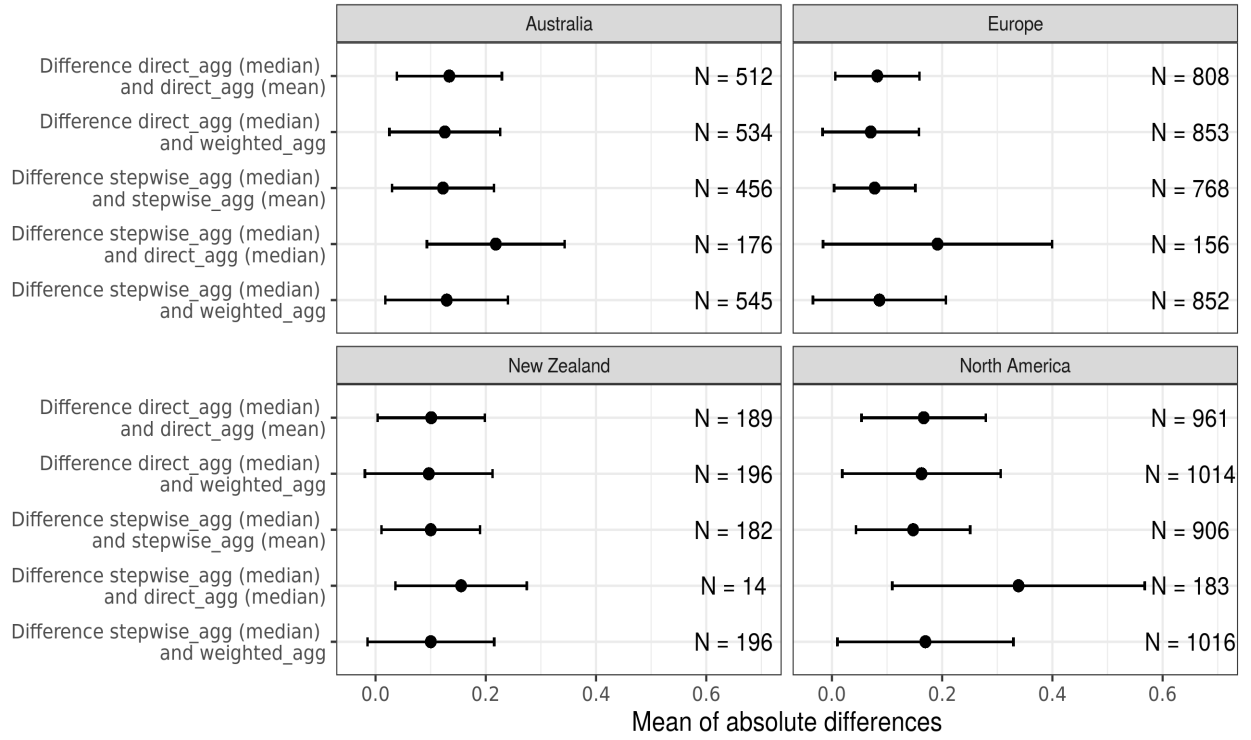## Comparison of the trait aggregation methods with each other

Figure 4: Means of absolute differences in trait affinities with standard deviations per region for all grouping features. Compared aggregation methods are displayed on the y-axis. N indicates the number of cases where differences occurred.

Re-analysis of Szöcs et al. 2014 using harmonized and aggregated grouping features.
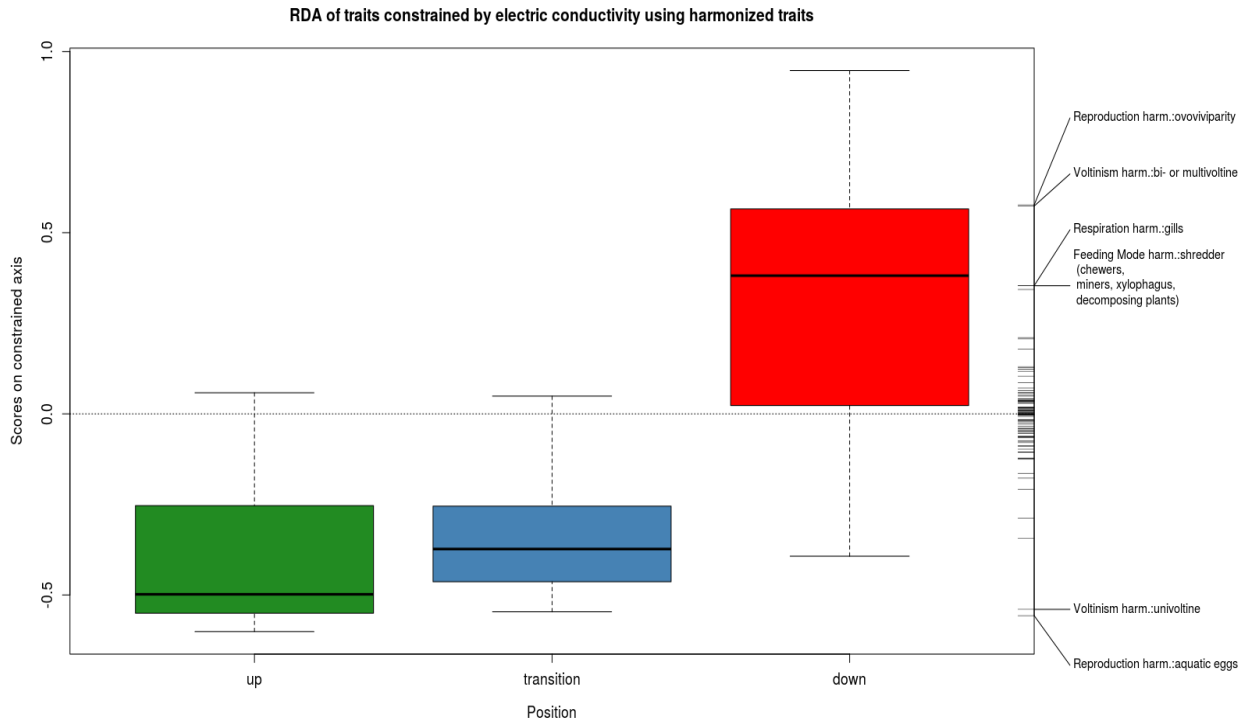

Figure 5: RDA of traits constrained by electric conductivity using harmonized grouping features. Boxplot of site scores along the conductivity axis (31.44% explained variance, p = 0.001, 1000 permutations). Rug on the left indicates trait scores on the conductivity axis. Only traits with a mahalanobis distance greater than 5.02 were labeled in accordance to the procedure in Szöcs et al. 2014.
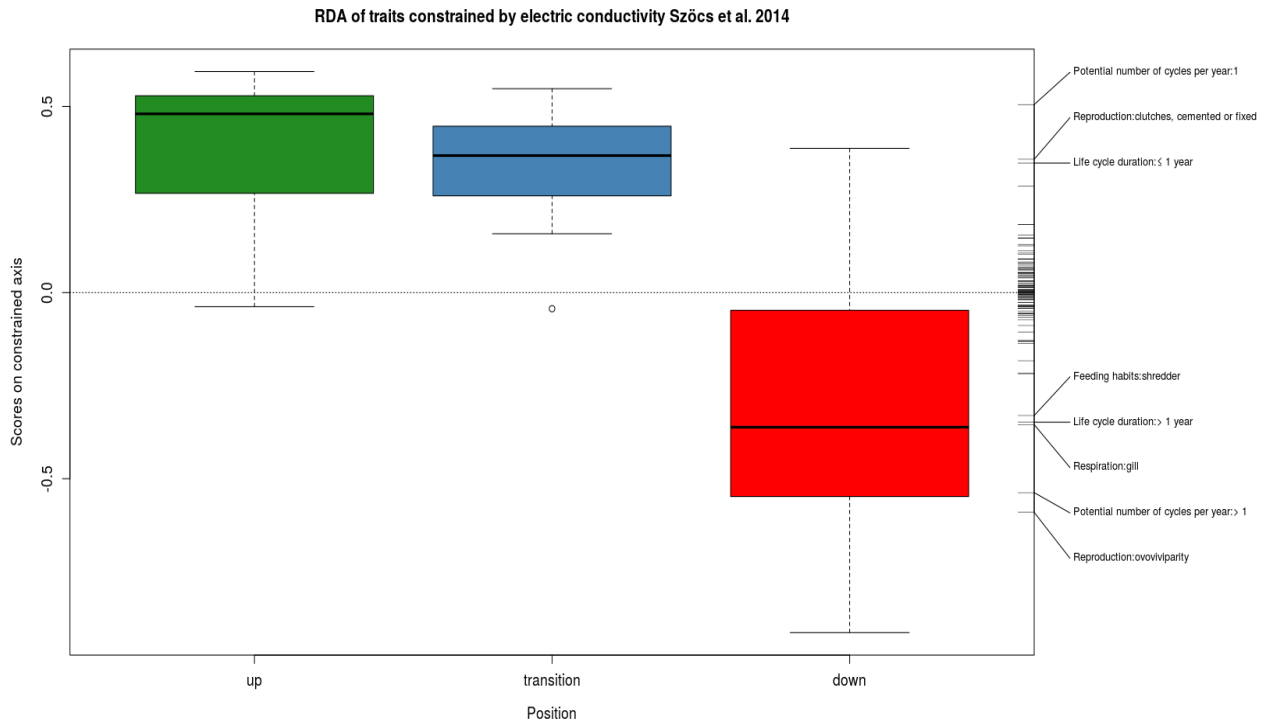
Figure 6: RDA of traits constrained by electric conductivity. Boxplot of site scores along the conductivity axis (30.09% explained variance, p = 0.001, 1000 permutations). Rug on the left indicates trait scores on the conductivity axis. Only traits with a mahalanobis distance greater than 5.02 were labeled.
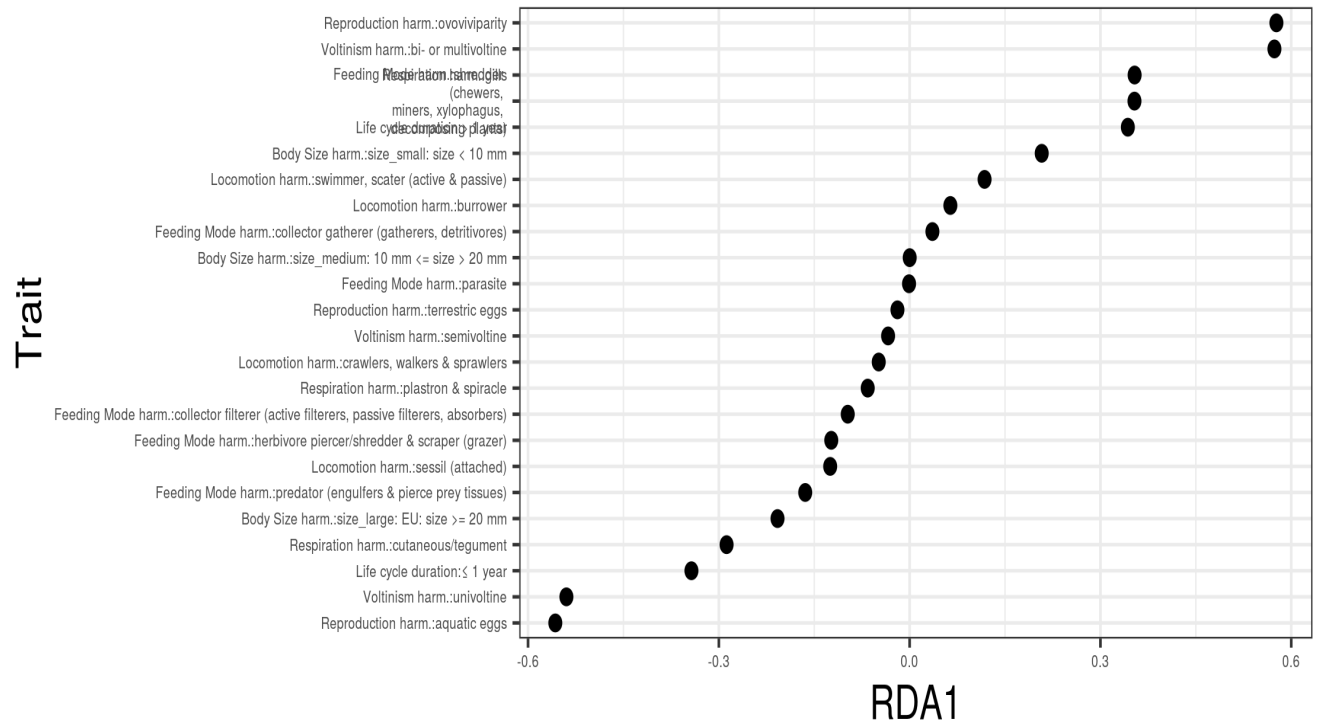
Trait distribution along first RDA axis

Figure 7: Trait scores on the first RDA axis for harmonized traits and traits of the grouping feature *life cycle duration*.
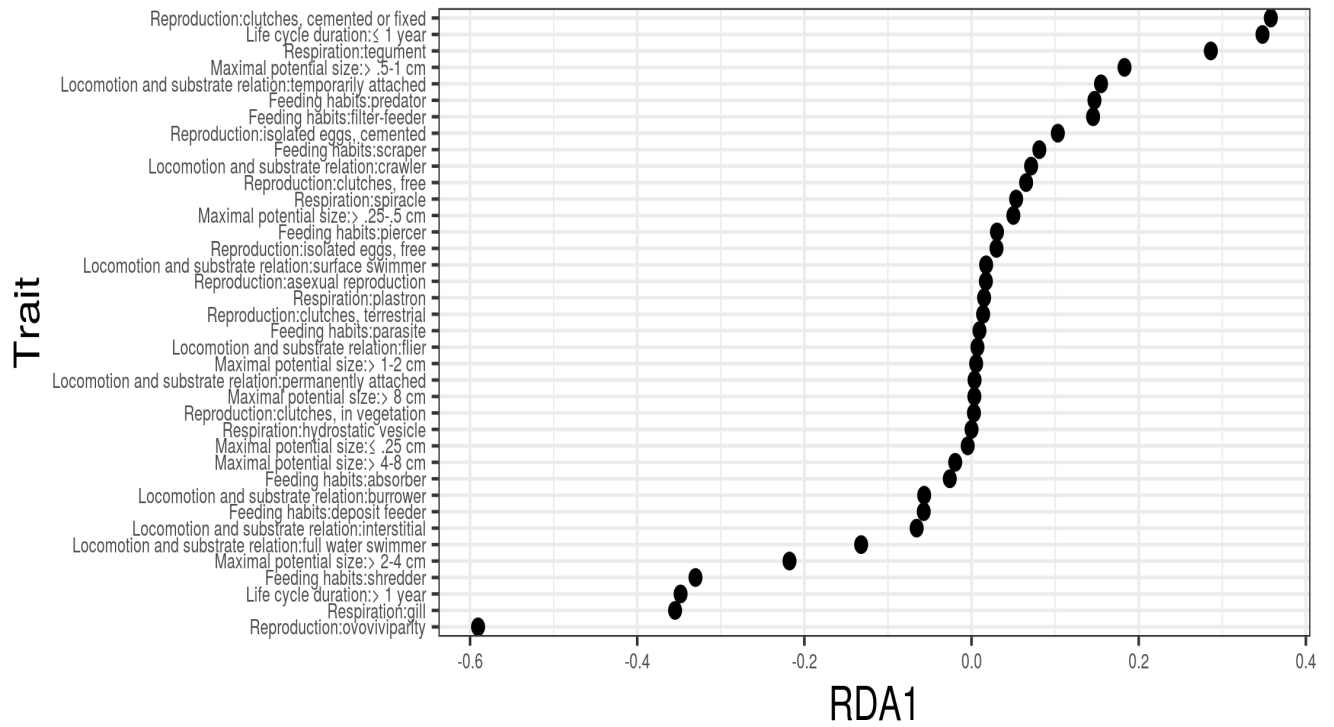
Figure 8: Trait scores on the first RDA axis for the traits responding to high salinity in Szöcs et al. 2014 .

Linear models of trait proportions

Linear models of trait proportions with harmonized traits:

Table 5: Results of linear models for the four selected harmonized traits and life cycle duration > 1 year. Trait proportions were logit transformed prior model building, estimates are on the logit scale. Although years were statistically not significant we kept this factor in the model to avoid temporal autocorrelation. Bold values indicate statistically significant effects ($p < 0.05$).

	Feeding mode: shredder	Life cycle duration: > 1 year	Voltinism: bi- or multivoltine	Reproduction: ovoviviparity	Respiration: gills
Intercept (= upstream)	**-1.041**	**-0.486**	0.375*	**-0.823**	0.092
Downstream	**0.926**	**0.605**	**1.376**	**1.684**	**0.854**
Downstream x 2008	-0.117	0.106	-0.235	-0.088	-0.317
Downstream x 2009	0.030	-0.056	0.001	0.245	0.180
Year 2008	-0.167	-0.115	0.033	-0.182	-0.151
Year 2009	0.175	0.086	-0.088	0.246	0.141

* p.value = 0.055

Linear models of trait proportions Szöcs et al. 2014:

Table 6: Results of linear models for the five selected traits for Szöcs et al. 2014. Trait proportions were logit transformed prior model building, estimates are on the logit scale. Although years were statistically not significant we kept this factor in the model to avoid temporal autocorrelation. Bold values indicate statistically significant effects ($p < 0.05$).

	Feeding habits: shredder	Life cycle duration: > 1 year	Cycles per year: > 1	Reproduction: ovoviviparity	Respiration: gills
Intercept (= upstream)	**-0.853**	**-0.478**	**0.603**	**-0.838**	0.111
Downstream	**0.819**	**0.594**	**1.297**	**1.679**	**0.839**
Downstream x 2008	-0.155	0.102	-0.227	-0.070	-0.314
Downstream x 2009	0.073	-0.053	-0.020	0.248	0.176
Year 2008	-0.122	-0.112	0.026	-0.192	-0.154
Year 2009	0.167	0.084	-0.104	0.250	0.139

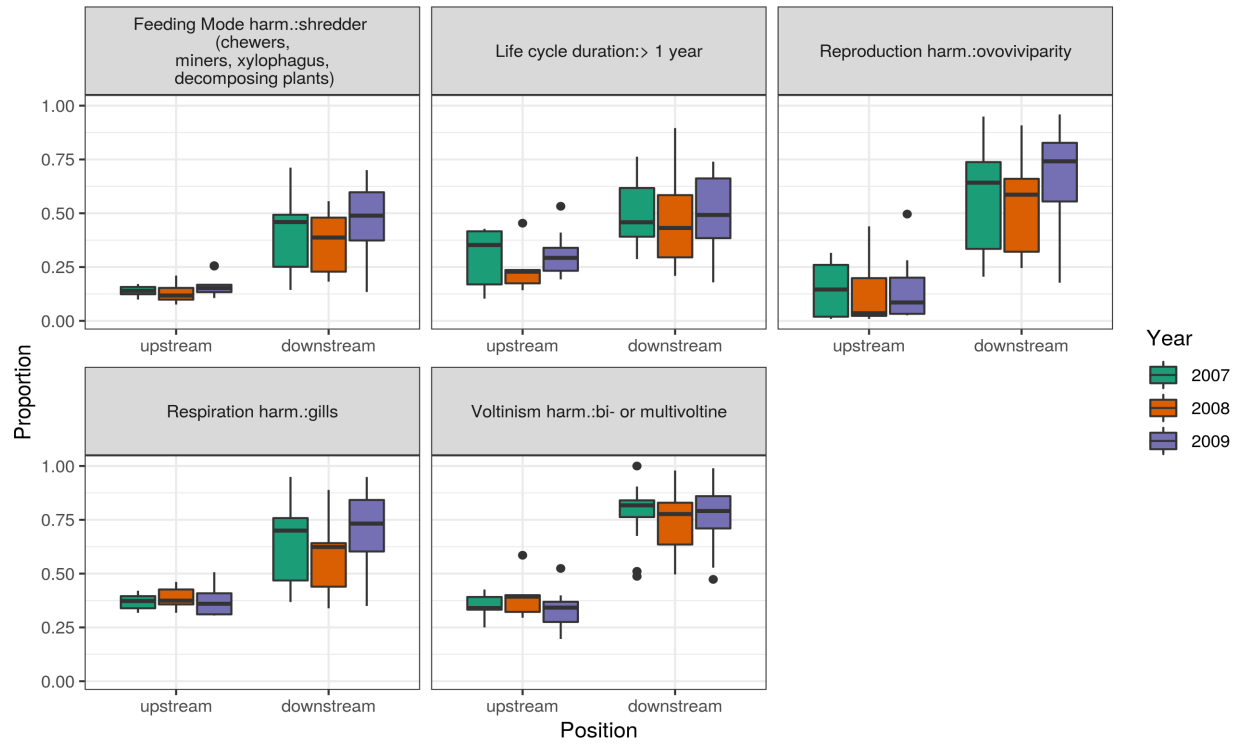# Trait proportions over time

Figure 9: Proportions for the four harmonized traits that have been promoted by salinization and life cycle duration > 1 year for down- and upstream sites.
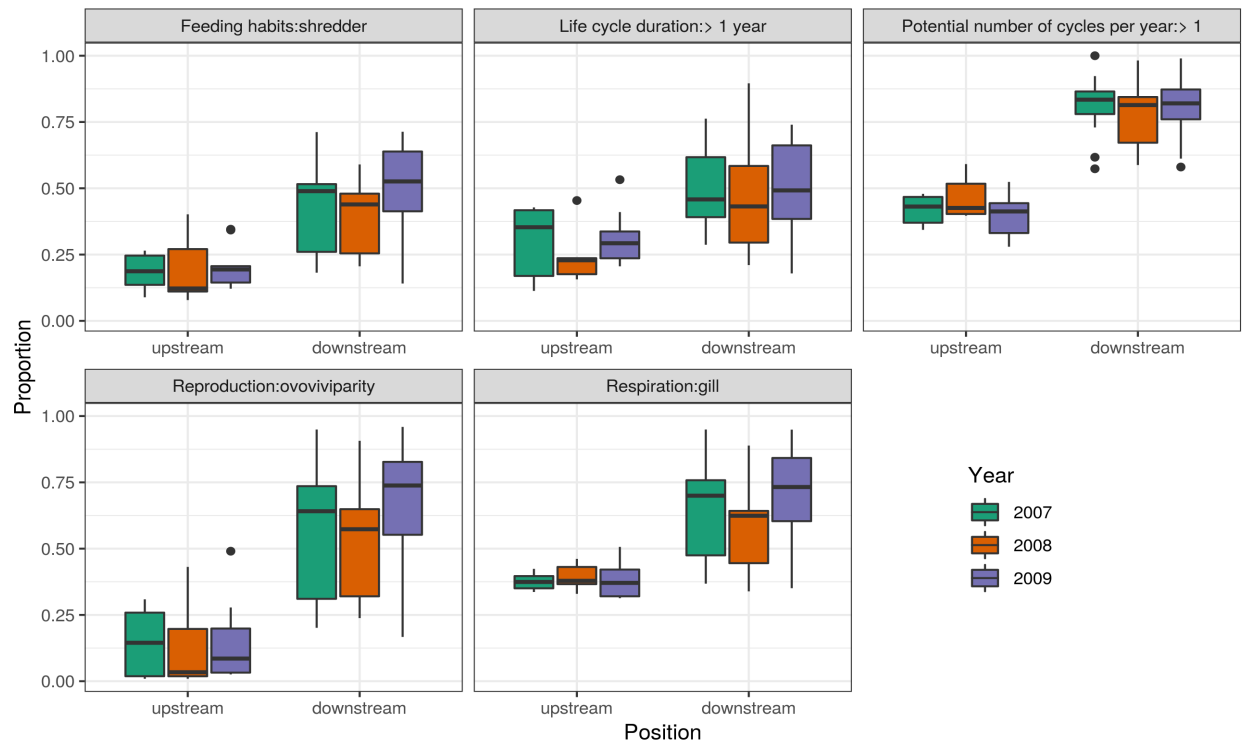
Figure 10: Proportions for five selected traits for down- and upstream sites (traits that have been promoted by salinization) from Szöcs et al. 2014.

Harmonization of the European trait databases

Table 7: Representation of traits per grouping feature and their harmonization for the European trait databases. The color coding indicates traits that have been harmonized. Cyan colored traits have not been used because they either represented ambiguous traits or traits that were not compatible with the traits of the other databases. Harmonization was done by assigning the maximum affinity of the allocated traits for the respective taxa to the harmonized trait.

Grouping feature	Freshwater ecology	Tachet	Harmonized traits
Voltinism	Semivoltine	Semivoltine	Semivoltine
Voltinism	Univoltine	Univoltine	Univoltine
Voltinism	Bivoltine	Polyvoltine	Bi/Multivoltine
Voltinism	Trivoltine		
Voltinism	Multivoltine		
Voltinism	Flexible		
Feeding Mode	Shredder	Shredder	Shredder
Feeding Mode	Miner	Deposit-feeder	Gatherer
Feeding Mode	Xylophagus	Absorber	Filterer
Feeding Mode	Gatherer	Filter-feeder	Herbivore
Feeding Mode	Active filterer	Scraper	Predator
Feeding Mode	Passive filterer	Predator	Parasite
Feeding Mode	Grazer	Parasite	
Feeding Mode	Predator	*Piercer (plants or animals)* [a]	
Feeding Mode	Parasite		
Feeding Mode	Other		
Locomotion	Swimming/scating	Surface swimmer	Swimmer
Locomotion	Swimming/diving	Full water swimmer	Burrower
Locomotion	Burrowing/boring	Burrower	Crawler
Locomotion		Interstitial	Sessil
Locomotion	Sprawling/walking	Crawler	
Locomotion	(semi) sessil	Temporarily attachted	
Locomotion	Other	Permanently attached	
Locomotion		Flier	
Respiration	Tegument	Tegument	Tegument
Respiration	Gill	Gill	Gills
Respiration	Plastron	Plastron	Plastron, spiracle
Respiration	Spiracle (aerial)	Spiracle (aerial)	
Respiration	Hydrostatic vesicle	Hydrostatic vesicle (aerial)	
Respiration	Tapping (air stores of aq. plants)		
Respiration	Excursion/Extension (to surface)		
Body size		<= 0.25cm	Small (< 1 cm)
Body size		> 0.25 - 0.5cm	Medium (>= 1cm - 2 cm)
Body size		> 0.5- 1cm	Large (>= 2 cm)

Body size		$> 1 - 2$ cm	
Body size		$2 - 4$ cm	
Body size		$4 - 8$ cm	
Body size		> 8 cm	
Reproduction	ovovivipar	ovoviviparity	ovoviviparity
Reproduction	free isolated eggs	isolated eggs, free	aquatic eggs
Reproduction	cemented isolated eggs	isolated eggs, cemented	terrestrial eggs
Reproduction	fixed clutches	clutches, cemented or fixed	
Reproduction	free clutches	clutches, free	
Reproduction	clutches in vegetation	clutches, in vegetation	
Reproduction	terrestrial clutches	clutches, terrestrial	
Reproduction	asexual	asexual reproduction	
Reproduction	parasitic		

a Taxa exhibiting this trait have been assigned to predators or herbivores based on a classification by Philippe Usseglio-Polatera.

Table 8: Comparison of trait definitions between invertebrate trait databases. Only traits that are differently described across databases are listed. The definition is quoted if it enables differences to be identified, otherwise the differences are described. The hyphen indicates a missing trait. Reproduction was captured in multiple grouping features per database. Hence, differences for reproduction have been described in the paper. Body form traits are not different between databases, except that the North America (Vieira) database contains the trait Bluff (blocky) which does not appear in the other databases.

Trait	Freshwaterecology	Tachet	North America (Twardochleb)	North America (Vieira)	Australia	New Zealand
Feeding shredder	"Feed from fallen leaves, plant tissues, CPOM"	"Eat coarse detritus, plants or *animal material*"	• "Shred decomposing vascular plant tissue" • Trait herbivore includes among others insect that shred *living aquatic plants*	Shredder	• Detrivore [a] • Trait herbivore includes among others the trait shredder	Shredders

	Predator	Piercer & engulfer	Predator	Engulfers ("ingest prey whole or in parts") & piercers ("prey tissues and suck fluids")	Carvers, engulfers & swallowers • Piercers (plants & animals) are an additional trait	"Eating from prey"
Feeding filter-feeder	No distinction between active and passive	No distinction between active and passive	No distinction between active and passive	No distinction between active and passive	No distinction between active and passive	Distinguishes between active and passive
Semivoltine	"< 1 reproductive cycle per year"	"< 1 generation per year"	"< 1 generation per year"	"< 1 generation per year"	"Life cycle lasts *at least* two years"	"One generation in two years"
Multivoltine	"> 1 reproductive cycles per year"	• 1-2 generations per year • bi/multivoltine • up to 5 generations per year • up to 10 generations per year	"> 1 generations per year"	"> 1 generations per year"	"Able to complete *at least* two successive generations per year"	"More than *three* generations per year" b

Locomotion type	Details	Description	Name	Definition	Group
Locomotion swimming	• Passive movement like floating or drifting (trait swimming/scating) • Active movement (trait swimming/diving)	• Surface swimmers (over and under the water surface) • Full water swimmers (e.g. Baetidae).	"Adapted for "fish-like" swimming" Swimmer	"Distinguishes swimmer and skater"	Swimmers (water column)
Locomotion burrowing	"Burrowing in *soft* substrates or boring in *hard* substrates"	• Burrowing "within the first centimeters of the benthic *fine* sediment" • Differentiates also the trait interstitial (endobenthic)	"Inhabiting *fine* sediment of streams and lakes" Burrower	"Moving deep into the substrate and thus avoiding flow"	Burrowers (in-fauna)
Locomotion sprawling & walking	"Sprawling or walking actively with legs, pseudopods or on a mucus"	-	Sprawling: "inhabiting the surface of floating leaves of vascular hydrophytes or fine sediments" Sprawler	-	-

Trait						
Locomotion crawling	-	"Crawling over the bottom substrate"	Defined as crawling on the surface of floating leaves or fine sediments on the bottom	-	Database contains traits crawler, sprawler, climber and clinger.	Crawlers (epibenthic)
Locomotion sessil	Does not distinguish temporarily and permanently attached	Distinguishes temporarily and permanently attached	Does not distinguish temporarily and permanently attached	Does not distinguish temporarily and permanently attached	Distinguishes temporarily and permanently attached	Does not distinguish temporarily and permanently attached
Respiration plastron & spiracle	Plastron and spiracle (aerial) are two separate traits	Definition includes respiration using air stores of aquatic plants	Plastron and spiracle combined into one trait	Distinguishes spiracular gills, plastron, atmospheric, spheric breathers and plant breathers	Plastron and spiracle (termed aerial) occur as separate and combined traits. Contains also traits: air (plants), atmospheric, and functional spiracles	Distinguishes plastron and spiracle (termed aerial)
Body size small	-	Multiple size classifications [d]	< 9 mm	< 9 mm	< 9 mm [a;c]	Multiple size classifications [e]
Body size medium	-		9 - 16 mm	9 - 16 mm	9 - 16 mm	
Body size large	-		> 16 mm	> 16 mm	> 16 mm	

a Traits from Botwe et al.

b Contains also bivoltine (two generations per year), trivoltine (three generations per year) and flexible.

c Contains a size trait with numeric size values. Contains also traits classifying size like Tachet and like the North American trait databases.

d Size classifications: $<= 0.25$ *cm*, $> 0.25 - 0.5$ *cm*, $0.5 - 1$ *cm*, $1 - 2$ *cm*, $2 - 4$ *cm*, $4 - 8$ *cm*, > 8 *cm*. No distinction into small, medium and large.

e Size classifications: $> 0.25 - 0.5$ *cm*, $0.5 - 1$ *cm*, $1 - 2$ *cm*, $2 - 4$ *cm*, $4 - 8$ *cm*. No distinction into small, medium and large.