New Zealand Freshwater Macroinvertebrate Trait Database

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Contents

Executive summary

- Species possess biological traits that reflect how they are born, live (including how they grow, feed, move, disperse and reproduce) and die.
- There is growing interest in the use of macroinvertebrate species traits as an assessment tool for monitoring human impacts on stream ecosystems.
- The use of species traits offers a fundamentally different way of examining ecosystem responses to human impacts than taxonomic-based measures, as traits reflect life history, physiology and the functional role that species play within the ecosystem and how disturbance affects these through direct effects on organism performance.
- Species traits may also be useful for establishing mechanistic linkages between biotic responses and environmental conditions.
- The New Zealand Freshwater Macroinvertebrate Trait Database comprises 16 biological traits, representing life history, morphology, mobility and resource acquisition trait categories of New Zealand's aquatic macroinvertebrates.
- An extensive review of the New Zealand and overseas published and grey literature was undertaken to derive trait information. Unpublished data, personal observations and expert opinion were also used to derive and/or confirm initial trait information and to update the database.
- Each trait is defined by a set of states or modalities, which describe the range of possible values for each trait.
- Once the trait information was compiled, an extensive process was undertaken to assign affinity scores for each taxon, for each trait modality. The affinity score represents the association that the taxon has with a particular trait modality.
- Because various sources of information are used to derive the traits, and taxa may show an association with more than one trait modality, 'fuzzy coding' is used to quantify the affinity of each taxon for each modality that contributed to a trait.
- The functional composition of a set of sites can be described in terms of trait % abundance, by multiplying the abundance (or log abundance) of species at the sites by the affinities of those species for the various trait modalities (i.e., the trait database).
- The New Zealand Freshwater Macroinvertebrate Trait Database has been used in a range of applications.

1 Introduction

Species possess biological traits that reflect how they are born, live (including how they grow, feed, move, disperse and reproduce) and die. We assume that these traits have evolved as a consequence of selective pressures exerted by the organism's environment (Southwood 1977, 1988). Certain suites of traits allow species to be successful in a given environment. Species that do not have the required traits do not survive and disappear from the community.

There is growing interest in the use of macroinvertebrate species traits as an assessment tool for monitoring human impacts on stream ecosystems (Dolédec et al. 2006; Dolédec et al. 1999; Stark & Phillips 2009; Statzner et al. 2005; Archaimbault et al. 2010; Magbanua et al. 2013; Phillips and Reid 2012a, b; Clapcott et al. 2017). The use of species traits offers a fundamentally different way of examining ecosystem responses to human impacts than taxonomic-based measures, as traits reflect life history, physiology and the functional role that species play within the ecosystem and how disturbance affects this through direct effects on organism performance (McGill et al. 2006). The habitat template model (Southwood 1977, 1988) provides the theoretical basis for this approach. It predicts that where environmental conditions are similar, species trait composition should also be similar, regardless of biogeographical differences in taxonomic composition. Townsend and Hildrew (1994) adapted this model for streams, suggesting that benthic communities should consist of species possessing traits well suited to both the temporal and spatial variability of their local habitats. This model has been used in numerous studies to examine the relationships between traits and environmental drivers (e.g., Scarsbrook & Townsend 1993; Statzner et al. 1997; Townsend & Scarsbrook 1997; Heino 2005; Beche et al. 2006). The approach is simple, intuitive and the effects of individual stressors are often a priori predictable. In general, traits have been found as effective, and in some cases, more effective, than traditional biomonitoring methods in differentiating human impacts (Dolédec et al. 2006; Magbanua et al. 2010; Rubach et al. 2010), even over large geographic areas (Charvet et al. 2000; Statzner et al. 2001; Lamouroux et al. 2004; Statzner et al. 2005; Dolédec et al. 2011).

Species traits may also be useful for establishing mechanistic linkages between biotic responses and environmental conditions (Baird et al. 2010; Culp et al. 2010; Van den Brink et al. 2010). For example, the kinds of food (energy) sources available at a site will determine the kinds of feeding mechanisms that will be successful. In contrast, taxonomic-based measures generally only indicate that an ecological change has occurred (Culp et al. 2010). Due to the mechanistic basis of the trait approach, the species trait approach has been proposed for use in ecological risk assessment (Baird et al. 2010; Culp et al. 2010; Van den Brink et al. 2010). A trait-based approach could also provide a framework for mechanistically connecting the occurrence of traits in a community to major environmental drivers, e.g., fine sediment (Pollard & Yuan 2010) or toxic contaminants (Liess et al. 2008). This mechanistic framework may help us better understand and predict response patterns associated with particular stressors, a goal of particular interest for environmental managers.

This report describes the basis for New Zealand Freshwater Macroinvertebrate Trait Database. It summarises the traits and modalities used, how these traits and modalities were selected, how species information was converted into affinity scores and the mechanics of calculating a trait by site matrix from a taxon by site (community composition) matrix. Finally, it lists examples of the use of trait-based assessments of macroinvertebrates in a variety of research, management and policy applications. The New Zealand Freshwater Macroinvertebrate Trait Database is located at https://www.niwa.co.nz/aquatic-invertebrate-traits-database.

2 Background to the New Zealand Freshwater Macroinvertebrate Trait Database

2.1 Trait categories and traits

The New Zealand Freshwater Macroinvertebrate Trait Database comprises 16 **biological traits**, representing life history, morphology, mobility and resource acquisition **trait categories** of New Zealand's aquatic macroinvertebrates (Table 2-1). These traits describe different aspects of the life history of organisms (e.g., size, number of reproductive cycles) or features that confer resilience or resistance beyond that provided by life history traits (e.g., attachment, body shape), as well as more general biological and physiological features (e.g., feeding habits, respiration). The choice of which traits to include was based on a review of earlier New Zealand studies (e.g., Townsend & Scarsbrook 1997), combined with those derived from a review of international literature at that time (e.g., Poff et al. 2006; Vieira et al. 2006). While a more extensive range of potential traits is possible (e.g., such as those listed in the USEPA trait database (Table 2-2), the limited availability of relevant data for New Zealand taxa restricted the potential range of traits for which information could be derived.

Table 2-1: Trait categories, traits and their descriptions included in the New Zealand Freshwater Macroinvertebrate Trait Database.

Trait category	Trait name	Description
Life history	Aquatic stages	Are all stages of the life cycle of the animal aquatic? E.g., all stages of Dytiscidae are aquatic, whereas only larvae of Megaloptera are aquatic.
	Egg/egg mass	Do the eggs float freely on the water surface or stream bed or are they cemented to rocks and other debris or to plant material? Are they retained within the body (protected)?
	Life duration	How long do adults live? Short (e.g., 1 day) to long (e.g., >1 year)?
	Number of reproductive cycles per individual	How many times does an animal reproduce before it dies?
	Oviposition site	Where are the eggs deposited? On or under water, on land or are they inserted into plants (endophytic)?
	Potential number of descendants per reproductive cycle	Generally measured as the number of eggs (or number of individuals if live-bearing) produced per reproductive cycle.
	Potential number of reproductive cycles per year (voltinism)	May be less than once a year (semi-voltine), once a year (univoltine) or greater than once a year (plurivoltine). This measure is known to vary with temperature and hence latitude.

Trait category	Trait name	Description
	Reproductive technique	May be sexual (male and female), asexual (budding or cloning) or hermaphroditic (male and female sexual organs present on the animal).
	Attachment to substrate	How does the animal move within its habitat? Does it swim, crawl, burrow or is it attached?
Mobility	Dissemination potential	How far can the larvae, pupae and adults move? Up to 10 m (low dissemination potential), 1 km (medium) or >1 km (high dissemination potential).
	Body flexibility	How flexible is the animal? Not flexible (<10°), low (>10–45°) or high (>45°)? E.g., snails are not flexible, worms have high flexibility.
	Body form	What is the shape of the animal? Is it streamlined, flattened (dorso-ventral or lateral), cylindrical or spherical?
Morphology	Potential maximum size	Refers to the maximum recorded size of the animal.
	Respiration of aquatic stages	How is oxygen acquired? If in dissolved form, then respiration may be via gills or general body surface (tegument and spiracles). If in gaseous form from the atmosphere, then a respiratory siphon, plastron (temporary air storage) or other structures may be used.
	Dietary preferences	Is a particular species or type of food required (e.g., wood feeder, periphyton) or is it more generalised?
Resource acquisition	Feeding habits	How does the animal feed? Is it a shredder, scraper, deposit-feeder, filter-feeder, predator or algal piercer?

Table 2-2: Trait categories and traits included in the US Freshwater Invertebrate Trait Database.[1]

Trait category	Traits included
Morphology	Includes body size, shape and armouring, respiration mode, morphological adaptations (suckers, friction, hooks, silk, ballast, hairy), and attachment.
Life history	Includes emergence behaviour including timing and synchronization, oviposition behaviour, fecundity, egg type, voltinism, development speed, adult lifespan, hatch time, ability to exit, and ability to survive desiccation.
Resource Acquisition Preference	Includes functional feeding group, habitat, flow preference, microhabitat substrate preference, and lateral and vertical habitat position in water column.
Mobility	Includes occurrence in drift, larval and adult dispersal distances including flying, crawling and swimming ability.
Tolerance	Includes thermal preference, oxygen, pH, salinity, turbidity and organic enrichment.

2.2 Compiling the trait information

A review of the New Zealand and overseas published and grey literature was undertaken to derive trait information for each taxon, with a focus on information at the MCI (Macroinvertebrate Community Index, Stark & Maxted 2007) level. This was primarily genus for insects, most crustaceans and molluscs, and family or higher level for some crustaceans and all "lower" taxa. Species-level information was derived wherever possible. Scientific publications, reports, taxonomic keys and notes were used to derive this information (Appendix A). In some cases, information at the family or, occasionally, order level was used. Species-level resolution is typically not necessary for trait-based analytical approaches used in bioassessment programs (Vieira et. al. 2006). Taxonomic resolution at the genus and family levels has resulted in successful application of traits to characterize aquatic communities for bioassessment purposes (Dolédec et. al. 1998, 2000; Gayraud et. al. 2003). In addition to the literature search, unpublished data, personal observations and expert opinion were used to derive and/or confirm initial trait information and to update the database. The latest update of the database largely reflects changes to affinity scores for some taxa based on personal observations, expert opinion and information derived from more recent publications (B. Smith, pers. comm., Feb 2018). In addition, the taxa list has increased from 202 to 495, primarily through the addition of species from Ephemeroptera, Plecoptera and Trichoptera.

[1] Sourced from https://www.epa.gov/risk/freshwater-biological-traits-database-traits#tab-1 on 19 February 2018.

2.3 Trait states or modalities

Each trait is defined by a set of **states or modalities**, which describe the range of possible values for each trait. For example, the trait "maximum potential size" was assigned the modalities <=5 mm, >5–10 mm, >10–20 mm, >20–40 mm and >40 mm. Similarly, non-numeric trait modalities can be allocated. For example, the trait "egg mass", which relates to oviposition site was assigned the modalities "free", "cemented" or "female bears eggs in/on body". A combination of numeric and non-numeric modalities is also possible. For example, "dissemination potential" includes the modalities "low (10 m)", "medium (1 km)" and "high (>1 km)". The cut-off points between modalities is guided by the range of possible values, identified through a review of literature, as well as expert opinion.

2.4 Trait affinity scores

Once the trait information was compiled, an extensive process was undertaken to assign affinity scores for each taxon, for each trait modality. The affinity score represents the association that the taxon has with a particular trait modality. Because various sources of information are used to derive the traits, and taxa may show an association with more than one modality, 'fuzzy coding' is used to quantify the affinity of each taxon for each modality that contributed to a trait (Chevenet et al. 1994). Fuzzy coding allows data from a variety of sources (e.g., quantitative, qualitative, observational) to be used and compared statistically. Affinities in the New Zealand traits database are coded using integers from 0 to 3, representing the strength of affinity for each trait modality. An affinity score of zero indicates no association of the taxon with a trait modality, whilst a score of three indicates a high affinity for a given trait modality. This approach also acknowledges the variability in traits that often occurs at different life stages, and that some taxa have broad preferences while others are more specialised. For example, a species that is predominantly a predator but feeds by scraping algae in early instars would be given an affinity of three for the feeding modality 'predator' and one for the modality 'scraper'. Fuzzy coding represents a more realistic characterization of trait states, especially for those organisms with ontogenetic shifts in trait states. Furthermore, fuzzy coding can be used to consolidate information on trait states at lower levels of taxonomic resolution. For example, if organisms are identified to the family level, trait affinity scores can be used to express the diversity of states occurring among the member genera. To give the same weight to each species and each trait, affinity scores typically are standardized so that the sum for a given species and a given trait equals one (Chevenet et al. 1994). We scored traits as zero for any modality of a given trait for which information was not available.

3 Using the New Zealand Freshwater Macroinvertebrate Trait Database

The functional composition of a set of sampling sites can be described in terms of trait % abundance, by multiplying the abundance (or log abundance) of species at the sites by the affinities of those species for the various trait modalities (i.e., the trait database). The resulting trait-by-site array contains the relative frequency of each modality per trait in each site (Figure 3-1).

Log abundance x site

Sample id	Acanthophlebia	Acarina	Acroperla
30818	0	0.30103	0
41543	0	0.30103	0
41813	0	0	0
41814	0	0	0

X

Species trait database

Taxon	SIZE1	SIZE2	SIZE3	SIZE4	SIZE5	DESC1	DESC2	DESC3	DESC4
Acanthophlebia	0	0	3	0	0	0	3	1	0
Acarina	3	1	0	0	0	0	3	0	0
Acroperla	0	0	3	0	0	0	3	0	0

=

Trait proportions x site

Sample id	SIZE1	SIZE2	SIZE3	SIZE4	SIZE5	DESC1	DESC2	DESC3	DESC4
30818	38%	15%	47%	0%	0%	53%	46%	1%	0%
41543	18%	54%	21%	8%	0%	19%	69%	9%	3%
41813	17%	39%	35%	3%	5%	22%	61%	11%	6%
41814	26%	46%	25%	2%	2%	28%	67%	5%	0%

Figure 3-1: How to calculate trait frequency. Source: Storey (2017).

Once the trait-by-site-array is calculated the dataset is ready for analysis. Some examples of the application of the New Zealand Freshwater Macroinvertebrate Trait Database (including earlier versions) are listed below:

- Assessment of landuse impacts at local (Doledec et al. 2006) and broad (Doledec et al. 2011) scales.
- Investigation of its potential as an indicator under the National Policy Statement on Freshwater Management 2014 (Clapcott et al. 2017).
- Assessment of the effects of landuse on multiple stressors (Wagenhoff et al. 2011, 2012; Magbanua et al. 2013; Lange et al. 2014).
- Differentiating effects of different farming practices on aquatic communities (Magbanua et al. 2010).
- Potential for application in Regional Council monitoring (Phillips & Reid 2012a, b).

- Use in explaining seasonal variation in the Macroinvertebrate Community Index (Stark & Phillips 2009).
- Testing the Habitat Template Theory (Scarsbrook & Townsend 1993; Townsend et al. 1997).

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Appendix A Traits database bibliography

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