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PRIMARY RESEARCH PAPER

# *dietr*: an R package for calculating fractional trophic levels from quantitative and qualitative diet data

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**Abstract** This article introduces an R package, *dietr*, which calculates fractional trophic levels from quantitative diet item and qualitative food item data following the routine implemented in *TrophLab* within the open source R environment. *dietr* is easy to use and can quickly calculate trophic levels for many diet records. In addition to calculating trophic levels following the *TrophLab* routines, users can also specify a taxonomic hierarchy and estimate trophic levels at multiple taxonomic levels in a single call of a function. Additionally, *dietr* works well with FishBase data obtained in R using *rfishbase* and comes with pre-made databases of prey trophic levels that users can utilize for estimating trophic levels. *dietr* can also calculate several prey electivity indices. I provide information on *dietr*'s performance and provide a use case example of how *dietr* can be used on an empirical dataset. Trophic levels for hundreds of specimens can be calculated in a few seconds and the flexibility of *dietr*'s input allows users to easily calculate trophic levels from their own data.

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## Introduction

Trophic levels of taxa are key for understanding a wide array of ecological processes, especially those shaping biological diversity (Post, 2002a). Studies utilizing trophic level data have provided valuable insights across a number of biological topics including macroevolution (Rojas et al., 2018; Borstein et al., 2019), ontogenetic changes in life-history (Wilbur et al., 1974; Mittelbach et al., 1988), ecological assembly (Leibold et al., 2004; Duffy et al., 2007; Marczak et al., 2007), food-web structure (Pimm et al., 1991; Williams & Martinez, 2004), fisheries management (Pauly et al., 1998; Essington et al., 2006), invasive species (Vander Zanden et al., 1999; Grosholz, 2002), and trophic modelling of ecosystems (Christensen & Pauly, 1992; Christensen & Pauly, 1993; Christensen & Walters, 2004). The main methods used to estimate trophic level are stomach contents analysis (Odum & Heald, 1975) or stable isotopes analysis (Post, 2002b). While both methods have their pros and cons, a discussion of which falls outside the scope of this paper, stomach contents are still commonly utilized to estimate trophic levels, either by themselves or in conjunction with stable isotope analyses as they can be highly complementary (Post, 2002b; Rybczynski et al., 2008; Polito et al., 2011; Mancinelli et al., 2013; Cresson et al., 2014). Because stomach contents analysis is common, diet data is widely available for many species through several literature and database resources (Jones et al., 2009; Wilman et al., 2014; Froese & Pauly, 2019; Palomares & Pauly, 2019).

Databases, such as FishBase (Froese & Pauly, 2019) and SeaLifeBase (Palomares & Pauly, 2019), provide a wealth of diet and trophic level data and are easily accessible through R using *rfishbase* (Boettiger et al., 2012). However, obtaining trophic level values from FishBase or *rfishbase* functions can be problematic and has some limitations as these databases may contain errors or biases (Sánchez-Hernández & Amundsen, 2018). For example, from FishBase records, multiple life-history stages across ontogeny may be included for an estimate of a species (e.g. *Plectropomus laevis* (Lacepède, 1801)), prey trophic levels may be incorrect due to entry errors causing a spurious trophic level calculation (e.g. *Macropharyngodon geoffroy* (Quoy & Gaimard, 1824), DietCode 2727 being artificially high), or species may have diet data but no calculated trophic level (e.g. *Deuterodon langei* Travassos, 1957, DietCode 52608). In some of the most extreme cases, some trophic levels for heterotrophs are incorrectly listed as equal to those of autotrophs in these databases (e.g. *Cottocomephorus grewingkii* (Dybowski, 1874), DietCode 2169). Consequently, users may want to re-calculate trophic levels for a species while removing certain life-history stages or re-calculate trophic levels when new data on the trophic levels of prey items becomes available. Additionally, users may want to calculate the trophic levels of taxa from newly collected diet data or from a study not incorporated in these databases.

Here, I introduce *dietr* (**Di**et **E**stimated **T**rophic Levels in **R**), a package that calculates trophic levels from diet or food item data implemented in the open source environment of R. *dietr* uses the TROPH routines described and implemented in *TrophLab* (Pauly et al., 2000). *TrophLab* is a program that estimates trophic levels from either quantitative (data in which the diet composition has been quantified) or qualitative (data in which the consumption of a prey type is documented) diet data. Two different routines are implemented to calculate trophic levels from these two types of data and are described in the implementation section below. Currently, *TrophLab* is only available as a Microsoft Access program and is not actively developed. *TrophLab* and its routines are also used by FishBase to calculate trophic levels of species in the FishBase database (Froese & Pauly, 2000; Froese & Pauly, 2019). In *dietr,* I offer a quick user-friendly interface to calculate trophic levels, as well as to incorporate hierarchies in trophic level calculations.

## Implementation

*dietr* is written in R (R Development Core Team, 2020), a popular language for analyzing biological data, and requires R version 3.6 or higher. It uses the existing R package *rfishbase* (Boettiger et al., 2012). For ease of use and fast vectorized calculations of trophic levels, the main inputs for *dietr* functions are data frames.

While the main functions in *dietr* calculate trophic levels, *dietr* also has functions that aid in formatting data from FishBase/SeaLifeBase to be compatible with *dietr* (Table 1). Specifically, the functions convert FishBase/SeaLifeBase diet and food item data obtained from *rfishbase* into a format that *dietr* can use. Diet data obtained from the *rfishbase diet* function retrieves data from FishBase/SeaLifeBase's diet tables, which contain quantitative diet data in which the percent composition of prey in the diet has been described. Food items retrieved by the *rfishbase fooditems* function accesses data from FishBase/SeaLifeBase's food items tables, which contain simple qualitative data on whether a prey item is consumed by a species. I use the term "prey items" in this paper to refer to unique prey types consumed (e.g. a species eaten), not the number or quantity of individual items consumed. The functions (*ConvertFishbaseDiet* and *ConvertFishbaseFood)* take the data frame produced by *rfishbase*'s *diet* and *fooditems* functions, respectively, as input, with an additional argument *ExcludeStage*, for which users can specify life-history stages (e.g. larvae, recruits, adults) they would like to exclude from the dataset. While users can use their own diet data with the remaining functions that are described below, the *ConvertFishbaseDiet* and *ConvertFishbasFood* functions allow users to download data from FishBase/SeaLifeBase that are already in a compatible form to use with *dietr*.

**Table 1** Functions and datasets available in the R package *dietr*

| Function or Dataset Name | Description |
|---|---|
| **Functions for Trophic Levels and Electivity Indices** | |
| DietTroph | Calculates trophic level from diet data |
| Electivity | Calculates forage index and several electivity indices |
| FoodTroph | Calculates trophic levels from food item data |
| **Optional Functions to Retrieve FishBase Data** | |
| ConvertFishbaseDiet | Converts diet data from FishBase/SeaLifeBase into a usable format for *dietr* |
| ConvertFishbaseFood | Converts food item data from FishBase/SeaLifeBase into a usable format for *dietr* |
| **Datasets** | |
| CortesPreyVals | Dataset containing trophic levels of prey items following Cortés (1999), which can be used in trophic level calculations |
| FishbasePreyVals | Dataset containing trophic levels of prey items following FishBase/*TrophLab* which can be used in trophic level calculations |
| Herichthys | Raw data from Magalhaes et al. (2015) described in the use case below and used in the tutorial in the vignette |
| Horn1982 | Data from Horn et al. (1982) containing prey consumption and prey availability data for two species used in examples for the Electivity function |

*dietr*'s *DietTroph* and *FoodTroph* functions perform trophic level calculations. The equations used to calculate trophic level are not different from those implemented in *TrophLab* and are discussed below for the two different routines (quantitative and qualitative, respectively). The function *DietTroph* calculates trophic level from quantitative diet data where the percent contributions of prey are known (i.e. volumetric, weight, etc.). The calculation of the trophic level is defined by Eq. 1. Here the trophic level of the focal species, $\mathrm{Troph_i}$, is calculated by adding 1 to the sum of the trophic level of the prey items weighted by their contribution in the diet, where $\mathrm{Troph_j}$ is the trophic level of prey item j, $\mathrm{DC_{ij}}$ is the proportion of item j in the diet of species i and G is the number of prey items consumed.

$$\mathrm{Troph}_i = 1 + \sum_{j=1}^{G} \mathrm{DC}_{ij} \times \mathrm{Troph}_j \tag{1}$$

As estimates of prey trophic levels may not be exact, the standard error around the estimate of the trophic level can be calculated with Eq. 2. Here, the standard error of the focal species $i$, $\mathrm{s.e.}_{\cdot i}$, is calculated as the square root of the sum of the product of the variance of the prey items trophic levels $\mathrm{s.e.}_{\cdot j}$ weighted by their respective contribution in the diet, $\mathrm{DC}_{ij}$ over 100.

$$\mathrm{s.e.}_{\cdot i} = \sqrt{\frac{\sum_{j=1}^{G} \mathrm{DC}_{ij} * \mathrm{s.e.}_{\cdot j}^{2}}{100}} \tag{2}$$

For qualitative data where only a list of food items appearing in the diet is known without knowledge of their percent contribution in the diet, a different procedure is performed for calculating the trophic level and standard error. This is implemented in the function *FoodTroph*. In the simplest of cases, where a species only consumes one type of prey, the trophic level is 1 added to the trophic level of the prey item and the standard error is equal to the standard error of the prey item. In cases where more than one type of prey is consumed, trophic level is calculated differently. First, prey items are randomly selected and ordered, and their simulated contribution to a diet, $P$, is calculated by Eq. 3 (Froese & Pauly, 2000). Here, $R$ denotes the ordered rank of the prey item and $G$ represents the total number of prey items consumed.

$$\log_{10} P = 2 - 1.9 \log_{10} R - 0.16 \log_{10} G \tag{3}$$

The simulated contribution of a diet items, $P$, calculated from Eq. 3 are then used to calculate the trophic level in Eq. 4, which is the sum of the products of the simulated contribution of prey items $P_i$ and their respective trophic levels divided by the sum of $P_{i.}$

$$\text{Troph} = \frac{\sum (P_i * \text{Troph}_i)}{\sum P_i} \tag{4}$$

The estimate of the standard error around the trophic level from food item data is defined by Eq. 5. Here, the standard error is the square root of the sum of the product of the variance of a prey item and the contribution of the prey item minus 1 divided by the sum of the contribution of the prey items, *P*, minus the total number of prey items, *G*. In *TrophLab*'s calculations of trophic level from food item data, the random sampling routine and calculation to estimate trophic level and standard error is repeated 100 times, with the final trophic level and standard error being the mean of these 100 calculations. While this number has been kept as the default in *dietr,* users may specify the number of iterations they would like to perform the routine.

$$\text{s.e.}_{\cdot i} = \sqrt{\frac{(\text{s.e.}_{\cdot 1})^2 * (P_1 - 1) + (\text{s.e.}_{\cdot 2})^2 * (P_2 - 1) \ldots (\text{s.e.}_{\cdot G})^2 * (P_G - 1)}{\sum P - G}} \tag{5}$$

As input, the *DietTroph* and *FoodTroph* functions require either a data frame of diet or food item data and a data frame containing the trophic levels of the prey items. The names used in the diet data must match those in the prey trophic levels and a value for the prey trophic levels must be supplied. While users can upload any set of prey trophic values for their calculations, I do provide the data object *FishBasePreyVals* that contains the same prey trophic levels found in *TrophLab*. This is formatted to work with data retrieved from FishBase using the *ConvertFishbaseDiet* and *ConvertFishbaseFood* functions. A vector of shared column names that contain the classification of the prey items also must be specified so diet items can be linked to prey trophic levels. The most unique feature, which is distinct from *TrophLab,* implemented in *dietr* is the option for users to specify a data frame containing a taxonomy to calculate trophic levels at different hierarchies. This data frame should increase from least inclusive to most inclusive from left to right. By specifying a taxonomy, users can calculate the trophic level at numerous levels (i.e. individual, population, species, etc.) in a single function call. For example, if users wished to calculate trophic levels at the individual, population, and species levels, *dietr* first calculates the trophic levels of each individual and from that data, calculates the mean trophic level for each population and the mean trophic level of the species.

If users have data on the availability of prey in a habitat in addition to diet data, they can use the *dietr* function *Electivity* for calculating various electivity indices used in dietary studies. Users simply need to read two data frames into R as input, one containing diet data and the other, prey availability. With a single execution of the function, users can calculate one or any combination of the following: forage ratio (Ivlev, 1961), Chesson's standardized forage ratio (Chesson, 1983), Ivlev's electivity index (Ivlev, 1961), Jacob's electivity index (Jacobs, 1974), Manly's alpha (Manly, 1974), Strauss' electivity index (Strauss, 1979), and Vanderploeg & Scavia's electivity index (Vanderploeg & Scavia, 1979). Users wishing to use these functions should consult the tutorial in the package vignette in R.

*dietr* is available through CRAN (https://cran.r-project.org/package=dietr) and is developed on GitHub (https://github.com/sborstein/dietr). New extensions in development and bug fixes can be seen under the issues section on the package GitHub page. For a more in-depth introduction to using *dietr* users should consult the vignette (package guide and tutorial) in R through vignette("*dietr*-vignette"), which provides instructions and a tutorial on how to use the functions and their respective options. Other details about the package can be accessed through the documentation via help("*dietr*").

## Methods

To test the accuracy of trophic levels estimated with *dietr,* I randomly sampled 1000 diets from FishBase using the *rfishbase* package. FishBase diets include studies in which the diet was quantitatively estimated by volume or weight. I then used the *DietTroph* function to estimate trophic levels using a database of prey trophic level values from FishBase/TrophLab available in the *dietr* package data object *FishbasePreyVals* which contains the same trophic level information for prey items that is available in *TrophLab*. It is important to note that while *dietr* has flexibility as far as allowing users to input their own trophic levels of prey for trophic level calculations, to directly compare trophic levels on FishBase, which were generated using *TrophLab*, it is necessary to use the same prey trophic levels for trophic level calculations. Thus, I conducted a correlation test in R between the trophic levels calculated using *dietr* to those on Fishbase. As the trophic levels of diet record on FishBase were calculated using *TrophLab*, and *dietr* implements the same trophic level calculation equations, one would expect a strong correlation between the two datasets if *dietr* is performing accurately. To assess speed, I used R's *system.time* function to measure the time in seconds it took *dietr* to perform.

Similarly, I compared trophic levels from qualitative food item data on FishBase to those calculated using *dietr*. To do this, I selected 1000 random species which had food item data and used the *dietr* function *FoodTroph* with prey trophic levels from the *FishbasePreyVals* data object in the *dietr* package. Again, the *FishbasePreyVals* were used to make a direct comparison to the trophic levels on FishBase, which are calculated with *TrophLab*. Speed of the function was assessed using R's *system.time* function.

To highlight a use case of *dietr*, I obtained data from a study by Magalhaes et al. (2015) on *Herichthys minckleyi* (Kornfield & Taylor, 1983), a cichlid endemic to the Endorheic basin of Cuatro Ciénegas, Coahuila, Mexico. This dataset, which is not on FishBase, reported the percent volumetric contribution of seven prey items in the diet of 422 *Herichthys minckleyi* with information on the lake and year in which they were collected within the Cuatro Ciénegas valley of Mexico. As an exploratory analysis, I used *dietr* to calculate trophic levels in a hierarchy by lake and year (2011/2012), lake regardless of year, and finally across all samples for the species. In cases where portions of the stomach contents were non-identifiable, the percentage dietary contribution was re-calculated from the identified items. As Magalhaes et al. (2015) did not calculate trophic levels in their study, they do not provide trophic levels for the prey consumed by *Herichthys minckleyi*. Additionally, the prey types are reported at broad taxonomic levels (e.g. gastropods, fish, macrophytes, etc.). Instead of arbitrarily assigning prey trophic values, I used the default taxonomic prey trophic levels from *TrophLab* for these prey items, which are available in *dietr* via the *FishbasePreyVals* data object. The data used in this analysis are available within the package and the code used in this analysis is shown in the *dietr* vignette. The vignette provides a tutorial on how users can create and format input data to calculate hierarchical trophic levels.

## Results

Trophic levels estimated with *dietr* were found to strongly correlate with trophic levels from FishBase ($r = 0.888$, $df = 998$, $P < 0.001$, Figure 1). Code execution time to measure trophic levels for these 1000 diet records was 2.76 s.

Trophic levels estimated using the *FoodTroph* function were highly correlated with the values reported on FishBase ($r = 0.989$, $df = 998$, $P < 0.001$, Figure 1). Code execution time to measure trophic levels for 1000 species was 11.08 seconds.

For the use case using stomach contents of *Herichthys minckleyi* from Magalhaes et al. (2015), mean trophic levels by lake and year ranged from 3.05 to 3.49 (Figure 2). By lake regardless of year, mean trophic levels ranged from 3.07 to 3.42. Across all individuals, trophic levels to range from 2.0 to 4.5, with the extremes of the range representing individuals that fed exclusively on autotrophs (trophic level 2) and fish (trophic level 4.5) respectively. The mean trophic level for *Herichthys minckleyi* across all individuals in the dataset was 3.21. Time to perform trophic level calculations for 422 individuals across the four hierarchical groupings took 0.33 seconds.

## Discussion

Generally, *dietr*'s ability and accuracy to calculate trophic levels yielded similar results to those calculated by *TrophLab* and stored on FishBase. However, some values calculated with *dietr* do differ from those listed on FishBase, which appears to be due to two factors. First, values differ due to database entry errors on FishBase. For example, the diet entry 2454 for *Clupea harengus* Linnaeus, 1758 has a trophic level of 1.35. Because minimum trophic levels for consumers is 2.0 (given autotrophs have a trophic level of 1), this value is impossible. It would suggest that this species is partially autotrophic. *dietr* estimates a trophic level of 3.09 for this species. When the diet data for this

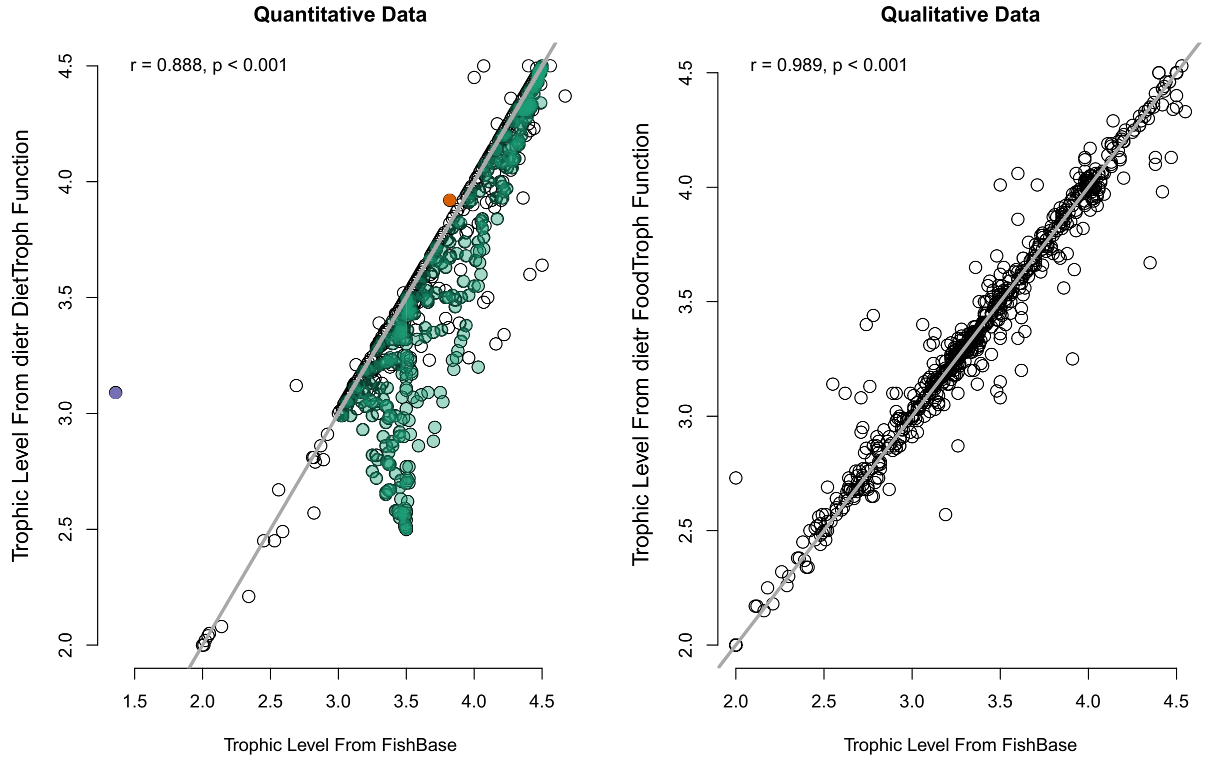

**Fig. 1** Correlation between trophic levels obtained from FishBase ($x$-axis in both plots) and those estimated by *dietr* ($y$-axis in both plots). Trophic levels estimated from quantitative diet data are shown on the left while trophic levels estimated from qualitative food item data appear on the right. The grey line represents the expected 1:1 relationship between the two sets of calculated trophic levels. Trophic levels calculated by *dietr* were comparable and strongly correlated to those on FishBase ($r = 0.888$, $P < 0.001$ for the quantitative dataset and $r = 0.989$, $P < 0.001$ for the qualitative dataset). For the quantitative dataset, outliers (see results for details) are highlighted as follows: One, in which FishBase has the incorrect trophic level suggesting the species is partially autotrophic in blue, a record using alternative prey trophic levels from Cortés (1999) in orange, and those from ICES (2012) which utilize a different trophic level for prey listed as "others" are listed in green. Note that the colors are transparent, so darker color represents more overlapping data points

record is entered into *TrophLab,* a trophic level of 3.09 is also calculated. Second, differences in trophic levels estimated by *dietr* and those stored on FishBase may be due to the use of unique prey trophic levels in trophic level calculations, which are listed in the *diet_items* table from *rfishbase* as *preyTroph*. As the database of prey trophic levels used for the *dietr* calculations were the same as those used in *TrophLab*, deviations from these values will cause differences in estimated trophic levels. For example, the largest differences in calculations are for a single reference (FishBase reference number 92354 (ICES 2012)). These records in FishBase have prey listed as "others", "others", and "n.a./others" in the "FoodI", "FoodII", and "FoodIII" prey categories, respectively. In some cases, this is the only item eaten (example DietCode 16956 for *Scomber scombrus* Linnaeus, 1758). If a single prey item is consumed, the trophic level is simply calculated as 1+trophic level of the prey item. In this case, the trophic level of the prey item according to the database of prey values in TrophLab should be 1.5, yielding a trophic level of 2.5. While *dietr* calculated a trophic level for this record as 2.5, this record has a trophic level of 3.5 on FishBase. This suggests a value of 2.5 was used as the trophic level for this prey for the calculation on FishBase. However, this is not noted anywhere in the FishBase database or in the metadata retrieved via *rfishbase*. Another good example of this is trophic levels on FishBase calculated from the data in Cortés (1999). While alternative prey trophic levels used in these calculations are not available through rfishbase, details in the metadata indicate that they do utilize an

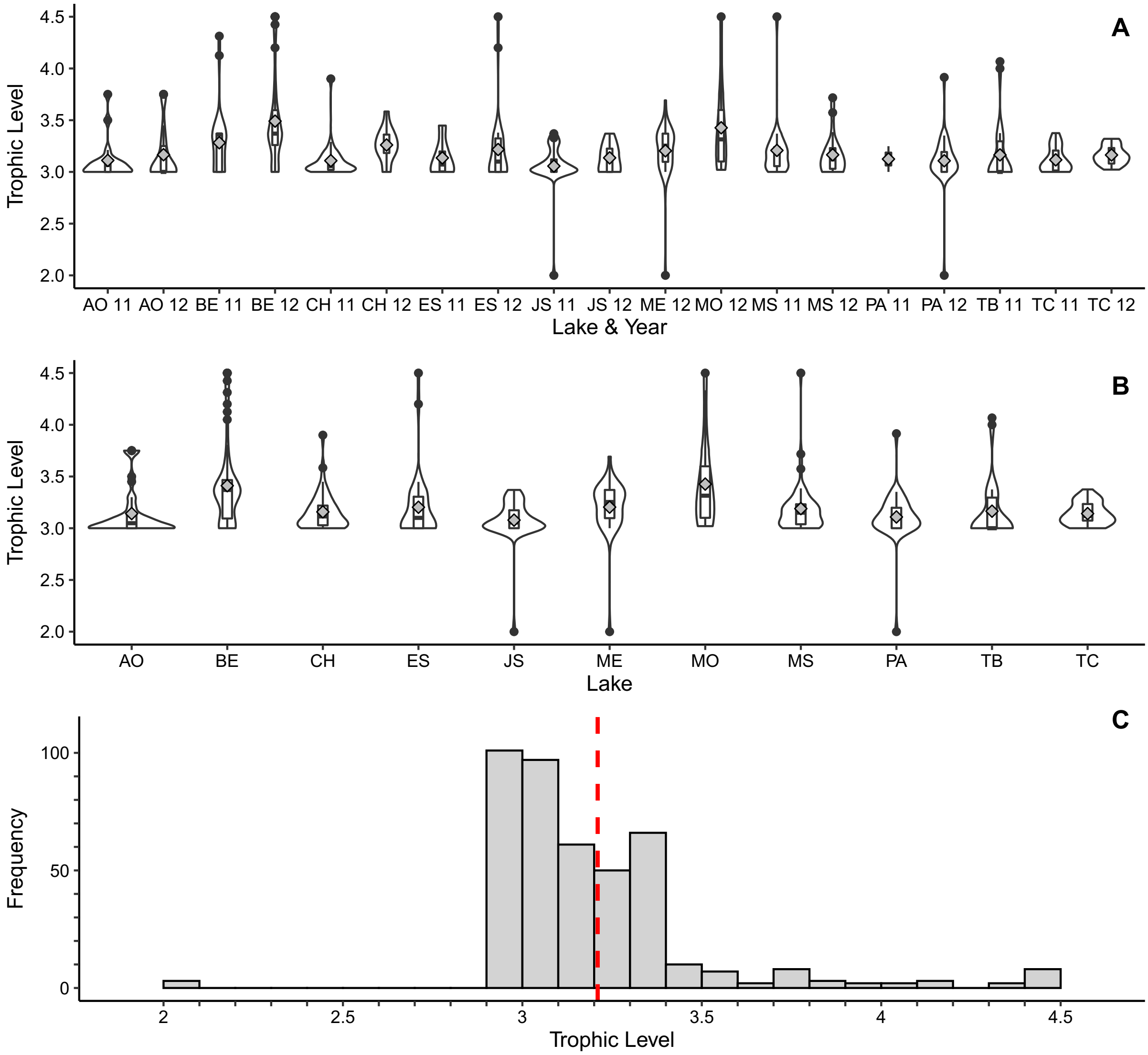

**Fig. 2** Hierarchical Trophic levels of *Herichthys minckley*i calculated using *dietr* from data in Magalhaes et al. (2015). **A** Violin plots of the trophic levels of *H. minckleyi* by lake regardless of year. Overlaid boxplots show the quantile ranges while the grey circle represents the mean. Lake abbreviations correspond as: Anteojo (AO), Becerra (BE), Churnice (CH), Excobedo (ES), Juan Santos (JS), Mojaral Este (ME), Mojaral Oeste (MO), Mezquites-Palpas (MS), Pozas Azules II (PA), Tierra Blanca (TB), and Tio Candido (TC). **B** Violin plots of trophic levels of *H. minckleyi* in eleven lakes between 2011 and 2012. Overlaid boxplots show the quantile ranges while the grey circle represents the mean. **C** Distribution of individual trophic levels of 422 *H. minckleyi* with the species mean displayed as a red vertical line

alternative set of trophic levels for prey, which can be confirmed by looking at original paper.

While these differences may seem concerning, they do not necessarily suggest that trophic levels calculated by *dietr* or those listed on FishBase (which are calculated with *TrophLab*) are more or less accurate. While FishBase does contain obvious errors in a handful of their trophic level records, such as trophic levels of 0 or trophic levels suggesting fishes are partially autotrophic as discussed above, *dietr* provides an alternative to use these diet data and recalculate the trophic levels of these erroneous records. Many of the FishBase records agree with those calculated by *dietr*. However, where differences occur, most can be easily explained by differences in the values of prey trophic levels used. If one enters in the diet data from the Cortés (1999) or ICES (2012) studies that can be retrieved from FishBase via *rfishbase* into *TrophLab* and uses the default prey values in *TrophLab* to calculate the trophic level, they are identical to those calculated by *dietr*. This suggests that the implementation of the equations to calculate trophic levels in *dietr* are behaving as expected. While some records for trophic levels on FishBase use alternative prey values that may be more specific or considered a better representation of the contribution of the prey in the diet, inconsistencies in the reporting of whether differing prey trophic levels were used in the metadata make assessing this difficult. Given the alternative prey values may not always be listed, it makes reproducing these calculations difficult. Additionally, it may also cause problems when comparing a broad number of records as it is possible that prey trophic levels across many studies may use different values for the same prey items.

While correlations between trophic levels estimated from food items reported by FishBase and *dietr* were very high, slight differences do occur. This is not necessarily surprising given that the routine to calculate trophic levels from food item data randomly samples food items, ranks them, and calculates trophic levels, with the final trophic level being the mean across 100 iterations. It is important to note that because of the sampling routine, it is possible, both in *dietr* and in *TrophLab* that repeating trophic calculations for the same record may yield slightly different results due to random sampling and ranking of prey items. It has been suggested that qualitative diet data as well as those based on frequency or percent number are not as good at estimating trophic levels and that estimates from studies where diet was quantified by weight or volume are preferred (Froese & Pauly, 2000; Stergiou & Karpouzi, 2002). Thus, it is strongly recommended that if *dietr* users have diet data that is either in percent weight or volume that they use the *DietTroph* function rather than the *FoodTroph* function to calculate trophic levels. While users with frequency or percent number data could use the *DietTroph* function, they should be cautious of the pitfalls of using these quantification methods for trophic level estimation using the *DietTroph* routine (Froese & Pauly, 2000; Stergiou & Karpouzi, 2002) and instead may wish to use the *FoodTroph* function. The *FoodTroph* function takes roughly four times as long to run as the *DietTroph* function, which is not surprising given the random sampling, ranking, and trophic level calculation occurring 100 times for each record. Therefore, the code is calculating 100,000 trophic levels in this amount of time (100 iterations × 1000 diet records). While I did not directly compare the timings of *dietr* to *TrophLab*, given users must manually enter data into *TrophLab* for each record, the simple input of data frames implemented in *dietr* provides a faster alternative to calculate trophic levels, especially when thousands of records are to be calculated.

While I compared *dietr* trophic level calculations to trophic levels on FishBase calculated with *TrophLab* to assess the accuracy of *dietr*, I believe *dietr* is most useful for data sets not derived from FishBase. *dietr* provides a quick, easy, and accurate way for users to calculate trophic levels from new diet data and provides users the flexibility to assign descriptive and accurate trophic levels for their calculations. While FishBase has a substantial amount of diet data, a vast amount of dietary studies are not included in the database. *dietr* provides users a way to calculate trophic levels from these datasets. The speed of *dietr* and simple input of data frames of diet data and prey trophic level data also make it ideal for calculating the trophic levels of many records in a single execution of the function, which may be useful for individuals conducting meta-analyses or studies with lots of individuals or taxa. The use case analyzing the diets of *Herichthys minckleyi* demonstrates the flexibility of *dietr* and highlights the ability of users to submit a hierarchy to calculate trophic levels across multiple groupings in a single execution of the function. This feature provides a simple method for users to follow a taxonomy and measure trophic levels and can be used to test various hypotheses. For example, users could measure individual, population, and species trophic levels simultaneously in a study looking at individual specialization and the niche variation hypothesis (Van Valen, 1965). This feature could also be used in other ways, like calculating trophic levels for species by year at a fishing ground to look at the mean trophic level change within the ecosystem over time (Pauly et al., 1998).

While I have shown that *dietr* properly implements the TROPH routine to calculate trophic levels, a major limitation to the accuracy of *dietr*'s trophic level calculations is the data itself. *dietr* is only as accurate as the data that is input into it. The more specific and accurate the estimation of the prey trophic level, the more accurate the trophic level calculation will be in a biological sense. While it may be difficult for some studies to use species-specific trophic levels for prey items, I would highly recommend users do so if possible, to provide the best estimates of trophic levels. While *dietr* has simple checks to ensure that quantitative diet data sums to 100% to accurately calculate trophic levels, it does not have a way to check the quality of the prey trophic level values as users can assign custom values that work best with their diet data. This could be problematic as incorrectly specified trophic levels of prey could yield biologically incorrect trophic level calculations. As *dietr* is implemented in an open source language and has a relatively simple structure for input, it will help aid the reproducibility of trophic ecological studies measuring trophic levels. Researchers using *dietr* could easily supply their code, diet data matrix, and prey trophic level values used for calculating trophic levels as supplemental data files supporting their research, aiding in reproducibility, and providing a data resource for future studies.

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**Data Availability** The code and data used to carry out the analysis are provided on the GitHub repository page for the package and are available here: https://github.com/sborstein/dietr.

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