

Phylogenetics

pez: phylogenetics for the environmental sciences

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Abstract

Summary: *pez* is an *R* package that permits measurement, modelling and simulation of phylogenetic structure in ecological data. *pez* contains the first implementation of many methods in *R*, and aggregates existing data structures and methods into a single, coherent package.

Availability and implementation: *pez* is released under the GPL v3 open-source license, available on the Internet from CRAN (<http://cran.r-project.org>). The package is under active development, and the authors welcome contributions (see <http://github.com/willpearse/pez>).

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1 Introduction

Community phylogenetics (or eco-phylogenetics) combines ecology and evolutionary biology, linking ecological phenomena with the evolutionary processes that generate species and their traits (see Webb *et al.*, 2002). This growing field has produced a number of statistical tools and software code to implement them (e.g. Kembel *et al.*, 2010), but this code is disparate and handles data differently, making routine data analyses challenging. In many cases, published methods are not formally implemented in a software package and are available only as supplementary materials to papers. Without active (public) maintenance, these valuable techniques are effectively lost to the scientific community.

Here, we present the *pez* *R* (R Core Team, 2015) package which provides an intuitive framework that merges existing tools and supports the development of the next generation of eco-phylogenetic methods. It is based around an *R* class (*comparative.comm*) that

links phylogenetic, community, environmental and trait data in a single object. With a *comparative.comm* object, one can presently calculate over 30 phylogenetic and trait diversity metrics (described in the documentation for *pez.metrics*), including more than 10 that were previously unavailable in *R*. *pez* additionally implements statistical models (Cavender-Bares *et al.*, 2004; Ives and Helmus, 2011; Rafferty and Ives, 2013) to infer the processes that underlie patterns in community phylogenetic and trait data. Users can also perform simulations under various community assembly and evolutionary processes, to help test hypotheses about the structure of biodiversity.

2 Description

2.1 Data manipulation and storage

pez provides a unified class to contain eco-phylogenetic data, and provides wrapper functions to manipulate the species and site

composition of community, trait, environmental and phylogenetic data. Using the *phy.build* family of functions, users can generate phylogenies for their dataset (making use of methods previously implemented in *phyloGenerator*; [Pearse and Purvis, 2013](#)). *pez* integrates and makes use of much existing R code ([Bortolussi et al., 2013](#); [Genz et al., 2013](#); [Koenker, 2015](#); [Labrière et al., 2014](#); [Oksanen et al., 2015](#); [Paradis et al., 2004](#)), and its *comparative.comm* class is directly compatible with all *caper* ([Orme et al., 2013](#)) code, easing comparative analysis of species trait data.

2.2 Metrics

Following the classification of [Pearse et al. \(2014\)](#), *pez* simplifies the calculation and comparison of over 30 metrics by grouping them into four categories: *shape*, *evenness*, *dispersion*, and *dissimilarity*. Shape metrics measure the structure of a community phylogeny, while evenness metrics additionally incorporate species abundances. Dispersion metrics are used to examine whether phylogenetic biodiversity in an assemblage differs from the expectation of random assembly from a given set of species—a species pool. Finally, dissimilarity metrics measure the pairwise difference in phylogenetic biodiversity between assemblages. This classification links directly onto the kind of data the investigator has at hand: assemblage occupancy (*shape*), assemblage abundance (*evenness*), source pool (*dispersion*) and assemblage comparisons (*dissimilarity*).

Other packages (notably *picante*; [Kembel et al., 2010](#)) allow for the calculation of some of the metrics contained within *pez*. *pez* unifies these metrics with other metrics not previously implemented under a common interface that can be extended to trait and transformed phylogenetic matrices (*sensu* [Letten and Cornwell, 2015](#)). For example, *pez* provides the first implementation of the *traitgram* framework ([Ackerly, 2009](#); [Cadotte et al., 2010](#)), allowing direct comparison of the extent of phylogenetic and functional trait community structure. *pez* also contains a flexible metric estimation and null-model generation suite (the *generic.metric* family), that can be used to easily compare different metrics and perhaps generate new *dispersion* metrics. New null models based around species' trait values (using *trait.asm*), and expected mean pairwise phylogenetic and trait distances (using *ConDivSim*) can also be simulated. The speed and ease by which *pez* allows for the user to compare many metrics is important because different metrics reveal separate aspects of eco-phylogenetic structure ([Cadotte et al., 2010](#)).

2.3 Statistical models

pez implements the [Cavender-Bares et al. \(2004\)](#) regression framework (*fingerprint.regression*), and extends it to include more metrics of trait evolution. While community phylogenetics has been criticised for relying on the assumption of niche conservatism to explain ecological assembly (e.g. [Mayfield and Levine, 2010](#)), this early (yet previously unavailable) approach does not rely on niche conservatism. Instead, it regresses the correlation between species' trait similarity and observed degree of co-occurrence against summary statistics of the evolution of those traits. The approach goes beyond simply describing the phylogenetic or ecological structure of an assemblage, and instead draws links between how traits have evolved and how they play-out in their present-day ecological context.

The *pglm* family of functions permit regression modelling of community ([Ives and Helmus, 2011](#)) and interaction network data ([Rafferty and Ives, 2013](#)) using the Phylogenetic Generalised Linear Mixed Model (PGLMM) framework. PGLMMs permit tests of the

mechanisms that underlie ecological and evolutionary structure in multiple communities. By fitting random effect terms that account for phylogenetic and trait co-variance, the user can statistically estimate how likely similar and dissimilar species are to (co-)occur as a function of their traits, environmental conditions, and the presence of interacting species.

2.4 Simulations

Hypothesis testing and the development of new eco-phylogenetic methods require simulation of data under known conditions, and *pez* contains functions to facilitate this. The *scape* family of functions (following [Helmus and Ives, 2012](#)) simulate species' distributions across environmental gradients. Species' environmental tolerances, range size and negative species interactions can be simulated to contain phylogenetic signal and generate patterns of phylogenetic structure at different spatial scales. The *sim.meta.phy.comm* family of functions simulate phylogeny, trait evolution and assemblage structure simultaneously across a landscape. Species' abundances across the landscape are proportional to the fit of each species' trait value to the conditions in each assemblage, and individuals migrate at random across the landscape. The *sim.meta.phy.comm* functions do not require the user to specify a phylogeny, and combined with the *phy.sim* family, provide a toolkit for the development of new simulation scenarios.

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