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pez: Phylogenetics for the Environmental Sciences

Short Structured Abstract

Summary

Pez is an *R* package that calculates >30 community phylogenetic metrics, statistically models phylogenetic, trait, and community data, and simulates community structure. It provides a common programmatic standard for the management and manipulation of eco-phylogenetic data in *R*.

Availability

‘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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Supplementary information

A vignette (available with the package) showing some of the package’s functions, and briefly describing the classification of community phylogenetic metrics.

Text

Introduction

Community phylogenetics is a subfield of ecology which links ecological phenomena (e.g., competition, ecosystem functioning) with the evolutionary processes that generate species and their traits (**Webb2002**; **Cavender-Bares2004**). This growing field has generated a number of statistical tools, such as >30 metrics of phylogenetic biodiversity, and software code and packages to implement such statistics (**Webb2008**; **Regetz2009**; **Kembel2010**; **Orme2013**; **Eastman2013**). However, existing code for these statistics is disparate and handles data differently making routine data analyses with different statistics by the end user challenging. Further, many statistics are not formally implemented in a particular software package and are available only as supplementary materials to papers which are not maintained or have public source code. Without active maintenance, these valuable statistics are effectively lost to the scientific community.

Pez provides an *R* class (*comparative.comm*) that integrates phylogenetic, community, environmental and trait data in as a single object. One can then calculate a large number of phylogenetic biodiversity metrics utilizing single functions. The implemented metrics are thematically organized into one of four classifications according to the framework outlined in **Pearse2014review** allowing the user to better understand the actual aspects of phylogenetic biodiversity they are calculating with any particular metric. As the structure of the package has been written to be flexible and intuitive, newly published metrics will continue to be incorporated in *Pez*.

Further, *Pez* implements and extends the regression framework presented by (**Cavender-Bares2004**) (**Cavender-Bares2006**). Finally, it provides functions that simulate ecological communities to exhibit varying degrees of phylogenetic and trait community structure. Together, the functions we have implemented in *Pez* will facilitate and speed the use of analysis of eco-phylogenetic datasets, and provide a common *R* framework for community phylogenetics.

| Function | Description |
|-------------------------------|--|
| <i>comparative.comm</i> | Object class to store community, phylogenetic, environmental, and trait data |
| <i>shape</i> | Calculates PSV^* (Helmus2007), PSR^* (Helmus2007), PD^* & MPD^* (Faith1992), Colless' Index* (Colless1982), γ^* (Pybus2000), Δ^* (Warwick1995), E_{ED} & H_{ed} (Cadotte2010), phylo-eigenvectors* (Diniz-Filho2011) |
| <i>evenness</i> | Calculates Δ (Warwick1995), Phylogenetic Entropy (Allen2009), PAE , IAC , H_{aed} , & E_{aed} (Cadotte2010), Rao's quadratic entropy* (Rao1982a), λ (Pagel1999), δ (Pagel1999), κ (Pagel1999), Simpson's XXX (XXX) |
| <i>dispersion</i> | SES_{MPD}/NRI^* (Webb2000 ; Webb2002 ; Kembel2009), SES_{MNTD}/NTT^* (Webb2000 ; Webb2002 ; Kembel2009), $INND$ (Ness2011), D^* (Fritz2010) |
| <i>dissimilarity</i> | UniFrac (Lozupone2005), PCD (Helmus2010), PhyloSor (Bryant2008), Rao's Q (Rao1982a) |
| <i>fingerprint.regression</i> | Compares phylogenetic, community co-existence, and trait similarity matrices using Mantel tests, quantile regressions, or linear models following (Cavender-Bares2004 ; Cavender-Bares2006). Completely re-implements all features previously available in <i>EcoPhyl</i> (XXX) |
| <i>scape</i> | Simulates community phylogenetic structure across a landscape, simulating phylogenetic repulsion, attraction, niche width, and range size (Helmus2012) |
| <i>trait.asm</i> | Simulated community structure based on species traits following Helmus2013 |
| Others? | classic.phy.signal (worth keeping?) - some stuff from willeerd? |

Table 1: Some of the functions available in *pez*. * indicates a metric whose code is based on existing *R* code. Note that calculation of Pagel's λ (**Pagel1999**), δ (**Pagel1999**), κ (**Pagel1999**) are calculated using the *ppls* function in *caper* (**Orme2013**).

Description

Data manipulation and storage

Pez extends the data manipulation and import/export features of *R*, and contains a unified class to contain all eco-phylogenetic data. It simplifies the process of ensuring community, trait, environmental, and phylogenetic data are compatible by overloading *R*'s standard row and column operators. This makes it simple to make consistent changes across datasets; for example, removing a species from the community data automatically trims it from the phylogeny, and removes its associated trait data. *Pez* was designed to be backwards-compatible with *caper*'s (**Orme2013**) *comparative.data* class, seamlessly permitting detailed comparative analysis of species trait data. The data of *comparative.comm* objects can also easily be extracted to be compatible with the functions of an existing community phylogenetics *R* package *picante*. The data structure of */emphpez* thus allows for fully integrated data analyses with existing and future eco-phylogenetic packages.

Metrics

Following the classification of **Pearse2014review** *pez* simplifies the calculation and comparison of a number of metrics by grouping them into four categories: *shape*, *evenness*, *dispersion*, and *dissimilarity*. Shape metrics measure the structure of a community phylogeny. Evenness metrics are shape metrics that incorporate a weighting with species' abundances. Dispersion metrics calculate the phylogenetic biodiversity expected given a source pool. Finally, dissimilarity differs from the former as they directly calculate the pairwise difference in phylogenetic biodiversity between assemblages. Table 1 gives an overview of the metrics that may be calculated in *pez*, speeding and easing the comparison of community phylogenetic metrics is important, since each can reveal radically different aspects of the structure of ecological assemblages (**Cadotte2010**).

Models

Model-based approaches are, in many ways, an advance over metrics that simply quantify phylogenetic pattern in ecological assemblages. Models explain phylogenetic structure across a number of assemblages simultaneously, maximising statistical power, and can incorporate phylogenetic, environmental, trait, and other information. *Pez* contains a complete re-implementation of all routines previously available in *EcoPhyl* (XXX)

that regress species co-existence matrices against environmental and, trait, and phylogenetic distance matrices (**Cavender-Bares2004**; **Cavender-Bares2006**). It extends these routines to include, for example, more modern measures of phylogenetic signal (*e.g.*, λ , *delta*, κ , *D*), and to examine differences in relationships among clades.

Simulation

Finally, *pez* contains functions to simulate communities under various models of community assembly and/or evolution. *scape* simulates community assembly over a region and allows the user to simultaneously model phylogenetic attraction and repulsion such that closely related species are generally found at sites of similar environment, just not at the same site. *metapop.sim* fits models of trait evolution and dispersal ability to a static landscape, evolving both a phylogeny, species traits, and the resulting distribution of species across the landscape.

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