

New version of R package ieggr. Download address:

<ftp://129.15.40.254/R.package/ieggr>

What is new in Version 2.1?

(1) alpha.g

This function can simultaneously calculate various taxonomic alpha diversity indexes, including "richness", "shannon", "simpson", "invsimpson", "fisher", "chao1", "ACE", "renyi", and "hill number".

(2) biolog

To calculate "area under the curve" from BioLog data and sort the results by substrates and plates. Written by Arthur.

(3) geochip.trans

This function can finish various options of GeoChip data scaling and/or transformation efficiently, and save files in the format required by our geochip analysis pipeline.

(4) iwd

a small tool in ieggr-tools. set work directory from a directory or file path (automatically remove "<file:///>") and show a message of current work directory. more efficient than setwd() and getwd().

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How to use?

(1) Download the .Zip file (for Windows) or .tar.gz file (for Mac or Linux) of the most recent vesion.

(2) Install other necessary packages (vegan, ape, seqinr) by

R-->Packages-->install Package. Or just run following codes in R:

```
pk=c("vegan","ape","seqinr");pkg=pk[!(pk %in%  
installed.packages()[,1])];if(length(pkg)!=0){install.packages(pkgs=pkg,repo  
s="http://cran.us.r-project.org")}
```

(3) Install this "ieggr" package in R, by click R-->Packages-->Install Package(s) by zip/tar.gz files

(4) Load the package by typing "library(ieggr)" in R.

(5) Enjoy the functions. Every function has help document. You can use help() or search the manual for details.

Att: current version will triggler conflict of some functions in R package {ade4} with R package {vegan}, but functions in {ieggr} are still good to go. i will fix this in later version.

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New function since Version 1.8

(1) cor.cate.env

Various correlation tests between each environment factor and each taxa category (can be each OTU, probe, gene, gene family, gene category, or whole).

Correlation tests include pearson, kendall, spearman, Mantel using different dissimilarity methods and correlation methods, and CCA analysis between each factor and each category.

See manual or help document of function "cor.cate.env" for details and examples.

New function since Version 1.7

(1) tree.color plot a colorful tree according to the colors you specified for every category (e.g. phylum, class, special group)

New functions since Version 1.6:

(1) mantel.n and manteln.partial

Mantel test for both positive and negative correlation. You can randomize within specified strata. You can count in diagonal elements if they are not zero (may be useful for distance-decay, time-decay or other analysis which count in dissimilarity at zero-time/distance-difference point)

(2) hillnum

Calculate Hill number, unified index for taxonomic, phylogenetic and functional alpha diversity. Anne Chao, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. Annu. Rev. Ecol. Evol. Syst. 2014. 45:297-324

(3) tree.path and tree.part

To list all nodes and edge length from root to each tip, and all the tips derived from each node in a phylogenetic tree. Useful to calculate tree-based diversity index, such as phylogenetic Hill number.

(4) cohend

Popular standardized effect size index. You can set paired comparison. You can get standard deviation of Cohen's d.

(5) data("color.MS2010")

Color palette from MicroSoft Office 2007-2010. You may use the color in your figures generated by R.

(6) col3.dist

Transform 3-column matrix to distance matrix. A reverse function of dist.3col.

New functions since Version 1.4:

(1) Community analysis:

bNTI.p to calculate beta NTI (null model test of phylogenetic beta diversity) by parallel computation

RC.p to calculate Raup-Crick value based on Bray-Curtis (null model

test of taxonomic beta diversity)
qp.js to quantify relative roles of different ecological processes
by using James Stegen's method (2015).

(2) Tools:

lazyopen a very simple way to open file of a type we usually use (.csv,
.txt, .nwk, .fasta, .fna, .RData, and .rda). just copy/paste file path or file name.

New function since version 1.3:

One important upgrade is a new code for Mantel test.

New function since version 1.2

(1) Community analysis:

dissm: pairwise dissimilarity test between treatments (using multiple methods at a time).

pdist.p: calculate phylogenetic distance matrix (especially from large dataset).

beta.g: various taxonomic/phylogenetic beta diversity indexes (using multiple methods at a time).

bmpd: betaMPD, a measure of phylogenetic beta diversity.

bmntd: betaMNTD, a measure of phylogenetic beta diversity.

(2) Tools:

open.file: open commonly used files (.csv, .txt, .nwk, .fasta, .fna, .RData).

save.file: save file as a commonly used type (.csv, .txt, .nwk, .fasta, .RData).

match.name: check whether the sample/species names are the same in different matrixes, or select
some samples/species from some matrixes.

dist.3col: transform distance matrix to 3-column matrix.