Package: popularitree (via r-universe)

August 18, 2024

Title Subsamples a tree to get popular taxa

Version 0.0.0.9000

Description Often you want to show a reduced summary tree. Taxa chosen
should span all the tree (for example, a tree of mammals should
not have just primates) but also be recognizable groups to your
audience. This lets you select a final tree size you want,
criteria you want to use, and finds the tree that maximizes the
criteria.

Depends R (>= 3.4.3)

Imports gtrendsR, picante, ape, taxize

Suggests testthat, rotl, geiger

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Repository https://phylotastic.r-universe.dev

RemoteUrl https://github.com/bomeara/popularitree

RemoteRef HEAD

RemoteSha ce3e5899c095dcaae55a5089ccbd182d8b7d0b1c

Contents

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generate_sample   *Generate a sample of species, weighted by their score*

Description

Generate a sample of species, weighted by their score

Usage

```
generate_sample(taxon_scores, ntax, phy, pd_weighting, min.prob = 0.01,
  max.prob = 0.99)
```

Arguments

taxon_scores	The vector of scores for taxa
ntax	The number of taxa you want returned
phy	Phylogeny to prune
pd_weighting	How much to weight the pd vs the popularity
min.prob	The minimum probability of sampling for a taxon
max.prob	The maximum probability of sampling for a taxon

Value

A list: selected=vector of names of sampled taxa to include, and score=sum of the taxon metrics for these taxa

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popularitree   *Get a smaller tree with popular taxa spanning the diversity*

Description

This assumes you will have a data.frame of popularity measures and then sum to combine the columns into a single measure.

Usage

```
popularitree(phy, ntax, measures, pd_weighting = 0.5, nrep = 10000)
```

Arguments

phy	A phylo object
ntax	The final number of taxa you want
measures	Data.frame of the measures of popularity
pd_weighting	How much to weight the pd vs the popularity
nrep	How many replicates to use

Value

A phylo object pruned to the number of taxa

Examples

```
big.phy <- rotl::get_study("ot_308")[[1]]
big.phy <- geiger::drop.random(big.phy, ape::Ntip(big.phy) - 20)
measures <- tree_compute_measures(big.phy)
small.phy <- popularitree(phy=big.phy, ntax=5, measures, nrep=100)
par(mfcol=c(1,3))
plot(big.phy)
plot(small.phy)
plot(tree_convert_to_common(small.phy))
```

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species_get_common	*Return common name if known, otherwise return scientific name*

Description

Return common name if known, otherwise return scientific name

Usage

```
species_get_common(species)
```

Arguments

species   Species name

Value

Common name (ideally) or species name

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species_gtrends_popularity	
	Get a sum of hits of a species relative to a standard

Description

Get a sum of hits of a species relative to a standard

Usage

```
species_gtrends_popularity(species, standard = "Myrmeocystus mexicanus",
  verbose = TRUE)
```

Arguments

species	The focal species to look at search interest over
standard	Since Google Trends always compares popularity, give a standard species to use
verbose	If TRUE, chat about what species is being examined

Value

The sum of relative hits over the time period

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species_ncbi_common_exists

Return 1 if a species has a common name in NCBI, 0 otherwise

Description

Return 1 if a species has a common name in NCBI, 0 otherwise

Usage

```
species_ncbi_common_exists(species)
```

Arguments

species	The focal species to examine

Value

1 or 0

Examples

```
species_ncbi_common_exists('Puma concolor')
species_ncbi_common_exists('Pomatomus saltatrix')
```

tree_compute_measures   *Compute popularity measures*

Description

Compute popularity measures

Usage

```
tree_compute_measures(phy)
```

Arguments

phy   An input phylogeny

Value

data.frame of measures

tree_convert_to_common

Convert tips to common names if possible

Description

Convert tips to common names if possible

Usage

```
tree_convert_to_common(phy)
```

Arguments

phy   A phylogeny

Value

Phylogeny with names changed

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