Package: invasible (via r-universe)

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Title Predicting Invasion Probabilities from Phylogenetic Data and Species Traits

Version 1.0.0

Description A phylogenetic modelling approach for predicting species invasion risk, out of a given pool of local species where a subset is known to be invasive elsewhere. The package uses phylogenetic signal estimation and phylogenetic linear and logistic models to estimate probabilities of being invasive based on phylogeny and any set of additional predictors. A ranking method is implemented to evaluate prioritisation strategies. A manuscript describing these methods, by Shahar Dubiner and Tamar Guy-Haim, is in preparation.

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Encoding UTF-8

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`fish_beginning_with_E` *Fish dataset with invasive status*

Description

A few fish species and their binary invasiveness status

Usage

```
fish_beginning_with_E
```

Format

A data frame with 2 variables:

Species Character species name

Invasive 0/1 indicator of invasiveness

Fake_continuous_trait a simulated predictor

Fake_categorical_trait another simulated predictor

Source

Example data.

`invasion_signal` *Compute phylogenetic signal and baseline invasion model*

Description

This function must be run before all prediction/evaluation steps.

Usage

```
invasion_signal(prepared)
```

Arguments

prepared	Output of prepare_invasible() #'

Details

1. Computes Fritz & Purvis D statistic
2. Fits phylogenetic logistic regression
3. Extracts phylogenetic dependence parameter (alpha)
4. Returns an "invasible_signal" object for prediction functions

Value

An object of class `invasible_signal`, a list containing:

phylo_model

predictors

prepared

tree

D

p_random ,

p_brownian

alpha

Examples

```
species_list <- fish_beginning_with_E
prep <- prepare_invasible(species_list)
signal <- invasion_signal(prep)
signal$D
signal$p_random
```

---

monitor_species *Simulated monitoring performance for predicted invaders*

Description

Evaluates the probability of :

1. Detecting at least one invasion within n given species, under ranked monitoring, i.e. the highest-probability n species, vs a random selection.
2. Given an invasion, detecting it within the n species, under ranked monitoring, i.e. the highest-probability n species, vs a random selection.

Usage

```
monitor_species(pred_out, plot = FALSE, max_n = 25)
```

Arguments

pred_out	Output from predict_invasible().
plot	Logical. If TRUE, returns ggplot objects.
max_n	Integer. Highest n value to be plotted (n=25 as default).

Value

a list containing:

results simulation results for each value of n

plot1 1st plot of results for each value until max_n

plot2 2nd plot of results for each value until max_n

dev

Examples

```
species_list <- fish_beginning_with_E
prep <- prepare_invasible(species_list,rho=1, predictors=c("Fake_continuous_trait"))
signal <- invasion_signal(prep)
pred <- predict_invasible(signal)
set.seed(10)
probs <- monitor_species(pred,plot=TRUE,max_n=16)
probs$plot1
probs$plot2
```

---

predict_invasible *Predict invasion risk and evaluate model performance*

Description

1. Fits a phylogenetic generalized linear mixed model (PGLMM) from the output of invasion_signal()
2. Calculates the probability of being invasive for all species, based on the phylogeny (and optionally species traits) given to the original prepare_invasible() function
3. Computes predictive performance metrics such as ROC AUC
4. Plots the predicted values for observed invasive species (1) vs non-invading species (0) (optional)

Usage

```
predict_invasible(signal, vcv_alpha = NULL, plot = FALSE, fam = "gaussian")
```

Arguments

signal	Output of invasion_signal()
vcv_alpha	Numeric, optional: set a value of alpha for OU model which is different to the value inherited from the invasion_signal() output
plot	Logical. If TRUE, returns diagnostic plot of observed vs predicted
fam	Character, Distribution family of the model (if other than "binomial")

Value

An object of class pred_output, a list containing:

model Fitted PGLMM model object.

predictions Data frame with observed and predicted values for all species.

ranked_predictions Candidate invasives ordered by decreasing probability.

roc ROC object

auc Numeric AUC (area under the curve) value.

plot ggplot object (if requested; run pred_output$plot to show).

Examples

```
species_list <- fish_beginning_with_E
prep <- prepare_invasible(species_list,rho=1, predictors=c("Fake_continuous_trait"))
signal <- invasion_signal(prep)
pred <- predict_invasible(signal,plot=TRUE)
pred$ranked_predictions
pred$auc
pred$plot
```

---

prepare_invasible *Prepare data and phylogeny for analyses (mandatory step)*

Description

Aligns species-level invasion data with a phylogeny and stores predictor information for downstream analyses.

Usage

```
prepare_invasible(
  df,
  tree = NULL,
  predictors = NULL,
  species_col = "Species",
  rho = 0.5,
  plot = FALSE
)
```

Arguments

df	Data frame containing at least a Species column formatted as "Genus_species", and an Invasive column (0: not invasive, 1: invasive).
tree	Optional object of class "phylo". If NULL, a phylogeny is retrieved from the Open Tree of Life.
predictors	Optional character vector of column names containing additional predictors. If NULL, no additional predictors are stored.
species_col	Character string giving the name of the species column. Defaults to "Species".
rho	Numeric value controlling the power parameter used for Grafen branch lengths. Defaults to 0.5.
plot	Logical. If TRUE, plots the resulting phylogeny as a fan tree using **phytools**.

Details

If no phylogeny is supplied, a tree is retrieved from the Open Tree of Life using **rotl**. Unmatched species names are removed with a warning. When multiple submitted names resolve to the same Open Tree taxon, the first occurrence is retained and subsequent occurrences are removed with a warning.

If a supplied phylogeny has species that are absent from the data, those tips are removed. Species present in the data but absent from the phylogeny are removed from the data with a warning.

If branch lengths are absent, Grafen branch lengths are added.

Value

An object of class "invasible_prepared" containing:

- data: the aligned data frame;
- tree: the aligned phylogeny;
- predictors: the supplied predictor names.

Examples

```
## Not run:
prep <- prepare_invasible(
  fish_beginning_with_E,
  rho = 1,
  predictors = c(
    "Fake_categorical_trait",
    "Fake_continuous_trait"
  )
)

prep$tree

## End(Not run)
```

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