

Package: invasible (via r-universe)

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Title Predicting Invasion Probabilities from Phylogenetic Data and Species Traits

Version 0.1.0

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	<i>Fish dataset with invasive status</i>
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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	<i>Compute phylogenetic signal and baseline invasion model</i>
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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(prepare)
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(prepare)
pred <- predict_invasible(signal)
set.seed(10)
probs <- monitor_species(pred, plot=TRUE, max_n=16)
probs$plot1
probs$plot2
```

predict_invasible	<i>Predict invasion risk and evaluate model performance</i>
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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)
```

Arguments

<code>signal</code>	Output of <code>invasion_signal()</code>
<code>vcv_alpha</code>	Numeric, optional: set a value of alpha for OU model which is different to the value inherited from the <code>invasion_signal()</code> output
<code>plot</code>	Logical. If TRUE, returns diagnostic plot of observed vs predicted

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(prepare)
pred <- predict_invasible(signal, plot=TRUE)
pred$ranked_predictions
pred$auc
pred$plot
```

<code>prepare_invasible</code>	<i>Prepare data and phylogeny for analyses (mandatory step)</i>
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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

<code>df</code>	Data frame containing at least a <code>Species</code> column formatted as "Genus_species", and an <code>Invasive</code> column (0: not invasive, 1: invasive).
<code>tree</code>	Optional object of class "phylo".
<code>predictors</code>	Optional character vector of column names (additional predictors beyond phylogeny; if NULL, models will be based on the tree alone).
<code>species_col</code>	Name of species column (default "Species" is recommended).
<code>rho</code>	Grafen branch length scaling parameter (default 0.5).
<code>plot</code>	Logical. If TRUE, visualizes the phylogeny in tree.

Details

If no phylogeny is supplied, a tree is retrieved from the Open Tree of Life using **rotl**; Grafen branch lengths are added if branch lengths are absent. We recommend providing a high-quality tree if available, and also recommend fully matching the species in the data and phylogeny.

Value

An object of class "invasible_prepared".

Examples

```
species_list <- fish_beginning_with_E
prep <- prepare_invasible(species_list, rho=1, plot=TRUE, predictors=
  c("Fake_categorical_trait", "Fake_continuous_trait"))
prep$tree
```

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