

# Package ‘invasible’

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**Title** Predicting Invasion Probabilities from Phylogenetic Data and Species Traits

**Version** 0.1.1

**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.

**License** GPL-3

**Encoding** UTF-8

**Imports** ape, caper, ggplot2, phylolm, phyr, phytools, pROC, rotl, stats

**RoxygenNote** 7.3.3

**NeedsCompilation** no

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fish\_beginning\_with\_E *Fish dataset with invasive status*

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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.

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invasion\_signal *Compute phylogenetic signal and baseline invasion model*

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**Description**

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

**Usage**

```
invasion_signal(prepared)
```

**Arguments**

prepared            Output of prepare\_invasive() #'

**Details**

1. Computes Fritz & Purvis D statistic
2. Fits phylogenetic logistic regression
3. Extracts phylogenetic dependence parameter (alpha)
4. Returns an "invasive\_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
```

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monitor\_species

*Simulated monitoring performance for predicted invaders*

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**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**

|                       |                                                                |
|-----------------------|----------------------------------------------------------------|
| <code>pred_out</code> | Output from <code>predict_invasible()</code> .                 |
| <code>plot</code>     | Logical. If TRUE, returns ggplot objects.                      |
| <code>max_n</code>    | 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
```

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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 = "binomial")
```

**Arguments**

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

**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
```

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|                   |                                                                 |
|-------------------|-----------------------------------------------------------------|
| prepare_invasible | <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 "invisible\_prepared".

### Examples

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

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## \* **datasets**

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