

Package: lump.split.pool.ENM (via r-universe)

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Title Comparing different ENM approaches

Version 0.2.4

Description Facilitate running simulations to compare different approaches for ecological niche modelling, namely splitting, lumping, and fit models with partial pooling. See <https://doi.org/10.1016/j.tree.2018.10.012> for more information.

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Encoding UTF-8

LazyData true

URL <https://github.com/Pakillo/lump.split.pool.ENM>

BugReports <https://github.com/Pakillo/lump.split.pool.ENM/issues>

Imports ape, gtools, arm, ggplot2, viridis, dplyr, broom, lme4, brms, MCMCglmm, tidyr, phytools

RoxygenNote 6.1.1

Repository <https://pakillo.r-universe.dev>

RemoteUrl <https://github.com/Pakillo/lump.split.pool.ENM>

RemoteRef HEAD

RemoteSha 9f33ffb78143c3122a607a974345f1ef6ec326bf

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<code>calculate_bias</code>	<i>Calculate bias after simulations</i>
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Description

Calculate bias after simulations

Usage

```
calculate_bias(simdf)
```

Arguments

`simdf` Data frame with simulation results, as produced by [run_sims](#).

Value

A tidy data frame with simulation details and resulting bias for each method tested.

<code>fit_bayesmix</code>	<i>Fit Bayesian mixed model (brms)</i>
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Description

Fit Bayesian mixed model (brms)

Usage

```
fit_bayesmix(simdata, delta = 0.95)
```

Arguments

`simdata` List generated by [simul_data](#).
`delta` `adapt_delta` parameter for brm

Value

A data frame with 4 columns (intercept estimate and standard error, and slope estimate and standard error), and as many rows as taxa.

<code>fit_lump</code>	<i>Fit lump model</i>
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Description

Fit lump model

Usage

```
fit_lump(simdata)
```

Arguments

`simdata` List generated by [simul_data](#).

Value

A data frame with 4 columns (intercept estimate and standard error, and slope estimate and standard error), and as many rows as taxa.

<code>fit_mixed</code>	<i>Fit mixed model (lme4)</i>
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Description

Fit mixed model (lme4)

Usage

```
fit_mixed(simdata)
```

Arguments

`simdata` List generated by [simul_data](#).

Value

A data frame with 4 columns (intercept estimate and standard error, and slope estimate and standard error), and as many rows as taxa.

`fit_pglmm`*Fit Bayesian phylogenetic mixed model (brms)*

Description

Fit Bayesian phylogenetic mixed model (brms)

Usage

```
fit_pglmm(simdata, delta = 0.95)
```

Arguments

`simdata` List generated by [simul_data](#).
`delta` `adapt_delta` parameter for brm

Value

A data frame with 2 columns (intercept and slope estimate), and as many rows as taxa.

`fit_split`*Fit split model*

Description

Fit split model

Usage

```
fit_split(simdata)
```

Arguments

`simdata` List generated by [simul_data](#).

Value

A data frame with 4 columns (intercept estimate and standard error, and slope estimate and standard error), and as many rows as taxa.

plot_niches	<i>Plot niches</i>
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Description

Plot niches

Usage

```
plot_niches(df = simdata$data2model, suitab.column = "suitab.invlogit")
```

Arguments

df	Data frame
suitab.column	Character. Name of the column containing suitability values

Value

A ggplot object

run_sims	<i>Run a number of simulations with fixed parameters</i>
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Description

Run a number of simulations with fixed parameters

Usage

```
run_sims(nsim = 10, nspp = NULL, nsite = NULL, min.K = NULL,
  delta = NULL, run.pglmm = TRUE, force.run = FALSE,
  out.dir = getwd())
```

Arguments

nsim	Number of replicate simulations to run
nspp	Number of taxa to simulate.
nsite	Number of sites (equal for all taxa)
min.K	Numeric Force minimum phylogenetic signal (Blomberg's K) for simulated intercepts and slopes?
delta	'adapt_delta' parameter for brm
run.pglmm	Logical. Run PGLMM? (default is TRUE).
force.run	Logical. If FALSE (the default) simulations will NOT be run if there is a simulation output file available with same parameters (nspp, nsite). If TRUE, simulations will run and the file will be overwritten.
out.dir	Path to folder where to simulations will be saved (in RDS format).

Value

A data.frame with nrow = nspp*nsim

run_simulation	<i>Run simulation</i>
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Description

Run simulation

Usage

```
run_simulation(nspp = NULL, nsite = NULL, min.K = NULL,
              delta = NULL, run.pglmm = TRUE)
```

Arguments

nspp	Number of taxa to simulate.
nsite	Number of sites (equal for all taxa)
min.K	Numeric Force minimum phylogenetic signal (Blomberg's K) for simulated intercepts and slopes?
delta	'adapt_delta' parameter for brm
run.pglmm	Logical. Run PGLMM? (default is TRUE).

Value

A data.frame

simul_data	<i>Simulate dataset</i>
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Description

Simulate dataset

Usage

```
simul_data(nspp = NULL, nsite = NULL, seed = NULL, min.K = NULL)
```

Arguments

nspp	Number of taxa
nsite	Number of sites
seed	Random seed
min.K	Numeric Force minimum phylogenetic signal (Blomberg's K) for simulated intercepts and slopes?

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Value

A dataframe

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