Package 'RPesto'

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Title Phylogenetic Estimation of Shifts in the Tempo of Origination

Version 0.1.6

Description Implements diversification analyses using the phylogenetic birth-death-shift model. It leverages belief propagation techniques to calculate branch-specific diversification rates, see Kopperud & Hoehna (2025) <doi:10.1093/sysbio/syaf041>.

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Encoding UTF-8

Imports tidytree, treeio, ape

Config/rextendr/version 0.4.2

SystemRequirements Cargo (Rust's package manager), rustc

Depends R (>= 4.2)

Config/roxygen2/version 8.0.0

NeedsCompilation yes

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RPesto-package — *RPesto: Phylogenetic Estimation of Shifts in the Tempo of Origination (in R)*

Description

Implements diversification analyses using the phylogenetic birth-death-shift model. It leverages belief propagation techniques to calculate branch-specific diversification rates, see Kopperud & Hoehna (2025) doi:10.1093/sysbio/syaf041.

References

- Kopperud, B. T., & Höhna, S. (2025). Phylogenetic Estimation of branch-specific Shifts in the Tempo of Origination. Systematic Biology, syaf041.
- Höhna, S., Freyman, W. A., Nolen, Z., Huelsenbeck, J. P., May, M. R., & Moore, B. R. (2019). A Bayesian approach for estimating branch-specific speciation and extinction rates. BioRxiv, 555805.

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fit_bds — *fits the bds model*

Description

fits the bds model

Usage

```
fit_bds(
  phy,
  sampling_fraction,
  lambda_hat,
  mu_hat,
  eta,
  num_speciation_classes = 6,
  num_extinction_classes = 6,
  lambda_sd = 0.587,
  mu_sd = 0.587,
```

```
  tol = 1e-06,
  condition_survival = TRUE,
  condition_root_speciation = TRUE,
  condition_marginal = FALSE,
  extinction_approximation = FALSE,
  verbose = FALSE,
  numthreads = 0
)
```

Arguments

phy	an object of type phylo
sampling_fraction	the probability that each species was sampled in the tree
lambda_hat	the overall scale of the log-normal base distribution for the speciation rates. If not specified, the function will estimate it using ML
mu_hat	the overall scale of the log-normal base distribution for the extinction rates. If not specified, the function will estimate it using ML
eta	the shift rate parameter. If not specified, the function will estimate it using ML
num_speciation_classes	the number of speciation rate class discretizations, such that rate categories is k = n_sp * n_mu
num_extinction_classes	the number of extinction rate class discretizations, such that rate categories is k = n_sp * n_mu
lambda_sd	the spread parameter for the log-normal base distribution
mu_sd	the spread parameter for the log-normal base distribution
tol	the local error threshold in the numerical ODE solver (per delta_t time step)
condition_survival	whether or not to condition on the survival of the left and right lineages descending from the root (default TRUE)
condition_root_speciation	whether or not to condition on that there was a speciation event at the root node (default TRUE)
condition_marginal	whether or condition using the marginal or per-category approach (default FALSE, i.e., to condition per rate category)
extinction_approximation	whether or not to approximate the extinction probability calculations, by assuming that rate shift events are not allowed on extinct lineages (default FALSE)
verbose	whether or not to print more information
numthreads	how many threads to use in likelihood calculation. If 0, then the program uses all available cores

Value

a list with three items: $model (the parameter estimates), $td (a tidytree object with branch-rate estimates), and $tip_rates (a data frame of the tip rates)

Examples

```
data("primates")

analysis <- fit_bds(primates, sampling_fraction = 0.6, numthreads = 2)
```

---

fit_cbd *fits the constant-rate birth-death model*

Description

fits the constant-rate birth-death model

Usage

```
fit_cbd(
  phy,
  sampling_fraction,
  tol = 1e-06,
  condition_survival = TRUE,
  condition_root_speciation = TRUE,
  verbose = FALSE
)
```

Arguments

phy	an object of type phylo
sampling_fraction	the probability that each species was sampled in the tree
tol	the local error threshold in the numerical ODE solver (per delta_t time step)
condition_survival	whether or not to condition on the survival of the left and right lineages descending from the root (default TRUE)
condition_root_speciation	whether or not to condition on that there was a speciation event at the root node (default TRUE)
verbose	whether or not to print more information

Value

a list with the maximum-likelihood parameter estimates of the speciation rate and the extinction rate

Phylogeny *Phylogeny*

Description

Constructs a phylogeny that lives in the "rust" part of the program

Usage

```
Phylogeny(newick)
```

Arguments

newick	a newick string

Examples

```
phy <- Phylogeny$new("((A:0.5,B:0.5):0.5,C:1.0);")

phy$print()

phy$write_newick()
```

primates *Primates phylogenetic tree*

Description

This tree is from Vos & Mooers (2006)

Usage

```
data(primates)
```

Format

An object of class phylo of length 5.

Details

Vos, R. and A. Mooers. 2006. A new dated supertree of the primates. in Inferring large phylogenies: the big tree problem (R Vos, Phd thesis). Simon Fraser University, Burnaby, British Columbia.

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