Package: RPesto (via r-universe)

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Title Phylogenetic Estimation of Shifts in the Tempo of Origination

Version 0.1.4.9000

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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Imports tidytree, treeio, ape

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SystemRequirements Cargo (Rust's package manager), rustc

Depends R (>= 4.2)

Config/pak/sysreqs cmake make libicu-dev libuv1-dev libclang-dev

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Contents

`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.

Author(s)

Maintainer: Bjørn Tore Kopperud <`kopperud@protonmail.com`>

Authors:

- Sebastian Höhna

`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,
  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
`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 constructor*

Description

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

Usage

```
Phylogeny(newick)
```

Arguments

`newick`	a newick string

Format

An object of class `environment` of length 10.

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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