Package 'CRABS'

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Title Congruent Rate Analyses in Birth-Death Scenarios

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Description Features tools for exploring congruent phylogenetic birth-death models. It can construct the pulled speciation- and net-diversification rates from a reference model. Given alternative speciation- or extinction rates, it can construct new models that are congruent with the reference model. Functionality is included to sample new rate functions, and to visualize the distribution of one congruence class. See also Louca & Pennell (2020) <doi:10.1038/s41586-020-2176-1>.

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License GPL-3

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URL https://github.com/afmagee/CRABS

NeedsCompilation no

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`CRABS-package` *CRABS: Congruent Rate Analyses in Birth-death Scenarios*

Description

Features tools for exploring congruent phylogenetic birth-death models. It can construct the pulled speciation- and net-diversification rates from a reference model. Given alternative speciation- or extinction rates, it can construct new models that are congruent with the reference model. Functionality is included to sample new rate functions, and to visualize the distribution of one congruence class. See also Louca & Pennell (2020) doi: 10.1038/s4158602021761.

References

- Louca, S., & Pennell, M. W. (2020). Extant timetrees are consistent with a myriad of diversification histories. Nature, 580(7804), 502-505.

Author(s)

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See Also

Useful links:

- https://github.com/afmagee/CRABS

`congruent.models` *Create a set of congruent models*

Description

Create a set of congruent models

Usage

```
congruent.models(
  model,
  mus = NULL,
  lambdas = NULL,
  keep_ref = TRUE,
  ode_solver = TRUE
)
```

Arguments

`model`	The reference model. An object of class "CRABS"
`mus`	A list of extinction-rate functions
`lambdas`	A list of speciation-rate functions
`keep_ref`	Whether or not to keep the reference model in the congruent set
`ode_solver`	Whether to use a numerical ODE solver to solve for lambda

Value

An object of class "CRABSset"

Examples

```
data(primates_ebd)
lambda <- approxfun(primates_ebd$time, primates_ebd$lambda)
mu <- approxfun(primates_ebd$time, primates_ebd$mu)

## A reference model
times <- seq(0, max(primates_ebd$time), length.out = 500)
model <- create.model(lambda, mu, times = times)

mu1 <- lapply(c(0.5, 1.5, 3.0), function(m) function(t) m)
```

```
model_set1 <- congruent.models(model, mus = mu1)

model_set1

lambda0 <- lambda(0.0) ## Speciation rates must all be equal at the present
bs <- c(0.0, 0.01, 0.02)
lambda1 <- lapply(bs, function(b) function(t) lambda0 + b*t)

model_set2 <- congruent.models(model, lambdas = lambda1)

model_set2
```

`crabs.loglikelihood` *Compute likelihood*

Description

Compute likelihood

Usage

```
crabs.loglikelihood(phy, model, rho = 1)
```

Arguments

`phy`	an object of class "phylo"
`model`	an object of class "CRABS"
`rho`	the taxon sampling fraction

Value

the log-likelihood of the tree given the model

Examples

```
library(ape)
lambda <- function(t) exp(0.3*t) - 0.5*t
mu <- function(t) exp(0.3*t) - 0.2*t - 0.8

model <- create.model(lambda, mu, times = seq(0, 3, by = 0.005))

set.seed(123)
phy <- rcoal(25)

crabs.loglikelihood(phy, model)
```

`create.model` *Computes the congruent class, i.e., the pulled rates.*

Description

Computes the congruent class, i.e., the pulled rates.

Usage

```
create.model(
  func_spec0,
  func_ext0,
  times = seq(from = 0, to = 5, by = 0.005),
  func_p_spec = NULL,
  func_p_div = NULL
)
```

Arguments

`func_spec0`	The speciation rate function (measured in time before present).
`func_ext0`	The extinction rate function (measured in time before present).
`times`	the time knots for the piecewise-linear rate functions
`func_p_spec`	the pulled speciation rate function
`func_p_div`	the pulled net-diversification rate function

Value

A list of rate functions representing this congruence class.

Examples

```
lambda1 <- function(t) exp(0.3*t) - 0.5*t + 1
mu1 <- function(t) exp(0.3*t) - 0.2*t + 0.2

model1 <- create.model(lambda1, mu1, times = seq(0, 5, by = 0.005))

model1

data("primates_ebd")

lambda2 <- approxfun(primates_ebd[["time"]], primates_ebd[["lambda"]])
mu2 <- approxfun(primates_ebd[["time"]], primates_ebd[["mu"]])
model2 <- create.model(lambda2, mu2, primates_ebd[["time"]])

model2
```

model2df *model2df*

Description

model2df

Usage

```
model2df(model, gather = TRUE, rho = 1, compute.pulled.rates = TRUE)
```

Arguments

model	an object of class "CRABS"
gather	boolean. Whether to return wide or long data frame
rho	the sampling fraction at the present. Used to calculate the pulled speciation rate
compute.pulled.rates	whether to compute the pulled rates

Value

a data frame

Examples

```
lambda <- function(t) 2.0 + sin(0.8*t)
mu <- function(t) 1.5 + exp(0.15*t)
times <- seq(from = 0, to = 4, length.out = 1000)
model <- create.model( lambda, mu, times = times)

model2df(model)
```

plot.CRABS *Plots the rate functions including the pulled rates.*

Description

Plots the rate functions including the pulled rates.

Usage

```
## S3 method for class 'CRABS'
plot(x, ...)
```

Arguments

x	An object of class "CRABS"
...	other parameters

Value

a patchwork object

Examples

```
data(primates_ebd)
lambda <- approxfun(primates_ebd$time, primates_ebd$lambda)
mu <- approxfun(primates_ebd$time, primates_ebd$mu)
times <- seq(0, max(primates_ebd$time), length.out = 500)

model <- create.model(lambda, mu, times = times)

plot(model)
```

---

plot.CRABSset *Plots the rate functions*

Description

Plots the rate functions

Usage

```
## S3 method for class 'CRABSset'
plot(x, ...)
```

Arguments

x	A list of congruent birth-death x
...	other parameters

Value

a patchwork object object

Examples

```
data(primates_ebd)
lambda <- approxfun(primates_ebd$time, primates_ebd$lambda)
mu <- approxfun(primates_ebd$time, primates_ebd$mu)
times <- seq(0, max(primates_ebd$time), length.out = 500)

model <- create.model(lambda, mu, times = times)

mus <- list(function(t) 0.2 + exp(0.01*t),
            function(t) 0.2 + sin(0.35*t) + 0.1*t,
            function(t) 1.0,
            function(t) 0.5 + 0.2*t)
models <- congruent.models(model, mus = mus)

plot(models)
```

---

primates *Primates phylogenetic tree*

Description

The example tree taken from the RevBayes tutorial website

Usage

```
data(primates)
```

Format

An object of class `phylo` of length 5.

---

primates_ebd *RevBayes Primates birth-death model*

Description

The results of a bayesian horseshoe markov random field (HSMRF) episodic birth-death model, fitted on the primates tree. One hundred episodes. Each estimate is the posterior median. The time unit is millions of years before the present.

Usage

```
data(primates_ebd)
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 100 rows and 3 columns.

primates_ebd_log *Primates birth-death model*

Description

See ?primates_ebd, but including posterior samples instead of a summary.

Usage

```
data(primates_ebd_log)
```

Format

An object of class tbl_df (inherits from tbl, data.frame) with 251 rows and 604 columns.

primates_ebd_tess *TESS Primates birth-death model*

Description

The results of a bayesian episodic birth-death model in the R-package TESS, fitted on the primates tree. One hundred episodes. Each estimate is the posterior median. The time unit is millions of years before the present.

Usage

```
data(primates_ebd_tess)
```

Format

An object of class tbl_df (inherits from tbl, data.frame) with 100 rows and 3 columns.

primates_ebd_treepar *TreePar Primates birth-death model*

Description

The results of a birth-death model in the R-package TreePar, fitted on the primates tree. The estimated model has two epochs, that are maximum-likelihood estimates. The time unit is millions of years before the present.

Usage

```
data(primates_ebd_treepar)
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 100 rows and 3 columns.

print.CRABS *Print method for CRABS object*

Description

Print method for CRABS object

Usage

```
## S3 method for class 'CRABS'
print(x, ...)
```

Arguments

x	and object of class CRABS
...	other arguments

Value

nothing

Examples

```
data(primates_ebd)
lambda <- approxfun(primates_ebd$time, primates_ebd$lambda)
mu <- approxfun(primates_ebd$time, primates_ebd$mu)
times <- seq(0, max(primates_ebd$time), length.out = 500)

model <- create.model(lambda, mu, times = times)

print(model)
```

print.CRABSposterior *Title*

Description

Title

Usage

```
## S3 method for class 'CRABSposterior'
print(x, ...)
```

Arguments

x	a list of CRABS objects
...	additional parameters

Value

nothing

Examples

```
data(primates_ebd_log)
posterior <- read.RevBayes(primates_ebd_log, max_t = 65, n_samples = 20)
print(posterior)
```

print.CRABSset *Print method for CRABSset object*

Description

Print method for CRABSset object

Usage

```
## S3 method for class 'CRABSset'
print(x, ...)
```

Arguments

x	an object of class CRABSset
...	other arguments

Value

nothing

Examples

```
data(primates_ebd)
lambda <- approxfun(primates_ebd$time, primates_ebd$lambda)
mu <- approxfun(primates_ebd$time, primates_ebd$mu)
times <- seq(0, max(primates_ebd$time), length.out = 500)

model <- create.model(lambda, mu, times = times)

mus <- list(function(t) 0.2 + exp(0.01*t),
            function(t) 0.2 + sin(0.35*t) + 0.1*t,
            function(t) 1.0,
            function(t) 0.5 + 0.2*t)
models <- congruent.models(model, mus = mus)

print(models)
```

---

print.CRABSsets *print.CRABSsets*

Description

print.CRABSsets

Usage

```
## S3 method for class 'CRABSsets'
print(x, ...)
```

Arguments

x	a list of (congruent) CRABS sets
...	additional parameters

Value

nothing

Examples

```
data(primates_ebd_log)

posterior <- read.RevBayes(primates_ebd_log, max_t = 65, n_samples = 10)

samples <- sample.congruence.class.posterior(posterior,
                                             num.samples = 5,
```

```
                                        rate.type = "extinction",
                                        rate0.median = 0.1,
                                        model = "MRF",
                                        max.rate = 1.0)

print(samples)
```

`read.RevBayes` *read RevBayes log file*

Description

read RevBayes log file

Usage

```
read.RevBayes(x, n_times, max_t = 100, n_samples = 20, summary_type = "none",
extinction_prefix = "extinction_rate.", speciation_prefix = "speciation_rate.")
```

Arguments

`x`	path to log, or data frame
`n_times`	number of time knots
`max_t`	tree height
`n_samples`	first n posterior samples
`summary_type`	either "none" for all the posterior samples, or "mean" or "median" for the posterior mean/median
`extinction_prefix`	the prefix string for the extinction rate column names. Must be unique
`speciation_prefix`	the prefix string for the speciation rate column names. Must be unique

Value

a set of CRABS models, each being a sample in the posterior

Examples

```
data(primates_ebd_log)
posterior <- read.RevBayes(primates_ebd_log, n_times = 500, max_t = 65, n_samples = 20)
```

`sample.basic.models` *Samples simple increase/decrease models through time with noise.*

Description

Samples simple increase/decrease models through time with noise.

Usage

```
sample.basic.models(
  times,
  rate0 = NULL,
  model = "exponential",
  direction = "decrease",
  noisy = TRUE,
  MRF.type = "HSMRF",
  monotonic = FALSE,
  fc.mean = 3,
  rate0.median = 0.1,
  rate0.logsd = 1.17481,
  mrf.sd.scale = 1,
  min.rate = 0,
  max.rate = 10
)
```

Arguments

`times`	the time knots
`rate0`	The rate at present, otherwise drawn randomly.
`model`	"MRF" for pure MRF model, otherwise MRF has a trend of type "exponential","linear", or "episodic<n>"
`direction`	"increase" or "decrease" (measured in past to present)
`noisy`	If FALSE, no MRF noise is added to the trajectory
`MRF.type`	"HSMRF" or "GMRF", type for stochastic noise.
`monotonic`	Whether the curve should be forced to always move in one direction.
`fc.mean`	Determines the average amount of change when drawing from the model.
`rate0.median`	When not specified, rate at present is drawn from a lognormal distribution with this median.
`rate0.logsd`	When not specified, rate at present is drawn from a lognormal distribution with this sd
`mrf.sd.scale`	scale the sd of the mrf process up or down. defaults to 1.0
`min.rate`	The minimum rate (rescaling fone after after drawing rates).
`max.rate`	The maximum rate (rescaling fone after after drawing rates).

Value

Speciation or extinction rate at a number of timepoints.

Examples

```
data("primates_ebd")

l <- approxfun(primates_ebd[["time"]], primates_ebd[["lambda"]])
mu <- approxfun(primates_ebd[["time"]], primates_ebd[["mu"]])
times <- primates_ebd[["time"]]

model <- create.model(l, mu, times)

mus <- sample.basic.models(times = times,
                           rate0 = 0.05,
                           "MRF",
                           MRF.type = "HSMRF",
                           fc.mean = 2.0,
                           min.rate = 0.0,
                           max.rate = 1.0)

model_set <- congruent.models(model, mus = mus)

model_set
```

---

sample.congruence.class

Stochastic exploration of congruent models.

Description

Stochastic exploration of congruent models.

Usage

```
sample.congruence.class(
  model,
  num.samples,
  rate.type = "both",
  sample.speciation.rates = NULL,
  sample.extinction.rates = NULL
)
```

Arguments

model	the reference model, an object of class "CRABS"
num.samples	The pulled diversification rate function (measured in time before present).
rate.type	either "extinction", "speciation", or "both"

`sample.speciation.rates`
: a function that when called returns a speciation rate function

`sample.extinction.rates`
: a function that when called returns a extinction rate function

Value

A named list with congruent rates.

Examples

```
data("primates_ebd")

l <- approxfun(primates_ebd[["time"]], primates_ebd[["lambda"]])
mu <- approxfun(primates_ebd[["time"]], primates_ebd[["mu"]])
times <- primates_ebd[["time"]]

model <- create.model(l, mu, primates_ebd[["time"]])

extinction_rate_samples <- function(){
   res <- sample.basic.models(times = times,
                              rate0 = 0.05,
                              model = "MRF",
                              MRF.type = "HSMRF",
                              fc.mean = 2.0,
                              min.rate = 0.0,
                              max.rate = 1.0)
   return(res)
}

samples <- sample.congruence.class(model,
                                   num.samples = 8,
                                   rate.type = "extinction",
                                   sample.extinction.rates = extinction_rate_samples)
```

---

sample.congruence.class.posterior

Stochastic exploration of congruent models for all samples in the posterior

---

Description

This function takes a posterior sample as input: a list of CRABS objects. It will then iterate over the samples, and for each posterior sample it will sample from the posterior class. It will sample using the `sample.basic.models` function, and all additional parameters are passed to `sample.basic.models`.

Usage

```
sample.congruence.class.posterior(
  posterior,
  num.samples,
  rate.type = "extinction",
  mu0.equal = FALSE,
  rate0 = NULL,
  ...
)
```

Arguments

posterior	a list of CRABS model objects
num.samples	The pulled diversification rate function (measured in time before present).
rate.type	either "extinction", "speciation", or "both"
mu0.equal	whether to propose alternative mu starting at mu0 equal to the posterior sample. default to FALSE
rate0	rate0 allows the user to fix the extinction rate at the present to a single value. defaults to NULL, for drawing it randomly
...	Arguments passed on to sample.basic.models
	times the time knots
	model "MRF" for pure MRF model, otherwise MRF has a trend of type "exponential","linear", or "episodic<n>"
	direction "increase" or "decrease" (measured in past to present)
	noisy If FALSE, no MRF noise is added to the trajectory
	MRF.type "HSMRF" or "GMRF", type for stochastic noise.
	monotonic Whether the curve should be forced to always move in one direction.
	fc.mean Determines the average amount of change when drawing from the model.
	rate0.median When not specified, rate at present is drawn from a lognormal distribution with this median.
	rate0.logsd When not specified, rate at present is drawn from a lognormal distribution with this sd
	mrf.sd.scale scale the sd of the mrf process up or down. defaults to 1.0
	min.rate The minimum rate (rescaling fone after after drawing rates).
	max.rate The maximum rate (rescaling fone after after drawing rates).

Value

A named list with congruent rates.

Examples

```
data(primates_ebd_log)

posterior <- read.RevBayes(primates_ebd_log, max_t = 65, n_samples = 10)

samples <- sample.congruence.class.posterior(posterior,
                                             num.samples = 5,
                                             rate.type = "extinction",
                                             rate0.median = 0.1,
                                             model = "MRF",
                                             max.rate = 1.0)

print(samples)
```

`sample.rates` *Sample custom functions through time.*

Description

Sample custom functions through time.

Usage

```
sample.rates(
  times,
  lambda0 = NULL,
  rsample = NULL,
  rsample0 = NULL,
  autocorrelated = FALSE
)
```

Arguments

`times`	the time knots
`lambda0`	The rate at present
`rsample`	Function to sample next rate
`rsample0`	Function to sample rate at present
`autocorrelated`	Should rates be autocorrelated?

Value

Sampled rate vector

Examples

```
data("primates_ebd")

l <- approxfun(primates_ebd[["time"]], primates_ebd[["lambda"]])
mu <- approxfun(primates_ebd[["time"]], primates_ebd[["mu"]])
times <- primates_ebd[["time"]]

model <- create.model(l, mu, times)

rsample <- function(n) runif(n, min = 0.0, max = 0.9)
mu <- sample.rates(times, 0.5, rsample = rsample)


model_set <- congruent.models(model, mus = mu)

model_set
```

`summarize.posterior` *Summarize trends in the posterior*

Description

Summarize trends in the posterior

Usage

```
summarize.posterior(posterior, threshold = 0.01, rate_name = "lambda",
return_data = FALSE, rm_singleton = FALSE, per_time = TRUE,
window_size = 1, relative_deltas = FALSE)
```

Arguments

`posterior`	a list of CRABS objects, each one representing a sample from the posterior
`threshold`	a threshold for when $\Delta\lambda i$ should be interpreted as decreasing, flat, or increasing
`rate_name`	either "lambda" or "mu" or "delta"
`return_data`	instead of plots, return the plotting dataframes
`rm_singleton`	whether or not to remove singletons. Pass starting at present, going towards ancient
`per_time`	whether to compute $\Delta\lambda i$ that are in units of per time, i.e. divide by Δt
`window_size`	the window size "k" in $\Delta\lambda i = \lambda i - \lambda(i - k)$
`relative_deltas`	whether to divide $\Delta\lambda i$ by the local lambda value

Value

a ggplot object

Examples

```
data(primates_ebd_log)

posterior <- read.RevBayes(primates_ebd_log, max_t = 65, n_samples = 10)

samples <- sample.congruence.class.posterior(posterior,
                                             num.samples = 5,
                                             rate.type = "extinction",
                                             rate0.median = 0.1,
                                             model = "MRF",
                                             max.rate = 1.0)

p <- summarize.posterior(samples, threshold = 0.05)
```

`summarize.trends` *Summarize trends in the congruence class*

Description

Summarize trends in the congruence class

Usage

```
summarize.trends(model_set, threshold = 0.005, rate_name = "lambda",
window_size = 1, method = "neighbour", per_time = TRUE, return_data = FALSE,
rm_singleton = FALSE, relative_deltas = FALSE, group_names = NULL)
```

Arguments

`model_set`	an object of type "CRABSset"
`threshold`	a threshold for when $\Delta\lambda i$ should be interpreted as decreasing, flat, or increasing
`rate_name`	either "lambda" or "mu" or "delta"
`window_size`	the window size "k" in $\Delta\lambda i = \lambda i - \lambda(i - k)$
`method`	default to "neighbour", i.e. to compare rate values at neighbouring time points.
`per_time`	whether to compute $\Delta\lambda i$ that are in units of per time, i.e. divide by Δt
`return_data`	instead of plots, return the plotting dataframes
`rm_singleton`	whether or not to remove singletons. Pass starting at present, going towards ancient
`relative_deltas`	whether to divide $\Delta\lambda i$ by the local lambda value
`group_names`	a vector of prefixes, if you want to group the models in a facet. For example 'c("reference", "model")'

Value

a patchwork object

Examples

```
data(primates_ebd)
lambda <- approxfun(primates_ebd$time, primates_ebd$lambda)
mu <- approxfun(primates_ebd$time, primates_ebd$mu)
times <- seq(0, max(primates_ebd$time), length.out = 500)

reference <- create.model(lambda, mu, times = times)

mus <- list(function(t) exp(0.01*t) - 0.01*t - 0.9,
            function(t) exp(-0.02*t) - 0.2,
            function(t) exp(-0.07*t) + 0.02*t - 0.5,
            function(t) 0.2 + 0.01*t,
            function(t) 0.2)


model_set <- congruent.models(reference, mus = mus)

p <- summarize.trends(model_set, 0.02)
```

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