

# Package ‘TESS’

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**Type** Package

**Title** Fast simulation of reconstructed phylogenetic trees under time-dependent birth-death processes

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**Depends** ape, coda, deSolve

**Description** TESS is a package for simulation of reconstructed phylogenetic trees under global, time-dependent birth-death processes. Speciation and extinction rates can be any function of time and mass-extinction events at specific times can be provided. Trees can be simulated either conditioned on the number of species, the time of the process, or both. Additionally, the likelihood equations are implemented for convenience and can be used for Maximum Likelihood (ML) estimation and Bayesian inference.

**License** GPL-3

**LazyLoad** yes

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TESS-package	<i>Fast simulation of reconstructed phylogenetic trees under time-dependent birth-death processes</i>
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## Description

TESS is a package for simulation of reconstructed phylogenetic trees under global, time-dependent birth-death processes. Speciation and extinction rates can be any function of time and mass-extinction events at specific times can be provided. Trees can be simulated either conditioned on the number of species, the time of the process, or both. Additionally, the likelihood equations are implemented for convenience and can be used for Maximum Likelihood (ML) estimation and Bayesian inference.

## Details

Package:	TESS
Type:	Package
Version:	1.2.1
Date:	2013-03-27
License:	GPL-3
LazyLoad:	yes

## Author(s)

Sebastian Hoehna  
 Maintainer: Sebastian Hoehna <hoehna@math.su.se>

## References

S. Hoehna: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. Submitted. 2012.

## See Also

ape

---

`cettiidae`*Cettiidae phylogeny from Alstroem et al. (2011)*

---

**Description**

This phylogeny describes the species relationship and divergence times of the bird family Cettiidae, published in Alstroem et al. (2011).

**Usage**

```
data(cettiidae)
```

**Format**

The phylogeny is stored as an object of class "phylo" which structure is described in the help page of the function [read.tree](#) of the package [ape](#).

**Source**

Astroem, P., Hoehna, S., Gelang, M., Ericson, P.G.P, and Olsson, U. (2011) Non-monophyly and intricate morphological evolution within the avian family Cettiidae revealed by multilocus analysis of a taxonomically densely sampled dataset, BMC Evolutionary Biology, 11:352.

**Examples**

```
data(cettiidae)
op <- par()
par(cex = 0.3)
plot(cettiidae)
par(op)
```

---

`globalBiDe.likelihood` *globalBiDe.likelihood: Probability density of a tree under a global, time-dependent birth-death process*

---

**Description**

`globalBiDe.likelihood` computes the probability of a reconstructed phylogenetic tree under time-dependent. The rates may be any positive function of time or a constant. Additionally, mass-extinction event can be provided and a random taxon sampling probability. You have several options for the start of the process (origin vs MRCA) and the condition of the process (time, survival or taxa; note that survival and taxa implicitly condition on the time too!). See equation (5) in the manuscript for more information. Note that constant rates lead to much faster computations. The likelihood can be computed for incompletely sampled trees. You need to give a sampling probability != 1.0. You have three options for the sampling strategy: `randomldiversifiedlage`. The detailed description of these can be found in the references.

**Usage**

```
globalBiDe.likelihood(tree, lambda, mu, massExtinctionTimes = c(),
  massExtinctionSurvivalProbabilities = c(), t.crit=c(),
  samplingProbability = 1, samplingStrategy = "random", MRCA = TRUE,
  CONDITION = "survival", log = TRUE)
```

**Arguments**

<code>tree</code>	The tree in 'phylo' format.
<code>lambda</code>	The speciation rate function or constant.
<code>mu</code>	The extinction rate function or constant.
<code>massExtinctionTimes</code>	The set of mass-extinction times after the start of the process.
<code>massExtinctionSurvivalProbabilities</code>	The set of survival probabilities for each speciation event. The set must have the same length as the set of mass-extinction times.
<code>t.crit</code>	Set of times when a critical change in the rate function happens, such as a jump in a stepwise discrete function.
<code>samplingProbability</code>	The probability for a species to be included in the sample.
<code>samplingStrategy</code>	The strategy how samples were obtained. Options are: randomldiversifiedlage.
<code>MRCA</code>	Does the process start with the most recent common ancestor? If not, the tree must have a root edge!
<code>CONDITION</code>	do we condition the process on timelurvivalntaxa?
<code>log</code>	log-likelihood?

**Value**

Returns the (log) probability of the tree, i.e. the likelihood of the parameters given the tree.

**Author(s)**

Sebastian Hoehna

**References**

Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted. Hoehna, S.: A Birth-Death Process with Decreasing Diversification Rate and Diversified Taxon Sampling. 2013, submitted. Hoehna, S. and Catalan, A.: Estimating Diversification Rates and Patterns in Mammals. 2013, submitted.

**Examples**

```

data(cettiidae)

l <- function(x) { if (x > 0.5 || x < 0.3) { return (1) } else { return (2) } }
e <- function(x) { if (x > 0.5 || x < 0.3) { return (0.95) } else { return (0.5) } }

globalBiDe.likelihood(cettiidae,l,e,MRCA=TRUE,log=TRUE)

# constant rate likelihood function
globalBiDe.likelihood(cettiidae,2.0,1.0,MRCA=TRUE,log=TRUE)

# constant rate pure birth likelihood function
globalBiDe.likelihood(cettiidae,2.0,0.0,MRCA=TRUE,log=TRUE)

```

---

```
globalBiDe.nTaxa.expected
```

*globalBiDe.nTaxa.expected: The expected number of taxa at present of a tree under a global, time-dependent birth-death process ( $E[N(T)]$ )*

---

**Description**

globalBiDe.nTaxa.expected computes the expected number of taxa at the present time  $T$  (the process start at time  $s$  and times increases until the present) under time-dependent. The rates may be any positive function of time or a constant. Additionally, mass-extinction event can be provided and a random taxon sampling probability. You have several options for the start of the process (origin vs MRCA). See equation (??) in the manuscript for more information. Note that constant rates (scalars) lead to much faster computations.

**Usage**

```
globalBiDe.nTaxa.expected(t_low,t_high,lambda,mu,massExtinctionTimes=c(),
  massExtinctionSurvivalProbabilities=c(),samplingProbability=1.0,MRCA=TRUE)
```

**Arguments**

t_low	The time when the process starts.
t_high	The time when the process end (e.g. the present).
lambda	The speciation rate function or constant.
mu	The extinction rate function or constant.
massExtinctionTimes	The set of mass-extinction times after the start of the process.
massExtinctionSurvivalProbabilities	The set of survival probabilities for each speciation event. The set must have the same length as the set of mass-extinction times.

samplingProbability

The probability for a species to be included in the sample.

MRCA

Does the process start with the most recent common ancestor? If not, the tree must have a root edge!

### Value

Returns the expected number of taxa.

### Author(s)

Sebastian Hoehna

### References

Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted

### Examples

```
l <- function(x) { if (x > 0.5 || x < 0.3) { return (1) } else { return (2) } }
e <- function(x) { if (x > 0.5 || x < 0.3) { return (0.95) } else { return (0.5) } }

globalBiDe.nTaxa.expected(0,5,1,e,MRCA=TRUE)
```

---

mammalia

*Dated family level mammalian phylogeny from Meredith et al. (2011): Impacts of the cretaceous terrestrial revolution and kpg extinction on mammal diversification.*

---

### Description

This phylogeny describes the species relationship and divergence times of the class Mammalia with 1-3 species included per family, published in Meredith et al. (2011).

### Usage

```
data(mammalia)
```

### Format

The phylogeny is stored as an object of class "phylo" which structure is described in the help page of the function [read.tree](#) of the package [ape](#).

**Source**

Meredith, R. et al. (2011): Impacts of the cretaceous terrestrial revolution and kpg extinction on mammal diversification. Science, 334:521-524

**Examples**

```
data(mammalia)
op <- par()
par(cex = 0.3)
plot(mammalia)
par(op)
```

---

sim.globalBiDe.age	<i>sim.globalBiDe.age: Simulate a reconstructed tree for a given age under a global, time-dependent birth-death process.</i>
--------------------	--

---

**Description**

sim.globalBiDe.age simulates a reconstructed phylogenetic tree under a global, time-dependent birth-death process conditioned on the age of the tree. The rates may be any positive function of time or a constant. The process starts at time 0 and goes forward in time, hence the rates and events should be interpreted in the time after the origin. Additionally, mass-extinction event can be provided and a random taxon sampling probability. It is possible to start either with the origin (1 species) or with the most recent common ancestor (2 species).

**Usage**

```
sim.globalBiDe.age(n, age, lambda, mu, massExtinctionTimes = c(),
  massExtinctionSurvivalProbabilities = c(), samplingProbability = 1,
  samplingStrategy = "random", MRCA = TRUE)
```

**Arguments**

n	Number of simulations.
age	The age of the tree, i.e. the time to simulate.
lambda	The speciation rate function or constant.
mu	The extinction rate function or constant.
massExtinctionTimes	The set of mass-extinction times after the start of the process.
massExtinctionSurvivalProbabilities	The set of survival probabilities for each speciation event. The set must have the same length as the set of mass-extinction times.
samplingProbability	The probability for a species to be included in the sample.
samplingStrategy	The strategy how samples were obtained. Options are: randomldiversified.
MRCA	Does the process start with the most recent common ancestor?

**Value**

Returns a tree in 'phylo' format.

**Author(s)**

Sebastian Hoehna

**References**

S. Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted

**Examples**

```
l <- function(x) { if (x > 0.5 || x < 0.3) { return (1) } else { return (2) } }
e <- function(x) { if (x > 0.5 || x < 0.3) { return (0.95) } else { return (0.5) } }

sim.globalBiDe.age(n=1,age=1,l,e,MRCA=TRUE)

# simulation under constant rates
sim.globalBiDe.age(n=1,age=1,2.0,1.0,MRCA=TRUE)
```

---

sim.globalBiDe.taxa    *sim.globalBiDe.taxa.taxa: Simulate a reconstructed tree for a given number of taxa under a global, time-dependent birth-death process.*

---

**Description**

sim.globalBiDe.taxa simulates a reconstructed phylogenetic tree under a global, time-dependent birth-death process conditioned on the number of taxa sampled. The rates may be any positive function of time or a constant. The process starts at time 0 and goes forward in time, hence the rates and events should be interpreted in the time after the origin. Additionally, mass-extinction event can be provided and a random taxon sampling probability. It is possible to start either with the origin (1 species) or with the most recent common ancestor (2 species).

**Usage**

```
sim.globalBiDe.taxa(n, nTaxa, max, lambda, mu, massExtinctionTimes = c(),
  massExtinctionSurvivalProbabilities = c(), samplingProbability = 1,
  samplingStrategy = "random", SURVIVAL = TRUE, MRCA = TRUE, t_crit = c())
```



**Arguments**

n	Number of simulations.
nTaxa	Number of species sampled.
max	Maximum time/height of the tree.
lambda	The speciation rate function or constant.
mu	The extinction rate function or constant.
massExtinctionTimes	The set of mass-extinction times after the start of the process.
massExtinctionSurvivalProbabilities	The set of survival probabilities for each speciation event. The set must have the same length as the set of mass-extinction times.
samplingProbability	The probability for a species to be included in the sample.
samplingStrategy	The strategy how samples were obtained. Options are: randomldiversified.
SURVIVAL	Do you want to condition on survival of the process?
MRCA	Does the process start with the most recent common ancestor?
t_crit	The critical time points when a jump in the rate function occurs. Only a help for the numerical integration routine.

**Value**

Returns a tree in 'phylo' format.

**Author(s)**

Sebastian Hoehna

**References**

S. Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted

**Examples**

```
l <- function(x) { if (x > 0.5 || x < 0.3) { return (1) } else { return (2) } }
e <- function(x) { if (x > 0.5 || x < 0.3) { return (0.95) } else { return (0.5) } }

sim.globalBiDe.taxa(n=1,nTaxa=10,max=10,l,e,MRCA=TRUE)

# simulation under constant rates
sim.globalBiDe.taxa(n=1,nTaxa=10,max=10,2.0,1.0,MRCA=TRUE)
```

---

sim.globalBiDe.taxa.age

*sim.globalBiDe.taxa.age: Simulate a reconstructed tree for a given age and number of taxa under a global, time-dependent birth-death process.*

---

## Description

sim.globalBiDe.taxa.age simulates a reconstructed phylogenetic tree under a global, time-dependent birth-death process conditioned on the age of the tree and number of taxa sampled. The rates may be any positive function of time or a constant. The process starts at time 0 and goes forward in time, hence the rates and events should be interpreted in the time after the origin. Additionally, mass-extinction event can be provided and a random taxon sampling probability. It is possible to start either with the origin (1 species) or with the most recent common ancestor (2 species).

## Usage

```
sim.globalBiDe.taxa.age(n, nTaxa, age, lambda, mu, massExtinctionTimes = c(),
  massExtinctionSurvivalProbabilities = c(), samplingProbability = 1,
  samplingStrategy = "random", MRCA = TRUE)
```

## Arguments

n	Number of simulations.
nTaxa	Number of species sampled.
age	The age of the tree, i.e. the time to simulate.
lambda	The speciation rate function or constant.
mu	The extinction rate function or constant.
massExtinctionTimes	The set of mass-extinction times after the start of the process.
massExtinctionSurvivalProbabilities	The set of survival probabilities for each speciation event. The set must have the same length as the set of mass-extinction times.
samplingProbability	The probability for a species to be included in the sample.
samplingStrategy	The strategy how samples were obtained. Options are: randomldiversified.
MRCA	Does the process start with the most recent common ancestor?

## Value

Returns a tree in 'phylo' format.

## Author(s)

Sebastian Hoehna

## References

S. Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted

## Examples

```
l <- function(x) { if (x > 0.5 || x < 0.3) { return (1) } else { return (2) } }
e <- function(x) { if (x > 0.5 || x < 0.3) { return (0.95) } else { return (0.5) } }

sim.globalBiDe.taxa.age(n=1, l, e, nTaxa=10, age=1, MRCA=TRUE)

# simulation under constant rates
sim.globalBiDe.taxa.age(n=1, 2.0, 1.0, nTaxa=10, age=1, MRCA=TRUE)
```

---

tess.mcmc

*tess.mcmc: Metropolis-Hastings algorithm.*


---

## Description

tess.mcmc constructs a Markov chain Monte Carlo algorithm (MCMC) by implementing a general Metropolis-Hastings algorithm. Any model can be used where the likelihood is known and thus can be passed in as an argument. The parameters have to be continuous. Proposals are taken from a normal distribution centered around the current value. The variance of the new proposed values is initialized with 1 but can be automatically optimized when using the option `adaptive = TRUE`. The algorithm creates samples from the posterior probability distribution and returns these as a CODA mcmc object.

## Usage

```
tess.mcmc(likelihoodFunction, priors, parameters, logTransforms, delta,
          iterations, burnin=round(iterations/3), thinning=1,
          adaptive=TRUE, verbose=FALSE)
```

## Arguments

likelihoodFunction	The log-likelihood function which will be called internally by likelihoodFunction(parameters).
priors	A list of functions of the log-prior-densities of each parameter.
parameters	The initial parameter value list.
logTransforms	A vector of booleans telling if log-transform for the parameters should be used (e.g. for rates).
delta	The variance of new proposed values.
iterations	The number of iterations for the MCMC.

burnin	The number of iterations to burn before starting the MCMC.
thining	The frequency of taking a sample of the parameters.
adaptive	Should we use adaptive MCMC?
verbose	Do you want detailed information during the run?

**Value**

Returns the posterior samples for the parameters.

**Author(s)**

Sebastian Hoehna

**References**

Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted

**Examples**

```

data(cettiidae)

likelihood <- function(params) {
  # We use the parameters as diversification rate and turnover rate.
  # Thus we need to transform first
  b <- params[1] + params[2]
  d <- params[2]

  lnL <- globalBiDe.likelihood(cettiidae,b,d,samplingProbability=1.0,log=TRUE)
  return (lnL)
}

prior_diversification <- function(x) { dexp(x,rate=0.1,log=TRUE) }
prior_turnover <- function(x) { dexp(x,rate=0.1,log=TRUE) }
priors <- c(prior_diversification,prior_turnover)

# Note, the number of iterations and the burnin is too small here and should be adapted for real analyses
samples <- tess.mcmc(likelihood,priors,runif(2,0,1),logTransforms=c(TRUE,TRUE),delta=c(0.1,0.1),iterations=100,
#plot(samples)
summary(samples)
colMeans(samples)

```

---

tess.PosteriorPrediction

*tess.PosteriorPrediction: Approximation of the posterior predictive distribution.*

---

### Description

tess.PosteriorPrediction calls the simulation function exactly once for each sampled parameter combination. In that way, posterior predictive simulations can be obtained.

### Usage

```
tess.PosteriorPrediction(simulationFunction, parameters)
```

### Arguments

simulationFunction      The simulation function which will be called internally by simulationFunction(parameters).

parameters              A matrix of parameters where the rows represent samples of parameters and the column the different parameters.

### Value

Returns samples simulated from the posterior predictive distribution.

### Author(s)

Sebastian Hoehna

### References

Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted

### Examples

```
# We first run an MCMC to obtain samples from the posterior distribution and then simulate the posterior predictive
# The bird phylogeny as the test data set
data(cettiidae)

# The log-likelihood function
likelihood <- function(params) {
  # We use the parameters as diversification rate and turnover rate.
  # Thus we need to transform first
  b <- params[1] + params[2]
  d <- params[2]

  lnL <- globalBiDe.likelihood(cettiidae,b,d,samplingProbability=1.0,log=TRUE)
```

```

    return (lnl)
  }

  prior_diversification <- function(x) { dexp(x,rate=0.1,log=TRUE) }
  prior_turnover <- function(x) { dexp(x,rate=0.1,log=TRUE) }
  priors <- c(prior_diversification,prior_turnover)

  # Note, the number of iterations and the burnin is too small here and should be adapted for real analyses
  samples <- tess.mcmc(likelihood,priors,c(1,0.1),c(TRUE,TRUE),c(0.1,0.1),10,10)

  tmrca <- max(branching.times(cettiidae))
  # The simulation function
  sim <- function(params) {
    # We use the parameters as diversification rate and turnover rate.
    # Thus we need to transform first
    b <- params[1] + params[2]
    d <- params[2]

    tree <- sim.globalBiDe.age(n=1,age=tmrca,b,d,samplingProbability=1.0)[[1]]
    return (tree)
  }

  trees <- tess.PosteriorPrediction(sim,samples)
  #plot(trees)

```

---

```
tess.PosteriorPredictiveTest
```

*tess.PosteriorPredictiveTest: Approximation of the posterior predictive distribution.*

---

## Description

tess.PosteriorPredictiveTest computes the values of the statistic for the posterior predictive simulations and computes the p-value for the observed statistic.

## Usage

```
tess.PosteriorPredictiveTest(samples,observation,statistic)
```

## Arguments

samples	Samples from the posterior predictive distribution.
observation	The observed value.
statistic	The function that computes the statistic.

## Value

Returns a list of the statistic for each sample.

**Author(s)**

Sebastian Hoehna

**References**

Hoehna, S.: Fast simulation of reconstructed phylogenies under global, time-dependent birth-death processes. 2012, submitted

**Examples**

```
# We first run an MCMC to obtain samples from the posterior distribution and then simulate the posterior prediction

# The bird phylogeny as the test data set
data(cettiidae)

# The log-likelihood function
likelihood <- function(params) {
  # We use the parameters as diversification rate and turnover rate.
  # Thus we need to transform first
  b <- params[1] + params[2]
  d <- params[2]

  lnL <- globalBiDe.likelihood(cettiidae,b,d,samplingProbability=1.0,log=TRUE)
  return (lnL)
}

prior_diversification <- function(x) { dexp(x,rate=0.1,log=TRUE) }
prior_turnover <- function(x) { dexp(x,rate=0.1,log=TRUE) }
priors <- c(prior_diversification,prior_turnover)

# Note, the number of iterations and the burnin is too small here and should be adapted for real analyses
samples <- tess.mcmc(likelihood,priors,c(1,0.1),c(TRUE,TRUE),c(0.1,0.1),10,10)

tmrca <- max(branching.times(cettiidae))
# The simulation function
sim <- function(params) {
  # We use the parameters as diversification rate and turnover rate.
  # Thus we need to transform first
  b <- params[1] + params[2]
  d <- params[2]

  # We need trees with at least three tips for the gamma-statistics
  repeat {
    tree <- sim.globalBiDe.age(n=1,age=tmrca,b,d,samplingProbability=1.0,MRCA=TRUE)[[1]]
    if (tree$Nnode > 1) break
  }
  return (tree)
}

# simulate trees from the posterior predictive distribution
trees <- tess.PosteriorPrediction(sim,samples)
```

```
# compute the posterior predictive test statistic
ppt <- tess.PosteriorPredictiveTest(trees,cettiidae,gammaStat)
# get the p-value of the observed test-statistic
ppt[[2]]
```

---

tess.steppingStoneSampling

*tess.steppingStoneSampling: Marginal likelihood estimation via Stepping-Stone-Sampling.*

---

### Description

tess.steppingStoneSampling uses a power posterior series and stepping-stone-sampling to estimate the marginal likelihood of a model.

### Usage

```
tess.steppingStoneSampling(likelihoodFunction,priors,parameters,logTransforms,
                           iterations,burnin=round(iterations/3),K=50)
```

### Arguments

likelihoodFunction	The log-likelihood function which will be called internally by likelihoodFunction(parameters).
priors	A list of functions of the log-prior-densities of each parameter.
parameters	The initial parameter value list.
logTransforms	A vector of booleans telling if log-transform for the parameters should be used (e.g. for rates).
iterations	The number of iterations for the MCMC.
burnin	The number of iterations to burn before starting the MCMC.
K	The number of stepping stones.

### Value

Returns the posterior samples for the parameters.

### Author(s)

Sebastian Hoehna

### References

Xie et al., 2011: Improving marginal likelihood estimation for Bayesian phylogenetic model selection  
 Baele et al., 2012: Improving the accuracy of demographic and molecular clock model comparison while accommodating phylogenetic uncertainty  
 Baele et al., 2013: Accurate Model Selection of Relaxed Molecular Clocks in Bayesian Phylogenetics



**Examples**

```
data(cettiidae)

likelihood <- function(params) {
  # We use the parameters as diversification rate and turnover rate.
  # Thus we need to transform first
  b <- params[1] + params[2]
  d <- params[2]

  lnL <- globalBiDe.likelihood(cettiidae,b,d,samplingProbability=1.0,log=TRUE)
  return (lnL)
}

prior_diversification <- function(x) { dexp(x,rate=0.1,log=TRUE) }
prior_turnover <- function(x) { dexp(x,rate=0.1,log=TRUE) }
priors <- c(prior_diversification,prior_turnover)

# Note, the number of iterations, the burnin and the number of stepping stones is too small here and should be adapted
marginalLikelihood <- tess.steppingStoneSampling(likelihood,priors,runif(2,0,1),c(TRUE,TRUE),10,10,K=4)
```

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