

# Package ‘hisse’

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**Description** Sets up and executes a HiSSE model (Hidden State Speciation and Extinction) on a phylogeny and character sets to test for hidden shifts in trait dependent rates of diversification. Beaulieu and O'Meara (2016) <doi:10.1093/sysbio/syw022>.

**License** GPL (>= 2)

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BisseToHisse	<i>BisseToHisse</i>
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## Description

A simple utility function for organizing parameters from diversitree to be in the right format for marginRecon function.

## Usage

```
BisseToHisse(lambda, mu, q01, q10)
```

## Arguments

lambda	a vector containing the parameter estimates for lambda0 and lambda1 from diversitree.
mu	a vector containing the parameter estimates for mu0 and mu1 from diversitree.
q01	the estimate of transition rate from state 0 to state 1 from diversitree.
q10	the estimate of transition rate from state 1 to state 0 from diversitree.

**Value**

A simple vector providing the proper format for BiSSE parameters and defaults in HiSSE for use in the `marginRecon` function.

**Author(s)**

Jeremy M. Beaulieu

**Examples**

```
bisse.pars <- c(0.1, 0.2, 0.03, 0.03, 0.01, 0.01)
hisse.par.vec <- BisseToHisse(lambda=c(0.1,0.2), mu=c(0.03,0.03), q01=0.01, q10=0.01)
```

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Compute Model Weights *Compute model weights*

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**Description**

Computes the Akaike model weights for a list of HiSSE or GeoHiSSE model fits.

**Usage**

```
GetModelWeight(...)
```

**Arguments**

... Any number of model fits of class 'hisse.fit' or 'geohisse.fit' separated by commas OR a single list object composed by the model fits.

**Details**

Function computes the model weight from their AIC values using the formula:

```
“delta <- mod.AIC - min( mod.AIC )”
```

```
“aicw <- exp( -0.5 * delta ) / sum( exp( -0.5 * delta ) )”
```

Function will return model names if these are provided in the call using '...' or a list object.

**Author(s)**

Daniel Caetano

fGeoHiSSE

*fast Hidden Geographic State Speciation and Extinction***Description**

Sets up and executes a GeoHiSSE model (Hidden Geographic State Speciation and Extinction) on a very large phylogeny and character distribution.

**Usage**

```
fGeoHiSSE(phy, data, f=c(1,1,1), turnover=c(1,2,3), extinct.frac=c(1,2),
hidden.areas=FALSE, trans.rate=NULL, assume.cladogenetic=TRUE,
condition.on.survival=TRUE, root.type="madfitz", root.p=NULL, sann=FALSE,
sann.its=10000, bounded.search=TRUE, max.tol=.Machine$double.eps^.50,
mag.san.start=0.5, starting.vals=NULL, turnover.upper=1000,
extinct.frac.upper=1000, trans.upper=100, restart.obj=NULL, ode.eps=0)
```

**Arguments**

phy	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
data	a matrix (or dataframe) with two columns containing species information. First column has the species names and second column has area codes. Values for the areas need to be 0, 1, or 2, where 0 is the widespread area ‘01’, 1 is endemic area ‘00’ and 2 is endemic area ‘11’. See ‘Details’.
f	vector of length 3 with the estimated proportion of extant species in state 1 (area ‘00’), state 2 (area ‘1’), and state 0 (widespread area ‘01’) that are included in the phylogeny. A value of c(0.25, 0.25, 0.5) means that 25 percent of species in areas ‘00’ and ‘11’ and 50 percent of species in area ‘01’ are included in the phylogeny. By default all species are assumed to be sampled.
turnover	a numeric vector of length equal to 3+(number of hidden.areas * 3). A fGeoSSE model has 3 turnover parameters: tau00, tau11 and tau01. A fGeoHiSSE model with one hidden area has 6 speciation parameters: tau00A, tau11A, tau01A, tau00B, tau11B, and tau01B, and so on. The length of the numeric vector needs to match the number of speciation parameters in the model.
extinct.frac	a numeric vector of length equal to 2+(number of hidden.areas * 2). A fGeoSSE model has 2 extinct fraction parameters: ef00 and ef11. A fGeoHiSSE model with one hidden area has 4 extinct.frac parameters: ef00A, ef11A, ef00B, and ef11B, and so on. The length of the numeric vector needs to match the number of extinct.frac parameters in the model.
hidden.areas	a logical indicating whether the model includes a hidden area. The default is FALSE.
trans.rate	provides the transition rate model. See function TransMatMakerfGeoHiSSE.
assume.cladogenetic	assumes that cladogenetic events occur at nodes. The default is TRUE.

<code>condition.on.survival</code>	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
<code>root.type</code>	indicates whether root summarization follow the procedure described by FitzJohn et al. 2009, “madfitz” or Herrera-Alsina et al. 2018, “herr_als”.
<code>root.p</code>	a vector indicating fixed root state probabilities. The default is NULL. Order of the areas in the vector need to follow: <code>root.p[1] = 1</code> (endemic area '0'); <code>root.p[2] = 2</code> (endemic area '1'); <code>root.p[3] = 0</code> (widespread area '01').
<code>sann</code>	a logical indicating whether a two-step optimization procedure is to be used. The first includes a simulate annealing approach, with the second involving a refinement using <code>subplex</code> . The default is FALSE.
<code>sann.its</code>	a numeric indicating the number of times the simulated annealing algorithm should call the objective function.
<code>bounded.search</code>	a logical indicating whether or not bounds should be enforced during optimization. The default is TRUE.
<code>max.tol</code>	supplies the relative optimization tolerance to <code>subplex</code> .
<code>mag.san.start</code>	Sets the extinction fraction to estimate the starting values for the diversification parameters. The equation used is based on Magallon and Sanderson (2001), and follows the procedure used in the original GeoSSE implementation.
<code>starting.vals</code>	a vector of starting values for the diversification parameters to be used instead of the default settings.
<code>turnover.upper</code>	sets the upper bound for the speciation parameters.
<code>extinct.frac.upper</code>	sets the upper bound for the extirpation parameters.
<code>trans.upper</code>	sets the upper bound for the transition rate parameters.
<code>restart.obj</code>	an object that contains everything to restart an optimization.
<code>ode.eps</code>	sets the tolerance for the integration at the end of a branch. Essentially if the sum of <code>compD</code> is less than this tolerance, then it assumes the results are unstable and discards them. The default is set to zero, but in testing a value of $1e-8$ can sometimes produce stable solutions for both easy and very difficult optimization problems.

## Details

This function sets up and executes a more complex and potentially faster version of the GeoHiSSE model. One of the main differences here is that the model allows up to 10 hidden categories, and implements a more efficient means of carrying out the branch calculation. Specifically, we break up the tree into carry out all descendent branch calculations simultaneously, combine the probabilities based on their shared ancestry, then repeat for the next set of descendent . In testing, we’ve found that as the number of taxa increases, the calculation becomes much more efficient. In future versions, we will likely allow for multicore processing of these calculations to further improve speed. Also, note this function will eventually completely replace the version of GeoSSE that is currently available.

The other main difference is that, like HiSSE, we employ a modified optimization procedure. In other words, rather than optimizing birth and death separately, fGeoHiSSE optimizes orthogonal transformations of these variables: we let  $\tau = \text{birth} + \text{death}$  define "net turnover", and we let  $\epsilon = \text{death} / \text{birth}$  define the "extinction fraction". This reparameterization alleviates problems associated with overfitting when birth and death are highly correlated, but both matter in explaining the diversity pattern.

To setup a model, users input vectors containing values to indicate how many free parameters are to be estimated for each of the variables in the model. This is done using the `turnover` and `extinct.frac` parameters. One needs to specify a value for each of the parameters of the model, when two parameters show the same value, then the parameters are set to be linked during the estimation of the model. For example, a fGeoHiSSE model with 1 hidden area and all free parameters has `turnover = 1:6`. The same model with speciation rates constrained to be the same for all hidden areas has `turnover = c(1,2,3,1,2,3)`. This same format applies to `extinct.frac`.

Once the model is specified, the parameters can be estimated using the subplex routine (default), or use a two-step process (i.e., `sann=TRUE`) that first employs a stochastic simulated annealing procedure, which is later refined using the subplex routine.

The "trans.rate" input is the transition model and has an entirely different setup than speciation and extirpation rates. See `TransMatMakerfGeoHiSSE` function for more details.

For user-specified "root.p", you should specify the probability for each area. If you are doing a hidden model, there will be six areas: 0A, 1A, 2A, 0B, 1B, 2B. So if you wanted to say the root had to be in area 0 (widespread distribution), you would specify "root.p = c(0.5, 0, 0, 0.5, 0, 0)". In other words, the root has a 50% chance to be in one of the areas 0A or 0B.

For the "root.type" option, we are currently maintaining the previous default of "madfitz". However, it was recently pointed out by Herrera-Alsina et al. (2018) that at the root, the individual likelihoods for each possible state should be conditioned prior to averaging the individual likelihoods across states. This can be set doing "herr\_als". It is unclear to us which is exactly correct, but it does seem that both "madfitz" and "herr\_als" behave exactly as they should in the case of character-independent diversification (i.e., reduces to likelihood of tree + likelihood of trait model). We've also tested the behavior and the likelihood differences are very subtle and the parameter estimates in simulation are nearly indistinguishable from the "madfitz" conditioning scheme. We provide both options and encourage users to try both and let us know conditions in which the result vary dramatically under the two root implementations. We suspect they do not.

Also, note, that in the case of "root.type=user" and "root.type=equal" are no longer explicit "root.type" options. Instead, either "madfitz" or "herr\_als" are specified and the "root.p" can be set to allow for custom root options.

## Value

GeoHiSSE returns an object of class `geohisse.fit`. This is a list with elements:

<code>\$loglik</code>	the maximum negative log-likelihood.
<code>\$AIC</code>	Akaike information criterion.
<code>\$AICc</code>	Akaike information criterion corrected for sample-size.
<code>\$solution</code>	a matrix containing the maximum likelihood estimates of the model parameters.
<code>\$index.par</code>	an index matrix of the parameters being estimated.
<code>\$f</code>	user-supplied sampling frequencies.

<code>\$hidden.areas</code>	a logical indicating whether hidden areas were included in the model.
<code>\$assume.cladogenetic</code>	a logical indicating whether cladogenetic events were allowed at nodes.
<code>\$condition.on.survival</code>	a logical indicating whether the likelihood was conditioned on the survival of two lineages and the speciation event subtending them.
<code>\$root.type</code>	indicates the user-specified root prior assumption.
<code>\$root.p</code>	indicates whether the user-specified fixed root probabilities.
<code>\$phy</code>	user-supplied tree
<code>\$data</code>	user-supplied dataset
<code>\$trans.matrix</code>	the user-supplied transition matrix
<code>\$max.tol</code>	relative optimization tolerance.
<code>\$starting.vals</code>	The starting values for the optimization.
<code>\$upper.bounds</code>	the vector of upper limits to the optimization search.
<code>\$lower.bounds</code>	the vector of lower limits to the optimization search.
<code>\$ode.eps</code>	The ode.eps value used for the estimation.

### Author(s)

Jeremy M. Beaulieu

### References

- Caetano, D.S., B.C. O'Meara, and J.M. Beaulieu. 2018. Hidden state models improve state-dependent diversification approaches, including biogeographic models. *Evolution*, 72:2308-2324.
- Beaulieu, J.M, and B.C. O'Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., W.P. Maddison, and S.P. Otto. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., P.E. Midford, and S.P. Otto. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., R.M. May, and P.H. Harvey. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

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GeoHiSSE

*Hidden Geographic State Speciation and Extinction*

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### Description

Sets up and executes a GeoHiSSE model (Hidden Geographic State Speciation and Extinction) on a phylogeny and character distribution.

**Usage**

```
GeoHiSSE(phy, data, f=c(1,1,1), speciation=c(1,2,3), extirpation=c(1,2),
hidden.areas=FALSE, trans.rate=NULL, assume.cladogenetic=TRUE,
condition.on.survival=TRUE, root.type="madfitz", root.p=NULL, sann=FALSE,
sann.its=10000, bounded.search=TRUE, max.tol=.Machine$double.eps^.50,
mag.san.start=0.5, starting.vals=NULL, speciation.upper=1000, extirpation.upper=1000,
trans.upper=100, ode.eps=0)
```

**Arguments**

phy	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
data	a matrix (or dataframe) with two columns containing species information. First column has the species names and second column has area codes. Values for the areas need to be 0, 1, or 2, where 0 is the widespread area ‘01’, 1 is endemic area ‘0’ and 2 is endemic area ‘1’. See ‘Details’.
f	vector of length 3 with the estimated proportion of extant species in state 1 (area ‘0’), state 2 (area ‘1’), and state 0 (widespread area ‘01’) that are included in the phylogeny. A value of c(0.25, 0.25, 0.5) means that 25 percent of species in areas ‘0’ and ‘1’ and 50 percent of species in area ‘01’ are included in the phylogeny. By default all species are assumed to be sampled.
speciation	a numeric vector of length equal to 3+(number of hidden.areas * 3). A GeoSSE model has 3 speciation parameters: s0, s1 and s01. A GeoHiSSE model with one hidden area has 6 speciation parameters: s0A, s1A, s01A, s0B, s1B, s01B. And so on. The length of the numeric vector needs to match the number of speciation parameters in the model. See ‘Details’.
extirpation	a numeric vector of length equal to 2+(number of hidden.areas * 2). A GeoSSE model has 2 extirpation parameters: x0 and x1. A GeoHiSSE model with one hidden area has 4 extirpation parameters: x0A, x1A, x0B, and x1B. And so on. The length of the numeric vector needs to match the number of extirpation parameters in the model. See ‘Details’.
hidden.areas	a logical indicating whether the model includes a hidden area. The default is FALSE.
trans.rate	provides the transition rate model. See function TransMatMakerGeoHiSSE.
assume.cladogenetic	assumes that cladogenetic events occur at nodes. The default is TRUE.
condition.on.survival	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
root.type	indicates whether root summarization follow the procedure described by FitzJohn et al. 2009, “madfitz” or Herrera-Alsina et al. 2018, “herr_als”.
root.p	a vector indicating fixed root state probabilities. The default is NULL. Order of the areas in the vector need to follow: root.p[1] = 1 (endemic area ‘0’); root.p[2] = 2 (endemic area ‘1’); root.p[3] = 0 (widespread area ‘01’).



<code>sann</code>	a logical indicating whether a two-step optimization procedure is to be used. The first includes a simulated annealing approach, with the second involving a refinement using <code>subplex</code> . The default is <code>FALSE</code> .
<code>sann.its</code>	a numeric indicating the number of times the simulated annealing algorithm should call the objective function.
<code>bounded.search</code>	a logical indicating whether or not bounds should be enforced during optimization. The default is <code>TRUE</code> .
<code>max.tol</code>	supplies the relative optimization tolerance to <code>subplex</code> .
<code>mag.san.start</code>	Sets the extinction fraction to estimate the starting values for the diversification parameters. The equation used is based on Magallon and Sanderson (2001), and follows the procedure used in the original GeoSSE implementation.
<code>starting.vals</code>	a vector of starting values for the diversification parameters to be used instead of the default settings.
<code>speciation.upper</code>	sets the upper bound for the speciation parameters.
<code>extirpation.upper</code>	sets the upper bound for the extirpation parameters.
<code>trans.upper</code>	sets the upper bound for the transition rate parameters.
<code>ode.eps</code>	sets the tolerance for the integration at the end of a branch. Essentially if the sum of <code>compD</code> is less than this tolerance, then it assumes the results are unstable and discards them. The default is set to zero, but in testing a value of <code>1e-8</code> can sometimes produce stable solutions for both easy and very difficult optimization problems.

## Details

This function sets up and executes the GeoHiSSE model. The model closely follows `diversitree`, although here we employ modified optimization procedures. As for data file format, GeoHiSSE expects a two column matrix or data frame, with the first column containing the species names and the second containing the area information. The area information need to be in the format of three numbers: 0 for area '01', 1 for area '0', and 2 for '1'. Please note that the code for the areas here differ from the `make.geosse` function of package `diversitree`. The order of the data file and the names in the "phylo" object need not be in the same order; `hisse` deals with this internally. Also, the character information MUST be 0, 1, or 2, otherwise, the function will return an error message.

To setup a model, users input vectors containing values to indicate how many free parameters are to be estimated for each of the variables in the model. This is done using the `speciation` and `extirpation` parameters. One needs to specify a value for each of the parameters of the model, when two parameters show the same value, then the parameters are set to be linked during the estimation of the model. For example, a GeoHiSSE model with 1 hidden area and all free parameters has `speciation = 1:6`. The same model with speciation rates constrained to be the same for all hidden areas has `speciation = c(1,2,3,1,2,3)`. This same format applies to `extirpation`. Please note that GeoHiSSE currently works with up to 4 hidden areas. The most complex model would be `speciation = 1:15` and `extirpation = 1:10`.

Once the model is specified, the parameters can be estimated using the `subplex` routine (default), or use a two-step process (i.e., `sann=TRUE`) that first employs a stochastic simulated annealing procedure, which is later refined using the `subplex` routine.

The “trans.rate” input is the transition model and has an entirely different setup than speciation and extirpation rates. See `TransMatMakerGeoHiSSE` function for more details.

For user-specified “root.p”, you should specify the probability for each area. If you are doing a hidden model, there will be six areas: 0A, 1A, 01A, 0B, 1B, 01B. So if you wanted to say the root had to be in area 0 (widespread distribution), you would specify “root.p = c(0.5, 0, 0, 0.5, 0, 0)”. In other words, the root has a 50% chance to be in one of the areas 0A or 0B.

For the “root.type” option, we are currently maintaining the previous default of “madfitz”. However, it was recently pointed out by Herrera-Alsina et al. (2018) that at the root, the individual likelihoods for each possible state should be conditioned prior to averaging the individual likelihoods across states. This can be set doing “herr\_als”. It is unclear to us which is exactly correct, but it does seem that both “madfitz” and “herr\_als” behave exactly as they should in the case of character-independent diversification (i.e., reduces to likelihood of tree + likelihood of trait model). We’ve also tested the behavior and the likelihood differences are very subtle and the parameter estimates in simulation are nearly indistinguishable from the “madfitz” conditioning scheme. We provide both options and encourage users to try both and let us know conditions in which the result vary dramatically under the two root implementations. We suspect they do not.

Also, note, that in the case of “root.type=user” and “root.type=equal” are no longer explicit “root.type” options. Instead, either “madfitz” or “herr\_als” are specified and the “root.p” can be set to allow for custom root options.

## Value

GeoHiSSE returns an object of class `geohisse.fit`. This is a list with elements:

<code>\$loglik</code>	the maximum negative log-likelihood.
<code>\$AIC</code>	Akaike information criterion.
<code>\$AICc</code>	Akaike information criterion corrected for sample-size.
<code>\$solution</code>	a matrix containing the maximum likelihood estimates of the model parameters.
<code>\$index.par</code>	an index matrix of the parameters being estimated.
<code>\$f</code>	user-supplied sampling frequencies.
<code>\$hidden.areas</code>	a logical indicating whether hidden areas were included in the model.
<code>\$assume.cladogenetic</code>	a logical indicating whether cladogenetic events were allowed at nodes.
<code>\$condition.on.survival</code>	a logical indicating whether the likelihood was conditioned on the survival of two lineages and the speciation event subtending them.
<code>\$root.type</code>	indicates the user-specified root prior assumption.
<code>\$root.p</code>	indicates whether the user-specified fixed root probabilities.
<code>\$timeslice</code>	indicates whether the user-specified timeslice that split the tree.
<code>\$phy</code>	user-supplied tree
<code>\$data</code>	user-supplied dataset
<code>\$trans.matrix</code>	the user-supplied transition matrix
<code>\$max.tol</code>	relative optimization tolerance.

`$starting.vals` The starting values for the optimization.  
`$upper.bounds` the vector of upper limits to the optimization search.  
`$lower.bounds` the vector of lower limits to the optimization search.  
`$ode.eps` The ode.eps value used for the estimation.

### Author(s)

Jeremy M. Beaulieu

### References

- Caetano, D.S., B.C. O’Meara, and J.M. Beaulieu. 2018. Hidden state models improve state-dependent diversification approaches, including biogeographic models. *Evolution*, 72:2308-2324.
- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., W.P. Maddison, and S.P. Otto. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Goldberg, E. E., L. T. Lancaster, and R. H. Ree. 2011. Phylogenetic Inference of Reciprocal Effects between Geographic Range Evolution and Diversification. *Syst. Biol.* 60:451-465.
- Maddison W.P., P.E. Midford, and S.P. Otto. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., R.M. May, and P.H. Harvey. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

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hisse

*Hidden State Speciation and Extinction*

---

### Description

Sets up and executes a HiSSE model (Hidden State Speciation and Extinction) on a phylogeny and character distribution.

### Usage

```
hisse(phy, data, f=c(1,1), hidden.states=TRUE, turnover.anc=c(1,1,0,0),
eps.anc=c(1,1,0,0), trans.rate=NULL, turnover.beta=c(0,0,0,0),
eps.beta=c(0,0,0,0), timeslice=NULL, condition.on.survival=TRUE,
root.type="madfitz", root.p=NULL, output.type="turnover", sann=FALSE,
sann.its=10000, bounded.search=TRUE, max.tol=.Machine$double.eps^.25,
starting.vals=NULL, turnover.upper=10000, eps.upper=3, trans.upper=100,
ode.eps=0)
```

**Arguments**

<code>phy</code>	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
<code>data</code>	a data matrix containing species information (see Details).
<code>f</code>	vector of length 2 with the estimated proportion of extant species in state 0 and 1 that are included in the phylogeny. A value of <code>c(0.25, 0.5)</code> means that 25 percent of species in state 0 and 50 percent of species in state 1 are included in the phylogeny. By default all species are assumed to be sampled.
<code>hidden.states</code>	a logical indicating whether the model includes a hidden state. The default is FALSE.
<code>turnover.anc</code>	a vector of length 4, indicating the free parameters associated with the net turnover rates. Default settings is a BiSSE model with fixed turnover rates for both observed states (see Details).
<code>eps.anc</code>	a vector of length 4, indicating the free parameters associated with the extinction fractions. Default settings is a BiSSE model with fixed extinction fractions for both observed states (see Details).
<code>trans.rate</code>	provides the transition rate model.
<code>turnover.beta</code>	a vector of length 4, indicating the free parameters associated with time-varying net turnover rates (see Details).
<code>eps.beta</code>	a vector of length 4, indicating the free parameters associated with time-varying extinction fractions (see Details).
<code>timeslice</code>	a user-supplied time to split the tree.
<code>condition.on.survival</code>	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
<code>root.type</code>	indicates whether root summarization follow the procedure described by FitzJohn et al. 2009, “madfitz” or Herrera-Alsina et al. 2018, “herr_als”.
<code>root.p</code>	a vector indicating fixed root state probabilities. The default is NULL.
<code>output.type</code>	indicates whether the rates should be printed onscreen as the optimized variables, “turnover”, transformed to reflect net diversification, “net.div”, or transformed to reflect $\lambda$ and $\mu$ , “raw”.
<code>sann</code>	a logical indicating whether a two-step optimization procedure is to be used. The first includes a simulate annealing approach, with the second involving a refinement using <code>subplex</code> . The default is FALSE.
<code>sann.its</code>	a numeric indicating the number of times the simulated annealing algorithm should call the objective function.
<code>bounded.search</code>	a logical indicating whether or not bounds should be enforced during optimization. The default is TRUE.
<code>max.tol</code>	supplies the relative optimization tolerance to <code>subplex</code> .
<code>starting.vals</code>	a vector of starting values to be used instead of the default settings. These are just three values given in the following order: turnover (1), extinction fraction (2), and a single transition rate (3)

<code>turnover.upper</code>	sets the upper bound for the turnover parameters. The default upper bound assumes an event occurs every 100 years.
<code>eps.upper</code>	sets the upper bound for the extinction fraction parameters.
<code>trans.upper</code>	sets the upper bound for the transition rate parameters.
<code>ode.eps</code>	sets the tolerance for the integration at the end of a branch. Essentially if the sum of <code>compD</code> is less than this tolerance, then it assumes the results are unstable and discards them. The default is set to zero, but in testing a value of $1e-8$ can sometimes produce stable solutions for both easy and very difficult optimization problems.

## Details

This function sets up and executes the HiSSE model. The model closely follows `diversitree`, although here we employ modified optimization procedures. For example, rather than optimizing birth and death separately, `hisse` optimizes orthogonal transformations of these variables: we let  $\text{tau} = \text{birth} + \text{death}$  define "net turnover", and we let  $\text{eps} = \text{death} / \text{birth}$  define the "extinction fraction". This reparameterization alleviates problems associated with overfitting when birth and death are highly correlated, but both matter in explaining the diversity pattern. As for data file format, `hisse` expects a two column matrix or data frame, with the first column containing the species names and the second containing the binary character information. Note that the order of the data file and the names in the "phylo" object need not be in the same order; `hisse` deals with this internally. Also, the character information should be binary and coded as 0 and 1, otherwise the function will misbehave. However, if the state for a species is unknown, a user can specify this with a 2, and the state will be considered maximally ambiguous.

To setup a model, users input vectors containing values to indicate how many free parameters are to be estimated for each of the variables in the model. For example, the "turnover.anc" input vector is set by default as  $c(1,1,0,0)$ . This means for state 0 and state 1, we are allowing one free parameter to define the net turnover rate (birth+death) in the model. This is essentially a BiSSE model with fixed turnover rates. Now, say we want to include separate turnover rates for both states we would simply input  $c(1,2,0,0)$ . The last two entries, which in the preceding example are set to zero, correspond to the hidden states; the third entry corresponds to a hidden state associated with observed state 0, such that 0A (hidden state absent) is the first entry, and 0B (hidden state present) is the third entry. So, to set up a model with three turnover rates, where we include a free parameter for a hidden state associated with state 0 we input  $c(1,2,3,0)$ . A full model would thus be  $c(1,2,3,4)$ , which corresponds to four separate net turnover rates, for states 0A (first entry), 1A (second entry), 0B (third entry), and 1B (fourth entry). Extinction fraction, or "eps.anc", follows the same format, though including a zero for a state we want to include in the model corresponds to no extinction, which is the Yule equivalent. In general, we follow this format to make it easier to generate a large set of nested models. Once the model is specified, the parameters can be estimated using the subplex routine (default), or use a two-step process (i.e., `sann=TRUE`) that first employs a stochastic simulated annealing procedure, which is later refined using the subplex routine.

The "trans.rate" input is the transition model and has an entirely different setup than turnover and extinction rates. See `TransMatMaker` function for more details.

For user-specified "root.p", you should specify the probability for each state. If you are doing a hidden model, there will be four states: 0A, 1A, 0B, 1B. So if you wanted to say the root had to be state 0, you would specify "root.p =  $c(0.5, 0, 0.5, 0)$ ".

For the “root.type” option, we are currently maintaining the previous default of “madfitz”. However, it was recently pointed out by Herrera-Alsina et al. (2018) that at the root, the individual likelihoods for each possible state should be conditioned prior to averaging the individual likelihoods across states. This can be set doing “herr\_als”. It is unclear to us which is exactly correct, but it does seem that both “madfitz” and “herr\_als” behave exactly as they should in the case of character-independent diversification (i.e., reduces to likelihood of tree + likelihood of trait model). We’ve also tested the behavior and the likelihood differences are very subtle and the parameter estimates in simulation are nearly indistinguishable from the “madfitz” conditioning scheme. We provide both options and encourage users to try both and let us know conditions in which the result vary dramatically under the two root implementations. We suspect they do not.

Also, note, that in the case of “root.type=user” and “root.type=equal” are no longer explicit “root.type” options. Instead, either “madfitz” or “herr\_als” are specified and the “root.p” can be set to allow for custom root options.

Finally, the options “.beta” and “timeslice” are included, but neither have been tested – needless to say, use at your own risk (but really, though, you should probably forget that these options exist for the time being). The “.beta” provides a means for testing for time-varying rates, whereas “timeslice” splits the tree to allow the process to vary before and after some user defined time period. These options will be further developed in due course.

## Value

`hisse` returns an object of class `hisse.fit`. This is a list with elements:

<code>\$loglik</code>	the maximum negative log-likelihood.
<code>\$AIC</code>	Akaike information criterion.
<code>\$AICc</code>	Akaike information criterion corrected for sample-size.
<code>\$solution</code>	a matrix containing the maximum likelihood estimates of the model parameters.
<code>\$index.par</code>	an index matrix of the parameters being estimated.
<code>\$f</code>	user-supplied sampling frequencies.
<code>\$hidden.states</code>	a logical indicating whether a hidden state was included in the model.
<code>\$condition.on.survival</code>	a logical indicating whether the likelihood was conditioned on the survival of two lineages and the speciation event subtending them.
<code>\$root.type</code>	indicates the user-specified root prior assumption.
<code>\$root.p</code>	indicates whether the user-specified fixed root probabilities.
<code>\$timeslice</code>	indicates whether the user-specified timeslice that split the tree.
<code>\$phy</code>	user-supplied tree
<code>\$data</code>	user-supplied dataset
<code>\$iterations</code>	number of iterations of the likelihood search that were executed.
<code>\$output.type</code>	the user-specified output.type to be printed on the screen.
<code>\$max.tol</code>	relative optimization tolerance.
<code>\$upper.bounds</code>	the vector of upper limits to the optimization search.
<code>\$lower.bounds</code>	the vector of lower limits to the optimization search.

**Author(s)**

Jeremy M. Beaulieu

**References**

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Herrera-Alsina L., van Els P., and Etienne R.S. 2018. Detecting the dependence of diversification on multiples traits from phylogenetic trees and trait data. *Systematic Biology* In press.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

**Examples**

```
library(diversitree)
pars <- c(0.1, 0.2, 0.03, 0.03, 0.01, 0.01)
set.seed(4)
phy <- tree.bisse(pars, max.t=30, x0=0)
sim.dat <- data.frame(names(phy$tip.state), phy$tip.state)
## Fit BiSSE equivalent:
trans.rates.bisse <- TransMatMaker(hidden.states=FALSE)
pp.bisse <- hisse(phy, sim.dat, hidden.states=FALSE, turnover.anc=c(1,2,0,0),
eps.anc=c(1,2,0,0), trans.rate=trans.rates.bisse)

## Now fit HiSSE equivalent with a hidden state for state 1:
trans.rates.hisse <- TransMatMaker(hidden.states=TRUE)
trans.rates.hisse <- ParDrop(trans.rates.hisse, c(2,3,5,7,8,9,10,12))
pp.hisse <- hisse(phy, sim.dat, hidden.states=TRUE, turnover.anc=c(1,2,0,3),
eps.anc=c(1,2,0,3), trans.rate=trans.rates.hisse)
```

---

hisse.null4

---

*Four state trait-independent Hidden State Speciation and Extinction*


---

**Description**

Sets up and executes a four state trait-independent HiSSE model (Hidden State Speciation and Extinction) on a phylogeny and character set.

**Usage**

```
hisse.null4(phy, data, f=c(1,1), turnover.anc=rep(c(1,2,3,4),2),
eps.anc=rep(c(1,2,3,4),2), trans.type="equal", condition.on.survival=TRUE,
root.type="madfitz", root.p=NULL, output.type="turnover", sann=FALSE,
sann.its=10000, bounded.search=TRUE, max.tol=.Machine$double.eps^.25,
starting.vals=NULL, turnover.upper=10000, eps.upper=3, trans.upper=100,
ode.eps=0)
```

**Arguments**

<code>phy</code>	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
<code>data</code>	a data matrix containing species information (see Details).
<code>f</code>	vector of length 2 with the estimated proportion of extant species in state 0 and 1 that are included in the phylogeny. A value of <code>c(0.25, 0.5)</code> means that 25 percent of species in state 0 and 50 percent of species in state 1 are included in the phylogeny. By default all species are assumed to be sampled.
<code>turnover.anc</code>	a vector of length 8, indicating the free parameters associated with the net turnover rates. Default setting assumes character independent diversification (see Details).
<code>eps.anc</code>	a vector of length 8, indicating the free parameters associated with the extinction fractions. Default setting assumes character independent diversification (see Details).
<code>trans.type</code>	provides the type of transition rate model. Currently this model allows two types: “equal”, the default, which assumes all transitions are equal, and “three.rate”, that assumes three rates (see Details).
<code>condition.on.survival</code>	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
<code>root.type</code>	indicates whether root summarization follow the procedure described by FitzJohn et al. 2009, “madfitz” or Herrera-Alsina et al. 2018, “herr_als”.
<code>root.p</code>	a vector indicating fixed root state probabilities. The default is NULL.
<code>output.type</code>	indicates whether the rates should be printed onscreen as the optimized variables, “turnover”, transformed to reflect net diversification, “net.div”, or transformed to reflect $\lambda$ and $\mu$ , “raw”.
<code>sann</code>	a logical indicating whether a two-step optimization procedure is to be used. The first includes a simulate annealing approach, with the second involving a refinement using <code>subplex</code> . The default is FALSE.
<code>sann.its</code>	a numeric indicating the number of times the simulated annealing algorithm should call the objective function.
<code>bounded.search</code>	a logical indicating whether or not bounds should be enforced during optimization. The default is TRUE.
<code>max.tol</code>	supplies the relative optimization tolerance to <code>subplex</code> .



<code>starting.vals</code>	a vector of starting values to be used instead of the default settings. These are just three values given in the following order: turnover (1), extinction fraction (2), and a single transition rate (3)
<code>turnover.upper</code>	sets the upper bound for the turnover parameters. The default upper bound assumes an event occurs every 100 years.
<code>eps.upper</code>	sets the upper bound for the extinction fraction parameters.
<code>trans.upper</code>	sets the upper bound for the transition rate parameters.
<code>ode.eps</code>	sets the tolerance for the integration at the end of a branch. Essentially if the sum of <code>compD</code> is less than this tolerance, then it assumes the results are unstable and discards them. The default is set to zero, but in testing a value of $1e-8$ can sometimes produce stable solutions for both easy and very difficult optimization problems.

## Details

This function sets up and executes a four-state trait independent HiSSE model. The model closely follows `hisse`.

Like `hisse`, users input vectors containing values to indicate how many free parameters are to be estimated for each of the variables in the model. However, the null-four model assumes that “`turnover.anc`” and “`eps.anc`” are linked between the two observed states. Thus, users are unlikely to alter the inputs much, aside from perhaps fixing “`turnover.anc`” or “`eps.anc`” to be equal across the four hidden states, where the “`turnover.anc`” input vector is set as `rep(c(1,1,1,1),2)`. For a Yule equivalent, the input vector for “`eps.anc`” would be `rep(c(0,0,0,0),2)`. For how to setup a null-two model see the example code below.

For user-specified “`root.p`”, you should specify the probability for each state. See help for “`hisse`” for more on other parameters for this function.

For the “`root.type`” option, we are currently maintaining the previous default of “`madfitz`”. However, it was recently pointed out by Herrera-Alsina et al. (2018) that at the root, the individual likelihoods for each possible state should be conditioned prior to averaging the individual likelihoods across states. This can be set doing “`herr_als`”. It is unclear to us which is exactly correct, but it does seem that both “`madfitz`” and “`herr_als`” behave exactly as they should in the case of character-independent diversification (i.e., reduces to likelihood of tree + likelihood of trait model). We’ve also tested the behavior and the likelihood differences are very subtle and the parameter estimates in simulation are nearly indistinguishable from the “`madfitz`” conditioning scheme. We provide both options and encourage users to try both and let us know conditions in which the result vary dramatically under the two root implementations. We suspect they do not.

Also, note, that in the case of “`root.type=user`” and “`root.type=equal`” are no longer explicit “`root.type`” options. Instead, either “`madfitz`” or “`herr_als`” are specified and the “`root.p`” can be set to allow for custom root options.

## Value

`hisse` returns an object of class `hisse.fit`. This is a list with elements:

<code>\$loglik</code>	the maximum negative log-likelihood.
<code>\$AIC</code>	Akaike information criterion.

\$AICc	Akaike information criterion corrected for sample-size.
\$solution	a matrix containing the maximum likelihood estimates of the model parameters.
\$index.par	an index matrix of the parameters being estimated.
\$f	user-supplied sampling frequencies.
\$condition.on.survival	a logical indicating whether the likelihood was conditioned on the survival of two lineages and the speciation event subtending them.
\$root.type	indicates the user-specified root prior assumption.
\$root.p	indicates whether the user-specified fixed root probabilities.
\$phy	user-supplied tree
\$data	user-supplied dataset
\$output.type	the user-specified output.type to be printed on the screen.
\$trans.type	the user-specified transition model.
\$trans.mat	the index matrix that specifies the free parameters in the transition model.
\$max.tol	relative optimization tolerance.
\$upper.bounds	the vector of upper limits to the optimization search.
\$lower.bounds	the vector of lower limits to the optimization search.

### Author(s)

Jeremy M. Beaulieu

### References

Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.

### Examples

```
## Not run
library(diversitree)
pars <- c(0.1, 0.2, 0.03, 0.03, 0.01, 0.01)
set.seed(4)
phy <- tree.bisse(pars, max.t=30, x0=0)
sim.dat <- data.frame(names(phy$tip.state), phy$tip.state)

## Fit null-four HiSSE:
pp.hisse.null <- hisse.null4(phy, sim.dat, turnover.anc=rep(c(1,2,3,4),2),
eps.anc=rep(c(1,2,3,4),2), trans.type="equal")

## Fit null-two HiSSE model:
trans.rates.hisse <- TransMatMaker(hidden.states=TRUE)
trans.rates.hisse <- ParDrop(trans.rates.hisse, c(3,5,8,10))
trans.rates.hisse[!is.na(trans.rates.hisse) & !trans.rates.hisse == 0] = 1
pp.hisse <- hisse(phy, sim.dat, hidden.states=TRUE, turnover.anc=c(1,1,2,2),
eps.anc=c(1,1,2,2), trans.rate=trans.rates.hisse)
```

---

makeHiSSELikelihood     *Export likelihood function for the HiSSE model*

---

### Description

Exports a likelihood function conditioned on the data and a named vector with the parameters for each of the models.

### Usage

```
makeHiSSELikelihood(phy, data, hidden.states=TRUE, null4=FALSE,
f=c(1,1), condition.on.survival=TRUE, root.type="madfitz", root.p=NULL, ode.eps=0)
```

### Arguments

phy	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
data	a data matrix containing species information (see Details).
hidden.states	whether the model has hidden states. This is ignored if the option “null4” is selected.
null4	used to select the null model for the full HiSSE model. This is a special model with 4 hidden states.
f	vector of length 2 with the estimated proportion of extant species in state 0 and 1 that are included in the phylogeny. A value of c(0.25, 0.5) means that 25 percent of species in state 0 and 50 percent of species in state 1 are included in the phylogeny. By default all species are assumed to be sampled.
condition.on.survival	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
root.type	indicates whether root summarization follow the procedure described by FitzJohn et al. 2009, “madfitz” or Herrera-Alsina et al. 2018, “herr_als”.
root.p	a vector indicating fixed root state probabilities. The default is NULL.
ode.eps	sets the tolerance for the integration at the end of a branch. Essentially if the sum of compD is less than this tolerance, then it assumes the results are unstable and discards them. The default is set to zero, but in testing a value of 1e-8 can sometimes produce stable solutions for both easy and very difficult optimization problems.

### Details

This function sets up and returns the likelihood for the HiSSE model together with a vector of parameters. The likelihood function is conditioned on the observed data and will return a value of loglikelihood given a vector of parameter values. The length of the parameter vector as well as the order of the parameter vector cannot be changed. The parameter values are provided in natural form

but are log-transformed for the likelihood evaluation. Please pay special attention to the length of the parameter vector and the names of the parameters provided by the “pars” element of the list.

When the option “null4” is set to TRUE, then the likelihood returned is for the HiSSE null model with 4 hidden states. The returned list will include an additional element named “trans.mat.guide” which can be used as a reference for the meaning of the 32 transition parameters. Note that the original model in “hisse.null4” usually sets all these transitions to a single value. This helps model estimation since information is limited to estimate distinct transition rates between parameters.

## Value

makeHiSSELikelihood returns a list with elements:

\$loglik	the likelihood function for the model. This has a single parameter ‘p’.
\$pars	a named vector for the likelihood function populated with 0 values.
\$trans.mat.guide	a reference matrix to understand the parameters returned by the “\$pars” vector. Only present if the “null4” option is set to TRUE.

## Author(s)

Jeremy M. Beaulieu and Daniel S. Caetano

## References

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

## Examples

```
library(diversitree)
library(hisse)
## Generate data:
pars <- c(0.1, 0.2, 0.03, 0.03, 0.01, 0.01)
set.seed(4)
phy <- tree.bisse(pars, max.t=30, x0=0)
sim.dat <- data.frame(names(phy$tip.state), phy$tip.state)
## Get lik function:
lik.hisse <- makeHiSSELikelihood(phy = phy, data = sim.dat, hidden.states = FALSE)
likf <- lik.hisse$log.lik
pars <- lik.hisse$pars
## Set the parameter values. Note that we have turnover and eps, not speciation and extinction!
pars <- setNames(c(0.1+0.03,0.2+0.03,0.03/0.1,0.03/0.2,0.01,0.01), names(pars))
```

```
## Compute the log-likelihood for the model.
likf(pars)
```

---

MarginRecon

*Ancestral State Estimation based on Marginal Reconstruction*


---

### Description

Estimates the likeliest states for both internal nodes and tips of a phylogeny using the marginal reconstruction algorithm.

### Usage

```
MarginRecon(phy, data, f, pars, hidden.states=TRUE, four.state.null=FALSE,
timeslice=NULL, condition.on.survival=TRUE, root.type="madfitz", root.p=NULL,
aic=NULL, verbose=TRUE, n.cores=NULL)
```

### Arguments

phy	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
data	a data matrix containing species information (see Details).
f	vector of length 2 with the estimated proportion of extant species in state 0 and 1 that are included in the phylogeny. A value of c(0.25, 0.5) means that 25 percent of species in state 0 and 50 percent of species in state 1 are included in the phylogeny. By default all species are assumed to be known.
pars	vector containing the MLE of the parameters.
hidden.states	a logical indicating whether the model includes a hidden state. The default is FALSE.
four.state.null	a logical indicating whether the model is the null-four model. The default is FALSE.
timeslice	a user-supplied time to split the tree.
condition.on.survival	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
root.type	indicates whether root prior assumption should be based on the procedure described by FitzJohn et al. 2009, “madfitz”, assumed equal, “equal”, or set to user, “user”.
root.p	a vector indicating fixed root state probabilities. The default is NULL.
aic	the AIC for the model being used for the reconstruction. This is used by the plotting function. The default is NULL.
verbose	a logical indicating whether progress should be printed to screen. The default is TRUE.
n.cores	specifies the number of independent processors to conduct the analysis.. The default is NULL.

## Details

In this implementation the marginal probability of state  $i$  for a focal node is simply the overall likelihood of the tree and data when the state of the focal node is fixed in state  $i$ . Note that the likeliest tip states can also be estimated: we observe state 1, but the underlying state could either be state 1A or 1B. Thus, for any given node or tip we traverse the entire tree as many times as there are states in the model. As the size of the tree grows, however, these repeated tree traversals can slow the calculation down considerably. For this reason, we allow the marginal calculation to be conducted in parallel across any number of independent computer processors.

For user-specified “root.p”, you should specify the probability for each state. If you are doing a hidden model, there will be four states: 0A, 1A, 0B, 1B. So if you wanted to say the root had to be state 0, you would specify “root.p = c(0.5, 0, 0.5, 0)”.

See help for “hisse” for more on other parameters for this function.

## Value

MarginRecon returns an object of class `hisse.states`. This is a list with elements:

<code>\$node.mat</code>	the marginal probabilities calculated for each node. They are ordered based on the elements in the edge matrix in “phylo” format.
<code>\$tip.mat</code>	the marginal probabilities calculated for each tip. They are ordered based on the order of tip labels in the tree.
<code>\$rate.mat</code>	a matrix that details the rates for each state combination. This is used by the plotting function.
<code>\$phy</code>	a phylogenetic tree in the “phylo” format that contains the states with the highest marginal probability at each internal node.

## Author(s)

Jeremy M. Beaulieu

## References

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters’ effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

## Examples

```
## Not run
library(diversitree)
pars <- c(0.1, 0.2, 0.03, 0.03, 0.01, 0.01)
```

```

set.seed(4)
phy <- tree.bisse(pars, max.t=30, x0=0)
sim.dat <- data.frame(names(phy$tip.state), phy$tip.state)
## Now fit HiSSE equivalent with a hidden state for state 1:
trans.rates.hisse <- TransMatMaker(hidden.states=TRUE)
trans.rates.hisse <- ParDrop(trans.rates.hisse, c(2,3,5,7,8,9,10,12))
pp.hisse <- hisse(phy, sim.dat, hidden.states=TRUE, turnover.anc=c(1,2,0,3),
eps.anc=c(1,2,0,3), trans.rate=trans.rates.hisse)
##Now reconstruct the likeliest states under this model:
pp <- MarginRecon(phy, sim.dat, f=c(1,1), pars=pp.hisse$solution,
hidden.states=TRUE)

```

---

MarginReconfGeoSSE      *fast Ancestral State Estimation based on Marginal Reconstruction for the GeoSSE and GeoHiSSE models.*

---

## Description

Estimates the likeliest states for both internal nodes and tips of a phylogeny using the marginal reconstruction algorithm.

## Usage

```

MarginReconfGeoSSE(phy, data, f, pars, hidden.areas=TRUE,
assume.cladogenetic=TRUE, condition.on.survival=TRUE,
root.type="madfitz", root.p=NULL, aic=NULL, verbose=TRUE,
n.cores=NULL, total.hidden=NULL)

```

## Arguments

phy	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
data	a data matrix containing species information (see Details).
f	vector of length 3 with the estimated proportion of extant species in area 00, 11, and 01 that are included in the phylogeny. A value of c(0.25, 0.5, 0.25) means that 25 percent of species in state 00 and 01 and 50 percent of species in state 11 are included in the phylogeny. By default all species are assumed to be known.
pars	vector containing the MLE of the parameters.
hidden.areas	a logical indicating whether the model includes hidden areas. The default is FALSE.
assume.cladogenetic	a logical indicating whether the model assumes that changes occur at the nodes. The default is TRUE. Setting this to FALSE will result in a different models from GeoSSE. Please check hisse::GeoHiSSE for more details.

<code>condition.on.survival</code>	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
<code>root.type</code>	indicates whether root prior assumption should based the procedure described by FitzJohn et al. 2009, “madfitz”, assumed equal, “equal”, or set to user, “user”.
<code>root.p</code>	a vector indicating fixed root state probabilities. The default is NULL.
<code>aic</code>	the AIC for the model being used for the reconstruction. This is used by the plotting function. The default is NULL.
<code>verbose</code>	a logical indicating whether progress should be printed to screen. The default is TRUE.
<code>n.cores</code>	specifies the number of independent processors to conduct the analysis.. The default is NULL.
<code>total.hidden</code>	specifies the number of hidden states assumed in the given model. By default it is NULL, which means it will evaluate all 10 possible hidden states.

## Details

In this implementation the marginal probability of area  $i$  for a focal node is simply the overall likelihood of the tree and data when the area of the focal node is fixed in area  $i$ . Note that the likeliest tip areas can also be estimated: we observe area 11, but the underlying area could either be area 11A or 11B. Thus, for any given node or tip we traverse the entire tree as many times as there are areas in the model. As the size of the tree grows, however, these repeated tree traversals can slow the calculation down considerably. For this reason, we allow the marginal calculation to be conducted in parallel across any number of independent computer processors.

For user-specified “root.p”, you should specify the probability for each area. If you are doing a hidden model, the number of parameters will depend on the number of hidden areas included. For a two classes model there are six areas: 00A, 11A, 01A, 00B, 11B, 01B. So if you wanted to say the root had to be area A, you would specify “root.p = c(0.5, 0, 0, 0.5, 0, 0)”. The root area is 00, but there is an equal chance for hidden area A or B.

See help for “fGeoHiSSE” for more on other parameters for this function.

## Value

MarginRecon returns an object of class `geohisse.states`. This is a list with elements:

<code>\$node.mat</code>	the marginal probabilities calculated for each node. They are ordered based on the elements in the edge matrix in “phylo” format.
<code>\$tip.mat</code>	the marginal probabilities calculated for each tip. They are ordered based on the order of tip labels in the tree.
<code>\$rate.mat</code>	a matrix that details the rates for each state combination. This is used by the plotting function.
<code>\$phy</code>	a phylogenetic tree in the “phylo” format that contains the states with the highest marginal probability at each internal node.



**Author(s)**

Jeremy M. Beaulieu

**References**

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Goldberg, E. E., L. T. Lancaster, and R. H. Ree. 2011. Phylogenetic Inference of Reciprocal Effects between Geographic Range Evolution and Diversification. *Syst. Biol.* 60:451-465.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters’ effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

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MarginReconGeoSSE	<i>Ancestral State Estimation based on Marginal Reconstruction for the GeoSSE and GeoHiSSE models.</i>
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**Description**

Estimates the likeliest states for both internal nodes and tips of a phylogeny using the marginal reconstruction algorithm.

**Usage**

```
MarginReconGeoSSE(phy, data, f, pars, hidden.areas=TRUE,
assume.cladogenetic=TRUE, condition.on.survival=TRUE,
root.type="madfitz", root.p=NULL, aic=NULL, verbose=TRUE,
n.cores=NULL)
```

**Arguments**

phy	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
data	a data matrix containing species information (see Details).
f	vector of length 2 with the estimated proportion of extant species in state 0 and 1 that are included in the phylogeny. A value of c(0.25, 0.5) means that 25 percent of species in state 0 and 50 percent of species in state 1 are included in the phylogeny. By default all species are assumed to be known.
pars	vector containing the MLE of the parameters.
hidden.areas	a logical indicating whether the model includes hidden areas. The default is FALSE.

<code>assume.cladogenetic</code>	a logical indicating whether the model assumes that changes occur at the nodes. The default is TRUE. Setting this to FALSE will result in a different models from GeoSSE. Please check <code>hisse::GeoHiSSE</code> for more details.
<code>condition.on.survival</code>	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
<code>root.type</code>	indicates whether root prior assumption should based the procedure described by FitzJohn et al. 2009, “madfitz”, assumed equal, “equal”, or set to user, “user”.
<code>root.p</code>	a vector indicating fixed root state probabilities. The default is NULL.
<code>aic</code>	the AIC for the model being used for the reconstruction. This is used by the plotting function. The default is NULL.
<code>verbose</code>	a logical indicating whether progress should be printed to screen. The default is TRUE.
<code>n.cores</code>	specifies the number of independent processors to conduct the analysis.. The default is NULL.

## Details

In this implementation the marginal probability of area  $i$  for a focal node is simply the overall likelihood of the tree and data when the area of the focal node is fixed in area  $i$ . Note that the likeliest tip areas can also be estimated: we observe area 1, but the underlying area could either be area 1A or 1B. Thus, for any given node or tip we traverse the entire tree as many times as there are areas in the model. As the size of the tree grows, however, these repeated tree traversals can slow the calculation down considerably. For this reason, we allow the marginal calculation to be conducted in parallel across any number of independent computer processors.

For user-specified “root.p”, you should specify the probability for each area. If you are doing a hidden model, the number of parameters will depend on the number of hidden areas included. For a two classes model there are six areas: A0, B0, AB0, A1, B1, AB1. So if you wanted to say the root had to be area A, you would specify “root.p = c(0.5, 0, 0, 0.5, 0, 0)”. There is ‘root area is A and there is an equal chance for hidden area A0 or A1’.

See help for “GeoHiSSE” for more on other parameters for this function.

## Value

MarginRecon returns an object of class `geohisse.states`. This is a list with elements:

<code>\$node.mat</code>	the marginal probabilities calculated for each node. They are ordered based on the elements in the edge matrix in “phylo” format.
<code>\$tip.mat</code>	the marginal probabilities calculated for each tip. They are ordered based on the order of tip labels in the tree.
<code>\$rate.mat</code>	a matrix that details the rates for each state combination. This is used by the plotting function.
<code>\$phy</code>	a phylogenetic tree in the “phylo” format that contains the states with the highest marginal probability at each internal node.

**Author(s)**

Jeremy M. Beaulieu

**References**

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Goldberg, E. E., L. T. Lancaster, and R. H. Ree. 2011. Phylogenetic Inference of Reciprocal Effects between Geographic Range Evolution and Diversification. *Syst. Biol.* 60:451-465.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters’ effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

**Examples**

## Need some examples here.

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MarginReconMiSSE	<i>Ancestral State Estimation based on Marginal Reconstruction for the MiSSE models.</i>
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**Description**

Estimates the likeliest states for both internal nodes and tips of a phylogeny using the marginal reconstruction algorithm.

**Usage**

```
MarginReconMiSSE(phy, f, pars, hidden.states=2,
condition.on.survival=TRUE, root.type="madfitz", root.p=NULL,
aic=NULL, verbose=TRUE, n.cores=NULL)
```

**Arguments**

- |      |  |
|------|--|
| phy  | a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.   |
| f    | the estimated proportion of extant species included in the phylogeny. A value of 0.50 means that 50 percent of species are contained in the. By default all species are assumed to be sampled. |
| pars | vector containing the MLE of the parameters.   |

<code>hidden.states</code>	a numeric indicating the number of shifts. The default is 2.
<code>condition.on.survival</code>	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
<code>root.type</code>	indicates whether root prior assumption should based the procedure described by FitzJohn et al. 2009, “madfitz”, assumed equal, “equal”, or set to user, “user”.
<code>root.p</code>	a vector indicating fixed root state probabilities. The default is NULL.
<code>aic</code>	the AIC for the model being used for the reconstruction. This is used by the plotting function. The default is NULL.
<code>verbose</code>	a logical indicating whether progress should be printed to screen. The default is TRUE.
<code>n.cores</code>	specifies the number of independent processors to conduct the analysis. The default is NULL.

### Details

In this implementation the marginal probability of state combination  $i$  for a focal node is simply the overall likelihood of the tree and data when the state of the focal node is fixed in state combination  $i$ .

See help for “MiSSE” for more on other parameters for this function.

### Value

MarginReconMiSSE returns an object of class `misse.states`. This is a list with elements:

<code>\$node.mat</code>	the marginal probabilities calculated for each node. They are ordered based on the elements in the edge matrix in “phylo” format.
<code>\$tip.mat</code>	the marginal probabilities calculated for each tip. They are ordered based on the order of tip labels in the tree.
<code>\$rate.mat</code>	a matrix that details the rates for each state combination. This is used by the plotting function.
<code>\$phy</code>	a phylogenetic tree in the “phylo” format that contains the states with the highest marginal probability at each internal node.

### Author(s)

Jeremy M. Beaulieu

### References

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.

Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters' effect on speciation and extinction. *Syst. Biol.* 56:701-710.

Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

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MarginReconMuHiSSE      *Ancestral State Estimation based on Marginal Reconstruction for the MuSSE and MuHiSSE models.*

---

### Description

Estimates the likeliest states for both internal nodes and tips of a phylogeny using the marginal reconstruction algorithm.

### Usage

```
MarginReconMuHiSSE(phy, data, f, pars, hidden.states=TRUE,
condition.on.survival=TRUE, root.type="madfitz", root.p=NULL,
aic=NULL, verbose=TRUE, n.cores=NULL)
```

### Arguments

phy	a phylogenetic tree, in ape "phylo" format and with internal nodes labeled denoting the ancestral selective regimes.
data	a matrix (or dataframe) with three columns. The first column containing the species names and the second and third containing the binary character information. Character "0" is on column 2 and character "1" is on column 3. A value of 0 means character absent and a value of 1 character present. The input of data follows a Pagel model. See 'Details'.
f	vector of length 4 with the estimated proportion of extant species in 00, 01, 10, and 11 that are included in the phylogeny. A value of c(0.50, 0.25, 0.125, 0.125) means that 50 percent of species in combination '00', 25 percent in '01' and 12.5 percent in '10' and '11'. By default all species are assumed to be sampled.
pars	vector containing the MLE of the parameters.
hidden.states	a logical indicating whether the model includes hidden states. The default is FALSE.
condition.on.survival	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
root.type	indicates whether root prior assumption should be based on the procedure described by FitzJohn et al. 2009, "madfitz", assumed equal, "equal", or set to user, "user".
root.p	a vector indicating fixed root state probabilities. The default is NULL.
aic	the AIC for the model being used for the reconstruction. This is used by the plotting function. The default is NULL.

verbose	a logical indicating whether progress should be printed to screen. The default is TRUE.
n.cores	specifies the number of independent processors to conduct the analysis.. The default is NULL.

### Details

In this implementation the marginal probability of state combination  $i$  for a focal node is simply the overall likelihood of the tree and data when the state of the focal node is fixed in state combination  $i$ . Note that the likeliest tip states can also be estimated: we observe state 00, but the underlying state could either be 00A or 00B. Thus, for any given node or tip we traverse the entire tree as many times as there are states in the model. As the size of the tree grows, however, these repeated tree traversals can slow the calculation down considerably. For this reason, we allow the marginal calculation to be conducted in parallel across any number of independent computer processors.

For user-specified “root.p”, you should specify the probability for each state combination. If you are doing a hidden model, the number of parameters will depend on the number of hidden states included. For a two classes model there are eight states: 00A, 01A, 10A, 11A, 00B, 01B, 10B, and 11B. So if you wanted to say the root had to be in state 00, you would specify “root.p = c(0.5, 0, 0, 0, 0.5, 0, 0, 0)”. There is 50 percent chance the root state is 00 and there is an equal chance for hidden state A or B.

See help for “MuHiSSE” for more on other parameters for this function.

### Value

MarginRecon returns an object of class `muhisse.states`. This is a list with elements:

<code>\$node.mat</code>	the marginal probabilities calculated for each node. They are ordered based on the elements in the edge matrix in “phylo” format.
<code>\$tip.mat</code>	the marginal probabilities calculated for each tip. They are ordered based on the order of tip labels in the tree.
<code>\$rate.mat</code>	a matrix that details the rates for each state combination. This is used by the plotting function.
<code>\$phy</code>	a phylogenetic tree in the “phylo” format that contains the states with the highest marginal probability at each internal node.

### Author(s)

Jeremy M. Beaulieu

### References

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters’ effect on speciation and extinction. *Syst. Biol.* 56:701-710.

Nakov, T., Beaulieu, J.M., and Alverson, A.J. 2018. Freshwater diatoms diversify faster than marine in both planktonic and benthic habitats. bioRxiv, doi: <https://doi.org/10.1101/406165>.

Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. Philos. Trans. R. Soc. Lond. B Biol. Sci. 344:305-311.

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 MiSSE

---

*Character-free State Speciation and Extinction*


---

## Description

Sets up and executes a MiSSE model (Missing State Speciation and Extinction) on a phylogeny.

## Usage

```
MiSSE(phy, f=1, turnover=c(1,2), eps=c(1,2), condition.on.survival=TRUE,
root.type="madfitz", root.p=NULL, sann=FALSE, sann.its=10000,
bounded.search=TRUE, max.tol=Machine$double.eps^.50, starting.vals=NULL,
turnover.upper=10000, eps.upper=3, trans.upper=100, restart.obj=NULL,
ode.eps=0)
```

## Arguments

phy	a phylogenetic tree, in ape “phylo” format and with internal nodes labeled denoting the ancestral selective regimes.
f	the estimated proportion of extant species included in the phylogeny. A value of 0.50 means that 50 percent of species are contained in the. By default all species are assumed to be sampled.
turnover	a numeric vector of length equal to the number of suspected rates in turnover. See ‘Details’.
eps	a numeric vector of length equal to the number of suspected rates in extinction fraction. See ‘Details’.
condition.on.survival	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
root.type	indicates whether root summarization follow the procedure described by FitzJohn et al. 2009, “madfitz” or Herrera-Alsina et al. 2018, “herr_als”.
root.p	a vector indicating fixed root state probabilities. The default is NULL.
sann	a logical indicating whether a two-step optimization procedure is to be used. The first includes a simulate annealing approach, with the second involving a refinement using subplex. The default is FALSE.
sann.its	a numeric indicating the number of times the simulated annealing algorithm should call the objective function.
bounded.search	a logical indicating whether or not bounds should be enforced during optimization. The default is TRUE.

<code>max.tol</code>	supplies the relative optimization tolerance to <code>subplex</code> .
<code>starting.vals</code>	a vector of starting values for the diversification parameters to be used instead of the default settings.
<code>turnover.upper</code>	sets the upper bound for the turnover parameters.
<code>eps.upper</code>	sets the upper bound for the eps parameters.
<code>trans.upper</code>	sets the upper bound for the transition rate parameters.
<code>restart.obj</code>	an object of class that contains everything to restart an optimization.
<code>ode.eps</code>	sets the tolerance for the integration at the end of a branch. Essentially if the sum of <code>compD</code> is less than this tolerance, then it assumes the results are unstable and discards them. The default is set to zero, but in testing a value of $1e-8$ can sometimes produce stable solutions for both easy and very difficult optimization problems.

## Details

One thing pointed out in the original HiSSE paper (Beaulieu & O’Meara, 2016) is that the trait-independent hisse model is basically a model for traits and a separate model for shifts in diversification parameters, much like BAMM (though without priors, discontinuous inheritance of extinction probability, or other mathematical foibles). The hidden states can drive different diversification processes, and the traits just evolve in a regular trait model. At that point, there is no harm in just dropping the trait (or analyzing separately) and just focusing on diversification driven by unknown factors. That is what this function does. It sets up and executes a completely trait-free version of a HiSSE model.

Thus, all that is required is a tree. The model allows up to 26 possible hidden states in diversification (denoted by A-Z). Transitions among hidden states are governed by a global transition rate,  $q$ . A "shift" in diversification denotes a lineage tracking some unobserved, hidden state. An interesting byproduct of this assumption is that distantly related clades can actually share the same discrete set of diversification parameters.

Note that "hidden state" is a shorthand. We do not mean that there is a single, discrete character that is solely driving diversification differences. There is some heritable "thing" that affects rates: but this could be a combination of body size, oxygen concentration, trophic level, and how many other species are competing in an area. This is true for HiSSE, but is especially important to grasp for MiSSE. It could be that there is some single discrete trait that drives everything; it’s more likely that a whole range of factors play a role, and we just slice them up into discrete categories, the same way we slice up mammals into carnivore / omnivore / herbivore or plants into woody / herbaceous when the reality is more continuous.

As with `hisse`, we employ a modified optimization procedure. In other words, rather than optimizing birth and death separately, MiSSE optimizes orthogonal transformations of these variables: we let  $\tau = \text{birth} + \text{death}$  define "net turnover", and we let  $\text{eps} = \text{death} / \text{birth}$  define the "extinction fraction". This reparameterization alleviates problems associated with overfitting when birth and death are highly correlated, but both matter in explaining the diversity pattern.

For the "root.type" option, we are currently maintaining the previous default of "madfitz". However, it was recently pointed out by Herrera-Alsina et al. (2018) that at the root, the individual likelihoods for each possible state should be conditioned prior to averaging the individual likelihoods across states. This can be set doing "herr\_als". It is unclear to us which is exactly correct, but it does



seem that both “madfitz” and “herr\_als” behave exactly as they should in the case of character-independent diversification (i.e., reduces to likelihood of tree + likelihood of trait model). We’ve also tested the behavior and the likelihood differences are very subtle and the parameter estimates in simulation are nearly indistinguishable from the “madfitz” conditioning scheme. We provide both options and encourage users to try both and let us know conditions in which the result vary dramatically under the two root implementations. We suspect they do not.

Also, note, that in the case of “root.type=user” and “root.type=equal” are no longer explicit “root.type” options. Instead, either “madfitz” or “herr\_als” are specified and the “root.p” can be set to allow for custom root options.

## Value

MiSSE returns an object of class `misse.fit`. This is a list with elements:

<code>\$loglik</code>	the maximum negative log-likelihood.
<code>\$AIC</code>	Akaike information criterion.
<code>\$AICc</code>	Akaike information criterion corrected for sample-size.
<code>\$solution</code>	a matrix containing the maximum likelihood estimates of the model parameters.
<code>\$index.par</code>	an index matrix of the parameters being estimated.
<code>\$f</code>	user-supplied sampling frequencies.
<code>\$hidden.states</code>	a logical indicating whether hidden states were included in the model.
<code>\$condition.on.survival</code>	a logical indicating whether the likelihood was conditioned on the survival of two lineages and the speciation event subtending them.
<code>\$root.type</code>	indicates the user-specified root prior assumption.
<code>\$root.p</code>	indicates whether the user-specified fixed root probabilities.
<code>\$phy</code>	user-supplied tree
<code>\$max.tol</code>	relative optimization tolerance.
<code>\$starting.vals</code>	The starting values for the optimization.
<code>\$upper.bounds</code>	the vector of upper limits to the optimization search.
<code>\$lower.bounds</code>	the vector of lower limits to the optimization search.
<code>\$ode.eps</code>	The <code>ode.eps</code> value used for the estimation.

## Author(s)

Jeremy M. Beaulieu

## References

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.

Herrera-Alsina L., van Els P., and Etienne R.S. 2018. Detecting the dependence of diversification on multiples traits from phylogenetic trees and trait data. *Systematic Biology* In press.

Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.

Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

Model averaged equilibrium frequencies

*Model average equilibrium frequencies*

### Description

Calculates the expected equilibrium frequencies under various hidden SSE models from a single model or a set of models and returns model averaged frequencies.

### Usage

```
GetModelAveEqFreqs(x, max.time, model.type="hisse", get.rates=FALSE,
rate.type="turnover", get.all.states=FALSE)
```

### Arguments

<code>x</code>	a <code>.fit</code> object, or a list of such objects. A list of model can only include models of one type.
<code>max.time</code>	a numeric value that indicates the duration of time when calculating equilibrium frequencies. (Not the maximum time that the function is allowed to run!)
<code>model.type</code>	indicates which set of models to calculate equilibrium frequencies for. Options are "hisse", "geohisse", or "muhisse"
<code>get.rates</code>	indicates whether you want model-averaged rates based on equilibrium. Default is FALSE, which means just the equilibrium frequencies are returned.
<code>rate.type</code>	if <code>get.rates=TRUE</code> , this specifies which type of rates to be returned. Default is "turnover", but options include "net.div" and "speciation".
<code>get.all.states</code>	indicates that you would like the equilibrium frequencies to be output for all observed and hidden state combinations. Note that under this option, the frequencies cannot be averaged across models.

### Details

Provides a data frame model-averaged equilibrium frequencies across a set of models. If, for example, you give it a single `geohisse.fit` object, it uses that; if you give it a list of them, it will model-average the results. The purpose of this approach is dealing with mixed signals among hidden states with respect to the observed states. We discuss this in detail in Caetano et al (2018).

Note, that this function does not work for model fits obtained from `fGeoHiSSE`. This will provided in the next version.

**Author(s)**

Jeremy M. Beaulieu

**References**

Caetano, D.S., B.C. O'Meara, and J.M. Beaulieu. 2018. Hidden state models improve state-dependent diversification approaches, including biogeographic models. *Evolution*, 72:2308-2324.

---

Model averaged rates    *Model average rates at tips and nodes*

---

**Description**

Summarizes reconstructions from a single model or a set of models and returns model averaged rates.

**Usage**

```
GetModelAveRates(x, AIC.weights=NULL, type=c("tips", "nodes", "both"),
bound.par.matrix=cbind(c(0,-1000,0,0,0),c(1000,1000,1000,3,1000)) )
```

**Arguments**

<code>x</code>	a <code>hisse.states</code> object, a <code>hisse.states.geosse</code> object, a <code>muhisse.states</code> or a list of such objects. A list of model can only include models of one type.
<code>AIC.weights</code>	a numeric vector with length equal to the number of models in the list 'x'. This is the AICw for each of the models to be averaged. If 'AIC.weights==NULL' (the default value) then function will compute the AICw for the models in the set from the \$aic value for each model.
<code>type</code>	one of "tips", "nodes", or "both" (the default). This controls whether only the averaged rates for the tips, nodes or both should be returned. If tips or nodes is chosen the output will be a matrix and if both are returned the output will be a list.
<code>bound.par.matrix</code>	A numeric matrix with exactly 5 rows and 2 columns to set the limits for the model parameters. First column is the minimum value and second column is the maximum value (both inclusive). The rows are the model parameter in this fixed order: turnover, net diversification, speciation, extinction fraction, and extinction.

**Details**

Provides a data frame model-averaged rates for all possible configurations of the model parameters (i.e., turnover, net.div, speciation, extinction, or extinction.fraction), either for all tips or for all nodes. As with the plotting function, if you give a single `hisse.state` object, it uses that, and the rates account for uncertainty in the marginal probabilities of the states; if you give it a list of them,

it will model-average the results (it assumes the trees are the same) in addition to accounting for uncertainty in the marginal probabilities at tips and nodes. If 'AIC.weights==NULL', then the models in the set do not require the '\$aic' element to compute the AICw. Otherwise the function will return an error message.

### Author(s)

Jeremy M. Beaulieu

### References

Beaulieu, J.M, and B.C. O'Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.

---

MuHiSSE

*Multicharacter Hidden State Speciation and Extinction*

---

### Description

Sets up and executes a MuHiSSE model (Multicharacter Hidden State Speciation and Extinction) on a phylogeny and character distribution.

### Usage

```
MuHiSSE(phy, data, f=c(1,1,1,1), turnover=c(1,2,3,4), eps=c(1,2,3,4),
hidden.states=FALSE, trans.rate=NULL, condition.on.survival=TRUE,
root.type="madfitz", root.p=NULL, sann=FALSE, sann.its=10000,
bounded.search=TRUE, max.tol=.Machine$double.eps^.50, starting.vals=NULL,
turnover.upper=10000, eps.upper=3, trans.upper=100, restart.obj=NULL,
ode.eps=0)
```

### Arguments

phy	a phylogenetic tree, in ape "phylo" format and with internal nodes labeled denoting the ancestral selective regimes.
data	a matrix (or dataframe) with three columns. The first column containing the species names and the second and third containing the binary character information. Character "0" is on column 2 and character "1" is on column 3. A value of 0 means character absent and a value of 1 character present. The input of data follows a Pagel model. See 'Details'.
f	vector of length 4 with the estimated proportion of extant species in 00, 01, 10, and 11 that are included in the phylogeny. A value of c(0.50, 0.25, 0.125, 0.125) means that 50 percent of species in combination '00', 25 percent in '01' and 12.5 percent in '10' and '11'. By default all species are assumed to be sampled.

turnover	a numeric vector of length equal to $4+(\text{number of hidden.states} * 4)$ . A MuSSE model has 4 speciation parameters: <code>lambda00</code> , <code>lambda01</code> , <code>lambda10</code> , and <code>lambda11</code> . A MuHiSSE model with one hidden states has 8 speciation parameters: <code>lambda0A</code> , <code>s1A</code> , <code>s01A</code> , <code>s0B</code> , <code>s1B</code> , <code>s01B</code> . And so on. The length of the numeric vector needs to match the number of speciation parameters in the model. See 'Details'.
eps	a numeric vector of length equal to $4+(\text{number of hidden.states} * 4)$ . A MuSSE model has 4 extinction parameters: <code>mu00</code> , <code>mu01</code> , <code>mu10</code> , and <code>mu11</code> . A MuHiSSE model with one hidden state has 8 extinction parameters: <code>mu00A</code> , <code>mu01A</code> , <code>mu10A</code> , <code>mu11A</code> , <code>mu00B</code> , <code>mu01B</code> , <code>mu10B</code> , and <code>mu11B</code> . And so on. The length of the numeric vector needs to match the number of extinction parameters in the model. See 'Details'.
hidden.states	a logical indicating whether the model includes a hidden states. The default is FALSE.
trans.rate	provides the transition rate model. See function <code>TransMatMakerMuHiSSE</code> .
condition.on.survival	a logical indicating whether the likelihood should be conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
root.type	indicates whether root summarization follow the procedure described by FitzJohn et al. 2009, "madfitz" or Herrera-Alsina et al. 2018, "herr_als".
root.p	a vector indicating fixed root state probabilities. The default is NULL.
sann	a logical indicating whether a two-step optimization procedure is to be used. The first includes a simulate annealing approach, with the second involving a refinement using <code>subplex</code> . The default is FALSE.
sann.its	a numeric indicating the number of times the simulated annealing algorithm should call the objective function.
bounded.search	a logical indicating whether or not bounds should be enforced during optimization. The default is TRUE.
max.tol	supplies the relative optimization tolerance to <code>subplex</code> .
starting.vals	a vector of starting values for the diversification parameters to be used instead of the default settings.
turnover.upper	sets the upper bound for the turnover parameters.
eps.upper	sets the upper bound for the eps parameters.
trans.upper	sets the upper bound for the transition rate parameters.
restart.obj	an object of class that contains everything to restart an optimization.
ode.eps	sets the tolerance for the integration at the end of a branch. Essentially if the sum of <code>compD</code> is less than this tolerance, then it assumes the results are unstable and discards them. The default is set to zero, but in testing a value of $1e-8$ can sometimes produce stable solutions for both easy and very difficult optimization problems.

## Details

This function sets up and executes a multiple state HiSSE model. The model allows up to 8 hidden categories (hidden states A-H), and implements a more efficient means of carrying out the branch calculation. Specifically, we break up the tree into carry out all descendent branch calculations simultaneously, combine the probabilities based on their shared ancestry, then repeat for the next set of descendents. In testing, we've found that as the number of taxa increases, the calculation becomes much more efficient. In future versions, we will likely allow for multicore processing of these calculations to further improve speed. We also note that there is vignette tha describes more details for running this particular function.

As for data file format, MuHiSSE expects a three column matrix or data frame, with the first column containing the species names and the second and third containing the binary character information. Note that the order of the data file and the names in the “phylo” object need not be in the same order; MuHiSSE deals with this internally. Also, the character information must be coded as 0 and 1, otherwise, the function will misbehave. However, if the state for a species is unknown for either character, a user can specify this with a 2, and the state will be considered maximally ambiguous for all relevant character combinations. For example, if character 1 is in state 0, but character 2 is provided a 2, then the program provides a probability of 1 for 00 and a probability of for 01.

As with *hisse*, we employ a modified optimization procedure. In other words, rather than optimizing birth and death separately, MuHiSSE optimizes orthogonal transformations of these variables: we let  $\tau = \text{birth} + \text{death}$  define “net turnover”, and we let  $\epsilon = \text{death} / \text{birth}$  define the “extinction fraction”. This reparameterization alleviates problems associated with overfitting when birth and death are highly correlated, but both matter in explaining the diversity pattern.

To setup a model, users input vectors containing values to indicate how many free parameters are to be estimated for each of the variables in the model. This is done using the `turnover` and `extinct.frac` parameters. One needs to specify a value for each of the parameters of the model, when two parameters show the same value, then the parameters are set to be linked during the estimation of the model. For example, a MuHiSSE model with 1 hidden state and all free parameters has `turnover = 1:8`. The same model with turnover rates constrained to be the same for all hidden states has `turnover = c(1, 2, 3, 4, 1, 2, 3, 4)`. This same format applies to `extinct.frac`.

The “`trans.rate`” input is the transition model and has an entirely different setup than speciation and extinction rates. See `TransMatMakerMuHiSSE` function for more details.

For user-specified “`root.p`”, you should specify the probability for each state combination. If you are doing a hidden model, there will be eight state combinations: 00A, 01A, 10A, 11A, 00B, 01B, 10B, 11B. So if you wanted to say the root had to be in state 00, and since you do not know the hidden state, you would specify “`root.p = c(0.5, 0, 0, 0, 0.5, 0, 0, 0)`”. In other words, the root has a 50% chance to be in one of the states to be 00A or 00B.

For the “`root.type`” option, we are currently maintaining the previous default of “`madfitz`”. However, it was recently pointed out by Herrera-Alsina et al. (2018) that at the root, the individual likelihoods for each possible state should be conditioned prior to averaging the individual likelihoods across states. This can be set doing “`herr_als`”. It is unclear to us which is exactly correct, but it does seem that both “`madfitz`” and “`herr_als`” behave exactly as they should in the case of character-independent diversification (i.e., reduces to likelihood of tree + likelihood of trait model). We've also tested the behavior and the likelihood differences are very subtle and the parameter estimates in simulation are nearly indistinguishable from the “`madfitz`” conditioning scheme. We provide both options and encourage users to try both and let us know conditions in which the result vary dramatically under the two root implementations. We suspect they do not.

Also, note, that in the case of “root.type=user” and “root.type=equal” are no longer explicit “root.type” options. Instead, either “madfitz” or “herr\_als” are specified and the “root.p” can be set to allow for custom root options.

### Value

MuHiSSE returns an object of class `muhisse.fit`. This is a list with elements:

<code>\$loglik</code>	the maximum negative log-likelihood.
<code>\$AIC</code>	Akaike information criterion.
<code>\$AICc</code>	Akaike information criterion corrected for sample-size.
<code>\$solution</code>	a matrix containing the maximum likelihood estimates of the model parameters.
<code>\$index.par</code>	an index matrix of the parameters being estimated.
<code>\$f</code>	user-supplied sampling frequencies.
<code>\$hidden.states</code>	a logical indicating whether hidden states were included in the model.
<code>\$condition.on.survival</code>	a logical indicating whether the likelihood was conditioned on the survival of two lineages and the speciation event subtending them.
<code>\$root.type</code>	indicates the user-specified root prior assumption.
<code>\$root.p</code>	indicates whether the user-specified fixed root probabilities.
<code>\$phy</code>	user-supplied tree
<code>\$data</code>	user-supplied dataset
<code>\$trans.matrix</code>	the user-supplied transition matrix
<code>\$max.tol</code>	relative optimization tolerance.
<code>\$starting.vals</code>	The starting values for the optimization.
<code>\$upper.bounds</code>	the vector of upper limits to the optimization search.
<code>\$lower.bounds</code>	the vector of lower limits to the optimization search.
<code>\$ode.eps</code>	The <code>ode.eps</code> value used for the estimation.

### Author(s)

Jeremy M. Beaulieu

### References

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Herrera-Alsina L., van Els P., and Etienne R.S. 2018. Detecting the dependence of diversification on multiples traits from phylogenetic trees and trait data. *Systematic Biology* In press.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.

Nakov, T., Beaulieu, J.M., and Alverson, A.J. 2018. Freshwater diatoms diversify faster than marine in both planktonic and benthic habitats. bioRxiv, doi: <https://doi.org/10.1101/406165>.

Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. Philos. Trans. R. Soc. Lond. B Biol. Sci. 344:305-311.

---

plot.geohisse.states *Plotting function geohisse.states objects*

---

## Description

A plotting function for visualizing changes in states and rates over a phylogeny

## Usage

```
## S3 method for class 'geohisse.states'
plot(x, rate.param = "net.div", type = "fan",
     show.tip.label = TRUE, fsize = 1.0, legend = TRUE, ...)
```

## Arguments

x	a hisse.states object or a list of such objects.
rate.param	indicates the type of rates to plot. Options include: “turnover”, “net.div”, “speciation”, “extinction”, “extinction.fraction”.
type	a character string specifying the type of phylogeny to be drawn. Options are “fan” (default) or “phylogram”.
show.tip.label	a logical indicating whether tip names should be included. Default is TRUE
fsize	sets the font size for the tip labels.
legend	indicates if the legend is to be plotted. TRUE or FALSE.
...	Additional parameters to control the plot. See “Details”.

## Details

Additional parameters can be defined using “...”:

“do.observed.only” is a logical indicating whether just the states should be plotted; for now, only TRUE works. “rate.colors” are user specified colors to be used for coloring rates. “state.colors” are user specified colors to be used for coloring states. A vector with the color for state 1 (endemic area '0'), state 2 (endemic area '1') and state 0 (widespread area '01'). Always in this order! “edge.width” is the width of the branches of the phylogeny. “width.factor” is the factor multiplying the “edge.width” to get the width of the branch for the states tree. Needs to be a numeric value between 0 and 1. “rate.range” is an optional two element vector. If present, specifies the range of rate values to use for plotting. “lims.percentage.correction” deals with cases where the limits are slightly smaller than the values due to imprecision issues. “legend.position” are the coordinates for placing the legend. “legend.cex” is the text size inside the legend. “legend.kernel” lets you specify the way the density plot or histogram is made for rates. A value of “auto” chooses what we think is the best option given your data, “hist” makes a histogram, “rectangular”, “gaussian”, and



others make a density plot. See `?density` for all non-“hist” options. “legend.bg” sets the color for the legend background. “mar” sets the margins for the plot. See more information in `'help(par)'`. “outline” is whether to plot an outline on the branches of the tree. Choose the color of the outline using the parameter `outline.color`. “outline.color” is the color for the outline. Defaults to “black”. “swap.underscore” sets whether to substitute all “\_” with “ ” on the labels for the tips.

This function is very similar to the `hisse::plot.hisse.states` function. See more details in help page for `hisse::plot.hisse.states` function.

### Author(s)

Brian O’Meara and Daniel Caetano

### References

Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.

---

plot.hisse.states      *Plotting function hisse.states objects*

---

### Description

A plotting function for visualizing changes in states and rates over a phylogeny

### Usage

```
## S3 method for class 'hisse.states'
plot(x, rate.param = "net.div", type = "fan",
     show.tip.label = TRUE, fsize = 1.0, legend = "tips", ...)
```

### Arguments

<code>x</code>	a <code>hisse.states</code> object or a list of such objects.
<code>rate.param</code>	indicates the type of rates to plot. Options include: “turnover”, “net.div”, “speciation”, “extinction”, “extinction.fraction”. The default is “net.div”.
<code>type</code>	a character string specifying the type of phylogeny to be drawn. Options are “fan” (default) or “phylogram”.
<code>show.tip.label</code>	a logical indicating whether tip names should be included.
<code>fsize</code>	sets the font size for the tip labels.
<code>legend</code>	indicates the type of legend. Options include: “none”, “traditional”, “tips”, “internal”, “all”.
<code>...</code>	Additional parameters to control the plot. See “Details”.

## Details

Provides phylogeny that shows a heat map of the diversification rate parameter you specify (which could be turnover, net.div, speciation, extinction, or extinction.fraction). The discrete state reconstruction appears as lines on top of the heat map. If you give a single `hisse.state` object, it uses that; if you give it a list of them, it will model-average the results (it assumes the trees are the same). Colors can be specified by sending a vector of colors to `rate.colors` or `state.colors` (the defaults are red to blue for rate and white to black for state). You can specify two or more colors: `c("red", "gray", "blue")` for example. By default the visualization uses the minimum rate on the tree for the minimum color, and the maximum rate for the maximum color, but you may want to use the same color scale across models, even if some of them have a smaller range than others. To do this, pass a vector with the minimum and maximum rate across all models to the visualization for all models and they will use the same scale. There are many options for adding a legend. A traditional legend showing what values a color corresponds to is “traditional”, like what `plotSimmap` will show in `phytools`. However, we can also use the legend to show the distribution of values, rather than just a key to color. “tips” shows a density plot of states or rates at tips, “internal” a distribution at internal nodes, and “all” at all nodes in the tree. For the density or histogram plots, you can let the package pick the best visualization or choose yourself whether to use a histogram or density plot, and if the latter, what kernel you want. The legend can be moved around the overall tree plot by using “`legend.position`”: this is a vector that specifies the “`fig`” argument to “`par`”: `c(x1, x2, y1, y2)`, where the values are the starting and ending positions as a fraction of the overall plot. By default, the legend starts at the lower left corner and continues up 20 the rest of the plot (`c(0, 0.2, 0, 0.2)`): by changing values, you can make the legend larger or smaller and change its position. The heatmap code is modified slightly from Liam Revell’s `phytools` package.

Additional parameters to control the plot: “`do.observed.only`” is a logical indicating whether just the states should be plotted; for now, only TRUE works. “`rate.colors`” sets user specified colors to be used for coloring rates. “`state.colors`” sets user specified colors to be used for coloring states. “`edge.width`” sets the width of the branches of the phylogeny. “`width.factor`” is the factor multiplying the `edge.width` to get the width of the branch for the states tree. Needs to be a numeric value between 0 and 1. “`rate.range`” is an optional two element vector. If present, specifies the range of rate values to use for plotting. “`lims.percentage.correction`” deals with cases where the limits are slightly smaller than the values due to imprecision issues. “`legend.position`” are the coordinates for placing the legend. “`legend.cex`” is the text size inside the legend. “`legend.kernel.rates`” used for `legend=tips`, `internal`, or `all`, lets you specify the way the density plot or histogram is made for rates. “`auto`” chooses what we think is the best option given your data, “`hist`” makes a histogram, “`rectangular`”, “`gaussian`”, and others make a density plot. See `?density` for all non-“`hist`” options. “`legend.kernel.states`” is as above, for states. “`legend.bg`” sets the color for the legend background. “`mar`” sets the margins for the plot. See more information in `'help(par)'`. “`outline`” sets whether to plot an outline on the branches of the tree. Choose the color of the outline using the parameter `outline.color`. “`outline.color`” sets the color for the outline. Defaults to “`black`”. “`swap.underscore`” defines whether to substitute all “`_`” with “” on the labels for the tips.

## Author(s)

Brian O’Meara and Daniel Caetano

## References

Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.

---

plot.misse.states      *Plotting function geohisse.states objects*

---

## Description

A plotting function for visualizing changes in states and rates over a phylogeny

## Usage

```
## S3 method for class 'misse.states'
plot(x, rate.param = "net.div", type = "fan",
     show.tip.label = TRUE, fsize = 1.0, legend = "tips", ...)
```

## Arguments

x	a misse.states object or a list of such objects.
rate.param	indicates the type of rates to plot. Options include: “turnover”, “net.div”, “speciation”, “extinction”, “extinction.fraction”.
type	a character string specifying the type of phylogeny to be drawn. Options are “fan” (default) or “phylogram”.
show.tip.label	a logical indicating whether tip names should be included. Default is TRUE
fsize	sets the font size for the tip labels.
legend	indicates if the legend is to be plotted. TRUE or FALSE.
...	Additional parameters to control the plot. See “Details”.

## Details

Additional parameters can be defined using “...”:

“do.observed.only” is a logical indicating whether just the states should be plotted; for now, only TRUE works. “rate.colors” are user specified colors to be used for coloring rates. “state.colors” are user specified colors to be used for coloring states. A vector with the color for states 00, 01, 10, and 11 (in this order). “edge.width” is the width of the branches of the phylogeny. “width.factor” is the factor multiplying the “edge.width” to get the width of the branch for the states tree. Needs to be a numeric value between 0 and 1. “rate.range” is an optional two element vector. If present, specifies the range of rate values to use for plotting. “lims.percentage.correction” deals with cases where the limits are slightly smaller than the values due to imprecision issues. “legend.position” are the coordinates for placing the legend. “legend.cex” is the text size inside the legend. “legend.kernel” lets you specify the way the density plot or histogram is made for rates. A value of “auto” chooses what we think is the best option given your data, “hist” makes a histogram, “rectangular”, “gaussian”, and others make a density plot. See ?density for all non-“hist” options. “legend.bg” sets the color for the legend background. “mar” sets the margins for the plot. See more information in

'help(par)'. "outline" is whether to plot an outline on the branches of the tree. Choose the color of the outline using the parameter outline.color. "outline.color" is the color for the outline. Defaults to "black". "swap.underscore" sets whether to substitute all "\_" with " " on the labels for the tips.

This function is very similar to the hisse::plot.hisse.states function. See more details in help page for hisse::plot.hisse.states function.

### Author(s)

Brian O'Meara and Daniel Caetano

### References

Beaulieu, J.M, and B.C. O'Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. Syst. Biol. 65:583-601.

---

plot.muhisse.states     *Plotting function muhisse.states objects*

---

### Description

A plotting function for visualizing changes in states and rates over a phylogeny

### Usage

```
## S3 method for class 'muhisse.states'
plot(x, rate.param = "net.div", type = "fan",
      show.tip.label = TRUE, fsize = 1.0, legend = TRUE, ...)
```

### Arguments

x	a muhisse.states object or a list of such objects.
rate.param	indicates the type of rates to plot. Options include: "turnover", "net.div", "speciation", "extinction", "extinction.fraction".
type	a character string specifying the type of phylogeny to be drawn. Options are "fan" (default) or "phylogram".
show.tip.label	a logical indicating whether tip names should be included. Default is TRUE
fsize	sets the font size for the tip labels.
legend	indicates if the legend is to be plotted. TRUE or FALSE.
...	Additional parameters to control the plot. See "Details".

**Details**

Additional parameters can be defined using "...":

"do.observed.only" is a logical indicating whether just the states should be plotted; for now, only TRUE works. "rate.colors" are user specified colors to be used for coloring rates. "state.colors" are user specified colors to be used for coloring states. A vector with the color for states 00, 01, 10, and 11 (in this order). "edge.width" is the width of the branches of the phylogeny. "width.factor" is the factor multiplying the "edge.width" to get the width of the branch for the states tree. Needs to be a numeric value between 0 and 1. "rate.range" is an optional two element vector. If present, specifies the range of rate values to use for plotting. "lims.percentage.correction" deals with cases where the limits are slightly smaller than the values due to imprecision issues. "legend.position" are the coordinates for placing the legend. "legend.cex" is the text size inside the legend. "legend.kernel" lets you specify the way the density plot or histogram is made for rates. A value of "auto" chooses what we think is the best option given your data, "hist" makes a histogram, "rectangular", "gaussian", and others make a density plot. See ?density for all non-"hist" options. "legend.bg" sets the color for the legend background. "mar" sets the margins for the plot. See more information in 'help(par)'. "outline" is whether to plot an outline on the branches of the tree. Choose the color of the outline using the parameter outline.color. "outline.color" is the color for the outline. Defaults to "black". "swap.underscore" sets whether to substitute all "\_" with " " on the labels for the tips.

This function is very similar to the `hisse::plot.hisse.states` function. See more details in help page for `hisse::plot.hisse.states` function.

**Author(s)**

Brian O'Meara and Daniel Caetano

**References**

Beaulieu, J.M, and B.C. O'Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.

---

SimToPhylo

*Convert simulated result to a tree*

---

**Description**

Converts the \$results element of the return to a phylo object

**Usage**

```
SimToPhylo(results, include.extinct=FALSE, drop.stem=TRUE)
```

**Arguments**

results	dataframe of results from SimulateHisse.
include.extinct	include (TRUE) or delete (FALSE) extinct terminal taxa.
drop.stem	include the lineage leading to the first saved speciation even (FALSE) or cull it (TRUE).

**Details**

This takes the `$results` object from a `SimulateHisse` run and converts it to an ape phylo object. If there are no taxa on the final tree, it returns NA; if there is one taxon, it returns a one taxon tree. This is behavior different from `diversitree`'s tree simulators, which returns NULL in both the zero and one taxon case. Extinct taxa can be pruned or not. For simulations starting with one taxon, and/or for simulations with some extinction, the final tree can have a time when there is a single lineage before it radiates into the crown group. This stem can be included or not. The tip states are stored in `$tip.state` in the returned tree.

**Value**

phylo                    a phylo object in cladewise order.

**Author(s)**

Brian O'Meara

**References**

Beaulieu, J.M, and B.C. O'Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.

**Examples**

```
simulated.result <- SimulateHisse(c(.3, .1), c(.1, 0),
matrix(c(NA, 0.2, .3, NA), nrow=2), max.taxa=35, x0=1)
par(mfcol=c(1,2))
plot(SimToPhylo(simulated.result$results, include.extinct=TRUE))
plot(SimToPhylo(simulated.result$results, include.extinct=FALSE))
```

---

SimulateGeoHiSSE

*Simulate under a GeoHiSSE model*

---

**Description**

Simulation function for the GeoHiSSE model

**Usage**

```
SimulateGeoHiSSE(pars, hidden.areas=1, x0="0A", max.taxa=Inf,
max.time=Inf, add.jumps=FALSE, add.extinction=FALSE,
include.extinct=FALSE, return.GeoHiSSE_pars=FALSE,
override.safeties=FALSE)
```

**Arguments**

<code>pars</code>	an object of class "GeoHiSSE_pars" generated by SimulateGeoHiSSE. See 'Details'.
<code>hidden.areas</code>	number of hidden areas in the model. Default is 1.
<code>x0</code>	a character value for the starting state. Default is "01A".
<code>max.taxa</code>	have the simulation stop at <code>max.taxa</code> surviving taxa.
<code>max.time</code>	have the simulation stop at <code>max.time</code> height (including stem).
<code>return.GeoHiSSE_pars</code>	whether to (only) return a "GeoHiSSE_pars" object in the correct format to use in this function. See 'Details'.
<code>add.jumps</code>	whether to include jump dispersals in the model. Both for returning the parameters of the model and model estimation. Default is FALSE.
<code>add.extinction</code>	whether to separate extirpation and extinction of endemic lineages. Both for returning the parameters of the model and model estimation. Default is FALSE.
<code>include.extinct</code>	whether the simulation should keep extinct lineages. Default is FALSE.
<code>override.safeties</code>	simulate even if there is no limit on number of taxa or depth of tree.

**Details**

This function uses `diversitree::tree.classe` function to simulate the tree under the GeoSSE model with hidden areas. The parameter `pars` is a list of class "GeoHiSSE\_pars" that can be generated using this same function. The best way is to first run `SimulateGeoHiSSE` with empty parameters and `return.GeoHiSSE_pars=TRUE` and with `hidden.areas` equal to the number of desired hidden areas in the model. This will return an object in list format with a set of four matrices. Each matrix controls a different set of parameters of the model. All parameters are set to 0 and parameters not used by the model are set to NA. To prepare the simulation, edit these matrices and change the desired parameter values. Leaving a parameter equal to 0 is the same as reducing the model by eliminating this parameter of the model.

**Value**

This returns a list, with the following elements:

<code>\$phy</code>	a phylogeny of class <code>phylo</code> .
<code>\$data</code>	a data matrix with the species names as the first column and the ranges (in 0, 1, and 2 format) as the second column.
<code>\$hidden.areas</code>	a named vector with the 'true' simulated ranges (include the hidden area information).
<code>\$sim.attempts</code>	number of times that the simulation tried before reaching desired termination condition.
<code>\$pars</code>	the parameters used for the simulation.
<code>\$classe.pars</code>	the parameters in 'make.classe' format for the 'diversitree' package.

**Author(s)**

Daniel Caetano

**Examples**

```
## Not run:
## Get the a list with the correct parameters to run the simulation:
pars <- SimulateGeoHiSSE(hidden.areas=1, return.GeoHiSSE_pars=TRUE)
## Edit the parameter values:
pars$model.pars[1:3,] <- 0.1
pars$model.pars[4:5,] <- 0.05
pars$model.pars[6:7,] <- 0.01
pars$q.01[1,2] <- pars$q.01[2,1] <- 0.01
pars$q.1[1,2] <- pars$q.1[2,1] <- 0.02
pars$q.2[1,2] <- pars$q.2[2,1] <- 0.02
## Run the simulation:
sim <- SimulateGeoHiSSE(pars=pars, hidden.areas=1, x0="01A", max.taxa=100)

## End(Not run)
```

---

 SimulateHisse

*Simulate under a HiSSE model*


---

**Description**

Flexible simulation function allowing checkpointing

**Usage**

```
SimulateHisse(turnover.rates, eps.values, transition.rates, max.taxa=Inf, max.t=Inf,
max.wall.time=Inf, x0, nstart=1, checkpoint.file=NULL, checkpoint.frequency=100,
checkpoint.start.object=NULL, override.safeties=FALSE)
```

**Arguments**

<code>turnover.rates</code>	a vector of turnover rates.
<code>eps.values</code>	a vector of extinction fractions.
<code>transition.rates</code>	a matrix of transition rates.
<code>max.taxa</code>	have the simulation stop at <code>max.taxa</code> surviving taxa.
<code>max.t</code>	have the simulation stop at <code>max.t</code> height (including stem).
<code>max.wall.time</code>	have the simulation stop at this many seconds of running.
<code>x0</code>	the starting state.
<code>nstart</code>	how many taxa you want to start from. Usual values are 1 (start with single lineage) or 2 (crown group).



`checkpoint.file`  
if you want to save progress (so you can restart from last saved point) include the name of a file.

`checkpoint.frequency`  
if there is a checkpoint file, frequency (in terms of number of steps: births, deaths, or transitions) at which this is saved.

`checkpoint.start.object`  
if you are starting from a `checkpointed.file`, the object loaded from that file. Typically called `checkpoint.result`.

`override.safeties`  
simulate even if there is no limit on number of taxa, depth of tree, or wall time.

## Details

Note that currently, the simulator assumes `turnover.rates`, `eps.values`, and `transition.rates` are in the same state order. Remember that `turnover.rates` are birth + death rates, and `eps.values` are death / birth rates.

We strongly advise putting some limits to stop the run. These can be any combination of `max.taxa`, `max.t`, and `max.wall.time`. For example, you could set up the run to stop when you hit 1000 taxa or 3600 seconds (one hour) of running on your computer, whichever comes first. If you want to run with no limits, you have to specify `override.safeties=TRUE`, and you should know what you're doing here (the runs might never finish). There is only one starting state ( $x_0$ ), which should be the index into the rate vectors, starting with 0: that is, if your states are 0A, 0B, 1A, and 1B,  $x_0=0$  would start in 0A,  $x_0=3$  would start in 1B. `nstart` lets you choose how many taxa to start with: it could be one lineage to start from a single taxon, in which case you'll have to wait some time for the first speciation event, or you could start with two, to start simulation with a clade of this size (though, if extinction is nonzero, you are not guaranteed to have the final crown group include both of these descendants). You can choose numbers higher than two, to start with, say, a 50-species polytomy. We're not sure why you would. You can add checkpointing: runs take a long time, and if it crashes, this will let you start from the same point in the last saved file (though with a different seed, unless you specify this yourself). If you want to save checkpoints as you go along, specify a file in `checkpoint.file`. Every `checkpoint.frequency` events, where an event is a speciation, extinction, or transition event, it will save current progress to a file. The smaller this value, the more frequently the simulation will be saved: fewer lost steps if you have to re-simulate, but slower during the run because it spends time writing to disk. If you want to start from a checkpointed analysis, load the file into R and then specify the object within R [not the file] containing the checkpointed results (by default, saved in an object called `checkpoint.result`) and the simulation will continue from that point.

Results are returned in a list, containing a dataframe with the outcome of the simulation (one row per edge in the tree, and containing information on the lengths, ancestor, tipward height from the original root, and state at the tipward end of the edge (you can get state at the rootward end by getting the tipward state of the ancestral edge). It may be of interest to know how many events of each type occurred, which is saved in `$birth.counts`, `$death.counts`, `$transition.counts`. The total number of surviving taxa is stored in `$n.surviving`.

The output can be returned as an ape phylo tree by passing the `$results` element of the final output to `SimToPhylo()`.

**Value**

This returns a list, with the following elements:

<code>\$results</code>	a dataframe containing the simulation output: states at nodes and tips, ancestor-descendant pairs, branch lengths.
<code>\$birth.counts</code>	a vector, in the same state order as <code>turnover.rates</code> et al., that includes the counts for the number of times species in each state speciated.
<code>\$death.counts</code>	same as <code>birth.counts</code> , but counting extinction events in each state.
<code>\$transition.counts</code>	matrix of counts of transitions from one state to another.
<code>\$n.surviving</code>	the number of taxa alive at the end of the simulation.

**Author(s)**

Brian O’Meara

**References**

Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.

**Examples**

```
simulated.result <- SimulateHisse(c(.3, .1), c(.1, 0),
matrix(c(NA, 0.2, .3, NA), nrow=2), max.taxa=35, x0=1)
par(mfcol=c(1,2))
plot(SimToPhylo(simulated.result$results, include.extinct=TRUE))
plot(SimToPhylo(simulated.result$results, include.extinct=FALSE))
```

---

SupportRegion

*Adaptive Sampling of the Likelihood Surface*

---

**Description**

Adaptively samples points for each parameter to obtain an estimate of the confidence intervals.

**Usage**

```
SupportRegion(hisse.obj, n.points=1000, scale.int=0.1, desired.delta=2,
min.number.points=10, output.type="turnover", hidden.states=TRUE,
condition.on.survival=TRUE, root.type="madfitz", root.p=NULL, verbose=TRUE)
```

**Arguments**

<code>hisse.obj</code>	an object of class <code>hisse.fit</code> that contains the MLE from a model run.
<code>n.points</code>	indicates the number of points to sample.
<code>scale.int</code>	the scaling multiplier that defines interval to randomly sample. By default the value is set to 0.1, meaning that values are drawn at random along an interval that encompasses 10 percent above and below the MLE.
<code>desired.delta</code>	defines the number $\ln L$ units away from the MLE to include. By default the value is set to 2.
<code>min.number.points</code>	sets the minimum number of points that can be returned. By default the value is set to 10.
<code>output.type</code>	indicates whether the rates should be printed onscreen as the optimized variables, “turnover”, transformed to reflect net diversification, “net.div”, or transformed to reflect $\lambda$ and $\mu$ , “raw”.
<code>hidden.states</code>	a logical indicating whether the model includes a hidden state. The default is TRUE.
<code>condition.on.survival</code>	a logical indicating whether the likelihood was conditioned on the survival of two lineages and the speciation event subtending them (Nee et al. 1994). The default is TRUE.
<code>root.type</code>	indicates whether root prior assumption should be based on the procedure described by FitzJohn et al. 2009, “madfitz”, assumed equal, “equal”, or set to user, “user”.
<code>root.p</code>	a vector indicating fixed root state probabilities. The default is NULL.
<code>verbose</code>	a logical indicating whether progress should be printed to the screen. The default is TRUE.

**Details**

This function provides a means for sampling the likelihood surface quickly to estimate confidence intervals that reflect the uncertainty in the MLE. The function starts with the MLE from the `hisse` run. It then uses a scaling multiplier to generate an interval by which to randomly alter each parameter. However, the algorithm was designed to “feel” the boundaries of the random search. In other words, when the algorithm begins to sample the hinterlands of the surface, it will know to restrict the boundary to allow sampling of more reasonable values based on the currently sampled set. The goal of this sampling process is to find points within some desired distance from the MLE; by default we assume this distance is  $2 \ln L$ . The confidence interval can be estimated directly from these points. The full set of points tried are also provided and can be used to generate contour plots (though, it is not entirely straightforward to do so – but certainly doable).

Note the `scale.int` option. This roughly sets the variance for sampling points. If this seems to take a long while to find enough points within the desired likelihood region consider reducing `scale.int` to either 0.05 or, in some cases, 0.01.

**Value**

`SupportRegion` returns an object of class `hisse.support`. This is a list with elements:

`$ci` the sampled confidence interval.  
`$points.within.region` the sampled points that within  $2\ln L$  units from the MLE.  
`$all.points` all points sampled by the adaptive sampler.

**Author(s)**

Jeremy M. Beaulieu

**References**

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

---

SupportRegionGeoSSE *Adaptive Sampling of the Likelihood Surface under GeoSSE*

---

**Description**

Adaptively samples points for each parameter to obtain an estimate of the confidence intervals.

**Usage**

```
SupportRegionGeoSSE(geohisse.obj, n.points=1000, scale.int=0.1, desired.delta=2,
min.number.points=10, verbose=TRUE)
```

**Arguments**

`geohisse.obj` an object of class `geohisse.fit` that contains the MLE from a model run.

`n.points` indicates the number of points to sample.

`scale.int` the scaling multiplier that defines interval to randomly sample. By default the value is set to 0.1, meaning that values are drawn at random along an interval that encompasses 10 percent above and below the MLE.

`desired.delta` defines the number  $\ln L$  units away from the MLE to include. By default the value is set to 2.

`min.number.points` sets the minimum number of points that can be returned. By default the value is set to 10.

`verbose` a logical indicating whether progress should be printed to the screen. The default is TRUE.

## Details

This function provides a means for sampling the likelihood surface quickly to estimate confidence intervals that reflect the uncertainty in the MLE. The function starts with the MLE from the hisse run. It then uses a scaling multiplier to generate an interval by which to randomly alter each parameter. However, the algorithm was designed to “feel” the boundaries of the random search. In other words, when the algorithm begins to sample the hinterlands of the surface, it will know to restrict the boundary to allow sampling of more reasonable values based on the currently sampled set. The goal of this sampling process is to find points within some desired distance from the MLE; by default we assume this distance is  $2 \ln \text{Lik}$ . The confidence interval can be estimated directly from these points. The full set of points tried are also provided and can be used to generate contour plots (though, it is not entirely straightforward to do so – but certainly doable).

Note the `scale.int` option. This roughly sets the variance for sampling points. If this seems to take a long while to find enough points within the desired likelihood region consider reducing `scale.int` to either 0.05 or, in some cases, 0.01.

## Value

`SupportRegion` returns an object of class `geohisse.support`. This is a list with elements:

`$ci`                    the sampled confidence interval.  
`$points.within.region`  
                           the sampled points that within  $2 \ln L$  units from the MLE.  
`$all.points`        all points sampled by the adaptive sampler.

## Author(s)

Jeremy M. Beaulieu

## References

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

---

SupportRegionMiSSE      *Adaptive Sampling of the Likelihood Surface under MiSSE*

---

### Description

Adaptively samples points for each parameter to obtain an estimate of the confidence intervals.

### Usage

```
SupportRegionMiSSE(misse.obj, n.points=1000, scale.int=0.1, desired.delta=2,
min.number.points=10, verbose=TRUE)
```

### Arguments

<code>misse.obj</code>	an object of class <code>misse.fit</code> that contains the MLE from a model run.
<code>n.points</code>	indicates the number of points to sample.
<code>scale.int</code>	the scaling multiplier that defines interval to randomly sample. By default the value is set to 0.1, meaning that values are drawn at random along an interval that encompasses 10 percent above and below the MLE.
<code>desired.delta</code>	defines the number $\ln L$ units away from the MLE to include. By default the value is set to 2.
<code>min.number.points</code>	sets the minimum number of points that can be returned. By default the value is set to 10.
<code>verbose</code>	a logical indicating whether progress should be printed to the screen. The default is TRUE.

### Details

This function provides a means for sampling the likelihood surface quickly to estimate confidence intervals that reflect the uncertainty in the MLE. The function starts with the MLE from the `hisse` run. It then uses a scaling multiplier to generate an interval by which to randomly alter each parameter. However, the algorithm was designed to “feel” the boundaries of the random search. In other words, when the algorithm begins to sample the hinterlands of the surface, it will know to restrict the boundary to allow sampling of more reasonable values based on the currently sampled set. The goal of this sampling process is to find points within some desired distance from the MLE; by default we assume this distance is  $2 \ln L$ . The confidence interval can be estimated directly from these points. The full set of points tried are also provided and can be used to generate contour plots (though, it is not entirely straightforward to do so – but certainly doable).

Note the `scale.int` option. This roughly sets the variance for sampling points. If this seems to take a long while to find enough points within the desired likelihood region consider reducing `scale.int` to either 0.05 or, in some cases, 0.01.

**Value**

SupportRegion returns an object of class `misse.support`. This is a list with elements:

`$ci`                    the sampled confidence interval.  
`$points.within.region`  
                           the sampled points that within  $2\ln L$  units from the MLE.  
`$all.points`        all points sampled by the adaptive sampler.

**Author(s)**

Jeremy M. Beaulieu

**References**

- Beaulieu, J.M, and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.

---

SupportRegionMuHiSSE    *Adaptive Sampling of the Likelihood Surface under MuHiSSE*

---

**Description**

Adaptively samples points for each parameter to obtain an estimate of the confidence intervals.

**Usage**

```
SupportRegionMuHiSSE(muhis.se.obj, n.points=1000, scale.int=0.1, desired.delta=2,
min.number.points=10, verbose=TRUE)
```

**Arguments**

`muhis.se.obj`        an object of class `muhis.se.fit` that contains the MLE from a model run.

`n.points`            indicates the number of points to sample.

`scale.int`          the scaling multiplier that defines interval to randomly sample. By default the value is set to 0.1, meaning that values are drawn at random along an interval that encompasses 10 percent above and below the MLE.

`desired.delta`     defines the number  $\ln L$  units away from the MLE to include. By default the value is set to 2.

<code>min.number.points</code>	sets the minimum number of points that can be returned. By default the value is set to 10.
<code>verbose</code>	a logical indicating whether progress should be printed to the screen. The default is TRUE.

### Details

This function provides a means for sampling the likelihood surface quickly to estimate confidence intervals that reflect the uncertainty in the MLE. The function starts with the MLE from the `hisse` run. It then uses a scaling multiplier to generate an interval by which to randomly alter each parameter. However, the algorithm was designed to “feel” the boundaries of the random search. In other words, when the algorithm begins to sample the hinterlands of the surface, it will know to restrict the boundary to allow sampling of more reasonable values based on the currently sampled set. The goal of this sampling process is to find points within some desired distance from the MLE; by default we assume this distance is  $2 \ln \text{Lik}$ . The confidence interval can be estimated directly from these points. The full set of points tried are also provided and can be used to generate contour plots (though, it is not entirely straightforward to do so – but certainly doable).

Note the `scale.int` option. This roughly sets the variance for sampling points. If this seems to take a long while to find enough points within the desired likelihood region consider reducing `scale.int` to either 0.05 or, in some cases, 0.01.

### Value

`SupportRegion` returns an object of class `muhisse.support`. This is a list with elements:

<code>\$ci</code>	the sampled confidence interval.
<code>\$points.within.region</code>	the sampled points that within $2 \ln L$ units from the MLE.
<code>\$all.points</code>	all points sampled by the adaptive sampler.

### Author(s)

Jeremy M. Beaulieu

### References

- Beaulieu, J.M., and B.C. O’Meara. 2016. Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Syst. Biol.* 65:583-601.
- FitzJohn R.G., Maddison W.P., and Otto S.P. 2009. Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. *Syst. Biol.* 58:595-611.
- Maddison W.P., Midford P.E., and Otto S.P. 2007. Estimating a binary characters effect on speciation and extinction. *Syst. Biol.* 56:701-710.
- Nakov, T., Beaulieu, J.M., and Alverson, A.J. 2018. Freshwater diatoms diversify faster than marine in both planktonic and benthic habitats. *bioRxiv*, doi: <https://doi.org/10.1101/406165>.
- Nee S., May R.M., and Harvey P.H. 1994. The reconstructed evolutionary process. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 344:305-311.



---

TranslateParsMakerGeoHiSSE

*Key to translate GeoHiSSE into ClaSSE*

---

## Description

Simulate key of parnames to translate between GeoHiSSE and ClaSSE models

## Usage

```
TranslateParsMakerGeoHiSSE(k, add.extinction, add.jumps)
```

## Arguments

`k` number of hidden states in the model. Minimum is 0 for a model without hidden states (i.e., GeoSSE).

`add.extinction` if the extinction parameter should be separated from extirpation.

`add.jumps` if jumps between endemic areas should be added.

## Details

Function will only return the parameters that are relevant for a GeoHiSSE model. The ClaSSE model will have many more parameters. The extra parameters of the ClaSSE model need to be all set to 0. The number of parameters of the correspondent ClaSSE model given the parameter `k` is given by:

$$(k+1)*3$$

## Value

Function returns a matrix of characters names. Column 'classe.pars' have the parameter names for a ClaSSE model and column 'geohisse.pars' have the parameter names for the matching GeoHiSSE model.

## Author(s)

Daniel Caetano

---

TransMatMaker      *Transition Rate matrix generator*

---

### Description

Generates and manipulates the index of the rate parameters to be optimized

### Usage

```
TransMatMaker(hidden.states=FALSE)
ParDrop(rate.mat.index=NULL, drop.par=NULL)
ParEqual(rate.mat.index=NULL, eq.par=NULL)
```

### Arguments

`hidden.states`    a logical indicating whether the underlying model includes hidden states. The default is FALSE.

`rate.mat.index`    A user-supplied rate matrix index to be manipulated.

`drop.par`            a vector of transitions to be dropped from the model.

`eq.par`              a vector of transitions pairs to be set equal.

### Details

Outputs the full index of the rate parameters that are to be optimized. The intention is that a user might want to see how the matrix is designed prior to an analysis and perhaps drop a few parameters beforehand due to some hypothesis that he or she might have. The resulting matrix is to be plugged directly into hisse.

### Value

Returns a rate matrix index

---

TransMatMakerGeoHiSSE    *Transition Rate matrix generator for the GeoHiSSE model*

---

### Description

Generates and manipulates the index of the transition rate parameters to be optimized.

### Usage

```
TransMatMakerGeoHiSSE(hidden.areas=0, make.null=FALSE, include.jumps=FALSE,
separate.extirpation=FALSE)
```

**Arguments**

<code>hidden.areas</code>	a numeric value with the number of hidden areas in the model. The canonical GeoSSE model has no hidden areas, so ' <code>hidden.areas=0</code> '. The default value is 0.
<code>make.null</code>	Sets the transition matrix to the null model such that (1) transition rates from endemic to widespread areas ( $A \rightarrow AB$ and $B \rightarrow AB$ ) are the same across all hidden areas and (2) the transition rates between hidden areas (such as $0A \leftrightarrow 1A$ ) are the same for all areas.
<code>include.jumps</code>	allows for $0 \rightarrow 1$ and $1 \rightarrow 0$ transitions.
<code>separate.extirpation</code>	allows for $01 \rightarrow 0$ and $01 \rightarrow 1$ transitions.

**Details**

Outputs the full index of the rate parameters that are to be optimized.

The intention is that a user might want to see how the matrix is designed prior to an analysis and perhaps drop a few parameters beforehand due to some hypothesis that she might have. The resulting matrix is to be plugged directly into GeoHiSSE.

**Value**

Returns a rate matrix index.

---

TransMatMakerMuHiSSE    *Transition Rate matrix generator for the MuHiSSE model*

---

**Description**

Generates and manipulates the index of the transition rate parameters to be optimized.

**Usage**

```
TransMatMakerMuHiSSE(hidden.traits=0, make.null=FALSE, include.diagonals=FALSE,
make.special.for.teo=FALSE)
```

**Arguments**

<code>hidden.traits</code>	a numeric value with the number of hidden states in the model. The canonical MuSSE model has no hidden states, so ' <code>hidden.states=0</code> '. The default value is 0.
<code>make.null</code>	Sets the transition matrix to the null model such that (1) transition rates are the same across all hidden states and (2) the transition rates between hidden states (such as $00A \leftrightarrow 01A$ ) are the same.
<code>include.diagonals</code>	allows for dual transitions, e.g., $00 \rightarrow 11$ and $11 \rightarrow 00$ transitions.
<code>make.special.for.teo</code>	Testing proof of concept for Teo.

**Details**

Outputs the full index of the rate parameters that are to be optimized.

The intention is that a user might want to see how the matrix is designed prior to an analysis and perhaps drop a few parameters beforehand due to some hypothesis that she might have. The resulting matrix is to be plugged directly into MuHiSSE.

**Value**

Returns a rate matrix index.

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