

Package ‘PCMBase’

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Type Package

Title Simulation and Likelihood Calculation of Phylogenetic Comparative Models

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Description Phylogenetic comparative methods represent models of continuous trait data associated with the tips of a phylogenetic tree. Examples of such models are Gaussian continuous time branching stochastic processes such as Brownian motion (BM) and Ornstein-Uhlenbeck (OU) processes, which regard the data at the tips of the tree as an observed (final) state of a Markov process starting from an initial state at the root and evolving along the branches of the tree. The PCMBase R package provides a general framework for manipulating such models. This framework consists of an application programming interface for specifying data and model parameters, and efficient algorithms for simulating trait evolution under a model and calculating the likelihood of model parameters for an assumed model and trait data. The package implements a growing collection of models, which currently includes BM, OU, BM/OU with jumps, two-speed OU as well as mixed Gaussian models, in which different types of the above models can be associated with different branches of the tree. The PCMBase package is limited to trait-simulation and likelihood calculation of (mixed) Gaussian phylogenetic models. The PCMFit package provides functionality for ML and Bayesian fit of these models to tree and trait data. The package web-site <<https://venelin.github.io/PCMBase/>> provides access to the documentation and other resources.

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is.MixedGaussian	<i>Check if an object is a ‘MixedGaussian’ PCM</i>
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Description

Check if an object is a ‘MixedGaussian’ PCM

Usage

```
is.MixedGaussian(x)
```

Arguments

x any object

Value

TRUE if x inherits from the S3 class ‘MixedGaussian’, FALSE otherwise.

is.PCM	<i>Check if an object is a PCM.</i>
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Description

Check if an object is a PCM.

Usage

```
is.PCM(x)
```

Arguments

x an object.

Value

TRUE if 'x' inherits from the S3 class "PCM".

MixedGaussian	<i>Create a multi-regime Gaussian model (MixedGaussian)</i>
---------------	---

Description

Create a multi-regime Gaussian model (MixedGaussian)

Usage

```
MixedGaussian(k, modelTypes, mapping,
  className = paste0("MixedGaussian_", do.call(paste0,
  as.list(mapping))), X0 = structure(0, class = c("VectorParameter",
  "_Global"), description = "trait values at the root"), ...,
  Sigmae_x = structure(0, class = c("MatrixParameter",
  "_UpperTriangularWithDiagonal", "_WithNonNegativeDiagonal", "_Global"),
  description =
  "Upper triangular Choleski factor of the non-phylogenetic variance-covariance"))
```

Arguments

k integer defining the number of traits.

modelTypes a character string vector with the class names of the model-types that can possibly be included (assigned to regimes) in the MixedGaussian, e.g. c("BM", "OU") (see also [PCMModels](#)).

mapping	a character string vector with elements from modelTypes or an integer vector with elements between 1 and length(modelTypes) mapping modelTypes to regimes, e.g. if modelTypes = c("BM", "OU") and mapping = c(a = 1, b = 1, c = 2, d = 1) defines an MixedGaussian with four different regimes with model-types BM3, BM3, OU3 and BM3, corresponding to each regime. mapping does not have to be a named vector. If it is a named vector, then all the names must correspond to valid regime names in a tree to which the model will be fit or simulated (member tree\$edge.regime should be a character vector). If it is not a named vector then the positions of the elements correspond to the regimes in their order given by the function PCMTreeUniqueRegimes called on a tree object.
className	a character string defining a valid S3 class name for the resulting MixedGaussian object. If not specified, a className is generated using the expression <code>paste0("MixedGaussian_", do.call(paste0, as.list(mapping)))</code> .
X0	specification for the global vector X0 to be used by all models in the MixedGaussian.
...	specifications for other _Global parameters coming after X0.
Sigmae_x	specification of a _Global Sigmae_x parameter. This is used by Submodels only if they have Sigmae_x_Omitted.

Details

If X0 is not NULL it has no sense to use model-types including X0 as a parameter (e.g. use BM1 or BM3 instead of BM or BM2). Similarly if Sigmae_x is not NULL there is no meaning in using model-types including Sigmae_x as a parameter, (e.g. use OU2 or OU3 instead of OU or OU1).

Value

an object of S3 class className inheriting from MixedGaussian, GaussianPCM and PCM.

See Also

[PCMTreeUniqueRegimes](#)
[PCMModels\(\)](#)

 PCM

Create a phylogenetic comparative model object

Description

This is the entry-point function for creating model objects within the PCMBase framework representing a single model-type with one or several model-regimes of this type associated with the branches of a tree. For mixed Gaussian phylogenetic models, which enable multiple model-types, use the [MixedGaussian](#) function.

Usage

```
PCM(model, modelTypes = class(model)[1], k = 1L, regimes = 1L,
     params = NULL, vecParams = NULL, offset = 0L, spec = NULL, ...)
```

Arguments

model	This argument can take one of the following forms: <ul style="list-style-type: none"> • a character vector of the S3-classes of the model object to be created (one model object can have one or more S3-classes, with the class PCM at the origin of the hierarchy); • an S3 object which's class inherits from the PCM S3 class. <p>The Details section explains how these two types of input are processed.</p>
modelTypes	a character string vector specifying a set (family) of model-classes, to which the constructed model object belongs. These are used for model-selection.
k	integer denoting the number of traits (defaults to 1).
regimes	a character or integer vector denoting the regimes.
params	NULL (default) or a list of parameter values (scalars, vectors, matrices, or arrays) or sub-models (S3 objects inheriting from the PCM class). See details.
vecParams	NULL (default) or a numeric vector the vector representation of the variable parameters in the model. See details.
offset	integer offset in vecParams; see Details.
spec	NULL or a list specifying the model parameters (see PCMSpecify). If NULL (default), the generic PCMSpecify is called on the created object of class model.
...	additional parameters intended for use by sub-classes of the PCM class.

Details

This is an S3 generic. The PCMBase package defines three methods for it:

- `PCM.PCM`: A default constructor for any object with a class inheriting from "PCM".
- `PCM.character`: A default PCM constructor from a character string specifying the type of model.
- `PCM.default`: A default constructor called when no other constructor is found. When called this constructor raises an error message.

Value

an object of S3 class as defined by the argument model.

See Also

[MixedGaussian](#)

Examples

```

# a Brownian motion model with one regime
modelBM <- PCM(model = "BM", k = 2)
# print the model
modelBM

# a BM model with two regimes
modelBM.ab <- PCM("BM", k = 2, regimes = c("a", "b"))
modelBM.ab

# print a single parameter of the model (in this case, the root value)
modelBM.ab$X0

# assign a value to this parameter (note that the brackets [] are necessary
# to preserve the parameter attributes):
modelBM.ab$X0[] <- c(5, 2)

PCMNumTraits(modelBM)
PCMNumRegimes(modelBM)
PCMNumRegimes(modelBM.ab)

# number of numerical parameters in the model
PCMPParamCount(modelBM)

# Get a vector representation of all parameters in the model
PCMPParamGetShortVector(modelBM)

# Limits for the model parameters:
lowerLimit <- PCMPParamLowerLimit(modelBM)
upperLimit <- PCMPParamUpperLimit(modelBM)

# assign the model parameters at random: this will use uniform distribution
# with boundaries specified by PCMPParamLowerLimit and PCMPParamUpperLimit
# We do this in two steps:
# 1. First we generate a random vector. Note the length of the vector equals PCMPParamCount(modelBM)
randomParams <- PCMPParamRandomVecParams(modelBM, PCMNumTraits(modelBM), PCMNumRegimes(modelBM))
randomParams
# 2. Then we load this random vector into the model.
PCMPParamLoadOrStore(modelBM, randomParams, 0, PCMNumTraits(modelBM), PCMNumRegimes(modelBM), TRUE)

print(modelBM)

PCMPParamGetShortVector(modelBM)

# generate a random phylogenetic tree of 10 tips
tree <- ape::rtree(10)

#simulate the model on the tree
traitValues <- PCMSim(tree, modelBM, X0 = modelBM$X0)

# calculate the likelihood for the model parameters, given the tree and the trait values
PCMLik(traitValues, tree, modelBM)

```



```
# create a likelihood function for faster processing for this specific model.
# This function is convenient for calling in optim because it recieves and parameter
# vector instead of a model object.
likFun <- PCMCreateLikelihood(traitValues, tree, modelBM)
likFun(randomParams)
```

PCMAbCdEf

Quadratic polynomial parameters A, b, C, d, E, f for each node

Description

An S3 generic function that has to be implemented for every model class. This function is called by [PCMLik](#).

Usage

```
PCMAbCdEf(tree, model, metaI = PCMInfo(NULL, tree, model, verbose),
  verbose = FALSE)
```

Arguments

tree	a phylo object with N tips.
model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
metaI	a list returned from a call to <code>PCMInfo(X, tree, model)</code> , containing meta-data such as N, M and k.
verbose	logical indicating if some debug-messages should printed.

PCMAApplyTransformation

Map a parametrization to its original form.

Description

This is an S3 generic that transforms the passed argument by applying the transformation rules for its S3 class.

This is an S3 generic. See ‘`PCMAApplyTransformation._CholeskiFactor`’ for an example.

Usage

```
PCMAApplyTransformation(o, ...)
```

Arguments

- o a PCM object or a parameter
- ... additional arguments that can be used by implementing methods.

Details

This function returns the same object if it is not transformable.

Value

a transformed version of o.

See Also

[is.Transformable](#)

PCMBaseIsADevRelease *Check if the PCMBase version correponds to a dev release*

Description

We define a dev release as having a sub-release, eg 0.9.15.5 is one whereas 0.9.16 is not. The number of components in the version can be changed through the argument numVersionComponents.

Usage

```
PCMBaseIsADevRelease(numVersionComponents = 4L)
```

Arguments

numVersionComponents
an integer, default 4.

Value

a logical

PCMCOLORpalette *A fixed palette of n colors*

Description

A fixed palette of n colors

Usage

```
PCMCOLORpalette(n, names)
```

Arguments

n an integer defining the number of colors in the resulting palette.
 names a character vector of length 'n'.

Value

A vector of character strings which can be used as color specifications by R graphics functions.

PCMCCond *Conditional distribution of a daughter node given its parent node*

Description

An S3 generic function that has to be implemented for every model class.

Usage

```
PCMCCond(tree, model, r = 1, metaI = PCMCInfo(NULL, tree, model,
  verbose), verbose = FALSE)
```

Arguments

tree a phylo object with N tips.
 model an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
 r an integer specifying a model regime
 metaI a list returned from a call to PCMCInfo(X, tree, model), containing meta-data such as N, M and k.
 verbose logical indicating if some debug-messages should be printed.

Value

an object of type specific to the type of model

PCMCond.GaussianPCM *Conditional distribution of a daughter node given its parent node*

Description

An S3 generic function that has to be implemented for every model class.

Usage

```
## S3 method for class 'GaussianPCM'
PCMCond(tree, model, r = 1, metaI = PCMIInfo(NULL,
  tree, model, verbose), verbose = FALSE)
```

Arguments

tree	a phylo object with N tips.
model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
r	an integer specifying a model regime
metaI	a list returned from a call to PCMIInfo(X, tree, model), containing meta-data such as N, M and k.
verbose	logical indicating if some debug-messages should be printed.

Value

For GaussianPCM models, a named list with the following members:

omega	d
Phi	
V	

PCMCondVOU *Variance-covariance matrix of an OU process with optional measurement error and jump at the start*

Description

Variance-covariance matrix of an OU process with optional measurement error and jump at the start

Usage

```
PCMCondVOU(H, Sigma, Sigmae = NULL, Sigmaj = NULL, xi = NULL,
  e_Ht = NULL,
  threshold.Lambda_ij = getOption("PCMBase.Threshold.Lambda_ij", 1e-08))
```

Arguments

H	a numerical k x k matrix - selection strength parameter.
Sigma	a numerical k x k matrix - neutral drift unit-time variance-covariance matrix.
Sigmae	a numerical k x k matrix - environmental variance-covariance matrix.
Sigmaj	is the variance matrix of the normal jump distribution (default is NULL).
xi	a vector of 0's and 1's corresponding to each branch in the tree. A value of 1 indicates that a jump takes place at the beginning of the branch. This argument is only used if Sigmaj is not NULL. Default is NULL.
e_Ht	a numerical k x k matrix - the result of the matrix exponential $\exp(-t*H)$.
threshold.Lambda_ij	a 0-threshold for $\text{abs}(\text{Lambda}_i + \text{Lambda}_j)$, where Lambda_i and Lambda_j are eigenvalues of the parameter matrix H. This threshold-values is used as a condition to take the limit time of the expression $(1 - \exp(-\text{Lambda}_{ij} * \text{time})) / \text{Lambda}_{ij}$ as $(\text{Lambda}_i + \text{Lambda}_j) \rightarrow 0$. You can control this value by the global option "PCMBase.Threshold.Lambda_ij". The default value (1e-8) is suitable for branch lengths bigger than 1e-6. For smaller branch lengths, you may want to increase the threshold value using, e.g. <code>options(PCMBase.Threshold.Lambda_ij=1e-6)</code> .

Value

a function of one numerical argument (time) and an integer indicating the branch-index that is used to check the corresponding element in xi.

PCMCreateLikelihood *Create a likelihood function of a numerical vector parameter*

Description

Create a likelihood function of a numerical vector parameter

Usage

```
PCMCreateLikelihood(X, tree, model, metaI = PCMInfo(X, tree, model),
  positiveValueGuard = Inf)
```

Arguments

X	a k x N numerical matrix with possible NA and NaN entries. Each column of X contains the measured trait values for one species (tip in tree). Missing values can be either not-available (NA) or not existing (NaN). These two values have are treated differently when calculating likelihoods: see PCMPresentCoordinates .
tree	a phylo object with N tips.

model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
metaI	a list returned from a call to <code>PCMInfo(X, tree, model)</code> , containing meta-data such as N, M and k.
positiveValueGuard	positive numerical value (default Inf), which serves as a guard for numerical error. Values exceeding this positiveGuard are most likely due to numerical error and <code>PCMOptions()\$PCMBase.Value.NA</code> is returned instead.

Details

It is possible to specify a function for the argument `metaI`. This function should have three parameters (`X`, `tree`, `model`) and should return a `metaInfo` object. (see [PCMInfo](#)).

Value

a function of a numerical vector parameter called `p` returning the likelihood of `X` given the `tree` and the `model` with parameter values specified by `p`.

<code>PCMDefaultObject</code>	<i>Generate a default object of a given PCM model type or parameter type</i>
-------------------------------	--

Description

This is an S3 generic. See, e.g. `'PCMDefaultObject.MatrixParameter'`.

Usage

```
PCMDefaultObject(spec, model, ...)
```

Arguments

spec	any object having a class attribute. The value of this object is not used, but its class is used for method-dispatch.
model	a PCM object used to extract attributes needed for creating a default object of class specified in <code>class(spec)</code> , such as the number of traits (<code>k</code>) or the regimes and the number of regimes;
...	additional arguments that can be used by methods.

Value

a parameter or a PCM object.

PCMDescribe *Human friendly description of a PCM*

Description

Human friendly description of a PCM

Usage

```
PCMDescribe(model, ...)
```

Arguments

model	a PCM model object
...	additional arguments used by implementing methods.

Details

This S3 generic function is intended to be specified for user models

Value

a character string

PCMDescribeParameters *Describe the parameters of a PCM*

Description

This is an S3 generic.

Usage

```
PCMDescribeParameters(model, ...)
```

Arguments

model	a PCM object.
...	additional arguments that can be used by implementing methods.

Value

a named list with character elements corresponding to each parameter.

PCMFixParameter	<i>Fix a parameter in a PCM model</i>
-----------------	---------------------------------------

Description

Fix a parameter in a PCM model

Usage

```
PCMFixParameter(model, name)
```

Arguments

model	a PCM object
name	a character string

Value

a copy of the model with added class `'_Fixed'` to the class of the parameter name

PCMGenerateParameterizations	<i>Generate possible parameterizations for a given type of model</i>
------------------------------	--

Description

A parameterization of a PCM of given type, e.g. OU, is a PCM-class inheriting from this type, which imposes some restrictions or transformations of the parameters in the base-type. This function generates the S3 methods responsible for creating such parameterizations, in particular it generates the definition of the methods for the two S3 generics `'PCMParentClasses'` and `'PCMSpecify'` for all parameterizations specified in the `'tableParameterizations'` argument.

Usage

```
PCMGenerateParameterizations(model,
  listParameterizations = PCMListParameterizations(model),
  tableParameterizations = PCMTableParameterizations(model,
  listParameterizations), env = .GlobalEnv,
  useModelClassNameForFirstRow = FALSE)
```


Arguments

<code>model</code>	a PCM object.
<code>listParameterizations</code>	a list or a sublist returned by <code>'PCMListParameterizations'</code> . Default: <code>'PCMListParameterizations(model)'</code> .
<code>tableParameterizations</code>	a data.table containing the parameterizations to generate. By default this is generated from <code>'listParameterizations'</code> using a call <code>'PCMTTableParameterizations(model, listParameterizations)'</code> . If specified by the user, this parameter takes precedence over <code>'listParameterizations'</code> and <code>'listParameterizations'</code> is not used.
<code>env</code>	an environment where the method definitions will be stored. Default: <code>'env = .GlobalEnv'</code> .
<code>useModelClassNameForFirstRow</code>	A logical specifying if the S3 class name of <code>'model'</code> should be used as a S3 class for the model defined in the first row of <code>'tableParameterizations'</code> . Default: <code>FALSE</code> .

Value

This function does not return a value. It only has a side effect by defining S3 methods in `'env'`.

PCMGetVecParamsRegimesAndModels

Get a vector of all parameters (real and discrete) describing a model on a tree including the numerical parameters of each model regime, the integer ids of the splitting nodes defining the regimes on the tree and the integer ids of the model classes associated with each regime.

Description

Get a vector of all parameters (real and discrete) describing a model on a tree including the numerical parameters of each model regime, the integer ids of the splitting nodes defining the regimes on the tree and the integer ids of the model classes associated with each regime.

Usage

```
PCMGetVecParamsRegimesAndModels(model, tree, ...)
```

Arguments

<code>model</code>	a PCM model
<code>tree</code>	a phylo object with an <code>edge.regime</code> member.
<code>...</code>	additional parameters passed to methods.

Details

This is an S3 generic. In the default implementation, the last entry in the returned vector is the number of numerical parameters. This is used to identify the starting positions in the vector of the first splitting node.

Value

a numeric vector concatenating the result

 PCMInfo

Meta-information about a tree associated with a PCM

Description

This function pre-processes the given tree and data in order to create meta-information used during likelihood calculation.

Usage

```
PCMInfo(X, tree, model, verbose = FALSE, preorder = NULL, ...)
```

Arguments

X	a $k \times N$ numerical matrix with possible NA and NaN entries. Each column of X contains the measured trait values for one species (tip in tree). Missing values can be either not-available (NA) or not existing (NaN). These two values have are treated differently when calculating likelihoods: see PCMPresentCoordinates .
tree	a phylo object with N tips.
model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
verbose	logical indicating if some debug-messages should printed.
preorder	an integer vector of row-indices in tree\$edge matrix as returned by PCMTreePreorder. This can be given for performance speed-up when several operations needing preorder are executed on the tree. Default : NULL.
...	additional arguments used by implementing methods.

Value

a named list with the following elements:

M	total number of nodes in the tree;
N	number of tips;
k	number of traits;
RTree	number of regimes on the tree (distinct elements of tree\$edge.regime);

RModel	number of regimes in the model (distinct elements of <code>attr(model, regimes)</code>);
p	number of free parameters describing the model;
r	an integer vector corresponding to <code>tree\$edge</code> with the regime for each branch in tree;
xi	an integer vector of 0's and 1's corresponding to the rows in <code>tree\$edge</code> indicating the presence of a jump at the corresponding branch;
pc	a logical matrix of dimension $k \times M$ denoting the present coordinates for each node;

This list is passed to [PCMLik](#).

PCMLik	<i>Likelihood of a multivariate Gaussian phylogenetic comparative model with non-interacting lineages</i>
--------	---

Description

The likelihood of a PCM represents the probability density function of observed trait values (data) at the tips of a tree given the tree and the model parameters. Seen as a function of the model parameters, the likelihood is used to fit the model to the observed trait data and the phylogenetic tree (which is typically inferred from another sort of data, such as an alignment of genetic sequences for the species at the tips of the tree). The [PCMLik](#) function provides a common interface for calculating the (log-)likelihood of different PCMs. Below we denote by N the number of tips, by M the total number of nodes in the tree including tips, internal and root node, and by k - the number of traits.

Usage

```
PCMLik(X, tree, model, metaI = PCMInfo(X, tree, model, verbose =
  verbose), log = TRUE, verbose = FALSE)
```

Arguments

X	a $k \times N$ numerical matrix with possible NA and NaN entries. Each column of X contains the measured trait values for one species (tip in tree). Missing values can be either not-available (NA) or not existing (NaN). These two values have are treated differently when calculating likelihoods: see PCMPresentCoordinates .
tree	a phylo object with N tips.
model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
metaI	a list returned from a call to <code>PCMInfo(X, tree, model)</code> , containing meta-data such as N, M and k.
log	logical indicating whether a log-likelihood should be calculated. Default is TRUE.
verbose	logical indicating if some debug-messages should be printed.

Details

For efficiency, the argument `metaI` can be provided explicitly, because this is not supposed to change during a model inference procedure such as likelihood maximization.

Value

a numerical value with named attributes as follows:

X0 A numerical vector of length `k` specifying the value at the root for which the likelihood value was calculated. If the model contains a member called `X0`, this vector is used; otherwise the value of `X0` maximizing the likelihood for the given model parameters is calculated by maximizing the quadratic polynomial ' $X0 * L_root * X0 + m_root * X0 + r_root$ '.

error A named list containing error information if a numerical or other logical error occurred during likelihood calculation (this is a list returned by [PCMParseErrorMessage](#)). If an error occurred during likelihood calculation, the default behavior is to return `NA` with a non-NULL error attribute. This behavior can be changed in using global options:

"PCMBase.Value.NA" Allows to specify a different NA value such as `-Inf` or `-1e20` which can be used in combination with `log = TRUE` when using `optim` to maximize the log-likelihood;

"PCMBase.Errors.As.Warnings" Setting this option to `FALSE` will cause any error to result in calling the `stop` R-base function. If not caught in a `tryCatch`, this will cause the inference procedure to abort at the occurrence of a numerical error. By default, this option is set to `TRUE`, which means that `getOption("PCMBase.Value.NA", as.double(NA))` is returned with an error attribute and a warning is issued.

See Also

[PCMInfo](#) [PCMAbCdEf](#) [PCMLmr](#) [PCMSim](#) [PCMCond](#) [PCMParseErrorMessage](#)

PCMListParameterizations

Specify the parameterizations for each parameter of a model

Description

This is an S3 generic.

Usage

```
PCMListParameterizations(model, ...)
```

Arguments

<code>model</code>	a PCM.
<code>...</code>	additional arguments used by implementing methods.

Value

a named list with list elements corresponding to each parameter in model. Each list element is a list of character vectors, specifying the possible S3 class attributes for the parameter in question. For an example, type 'PCMListParameterizations.BM' to see the possible parameterizations for the BM model.

 PCMLmr

Quadratic polynomial parameters L, m, r

Description

Quadratic polynomial parameters L, m, r

Usage

```
PCMLmr(X, tree, model, metaI = PCMInfo(X, tree, model, verbose =
  verbose), root.only = TRUE, verbose = FALSE)
```

Arguments

X	a $k \times N$ numerical matrix with possible NA and NaN entries. Each column of X contains the measured trait values for one species (tip in tree). Missing values can be either not-available (NA) or not existing (NaN). These two values have are treated differently when calculating likelihoods: see PCMPresentCoordinates .
tree	a phylo object with N tips.
model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
metaI	a list returned from a call to PCMInfo(X, tree, model), containing meta-data such as N, M and k.
root.only	logical indicatin whether to return the calculated values of L,m,r only for the root or for all nodes in the tree.
verbose	logical indicating if some debug-messages should printed.

Value

A list with the members A,b,C,d,E,f,L,m,r for all nodes in the tree or only for the root if root.only=TRUE.

```

PCMapModelTypesToRegimes
  #' Regimes in a model #' @param model a PCM object #'
  @param tree a phylo object or NULL. If the regimes in the model
  are integers and tree is not NULL, #' then these integers are
  used as indexes in PCMTreeUniqueRegimes(tree). Default NULL.
  #' @return a character or an integer vector giving the regime
  names of the models #' @export PCMRegimes <- function(model,
  tree = NULL, preorder = if(is.null(tree)) NULL else PCMTreePre-
  order(tree)) UseMethod("PCMRegimes", model)

```

Description

```

#' @export PCMRegimes.PCM <- function(model, tree = NULL, preorder = if(is.null(tree)) NULL
else PCMTreePreorder(tree)) r <- attr(model, "regimes") if(is.integer(r) && !is.null(tree)) PCMTree-
UniqueRegimes(tree, preorder)[r] else r

```

Integer vector giving the model type index for each regime

Usage

```
PCMapModelTypesToRegimes(model, tree, ...)
```

Arguments

model	a PCM model
tree	a phylo object with an edge.regime member
...	additional parameters passed to methods

Details

This is a generic S3 method. The default implementation for the basic class PCM returns a vector of 1's, because it assumes that a single model type is associated with each regime. The implementation for multi-regime models (MRG) returns the mapping attribute of the MRG object reordered to correspond to PCMTreeUniqueRegimes(tree).

Value

an integer vector with elements corresponding to the elements in PCMTreeUniqueRegimes(tree)

PCMMean	<i>Expected mean vector at each tip conditioned on a trait-value vector at the root</i>
---------	---

Description

Expected mean vector at each tip conditioned on a trait-value vector at the root

Usage

```
PCMMean(tree, model, X0 = model$X0, metaI = PCMInfo(NULL, tree, model,
  verbose), internal = FALSE, verbose = FALSE)
```

Arguments

tree	a phylo object with N tips.
model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
X0	a k-vector denoting the root trait
metaI	a list returned from a call to PCMInfo(X, tree, model), containing meta-data such as N, M and k.
internal	a logical indicating if the per-node mean vectors should be returned (see Value). Default FALSE.
verbose	logical indicating if some debug-messages should be printed.

Value

If `internal` is FALSE (default), then a $k \times N$ matrix `Mu`, such that `Mu[, i]` equals the expected mean k -vector at tip i , conditioned on `X0` and the tree. Otherwise, a $k \times M$ matrix `Mu` containing the mean vector for each node.

Examples

```
# a Brownian motion model with one regime
modelBM <- PCM(model = "BM", k = 2)
# print the model
modelBM
# assign the model parameters at random: this will use uniform distribution
# with boundaries specified by PCMPParamLowerLimit and PCMPParamUpperLimit
# We do this in two steps:
# 1. First we generate a random vector. Note the length of the vector equals PCMPParamCount(modelBM)
randomParams <- PCMPParamRandomVecParams(modelBM, PCMNumTraits(modelBM), PCMNumRegimes(modelBM))
randomParams
# 2. Then we load this random vector into the model.
PCMPParamLoadOrStore(modelBM, randomParams, 0, PCMNumTraits(modelBM), PCMNumRegimes(modelBM), TRUE)
```

```
# create a random tree of 10 tips
tree <- ape::rtree(10)
PCMMean(tree, modelBM)
```

PCMMeanAtTime *Calculate the mean at time t, given X0, under a PCM model*

Description

Calculate the mean at time t, given X0, under a PCM model

Usage

```
PCMMeanAtTime(t, model, X0 = model$X0, regime = 1L, verbose = FALSE)
```

Arguments

t	positive numeric denoting time
model	a PCM model object
X0	a numeric vector of length k, where k is the number of traits in the model (Defaults to model\$X0).
regime	an integer or a character denoting the regime in model for which to do the calculation; (Defaults to 1L meaning the first regime in the model)
verbose	a logical indicating if (debug) messages should be written on the console (Defaults to FALSE).

Value

A numeric vector of length k

Examples

```
# a Brownian motion model with one regime
modelBM <- PCM(model = "BM", k = 2)
# print the model
modelBM
# assign the model parameters at random: this will use uniform distribution
# with boundaries specified by PCMPParamLowerLimit and PCMPParamUpperLimit
# We do this in two steps:
# 1. First we generate a random vector. Note the length of the vector equals PCMPParamCount(modelBM)
randomParams <- PCMPParamRandomVecParams(modelBM, PCMPParamCount(modelBM), PCMPParamCount(modelBM))
randomParams
# 2. Then we load this random vector into the model.
PCMPParamLoadOrStore(modelBM, randomParams, 0, PCMPParamCount(modelBM), PCMPParamCount(modelBM), TRUE)

# PCMMeanAtTime(1, modelBM)

# note that the variance at time 0 is not the 0 matrix because the model has a non-zero
# environmental deviation
PCMMeanAtTime(0, modelBM)
```

PCMModels	<i>Get a list of PCM models currently implemented</i>
-----------	---

Description

Get a list of PCM models currently implemented

Usage

```
PCMModels(pattern = NULL, parentClass = NULL, ...)
```

Arguments

pattern	a character string specifying an optional for the model-names to search for.
parentClass	a character string specifying an optional parent class of the models to look for.
...	additional arguments used by implementing methods.

Details

The function is using the S3 api function [methods](#) looking for all registered implementations of the function [PCMSpecify](#).

Value

a character vector of the model classes found.

Examples

```
PCMModels()
PCMModels("^OU")
```

PCMNumRegimes	<i>Number of regimes in a model</i>
---------------	-------------------------------------

Description

Number of regimes in a model

Usage

```
PCMNumRegimes(model)
```

Arguments

model	a PCM object
-------	--------------

Value

an integer

PCMNumTraits	<i>Number of traits modeled by a PCM</i>
--------------	--

Description

Number of traits modeled by a PCM

Usage

```
PCMNumTraits(model)
```

Arguments

model a PCM object

Value

an integer

PCMOptions	<i>Global options for the PCMBase package</i>
------------	---

Description

Global options for the PCMBase package

Usage

```
PCMOptions()
```

Value

a named list with the currently set values of the following global options:

- `PCMBase.Value.NA` NA value for the likelihood; used in `GaussianPCM` to return this value in case of an error occurring during likelihood calculation. By default, this is set to `as.double(NA)`.
- `PCMBase.Errors.As.Warnings` a logical flag indicating if errors (occurring, e.g. during likelihood calculation) should be treated as warnings and added as an attribute "error" to returned likelihood values. Default `TRUE`.
- `PCMBase.Threshold.Lambda_ij` a 0-threshold for $\text{abs}(\text{Lambda}_i + \text{Lambda}_j)$, where Lambda_i and Lambda_j are eigenvalues of the parameter matrix H of an OU or other model. Default `1e-8`. See [PCMPExpMeanExp](#).

- `PCMBase.Threshold.SV` A 0-threshold for $\min(\text{svdV})/\max(\text{svdV})$, where `svdV` is the vector of eigenvalues of the matrix `V` for a given branch. The `V` matrix is considered singular if it has eigenvalues equal to 0 or when the ratio $\min(\text{svdV})/\max(\text{svdV})$ is below `PCMBase.Threshold.SV`. Default is $1e-6$. Treatment of branches with singular `V` matrix is defined by the option `PCMBase.Skip.Singular`.
- `PCMBase.Threshold.Skip.Singular` A double indicating if a branch of shorter length with singular matrix `V` should be skipped during likelihood calculation. Setting this option to a higher value, together with a `TRUE` value for the option `PCMBase.Skip.Singular` will result in tolerating some parameter values resulting in singular variance covariance matrix of the transition distribution. Default $1e-4$.
- `PCMBase.Skip.Singular` A logical value indicating whether branches with singular matrix `V` and shorter than `getOption("PCMBase.Threshold.Singular.Skip")` should be skipped during likelihood calculation, adding their children `L,m,r` values to their parent node. Default `TRUE`. Note, that setting this option to `FALSE` may cause some models to stop working, e.g. the White model. Setting this option to `FALSE` will also cause errors or NA likelihood values in the case of trees with very short or 0-length branches.
- `PCMBase.Tolerance.Symmetric` A double specifying the tolerance in tests for symmetric matrices. Default $1e-8$; see also [isSymmetric](#).
- `PCMBase.Lmr.mode` An integer code specifying the parallel likelihood calculation mode.
- `PCMBase.ParamValue.LowerLimitDefault` lower limit value for parameters, default setting is -10.0 .
- `PCMBase.ParamValue.LowerLimit.NonNegativeDiagonalDefault` lower limit value for parameters corresponding to non-negative diagonal elements of matrices, default setting is 0.0 .
- `PCMBase.ParamValue.UpperLimitDefault` upper limit value for parameters, default setting is 10.0 .

Examples

```
PCMOptions()
```

```
PCMPairSums
```

```
Sums of pairs of elements in a vector
```

Description

Sums of pairs of elements in a vector

Usage

```
PCMPairSums(lambda)
```

Arguments

`lambda` a numeric vector

Value

a squared symmetric matrix with $\text{elem}_{ij} = \lambda_i + \lambda_j$.

 PCMPParam

Module PCMPParam

Description

Global and S3 generic functions for manipulating model parameters. The parameters in a PCM are named objects with a class attribute specifying the main type and optional properties (tags).

S3 generic functions:

PCMPParamCount() Counting the number of actual numeric parameters (used, e.g. for calculating information scores, e.g. AIC);

PCMPParamLoadOrStore(), PCMPParamLoadOrStore() Storing/loading a parameter to/from a numerical vector;

PCMPParamLowerLimit(), PCMPParamUpperLimit() Specifying parameter upper and lower limits;

PCMPParamRandomVecParams() Generating a random parameter vector;

For all the above properties, check-functions are defined, e.g. 'is.Local(o)', 'is.Global(o)', 'is.ScalarParameter(o)', 'is.VectorParameter', etc.

 PCMPParamCount

Count the number of free parameters associated with a PCM or a PCM-parameter

Description

Count the number of free parameters associated with a PCM or a PCM-parameter

Usage

```
PCMPParamCount(o, countRegimeChanges = FALSE, countModelTypes = FALSE,
  offset = 0L, k = 1L, R = 1L, parentModel = NULL)
```

Arguments

o	a PCM model object or a parameter of a PCM object
countRegimeChanges	logical indicating if regime changes should be counted. If TRUE, the default implementation would add $\text{PCMNumRegimes}(\text{model}) - 1$. Default FALSE.
countModelTypes	logical indicating whether the model type should be counted. If TRUE the default implementation will add +1 only if there are more than one modelTypes ($\text{length}(\text{attr}(\text{model}, \text{"modelTypes"}, \text{exact} = \text{TRUE})) > 1$), assuming that all regimes are regimes of the same model type (e.g. OU). The implementation for MRG models will add +1 for every regime if there are more than one modelTypes. Default FALSE.
offset	an integer denoting an offset count from which to start counting (internally used). Default: 0.
k	an integer denoting the number of modeled traits. Default: 1.
R	an integer denoting the number of regimes in the model. Default: 1.
parentModel	NULL or a PCM object. Default: NULL.

Value

an integer

PCMParamGetShortVector

Get a vector of the variable numeric parameters in a model

Description

The short vector of the model parameters does not include the nodes in the tree where a regime change occurs, nor the the model types associated with each regime.

Usage

```
PCMParamGetShortVector(o, k = 1L, R = 1L, ...)
```

Arguments

o	a PCM model object or a parameter of a PCM object
k	an integer denoting the number of modeled traits. Default: 1.
R	an integer denoting the number of regimes in the model. Default: 1.
...	other arguments that could be used by implementing methods.

Value

a numeric vector of length equal to $\text{'PCMParamCount}(\text{o}, \text{FALSE}, \text{FALSE}, \text{0L}, \text{k}, \text{R})\text{'}$.

PCMPParamLoadOrStore *Load (or store) a PCM parameter from (or to) a vector of the variable parameters in a model.*

Description

Load (or store) a PCM parameter from (or to) a vector of the variable parameters in a model.

Usage

```
PCMPParamLoadOrStore(o, vecParams, offset, k, R, load, parentModel = NULL)
```

Arguments

o	a PCM model object or a parameter of a PCM object
vecParams	a numeric vector.
offset	an integer denoting an offset count from which to start counting (internally used). Default: 0.
k	an integer denoting the number of modeled traits. Default: 1.
R	an integer denoting the number of regimes in the model. Default: 1.
load	logical indicating if parameters should be loaded from vecParams into o (TRUE) or stored to vecParams from o (FALSE).
parentModel	NULL or a PCM object. Default: NULL.

Details

This S3 generic function has both, a returned value and side effects.

Value

an integer equaling the number of elements read from vecParams. In the case of type=="custom", the number of indices bigger than offset returned by the function indices(offset, k).

PCMPParamLowerLimit *The lower limit for a given model or parameter type*

Description

This is an S3 generic function.

Usage

```
PCMPParamLowerLimit(o, k, R, ...)
```

Arguments

- o an object such as a VectorParameter a MatrixParameter or a PCM.
- k integer denoting the number of traits
- R integer denoting the number of regimes in the model in which o belongs to.
- ... additional arguments (optional or future use).

Value

an object of the same S3 class as o representing a lower limit for the class.

PCMPParamRandomVecParams

Generate a random parameter vector for a model using uniform distribution between its lower and upper bounds.

Description

Generate a random parameter vector for a model using uniform distribution between its lower and upper bounds.

Usage

```
PCMPParamRandomVecParams(o, k, R, n = 1L, argsPCMPParamLowerLimit = NULL,
  argsPCMPParamUpperLimit = NULL)
```

Arguments

- o a PCM model object or a parameter
- k integer denoting the number of traits.
- R integer denoting the number of regimes.
- n an integer specifying the number of random vectors to generate
- argsPCMPParamLowerLimit, argsPCMPParamUpperLimit
 named lists of arguments passed to PCMPParamLowerLimit and PCMPParamUpperLimit.

Value

if $n = 1$, a numeric vector of length `PCMPParamCount(o)`; if $n > 1$, a numeric matrix of dimension $n \times \text{PCMPParamCount}(o)$.

See Also

PCMPParamLimits PCMPParamGetShortVector

PCMPParamSetByName *Set model parameters from a named list*

Description

Set model parameters from a named list

Usage

```
PCMPParamSetByName(model, params, inplace = TRUE,
  replaceWholeParameters = FALSE, ...)
```

Arguments

model	a PCM model object
params	a named list with elements among the names found in model
inplace	logical indicating if the parameters should be set "inplace" for the model object in the calling environment or a new model object with the parameters set as specified should be returned. Defaults to TRUE.
replaceWholeParameters	logical, by default set to FALSE. If TRUE, the parameters will be completely replaced, meaning that their attributes (e.g. S3 class) will be replaced as well (dangerous).
...	other arguments that can be used by implementing methods.

Value

If `inplace` is TRUE, the function only has a side effect of setting the parameters of the model object in the calling environment; otherwise the function returns a modified copy of the model object.

PCMPParamType *Parameter types*

Description

The parameter types are divided in the following categories:

Main type These are the "ScalarParameter", "VectorParameter" and "MatrixParameter" classes. Each model parameter must have a main type.

Scope/Omission These are the "_Global" and "_Omitted" classes. Every parameter can be global for all regimes or local for a single regime. If not specified, local scope is assumed. In some special cases a parameter (e.g. Sigmae) can be omitted from a model. This is done by adding "_Omitted" to its class attribute.

Constancy (optional) These are the "_Fixed", "_Ones", "_Identity" and "_Zeros" classes.

Transformation (optional) These are the "_Transformable", "_CholeskiFactor" and "_Schur" classes.

Other properties (optional) These are the "_NonNegative", "_WithNonNegativeDiagonal", "_LowerTriangular", "_AllEqual", "_ScalarDiagonal", "_Symmetric", "_UpperTriangular", "_LowerTriangularWithDiagonal" and "_UpperTriangularWithDiagonal" classes.

Usage

is.Local(o)

is.Global(o)

is.ScalarParameter(o)

is.VectorParameter(o)

is.MatrixParameter(o)

is.WithCustomVecParams(o)

is.Fixed(o)

is.Zeros(o)

is.Ones(o)

is.Identity(o)

is.AllEqual(o)

is.NonNegative(o)

is.Diagonal(o)

is.ScalarDiagonal(o)

is.Symmetric(o)

is.UpperTriangular(o)

is.UpperTriangularWithDiagonal(o)

is.WithNonNegativeDiagonal(o)

is.LowerTriangular(o)

is.LowerTriangularWithDiagonal(o)

is.Omitted(o)

is.CholeskiFactor(o)

is.Schur(o)

is.Transformable(o)

is.Transformed(o)

is.SemiPositiveDefinite(o)

Arguments

o an object, i.e. a PCM or a parameter object.

Value

logical indicating if the object passed is from the type appearing in the function-name.

Functions

- is.Local:
- is.Global:
- is.ScalarParameter:
- is.VectorParameter:
- is.MatrixParameter:
- is.WithCustomVecParams:
- is.Fixed:
- is.Zeros:
- is.Ones:
- is.Identity:
- is.AllEqual:
- is.NonNegative:
- is.Diagonal:
- is.ScalarDiagonal:
- is.Symmetric:
- is.UpperTriangular:
- is.UpperTriangularWithDiagonal:
- is.WithNonNegativeDiagonal:
- is.LowerTriangular:
- is.LowerTriangularWithDiagonal:
- is.Omitted:
- is.CholeskiFactor:

- `is.Schur`:
- `is.Transformable`:
- `is.Transformed`:
- `is.SemiPositiveDefinite`:

PCMPParamUpperLimit *The upper limit for a given model or parameter type*

Description

This is an S3 generic function.

Usage

```
PCMPParamUpperLimit(o, k, R, ...)
```

Arguments

<code>o</code>	an object such as a <code>VectorParameter</code> a <code>MatrixParameter</code> or a <code>PCM</code> .
<code>k</code>	integer denoting the number of traits
<code>R</code>	integer denoting the number of regimes in the model in which <code>o</code> belongs to.
<code>...</code>	additional arguments (optional or future use).

Value

an object of the same S3 class as `o` representing an upper limit for the class.

PCMParentClasses *Parent S3 classes for a model class*

Description

Parent S3 classes for a model class

Usage

```
PCMParentClasses(model)
```

Arguments

<code>model</code>	an S3 object.
--------------------	---------------

Details

This S3 generic function is intended to be specified for user models. This function is called by the 'PCM.character' method to determine the parent classes for a given model class.

Value

a vector of character string denoting the names of the parent classes

PCMParseErrorMessage *Extract error information from a formatted error message.*

Description

The function searches `x` for a pattern matching the format 'ERR:5-alphanumeric-character-code:project-name:source-file:error-specifics:'. Specifically it searches for a regular expression pattern "ERR:[0-9a-zA-Z]+:[^:]+:[^:]+:[^:]+:[^:]*:".

Usage

PCMParseErrorMessage(`x`)

Arguments

`x` character string representing the error message.

Value

a named list with the parsed error information or NULL, if no match was found. The elements of this list are named as follows:

<code>type</code>	The type of the error message. Usually this is ERROR, but could be WARNING or anything else.
<code>icode</code>	An alphanumeric code of the error.
<code>project</code>	The name of the project locating the code that raised the error.
<code>file</code>	The name of the source-file containing the code that raised the error.
<code>fun</code>	The name of the function raising the error
<code>info</code>	A character string containing additional error-specific information
<code>msg</code>	A verbal description of the error.

PCMPEpxMeanExp	<i>Create a function of time that calculates $(1-\exp(-\lambda_{ij} \cdot \text{time})) / \lambda_{ij}$ for every element λ_{ij} of the input matrix Λ_{ij}.</i>
----------------	---

Description

Create a function of time that calculates $(1-\exp(-\lambda_{ij} \cdot \text{time})) / \lambda_{ij}$ for every element λ_{ij} of the input matrix Λ_{ij} .

Usage

```
PCMPEpxMeanExp(Lambda_ij,
  threshold.Lambda_ij = getOption("PCMBase.Threshold.Lambda_ij", 1e-08))
```

Arguments

`Lambda_ij` a squared numerical matrix of dimension $k \times k$

`threshold.Lambda_ij` a 0-threshold for $\text{abs}(\Lambda_i + \Lambda_j)$, where Λ_i and Λ_j are eigenvalues of the parameter matrix H . This threshold-value is used as a condition to take the limit time of the expression $(1-\exp(-\Lambda_{ij} \cdot \text{time})) / \Lambda_{ij}$ as $(\Lambda_i + \Lambda_j) \rightarrow 0$. You can control this value by the global option "PCMBase.Threshold.Lambda_ij". The default value (1e-8) is suitable for branch lengths bigger than 1e-6. For smaller branch lengths, you may want to increase the threshold value using, e.g. `options(PCMBase.Threshold.Lambda_ij=1e-6)`.

Details

the function $(1-\exp(-\lambda_{ij} \cdot \text{time})) / \lambda_{ij}$ corresponds to the product of the CDF of an exponential distribution with rate λ_{ij} multiplied by its mean value (mean waiting time).

Value

a function of time returning a matrix with entries formed from the above function or the limit, time, if $|\Lambda_{ij}| \leq \text{threshold}$.

 PCMLambdaP_1

Eigen-decomposition of a matrix H

Description

Eigen-decomposition of a matrix H

Usage

PCMLambdaP_1(H)

Arguments

H a numeric matrix

Details

The function fails with an error message if H is defective, that is, if its matrix of eigenvectors is computationally singular. The test for singularity is based on the [rcond](#) function.

Value

a list with elements as follows:

lambda	a vector of the eigenvalues of H
P	a squared matrix with column vectors, the eigenvectors of H corresponding to the eigenvalues in lambda
P_1	the inverse matrix of P
.	

 PCMPlotGaussianDensityGrid2D

A 2D Gaussian distribution density grid in the form of a ggplot object

Description

A 2D Gaussian distribution density grid in the form of a ggplot object

Usage

```
PCMPlotGaussianDensityGrid2D(mu, Sigma, xlim, ylim, xNumPoints = 100,
  yNumPoints = 100, ...)
```

Arguments

<code>mu</code>	numerical mean vector of length 2
<code>Sigma</code>	numerical 2 x 2 covariance matrix
<code>xlim, ylim</code>	numerical vectors of length 2
<code>xNumPoints, yNumPoints</code>	integers denoting how many points should the grid contain for each axis.
<code>...</code>	additional arguments passed to <code>ggplot</code>

Value

a `ggplot` object

`PCMPlotGaussianSample2D`

A 2D sample from Gaussian distribution

Description

A 2D sample from Gaussian distribution

Usage

```
PCMPlotGaussianSample2D(mu, Sigma, numPoints = 1000, ...)
```

Arguments

<code>mu</code>	numerical mean vector of length 2
<code>Sigma</code>	numerical 2 x 2 covariance matrix
<code>numPoints</code>	an integer denoting how many points should be randomly sampled (see details).
<code>...</code>	additional arguments passed to <code>ggplot</code> .

Details

This function generates a random sample of `numPoints` 2d points using the function `rmvnorm` from the `mvtnorm` R-package. Then it produces a `ggplot` on the generated points.

Value

a `ggplot` object

PCMPLOTMath	<i>Beautiful model description based on plotmath</i>
-------------	--

Description

This is an S3 generic that produces a plotmath expression for its argument.

Usage

```
PCMPLOTMath(o, roundDigits = 2, transformChol = FALSE)
```

Arguments

<code>o</code>	a PCM or a parameter object.
<code>roundDigits</code>	an integer, default: 2.
<code>transformChol</code>	a logical indicating if Choleski transformation should be applied to Choleski-factor parameters prior to generating the plotmath expression.

Value

a character string.

PCMPLOTTraitData2D	<i>Scatter plot of 2-dimensional data</i>
--------------------	---

Description

Scatter plot of 2-dimensional data

Usage

```
PCMPLOTTraitData2D(X, tree, labeledTips = NULL, sizeLabeledTips = 8,
  palette = PCMPColorPalette(PCMPtreeNumUniqueRegimes(tree),
  PCMPtreeUniqueRegimes(tree)), scaleSizeWithTime = !is.ultrametric(tree))
```

Arguments

<code>X</code>	a $k \times N$ matrix
<code>tree</code>	a phylo object
<code>labeledTips</code>	a vector of tip-numbers to label (NULL by default)
<code>sizeLabeledTips</code>	passed <code>geom_text</code> to specify the size of tip-labels for the trait-points.
<code>palette</code>	a named vector of colors

scaleSizeWithTime

logical indicating if the size and the transparency of the points should reflect the distance from the present (points that are farther away in time with respect to the present moment, i.e. closer to the root of the tree, are displayed smaller and more transparent.). By default this is set to `!is.ultrametric(tree)`.

Value

a ggplot object

PCMPresentCoordinates *Determine which traits are present (active) on each node of the tree*

Description

For every node (root, internal or tip) in tree, build a logical vector of length k with TRUE values for every present coordinate. Non-present coordinates arise from NA-values in the trait data. These can occur in two cases:

Missing measurements for some traits at some tips: the present coordinates are FALSE for the corresponding tip and trait, but are full for all traits at all internal and root nodes.

non-existent traits for some species: the FALSE present coordinates propagate towards the parent nodes - an internal or root node will have a present coordinate set to FALSE for a given trait, if all of its descendants have this coordinate set to FALSE.

These two cases have different effect on the likelihood calculation: missing measurements (NA) are integrated out at the parent nodes; while non-existent traits (NaN) are treated as reduced dimensionality of the vector at the parent node.

Usage

```
PCMPresentCoordinates(X, tree, metaI)
```

Arguments

X	numeric $k \times N$ matrix of observed values, with possible NA entries. The columns in X are in the order of <code>tree\$tip.label</code>
tree	a phylo object
metaI	The result of calling <code>PCMInfo</code> .

Value

a $k \times M$ logical matrix which can be passed as a `pc` argument to the `PCMLik` function. The function fails in case when all traits are NAs for some of the tips. In that case an error message is issued "ERR:02001:PCMBase:PCM.R:PCMPresentCoordinates:: Some tips have 0 present coordinates. Consider removing these tips."

See Also

[PCMLik](#)

 PCMRegimes

Regimes in a model

Description

Regimes in a model

Usage

PCMRegimes(model)

Arguments

model a PCM object

Value

a character or an integer vector giving the regime names in the model

PCMSim

Simulation of a phylogenetic comparative model on a tree

Description

Generate trait data on a tree according to a multivariate stochastic model with one or several regimes

Usage

```
PCMSim(tree, model, X0, metaI = PCMInfo(X = NULL, tree = tree, model =
  model, verbose = verbose), verbose = FALSE)
```

Arguments

tree a phylo object specifying a rooted tree.
 model an S3 object specifying the model (see Details).
 X0 a numeric vector of length k (the number of traits) specifying the trait values at the root of the tree.
 metaI a named list containing meta-information about the data and the model.
 verbose a logical indicating if informative messages should be written during execution.

Details

Internally, this function uses the [PCMCond](#) implementation for the given model class.

Value

numeric $M \times k$ matrix of values at all nodes of the tree, i.e. root, internal and tip, where M is the number of nodes: $M = \dim(\text{tree}\$edge)[1] + 1$, with indices from 1 to $N = \text{length}(\text{tree}\$tip.label)$ corresponding to tips, $N+1$ corresponding to the root and bigger than $N+1$ corresponding to internal nodes. The function will fail in case that the length of the argument vector $X0$ differs from the number of traits specified in $\text{metaI}\$k$. Error message: "ERR:02002:PCMBase:PCM.R:PCMSim::X0 must be of length ...".

See Also

[PCMLik](#) [PCMInfo](#) [PCMCond](#)

PCMSpecify

Parameter specification of PCM model

Description

The parameter specification of a PCM model represents a named list with an entry for each parameter of the model. Each entry in the list is a structure defining the S3 class of the parameter and its verbal description. This is an S3 generic. See 'PCMSpecify.OU' for an example method.

Usage

```
PCMSpecify(model, ...)
```

Arguments

`model` a PCM model object.
`...` additional arguments used by implementing methods.

Value

a list specifying the parameters of a PCM.

PCMTableParameterizations

Cartesian product of possible parameterizations for the different parameters of a model

Description

This function generates a data.table in which each column corresponds to one parameter of model and each row corresponds to one combination of parameterizations for the model parameters, such that the whole table corresponds to the Cartesian product of the lists found in 'listParameterizations'. Usually, subsets of this table should be passed to 'PCMGenerateParameterizations'

Usage

```
PCMTableParameterizations(model,
  listParameterizations = PCMListParameterizations(model, ...), ...)
```

Arguments

`model` a PCM object.

`listParameterizations` a list returned by a method for 'PCMListParameterizations'. Default: 'PCMListParameterizations(model, ...)'.
`...` additional arguments passed to 'PCMListParameterizations(model, ...)'.
`...`

Value

a data.table object.

PCMTreeDropClade	<i>Drop a clade from a phylogenetic tree</i>
------------------	--

Description

Drop a clade from a phylogenetic tree

Usage

```
PCMTreeDropClade(tree, cladeRootNode, tableAncestors = NULL, X = NULL,
  returnPhylo = is.null(X), errorOnMissing = FALSE)
```

Arguments

`tree` a phylo object

`cladeRootNode` a character string denoting the label or an integer denoting a node in the tree

`tableAncestors` an integer matrix returned by a previous call to PCMTreeTableAncestors(tree) or NULL.

`X` an optional k x N matrix with trait value vectors for each tip in tree.

`returnPhylo` logical indicating if only the phylo object associated with the tree after dropping the clade should be returned. Defaults to is.null(X)

`errorOnMissing` logical indicating if an error should be raised if cladeRootNode is not among the nodes in tree. Default FALSE, meaning that if cladeRootNode is not a node in tree the tree (and X if returnPhylo is FALSE) is/are returned unchanged.

Value

If returnPhylo is TRUE, a phylo object associated with the remaining tree after dropping the clade, otherwise, a list with two named members :

- tree the phylo object associated with the remaining tree after dropping the clade
- X the submatrix of X with columns corresponding to the tips in the remaining tree

See Also

PCMTreeSpliAtNode PCMTreeDropClade

PCMTreeDtNodeRegimes *A data.table of the tips with their assigned regime*

Description

A data.table of the tips with their assigned regime

Usage

PCMTreeDtNodeRegimes(tree)

Arguments

tree a phylo object with node-labels and regimes

PCMTreeEdgeTimes *A matrix with the begin and end time from the root for each edge in tree*

Description

A matrix with the begin and end time from the root for each edge in tree

Usage

PCMTreeEdgeTimes(tree)

Arguments

tree a phylo

PCMTreeEvalNestedEDxOnTree

Perform nested extractions or drops of clades from a tree

Description

Perform nested extractions or drops of clades from a tree

Usage

```
PCMTreeEvalNestedEDxOnTree(expr, tree)
```

Arguments

expr	a character string representing an R expression of nested calls of functions $E(x, node)$ denoting extracting the clade rooted at node from the tree x , or $D(x, node)$, denoting dropping the clade rooted at node from the tree x . These calls can be nested, i.e. x can be either the symbol x (corresponding to the original tree passed as argument) or a nested call to d or e .
tree	a phylo object with named tips and internal nodes

Value

the resulting phylo object from evaluating `expr` on `tree`.

PCMTreeExtractBackboneRegimes

Prune the tree leaving one tip for each regime

Description

Prune the tree leaving one tip for each regime

Usage

```
PCMTreeExtractBackboneRegimes(tree)
```

Arguments

tree	a phylo with set node-labels and regimes
------	--

Value

a pruned version of `tree`

See Also

PCMTreeSetLabels PCMTreeSetRegimes

PCMTreeExtractClade *Extract a clade from phylogenetic tree*

Description

Extract a clade from phylogenetic tree

Usage

```
PCMTreeExtractClade(tree, cladeRootNode, tableAncestors = NULL,
  X = NULL, returnPhylo = is.null(X))
```

Arguments

tree	a phylo object
cladeRootNode	a character string denoting the label or an integer denoting a node in the tree.
tableAncestors	an integer matrix returned by a previous call to PCMTreeTableAncestors(tree) or NULL.
X	an optional k x N matrix with trait value vectors for each tip in tree.
returnPhylo	logical indicating if only the phylo object associated with the clade should be returned. Defaults to is.null(X)

Value

If returnPhylo is TRUE, a phylo object associated with the clade, otherwise, a list with two named members :

- treethe phylo object associated with the clade
- Xthe submatrix of X with columns corresponding to the tips in the clade

See Also

PCMTreeSpliAtNode PCMTreeDropClade

PCMTreeGetBranchLength

The length of the branch leading to a node

Description

The length of the branch leading to a node

Usage

```
PCMTreeGetBranchLength(tree, daughterId)
```

Arguments

tree a phylo object.
 daughterId an integer denoting the id of a daughter node

Value

a double denoting the length of the branch leading to daughterId

PCMTreeGetDaughters *A vector of the daughter nodes for a given parent node id in a tree*

Description

A vector of the daughter nodes for a given parent node id in a tree

Usage

```
PCMTreeGetDaughters(tree, parentId)
```

Arguments

tree a phylo object.
 parentId an integer denoting the id of the parent node

Value

an integer vector of the direct descendants of parentId

PCMTreeGetLabels *Get a vector of the tip and node labels in a tree*

Description

Get a vector of the tip and node labels in a tree

Usage

```
PCMTreeGetLabels(tree)
```

Arguments

tree a phylo object

Value

a character vector

PCMTreeGetParent *The parent node id of a daughter node in a tree*

Description

The parent node id of a daughter node in a tree

Usage

```
PCMTreeGetParent(tree, daughterId)
```

Arguments

tree a phylo object.
daughterId an integer denoting the id of the daughter node

Value

an integer denoting the parent of daughterId

PCMTreeGetRegimeForNode
Get the regime of the branch leading to a node or a tip

Description

Get the regime of the branch leading to a node or a tip

Usage

```
PCMTreeGetRegimeForNode(tree, node)
```

Arguments

tree a phylo object with an edge.regime member denoting regimes.
node an integer denoting the node

Value

a character or an integer denoting the regime of the branch leading to the node, according to tree\$edge.regime

 PCMTreeGetStartingNodesRegimes

Get the starting branch' nodes for each regime on a tree

Description

Get the starting branch' nodes for each regime on a tree

Usage

```
PCMTreeGetStartingNodesRegimes(tree, preorder = PCMTreePreorder(tree))
```

Arguments

tree	a phylo object with an edge.regime member denoting regimes. The function assumes that each regime covers a linked set of branches on the tree.
preorder	an integer vector of row-indices in tree\$edge as returned by PCMTreePreorder . Defaults to <code>PCMTreePreorder(tree)</code> . Specifying this argument may improve performance if <code>PCMTreePreorder</code> had to be called earlier.

Details

We call a starting branch the first branch from the root to the tips with a given regime. A starting node is the node at which a starting branch ends.

Value

an integer with elements equal to the starting nodes for each regime in regimes.

See Also

[PCMTreeSetRegimes](#)

 PCMTreeGetTipsInRegime

Get the tips belonging to a regime tree

Description

Get the tips belonging to a regime tree

Usage

```
PCMTreeGetTipsInRegime(tree, regime)
```

Arguments

tree	a phylo object with an edge.regime member
regime	a character or integer belonging to tree\$edge.regime

Value

an integer vector with the ids of the tips belonging to regime

PCMTreeInsertSingletons

Insert singleton nodes on chosen edges

Description

Insert singleton nodes on chosen edges

Usage

```
PCMTreeInsertSingletons(tree, nodes, positions)
```

```
PCMTreeInsertSingletonsAtEpoch(tree, epoch, minLength = 0.1)
```

Arguments

tree	a phylo object
nodes	an integer vector denoting the terminating nodes of the edges on which a singleton node is to be inserted
positions	a positive numeric vector of the same length as nodes denoting the root-ward distances from nodes at which the singleton nodes should be inserted.
epoch	a numeric indicating a distance from the root at which a singleton node should be inserted in all lineages that are alive at that time.
minLength	a numeric indicating the minimum allowed branch-length after dividing a branch by insertion of a singleton nodes. No singleton node is inserted if this would result in a branch shorter than 'minLength'. Note that this condition is checked only in 'PCMTreeInsertSingletonsAtEpoch'.

Value

a modified version of tree with inserted singleton nodes at the specified locations

Functions

- PCMTreeInsertSingletonsAtEpoch:

See Also

[PCMTreeEdgeTimes](#) [PCMTreeLocateEpochOnBranches](#) [PCMTreeLocateMidpointsOnBranches](#)

PCMTreeJumps

Jumps in modeled traits associated with branches in a tree

Description

Jumps in modeled traits associated with branches in a tree

Usage

```
PCMTreeJumps(tree)
```

Arguments

tree a phylo object

Value

an integer vector of 0's and 1's with entries correspondin to the denoting if a jump took place at the beginning of a branch.

PCMTreeListCladePartitions

A list of all possible partitions of a tree with a number of splitting nodes

Description

A list of all possible partitions of a tree with a number of splitting nodes

Usage

```
PCMTreeListCladePartitions(tree, nNodes, minCladeSize = 0,
  tableAncestors = NULL, verbose = FALSE)
```

Arguments

tree a phylo object

nNodes an integer giving the number of partitioning nodes. There would be nNodes+1 blocks in each partition (see details).

minCladeSize integer indicating the minimum number of tips allowed in a clade.

tableAncestors NULL (default) or an integer matrix returned by a previous call to PCMTreeTableAncestors(tree).

verbose a logical indicating if informative messages should be printed to the console.

Details

Each subset of `nNodes` distinct internal or tip nodes defines a partitioning of the branches of the tree into `nNodes+1` blocks. This function generates partitions in which `nNode` of the blocks are monophyletic complete groups (clades), while the `(nNodes+1)`'th block is a subtree originating at the root with tips ending at the rooting nodes of the `nNode` clades, eventually containing a clade of tips.

Value

a list of integer `nNodes`-vectors.

PCMTreeListDescendants

A list of the descendants for each node in a tree

Description

A list of the descendants for each node in a tree

Usage

```
PCMTreeListDescendants(tree,  
  tableAncestors = PCMTreeTableAncestors(tree))
```

Arguments

`tree` a phylo object
`tableAncestors` an integer matrix resulting from a call to `PCMTreeTableAncestors(tree)`.

Details

This function has time and memory complexity $O(M^2)$, where M is the number of nodes in the tree. It can take several minutes and gigabytes of memory on trees of more than 10000 tips.

Value

a list with unnamed elements in the order of nodes in the tree. Each element is an integer vector containing the descendant nodes (in increasing order) of the node identified by its index-number in the list.

PCMTreeListRootPaths *A list of the path to the root from each node in a tree*

Description

A list of the path to the root from each node in a tree

Usage

```
PCMTreeListRootPaths(tree, tableAncestors = PCMTreeTableAncestors(tree))
```

Arguments

tree a phylo object
tableAncestors an integer matrix resulting from a call to PCMTreeTableAncestors(tree).

Details

This function has time and memory complexity $O(M^2)$, where M is the number of nodes in the tree. It can take several minutes and gigabytes of memory on trees of more than 10000 tips.

Value

a list with unnamed elements in the order of nodes in the tree. Each element is an integer vector containing the ancestors nodes on the path from the node (i) to the root of the tree in that order (the first element in the vector is the parent node of i and so on).

PCMTreeLocateEpochOnBranches

Find the crossing points of an epoch-time with each lineage of a tree

Description

Find the crossing points of an epoch-time with each lineage of a tree

Usage

```
PCMTreeLocateEpochOnBranches(tree, epoch)
```

Arguments

tree a phylo
epoch a positive numeric ing tip-ward distance from the root

Value

a named list with an integer vector element "nodes" denoting the ending nodes for each branch crossing epoch and numeric vector element "positions" denoting the root-ward offset from each node in nodes.

PCMTreeLocateMidpointsOnBranches

Find the middle point of each branch longer than a threshold

Description

Find the middle point of each branch longer than a threshold

Usage

```
PCMTreeLocateMidpointsOnBranches(tree, threshold = 0)
```

Arguments

tree	a phylo
threshold	a positive numeric; only branches longer than threshold will be returned; Default 0.

Value

a named list with an integer vector element "nodes" denoting the ending nodes for each branch crossing epoch and numeric vector element "positions" denoting the root-ward offset from each node in nodes.

PCMTreeMatchLabels

Get the node numbers associated with tip- or node-labels in a tree

Description

Get the node numbers associated with tip- or node-labels in a tree

Usage

```
PCMTreeMatchLabels(tree, labels)
```

Arguments

tree	a phylo object
labels	a character vector with valid tip or node labels from tree

Value

an integer vector giving the tip- or node- integer indices corresponding to labels.

PCMTreeMatchRegimesWithModel

Regimes associated with branches in a tree

Description

Regimes associated with branches in a tree

Usage

```
PCMTreeMatchRegimesWithModel(tree, model,
  preorder = PCMTreePreorder(tree))
```

Arguments

tree	a phylo object
model	a PCM object
preorder	an integer vector of row-indices in tree\$edge matrix as returned by PCMTreePreorder. This can be given for performance speed-up when several operations needing preorder are executed on the tree. Default : PCMTreePreorder(tree).

Value

an integer vector with entries corresponding to the rows in tree\$edge denoting the regime on each branch in the tree as an index in PCMRegimes(model).

PCMTreeMatrixNodesInSameRegime

Which nodes in a tree belong to the same regime?

Description

Which nodes in a tree belong to the same regime?

Usage

```
PCMTreeMatrixNodesInSameRegime(tree, upperTriangle = TRUE,
  returnVector = TRUE)
```

Arguments

tree	a phylo object with an existing edge.regime
upperTriangle	logical indicating if all duplicated entries and diagonal entries could be set to NA (by default TRUE).
returnVector	logical indicating if a vector instead of a matrix should be returned (corresponding to calling as.vector on the resulting matrix and removing NAs). Default: TRUE

Value

a $M \times M$ logical matrix with TRUE on the diagonal and for each couple of tips that belong to the same dagonal. if returnVector is TRUE (default) only a vector of the non-NA entries will be returned.

PCMTreeMatrixTipsInSameRegime

Which tips in a tree belong to the same regime?

Description

Which tips in a tree belong to the same regime?

Usage

```
PCMTreeMatrixTipsInSameRegime(tree, upperTriangle = TRUE,
  returnVector = TRUE)
```

Arguments

tree	a phylo object with an existing edge.regime
upperTriangle	logical indicating if all duplicated entries and diagonal entries could be set to NA (by default TRUE).
returnVector	logical indicating if a vector instead of a matrix should be returned (corresponding to calling as.vector on the resulting matrix and removing NAs). Default: TRUE

Value

a $N \times N$ logical matrix with TRUE on the diagonal and for each couple of tips that belong to the same dagonal. if returnVector is TRUE (default) only a vector of the non-NA entries will be returned.

PCMTreeNearestNodesToEpoch

Find the nearest node to a given time from the root (epoch) on each lineage crossing this epoch

Description

Find the nearest node to a given time from the root (epoch) on each lineage crossing this epoch

Usage

```
PCMTreeNearestNodesToEpoch(tree, epoch)
```

Arguments

tree	a phylo
epoch	a positive numeric

Value

an integer vector

PCMTreeNodeTimes	<i>Calculate the time from the root to each node of the tree</i>
------------------	--

Description

Calculate the time from the root to each node of the tree

Usage

```
PCMTreeNodeTimes(tree, tipsOnly = FALSE)
```

Arguments

tree	an object of class phylo
tipsOnly	Logical indicating whether the returned results should be truncated only to the tips of the tree.

Value

A vector of size the number of nodes in the tree (tips, root, internal) containing the time from the root to the corresponding node in the tree.

PCMTreeNumNodes	<i>Number of all nodes in a tree</i>
-----------------	--------------------------------------

Description

Number of all nodes in a tree

Usage

```
PCMTreeNumNodes(tree)
```

Arguments

tree	a phylo object
------	----------------

Details

Wrapper for `nrow(tree$edge) + 1`

Value

the number of nodes in tree including root, internal and tips.

PCMTreeNumTips	<i>Wrapper for <code>length(tree\$tip.label)</code></i>
----------------	---

Description

Wrapper for `length(tree$tip.label)`

Usage

`PCMTreeNumTips(tree)`

Arguments

`tree` a phylo object

Value

the number of tips in tree

PCMTreeNumUniqueRegimes	<i>Number of unique regimes on a tree</i>
-------------------------	---

Description

Number of unique regimes on a tree

Usage

`PCMTreeNumUniqueRegimes(tree)`

Arguments

`tree` a phylo object

Value

the number of different regimes encountered on the tree branches

PCMTreePlot	<i>Plot a tree with regimes</i>
-------------	---------------------------------

Description

Plot a tree with regimes

Usage

```
PCMTreePlot(tree,
  palette = PCMColorPalette(PCMTreeNumUniqueRegimes(tree),
    PCMTreeUniqueRegimes(tree)), ...)
```

Arguments

tree	a phylo with set labels and regimes
palette	a named vector of colors corresponding to the regimes in tree
...	Arguments passed to ggtree, e.g. layout = 'fan', open.angle = 8, size=.25.

Note

Currently, the ggtree package is not on CRAN and therefore it is not explicitly imported by PCM-Base.

PCMTreePostorder	<i>Post-order tree traversal</i>
------------------	----------------------------------

Description

Post-order tree traversal

Usage

```
PCMTreePostorder(tree)
```

Arguments

tree	a phylo object with possible singleton nodes (i.e. internal nodes with one daughter node)
------	---

Value

a vector of indices of edges in tree\$edge in post-order.

PCMTreePreorder	<i>Pre-order tree traversal</i>
-----------------	---------------------------------

Description

Pre-order tree traversal

Usage

```
PCMTreePreorder(tree)
```

Arguments

tree	a phylo object with possible singleton nodes (i.e. internal nodes with one daughter node)
------	---

Value

a vector of indices of edges in tree\$edge in pre-order.

PCMTreeSetDefaultRegime	
-------------------------	--

Set a default edge.regime member of the passed tree object

Description

This function sets or overwrites the current member edge.regime in tree with one of the following:

- rep(regime[1], length(tree\$edge.length))if regime is a character or an integer
- rep(PCMRegimes(regime)[1], length(tree\$edge.length))if regime is a PCM model

Note that the function modifies the passed tree object inplace.

Usage

```
PCMTreeSetDefaultRegime(tree, regime)
```

Arguments

tree	a phylo object
regime	a character, an integer or PCM model object

Value

This function does not return a value but has a side effect on the passed tree object.

PCMTreeSetLabels *Set tip and internal node labels in a tree*

Description

Set tip and internal node labels in a tree

Usage

```
PCMTreeSetLabels(tree, labels = as.character(1:PCMTreeNumNodes(tree)),
  inplace = TRUE)
```

Arguments

tree	a phylo object
labels	a character vector in the order 1:PCMTreeNumNodes(tree) as denoted in the tree\$edge matrix.
inplace	a logical indicating if the change should be done in place on the object in the calling environment (in this case tree must not be a temporary object, e.g. returned by another function call). Default is TRUE.

Value

if inplace = FALSE, a copy of tree with set or modified tree\$tip.label and tree\$node.label, otherwise nothing.

PCMTreeSetRegimes *Assign regimes on a tree given a set of starting branches*

Description

Assign regimes on a tree given a set of starting branches

Usage

```
PCMTreeSetRegimes(tree, nodes, regimes = as.integer(1:(length(nodes) +
  1)), inplace = TRUE)
```

Arguments

tree	a phylo object
nodes	a character vector containing tip or node labels or an integer vector denoting tip or internal nodes in tree - the regimes change at the start of the branches leading to these nodes.
regimes	an integer or character vector of length equal to length(nodes) + 1 containing the regime-names to be assigned for each regime. If NULL the regime names will be the integers 1:(length(nodes) + 1).
inplace	a logical indicating if the change should be done to the tree in the calling environment (TRUE) or a copy of the tree with set edge.regime member should be returned (FALSE). Default is TRUE.

Details

It is assumed that each regime "paints" a linked subset of branches on a tree. Thus, each regime is fully described by its starting branch. The descendant branches inherit this regime until reaching a tip or a node that is present in the nodes parameter.

Value

If inplace is TRUE nothing, otherwise a copy of the tree with set edge.regime member.

See Also

[PCMTreeGetStartingNodesRegimes](#)

PCMTreeSplitAtNode	<i>Slit a tree at a given internal node into a clade rooted at this node and the remaining tree after dropping this clade</i>
--------------------	---

Description

Slit a tree at a given internal node into a clade rooted at this node and the remaining tree after dropping this clade

Usage

```
PCMTreeSplitAtNode(tree, node,
  tableAncestors = PCMTreeTableAncestors(tree), X = NULL)
```

Arguments

tree	a phylo object
node	an integer or character indicating a root, internal or tip node
tableAncestors	an integer matrix returned by a previous call to PCMTreeTableAncestors(tree) or NULL.
X	an optional k x N matrix with trait value vectors for each tip in tree.

Details

In the current implementation, the `edge.jump` and `edge.regime` members of the tree will be discarded and not present in the clade.

TODO: `preserveRegimes` and `preserve regimes`

Value

A list containing two named phylo objects:

- `clade` The subtree (clade) starting at node.
- `Xclade` The portion of X attributable to the tips in clade; NULL if X is NULL.
- `rest` The tree resulting after dropping all tips in the clade.
- `Xrest` The portion of X attributable to the tips in rest; NULL if X is NULL.

PCMTreeTableAncestors *A matrix (table) of ancestors/descendants for each node in a tree*

Description

A matrix (table) of ancestors/descendants for each node in a tree

Usage

```
PCMTreeTableAncestors(tree, preorder = PCMTreePreorder(tree))
```

Arguments

<code>tree</code>	a phylo object
<code>preorder</code>	an integer vector returned by a previous call to <code>PCMTreePreorder(tree)</code> . Default <code>PCMTreePreorder(tree)</code> .

Details

This function has time and memory complexity $O(M^2)$, where M is the number of nodes in the tree. It can take several minutes and gigabytes of memory on trees of more than 10000 tips.

Value

an integer square matrix of size $M \times M$ where M is the number of nodes in the tree. Element j on row i is 0 if j is not an ancestor of i or a positive integer equal to the position of j on the path from the root to i if j is an ancestor of i.

PCMTreeToString	<i>A character representation of a phylo object.</i>
-----------------	--

Description

A character representation of a phylo object.

Usage

```
PCMTreeToString(tree, includeLengths = FALSE,
  includeStartingNodesRegimes = FALSE)
```

Arguments

tree	a phylo object.
includeLengths	logical. Default: FALSE.
includeStartingNodesRegimes	logical. Default: FALSE.

Value

a character string.

PCMTreeUniqueRegimes	<i>Unique regimes on a tree in the order of occurrence from the root to the tips (preorder)</i>
----------------------	---

Description

Unique regimes on a tree in the order of occurrence from the root to the tips (preorder)

Usage

```
PCMTreeUniqueRegimes(tree, preorder = PCMTreePreorder(tree))
```

Arguments

tree	a phylo object with an additional member <code>edge.regime</code> which should be a character or an integer vector of length equal to the number of branches.
preorder	an integer vector of row-indices in <code>tree\$edge</code> matrix as returned by <code>PCMTreePreorder</code> . This can be given for performance speed-up when several operations needing <code>preorder</code> are executed on the tree. Default : <code>PCMTreePreorder(tree)</code> .

Value

a character or an integer vector depending on `tree$edge.regime`.

PCMUnfixParameter *Unfix a parameter in a PCM model*

Description

Unfix a parameter in a PCM model

Usage

```
PCMUnfixParameter(model, name)
```

Arguments

model	a PCM object
name	a character string

Value

a copy of the model with removed class `'_Fixed'` from the class of the parameter name

PCMVar *Expected variance-covariance matrix for each couple of tips (i,j)*

Description

Expected variance-covariance matrix for each couple of tips (i,j)

Usage

```
PCMVar(tree, model, W0 = matrix(0, PCMNumTraits(model),
  PCMNumTraits(model)), metaI = PCMInfo(NULL, tree, model, verbose),
  internal = FALSE, verbose = FALSE)
```

Arguments

tree	a phylo object with N tips.
model	an S3 object specifying both, the model type (class, e.g. "OU") as well as the concrete model parameter values at which the likelihood is to be calculated (see also Details).
W0	a numeric matrix denoting the initial k x k variance covariance matrix at the root (default is the k x k zero matrix).
metaI	a list returned from a call to <code>PCMInfo(X, tree, model)</code> , containing meta-data such as N, M and k.
internal	a logical indicating if the per-node variance-covariances matrices for the internal nodes should be returned (see Value). Default FALSE.
verbose	logical indicating if some debug-messages should be printed.

Value

If `internal` is `FALSE`, a $(k \times N) \times (k \times N)$ matrix `W`, such that $k \times k$ block $W[((i-1)*k)+(1:k), ((j-1)*k)+(1:k)]$ equals the expected covariance matrix between tips i and j . Otherwise, a list with an element 'W' as described above and a $k \times M$ matrix element 'Wii' containing the per-node variance covariance matrix for each node: The $k \times k$ block $Wii[, (i-1)*k + (1:k)]$ represents the variance covariance matrix for node i .

Examples

```
# a Brownian motion model with one regime
modelBM <- PCM(model = "BM", k = 2)
# print the model
modelBM
# assign the model parameters at random: this will use uniform distribution
# with boundaries specified by PCMPParamLowerLimit and PCMPParamUpperLimit
# We do this in two steps:
# 1. First we generate a random vector. Note the length of the vector equals PCMPParamCount(modelBM)
randomParams <- PCMPParamRandomVecParams(modelBM, PCMPParamCount(modelBM), PCMPParamUpperLimit(modelBM))
randomParams
# 2. Then we load this random vector into the model.
PCMPParamLoadOrStore(modelBM, randomParams, 0, PCMPParamCount(modelBM), PCMPParamUpperLimit(modelBM), TRUE)

# create a random tree of 10 tips
tree <- ape::rtree(10)
covMat <- PCMVar(tree, modelBM)
```

PCMVarAtTime	<i>Calculate the variance covariance $k \times k$ matrix at time t, under a PCM model</i>
--------------	---

Description

Calculate the variance covariance $k \times k$ matrix at time t , under a PCM model

Usage

```
PCMVarAtTime(t, model, W0 = matrix(0, PCMPParamCount(model),
  PCMPParamCount(model)), regime = 1L, verbose = FALSE)
```

Arguments

<code>t</code>	positive numeric denoting time
<code>model</code>	a PCM model object
<code>W0</code>	a numeric matrix denoting the initial $k \times k$ variance covariance matrix at the root (default is the $k \times k$ zero matrix).
<code>regime</code>	an integer or a character denoting the regime in model for which to do the calculation; (Defaults to 1L meaning the first regime in the model)
<code>verbose</code>	a logical indicating if (debug) messages should be written on the console (Defaults to FALSE).

Value

A numeric $k \times k$ matrix

Examples

```
# a Brownian motion model with one regime
modelBM <- PCM(model = "BM", k = 2)
# print the model
modelBM
# assign the model parameters at random: this will use uniform distribution
# with boundaries specified by PCMPParamLowerLimit and PCMPParamUpperLimit
# We do this in two steps:
# 1. First we generate a random vector. Note the length of the vector equals PCMPParamCount(modelBM)
randomParams <- PCMPParamRandomVecParams(modelBM, PCMPParamCount(modelBM), PCMPParamLowerLimit(modelBM), PCMPParamUpperLimit(modelBM))
randomParams
# 2. Then we load this random vector into the model.
PCMPParamLoadOrStore(modelBM, randomParams, 0, PCMPParamCount(modelBM), PCMPParamLowerLimit(modelBM), PCMPParamUpperLimit(modelBM), TRUE)

# PCMPVarAtTime(1, modelBM)

# note that the variance at time 0 is not the 0 matrix because the model has a non-zero
# environmental deviation
PCMPVarAtTime(0, modelBM)
```

 White

White Gaussian PCM ignoring phylogenetic history

Description

White model ignoring phylogenetic history, treating trait values as independent samples from a k -variate Gaussian.

Details

Calculating likelihoods for this model does not work if the global option `PCMPBase.Singular.Skip` is set to `FALSE`.

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