

Package ‘phybaseR’

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Type Package

Title phybaseR: An R package to easily create and run PhyBaSE models

Version 1.0

Description Provides tools for specifying and fitting Phylogenetic Bayesian Structural Equation Models (PhyBaSE) using JAGS. PhyBaSE models allow causal inference in phylogenetic comparative analyses, accounting for phylogenetic uncertainty and handling missing data. Implements and expands on the methods described in von Hardenberg and Gonzalez-Voyer (2025) <[doi:10.1111/2041-210X.70044](https://doi.org/10.1111/2041-210X.70044)>.

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LazyData true

Imports rjags, ape, ggm, coda, stats, parallel, utils

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|------------------|---|
| equations_to_dag | <i>Convert phybaseR equations to ggm DAG adjacency matrix</i> |
|------------------|---|

Description

Convert phybaseR equations to ggm DAG adjacency matrix

Usage

```
equations_to_dag(equations)
```

Arguments

| | |
|-----------|------------------|
| equations | List of formulas |
|-----------|------------------|

Value

Named adjacency matrix in ggm format

| | |
|--------------------------|---|
| extract_bidirected_edges | <i>Extract bidirected edges (induced correlations) from MAG</i> |
|--------------------------|---|

Description

Extract bidirected edges (induced correlations) from MAG

Usage

```
extract_bidirected_edges(mag)
```

Arguments

| | |
|-----|--------------------------------------|
| mag | MAG adjacency matrix from DAG.to.MAG |
|-----|--------------------------------------|

Value

List of variable pairs with induced correlations

mag_basis_to_formulas *Convert MAG basis set to phybaseR formula format*

Description

Convert MAG basis set to phybaseR formula format

Usage

```
mag_basis_to_formulas(basis_set)
```

Arguments

basis_set Basis set from basiSet.mag()

Value

List of formulas with test_var attribute

phybase_compare *Compare PhyBaSE Models*

Description

A unified function to either (1) compare previously fitted models, or (2) run multiple model specifications in parallel and then compare them.

Usage

```
phybase_compare(
  ...,
  model_specs = NULL,
  data = NULL,
  tree = NULL,
  n.cores = 1,
  cl = NULL,
  sort = TRUE
)
```

Arguments

| | |
|-------------|---|
| ... | For comparing fitted models: individual fitted model objects of class "phybase". For running models: additional arguments passed to phybase_run (e.g., n.iter). |
| model_specs | A named list of model specifications to run (Mode 2). Each element should be a list containing arguments for phybase_run. Alternatively, this argument can accept the first fitted model object (Mode 1). |
| data | The dataset (required for Mode 2). Alternatively, the second fitted model object (Mode 1). |

| | |
|---------|---|
| tree | The phylogenetic tree (optional for Mode 2). Alternatively, the third fitted model object (Mode 1). |
| n.cores | Number of cores for parallel execution (Mode 2). Default is 1. |
| cl | Optional cluster object (Mode 2). |
| sort | Logical. If TRUE (default), sort comparison table by WAIC. |

Details

Mode 1: Compare Fitted Models Call `phybase_compare(fit1, fit2)` or `phybase_compare(models = list(fit1, fit2))`. Extracts WAIC (with SE) from each model and ranks them.

Mode 2: Run and Compare Call `phybase_compare(model_specs = list(m1=..., m2=...), data=data, tree=tree)`. This runs the models in parallel and returns the comparison.

Value

If comparing fitted models: A class "phybase_comparison" object (data frame) with WAIC rankings.

If running models: A list containing:

| | |
|------------|-------------------------------|
| results | List of fitted model objects. |
| comparison | The comparison data frame. |

Examples

```
## Not run:
# Mode 1: Compare existing fits
phybase_compare(fit1, fit2)

# Mode 2: Run and compare
specs <- list(m1 = list(equations = list(Y ~ X)), m2 = list(equations = list(Y ~ X + Z)))
res <- phybase_compare(specs, data = df, tree = tr, n.cores = 2)
print(res$comparison)

## End(Not run)
```

phybase_dsep

Extract d-separation statements from a structural equation model

Description

This function takes a set of structural equations defining a causal model and returns the conditional independence statements (d-separation or m-separation tests) implied by the model structure. If latent variables are specified, the function uses the MAG (Maximal Ancestral Graph) approach by Shipley and Douma (2021) to account for unmeasured latent variables.

Usage

```
phybase_dsep(equations, latent = NULL, quiet = FALSE)
```

Arguments

| | |
|------------------------|--|
| <code>equations</code> | A list of model formulas (one per structural equation), e.g., <code>list(Y ~ X1 + X2, Z ~ Y)</code> . |
| <code>latent</code> | Optional character vector of latent (unmeasured) variable names. If provided, the function converts the DAG to a MAG and returns m-separation tests. |
| <code>quiet</code> | Logical; if FALSE (default), print the basis set and MAG structure. If TRUE, suppress informational output. |

Details

The function implements the basis set approach to d-separation testing (Shipley 2000, 2009, 2016). For standard DAGs without latent variables, it identifies pairs of non-adjacent variables and creates conditional independence tests.

When latent variables are specified, the function uses the DAG-to-MAG conversion (Shipley & Douma 2021) to identify m-separation statements and induced correlations among observed variables that arise from shared latent common causes.

Value

If `latent` is NULL, returns a list of formulas representing conditional independence tests. If `latent` is specified, returns a list with:

- `tests`: List of m-separation test formulas
- `correlations`: List of variable pairs with induced correlations

References

- Shipley, B. (2000). A new inferential test for path models based on directed acyclic graphs. *Structural Equation Modeling*, 7(2), 206-218.
- Shipley, B. (2009). Confirmatory path analysis in a generalized multilevel context. *Ecology*, 90(2), 363-368.
- Shipley, B. (2016). *Cause and Correlation in Biology* (2nd ed.). Cambridge University Press.
- Shipley, B., & Douma, J. C. (2021). Testing Piecewise Structural Equations Models in the Presence of Latent Variables and Including Correlated Errors. *Structural Equation Modeling: A Multidisciplinary Journal*, 28(4), 582–589. <https://doi.org/10.1080/10705511.2020.1871355>

Examples

```
# Standard DAG
equations <- list(LS ~ BM, NL ~ BM + RS, DD ~ NL)
ind_tests <- phybase_dsep(equations)

# With latent variable
equations_latent <- list(X ~ Quality, Y ~ Quality)
result <- phybase_dsep(equations_latent, latent = "Quality")
# result$tests: m-separation tests
# result$correlations: induced correlation between X and Y
```

phybase_format_data *Format Data for PhyBaSE Analysis*

Description

Converts data from long format (one row per observation) to the list format required by [phybase_run](#).

Usage

```
phybase_format_data(data, species_col = "SP", tree)
```

Arguments

| | |
|-------------|---|
| data | A data.frame in long format with one row per observation. |
| species_col | Name of the column containing species identifiers (default: "SP"). |
| tree | A phylogenetic tree (class phylo). Required to determine species order. |

Details

This function handles:

- Different numbers of replicates per species (creates rectangular matrix with NA padding)
- Missing values (NA)
- Automatic alignment with phylogenetic tree tip labels

When species have different numbers of replicates, the function creates a matrix with dimensions (number of species) x (maximum number of replicates). Species with fewer replicates are padded with NA values.

Species in the tree but not in the data will have all NA values. Species in the data but not in the tree will be excluded with a warning.

Value

A named list where each element is either:

- A numeric vector (if all species have exactly 1 observation)
- A numeric matrix with species in rows and replicates in columns

Species are ordered to match `tree$tip.label`.

Examples

```
## Not run:
# Example data in long format
data_long <- data.frame(
  SP = c("sp1", "sp1", "sp1", "sp2", "sp2", "sp3"),
  BM = c(1.2, 1.3, 1.1, 2.1, 2.2, 1.8),
  NL = c(0.5, 0.6, NA, 0.7, 0.8, 0.9)
)

tree <- ape::read.tree(text = "(sp1:1,sp2:1,sp3:1);")
data_list <- phybase_format_data(data_long, species_col = "SP", tree = tree)
```

```
# Use with phybase_run
fit <- phybase_run(data = data_list, tree = tree, equations = list(NL ~ BM))

## End(Not run)
```

phybase_loo

Calculate LOO-CV for a PhyBaSE Model

Description

Calculates Leave-One-Out Cross-Validation using Pareto Smoothed Importance Sampling (PSIS-LOO) for a fitted PhyBaSE model.

Usage

```
phybase_loo(model, ...)
```

Arguments

| | |
|-------|--|
| model | A fitted model object of class "phybase" returned by phybase_run . |
| ... | Additional arguments passed to <code>loo::loo()</code> . |

Details

LOO-CV (Leave-One-Out Cross-Validation) uses Pareto Smoothed Importance Sampling to approximate leave-one-out predictive performance without refitting the model N times. This is particularly useful for:

- Model comparison when models have different numbers of latent variables
- Identifying influential observations (via Pareto k diagnostics)
- Robust predictive performance assessment

****Pareto k diagnostics**:**

- $k < 0.5$: Excellent (all estimates reliable)
- $0.5 < k < 0.7$: Good (estimates okay)
- $0.7 < k < 1$: Problematic (estimates unreliable)
- $k > 1$: Very problematic (refit model excluding these observations)

****Note on implementation**:** This function computes pointwise log-likelihoods from the posterior samples. For phylogenetic models, this is done by evaluating the multivariate normal log-likelihood for each observation given the posterior parameter values.

Value

A loo object containing:

| | |
|-------------|---|
| estimates | Table with ELPD (expected log pointwise predictive density), LOO-IC, and <code>p_loo</code> |
| diagnostics | Pareto k diagnostic values for each observation |
| pointwise | Pointwise contributions to LOO-IC |

Examples

```
## Not run:
fit <- phybase_run(data, tree, equations)
loo_result <- phybase_loo(fit)
print(loo_result)

# Check for problematic observations
plot(loo_result)

# Compare models
loo_compare(loo_result1, loo_result2)

## End(Not run)
```

| | |
|---------------------|------------------------------------|
| phybase_loo_compare | <i>Compare Models Using LOO-CV</i> |
|---------------------|------------------------------------|

Description

Wrapper for `loo::loo_compare()` to compare multiple PhyBaSE models.

Usage

```
phybase_loo_compare(...)
```

Arguments

... Two or more loo objects from `phybase_loo()`.

Value

A comparison table ranking models by expected out-of-sample predictive accuracy.

Examples

```
## Not run:
loo1 <- phybase_loo(fit1)
loo2 <- phybase_loo(fit2)
phybase_loo_compare(loo1, loo2)

## End(Not run)
```

| | |
|---------------|--|
| phybase_model | <i>Generate a JAGS model string for Phylogenetic Bayesian SEM (Phy-BaSE)</i> |
|---------------|--|

Description

This function builds the model code to be passed to JAGS based on a set of structural equations. It supports both single and multiple phylogenetic trees (to account for phylogenetic uncertainty). Missing values are handled both in the response and predictor variables treating all of them as stochastic nodes.

Usage

```
phybase_model(
  equations,
  multi.tree = FALSE,
  variability = NULL,
  distribution = NULL,
  vars_with_na = NULL,
  induced_correlations = NULL,
  latent = NULL,
  standardize_latent = TRUE,
  optimise = TRUE,
  structure_names = NULL
)
```

Arguments

| | |
|--------------|---|
| equations | A list of model formulas. |
| multi.tree | Logical; if TRUE, incorporates phylogenetic uncertainty by sampling across a set of trees. |
| variability | Optional character vector or named character vector of variable names that have measurement error or within-species variability. If named, the names should be the variable names and the values should be the type of variability: "se" (for mean and standard error) or "reps" (for repeated measures). If unnamed, it defaults to "se" for all specified variables. <ul style="list-style-type: none"> "se": Expects Var_mean and Var_se in the data. The model fixes observation error: $\text{Var_mean} \sim \text{dnorm}(\text{Var}, 1/\text{Var_se}^2)$. "reps": Expects Var_obs (matrix) and N_reps_Var (vector) in the data. The model estimates observation error: $\text{Var_obs}[i, j] \sim \text{dnorm}(\text{Var}[i], \text{Var_tau})$. |
| distribution | Optional named character vector specifying the distribution for response variables. Default is "gaussian" for all variables. Supported values: "gaussian", "binomial", "multinomial". For "binomial" variables, the model uses a logit link and a Bernoulli likelihood, with phylogenetic correlation modeled on the latent scale. |
| vars_with_na | Optional character vector of response variable names that have missing data. These variables will use element-wise likelihoods instead of multivariate normal. |

| | |
|-----------------------------------|---|
| <code>induced_correlations</code> | Optional list of variable pairs with induced correlations from latent variables. Each element should be a character vector of length 2 specifying the pair of variables that share a latent common cause. |
| <code>latent</code> | Optional character vector of latent variable names. |
| <code>standardize_latent</code> | Logical (default TRUE). If TRUE, standardizes latent variables to unit variance. |
| <code>optimise</code> | Logical. If TRUE (default), use random effects formulation for 4.6× speedup. If FALSE, use original marginal covariance formulation. |
| <code>structure_names</code> | (Internal) Character vector of names for multiple trees/structures. |

Details

The generated model includes:

- Linear predictors and multivariate normal likelihoods for each response variable.
- Priors for intercepts (α), slopes (β), lambda parameters (λ), and residual precisions (τ).
- Phylogenetic covariance modeled via a single VCV matrix (when `multi.tree = FALSE`) or a 3D array `multiVCV[, , K]` with categorical sampling across trees (when `multi.tree = TRUE`).
- (Optional) Observation models for variables with measurement error:
 - Type "se": $\text{Var_mean} \sim \text{dnorm}(\text{Var}, 1/\text{Var_se}^2)$
 - Type "reps": $\text{Var_obs}[i, j] \sim \text{dnorm}(\text{Var}[i], \text{Var_tau})$
- (Optional) Generalized linear mixed models for non-Gaussian responses (e.g., binomial).
- (Optional) Element-wise likelihoods for response variables with missing data.

Value

A list with two elements:

- `model`: A character string containing the JAGS model code.
- `parameter_map`: A data frame mapping response variables to their predictors and parameter names.

Examples

```
eqs <- list(BR ~ BM, S ~ BR, G ~ BR, L ~ BR)
cat(phybase_model(eqs, multi.tree = TRUE)$model)
```

phybase_run

Run a Phylogenetic Bayesian Structural Equation model (PhyBaSE)

Description

Run a Phylogenetic Bayesian Structural Equation model (PhyBaSE)

Usage

```
phybase_run(
  data,
  equations,
  id_col = NULL,
  structure = NULL,
  tree = NULL,
  monitor = NULL,
  n.chains = 3,
  n.iter = 12500,
  n.burnin = n.iter/5,
  n.thin = 10,
  DIC = TRUE,
  WAIC = FALSE,
  n.adapt = n.iter/5,
  quiet = FALSE,
  dsep = FALSE,
  variability = NULL,
  distribution = NULL,
  latent = NULL,
  latent_method = c("correlations", "explicit"),
  standardize_latent = TRUE,
  parallel = FALSE,
  n.cores = 1,
  cl = NULL,
  ic_recompile = TRUE,
  optimise = TRUE
)
```

Arguments

- | | |
|-----------|---|
| data | <p>Data for the model. Accepts:</p> <ul style="list-style-type: none"> • <code>data.frame</code>: A data frame with variables as columns. Variables needed for the model are automatically extracted from the equations. Extra columns are ignored. • <code>list</code>: A named list where each element is a vector of values (traditional format for backward compatibility). |
| equations | A list of model formulas describing the structural equation model. |
| id_col | <p>Character string specifying the column name in a data.frame containing unit identifiers (species, individuals, sites, etc.). This is used to:</p> <ul style="list-style-type: none"> • Match data rows to tree tip labels (for phylogenetic models) |

| | |
|-------------|---|
| | <ul style="list-style-type: none"> • Handle repeated measures (multiple rows per unit share the same covariance) <p>If NULL (default): uses meaningful row names if available. Ignored when data is already a list.</p> |
| structure | <p>The covariance structure for the model. Accepts:</p> <ul style="list-style-type: none"> • "phylo" object: Phylogenetic tree (Standard PGLS/PhyloSEM). • "multiPhylo" object: List of trees (incorporates phylogenetic uncertainty). • NULL: Independent model (Standard SEM, no covariance structure). • matrix: Custom covariance or precision matrix (e.g., spatial connectivity, kinship). |
| tree | (Deprecated alias for structure). A single phylogenetic tree of class "phylo" or a list of trees. Use structure instead for new code. |
| monitor | <p>Parameter monitoring mode. Options:</p> <ul style="list-style-type: none"> • "interpretable" (default): Monitor only scientifically meaningful parameters: intercepts (alpha), regression coefficients (beta), phylogenetic signals (lambda) for responses, and WAIC terms. Excludes variance components (tau) and auxiliary predictor parameters. • "all": Monitor all model parameters including variance components and implicit equation parameters. • Custom vector: Provide a character vector of specific parameter names to monitor. • NULL: Auto-detect based on model structure (equivalent to "interpretable"). |
| n.chains | Number of MCMC chains (default = 3). |
| n.iter | Total number of MCMC iterations (default = 12500). |
| n.burnin | Number of burn-in iterations (default = n.iter / 5). |
| n.thin | Thinning rate (default = 10). |
| DIC | <p>Logical; whether to compute DIC using <code>dic.samples()</code> (default = TRUE). **Note**: DIC penalty will be inflated for models with measurement error or repeated measures because latent variables are counted as parameters (penalty ~ structural parameters + N). For model comparison, use WAIC or compare mean deviance across models with similar structure.</p> |
| WAIC | <p>Logical; whether to sample values for WAIC and deviance (default = FALSE). WAIC is generally more appropriate than DIC for hierarchical models with latent variables.</p> |
| n.adapt | Number of adaptation iterations (default = n.iter / 5). |
| quiet | Logical; suppress JAGS output (default = FALSE). |
| dsep | Logical; if TRUE, monitor only the first beta in each structural equation (used for d-separation testing). |
| variability | <p>Optional specification for variables with measurement error or within-species variability. **AUTO-DETECTION**: If a variable X has a corresponding column X_se (standard errors), X_obs (repeated measures), or is provided as a matrix, variability is automatically detected.</p> <p>**Manual specification** (for non-standard column names):</p> <ul style="list-style-type: none"> • Simple: <code>list(X = "se", Y = "reps")</code> - uses standard X_se/Y_obs naming • Custom columns: <code>list(X = list(type = "se", se_col = "X_SD"))</code> - specify custom column names |

| | |
|---------------------------------|--|
| | <ul style="list-style-type: none"> • For SE: <code>se_col</code> (SE column), <code>mean_col</code> (mean column, optional) • For reps: <code>obs_col</code> (observations matrix column) |
| <code>distribution</code> | <p>Optional named character vector specifying the distribution for response variables. Default is "gaussian" for all variables. Supported values:</p> <ul style="list-style-type: none"> • "gaussian" (default) • "binomial" (binary data) • "multinomial" (unordered categorical > 2 levels) • "ordinal" (ordered categorical > 2 levels) • "poisson" (count data) • "negbinomial" (overdispersed count data) <p>Example: <code>distribution = c(Gregarious = "binomial")</code>.</p> |
| <code>latent</code> | Optional character vector of latent (unmeasured) variable names. If specified, the model will account for induced correlations among observed variables that share these latent common causes. |
| <code>latent_method</code> | <p>Method for handling latent variables (default = "correlations").</p> <ul style="list-style-type: none"> • "correlations": MAG approach - marginalize latent variables and estimate induced correlations (ρ) between observed variables that share latent parents. • "explicit": Model latent variables as JAGS nodes and estimate structural paths from latents to observed variables. |
| <code>standardize_latent</code> | Logical; if TRUE and <code>latent_method = "explicit"</code> , adds standardized priors ($N(0, 1)$) to latent variables to identify scale and location. This improves convergence and makes regression coefficients interpretable as standardized effects. Only applicable when using explicit latent variable modeling (default = TRUE). |
| <code>parallel</code> | Logical; if TRUE, run MCMC chains in parallel (default = FALSE). Note: Requires <code>n.cores > 1</code> to take effect. |
| <code>n.cores</code> | Integer; number of CPU cores to use for parallel chains (default = 1). Only used when <code>parallel = TRUE</code> . |
| <code>cl</code> | Optional; a cluster object created by <code>parallel::makeCluster()</code> . If NULL, a cluster will be created and destroyed automatically. |
| <code>ic_recompile</code> | Logical; if TRUE and <code>parallel = TRUE</code> , recompile the model after parallel chains to compute DIC/WAIC (default = TRUE). This adds a small sequential overhead but enables information criteria calculation. |
| <code>optimise</code> | Logical; if TRUE (default), use the optimized random effects formulation for phylogenetic models. This is significantly faster (5-10x) and more numerically stable. If FALSE, use the traditional marginal formulation (slower, but provided for comparison). |

Value

A list of class "phybase" with model output and diagnostics.

phybase_waic

Calculate WAIC with Standard Errors for a PhyBaSE Model

Description

Calculates the Widely Applicable Information Criterion (WAIC) with standard errors for a fitted PhyBaSE model using pointwise log-likelihoods.

Usage

```
phybase_waic(model)
```

Arguments

model A fitted model object of class "phybase" returned by [phybase_run](#) with WAIC = TRUE.

Details

This function implements WAIC following Vehtari et al. (2017). It requires that the model was run with WAIC = TRUE to monitor pointwise log-likelihoods.

Value

A data frame with columns Estimate and SE containing:

| | |
|-----------|--|
| elpd_waic | Expected log pointwise predictive density (higher is better) |
| p_waic | Effective number of parameters |
| waic | The WAIC value (lower is better for model comparison) |

The returned object also has a pointwise attribute containing individual observation contributions for model comparison.

WAIC Definition

The Widely Applicable Information Criterion (WAIC) is calculated as:

$$WAIC = -2 \times (lppd - p_{waic})$$

where:

- $lppd = \sum_{i=1}^N \log(\frac{1}{S} \sum_{s=1}^S \exp(\log_{lik_{is}}))$ is the log pointwise predictive density
- $p_{waic} = \sum_{i=1}^N \text{var}(\log_{lik_{is}})$ is the effective number of parameters

****WAIC Algorithm**:**

1. **lpd** (log pointwise predictive density): For each observation i , compute $\log(\text{mean}(\exp(\log_{lik_i})))$ across MCMC samples
2. **p_waic**: For each observation i , compute $\text{var}(\log_{lik_i})$ across MCMC samples
3. **elpd_waic**: $lpd_i - p_{waic_i}$ for each observation
4. **waic**: $-2 \times \sum \text{elpd_waic}_i$

Standard Errors

Standard errors for WAIC are calculated using the pointwise contributions:

$$SE(WAIC) = \sqrt{N \times \text{var}(waic_i)}$$

where $waic_i = -2 \times (lppd_i - p_{waic,i})$.

References

Vehtari, A., Gelman, A., & Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*, 27(5), 1413-1432.

Examples

```
## Not run:
# Fit model with WAIC monitoring
fit <- phybase_run(data, tree, equations, WAIC = TRUE)

# View WAIC with standard errors
fit$WAIC
#           Estimate    SE
# elpd_waic   -617.3   12.4
# p_waic       12.3    3.1
# waic        1234.5   24.8

# Compare two models
fit1$WAIC
fit2$WAIC
# Model with lower WAIC is preferred
# Difference is significant if |WAIC1 - WAIC2| > 2 * sqrt(SE1^2 + SE2^2)

## End(Not run)
```

rhino.dat

Rhinograd life-history data

Description

A dataset containing simulated life-history trait data for 100 Rhinograd species. This data is used to demonstrate phylogenetic Bayesian structural equation modeling with the phybaseR package.

Usage

```
rhino.dat
```

Format

A data frame with 100 rows (one per species) and 6 columns:

SP Character. Species names matching the tip labels in rhino.tree

BM Numeric. Body mass (standardised)

LS Numeric. Litter size (standardised)

NL Numeric. Nose length (standardised)

DD Numeric. Dispersal distance (standardised)

RS Numeric. Range size (standardised)

Details

This simulated dataset represents life-history traits for hypothetical Rhinograd species. The data can be used to test causal hypotheses about life-history evolution using phylogenetic structural equation models.

Example causal model (Model 8 from Gonzalez-Voyer and von Hardenberg (2014)):

- Body mass (BM) affects litter size (LS)
- Body mass (BM) and range size (RS) affect nose length (NL)
- Nose length (NL) affects dispersal distance (DD)

Source

Simulated data for Gonzalez-Voyer & von Hardenberg (2014)

References

Gonzalez-Voyer, A., & von Hardenberg, A. (2014). An introduction to phylogenetic path analysis. In: Modern phylogenetic comparative methods and their application in evolutionary biology (pp. 201–229). Springer.

Examples

```
data(rhino.dat)
head(rhino.dat)
summary(rhino.dat)
```

rhino.tree

Rhinograd phylogenetic tree

Description

A phylogenetic tree (phylo object) for 100 simulated Rhinograd species. This tree is used to demonstrate phylogenetic Bayesian structural equation modeling with the phybaseR package.

Usage

```
rhino.tree
```

Format

A phylo object (from the ape package) with 100 tips and 99 internal nodes. The tree has been scaled so that the root age is 1.0.

Details

Rhinograds are hypothetical mammals used as examples in phylogenetic comparative methods. This simulated tree represents the evolutionary relationships among 100 Rhinograd species.

Source

Simulated data for Gonzalez-Voyer and von Hardenberg (2014)

References

Gonzalez-Voyer, A., & von Hardenberg, A. (2014). An introduction to phylogenetic path analysis. In: Modern phylogenetic comparative methods and their application in evolutionary biology (pp. 201–229). Springer.

Examples

```
data(rhino.tree)
plot(rhino.tree)
```

summary.phybase

Summary for PhyBaSE Model

Description

Summarizes the output of a PhyBaSE model run.

Usage

```
## S3 method for class 'phybase'
summary(object, ...)
```

Arguments

| | |
|--------|---|
| object | A fitted model object of class "phybase". |
| ... | Additional arguments passed to summary.mcmc . |

Value

A summary object containing statistics for the monitored parameters. If dsep = TRUE was used in phybase_run, the summary focuses on the conditional independence tests.

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