

Package: ShiVa (via r-universe)

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Type Package

Title Detection of Evolutionary Shifts in Both Optimal Value and Variance

Version 1.1.1

Description Implements statistical methods for detecting evolutionary shifts in both the optimal trait value (mean) and evolutionary diffusion variance. The method uses an L1-penalized optimization framework to identify branches where shifts occur, and the shift magnitudes. It also supports the inclusion of measurement error. For more details, see Zhang, Ho, and Kenney (2023) <[doi:10.48550/arXiv.2312.17480](https://doi.org/10.48550/arXiv.2312.17480)>.

License GPL (>= 3)

Encoding UTF-8

LazyData true

Depends R (>= 3.6.0)

Imports glmnet, psych, ape, phylolm, MASS, igraph

Suggests knitr, rmarkdown

VignetteBuilder knitr

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Config/pak/sysreqs libgmp-dev libxml2-dev

Repository <https://wenshaz.r-universe.dev>

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backward_correction *Backward Selection for Shift Correction*

Description

Backward Selection for Shift Correction

Usage

```
backward_correction(
  tree,
  Y,
  alpha,
  sv_mean,
  sv_var,
  criterion = "BIC",
  original_model = NULL,
  measurement_error = FALSE,
  verbose = FALSE
)
```

Arguments

tree	Phylogenetic tree.
Y	Trait values.
alpha	Selection strength.
sv_mean	Mean shift branches.
sv_var	Variance shift branches.
criterion	"BIC", "mBIC", or "pBIC".
original_model	Optional pre-fitted model.
measurement_error	Logical.
verbose	Logical.

Value

Refined model.

fit_OU_mean_var	<i>Fit OU Model with Shifts in Mean and Variance</i>
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Description

Refit with known shift locations. Uses iterative coordinate descent.

Usage

```
fit_OU_mean_var(
  tree,
  Y,
  alpha,
  sv_mean,
  sv_var,
  max.steps = 1000,
  t = 0.01,
  thres = 0.01,
  measurement_error = FALSE,
  verbose = FALSE
)
```

Arguments

tree	Phylogenetic tree.
Y	Trait values.
alpha	Selection strength.
sv_mean	Branch indices with mean shifts.
sv_var	Branch indices with variance shifts.
max.steps	Max iterations. Default 1000.
t	Step size. Default 0.01.
thres	Convergence threshold. Default 0.01.
measurement_error	Logical.
verbose	Print convergence info. Default FALSE.

Value

Fitted model list.

`generate_design_matrix`*Generate Design Matrix*

Description

Constructs a design matrix for a given phylogenetic tree.

Usage

```
generate_design_matrix(tree, type = "simpX", alpha = 0)
```

Arguments

<code>tree</code>	A phylogenetic tree of class <code>phylo</code> .
<code>type</code>	A character string: "simpX" or "orgX".
<code>alpha</code>	Selection strength (only for type = "orgX").

Value

A design matrix `X`.

`get_mean_var_shifts`*Estimate Shifts in Mean and Variance (LASSO)*

Description

L1-penalised estimation of shifts.

Usage

```
get_mean_var_shifts(  
  Y,  
  tree,  
  alpha,  
  lambda1,  
  lambda2,  
  max.steps = 1000,  
  t = 0.01,  
  penalty = "L1",  
  thres = 0.01,  
  sigma2 = NULL,  
  measurement_error = FALSE,  
  verbose = FALSE  
)
```

Arguments

Y	Trait values.
tree	Phylogenetic tree.
alpha	Selection strength.
lambda1	Penalty for mean shifts.
lambda2	Penalty for variance shifts.
max.steps	Max iterations.
t	Step size.
penalty	"L1" or "None".
thres	Convergence threshold.
sigma2	Optional initial sigma2.
measurement_error	Logical.
verbose	Print convergence info. Default FALSE.

Value

List with detected shifts and parameter estimates.

get_mean_var_shifts_model_selection

Model Selection for Shifts in Mean and Variance

Description

Model Selection for Shifts in Mean and Variance

Usage

```
get_mean_var_shifts_model_selection(  
  Y,  
  tree,  
  alpha,  
  lambda1_list = NULL,  
  lambda2_list = exp(1:10 - 6),  
  criterion = "BIC",  
  max.steps = 300,  
  nfolds = 5,  
  top_k = 3,  
  measurement_error = FALSE,  
  verbose = FALSE  
)
```

Arguments

Y	Trait values.
tree	Phylogenetic tree.
alpha	Selection strength.
lambda1_list	Candidate lambda1 values.
lambda2_list	Candidate lambda2 values.
criterion	"BIC", "mBIC", or "pBIC".
max.steps	Max iterations.
nfolds	CV folds.
top_k	Top candidates for backward correction.
measurement_error	Logical.
verbose	Logical. Default FALSE.

Value

List with best_model and score_summary.

OU.vcv

OU.vcv

Description

Generate covariance matrix for OU process.

Usage

```
OU.vcv(tree, alpha)
```

Arguments

tree	phylogenetic tree
alpha	selection strength

Value

Covariance matrix V.

plot.ShiftModel *Plot Method for ShiftModel Objects*

Description

Plots a phylogenetic tree with detected shifts highlighted.

Usage

```
## S3 method for class 'ShiftModel'  
plot(x, title = "", ...)
```

Arguments

x	A ShiftModel object.
title	Plot title.
...	Additional arguments passed to plot.phylo.

Value

No return value (side effect: plot).

print.summary.ShiftModel
Print Method for Summary of ShiftModel

Description

Print Method for Summary of ShiftModel

Usage

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

Arguments

x	A summary.ShiftModel object.
...	Unused.

Value

No return value (side effect: console output).

Description

Detects evolutionary shifts in both optimal trait values and diffusion variance under an Ornstein-Uhlenbeck process. Optionally refits alpha after shift detection.

Usage

```
ShiVa(
  Y,
  tree,
  alpha = NULL,
  t = 0.01,
  lambda1_list = NULL,
  lambda2_list = exp(1:10 - 6),
  criterion = "BIC",
  max.steps = 300,
  nfolders = 5,
  top_k = 3,
  measurement_error = FALSE,
  refit_alpha = TRUE,
  verbose = FALSE
)
```

Arguments

Y	Trait values at tips.
tree	Phylogenetic tree of class phylo.
alpha	Selection strength. If NULL, estimated via phyloIm.
t	Step size. Default 0.01.
lambda1_list	Candidate lambda1 values.
lambda2_list	Candidate lambda2 values. Default $\exp(1:10 - 6)$.
criterion	"BIC", "mBIC", or "pBIC". Default "BIC".
max.steps	Max iterations. Default 300.
nfolders	CV folds. Default 8.
top_k	Top candidates for backward correction. Default 10.
measurement_error	Logical. Default FALSE.
refit_alpha	Logical. If TRUE, refit alpha after detection. Default TRUE.
verbose	Logical. Default FALSE.

Value

List with best_model and score_summary.

soft_thresholding	<i>Soft Thresholding</i>
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Description

Soft Thresholding

Usage

```
soft_thresholding(z, lambda)
```

Arguments

z	Numeric value.
lambda	Threshold level.

Value

Thresholded value.

summary.ShiftModel	<i>Summary of a ShiVa Shift Model</i>
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Description

Summary of detected shifts and fitted parameters.

Usage

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

Arguments

object	A ShiftModel object.
...	Unused.

Value

A summary.ShiftModel object.

update_step_gamma *Update Step for Gamma*

Description

Update Step for Gamma

Usage

```
update_step_gamma(gamma_k, X_k, Sigma, r, lambda2, t, penalty, V, q_k)
```

Arguments

gamma_k	Current gamma value.
X_k	Column of design matrix.
Sigma	Current covariance matrix.
r	Residual vector.
lambda2	Penalty parameter.
t	Step size.
penalty	"L1" or "None".
V	Baseline covariance matrix.
q_k	Element of design vector q.

Value

List with updated gamma_k and Sigma.

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