

Package ‘PSIMEX’

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Type Package

Title SIMEX Algorithm on Pedigree Structures

Version 1.1

Depends MCMCglmm, plotrix, pedigree, knitr

Suggests AICcmodavg, psych

VignetteBuilder knitr

Date 2017-08-23

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Description Generalization of the SIMEX algorithm from Cook & Stefanski (1994) <doi:10.2307/2290994> for the calculation of inbreeding depression or heritability on pedigree structures affected by missing or misassigned paternities. It simulates errors and tracks the behavior of the estimate as a function of the error proportion. It extrapolates back a true value corresponding to the null error rate.

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PSIMEX-package	<i>SIMEX Algorithm on Pedigree Structures</i>
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Generalization of the SIMEX algorithm from Cook & Stefanski (1994) <doi:10.2307/2290994> for the calculation of inbreeding depression or heritability on pedigree structures affected by missing or misassigned paternities. It simulates errors and tracks the behavior of the estimate as a function of the error proportion. It extrapolates back a true value corresponding to the null error rate.

Details

The DESCRIPTION file:

```

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VignetteBuilder: knitr
Date:         2017-08-23
Author:       Erica Ponzi
Maintainer:   Erica Ponzi <erica.ponzi@uzh.ch>
Description:  Generalization of the SIMEX algorithm from Cook & Stefanski (1994) <doi:10.2307/2290994> for the
License:      GPL (>= 2)
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```

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initial	Calculation of the initial error prone value for inbreeding depression
initial_herit	Calculation of the initial error prone value for heritability
pedigree	Pedigree data
plot.Psimex	A plot illustrating the extrapolation phase of the P-SIMEX algorithm
plot.simul.Psimex	A plot illustrating the simulation phase of the P-SIMEX algorithm
simul.na	Simulation phase for the P-SIMEX with missing paternities.
simul.na.bottom	Simulation phase for P-SIMEX on inbreeding depression with missing paternities and errors in the last generations of the pedigree.
simul.na.bottom.herit	Simulation phase for P-SIMEX on heritability with missing paternities and errors in the last generations of the pedigree.
simul.na.top	Simulation phase for P-SIMEX on inbreeding depression with missing paternities and errors in the first generations of the pedigree.
simul.na.top.herit	Simulation phase for P-SIMEX on heritability with missing paternities and errors in the first generations of the pedigree.
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simul.na.uni.herit	Simulation phase for P-SIMEX on heritability with missing paternities and uniform errors.
simul.replace	Simulation phase for the P-SIMEX with misassignment error.
simul.replace.similar	Simulation phase for P-SIMEX on inbreeding depression with misassignment error and replacement with similar individuals.
simul.replace.similar.herit	Simulation phase for P-SIMEX on heritability with misassignment error and replacement with similar individuals.
simul.replace.uni	Simulation phase for P-SIMEX on inbreeding depression with misassignment error and uniform replacement.
simul.replace.uni.herit	Simulation phase for P-SIMEX on heritability with misassignment error and uniform

replacement.

Further information is available in the following vignettes:

PSIMEXvignette PSIMEX (source, pdf)

~~ An overview of how to use the package, including the most important functions ~~

Author(s)

Erica Ponzi

Maintainer: Erica Ponzi <erica.ponzi@uzh.ch>

data	<i>Trait data</i>
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Description

Simulated trait records data for the package P-SIMEX. It contains information on each individual's trait and covariates.

Usage

data

Format

"sex" "f_inb" "animal.id" "id" "year" "animal" "y"

sex: Sex of the individual
 f_inb: Inbreeding coefficient of the individual (it can also be calculated from the pedigree)
 id: Individual's id
 animal.id: Individual's id (duplicate for animal model)
 animal: Individual's id (duplicate for animal model)
 year: Generation number of the individual in the pedigree (it can also be extracted from the pedigree)
 y: Individual's trait record

extrapolation	<i>Extrapolation phase for the SIMEX algorithm on pedigrees</i>
---------------	---

Description

Starting from the simulated values obtained in the previous SIMEX phase, it computes averages across all simulations for each error rate and fits a function of the estimate in terms of error rate. From this function it extrapolates the value corresponding to the null error rate. The fitted function can be linear, quadratic, cubic or non linear.

Usage

```
extrapolation(results, lambda, lambda0, estimate0, fitting.method, B, parameter)
```

Arguments

results	A dataset with \$100\$ or B values for each error rate given by the simulation part of the algorithm.
lambda	A numerical vector containing the error rates.
lambda0	The initial error rate.
estimate0	The initial error prone estimate.
fitting.method	A string or a vector of strings containing the fitting methods for the function. It can be: 'line', 'quad', 'nonl' or 'cubi'.
B	The number of simulation for each error rate.
parameter	A string containing the parameter of interest P-SIMEX is performed on. It can be either 'inbreeding' or 'heritability'.

Value

For inbreeding a list:

inb_pred	Inbreeding depression extrapolated error free value
inb_pred_se	Standard error of the error free value: regression component
se_pred	Standard error of the error free value: sampling error component
var	Total variance of the error free value
AIC	The AIC of the fitted function

For heritability a list:

h_pred	Heritability extrapolated error free value
h_pred_se	Standard error of the error free value: regression component
se_pred	Standard error of the error free value: sampling error component
var	Total variance of the error free value
VA_pred	Extrapolated value for the additive genetic variance
VE_pred	Extrapolated value for the environmental variance
AIC	The AIC of the fitted function

Author(s)

Erica Ponzi

fit.nls	<i>Fitting a non linear function on the data</i>
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Description

It fits a non linear function on a set of data

Usage

```
fit.nls(lambda, p.names, estimates)
```

Arguments

lambda	A vector containing the x axis points
p.names	Name of the y axis variables to be fitted
estimates	Y axis variables to be fitted

Value

A list containing the fitted functions of the function in the null value on the x axis. It contains one function per variable to be estimated.

Author(s)

Erica Ponzi

initial	<i>Calculation of the initial error prone value for inbreeding depression</i>
---------	---

Description

This function calculates the starting point for the P-SIMEX on inbreeding depression with the initial error in the pedigree.

Usage

```
initial(model, data, pedigree)
```

Arguments

model	An object specifying the model to calculate inbreeding depression. It can be a lm or glm.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model.
pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.

Value

A list:

model	The correct expression of the model to calculate inbreeding depression
inb0	The starting value of inbreeding depression
se0	The starting standard error of inbreeding depression
pval0	The starting p-value of inbreeding depression
mean_inb0	The starting mean value of inbreeding coefficient
median_inb0	The starting median value of inbreeding coefficient
var_inb0	The starting variance of inbreeding coefficient

Author(s)

Erica Ponzi

initial_herit	<i>Calculation of the initial error prone value for heritability</i>
---------------	--

Description

This function calculates the starting point for the P-SIMEX on heritability with the initial error in the pedigree.

Usage

```
initial_herit(model, data, pedigree)
```

Arguments

model	An object specifying the model to calculate inbreeding depression. It can be a lm or glm.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model.
pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.

Value

A list:

h0	The starting value of heritability
seh0	The starting standard error of heritability
VA0	The starting value of additive genetic variance
VE0	The starting value of environmental variance

Author(s)

Erica Ponzi

pedigree	<i>Pedigree data</i>
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Description

Simulated pedigree structure for the package P-SIMEX. It contains information on each individual's parents, as well its sex and generation.

Usage

```
pedigree
```

Format

id:	Individual's id
father:	Individual's father's id
mother:	Individual's mother's id
sex:	Sex of the individual
generation:	Generation number of the individual in the pedigree

plot.Psimex	<i>A plot illustrating the extrapolation phase of the P-SIMEX algorithm</i>
-------------	---

Description

This function produces a plot with the corrected estimate of interest and its 95 % confidence intervals.

Usage

```
plot.Psimex(results, extrapolation_results, lambda, lambda0, estimate0,
            parameter, fitting.method)
```

Arguments

results	A dataset containing the simulated values. It is the output of simul.replace or simul.na.
extrapolation_results	A dataset containing the extrapolated values. It is the output of extrapolation.
lambda	A vector of real numbers containing the error proportions to be generated.
lambda0	A real number specifying the initial error proportion.

estimate0	The initial naive estimate of the parameter
parameter	A string specifying the parameter of interest. It must be 'inbreeding' or 'heritability'.
fitting.method	A string or a vector of strings specifying the extrapolation functions to be fitted. It must be 'linear', 'quadratic', 'nonlinear' or 'cubic'.

Author(s)

Erica Ponzi

plot.simul.Psimex	<i>A plot illustrating the simulation phase of the P-SIMEX algorithm</i>
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Description

This function produces a plot with the estimate of interest and its 95 % confidence intervals as a function of the error proportion.

Usage

```
plot.simul.Psimex(results, lambda, lambda0, estimate0, parameter)
```

Arguments

results	A dataset containing the simulated values. It is the output of simul.replace or simul.na.
lambda	A vector of real numbers containing the error proportions to be generated.
lambda0	A real number specifying the initial error proportion.
estimate0	The initial naive estimate of the parameter
parameter	A string specifying the parameter of interest. It must be 'inbreeding' or 'heritability'.

Author(s)

Erica Ponzi

Psimex

*Pedigree SIMEX***Description**

This function performs the P-SIMEX on a given dataset and a given pedigree. The parameter of interest can be either heritability or inbreeding depression and the error structure can be chosen between missing or misassigned paternities. In the missing case, the error can be simulated uniformly across the pedigree or just in the first or last generations, choosing the number of them. In the misassignment case, the error can be simulated by replacing fathers with random individuals or with similar individuals. After simulation, extrapolation is performed and a correct estimate is given together with its standard error according to the chosen function (linear, quadratic or non linear)

Usage

```
Psimex(pedigree0, data, lambda, lambda0, B = 100, model,
       parameter = "inbreeding", error = "misassignment", way = "uniform",
       fitting.method = "quadratic", ntop = NA, nbottom = NA,
       prior, nitt, thin, burnin)
```

Arguments

pedigree0	A dataset containing the initial pedigree structure. It must have five columns: id, parent1, parent2, sex, generation.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
lambda	A vector of real numbers specifying the error proportion to be generated.
lambda0	A real number specifying the initial error rate.
B	An integer specifying the number of simulations to be run for each error level.
model	An object specifying the model which has to be fitted to calculate the parameter of interest. It can be a lm or glm for inbreeding depression and a MCMCglmm for heritability.
parameter	A string specifying the parameter of interest. It must be 'inbreeding' or 'heritability'.
error	A string specifying the type of error. It must be 'missing' or 'misassignment'.
way	A string specifying how errors are generated. It must be 'uniform' or 'similar' for the misassignment error or 'uniform', 'top' or 'bottom' for the missing case.
fitting.method	A string or a vector of strings specifying the extrapolation functions to be fitted. It must be 'linear', 'quadratic', 'nonlinear' or 'cubic'.
ntop	An integer specifying the number of the first generations to add errors to. It must be specified when the parameter 'way' is 'top'
nbottom	An integer specifying the number of the last generations to add errors to. It must be specified when the parameter 'way' is 'bottom'

prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

A list:

description	A string describing the analysed case
error	A string describing the kind of error
fitting.method	A string or a vector of strings describing the extrapolation functions
way	A string describing the way of simulating the error
simul_data	A list of simulated data, it's the output of one of the simulation functions 'simul.replace' or 'simul.na'
extrapolated_data	A list of extrapolated data, it's the output of the extrapolation function
lambda	The vector of the simulated error proportions
lambda0	The initial error proportion
starting.value	The initial error prone value of the parameter

Author(s)

Erica Ponzi

Examples

```
## Seed
set.seed(49494)

# extract data
data(pedigree)
data(data)
pedigree0 <- pedigree

# inbreeding depression case

# fixed error proportions
lambda <- c(0.2, 0.3, 0.4, 0.5, 0.6)
# initial error proportion
lambda0 <- 0.1
# model used to compute inbreeding depression
model <- lm(y~sex+f_inb, data = data)

# PSIMEX
results <- Psimex(pedigree0, data,
                  lambda, lambda0, B = 100,
                  model, parameter = "inbreeding",
```

```

        error = "missing", way = "uniform",
        fitting.method = c("quadratic", "linear"),
        ntop = NA, nbottom = NA,
        prior, nitt, thin, burnin)
results$description
results$error
results$fitting.method
results$way

results$extrapolated_data
results$lambda
results$lambda0
results$starting.value

## Not run:
# heritability case
## Seed
set.seed(49494)

# extract data
data(pedigree)
data(data)
pedigree0 <- pedigree

# fixed error proportions
lambda <- c(0.2, 0.3, 0.4, 0.5, 0.6)
# initial error proportion
lambda0 <- 0.1

# model to compute heritability (MCMCglmm)
# prior specification
prior <- list(G=list(G1=list(V=matrix(1/3),n=1),
                    G2=list(V=matrix(1/3),n=1)),
            R=list(V=matrix(1/3),n=1))

#to fulfill MCMCglmm requirements
pedigree <- pedigree0[ , c(1,2,3)]
names(pedigree) <- c("animal", "dam", "sire")
ord <- orderPed(pedigree)
pedigree <- pedigree[order(ord),]

# model specification
model <- MCMCglmm(y~1+sex, random = ~animal+id,
                pedigree = pedigree, data = data,
                prior = prior, nitt = 20000, thin = 100, burnin = 1000,
                verbose = FALSE)

# PSIMEX
results1 <- Psimex(pedigree0, data,
                 lambda, lambda0, B = 10,
                 model, parameter = "heritability",
                 error = "missing", way = "uniform",
                 fitting.method = "quadratic",

```

```

      ntop = NA, nbottom = NA,
      prior = prior, nitt = 20000, thin = 100, burnin = 1000)

results1$description
results1$error
results1$fitting.method
results1$way

results1$extrapolated_data
results1$lambda
results1$lambda0
results1$starting.value

## End(Not run)

```

simul.na

Simulation phase for the P-SIMEX with missing paternities.

Description

This function calls the proper simulation function for the parameter of interest with missing paternities.

Usage

```
simul.na(pedigree, pedigree0, lambda, lambda0, B, data,
model, parameter, way, ntop, nbottom, prior, nitt, thin, burnin)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
pedigree0	A dataset containing the initial pedigree structure. It must have five columns: id, parent1, parent2, sex, generation.
lambda	A vector of real numbers specifying the error proportion to be generated.
lambda0	A real number specifying the initial error rate.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	An object specifying the model to calculate the parameter of interest. It can be a lm or glm for inbreeding depression and a MCMCglmm for heritability.
parameter	A string specifying the parameter of interest. It must be 'inbreeding' or 'heritability'.
way	A string specifying how errors are generated. It must be 'uniform' or 'similar'.

ntop	An integer specifying the number of the first generations where to generate errors, when the parameter 'way' is 'top'.
nbottom	An integer specifying the number of the last generations where to generate errors, when the parameter 'way' is 'bottom'.
prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

For inbreeding a list:

inb	A dataset containing all the simulated values for inbreeding depression
se_inb	A dataset containing all the simulated standard errors for inbreeding depression
pval	A dataset containing all the simulated p-values for inbreeding depression
mean_inb	A dataset containing all the simulated values for inbreeding coefficient mean
median_inb	A dataset containing all the simulated values for inbreeding coefficient median
var_inb	A dataset containing all the simulated values for inbreeding coefficient variance

For heritability a list:

h	A dataset containing all the simulated values for heritability
se_h	A dataset containing all the simulated standard errors for heritability
VA	A dataset containing all the simulated values for additive variance
VE	A dataset containing all the simulated values for environmental variance

Author(s)

Erica Ponzi

simul.na.bottom	<i>Simulation phase for P-SIMEX on inbreeding depression with missing paternities and errors in the last generations of the pedigree.</i>
-----------------	---

Description

The function generates increasing amount of errors to the pedigree structure and calculates inbreeding depression for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated within the last nbottom generations of pedigree by eliminating fathers.

Usage

```
simul.na.bottom(pedigree, pedigree0, lambda, B, data, model, nbottom)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
pedigree0	A dataset containing the initial pedigree structure. It must have five columns: id, parent1, parent2, sex, generation.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class model used to calculate inbreeding depression.
nbottom	An integer specifying the number of the last generations where to generate errors.

Value

A list:

inb	A dataset containing all the simulated values for inbreeding depression
se_inb	A dataset containing all the simulated standard errors for inbreeding depression
pval	A dataset containing all the simulated p-values for inbreeding depression
mean_inb	A dataset containing all the simulated values for inbreeding coefficient mean
median_inb	A dataset containing all the simulated values for inbreeding coefficient median
var_inb	A dataset containing all the simulated values for inbreeding coefficient variance

Author(s)

Erica Ponzi

simul.na.bottom.herit *Simulation phase for P-SIMEX on heritability with missing paternities and errors in the last generations of the pedigree.*

Description

The function generates increasing amount of errors to the pedigree structure and calculates heritability for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated within the last nbottom generations of pedigree by eliminating fathers.

Usage

```
simul.na.bottom.herit(pedigree, pedigree0, lambda, B,
  data, model, nbottom, prior, nitt, thin, burnin)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
pedigree0	A dataset containing the initial pedigree structure.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class MCMCglmm used to calculate heritability.
nbottom	An integer specifying the number of the last generations where to generate errors.
prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

A list:

h	A dataset containing all the simulated values for heritability
se_h	A dataset containing all the simulated standard errors for heritability
VA	A dataset containing all the simulated values for additive variance
VE	A dataset containing all the simulated values for environmental variance

Author(s)

Erica Ponzi

simul.na.top

Simulation phase for P-SIMEX on inbreeding depression with missing paternities and errors in the first generations of the pedigree.

Description

The function generates increasing amount of errors to the pedigree structure and calculates inbreeding depression for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated within the first ntop generations of pedigree by eliminating fathers.

Usage

```
simul.na.top(pedigree, pedigree0, lambda, B, data, model, ntop)
```


Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
pedigree0	A dataset containing the initial pedigree structure. It must have five columns: id, parent1, parent2, sex, generation.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class model used to calculate inbreeding depression.
ntop	An integer specifying the number of the first generations where to generate errors.

Value

A list:

inb	A dataset containing all the simulated values for inbreeding depression
se_inb	A dataset containing all the simulated standard errors for inbreeding depression
pval	A dataset containing all the simulated p-values for inbreeding depression
mean_inb	A dataset containing all the simulated values for inbreeding coefficient mean
median_inb	A dataset containing all the simulated values for inbreeding coefficient median
var_inb	A dataset containing all the simulated values for inbreeding coefficient variance

Author(s)

Erica Ponzi

simul.na.top.herit	<i>Simulation phase for P-SIMEX on heritability with missing paternities and errors in the first generations of the pedigree.</i>
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Description

The function generates increasing amount of errors to the pedigree structure and calculates heritability for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated within the first ntop generations of pedigree by eliminating fathers.

Usage

```
simul.na.top.herit(pedigree,pedigree0, lambda, B,
data, model, ntop, prior, nitt,thin,burnin)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
pedigree0	A dataset containing the initial pedigree structure.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class MCMCglmm used to calculate heritability.
ntop	An integer specifying the number of the first generations where to generate errors.
prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

A list:

h	A dataset containing all the simulated values for heritability
se_h	A dataset containing all the simulated standard errors for heritability
VA	A dataset containing all the simulated values for additive variance
VE	A dataset containing all the simulated values for environmental variance

Author(s)

Erica Ponzi

simul.na.uni

Simulation phase for P-SIMEX on inbreeding depression with missing paternities and uniform errors.

Description

The function generates increasing amount of errors to the pedigree structure and calculates inbreeding depression for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated with the same probability across the all pedigree by eliminating fathers.

Usage

```
simul.na.uni(pedigree, lambda, B, data, model)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class model used to calculate inbreeding depression.

Value

A list:

inb	A dataset containing all the simulated values for inbreeding depression
se_inb	A dataset containing all the simulated standard errors for inbreeding depression
pval	A dataset containing all the simulated p-values for inbreeding depression
mean_inb	A dataset containing all the simulated values for inbreeding coefficient mean
median_inb	A dataset containing all the simulated values for inbreeding coefficient median
var_inb	A dataset containing all the simulated values for inbreeding coefficient variance

Author(s)

Erica Ponzi

simul.na.uni.herit	<i>Simulation phase for P-SIMEX on heritability with missing paternities and uniform errors.</i>
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Description

The function generates increasing amount of errors to the pedigree structure and calculates heritability for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated with the same probability across the all pedigree by eliminating fathers.

Usage

```
simul.na.uni.herit(pedigree, lambda, B, data,
model, prior, nitt, thin, burnin)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class MCMCglmm used to calculate heritability.
prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

A list:

h	A dataset containing all the simulated values for heritability
se_h	A dataset containing all the simulated standard errors for heritability
VA	A dataset containing all the simulated values for additive variance
VE	A dataset containing all the simulated values for environmental variance

Author(s)

Erica Ponzi

simul.replace

Simulation phase for the P-SIMEX with misassignment error.

Description

This function calls the proper simulation function for the parameter of interest with misassigned paternities.

Usage

```
simul.replace(pedigree, lambda, lambda0, B, data,
             model, parameter, way, prior, nitt, thin, burnin)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
lambda	A vector of real numbers specifying the error proportion to be generated.
lambda0	A real number specifying the initial error rate.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	An object specifying the model to calculate the parameter of interest. It can be a lm or glm for inbreeding depression and a MCMCglmm for heritability.
parameter	A string specifying the parameter of interest. It must be 'inbreeding' or 'heritability'.
way	A string specifying how errors are generated. It must be 'uniform' or 'similar'.
prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

For inbreeding a list:

inb	A dataset containing all the simulated values for inbreeding depression
se_inb	A dataset containing all the simulated standard errors for inbreeding depression
pval	A dataset containing all the simulated p-values for inbreeding depression
mean_inb	A dataset containing all the simulated values for inbreeding coefficient mean
median_inb	A dataset containing all the simulated values for inbreeding coefficient median
var_inb	A dataset containing all the simulated values for inbreeding coefficient variance

For heritability a list:

h	A dataset containing all the simulated values for heritability
se_h	A dataset containing all the simulated standard errors for heritability
VA	A dataset containing all the simulated values for additive variance
VE	A dataset containing all the simulated values for environmental variance

Author(s)

Erica Ponzi

simul.replace.similar *Simulation phase for P-SIMEX on inbreeding depression with misassignment error and replacement with similar individuals.*

Description

The function generates increasing amount of errors to the pedigree structure and calculates inbreeding depression for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated by replacing fathers with the most similar individual from the same generation.

Usage

```
simul.replace.similar(pedigree, lambda, B, data, model)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class model used to calculate heritability.

Value

A list:

inb	A dataset containing all the simulated values for inbreeding depression
se_inb	A dataset containing all the simulated standard errors for inbreeding depression
pval	A dataset containing all the simulated p-values for inbreeding depression
mean_inb	A dataset containing all the simulated values for inbreeding coefficient mean
median_inb	A dataset containing all the simulated values for inbreeding coefficient median
var_inb	A dataset containing all the simulated values for inbreeding coefficient variance

Author(s)

Erica Ponzi

```
simul.replace.similar.herit
```

Simulation phase for P-SIMEX on heritability with misassignment error and replacement with similar individuals.

Description

The function generates increasing amount of errors to the pedigree structure and calculates heritability for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated by replacing fathers with the most similar individual from the same generation.

Usage

```
simul.replace.similar.herit(pedigree, lambda, B, data,
model, prior, nitt, thin, burnin)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class MCMCglmm used to calculate heritability.
prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

A list:

h	A dataset containing all the simulated values for heritability
se_h	A dataset containing all the simulated standard errors for heritability
VA	A dataset containing all the simulated values for additive variance
VE	A dataset containing all the simulated values for environmental variance

Author(s)

Erica Ponzi

simul.replace.uni	<i>Simulation phase for P-SIMEX on inbreeding depression with misassignment error and uniform replacement.</i>
-------------------	--

Description

The function generates increasing amount of errors to the pedigree structure and calculates inbreeding depression for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated with the same probability across the all pedigree by replacing fathers with other individuals from the same generation.

Usage

```
simul.replace.uni(pedigree, lambda, B, data, model)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class model used to calculate inbreeding depression.

Value

A list:

inb	A dataset containing all the simulated values for inbreeding depression
se_inb	A dataset containing all the simulated standard errors for inbreeding depression
pval	A dataset containing all the simulated p-values for inbreeding depression
mean_inb	A dataset containing all the simulated values for inbreeding coefficient mean
median_inb	A dataset containing all the simulated values for inbreeding coefficient median
var_inb	A dataset containing all the simulated values for inbreeding coefficient variance

Author(s)

Erica Ponzi

 simul.replace.uni.herit

Simulation phase for P-SIMEX on heritability with misassignment error and uniform replacement.

Description

The function generates increasing amount of errors to the pedigree structure and calculates heritability for each simulation. For each level of the error proportion, a number of simulation equal to B are repeated. Errors are generated with the same probability across the all pedigree by replacing fathers with other individuals from the same generation.

Usage

```
simul.replace.uni.herit(pedigree, lambda, B, data,
  model, prior, nitt, thin, burnin)
```

Arguments

pedigree	A dataset containing the initial pedigree structure. It must have three columns: id, parent1, parent2.
lambda	A vector of real numbers specifying the error proportion to be generated.
B	An integer specifying the number of simulations to be run for each error level.
data	A dataset containing the phenotypic measurements on the population and the covariates which are included in the model. The trait should be named differently than 'trait' (see MCMCglmm)
model	A object of class MCMCglmm used to calculate heritability.
prior	Prior distribution for MCMCglmm model
nitt	Number of iterations for MCMCglmm model
thin	Thinning interval for MCMCglmm model
burnin	Burn in period for MCMCglmm model

Value

A list:

h	A dataset containing all the simulated values for heritability
se_h	A dataset containing all the simulated standard errors for heritability
VA	A dataset containing all the simulated values for additive variance
VE	A dataset containing all the simulated values for environmental variance

Author(s)

Erica Ponzi

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