Package 'pedantics'

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Type Package

Title Functions to Facilitate Power and Sensitivity Analyses for Genetic Studies of Natural Populations

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Depends R (>= 2.4.0), MasterBayes, MCMCglmm, kinship2, grid, genetics

Imports mvtnorm

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Description Functions for sensitivity and power analysis, for calculating statistics describing pedigrees from wild populations, and for viewing pedigrees.

License GPL-2 | GPL-3

LazyLoad yes

Repository CRAN

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R topics documented:

`pedantics-package` *Tools to facilitate quantitative genetic studies of natural populations, especially with respect to the use of pedigrees in such problems.*

Description

`pedantix` contains three types of functions. The first are functions specifically designed to aid power and sensitivity analyses for quantitative genetic studies, particulary with thought to accommodating the proglems and data structures that arise in data from natural populations. There are basic utility functions for manipulating pedigrees. Finally there are functions for visualizing and statistically characterizing pedigrees.

Details

Package:	pedantics
Type:	Package
Version:	1.01
Date:	2009-07-21
License:	GPL-2 | GPL-3
LazyLoad:	yes

See the tutorial, pedantics-Tutorial.pdf for detailed example analyses using `pedantics`

Author(s)

Michael Morrissey <michael.morrissey@ed.ac.uk>

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References

Morrissey et al. 2007. Journal of Evolutionary Biology 20:2309-2321., Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

`drawPedigree` *Produce a graphical representation of a pedigree*

Description

Plots a pedigree, with options specific to considerations for pedigrees used to for quantitative genetic inferencein natural populations. Pedigrees containing only those individuals that are informative with respect to (genetic) variation in an arbitrary trait can be plotted, potentially overlain on a complete pedigree. Functions also exist to plot various types of pedgiree links associated with focal individuals.

Usage

```
drawPedigree(Ped, cohorts = NULL, sex = NULL, dat = NULL, dots = "n",
             plotfull = "y", writeCohortLabels = "n", links = "all",
             sexInd = c(0, 1), dotSize = 0.001, dataDots = "n",
             dataDots.cex = 2, cohortLabs.cex = 1, retain="informative",
             focal=NULL, sexColours=c('red','blue'), ...)
```

Arguments

Ped	An ordered pedigree with 3 columns: id, dam, sire
cohorts	An optional numeric vector of the same length as the pedigree designating, for example cohort afinities or birth years
sex	An optional numeric vector of the same length as the pedigree containing the sexes (may be unknown) of all indivduals with entries in the pedigree. Defaults (modifiable with sexInd) are 0=male and 1=female
dat	An optional vector or data frame containg indicators of data availablility. If dat contains only ones and zeros, then any individual with any entry of one will be considered as having data records. If data contains values other than ones and zeros, individuals in the pedigree with rows in data that contain at least one available record, i.e., one data record is not NA, will be treated as having data.
dots	If 'y', then a dot will be printed representing each individual in the pedigree. If sexes are available, dots will be colour coded by sex.
plotfull	To be used when dat is supplied. If 'y' (the default), individuals in the pedigree that are uninformative with respect to the available data have their pedigree links plotted in gray.
writeCohortLabels	To be used when cohorts is used. Will plot the cohort values on the left hand side of the pedigree image.
links	Default is 'all', other values are 'mums' to print only maternal pedigree links and 'dads' to print only paternal pedigree links.
sexInd	To be used with if sex is supplied and if the vector of sex specifiers differs from the default.
dotSize	Set the dot size bigger or smaller
dataDots	Will print dots over the dots denoting indivdiuals, but denoting individuals with available data as indicated by dat.
dataDots.cex	controls the size of dataDots relative to dots.
cohortLabs.cex	controls the size of cohort lables.
retain	When those pedigree links only informative relative to phenotypic data availability are to be plotted, this controls whether or not a pruned pedigree based on phenotypic data is plotted (if set to "pruned"), or whether strictly only those informative pedigree links are plotted (the default)
focal	An optional list containing the id of an individual and the kinds of relatives of the focal individual to which to plot pedigree links. Available types are 'offspring','descendents','parents',,ancestors', and 'kin'.

sexColours	The colours that will be used to draw points and or lines associated with males and females.
...	Additional graphical parameters.

Author(s)

Michael Morrissey <michael.morrissey@st-andrews.ac.uk>

References

Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

See Also

fixPedigree to prepare pedigrees that may not explicitly contain records for all individuals (i.e., where founding individuals may only appear in the dam or sire column).)

Examples

```
data(gryphons)
pedigree<-fixPedigree(gryphons[,1:3])

## draw the gryphon pedigree by pedigree depth
drawPedigree(pedigree)

## draw the gryphon pedigree by cohort
# drawPedigree(pedigree,cohorts=gryphons$cohort,writeCohortLabels='y',
#                                                 cohortLabs.cex=1)

## Not run:

## draw the gryphon pedigree by cohort with only maternal links
drawPedigree(pedigree,cohorts=gryphons$cohort,links='mums')

## draw the gryphon pedigree by cohort with colour only for those
## indiduals that are informative relative to the quantitative
## genetics of a hypothetical trait only measured for individuals
## in the last two cohorts, emphasize the phenotyped individuals
## with large black dots, and all other individuals with dots
## colour coded by sex:
dataAvailability<-(gryphons$cohort>=(max(gryphons$cohort)-1))+0

# not run
# drawPedigree(pedigree,cohorts=gryphons$cohort,sex=gryphons$sex,
#   dots='y',dat=dataAvailability,writeCohortLabels='y',dataDots='y')


## End(Not run)
```

`fixPedigree` *Manipulating pedigrees to prepare them for requirements of subsequent analyses*

Description

Prepares a pedigree to conform with requirements of many softwares used in quantitative genetic analysis, as well as for many of the functions in pedantics.

Usage

```
fixPedigree(Ped, dat = NULL)
```

Arguments

`Ped`	An ordered pedigree with 3 columns: id, dam, sire
`dat`	An optional data frame, the same length as the pedigree

Value

Returns a pedigree in which all individuals that exsit in the dam and sire columns are represented by their own record lines, occurring before the records of their first offspring. If data are supplied, then fixPedigree will return a dataframe, the first two columns are the 'fixed' pedigree, and the following columns of which contain appropriately reordered data.

Author(s)

Michael Morrissey <michael.morrissey@ed.ac.uk>

References

Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

Examples

```
##  a valid pedigree, i.e., no loops, no bisexuality, etc.,
## but where not all parents have a record line, and where
## parents do not necessarily occur before their offspring:
pedigree<-as.data.frame(matrix(c(
  10,1,2,
  11,1,2,
  12,1,3,
  13,1,3,
  14,4,5,
  15,6,7,
  4,NA,NA,
  5,NA,NA,
```

```
  6,NA,NA,
  7,NA,NA),10,3,byrow=TRUE))
names(pedigree)<-c("id","dam","sire")
pedigree
fixedPedigree<-fixPedigree(Ped=pedigree)
fixedPedigree
```

`fpederr` *Simulates a pedigree with errors and missing data from a complete pedigree.*

Description

Implements the 'forward' approach to producing pairs of pedigrees for power and sensitivity analyses.

Usage

```
fpederr(truePedigree, founders = NULL, sex = NULL, samp = NULL,
          sireE = NULL, damE = NULL, sireA = NULL, damA = NULL,
          cohort = NULL, first = NULL, last = NULL, monoecey = 0,
          modifyAssumedPedigree = 0)
```

Arguments

`truePedigree`	A complete pedigree with records for all individuals and parental ID's for all non-founders
`founders`	A vector the same length as the pedigree containing indicator variables 1 = founder, 0 = non-founder
`sex`	A vector the same length as the pedigree indicating sex, 0=male, 1=female, any other value = unknown sex
`samp`	A vector the same length as the pedigree indicating whether or not each individual is sampled (1), or an unsampled dummy individual (0).
`sireE`	Value(s) indicating the paternal error rate. If it is a single number (between 0 and 1), it is applied to the entire pedigree; if it is a vector the length of the pedigree, then probabilities can vary among individuals.
`damE`	Value(s) indicating the maternal error rate. If it is a single number (between 0 and 1), it is applied to the entire pedigree; if it is a vector the length of the pedigree, then probabilities can vary among individuals.
`sireA`	Value(s) indicating the paternal pedigree link assignment rate. If it is a single number (between 0 and 1), it is applied to the entire pedigree; if it is a vector the length of the pedigree, then probabilities can vary among individuals.
`damA`	Value(s) indicating the maternal pedigree link assignment rate. If it is a single number (between 0 and 1), it is applied to the entire pedigree; if it is a vector the length of the pedigree, then probabilities can vary among individuals.

`cohort` A numeric vector the same length as the pedigree containing cohorts

`first` A numeric vector the same length as the pedigree indicating the first cohort for which an individual is to be considered a potential parent

`last` A numeric vector the same length as the pedigree indicating the last cohort for which an individual is to be considered a potential parent

`monoecey` An indicator specifying whether or not bisexuality is allowed (0=no (default), 1=yes)

`modifyAssumedPedigree`
An indicator variable specifying whether or not an assumed pedigree with errors but no missing links should be supplied.

Value

`assumedPedigree`
A pedigree differing from the supplied pedigree so as to mimic patterns of pedigree errors and missing data that might occur in a real study.

`truePedigree` Echos the pedigree supplied.

`supplementalPedigree`
(optional) a 'assumed' pedigree containing errorsbut no missing links.

Author(s)

Michael Morrissey <michael.morrissey@ed.ac.uk>

References

Morrissey et al. 2007. Journal of Evolutionary Biology 20:2309-2321., Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

See Also

rpederr,fpederr

Examples

```
testData<-as.data.frame(matrix(c(
1,NA,NA,1,1,1,2,2,
2,NA,NA,1,1,1,2,2,
3,NA,NA,1,1,1,2,2,
4,NA,NA,1,0,1,2,2,
5,NA,NA,1,0,1,2,2,
6,1,4,0,-1,2,3,3,
7,1,4,0,-1,2,3,3,
8,1,4,0,-1,2,3,3,
9,1,4,0,-1,2,3,3,
10,2,5,0,-1,2,3,3,
11,2,5,0,-1,2,3,3,
12,2,5,0,-1,2,3,3,
```

```
13,2,5,0,-1,2,3,3,
14,3,5,0,-1,2,3,3,
15,3,5,0,-1,2,3,3,
16,3,5,0,-1,2,3,3,
17,3,5,0,-1,2,3,3),
17,8,byrow=TRUE))

names(testData)<-c("id","dam","sire","founder","sex",
                                   "cohort","first","last")
pedigree<-as.data.frame(cbind(testData$id,testData$dam,
                                            testData$sire))
for(x in 1:3) pedigree[,x]<-as.factor(pedigree[,x])
names(pedigree)<-c("id","dam","sire")
pedigree

## some missing sire links:
fpederr(truePedigree=pedigree,founders=testData$founder,
        sex=testData$sex,sireA=0.5,cohort=testData$cohort,
        first=testData$first,last=testData$last)$assumedPedigree

## some erroneous sire links:
fpederr(truePedigree=pedigree,founders=testData$founder,
        sex=testData$sex,sireE=0.5,cohort=testData$cohort,
        first=testData$first,last=testData$last)$assumedPedigree
```

`genomesim` *A function to simulate QTL and/or SNP data.*

Description

Simulates a chromosome of arbitrary length with arbitrary numbers, types, and spacings of genetic loci over arbitrary pedigrees.

Usage

```
genomesim(pedigree, founders=NULL, positions=NULL, initHe=NULL,
             mutationType=NULL, mutationRate=NULL, phenotyped=NULL,
             founderHaplotypes=NULL, genotyped=NULL, returnG='n',
             initFreqs=NULL)
```

Arguments

`pedigree`	A pedigree
`founders`	A vector of indicator variables denoting founder status (1=founder, 0=non-founder)
`positions`	Genome locations in cM for markers
`initHe`	Initial levels of expected heterozygosity
`mutationType`	A vector of locus types - see details
`mutationRate`	A vector of mutation rates

`founderHaplotypes`
: A matrix or dataframe containing founder haplotypes

`phenotyped`
: A vector of IDs of those individuals for which to return phenotypic data

`genotyped`
: A vector of IDs of those individuals for which to return genotypic data

`returnG`
: If 'y' then genotypic data for all loci (including `cIAM` loci) will be returned.

`initFreqs`
: A list of allele frequencies for all loci. If `initFreqs` is specified, it will override information from `initHe`. `extractA` from package `MasterBayes` can be used to obtain obtain `initFreqs` form a sample of genotypes. For `cIAM` loci, allele names in `initFreqs` should be allelic substitution effects.

Details

Valid mutation types are 'Micro', 'Dom', 'dIAM' and 'cIAM', for microsatellite, dominant (AFLP), discrete infinite alleles mutation model loci (SNPs), and continuous infinite alleles mutation model loci (polymorphisms effecting phenotypic variation). cIAM loci have mutational allelic substitution effects taken drawn from a normal distribution with mean 0 and variance 1.

Value

`Phenotypes`
: A vector of phenotypes. Calculated as the sum of all allelic effects. Scaling is currently left to be done post-hoc.

`MarkerData`
: A vector of marker genotypes, i.e. alleles at all loci except those designated 'cIAM'

Author(s)

Michael Morrissey <michael.morrissey@st-andrews.ac.uk>

References

Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

See Also

`phensim`

Examples

```
testData<-as.data.frame(matrix(c(
1,NA,NA,1,1,1,2,2,
2,NA,NA,1,1,1,2,2,
3,NA,NA,1,1,1,2,2,
4,NA,NA,1,0,1,2,2,
5,NA,NA,1,0,1,2,2,
6,1,4,0,-1,2,3,3,
7,1,4,0,-1,2,3,3,
8,1,4,0,-1,2,3,3,
9,1,4,0,-1,2,3,3,
```

```
10,2,5,0,-1,2,3,3,
11,2,5,0,-1,2,3,3,
12,2,5,0,-1,2,3,3,
13,2,5,0,-1,2,3,3,
14,3,5,0,-1,2,3,3,
15,3,5,0,-1,2,3,3,
16,3,5,0,-1,2,3,3,
17,3,5,0,-1,2,3,3),
17,8,byrow=TRUE))

names(testData)<-c("id","dam","sire","founder","sex",
                                   "cohort","first","last")
pedigree<-as.data.frame(cbind(testData$id,testData$dam,
                                              testData$sire))
for(x in 1:3) pedigree[,x]<-as.factor(pedigree[,x])
names(pedigree)<-c("id","dam","sire")
pedigree

##make up some microsatellite and gene allele frquencies:
sampleGenotypes<-as.data.frame(matrix(c(
                  1,2,-1.32,0.21,2,1,0.21,0.21),2,4,byrow=TRUE))
testFreqs<-extractA(sampleGenotypes)

## note that alleles at the gene locus are given as their
## allelic substitution effects:
testFreqs

## simulate data for these indivdiuals based on a single QTL
## with two equally alleles with balanced frequencies in the
## founders, linked (2 cM) to a highly  polymorphic microsatellite:
genomesim(pedigree=pedigree,founders=testData$founder,positions=c(0,2),
     mutationType=c('Micro','cIAM'),mutationRate=c(0,0),
     initFreqs=testFreqs,returnG='y')
## since we specified returnG='y', we can check that
## the phenotypes add up to the
## allelic substitution effects for the second locus.
```

---

gryphons *Example dataset for pedantics examples and titorial*

Description

This contains pedigree and life history data of a fictional population. The data are relevent to power and sensitivity analyses for quantitative genetic studies of natural populations.

Usage

```
gryphons
```

Format

A table.

`makePedigreeFactor` *Converts a numeric pedigee to a pedigree with factors*

Description

Some internal `pedantics` modules require that pedigrees be specified only by numerical values, including numerical values for missing data, this converts them back to factors

Usage

```
makePedigreeFactor(id, sire, dam, key)
```

Arguments

`id`	Numeric individual identifiers
`sire`	Numeric sire codes
`dam`	Numeric dam codes
`key`	A dataframe, as produced by `makePedigreeNumeric`, specifying factor codes for numeric values in is, sire, and dam

Value

returns the pedigree with all ids specified as factors according to key

Author(s)

Michael Morrissey <michael.morrissey@st-andrews.ac.uk>

References

Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

See Also

`makePedigreeNumeric`

Examples

```
## first we'll implement the example from makePedigreeNumeric(),
## and use makePedigreeFactor() to turn it back again:

pedigree<-as.data.frame(matrix(c(
"m1",NA,NA,
"m2",NA,NA,
"m3",NA,NA,
"d4",NA,NA,
"d5",NA,NA,
"o6","m1","d4",
"o7","m1","d4",
"o8","m1","d4",
"o9","m1","d4",
"o10","m2","d5",
"o11","m2","d5",
"o12","m2","d5",
"o13","m2","d5",
"o14","m3","d5",
"o15","m3","d5",
"o16","m3","d5",
"o17","m3","d5"),17,3,byrow=TRUE))

names(pedigree)<-c("id","dam","sire")
for(x in 1:3) pedigree[,x]<-as.factor(pedigree[,x])

## make the test pedigree numeric with NAs denoted by -1
test<-makePedigreeNumeric(id=as.character(pedigree[,1]),
                          dam=as.character(pedigree[,2]),
                          sire=as.character(pedigree[,3]),
                          missingVal=-1)

test$numericPedigree

test$idKey

## and turn it back again
makePedigreeFactor(id=test$numericPedigree$id,
                          dam=test$numericPedigree$dam,
                          sire=test$numericPedigree$sire,
                          key=test$idKey)
```

`makePedigreeNumeric` *Converts a pedigree with individuals specified as factors to a numeric pedigree*

Description

Some internal pedantics modules require that pedigrees be specified only by numerical values, including numerical values for missing data, this provides that conversion

Usage

```
makePedigreeNumeric(id, sire, dam, missingVal = NULL)
```

Arguments

id	Individual identifiers - pass using as.character()
sire	Sire codes - pass using as.character()
dam	Dam codes - pass using as.character()
missingVal	the indicator that should be substituted for missing values

Value

numericPedigree	The factor pedigree in numeric form
idKey	A key to facilitate conversion back to the original identifiers

Author(s)

Michael Morrissey <michael.morrissey@st-andrews.ac.uk>

References

Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

See Also

makePedigreeFactor

Examples

```
pedigree<-as.data.frame(matrix(c(
"m1",NA,NA,
"m2",NA,NA,
"m3",NA,NA,
"d4",NA,NA,
"d5",NA,NA,
"o6","m1","d4",
"o7","m1","d4",
"o8","m1","d4",
"o9","m1","d4",
"o10","m2","d5",
"o11","m2","d5",
"o12","m2","d5",
"o13","m2","d5",
```

```
"o14","m3","d5",
"o15","m3","d5",
"o16","m3","d5",
"o17","m3","d5"),17,3,byrow=TRUE))
names(pedigree)<-c("id","dam","sire")
for(x in 1:3) pedigree[,x]<-as.factor(pedigree[,x])

## make the test pedigree numeric with NAs denoted by -1
makePedigreeNumeric(id=as.character(pedigree[,1]),
                          dam=as.character(pedigree[,2]),
                          sire=as.character(pedigree[,3]),
                          missingVal=-1)
```

`microsim` *Simulates microsatellite data across a pedigree.*

Description

Uses a pedgiree with parents identified for all non-founding individuas and simulates microsatellite genotypes

Usage

```
microsim(pedigree, genFreqs = NULL, genotypesSample = NULL,
        knownGenotypes = NULL,records = NULL, eRate1 = 0,
        eRate2 = 0, eRate3 = 0)
```

Arguments

`pedigree`	A pedigree
`genFreqs`	(optional) A list of allele frequencies, can be produced with `extractA` in `MasterBayes`
`genotypesSample`	(required if `genFreqs` is not supplied) a sample of genotypes from which to estimate population allele frequencies
`knownGenotypes`	(not yet implemented) a data frame of genotypes for (potentially a subset) of founder individuals
`records`	Record availability, see details.
`eRate1`	The rate of genotypic substitution errors, i.e., when a true genotype at a given locus is replaced by a pair of alleles selected at random based on the population allele frequencies
`eRate2`	The rate of allelic substitution errors, i.e. when an allele is erroneously replaced at a given locus by an allele chosen at random based on the population allele frequencies
`eRate3`	The rate of large allele dropouts, simulated by setting the value of the larger allele at a locus to the value of the smaller allele

Details

Error rates and data availability rates can be specified as either (1) single values to be applied to all individuals and all loci, (2) as a vector the same length as the number of loci, representing locus-specific rates to be applied uniformly to all individuals, or (3) as data frames with rows for each individual and columns for each locus. In the third option, observed patterns of data availability can be simulated by supplying 0s and 1s for missing and available individual genotypes, respectively.

Value

`trueGenotypes` A data frame of true genotypes

`observedGenotypes`
A data frame of plausible observed genotypes, given specified patterns of missingness and errors.

Author(s)

Michael Morrissey <michael.morrissey@ed.ac.uk>

References

Morrissey et al. 2007. Journal of Evolutionary Biology 20:2309-2321., Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

Examples

```
pedigree<-as.data.frame(matrix(c(
"m1",NA,NA,
"m2",NA,NA,
"m3",NA,NA,
"d4",NA,NA,
"d5",NA,NA,
"o6","m1","d4",
"o7","m1","d4",
"o8","m1","d4",
"o9","m1","d4",
"o10","m2","d5",
"o11","m2","d5",
"o12","m2","d5",
"o13","m2","d5",
"o14","m3","d5",
"o15","m3","d5",
"o16","m3","d5",
"o17","m3","d5"),17,3,byrow=TRUE))
names(pedigree)<-c("id","dam","sire")
for(x in 1:3) pedigree[,x]<-as.factor(pedigree[,x])

## some sample genotypes, very simple, two markers with He = 0.5
sampleGenotypes<-as.data.frame(matrix(c(
                  1,2,1,2,2,1,2,1),2,4,byrow=TRUE))
## locus names
```

```
names(sampleGenotypes)<-c("loc1a","loc1b","loc2a","loc2b")

## simulate some genotypes
microsim(pedigree=pedigree,genotypesSample=sampleGenotypes)
```

---

pedigreeStats *Calculates a range of statistics of pedigrees.*

Description

Statistics are those that will hopefully be useful for describing pedigrees to be used in quantitative genetic analyses of natural populations. This module will be most useful when cohort affinities for all individuals can be provided. All outputs are produced in a numerical form as well as in graphical summaries.

Usage

```
pedigreeStats(Ped, cohorts = NULL, dat = NULL,
              retain='informative', graphicalReport = "y",
              includeA=TRUE,lowMem=FALSE,grContrast=FALSE)
```

Arguments

Ped	A pedigree
cohorts	(Optional) Cohort affinities for members of the pedigree
dat	(Optional) Available data based upon which the pedigree can be pruned for just informative individuals
retain	The default value ('informative') results in pedigree being pruned to only those indivduals who's records contribute to estimation of quantitative genetic parameters with respect to the available data specified in dat. Otherwise, specifying a value of 'ancestors' will result in the inclusion of all ancestors of phenotyped individuals.
graphicalReport	Controls whether or not grphical output is produced.
includeA	If TRUE, additive genetic relatedness matrix is returned.
lowMem	If TRUE, then stats based on calculation of A are not performed.
grContrast	If TRUE, then uglier shades of red and blue are used to denote male and female statistics in graphical reports, but these colours provide better contrast in greyscale.

Value

`totalMaternities`
: Total number of maternities defined by the pedigree.

`totalPaternities`
: Total number of paternities defined by the pedigree.

`totalFullSibs`
: Total number of pair-wise full sib relationships defined by the pedigree.

`totalMaternalSibs`
: Total number of pair-wise maternal sib relationships defined by the pedigree. To get the number of maternal half sibs, subtract totalFullSibs.

`totalPaternalSibs`
: Total number of pair-wise paternal sib relationships defined by the pedigree. To get the number of paternal half sibs, subtract totalFullSibs.

`totalMaternalGrandmothers`
: Total number of maternal grandmothers defined by the pedigree.

`totalMaternalGrandfathers`
: Total number of maternal grandfathers defined by the pedigree.

`totalPaternalGrandmothers`
: Total number of paternal grandmothers defined by the pedigree.

`totalPaternalGrandfathers`
: Total number of paternal grandfathers defined by the pedigree.

`pedigreeDepth`
: The pedidigree pedth, i.e. maximum number of ancestral generations, for each individual.

`inbreedingCoefficients`
: Individual inbreeding coefficients

`maternalSibships`
: Sibship size of each individual appearing the the dam column of the pedigree.

`paternalSibships`
: Sibship size of each individual appearing the the sire column of the pedigree.

`cumulativeRelatedness`
: Proportion of pair-wise relatedness values less than values ranging from 0 to 1.

`relatednessCategories`
: Discretized distribution of relatedness.

`analyzedPedigree`
: Returns the pedigree.

`sampleSizesByCohort`
: (Optional) Numer of individuals belonging to each cohort.

`maternitiesByCohort`
: (Optional) Number of assigned maternities by offspring cohort.

`paternitiesByCohort`
: (Optional) Number of assigned paternities by offspring cohort.

`fullSibsByCohort`
: (Optional) Number of pair-wise full sib relationships by cohort - note the sum of these need not be equal to totalFullSibs in pedigrees of long-lived organisms.

`maternalSibsByCohort`
: (Optional) Number of pair-wise maternal sib relationships by cohort - note the sum of these need not be equal to totalMaternalSibs in pedigrees of long-lived organisms.

`paternalSibsByCohort`
: (Optional) Number of pair-wise paternal sib relationships by cohort - note the sum of these need not be equal to totalPaternalSibs in pedigrees of long-lived organisms.

`maternalGrandmothersByCohort`
: (Optional) Numbers of maternal grandmother assignments by offspring cohort.

`maternalGrandfathersByCohort`
: (Optional) Numbers of maternal grandmother assignments by offspring cohort.

`paternalGrandmothersByCohort`
: (Optional) Numbers of paternal grandfather assignments by offspring cohort.

`paternalGrandfathersByCohort`
: (Optional) Numbers of paternal grandfather assignments by offspring cohort.

`cumulativePedigreeDepth`
: (Optional) Distributions of pedigree depth by cohort.

`meanRelatednessAmongCohorts`
: (Optional) Mean relatedness among cohorts.

`cohorts`
: (Optional) Returns cohort designations.

Graphical summaries of a number of these summary statistics are printed to the console when codegraphicalReports=='y'.

Author(s)

Michael Morrissey <michael.morrissey@ed.ac.uk>

References

Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

See Also

`fixPedigree`

Examples

```
## Not run:

data(gryphons)
pedigree<-gryphons[,1:3]

gryphonsPedigreeSummary<-pedigreeStats(pedigree,
                      cohorts=gryphons$cohort,graphicalReport='n')
```

```
gryphonsPedigreeSummary$totalMaternities
gryphonsPedigreeSummary$totalPaternities

gryphonsPedigreeSummary$maternitiesByCohort
gryphonsPedigreeSummary$paternitiesByCohort


## End(Not run)
```

`pedStatSummary` *Post-processes output from pedigreeStats*

Description

Generates a manageable summary of pedigree-wide statistics reported by pedigreeStats, either for a single pedigree or for a comparison between pedigrees

Usage

```
pedStatSummary(pedStats,pedStats2=NULL)
```

Arguments

`pedStats`	An output data list from pedgireeStats
`pedStats2`	An optional output data list from pedgireeStats

Value

Returns a table of numbers of records, maternities, paternities, pairwise sibship relationships, numbers of different classes of grand-parental relationships, pedigree depth, number of founders, mean subship sizes, simple statistics of numbers of inbred and non-inbred indivdiuals, and proportions of pairwise relationship coefficients equal to or greater than several thresholds.

Author(s)

Michael Morrissey <michael.morrissey@st-andrews.ac.uk>

References

Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

phensim *A function to simulated phenotypic data*

Description

Simulates phenotypic data across arbitrary pedigrees. phensim simulate direct, maternal and paternal genetica and environmental effects for an arbitrary number of traits with arbitrary patterns of missing data.

Usage

```
phensim(pedigree, traits = 1, randomA = NULL, randomE = NULL,
        parentalA = NULL, parentalE = NULL, sampled = NULL,
              records = NULL, returnAllEffects = FALSE)
```

Arguments

pedigree	A pedigree
traits	The number of traits for which data should be simulated.
randomA	An additive genetic covariance matrix, with dimensions a multiple of traits - see details
randomE	An additive environmental covariance matrix, with dimensions a multiple of traits - see details
parentalA	A vector indicating which effects in randomA (if any) to treat as parental effects
parentalE	A vector indicating which effects in randomE (if any) to treat as parental effects
sampled	A vector indicating which individuals are sampled
records	A single value, array of matrix specifying data record availability - see details
returnAllEffects	If TRUE then all individual breeding values and environmental effects are returned

Details

randomA and randomE are square matrices with dimension equal to the sum of the number direct and indirect effects. This must be a multiple of the number of traits, i.e. if an indirect effect is to be simulated for only one of multiple traits, those traits with no indirect effect should be included with (co)variances of zero.

parentalA and parentalE are optional vectors of characters indicating which trait positions in randomA and randomE are to be treated as indirect effects, and which effects to treat as maternal or paternal. Valid values are 'd', 'm', and 'p', for direct, maternal indirect and paternal indirect effects, respectively.

records can be specified either (1) as asingle value to be applied to all individuals and traits, (2) as a vector the same length as the number of traits, representing trait-specific rates to be applied uniformly to all individuals, or (3) as data frames with rows for each individual and columns for each trait. In the third option, observed patterns of data availability can be simulated by supplying 0s and 1s for missing and available individual genotypes, respectively.

Value

phenotypes	A dataframe containing phenotypes for all indivduals specified to have records.
allEffects	(optional) A dataframe with all direct and indirect genetic and environmental effects.

Author(s)

Michael Morrissey <michael.morrissey@st-andrews.ac.uk>

References

Morrissey et al. 2007. Journal of Evolutionary Biology 20:2309-2321., Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

Examples

```
## make up a pedigree
id<-   c("a1","a2","a3","a4","a5","a6","a7","a8","a9")
dam<-  c(NA,NA,NA,"a1","a1","a1","a4","a4","a4")
sire<- c(NA,NA,NA,"a2","a2","a2","a5","a6","a6")
pedigree<-as.data.frame(cbind(id,sire,dam))

traits<-2
## no correlations
randomA<-diag(4)
randomE<-diag(4)
parentalA<-c("d","d","m","m")
parentalE<-c("d","d","m","m")

## generate phenoypic data based on this architecture
phensim(pedigree=pedigree,traits=2,randomA=randomA,randomE=randomE,
          parentalA=parentalA,parentalE=parentalE)

## let's do it again but see how the phenotypes were composed
phensim(pedigree=pedigree,traits=2,randomA=randomA,randomE=randomE,
          parentalA=parentalA,parentalE=parentalE,returnAllEffects=TRUE)
```

---

rpederr *Permutes a pedigree to create a plausible complete pedigree*

Description

Given estimates of indivdiual life histories and rates and patterns of errors in pedigree links, rpederr probabilistically assigns "true" parents given an incomplete and potentially eroneous pedigree.

Usage

```
rpederr(assumedPedigree, founders = NULL, sex = NULL, samp = NULL,
         sireE = NULL, damE = NULL, sireS = NULL, damS = NULL,
         cohort = NULL, first = NULL, last = NULL, monoecey = 0,
         modifyAssumedPedigree = 0)
```

Arguments

assumedPedigree	A pedigree
founders	A vector of indicator variables denoting founder status (1=founder, 0=non-founder)
sex	A vector of indicator variables denoting sex (0=male,1=female,anything else=unknown)
samp	A vector denoting whether or not individuals are sampled (1), or dummy individuals (0) added to the pedigree for the purpose of simulating potential "true" pedigree links that go outside the sampled population
sireE	Sire assignment error rates, see details
damE	Dam assignment error rates, see details
sireS	Proportion of "true" simulated sires that are to be taken from the unsampled portion of the pedgiree.
damS	Proportion of "true" simulated dams that are to be taken from the unsampled portion of the pedgiree.
cohort	A numeric vector the same length as the pedigree containing cohorts
first	A numeric vector the same length as the pedigree indicating the first cohort for which an individual is to be considered a potential parent
last	A numeric vector the same length as the pedigree indicating the last cohort for which an individual is to be considered a potential parent
monoecey	An indicator specifying whether or not bisexuality is allowed (0=no (default), 1=yes)
modifyAssumedPedigree	An indicator variable specifying whether or not an assumed pedigree with errors but no missing links should be supplied.

Value

assumedPedigree	echos the supplied pedigree
truePedigree	A plausible pedigree with no errors and no missing links
supplementalPedigree	A plausible pedigree with errors but no missing links

Author(s)

Michael Morrissey <michael.morrissey@st-andrews.ac.uk>

References

Morrissey et al. 2007. Journal of Evolutionary Biology 20:2309-2321., Morrissey, M.B, and A.J. Wilson, 2009. pedantics, an R package for pedigree-based genetic simulation, and pedigree manipulation, characterisation, and viewing. Molecular Ecology Resources.

Examples

```
id<-   c("a1","a2","a3","a4","a5","a6","a7","a8","a9")
dam<-  c(NA,NA,NA,"a1","a1","a1","a4","a4","a4")
sire<- c(NA,NA,NA,NA,NA,NA,"a5","a5","a5")
found<-c(1,1,1,0,0,0,0,0,0)
samp<- c(1,1,1,1,1,1,1,1,1)
sex<-  c(1,0,0,1,0,0,1,0,0)
dade<- rep(0,9)
mume<- rep(0,9)
dads<- rep(1,9)
mums<- rep(1,9)
cohort<-c(1,1,1,2,2,2,3,3,3)
first<-c(2,2,2,3,3,3,4,4,4)
last<-c(2,2,2,3,3,3,4,4,4)
pedigree<-as.data.frame(cbind(id,sire,dam))

### don't simulate any errors, just fill in the missing sires
rpederr(assumedPedigree=pedigree,founders=found,sex=sex,
                  samp=samp,cohort=cohort,first=first,last=last)

## fill in the missing sires, and additionally simulate a problem
## with the second maternal sibship note that it is probabilistic,
## so this example may need to be run a couple of times before the
## error comes up, given the very small example dataset
fatherErrors<-c(0,0,0,0,0,0,0.8,0.8,0.8)
rpederr(assumedPedigree=pedigree,founders=found,sex=sex,samp=samp,
           sireE=fatherErrors,cohort=cohort,first=first,last=last)
```

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