Package ‘Mangrove’

July 21, 2025

Type Package

Title Risk Prediction on Trees

Version 1.21

Date 2017-02-22

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Description Methods for performing genetic risk prediction from genotype data. You can use it to perform risk prediction for individuals, or for families with missing data.

License GPL (>= 2)

Suggests kinship2

LazyLoad yes

Depends R (>= 2.10)

Repository CRAN

Date/Publication 2017-02-22 17:15:37

NeedsCompilation no

Contents

`Mangrove-package` *Mangrove: Risk prediction on trees*

Description

`Mangrove` is an R package for performing genetic risk prediction from genotype data. You can use it to perform risk prediction for individuals, or for families with missing data.

Details

Package:	Mangrove
Type:	Package
Version:	1.21
Date:	2017-02-22
License:	GPL (>= 2)
LazyLoad:	yes

For a detailed example of how to use `Mangrove`, see `vignette("Mangrove")`.

Author(s)

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Examples

```
data(exampleORs)
data(famped)
tree <- initialiseTree()
tree$addPed(famped,exampleORs)
sam <- tree$getPrevs(exampleORs,K=0.02)
plotNaivePrev(famped,0.02)
plot(sam)
```

`getVarExp` *Calculating liability-scale variance explained by genetic risk variants*

Description

These functions calculate the variance explained on the liability scale by the genetic risk variants described by a `MangroveORs` object.

Usage

```
getVarExp(ORs, K)
getVarExpSim(ORs,K,iter=1000)
```

Arguments

`ORs`	An object of class `MangroveORs`
`K`	The prevalence of the disease.
`iter`	The number of individuals sampled for variance estimation.

Details

`getVarExp` calculates the variance explained analytically, by converting the odds ratios to liability-scale units, and combining them together additively. `getVarExpSim` simulates genotypes from the allele frequencies, performs risk prediction on them, converts the resulting posteriors to liabilities, and directly measures the variance of the sample.

Value

The proportion of variance explained, as a single numeric value.

Examples

```
data(exampleORs)
getVarExp(exampleORs,0.02)
getVarExpSim(exampleORs,0.02)
```

`MangroveBetas` *The MangroveBetas class*

Description

Functions to read in and use MangroveBetas objects

Usage

```
readBetas(betafile,header=TRUE)

## S3 method for class 'MangroveBetas'
print(x, ...)
## S3 method for class 'MangroveBetas'
summary(object, ...)
## S3 method for class 'MangroveBetas'
plot(x, ...)
```

Arguments

`betafile`	The location of a beta file to read in
`header`	Logical. Indicates whether the betafile above has a header.
`x`	A `MangroveBetas` object
`object`	A `MangroveBetas` object
`...`	Additional arguments to be passed to downstream methods.

Details

A `MangroveBetas` object is used to hold the risk alleles, beta values and frequencies for a set of genetic variants used to predict a quantitative trait. You can read a beta file from disk using `readBetas`.

The format of the beta file is a text file with 4 columns. The first should be the variant ID, the second the risk allele, the third the additive beta value and the fourth the frequency.

The `print` method shows the data that the object holds. The `summary` method gives some measures of how predictive the variants are, including the variance explained by the variants in the object. The `plot` method show the cumulative variance explained as the variants are added in one-at-a-time (in order of most-to-least variance explained).

See `vignette("Mangrove")` for an example of a beta file, and usage of a beta object.

Value

An object of class `MangroveBetas` for `readBetas`. Nothing is returned for the methods.

See Also

`MangroveContPreds` for performing quantitative trait prediction using this object.

Examples

```
data(exampleBetas)
summary(exampleBetas)
plot(exampleBetas)
```

`MangroveContPreds` *The MangroveContPreds class*

Description

Methods to generate, summarise and apply MangroveContPreds objects

Usage

```
calcBetas(ped,betas)
applyBetas(contpred,mu,sigma)

## S3 method for class 'MangroveContPreds'
print(x, ...)
## S3 method for class 'MangroveContPreds'
summary(object, ...)
## S3 method for class 'MangroveContPreds'
plot(x, ...)
```

Arguments

`ped`	A `MangrovePed` object
`betas`	A `MangroveBetas` object
`contpred`	A `MangroveContPreds` object
`object`	A `MangroveContPreds` object
`x`	A `MangroveContPreds` object
`mu`	The population mean of the quantitative trait being predicted
`sigma`	The population standard deviation of the quantitative trait being predicted
`...`	Arguments to be passed on to downstream methods.

Details

`MangroveContPreds` objects are used to hold quantitative (or continuous) trait predictions for a number of individuals. This object contains the beta value for the trait (i.e. the person's value of the trait on a scale with the population mean being zero and the population standard deviation being one). You can generate per-individual beta values from a pedigree object and some per-variant beta values using `calcBetas`, and you can transform these to quantitative trait predictions given a population mean and standard deviation using `applyBetas`.

The `print` method writes the beta value for each individual to screen. The `summary` method gives some quantile information, and the `plot` method plots a histogram of predicted values, which should be approximately normal.

Value

`calcBetas` returns a `MangroveContPreds` object, `applyBetas` returns a numeric vector containing posterior probabilities. The methods do not return anything.

See Also

`MangroveRiskPreds` for doing risk prediction for binary traits.

Examples

```
data(contped)
data(exampleBetas)
predbetas <- calcBetas(contped,exampleBetas)

summary(predbetas)
plot(predbetas)

contpreds <- applyBetas(predbetas,162,6.4)
```

`MangroveExamples` *Example data for the Mangrove vignette*

Description

Examples of the `MangroveORs`, `MangroveBetas` and `MangrovePed` classes from the `Mangrove` package. To be used in combination with the Mangrove vignette.

Usage

```
data(ccped)
data(famped)
data(exampleORs)
data(contped)
data(exampleBetas)
```

Details

See vignette("Mangrove") for details on these example objects.

Examples

```
data(ccped)
summary(ccped)

data(contped)
summary(contped)

data(famped)
summary(famped)

data(exampleORs)
summary(exampleORs)

data(exampleBetas)
summary(exampleBetas)
```

`MangroveORs` *The MangroveORs class*

Description

Functions to read in and use MangroveORs objects

Usage

```
readORs(ORfile,header=TRUE)

## S3 method for class 'MangroveORs'
print(x, ...)
## S3 method for class 'MangroveORs'
summary(object, K = NULL, ...)
## S3 method for class 'MangroveORs'
plot(x, K = NULL, ...)
```

Arguments

`ORfile`	The location of an odds ratio file to read in
`header`	Logical. Indicates whether the ORfile above has a header.
`x`	A `MangroveORs` object
`object`	A `MangroveORs` object
`K`	The prevalence of the disease that the odds ratios predict. If NULL, data is returned for a few example prevalences.
`...`	Additional arguments to be passed to downstream methods.

Details

A `MangroveORs` object is used to hold the risk alleles, odds ratios and frequencies for a set of genetic variants used to predict disease. You can read an odds ratio file from disk using `readORs`.

The format of the odds ratio file is a text file with 4 or 5 columns. If the file has 4 columns, the first should be the variant ID, the second the risk allele, the third the additive odds ratio and the fourth the frequency. If 5 columns exist, column three is the heterozygous odds ratio, column four is the homozygous risk odds ratio, and five is the allele frequency.

The `print` method shows the data that the object holds. The `summary` method gives some measures of how predictive the variants are, including the variance explained by the variants in the object on the liability scale. The `plot` method show the cumulative variance explained on the liability scale as the variants are added in one-at-a-time (in order of most-to-least variance explained).

See `vignette("Mangrove")` for an example of an odds ratio file, and usage of an odds ratio object.

Value

An object of class `MangroveORs` for `readORs`. Nothing is returned for the methods.

See Also

`MangroveRiskPreds` for performing risk prediction using this object, and `getVarExp` for more on assessing variance explained.

Examples

```
data(exampleORs)
summary(exampleORs)
plot(exampleORs)
```

`MangrovePed` *The MangrovePed class*

Description

Functions to read in and summarise MangrovePed objects

Usage

```
readPed(prefix)

## S3 method for class 'MangrovePed'
summary(object, ...)
## S3 method for class 'MangrovePed'
print(x, ...)
## S3 method for class 'MangrovePed'
plot(x, ...)
```

Arguments

`prefix`	The prefix for the file locations of a pair pedigree and map files, such as produced by the program `Plink`. Requires prefix.ped and prefix.map to both exist.
`x`	An object of class `MangrovePed`
`object`	An object of class `MangrovePed`
`...`	Arguments to be passed on to other methods.

Details

A MangrovePed object holds genotypes and family relationships for a number of individuals. You can read in such data from a Plink pedigree file using `readPed`.

You can show the raw pedigree data using the `print` method and get summary information (such as number of samples, cases and variants) using the `summary` method. The `plot` function produces an error.

Value

For `readPed`, an object of class `MangrovePed`. For methods, nothing is returned.

See Also

`MangroveORs`, `MangroveTree`.

Examples

```
data(famped)
summary(famped)
print(famped)
```

`MangroveRiskPreds` *The MangroveRiskPreds class*

Description

Methods to generate, summarise and apply MangroveRiskPreds objects

Usage

```
calcORs(ped,ORs)
applyORs(riskpred,K)

## S3 method for class 'MangroveRiskPreds'
print(x, ...)
## S3 method for class 'MangroveRiskPreds'
summary(object, ...)
## S3 method for class 'MangroveRiskPreds'
plot(x, ...)
```

Arguments

`ped`	A `MangrovePed` object
`ORs`	A `MangroveORs` object
`riskpred`	A `MangroveRiskPreds` object
`object`	A `MangroveRiskPreds` object
`x`	A `MangroveRiskPreds` object
`K`	The prevalence of the disease being predicted.
`...`	Arguments to be passed on to downstream methods.

Details

`MangroveRiskPreds` objects are used to hold risk predictions for a number of individuals. This object contains the odds ratio for each individual of developing the disease, relative to the population average. You can generate risk predictions from a pedigree object and some per-variant odds ratios using `calcORs`, and you can use these to calculate posterior probabilities of developing the disease given a prevalence using `applyORs`.

The `print` method writes the odds ratio for each individual to screen. The `summary` method gives some quantile information, and the `plot` method prints a histogram of log odds ratios, which should be approximately normal.

Value

`calcORs` returns a `MangroveRiskPreds` object, `applyORs` returns a numeric vector containing posterior probabilities. The methods do not return anything.

See Also

`MangroveTree` for doing risk prediction for a whole family. `MangroveContPreds` for doing quantitative trait prediction.

Examples

```
data(ccped)
data(exampleORs)
ccors <- calcORs(ccped,exampleORs)

summary(ccors)
plot(ccors)

ccposts <- applyORs(ccors,0.02)
```

`MangroveSample` *The MangroveSample class*

Description

Functions for manipulating MangroveSample objects

Usage

```
## S3 method for class 'MangroveSample'
print(x,...)
## S3 method for class 'MangroveSample'
summary(object, ...)
## S3 method for class 'MangroveSample'
plot(x,...)
```

Arguments

`x`	A `MangroveSample` object.
`object`	A `MangroveSample` object.
`...`	Further arguments to be passed on to downstream methods.

Details

MangroveSample objects are produced from a `MangroveTree` object via a call to `tree$getPrevs`. They contain samples from the posterior distribution of number of affecteds in a family conditional on that family's genotypes.

The `print` method writes all the samples to screen. You can plot the distribution of number of affecteds using the `plot` method (which calls `plotSampledPrev`), and perform a significance test for whether the observed number of affecteds is greater than would be expected using the `summary` method.

You can see a detailed example of how these methods are applied by calling `vignette("Mangrove")`

Value

None of the methods return anything.

See Also

`MangroveTree` to generate `MangroveSample` objects. `plotSampledPrev` for more on plotting expected distributions.

Examples

```
data(famped)
data(exampleORs)
tree <- initialiseTree()
tree$addPed(famped,exampleORs)
sam <- tree$getPrevs(exampleORs,0.02)

summary(sam)
plot(sam)
```

`MangroveTree` *The MangroveTree class*

Description

Functions to create, populate, summarise and utilise MangroveTree objects.

Usage

```
initialiseTree()

# Member functions:
# tree$addPed(ped,ORs)
# tree$getPrevs(ORs = NULL,K = NULL,overwrite=FALSE,iter=1000)

## S3 method for class 'MangroveTree'
print(x,...)
## S3 method for class 'MangroveTree'
summary(object,...)
## S3 method for class 'MangroveTree'
plot(x,...)
```

Arguments

`tree`	An object of class `MangroveTree`
`x`	An object of class `MangroveTree`
`object`	An object of class `MangroveTree`
`ped`	An object of class \codeMangrovePed
`ORs`	An object of class `MangroveORs`
`K`	The prevalence of the disease (between 0 and 1, or NULL if not known)
`overwrite`	Logical. If set to FALSE, and sampling has already been performed, then existing samples will be used. If TRUE, sampling is performed again.
`iter`	Number of samples to draw from the posterior distribution of number of affecteds.
`...`	Arguments to be passed on to other methods.

Details

The MangroveTree class is used for holding family trees, and for performing risk prediction on them. The `initialiseTree` function creates an empty tree, and the `tree$addPed` populates it from genetic data. You can then sample from the posterior distribution of number of affecteds using the `tree$getPrevs` function.

The `print` method writes a text version of the tree to screen, and the `summary` method writes some basic information about what the tree contains, along with what calculations have and have not been performed on it. The `plot` method is not implemented, and throws an error message.

To see an example of the use of this class, use `vignette("Mangrove")`.

Value

For `initialiseTree`, an empty object of class `MangroveTree`. For the `tree$getPrevs` class function, an object of class `MangroveSample`.

For all other functions, nothing is returned.

See Also

`MangrovePed`, `MangroveORs`, `MangroveSample`

Examples

```
data(famped)
data(exampleORs)

tree <- initialiseTree()
tree$addPed(famped,exampleORs)

print(tree)
summary(tree)

sam <- tree$getPrevs(exampleORs,K=0.02)
summary(sam)
```

`plotNaivePrev` *Plotting expected*

Description

Two functions for plotting the expected distribution of affecteds in a family, either assuming no genetic risk factors, or using sampled from a custom distribution of affecteds (such as produced by `MangroveTree`).

Usage

```
plotNaivePrev(ped,K,maxN = NULL,...)
plotSampledPrev(samples, obs_prev, exp_prev, maxN = NULL, ...)
```

Arguments

`ped`	A `MangrovePed` object.
`K`	The prevalence of the disease.
`samples`	Samples from the distribution of number of affecteds.
`obs_prev`	The number of affecteds actually observed.
`exp_prev`	The expected number of affecteds under a naive model.
`maxN`	The maximum number of affecteds to be shown on the graph. If `NULL`, an appropriate maximum is selected from the data.
`...`	Additional arguments to `plot`.

Details

These functions are used to assess how "unusual" a family is in terms of the number of affected individuals it contains. `plotNaivePrev` plots the distribution of affected individuals in the family assuming no genetic risk factors (i.e. under a binomial model). `plotSampledPrev` is more general, and takes in a set of samples from the expected distribution.

Note that `plotSampledPrev` is called by `plot.MangroveSample` to plot the results of a MangroveTree sampling. It will be easier to use the `print.MangroveSample` method rather than using `plotSampledPrev` under most circumstances.

Value

Neither function returns anything.

See Also

`MangroveSample`

Examples

```
data(famped)

plotNaivePrev(famped,0.02) # is this unexpected for a 2% disease?
plotNaivePrev(famped,0.04) # how about for a 4% disease?
```

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