Package ‘linkim’

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Type Package

Title Linkage information based genotype imputation method

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Description A linkage information based method for imputing missing diploid genotypes

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`linkim-package` *Linkage information based genotype imputation method*

Description

A linkage information based method for imputing missing diploid genotypes

Details

Package:	linkim
Type:	Package
Version:	1.0
Date:	2014-01-14
License: GPL(>= 2)	

Author(s)

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`barley` *A barley genotype dataset*

Description

A data frame of barley genotypes with genetic distance

Usage

```
data(barley)
```

Format

A data frame with 100 observations on the following 36 variables(barley SNP markers).

The first row is the genetic distance.

Examples

```
data(barley)
```

`link.im` *Linkage information based genotype imputation method*

Description

A linkage information based method for imputing missing diploid genotypes

Usage

```
link.im(data, r, char = NULL, oneside = NULL, twoside = NULL, trace = NULL,...)
```

Arguments

`data`	A data frame of genotypes. The type of genotype for each marker should be consistent.
`r`	Vector of recombination fraction or genetic distance.
`char`	Types of genotypes in the input data.
`oneside`	One flanking marker? Default TRUE.
`twoside`	Two flanking markers? Default TRUE.
`trace`	Show computation trace? Default FALSE.
`...`	Other arguments for future methods

Value

It returns a matrix of inputed genotype data frame.

References

Yi Xu, Yajun Wu, Michael G. Gonda and Jixiang Wu. A Linkage Based Imputation Method for Missing SNP Markers in Association Mapping (To be submitted)

Examples

```
data(barley)
dat <- barley[,-1]
r <- as.numeric(dat[1,])
data <- dat[-1,]
new.data <- link.im(data,r)
```

`pgdata` *Proportions of genotypes and distribution of missing values*

Description

Computes the proportions of genotypes in each columne, and plots the distribuition of missingness of the data.

Usage

```
pgdata(data, plot = NULL, type = NULL,...)
```

Arguments

`data`	A data frame of genotypes
`plot`	Plots the proportions of genotypes or missing values? Default FALSE.
`type`	Plot types, if type = "barplot" this is the barplot of proportions of missing values; if type= "stacked" this is the stacked barplot of proportions of missing values and genotypes; if type= "dist" this is the dot plot of missing values distribution. Default is not plot.
`...`	Other arguments for future methods

Value

It returns a matrix of proportions of genotypes and missing values for each column

Examples

```
data(barley)
data <- barley[-1:-2,-1]
pro <- pgdata(data)
pro <- pgdata(data,plot=TRUE,type="dist")
pro <- pgdata(data,plot=TRUE,type="barplot")
pro <- pgdata(data,plot=TRUE,type="stacked")
```

`sing.im` *Single imputation method*

Description

Imputes the missing value based on the observed data proportions.

Usage

```
sing.im(data,  ...)
```

Arguments

`data`	An input data frame
`...`	Other arguments for future methods

References

Peter A. Lachenbruch (2011) Variable selection when missing values are present: a case study. Statistical Methods in Medical Research 20:429-444

Examples

```
set.seed(123)
data <- matrix(sample(x=c(0,1,2,3),size=48,replace=TRUE),,4)
data[c(5,6,12),2] <- NA
data[c(4,12),3] <- NA
data[c(5,6),4] <- NA
sing.im(data)
sing.im(data,index=TRUE)
```

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