Package 'PAS'

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Type Package

Title Polygenic Analysis System (PAS)

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Description An R package for polygenic trait analysis.

Depends R (>= 2.10), glmnet

License GPL (>= 2)

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R topics documented:

PAS-package *Polygenic Analysis System (PAS)*

Description

The PAS package was developed to implement the method and algorithm developed by Zhiqiu Hu, Shizhong Xu, Zhiquan Wang, and Rongcai Yang for genomic value prediction. Although the current version of the package only provided functions for the bin model analysis (Hu et al., 2012), the package will be developed continuously to incorporate new methods of genomic value prediction that will be introduced by the authors in the near future.

updates:
1. A new option *foldid* was added into the binmod function to allow users assigning foldid for cross-validations;
2. A new output item *obj$optimal$map.binsnp* was added bridging the bin map and the snp map in a binmod object.

Details

Package:	PAS
Type:	Package
Version:	1.0
Date:	2012-04-12
License:	GPL (>2.0)

Author(s)

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References

bin model
Zhiqiu Hu, Zhiquan Wang, and Shizhong Xu (2012) An infinitesimal model for quantitative trait genomic value prediction. PloS ONE 7: e41336.

binmod.plot *plot function*

Description

Generate figures using an object created by the binmod function.

Usage

```
## S3 method for class 'binmod'
plot(x, file=NULL, width=7, height=5, getdata=FALSE, ...)
```

Arguments

x	An object generated by the binnod function.
file	The prefix of the figure files to be saved.
width	width of the figures (inch).
height	height of the figures (inch).
getdata	A logic indicator. The default value is FALSE, which mean not to return the data for plotting.
...	Further graphical parameters may also be supplied as arguments.

Examples

```
#load PAS library
library (PAS)
#load the demo data
data(beef)
#conduct bin model analysis and plotting the result.
plot(binmod(x, y, map))
```

binmod.predict *predict*

Description

Extract predicted genomic breeding values from the 10-fold cross-validation result that has been saved in a binmod object, or predict the breeding values for a new sample.

Usage

```
## S3 method for class 'binmod'
predict(object, newx=NULL, ...)
```

Arguments

object	An object generated by the binnod function.
newx	The numeric genotype indicator matrix of a new sample, which need to be coded in the same way as the genotypicdata generating the binmod object.
...	Further parameters may also be supplied as arguments.

Examples

```
#load PAS library
library(PAS)
#load the demo data
data(beef)
#conduct bin model analysis.
binmod.result=binmod(x, y, map)
#generate a new sample by sampling 20 individuals from the demo data
x0=x[sample(1:NROW(x) , 20), ]
#predict the genomic values of the new sample.
predict(binmod.result, newx=x0)
```

PAS.binmod *binmod*

Description

This is the main function for bin model analysis.

Usage

```
binmod(x, y, map, beta0=NA, binsizelist=-1, full.search=FALSE, foldid=NA, ...)
```

Arguments

x	input matrix, of dimensions nobs*nvars; each row is a observation vector of an individual and each column is a genotypic indicator vector for a molecular marker.
y	a matrix of response variable (phenotypic observations), of dimensions nobs*1.
map	A data frame for linkage map or physical map.
beta0	Estimated SNP effects obtained by univariate analysis. By default, the glm function in R will be called by the binmod to calculate the estimates of effects.
binsizelist	A list of binsizes to be considered in the analysis. A default list will be generated if the option was ignored or an invalid list has been specified.
full.search	A logic indicator selecting search strategies. If FALSE was assigned, the binmod will complete the running as soon as the optimal binsize was found. Otherwise, analysis will be conducted for all binsizes on the list.
foldid	An optional vector of values between 1 and nfold identifying what fold each observation is in. If not supplied, a random vector is generated under nfold=10.
...	Other parameters need to be passed to glmnet/r and glm/r.

Details

The function invokes binmod analysis for genomic value prediction. The default settings are strongly suggested for new users.

Value

`grid` information of all searched binsizes

`grid$mselist` a 'data.frame': nbinsizes of 4 variables # A list of mean square errors

`grid$mselist$binsize`
size settings of the bins, eight in bp or cM.

`grid$mselist$mse`
mean square error

`grid$mselist$mse_std`
the standard deviation of MSEs

`grid$mselist$nbin`
number of bins under the binsize setting

`grid$optbinsize`
optimal binsize

`grid$optid` order of the optimal binsize in the grid

`optimal` result obtained under the optimal binsize

`optimal$predict`
phentypic values and its' predicted values under the optimal model.

`optimal$predict$y`
original phenotypic observations

`optimal$predict$yp_cv`
predictions by 10-fold cross-validation.

`optimal$beta` estimated bin parameters

`optimal$beta$beta`
bin effect

`optimal$beta$SSx`
sum of square of bin indicator

`optimal$beta$Se`
residual error

`optimal$beta$Sb`
estimating error of bin effect

`optimal$beta$Wald`
Wald-test statistics

`optimal$beta$LOD`
LOD-test statistics

`optimal$xbin` indicator matrix of the bins under the optimal binsize

`optimal$map` 'data.frame': of 5 variables: #bin map

`optimal$map$chr`
chromosome id

`optimal$map$pos`
: bin position

`optimal$map$pos_id`
: mean of the orders of markers in the bin

`optimal$map$start_id`
: the order the first maker in a bin

`optimal$map$end_id`
: the order the last maker in a bin

`optimal$binsize`
: optimal binsize

`optimal$cv` cross-validation results

`optimal$cv$binsize`
: binsize

`optimal$cv$nbin`
: number of bins under the binsize setting

`optimal$cv$mse` mean squared error obtained from cross-validation

`optimal$cv$r` Pearson's correlation coefficient obtained from cross-validation

`snp` SNP information

`snp$map` linkage map or physical map

`snp$map$chr` chromosome id

`snp$map$pos` marker position

`snp$map$pos_id` marker order

`snp$effect` single marker analysis result

`snp$effect$beta`
: SNP effect

`snp$effect$SSx` sum of square of genotypic indicator

`snp$effect$Se` residual variance

`snp$effect$Sb` estimating error of marker effect

`snp$effect$Wald`
: Wald-test statistics

`snp$effect$LOD` LOD test statistics

`snp$mapinfo` a brief summary of the map

`snp$mapinfo$chr`
: chromosome id

`snp$mapinfo$start`
: the position of the first marker on the chromosome

`snp$mapinfo$end`
: the position of the last marker on the chromosome

`snp$mapinfo$length`
: length of the chromosome

`snp$mapinfo$nmark`
: number of markers on the chromosome

`snp$mapinfo$aver`
: average interval of the chromosome

`snp$mapinfo$min.interval`
: the smallest interval size on the chromosome

`cvfit`
: A cv.glmnet project. See manual of glmnet for details.

References

Zhiqiu Hu, Zhiquan Wang, and Shizhong Xu (2012) An infinitesimal model for quantitative trait genomic value prediction. PloS ONE

Examples

```
#load PAS library
library (PAS)
#load the demo data
data (beef)
#perform binmod analysis under the default settings.
binmod.result=binmod (x , y , map)
#plot binmod result
plot(binmod.result)
str(binmod.result)
#Output the predicted phenotypic values that was obtained
#by 10-fold cross validation .
predict(binmod.result)
#predict the phenotypic values for new individuals
x1=x[sample(1:NROW(x) , 20), ]
bin.pred.x1=predict(binmod.result, newx=x1)
str(bin.pred.x1)
```

PAS.binmod.beef *beef data*

Description

The data are provide for demonstration purpose only.

Value

`x` genotypic data. int [1:836, 1:300] 0 0 0 -1 -1 -1 -1 0 0 0 ...

`y` phenotypic data. int [1:836, 1] 768 157 508 614 590 777 505 243 509 351 ...

`map` physical map: 'data.frame': 300 obs. of 2 variables:
$ chr: num 1 1 1 1 ...
$ pos: int 113641 244698 369418 447277 ..

Examples

```
#load PAS library
library (PAS)
#load example data
data(beef)
str(x)
str(y)
str(map)
```

`PAS.binmod.print` *binmod.print*

Description

Show a terse summarize for a binmod object.

Usage

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

Arguments

`x`	An binmod object.
`...`	Further parameters may also be supplied as arguments.

Examples

```
#load PAS library
library (PAS)
#load the demo data
data (beef)
#conduct bin model analysis.
binmod.result=binmod (x, y, map)
print(binmod.result)
#show structure of a binmod object
str(binmod.result)
```

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