Package ‘PAS’

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Author Zhiqiu Hu; Shizhong Xu; Zhiquan Wang; Rongcai Yang
Maintainer Zhiqiu Hu <zhiqiu.hu@gmail.com>
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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

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Author(s)

Zhiqiu Hu, Shizhong Xu, Zhiquan Wang, Rong-cai Yang

Maintainer: Zhiqiu Hu <Zhiqiu.hu@gmail.com>

References

bin model
**binmod.plot**

**plot function**

**Description**
Generate figures using an object created by the binmod function.

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

**Arguments**
- `x` An object generated by the binmod 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**
```r
#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**
```r
## 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

```r
#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)
```

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)

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

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

Description

Show a terse summarize for a binmod object.

Usage

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

Arguments

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

Examples

```r
#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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