

# Package ‘PAS’

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**Type** Package

**Title** Polygenic Analysis System (PAS)

**Version** 1.2.5

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**Description** An R package for polygenic trait analysis.

**Depends** R (>= 2.10), glmnet

**License** GPL (>= 2)

**URL** <http://statgen.ucr.edu>, <http://www.ualberta.ca/~zhiqiu1>

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PAS-package

*Polygenic Analysis System (PAS)*

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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

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

## Author(s)

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

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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.

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binmod.plot	<i>plot function</i>
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### 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 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

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

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binmod.predict	<i>predict</i>
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### 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 binmod 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)
```

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PAS.binmod

*binmod*


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**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        phenotypic 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\$nbins 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\$mark 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)

```

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PAS.binmod.beef	<i>beef data</i>
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## 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)
```

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PAS.binmod.print	<i>binmod.print</i>
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**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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