

Package: GAGBLUP (via r-universe)

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Type Package

Title Genetic Algorithm Assisted Genomic Best Liner Unbiased Prediction

Version 1.0

Description Performs genetic algorithm (Scrucca, L (2013) <[doi:10.18637/jss.v053.i04](https://doi.org/10.18637/jss.v053.i04)>) assisted genomic best liner unbiased prediction for genomic selection. It also provides a binning method in natural population for genomic selection under the principle of linkage disequilibrium for dimensional reduction.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Depends R (>= 4.1.0)

Imports GA, foreach, doParallel

NeedsCompilation no

Repository CRAN

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bin	<i>Binning Genotypes for Dimensional Reduction</i>
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Description

Binning the original genotypes into bins for dimensional reduction under the principle of linkage disequilibrium.

Usage

```
bin(genotype = genotype, binvar = 0.15)
```

Arguments

genotype	a matrix for genotypes in numeric format, coded as 1, 0 and -1, with individuals in rows and markers in cols.
binvar	a hyper-parameter between 0 and 1, the closer to 0, the fewer bins yields. Users can choose binvar based on the required number of bins, default is 0.15.

Value

A list with following information is returned: \$bins_genotypes binned genotypes \$bins_range start and stop of each bin

Examples

```
## load example data from GAGBLUP package
data(genotype)
## binning genotypes
bins <- bin(genotype,0.2)
```

bins	<i>binned genotypes</i>
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Description

Binned genotypes of 410 maize hybrids.

Usage

```
bins
```

Format

A data frame with 410 rows and 810 variables.

gagblup	<i>Genetic algorithm assisted genomic best liner unbiased prediction for genomic selection</i>
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Description

Performs genomic selection with genetic algorithm assisted genomic best liner unbiased prediction

Usage

```
gagblup(
  genotype,
  phenotype,
  fit_fun = "HAT",
  maxiter = 2000,
  nfold = 10,
  nTimes = 1,
  seed = 123,
  n_core = 1
)
```

Arguments

genotype	a matrix for genotypes in numeric format, with individuals in rows and markers in cols.
phenotype	a vector of phenotype, missing (NA) values are not allowed.
fit_fun	the fitness function. There are four options: fitness = "AIC"/"BIC"/"FIT"/"HAT", default is "HAT"
maxiter	max number of iterations for GAGBLUP, default is 2000
nfold	the number of folds. Default is 10.
nTimes	the number of independent replicates for the cross-validation. Default is 1.
seed	the random number. Default is 123.
n_core	the number of CPU to be used, default is 1.

Value

A list with following information is returned: \$R2 the squared pearson correlation coefficient between the true value and the predicted value, \$predicted_value the predicted value and the true value of the phenotype, \$marker_selection a vector of the selected markers, with 1 indicates selected, 0 indicates not selected.

Examples

```
## load example data from GAGBLUP package
data(phenotype)
data(bins)
phenotype <- phenotype[1:200,3]
result <- gagblup(bins[1:200,],phenotype,fit_fun='HAT',maxiter=1,nfold=2,nTimes=1,seed=123,n_core=1)
```

genotype	<i>Genotype in Numeric Format</i>
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Description

Genotypic data of 410 maize hybrids with 4906 SNPs.

Usage

```
genotype
```

Format

A data frame with 410 rows and 4906 variables.

phenotype	<i>Phenotypic data of 410 hybrids</i>
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Description

This dataset contains phenotypic data of 410 hybrids for grain yield in maize.

Usage

```
phenotype
```

Format

A data frame with 410 rows and 3 variables:

M The names of male parents.

F The names of female parents.

GY The grain yield of hybrids.

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