Package 'StageWise'

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Title Two-stage analysis of multi-environment trials for genomic selection

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Description Two-stage analysis of multi-environment trials for genomic selection

Depends R (>= 4.0)

License GPL-3

LazyData true

RoxygenNote 7.1.1

Encoding UTF-8

Imports Matrix, ggplot2, methods, asreml, ggrepel, rlang

Suggests knitr, rmarkdown

Collate 'Stage1.R'
'Stage2.R'
'blup.R'
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'gwas_threshold.R'
'manhattan_plot.R'
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'read_geno.R'
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R topics documented:

`blup` *BLUP*

Description

BLUP

Usage

```
blup(data, geno = NULL, what, index.coeff = NULL, gwas.ncore = 0L)
```

Arguments

`data`	object of `class_prep` from `blup_prep`
`geno`	object of `class_geno` from `read_geno`
`what`	"id" or "marker"
`index.coeff`	index coefficients for the locations or traits
`gwas.ncore`	Integer indicating number of cores to use for GWAS (default is 0 for no GWAS). Requires `what="markers"`.

Details

Argument `what="id"` leads to prediction of breeding values (BV) and genotypic values (GV), including the average fixed effect of the environments and any fixed effect markers. For argument `what="marker"`, fixed effects are not included in the BLUP. Argument `index.coeff` should be a named vector, matching the names of the locations or traits. Index coefficients are normalized to have unit sum.

Value

Data frames of BLUPs

blup_prep *Prepare data for BLUP*

Description

Prepare data for BLUP

Usage

```
blup_prep(data, vcov = NULL, geno = NULL, vars, mask = NULL)
```

Arguments

data	data frame of BLUEs from Stage 1
vcov	list of variance-covariance matrices for the BLUEs
geno	object of class_geno from read_geno
vars	object of class_var from Stage2
mask	(optional) data frame with column "id" and optional columns "env", "trait"

Details

The argument mask can be used to mask all observations for a particular individual, or by including a column named 'env', only the observations in particular environments can be masked. This is useful for cross-validation to test the accuracy of predicting into new environments.

Value

Object of class_prep

class_geno-class *S4 class for marker genotype data*

Description

S4 class for marker genotype data

Slots

map Marker map positions

coeff Coefficients of the marker effects (dim: indiv x marker)

scale Scaling factor between markers and indiv

G Additive (genomic) relationship matrix

eigen.G list of eigenvalues and eigenvectors

class_prep-class *S4 class to prepare for blup*

Description

S4 class to prepare for blup

Slots

`y` Stage 1 BLUEs

`Z` Incidence matrix for random effects

`id` genotype identifiers

`var.u` variance of random effects

`Vinv` inverted covariance matrix of the Stage 1 BLUEs

`Pmat` P matrix from Searle

`fixed` fixed effect estimates

`random` random effect estimates

`add` logical whether additive effects predicted

`loc.env` data frame with loc, env

`fixed.marker` names of fixed effect markers

class_var-class *S4 class for variances*

Description

S4 class for variances

Slots

`add` additive

`g.resid` genetic residual

`resid` residual

`meanG` mean of diagonal of G

`meanOmega` mean of diagonal of Omega

`fixed.marker.var` variance of marker fixed effects

`fixed.marker.cov` contribution of marker fixed effects to additive covariance between locations

gwas_threshold *Compute GWAS discovery threshold*

Description

Compute GWAS discovery threshold

Usage

```
gwas_threshold(geno, n.core = 1, alpha = 0.05)
```

Arguments

geno	object of class_geno
n.core	number of cores to use
alpha	genome-wide significance level

Details

Uses a Bonferroni-type correction based on an effective number of markers that accounts for LD (Moskvina and Schmidt, 2008).

Value

-log10(p) threshold

References

Moskvina V, Schmidt KM (2008) On multiple-testing correction in genome-wide association studies. Genetic Epidemiology 32:567-573. doi:10.1002/gepi.20331

manhattan_plot *Create Manhattan plot*

Description

Create Manhattan plot

Usage

```
manhattan_plot(data, chrom = NULL, thresh = NULL, rotate = FALSE)
```

Arguments

data	data frame with columns for marker, chrom, position, and gwas.score
chrom	optional, to plot only one chromosome
thresh	optional, to include horizontal line at discovery threshold
rotate	TRUE/FALSE whether to rotate x-axis labels to be perpendicular

Details

Assumes position in bp

Value

ggplot2 object

`quantile` *G matrix quantile*

Description

G matrix quantile

Arguments

`x`	object of `class_geno`
`prob`	probability

Details

Unlike the S3 method, `prob` must have length = 1

Value

data frame with the quantile of the G matrix coefficients for each id

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`read_geno` *Read marker genotype data*

Description

Read marker genotype data

Usage

```
read_geno(filename, ploidy, map, eigen.tol = 1e-09)
```

Arguments

`filename`	Name of CSV file
`ploidy`	2,4,6,etc. (even numbers)
`map`	TRUE/FALSE
`eigen.tol`	1e-9

Details

When `map=TRUE`, first three columns of the file are marker, chrom, position. When `map=FALSE`, the first column is marker. Subsequent columns contain the allele dosage for individuals/clones, coded 0,1,2,...ploidy (fractional values are allowed). Additive coefficients are computed by subtracting the population mean from each marker, and the additive (genomic) relationship matrix is computed as G = tcrossprod(coeff)/scale. The scale parameter ensures the mean of the diagonal elements of G equals 1 under panmictic equilibrium. Missing genotype data is replaced with the population mean. For numerical conditioning, eigenvalues of G smaller than `eigen.tol` are replaced by `eigen.tol`.

Value

Variable of class `class_geno`.

`Stage1` *Stage 1 analysis of multi-environment trials*

Description

Computes genotype BLUEs within each environment using ASReml-R

Usage

```
Stage1(
  filename,
  traits,
  effects = NULL,
  silent = TRUE,
  workspace = "500mb",
  pworkspace = "500mb"
)
```

Arguments

`filename`	Name of CSV file
`traits`	trait names (see Details)
`effects`	data frame specifying other effects in the model (see Details)
`silent`	TRUE/FALSE, whether to suppress ASReml-R output
`workspace`	memory limit for ASRreml-R variance estimation
`pworkspace`	memory limit for ASRreml-R BLUE computation

Details

The input file must have one column labeled "id" for the individuals and one labeled "env" for the environments. The data for each environment are analyzed independently with a linear mixed model. Although not used in Stage1, to include a genotype x location effect in `Stage2`, a column labeled "loc" should be present in the input file.

Including multiple traits in `trait` triggers a multivariate analysis, but for computational reasons, only 2 traits are analyzed at a time. With more than 2 traits, the software analyzes all pairs of traits. For single trait analysis, broad-sense H2 on a plot basis is computed from the variance components

for each env, with genotype as a random effect. The residuals from this analysis are also returned as a table and plots.

Argument `effects` is used to specify other i.i.d. effects besides genotype and has three columns: name, fixed, factor. The "name" column is a string that must match a column in the input file. The fixed column is a logical variable to indicate whether the effect is fixed (TRUE) or random (FALSE). The factor column is a logical variable to indicate whether the effect is a factor (TRUE) or numeric (FALSE).

Missing response values are omitted for single-trait analysis but retained for multi-trait analysis (unless both traits are missing), to allow for prediction in Stage 2. By default, the workspace and pworkspace limits for ASReml-R are set at 500mb. If you get an error about insufficient memory, try increasing the appropriate value (workspace for variance estimation and pworkspace for BLUE computation).

Value

List containing

blue data frame of BLUEs for all environments

vcov list of variance-covariance matrices for the BLUEs, one per env

H2 broad-sense H2 on a plot basis (only for single trait)

resid list containing boxplot, qqplot, and table of residuals (only for single trait)

`Stage2` *Stage 2 analysis of multi-environment trials*

Description

Stage 2 analysis of multi-environment trials

Usage

```
Stage2(
  data,
  vcov = NULL,
  geno = NULL,
  fix.eff.marker = NULL,
  silent = TRUE,
  workspace = "500mb"
)
```

Arguments

`data`	data frame of BLUEs from Stage 1 (see Details)
`vcov`	list of variance-covariance matrices for the BLUEs
`geno`	output from `read_geno`
`fix.eff.marker`	markers in `geno` to include as additive fixed effect covariates
`silent`	TRUE/FALSE, whether to suppress ASReml-R output
`workspace`	Memory limit for ASRreml-R variance estimation

Details

Stage 2 of the two-stage approach described by Damesa et al. 2017, using ASReml-R for variance component estimation. The variable `data` has three mandatory column: id, env, BLUE. Optionally, `data` can have a column labeled "loc", which changes the main effect for genotype into a separable genotype-within-location effect, using a FA2 covariance model for the locations. Optionally, `data` can have a column labeled "trait", which introduces an unstructured covariance model for the traits. The multi-location and multi-trait analyses cannot be combined. Missing data are allowed in the multi-trait but not the single-trait analysis. The argument `geno` is used to partition genetic values into additive and non-additive (g.resid) components. Any individuals in `data` that are not present in `geno` are discarded.

The argument `vcov` is used to partition the macro- and micro-environmental variation, which are called GxE and residual in the output. `vcov` is a named list of variance-covariance matrices for the BLUEs within each environment, with id on the rownames. The order in `vcov` and `data` should match. Both `data` and `vcov` can be created using the function `Stage1`.

Because ASReml-R can only use relationship matrices defined in the global environment, this function creates and then removes global variables when either `vcov` or `geno` is used. By default, the workspace memory for ASReml-R is set at 500mb. If you get an error about insufficient memory, try increasing it. ASReml-R version 4.1.0.148 or later is required.

Value

List containing

aic AIC

vars variances, as variable of class `class_var`

fixed Fixed effect estimates for env and markers

random Random effect predictions

uniplot uniplot of the genetic correlation between locations

References

Damesa et al. 2017. Agronomy Journal 109: 845-857. doi:10.2134/agronj2016.07.0395

`summary` *Summarize variances and correlations*

Description

Summarize variances and correlations

Arguments

`object`	object of `class_var`

Details

When reporting the partitioning of variance, the variance component for the additive effect is multiplied by the mean diagonal of the G matrix.

Value

For univariate analysis, a matrix of variances. For multi-location or multi-trait analysis, a list containing the variance matrix and the correlation matrix.

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