

Package ‘StageWise’

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

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Description Fully efficient, two stage analysis of multi-environment trials, including directional dominance and multi-trait genomic selection

Depends R (>= 4.0)

License GPL-3

LazyData true

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Encoding UTF-8

Imports Matrix, ggplot2, methods, ggrepel, rlang, ggpubr, SpATS, spam, AGHmatrix, MASS, CVXR, ggforce

Suggests knitr, rmarkdown, asreml

Collate 'Stage1.R'
'Stage2.R'
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'blup_prep.R'
'class_geno.R'
'class_genoD.R'
'class_prep.R'
'class_var.R'
'corr.R'
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| | |
|------|-------------|
| blup | <i>BLUP</i> |
|------|-------------|

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 | One of the following: AV, BV, GV, AM, DM. See Details. |
| index.coeff | named vector of index coefficients for the locations or traits |
| gwas.ncore | Integer indicating number of cores to use for GWAS (default is 0 for no GWAS). |

Details

The argument `what` takes 5 possible values: "AV" (additive value), "BV" (breeding value), "GV" (genotypic value), "AM" (additive marker effect), and "DM" (dominance marker effect). "Values" refer to predictions for individuals, as opposed to markers. Predicted values include the average fixed effect of the environments, whereas predicted marker effects do not. Argument `index.coeff` is a named vector (matching the names of the locations or traits), and the values are interpreted for standardized traits.

Value

Data frame of BLUPs

| | |
|-----------|------------------------------|
| blup_prep | <i>Prepare data for BLUP</i> |
|-----------|------------------------------|

Description

Prepare data for BLUP

Usage

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

Arguments

| | |
|--------|--|
| data | data frame of BLUEs from Stage 1 |
| vcov | list of variance-covariance matrices for the BLUEs |
| geno | object of <code>class_geno</code> from <code>read_geno</code> |
| vars | object of <code>class_var</code> from <code>Stage2</code> |
| mask | (optional) data frame with possible columns "id", "env", "trait" |
| method | (optional) "MME", "Vinv", NULL (default). see Details |

Details

The method argument can be used to control how the linear system is solved. "MME" leads to inversion of the MME coefficient matrix, while "Vinv" leads to inversion of the overall var-cov matrix for the response vector. If NULL, the software uses whichever method involves inverting the smaller matrix. If the number of random effects (m) is less than the number of BLUEs (n), "MME" is used.

For the multi-location model, if all of the environments for a location are masked, the average of the other locations is used when computed average fixed effects.

Value

Object of `class_prep`

| | |
|-------------------|--|
| class_genos-class | <i>S4 class for marker genotype data</i> |
|-------------------|--|

Description

S4 class for marker genotype data

Slots

ploidy ploidy
 map Marker map positions
 coeff Coefficients of the marker effects (dim: indiv x marker)
 scale Scaling factor between markers and indiv
 G Additive relationship matrix (from markers and potentially also pedigree)
 eigen.G list of eigenvalues and eigenvectors

| | |
|--------------------|---|
| class_genosD-class | <i>S4 class for marker genotype data with dominance</i> |
|--------------------|---|

Description

S4 class for marker genotype data with dominance

Slots

ploidy ploidy
 map Marker map positions
 coeff Coefficients of the additive marker effects (dim: indiv x marker)
 scale Scaling factor between markers and indiv for additive effects
 G Additive relationship matrix (from markers and potentially also pedigree)
 eigen.G list of eigenvalues and eigenvectors for G
 coeff.D coefficients of the dominance marker effects (dim: indiv x marker)
 scale.D Scaling factor between markers and indiv for dominance effects
 D Dominance relationship matrix
 eigen.D list of eigenvalues and eigenvectors for D
 Fg genomic inbreeding coefficient

| | |
|------------------|-------------------------------------|
| class_prep-class | <i>S4 class to prepare for blup</i> |
|------------------|-------------------------------------|

Description

S4 class to prepare for blup

Slots

id genotype identifiers
 ploidy ploidy
 var.u variance of random effects
 var.uhat variance of BLUPs
 avg.env average fixed effect of the environments
 heterosis regression coefficients for inbreeding
 fixed.marker fixed marker effects
 B var-cov matrix for fixed effects
 random random effect estimates
 add matrix of additive variances from [class_var](#)
 g.iid matrix of g.iid variances from [class_var](#)
 dom matrix of dominance variances from [class_var](#)

| | |
|-----------------|-------------------------------|
| class_var-class | <i>S4 class for variances</i> |
|-----------------|-------------------------------|

Description

S4 class for variances

Slots

add additive
 g.iid iid genotype effect
 dom dominance
 resid residual
 diagG average diagonal element of the G matrix
 diagD average diagonal element of the D matrix
 vars variances for reporting
 B var-cov matrix of fixed effects for gain
 fix.eff.marker names of fixed effect markers

| | |
|------|---------------------------|
| corr | <i>Trait correlations</i> |
|------|---------------------------|

Description

Trait correlations

Usage

```
corr(vars, traits = NULL, effect = NULL)
```

Arguments

| | |
|--------|---|
| vars | object of <code>class_var</code> from <code>Stage2</code> |
| traits | pair of traits |
| effect | name of effect |

Details

Use either the argument `traits` or `effect`, not both. Using `traits` leads to a partitioning of the total correlation between those two traits, based on path analysis. Using `effect` displays the correlation between all traits for that effect. Use the `summary` command to see the names of the possible effects.

Value

matrix

| | |
|------|---------------------|
| gain | <i>Genetic gain</i> |
|------|---------------------|

Description

Genetic gain for breeding values

Usage

```
gain(input, traits = NULL, coeff = NULL, restricted = NULL, solver = "ECOS")
```

Arguments

| | |
|------------|---|
| input | either object of <code>class_prep</code> or <code>quad.mat</code> returned by this function |
| traits | optional, plots ellipse tradeoff |
| coeff | optional, index coefficients expressed in genetic standard deviation units |
| restricted | data frame of restricted traits see <code>Details</code> |
| solver | name of convex solver (default is "ECOS") |

Details

Optional argument `restricted` is a data frame with columns "trait" and "sign", where the options for sign are "=", ">", "<", representing equal to zero, non-negative, and non-positive.

Value

List containing

quad.mat quadratic matrix for the ellipsoid

plot ellipse plot

table data frame with gain and coefficients for the traits

| | |
|----------------|---|
| gwas_threshold | <i>Compute GWAS discovery threshold</i> |
|----------------|---|

Description

Compute GWAS discovery threshold

Usage

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

Arguments

| | |
|----------------------------|--------------------------------------|
| <code>geno</code> | object of class_geno |
| <code>alpha</code> | genome-wide significance level |
| <code>exclude.chrom</code> | chromosomes to exclude |
| <code>n.core</code> | number of cores to use |

Details

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

Value

$-\log_{10}(p)$ 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.label = FALSE)
```

Arguments

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

Details

Assumes position in bp

Value

ggplot2 object

| | |
|---------|---|
| predict | Predict individual values from marker effects |
|---------|---|

Description

Predict individual values from marker effects

Arguments

| | |
|----------------|---|
| object | object of <code>class_geno</code> |
| marker.effects | data frame with columns "marker" and "effect" |

Details

Use the `blup` function with `what="AM"` or `"DM"` to generate the data frame for `marker.effects`.

Value

data frame with columns "id" and "value"

| | |
|----------|--------------------------|
| quantile | <i>G matrix quantile</i> |
|----------|--------------------------|

Description

G matrix quantile

Arguments

| | |
|------|-----------------------------------|
| x | object of <code>class_geno</code> |
| 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

| | |
|-----------|----------------------------------|
| read_geno | <i>Read marker genotype data</i> |
|-----------|----------------------------------|

Description

Read marker genotype data

Usage

```
read_geno(
  filename,
  ploidy,
  map,
  min.minor.allele = 5,
  w = 1e-05,
  ped = NULL,
  dominance = FALSE
)
```

Arguments

| | |
|------------------|--|
| filename | Name of CSV file with marker allele dosage |
| ploidy | 2,4,6,etc. (even numbers) |
| map | TRUE/FALSE |
| min.minor.allele | threshold for marker filtering (see Details) |
| w | blending parameter (see Details) |
| ped | optional, pedigree data frame with 3 or 4 columns (see Details) |
| dominance | TRUE/FALSE whether to include dominance covariance (see Details) |

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). The input file for diploids can also be coded using -1,0,1 (fractional values allowed). Additive coefficients are computed by subtracting the population mean from each marker, and the additive (genomic) relationship matrix is computed as $G = \text{tcrossprod}(\text{coeff})/\text{scale}$. 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.

G can be blended with the pedigree relationship matrix (A) by providing a pedigree data frame in `ped` and blending parameter w . The blended relationship matrix is $H = (1-w)G + wA$. The first three columns of `ped` are `id`, `parent1`, `parent2`. Missing parents must be coded `NA`. An optional fourth column in binary (0/1) format can be used to indicate which ungenotyped individuals should be included in the H matrix. If there is no fourth column, only genotyped individuals are included. If a vector of w values is provided, the function returns a list of `class_geno` objects.

If the A matrix is not used, then G is blended with the identity matrix (times the mean diagonal of G) to improve numerical conditioning for matrix inversion. The default for w is $1e-5$, which is somewhat arbitrary and based on tests with the vignette dataset.

When `dominance=FALSE`, non-additive effects are captured using a residual genetic effect, with zero covariance. If `dominance=TRUE`, a (digenic) dominance covariance matrix is used instead.

The argument `min.minor.allele` specifies the minimum number of individuals that must contain the minor allele. Markers that do not meet this threshold are discarded.

Value

Variable of class `class_geno`.

Stage1

Stage 1 analysis of multi-environment trials

Description

Computes genotype BLUES for each experiment

Usage

```
Stage1(
  filename,
  traits,
  effects = NULL,
  solver = "asreml",
  spline = NULL,
  silent = TRUE,
  workspace = c("500mb", "500mb")
)
```

Arguments

| | |
|-----------|--|
| filename | Name of CSV file |
| traits | trait names (see Details) |
| effects | data frame specifying other effects in the model (see Details) |
| solver | one of the following: "asreml", "spats" |
| spline | vector of variable names for 2D spline with SpATS |
| silent | TRUE/FALSE, whether to suppress REML output |
| workspace | memory limits for ASRreml-R |

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.

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).

Argument solver specifies which software to use for REML. Current options are "asreml" and "spats". For "spats", the argument spline must be a vector of length two, with the names of the x and y variables (respectively) for the 2D spline.

The heritability and residuals in the output are based on a random effects model for id.

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.

Argument workspace is a vector of length two containing the workspace and pworkspace limits for ASReml-R, with default values of 500mb. If you get an error about insufficient memory, try increasing the appropriate value (workspace for variance estimation and pworkspace for BLUE computation).

For multiple traits, only "asreml" is supported, and only the BLUE model is run, so the returned object does not contain H2.

If the input file has a column "expt", this indicates multiple experiments within environment, which may be needed when using spatial analyses. Each experiment is first analyzed separately, and then the BLUEs from all experiments in one env are jointly analyzed to compute a single BLUE per env. The estimation errors from each experiment are propagated into the multi-expt model.

Value

List containing

blue data frame of BLUEs

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

fit data frame with broad-sense H2 (plot basis) and/or AIC

resid For single trait, list of diagnostic plots and data frame of residuals. For multi-trait, list of resid var-cov matrices.

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",
  dominance = FALSE
)
```

Arguments

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

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 uses an unstructured covariance model. 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 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` for rownames (single trait) or `id:trait`. 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** variance components for `blup_prep`, as variable of class `class_var`
 - fixed** Fixed effect estimates for env and markers
 - random** Random effect predictions
 - loadings** scaled loadings for the FA2 multi-loc model

References

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

| | |
|--------------|---|
| summary.geno | Summarize information about genomic relationships |
|--------------|---|

Description

Summarize information about genomic relationships

Arguments

object object of `class_geno`

Details

First column contains diagonal elements of the G matrix. For objects with dominance, second column contains the genomic inbreeding coefficients (scaled row-sum of the D matrix).

Value

data frame

| | |
|-------------|-------------------------------------|
| summary.var | Displays variances and correlations |
|-------------|-------------------------------------|

Description

Displays variances and correlations

Arguments

object object of `class_var`
digits number of digits for rounding

Details

For a single trait, the 'var' output is a data frame with two columns of information for the various effects: the first is the variance and the second is the proportion of variance explained (PVE), excluding the environment effect. For multiple locations or traits, the 'cor' output is the correlation matrix for additive effects (does not include fixed effect markers). For multiple traits, the variance and PVE results are returned as separate data frames.

Value

List output that varies depending on the situation (see Details)

| | |
|---------|--|
| uniplot | <i>Uniplot for multi-location models</i> |
|---------|--|

Description

Displays scaled loadings of the FA2 model

Usage

```
uniplot(loadings, nudge = 0.1)
```

Arguments

- loadings scaled factor loadings, from [Stage2](#).
- nudge distance to nudge labels

Details

The squared radius for each point is the proportion of genetic variance explained by the latent factors. For points on the unit circle, the cosine of the subtended angle equals the correlation.

Value

ggplot2 object

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