

Package: heritable (via r-universe)

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Title Heritability Estimation from Linear Mixed Models

Version 0.2.0

Description Provides flexible estimation of broad- and narrow-sense heritability from linear mixed models fitted with 'asreml' or 'lme4'. Implements commonly used estimators, including the Standard, Cullis, Oakey, Piepho, and Delta methods. Supports complex model structures, marginal and environment-specific heritability for genotype-by-environment models, and confidence intervals based on parametric bootstrap. The implemented estimators include methods discussed by Schmidt et al. (2019) <[doi:10.1534/genetics.119.302134](https://doi.org/10.1534/genetics.119.302134)>.

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Imports asremlPlus, boot, cli, irlba, MASS, Matrix, methods, reformulas, stringr, vctrs

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bootstrap_asreml	<i>Parametric bootstrap for an asreml model.</i>
------------------	--

Description

Simulate $\hat{y} \sim N(X\hat{\beta}, V)$ according to the current asreml fit and then refit to obtain the targeted statistics.

Usage

```
bootstrap_asreml(
  model,
  FUN,
  nsim = 1,
  use.u = FALSE,
  source = list(),
  seed = NULL,
  ...
)
```

Arguments

<code>model</code>	An asreml fitted model. Must be fitted with <code>model.frame = TRUE</code> .
<code>FUN</code>	A function with signature <code>function(fit)</code> returning a scalar (the statistic to bootstrap).
<code>nsim</code>	Integer. Number of bootstrap replicates.
<code>use.u</code>	A logical indicating whether to resample random effects, or only resample residuals.
<code>source</code>	The known genomic relationship matrix (GRM) used in <code>model</code> fitted using <code>asreml::vm()</code> , provided as a named list. When not provided (an empty list by default), the GRM variable used for <code>vm</code> calling will be searched in the global environment.
<code>seed</code>	Optional integer seed for reproducibility.
<code>...</code>	Additional arguments passed to <code>boot::boot()</code> .

Details

Fits parametric bootstrap replicates for an asreml model by:

- Extracting the fixed-effect fit $\hat{y} = X * \beta$.
- Extracting $V = \text{Var}(y)$ on the observation scale,
- Simulating new responses $y^* = \hat{y} + L \%*\% z$ where L is a Cholesky factor of V ,
- Refitting the same asreml call on each simulated dataset,
- Returning a boot object.

Value

A boot object.

Examples

```
## Not run:
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_asreml <- asreml(
  fixed = y ~ rep * pseudo_var1,
  random = ~gen,
  sparse = ~pseudo_var2,
```

```

    data = lettuce_subset,
    trace = FALSE
  )

  b <- bootstrap_asreml(
    lettuce_asreml,
    R = 200,
    statistic = function(fit) coef(fit)$fixed["(Intercept)", "effect"],
    seed = 1
  )
  boot::boot.ci(b, type = "perc")

## End(Not run)

```

confint.heritable	<i>Bootstrap confidence interval for heritability</i>
-------------------	---

Description

Computes a confidence interval for a heritability estimate using parametric bootstrap of the underlying mixed model. Parallel computing is supported through [boot::boot\(\)](#)

Usage

```

## S3 method for class 'heritable'
confint(
  object,
  parm = NULL,
  level = 0.95,
  B = 100,
  random_effect = c("resample", "conditional"),
  type = c("basic", "norm", "perc"),
  return_model = TRUE,
  seed = NULL,
  ...
)

```

Arguments

object	A heritability object returned by H2() (broad-sense) h2() (narrow-sense). The object must store the fitted model as an attribute.
parm	a specification of which methods are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all methods are considered.
level	Confidence level.
B	Integer. Number of bootstrap replicates.
random_effect	Character. Strategy for handling random effects. "resample" Resample random effects to propagate uncertainty.

	"conditional" Condition on estimated random effects.
type	Character. Bootstrap interval type; one of "basic", "norm", or "perc".
return_model	Logical. Whether to return to the boot object.
seed	Optional random seed.
...	Additional arguments passed to the bootstrap routine. Check <code>boot::boot()</code> , as well as the examples below for parallel computation

Value

A matrix of confidence intervals.

See Also

`boot::boot()`, `H2()`

Examples

```
## Not run:
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_asreml <- asreml(
  fixed = y ~ rep * pseudo_var1,
  random = ~gen,
  sparse = ~pseudo_var2,
  data = lettuce_subset,
  trace = FALSE
)

my_H2 <- H2(lettuce_asreml, "gen", c("Cullis", "Standard"))

my_ci <- confint(my_H2)

# Get bootstrap model
boot_mod <- attr(my_ci, "boot_mod")
boot_mod$t # Check bootstrap statistics

# Parallel computing (On Windows)
# Note that for asreml, `ncpus` can't be larger than the number of asreml
# license available
confint(my_H2, parallel = "snow", ncpus = 3)

# Parallel computing (On non-Windows)
confint(my_H2, parallel = "multicore", ncpus = 3)

## End(Not run)
```

`get_fixed_fit_asreml` *Fixed-effects-only fitted values from an asreml model*

Description

Returns the fitted values based on fixed effects only ($\hat{y} = X\hat{\beta}$), excluding all random effects.

Usage

```
get_fixed_fit_asreml(model, source = list())
```

Arguments

<code>model</code>	An object of class "asreml", fitted with <code>model.frame = TRUE</code> .
<code>source</code>	The known genomic relationship matrix (GRM) used in <code>model</code> fitted using <code>asreml::vm()</code> , provided as a named list. When not provided (an empty list by default), the GRM variable used for <code>vm</code> calling will be searched in the global environment.

Details

This function reconstructs the fixed-effect design matrix from the stored model frame and multiplies it by the estimated fixed coefficients. Sparse fixed terms (if any) are included.

Random effects (BLUPs) are not included.

Value

A numeric vector of length N , giving the fixed-effects-only fitted value for each observation.

H2 *Calculate broad-sense or narrow sense heritability from model object*

Description

A case-specific wrapper for calculating broad / narrow sense heritability.

- The lowercase prefix `h2_` refers to the wrapper or subfunctions e.g. `h2_Oakey()` for calculating narrow sense heritability
- The upper case prefix `H2_` refers to the wrapper or subfunctions e.g. `H2_Delta()` for calculating broad sense heritability

Usage

```

h2(model,
    target,
    method = c("Cullis", "Oakey", "Piepho", "Delta", "Standard"),
    options = NULL,
    marginal = TRUE,
    stratification = NULL,
    source = list(),
    vc = NULL,
    ...)

H2(model,
    target,
    method = c("Cullis", "Oakey", "Piepho", "Delta", "Standard"),
    options = NULL,
    marginal = TRUE,
    stratification = NULL,
    source = list(),
    vc = NULL,
    ...
)

```

Arguments

<code>model</code>	Model object of class <code>lmerMod/merMod</code> or <code>asreml</code>
<code>target</code>	The name of the random effect for which heritability is to be calculated.
<code>method</code>	Character vector of name of method to calculate heritability. See details.
<code>options</code>	NULL by default, for internal checking of model object before calculations
<code>marginal</code>	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
<code>stratification</code>	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
<code>source</code>	The known genomic relationship matrix (GRM) used in <code>model</code> fitted using <code>asreml::vm()</code> , provided as a named list. When not provided (an empty list by default), the GRM variable used for <code>vm</code> calling will be searched in the global environment. Ignored for broad-sense and <code>lmerMod</code> methods
<code>vc</code>	A list of precomputed variance components. Should be in the same structure as the output of <code>var_comp()</code>
<code>...</code>	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

The following methods are currently implemented for narrow-sense heritability `h2(method = "XX")`:

- "Cullis":

$$H_{Cullis}^2 = 1 - \frac{PEV_{\Delta..}^{BLUP}}{2\sigma_g^2}$$

- "Oakey":

$$H_{Oakey}^2 = \frac{\sum_{i=n_z+1}^{n_g} \lambda_i}{\sum_{n_g}^{\lambda_i \neq 0}}$$

- "Piepho":

$$H_{Piepho}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \overline{PEV_{BLUE_g}}/2}$$

- "Delta":

$$H_{\Delta ij}^2 = 1 - \frac{PEV_{\Delta ij}^{BLUP}}{\text{Var}(g_i - g_j)}$$

- "Standard":

$$H_{Standard}^2 = \frac{\text{Var}(g_i - g_j)}{\text{Var}(y_{i..} - y_{j..})}$$

- "Reliability":

$$\bar{r}^2 = \frac{1}{n_g} \sum_{i=1}^{n_g} \left(1 - \frac{\text{var}(\hat{g}_i^{BLUP})}{\text{var}(g_i)} \right)$$

"Reliability" is not part of the default method set but can be requested explicitly. Use `h2_Reliability_by_genotype()` / `H2_Reliability_by_genotype()` to obtain the per-genotype values r_i^2 instead of their mean.

The following methods are currently implemented for broad-sense heritability H2(method = "XX"):

- "Cullis":

$$H_{Cullis}^2 = 1 - \frac{PEV_{\Delta..}^{BLUP}}{2\sigma_g^2}$$

- "Oakey":

$$H_{Oakey}^2 = \frac{\sum_{i=n_z+1}^{n_g} \lambda_i}{\sum_{n_g}^{\lambda_i \neq 0}}$$

- "Piepho":

$$H_{Piepho}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \overline{PEV_{BLUE_g}}/2}$$

- "Delta":

$$H_{\Delta ij}^2 = 1 - \frac{PEV_{\Delta ij}^{BLUP}}{2\sigma_g^2}$$

- "Standard":

$$H_{Standard}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{1}{n_g} \sum_{n_g}^{i=1} \sigma_p^2 / n_{gi}}$$

- "Reliability":

$$\bar{r}^2 = \frac{1}{n_g} \sum_{i=1}^{n_g} \left(1 - \frac{\text{var}(\hat{g}_i^{BLUP})}{\text{var}(g_i)} \right)$$

For further details of a specific method - take a look at helpfile for each subfunctions `?H2_Cullis`

Value

A named numeric vector, length matching number of methods supplied

References

- Cullis, B. R., Smith, A. B., & Coombes, N. E. (2006). On the design of early generation variety trials with correlated data. *Journal of Agricultural, Biological, and Environmental Statistics*, 11(4), 381–393. <https://doi.org/10.1198/108571106X154443>
- Oakey, H., Verbyla, A., Pitchford, W., Cullis, B., & Kuchel, H. (2006). Joint modeling of additive and non-additive genetic line effects in single field trials. *Theoretical and Applied Genetics*, 113(5), 809–819. <https://doi.org/10.1007/s00122-006-0333-z>
- Schmidt, P., Hartung, J., Rath, J., & Piepho, H.-P. (2019). Estimating Broad-Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. *Crop Science*, 59(2), 525–536. <https://doi.org/10.2135/cropsci2018.06.0376>
- Piepho, H.-P., & Möhring, J. (2007). Computing Heritability and Selection Response From Unbalanced Plant Breeding Trials. *Genetics*, 177(3), 1881–1888. <https://doi.org/10.1534/genetics.107.074229>
- Falconer, D. S., & Mackay, T. F. C. (1996). *Introduction to quantitative genetics* (4th ed.). Longman.

See Also

[H2_Cullis\(\)](#), [H2_Oakey\(\)](#), [H2_Delta\(\)](#), [H2_Piepho\(\)](#), [H2_Standard\(\)](#), [h2_Oakey\(\)](#), [h2_Delta\(\)](#), [h2_Standard\(\)](#)

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2(lettuce_lme4, target = "gen", method = c("Standard", "Delta"))

# asreml model (Requires license)
## Not run:
lettuce_asreml <- asreml::asreml(fixed = y ~ rep,
                                random = ~ gen,
                                data = lettuce_subset,
                                trace = FALSE
                                )

H2(lettuce_asreml, target = "gen", method = c("Standard", "Delta"))

## End(Not run)
```

H2_Cullis

Calculate Cullis' heritability from model object

Description

Compute "generalised heritability" for unbalanced experimental designs. See Cullis, Smith and Coombes (2006) for derivation.

Usage

```
H2_Cullis(model,
          target,
          options = NULL,
          marginal = TRUE,
          stratification = NULL,
          vc = NULL,
          ...)
h2_Cullis(model,
          target,
          options = NULL,
          marginal = TRUE,
          stratification = NULL,
          vc = NULL,
          ...)
```

Arguments

model	Model object of class lmerMod/merMod or asreml
target	The name of the random effect for which heritability is to be calculated.
options	NULL by default, for internal checking of model object before calculations
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
vc	A list of precomputed variance components. Should be in the same structure as the output of <code>var_comp()</code>
...	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

The equation for Cullis heritability is as follow

$$H_{Cullis}^2 = 1 - \frac{PEV_{\Delta_{ij}}^{BLUP}}{2\sigma_g^2}$$

where:

- PEV is the prediction error variance matrix of the pairwise differences among BLUPS
- σ^2 is the variance attributed to differences between genotype

Value

Numeric value

References

Cullis, B. R., Smith, A. B., & Coombes, N. E. (2006). On the design of early generation variety trials with correlated data. *Journal of Agricultural, Biological, and Environmental Statistics*, 11(4), 381–393. <https://doi.org/10.1198/108571106X154443>

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Cullis(lettuce_lme4, target = "gen")

# asreml model (Requires license)
## Not run:
lettuce_asreml <- asreml::asreml(fixed = y ~ rep,
                                random = ~ gen,
                                data = lettuce_subset,
                                trace = FALSE
                                )

H2_Cullis(lettuce_asreml, target = "gen")

## End(Not run)
```

H2_Cullis_parameters *Calculate Cullis heritability using variance parameters*

Description

Compute the Cullis heritability for genotype means using the average variance of pairwise differences of best linear unbiased predictors (BLUPs).

Usage

```
H2_Cullis_parameters(vd_BLUP_avg, vc_g)
```

Arguments

- vd_BLUP_avg
- Numeric. Average variance of pairwise differences among BLUPs
- vc_g
- Numeric. Genotype variance component

Details

The equation for Cullis heritability is as follow

$$H^2_{Cullis} = 1 - \frac{PEV_{\Delta ij}^{BLUP}}{2\sigma_g^2}$$

where:

- *PEV* is the prediction error variance matrix of the pairwise differences among BLUPS
- σ^2 is the variance attributed to differences between genotype

Value

Numeric value

References

Cullis, B. R., Smith, A. B., & Coombes, N. E. (2006). On the design of early generation variety trials with correlated data. *Journal of Agricultural, Biological, and Environmental Statistics*, 11(4), 381–393. <https://doi.org/10.1198/108571106X154443>

Examples

```
H2_Cullis_parameters(vd_BLUP_avg = 0.25, vc_g = 0.8)
```

H2_Delta	<i>Calculate average heritability of differences between genotypes from model object</i>
----------	--

Description

Instead of computing heritability on a "entry-mean" basis, this method calculates heritability using "entry-differences". Entry here is referring to the genotype, line or variety of interest. See reference for origin and interpretation of h2/H2_Delta and it's variants

Usage

```

h2_Delta(model,
          target,
          type = c("BLUP", "BLUE"),
          options = NULL,
          marginal = TRUE,
          stratification = NULL,
          vc = NULL,
          ...)

H2_Delta(model,
          target,
          type = c("BLUP", "BLUE"),
          options = NULL,
          marginal = TRUE,
          stratification = NULL,
          vc = NULL,
          ...)

```

Arguments

model	Model object of class lmerMod/merMod or asreml
target	The name of the random effect for which heritability is to be calculated.
type	character, whether heritability is calculated using BLUEs or BLUPs
options	NULL by default, for internal checking of model object before calculations
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
vc	A list of precomputed variance components. Should be in the same structure as the output of <code>var_comp()</code>
...	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

The broad-sense heritability of differences between genotypes is given by:

$$H_{\Delta..}^2 = 1 - \frac{PEV_{\Delta..}^{BLUP}}{2\sigma_g^2}$$

where:

- $PEV_{\Delta..}^{BLUP}$ is the mean of the prediction error variance matrix for the pairwise differences among BLUPs (BLUEs if method = "BLUE") across all genotypes

- σ^2 is the variance attributed to differences between genotype

The narrow-sense heritability of differences between genotypes is given by:

$$h_{\Delta ij}^2 = 1 - \frac{PEV_{\Delta ij}^{BLUP}}{\text{Var}(g_i - g_j)}$$

where:

- g_i is the random effect of the i^{th} genotype

See reference page 995 - 997 for full derivation of this heritability measure and related variants

Value

Numeric

References

Schmidt, P., Hartung, J., Rath, J., & Piepho, H.-P. (2019). Estimating Broad-Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. *Crop Science*, 59(2), 525–536. <https://doi.org/10.2135/cropsci2018.06.03>

See Also

[h2_Delta_by_genotype\(\)](#), [H2_Delta_by_genotype\(\)](#), [h2_Delta_pairwise\(\)](#), [H2_Delta_pairwise\(\)](#)

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Delta(lettuce_lme4, target = "gen", type = "BLUP")

# asreml model (Requires license)
## Not run:
lettuce_asreml <- asreml::asreml(fixed = y ~ rep,
                                random = ~ gen,
                                data = lettuce_subset,
                                trace = FALSE
                                )

H2_Delta(lettuce_asreml, target = "gen", type = "BLUP")

## End(Not run)
```

H2_Delta_by_genotype	<i>Calculate heritability of differences for a given genotype from model object</i>
----------------------	---

Description

Instead of computing heritability on a "entry-mean" basis, this method calculates heritability using "entry-differences". Entry here is referring to the genotype, line or variety of interest. See reference for origin and interpretation of h2/H2_Delta_by_genotype and it's variants

Usage

```
h2_Delta_by_genotype(model,
  target,
  type = c("BLUP", "BLUE"),
  options = NULL,
  marginal = TRUE,
  stratification = NULL,
  vc = NULL,
  ...)
H2_Delta_by_genotype(model,
  target,
  type = c("BLUP", "BLUE"),
  options = NULL,
  marginal = TRUE,
  stratification = NULL,
  vc = NULL,
  ...)
```

Arguments

model	Model object of class lmerMod/merMod or asreml
target	The name of the random effect for which heritability is to be calculated.
type	character, whether heritability is calculated using BLUEs or BLUPs
options	NULL by default, for internal checking of model object before calculations
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
vc	A list of precomputed variance components. Should be in the same structure as the output of <code>var_comp()</code>
...	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

The broad-sense heritability of differences between genotypes is given by:

$$H_{\Delta..}^2 = 1 - \frac{PEV_{\Delta..}^{BLUP}}{2\sigma_g^2}$$

where:

- $PEV_{\Delta..}^{BLUP}$ is the mean of the prediction error variance matrix for the pairwise differences among BLUPs (BLUEs if method = "BLUE") across all genotypes
- σ^2 is the variance attributed to differences between genotype

The narrow-sense heritability of differences between genotypes is given by:

$$h_{\Delta ij}^2 = 1 - \frac{PEV_{\Delta ij}^{BLUP}}{\text{Var}(g_i - g_j)}$$

where:

- g_i is the random effect of the i^{th} genotype

See reference page 995 - 997 for full derivation of this heritability measure and related variants

Value

Numeric

Named list, with each element containing a named numeric vector

References

Schmidt, P., Hartung, J., Rath, J., & Piepho, H.-P. (2019). Estimating Broad-Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. *Crop Science*, 59(2), 525–536. <https://doi.org/10.2135/cropsci2018.06.03>

See Also

[h2_Delta\(\)](#), [H2_Delta\(\)](#), [h2_Delta_pairwise\(\)](#), [H2_Delta_pairwise\(\)](#)

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Delta_by_genotype(lettuce_lme4, target = "gen", type = "BLUP")

# asreml model (Requires license)
## Not run:
lettuce_asreml <- asreml::asreml(fixed = y ~ rep,
                                random = ~ gen,
                                data = lettuce_subset,
                                trace = FALSE)
```

```

    )

H2_Delta_by_genotype(lettuce_asrem1, target = "gen", type = "BLUP")

## End(Not run)

```

H2_Delta_pairwise	<i>Calculate pairwise heritability of differences between genotypes from model object</i>
-------------------	---

Description

Instead of computing heritability on a "entry-mean" basis, this method calculates heritability using "entry-differences". Entry here is referring to the genotype, line or variety of interest. See reference for origin and interpretation of h2/H2_Delta_pairwise and it's variants

Usage

```

h2_Delta_pairwise(model,
                  target,
                  type = c("BLUP", "BLUE"),
                  options = NULL,
                  marginal = TRUE,
                  stratification = NULL,
                  vc = NULL,
                  ...)
H2_Delta_pairwise(model,
                  target,
                  type = c("BLUP", "BLUE"),
                  options = NULL,
                  marginal = TRUE,
                  stratification = NULL,
                  vc = NULL,
                  ...)

```

Arguments

model	Model object of class lmerMod/merMod or asrem1
target	The name of the random effect for which heritability is to be calculated.
type	character, whether heritability is calculated using BLUEs or BLUPs
options	NULL by default, for internal checking of model object before calculations
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.

`vc` A list of precomputed variance components. Should be in the same structure as the output of `var_comp()`

`...` Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Value

A `dspMatrix`

References

Schmidt, P., Hartung, J., Rath, J., & Piepho, H.-P. (2019). Estimating Broad-Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. *Crop Science*, 59(2), 525–536. <https://doi.org/10.2135/cropsci2018.06.03>

See Also

`h2_Delta_by_genotype()`, `H2_Delta_by_genotype()`, `h2_Delta()`, `H2_Delta()`

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Delta_pairwise(lettuce_lme4, target = "gen", type = "BLUP")

# asreml model (Requires license)
## Not run:
lettuce_asreml <- asreml::asreml(fixed = y ~ rep,
                                random = ~ gen,
                                data = lettuce_subset,
                                trace = FALSE
                                )

H2_Delta_pairwise(lettuce_asreml, target = "gen", type = "BLUP")

## End(Not run)
```

H2_Delta_parameters	<i>Calculate heritability of pairwise differences using variance parameters</i>
---------------------	---

Description

Compute broad-sense heritability of differences using the variance of differences between two BLUPs/BLUEs

Usage

```
H2_Delta_parameters(delta_g, delta_pev, type = c("BLUP", "BLUE"))
```

Arguments

<code>delta_g</code>	Numeric. Genotypic variance-covariance matrix.
<code>delta_pev</code>	Matrix. Variance of pairwise differences among BLUES or BLUPs
<code>type</code>	Character. Either BLUES or BLUPS used to compute the variance of pairwise differences.

Details

See `H2_Delta()` and reference for full derivation and equation for heritability Delta

Value

Matrix of pairwise heritability of differences among BLUES or BLUPs

References

Schmidt, P., Hartung, J., Rath, J., & Piepho, H.-P. (2019). Estimating Broad-Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. *Crop Science*, 59(2), 525–536. <https://doi.org/10.2135/cropsci2018.06.03>

Examples

```
H2_Delta_parameters(delta_g = diag(0.15, 2, 2),
                    delta_pev = matrix(c(NA, 0.2, 0.2, NA), 2, 2),
                    type = "BLUP"
                    )
```

H2_Oakey

Calculate Oakey's heritability from model object

Description

Compute heritability for genotype means using the variance–covariance matrix of the genotype BLUPs as described by Oakey et al. (2006).

Usage

```
h2_Oakey(model,
          target,
          options = NULL,
          marginal = TRUE,
          stratification = NULL,
          vc = NULL,
          ...)
H2_Oakey(model,
          target,
          options = NULL,
```

```

marginal = TRUE,
stratification = NULL,
vc = NULL,
...)

```

Arguments

model	Model object of class lmerMod/merMod or asreml
target	The name of the random effect for which heritability is to be calculated.
options	NULL by default, for internal checking of model object before calculations
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
vc	A list of precomputed variance components. Should be in the same structure as the output of <code>var_comp()</code>
...	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

$$h_{Oakey}^2 = \frac{\sum_{i=n_z+1}^{n_g} \lambda_i}{\sum_{n_g} \lambda_i \neq 0}$$

where:

- n_g is the number of genotypes
- n_z is the number of zero eigenvalues
- λ_i is the i th eigenvalue of the matrix $I_m - G^{-1}C^{gg}$
- σ^2 is the variance attributed to differences between genotype

See pages 813 and 818 of the reference for full derivation and explanation for Oakey's heritability

Value

Numeric

References

Oakey, H., Verbyla, A., Pitchford, W., Cullis, B., & Kuchel, H. (2006). Joint modeling of additive and non-additive genetic line effects in single field trials. *Theoretical and Applied Genetics*, 113(5), 809–819. <https://doi.org/10.1007/s00122-006-0333-z>

See Also

[H2_Oakey\(\)](#), [h2_Oakey\(\)](#)

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Oakey(lettuce_lme4, target = "gen")
```

H2_Oakey_parameters	<i>Calculate Oakey's heritability using variance parameters</i>
---------------------	---

Description

Rather than providing a model object, supply the necessary components to compute this heritability measure.

Usage

```
H2_Oakey_parameters(Gg_inv, C22_g)
```

Arguments

Gg_inv	The inverse of the genotypic variance-covariance matrix.
C22_g	Prediction error variance matrix associated with the genotype effects.

Value

Numeric value

Examples

```
Gg_inv = diag(1/0.15, 3, 3)
C22_g <- matrix(
  c(
    0.08, 0.01, 0.00,
    0.01, 0.07, 0.01,
    0.00, 0.01, 0.09
  ),
  nrow = 3, byrow = TRUE
)
H2_Oakey_parameters(Gg_inv, C22_g)
```

H2_Piepho	<i>Calculate Piepho's heritability from model object Compute Piepho's heritability using variance differences between genotype BLUEs</i>
-----------	--

Description

Calculate Piepho's heritability from model object Compute Piepho's heritability using variance differences between genotype BLUEs

Usage

```
H2_Piepho(model,
           target,
           options = NULL,
           marginal = TRUE,
           stratification = NULL,
           vc = NULL,
           ...)
h2_Piepho(model,
           target,
           options = NULL,
           marginal = TRUE,
           stratification = NULL,
           vc = NULL,
           ...)
```

Arguments

model	Model object of class lmerMod/merMod or asreml
target	The name of the random effect for which heritability is to be calculated.
options	NULL by default, for internal checking of model object before calculations
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
vc	A list of precomputed variance components. Should be in the same structure as the output of var_comp()
...	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

The equation for Piepho's heritability is as follows:

$$H_{Piepho}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \overline{PEV_{BLUE_g}}/2}$$

where:

- $\overline{PEV_{BLUE_g}}$ is the prediction error variance matrix for genotype BLUEs
- σ_g^2 is the variance attributed to differences between genotype

See reference for full derivation and details.

Value

Numeric

References

Piepho, H.-P., & Möhring, J. (2007). Computing Heritability and Selection Response From Unbalanced Plant Breeding Trials. *Genetics*, 177(3), 1881–1888. <https://doi.org/10.1534/genetics.107.074229>

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Piepho(lettuce_lme4, target = "gen")

# asreml model (Requires license)
## Not run:
lettuce_asreml <- asreml::asreml(fixed = y ~ rep,
                                random = ~ gen,
                                data = lettuce_subset,
                                trace = FALSE
                                )

H2_Piepho(lettuce_asreml, target = "gen")

## End(Not run)
```

H2_Piepho_parameters *Calculate Piepho's heritability using variance parameters*

Description

Compute Piepho's heritability using the variance of differences between two BLUES.

Usage

```
H2_Piepho_parameters(vc_g, vd_BLUE_avg)
```

Arguments

vc_g	Numeric. Genotype variance component
vd_BLUE_avg	Numeric. Mean variance of pairwise differences among BLUES

Details

The equation for Piepho's heritability is as follows:

$$H_{Piepho}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \overline{PEV_{BLUE_g}}/2}$$

where:

- $\overline{PEV_{BLUE_g}}$ is the prediction error variance matrix for genotype BLUES
- σ_g^2 is the variance attributed to differences between genotype

Value

Numeric value

References

Piepho, H.-P., & Möhring, J. (2007). Computing Heritability and Selection Response From Unbalanced Plant Breeding Trials. *Genetics*, 177(3), 1881–1888. <https://doi.org/10.1534/genetics.107.074229>

Examples

```
H2_Piepho_parameters(vc_g = 0.25, vd_BLUE_avg = 0.68)
```

H2_Reliability	<i>Calculate reliability from model object</i>
----------------	--

Description

Compute the reliability (r^2 , also known as the coefficient of determination) of the genotype BLUPs, as described by Schmidt et al. (2019). `h2_Reliability()` / `H2_Reliability()` return the overall (mean) reliability $\bar{r}^2$, while `h2_Reliability_by_genotype()` / `H2_Reliability_by_genotype()` return the per-genotype values r_i^2 .

Usage

```
H2_Reliability(
  model,
  target,
  options = NULL,
  marginal = TRUE,
  stratification = NULL,
  vc = NULL,
  ...
)

H2_Reliability_by_genotype(
  model,
  target,
  options = NULL,
  marginal = TRUE,
  stratification = NULL,
  vc = NULL,
  ...
)

h2_Reliability(
  model,
  target,
  options = NULL,
  marginal = TRUE,
  stratification = NULL,
  vc = NULL,
  ...
)

h2_Reliability_by_genotype(
  model,
  target,
  options = NULL,
  marginal = TRUE,
```

```

    stratification = NULL,
    vc = NULL,
    ...
)

```

Arguments

<code>model</code>	Model object of class <code>lmerMod</code> / <code>merMod</code> or <code>asreml</code>
<code>target</code>	The name of the random effect for which heritability is to be calculated.
<code>options</code>	NULL by default, for internal checking of model object before calculations
<code>marginal</code>	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
<code>stratification</code>	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with <code>target</code> .
<code>vc</code>	A list of precomputed variance components. Should be in the same structure as the output of <code>var_comp()</code>
<code>...</code>	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

The reliability of the i th genotype is

$$r_i^2 = 1 - \frac{\text{var}(\hat{g}_i^{BLUP})}{\text{var}(g_i)}$$

where $\text{var}(\hat{g}_i^{BLUP})$ is the i th diagonal element of the prediction error variance matrix $C_{22(g)}$ and $\text{var}(g_i)$ is the i th diagonal element of the genotypic variance-covariance matrix $G_{(g)}$. As only the diagonal elements are used, r_i^2 ignores the off-diagonal elements (covariances) of both matrices. The overall reliability is the mean across genotypes,

$$\bar{r}^2 = \frac{1}{n_g} \sum_{i=1}^{n_g} r_i^2.$$

Value

`h2_Reliability()` / `H2_Reliability()` return a numeric value; `h2_Reliability_by_genotype()` / `H2_Reliability_by_genotype()` return a named numeric vector.

References

- Schmidt, P., Hartung, J., Bennewitz, J., & Piepho, H.-P. (2019). Heritability in Plant Breeding on a Genotype-Difference Basis. *Genetics*, 212(4), 991–1008. <https://doi.org/10.1534/genetics.119.302134>
- Mrode, R. A. (2014). *Linear Models for the Prediction of Animal Breeding Values* (3rd ed.). CABI.

See Also

[H2_Reliability_parameters\(\)](#)

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Reliability(lettuce_lme4, target = "gen")
H2_Reliability_by_genotype(lettuce_lme4, target = "gen")
```

H2_Reliability_parameters

Calculate reliability using variance parameters

Description

Compute the reliability (r^2 , also known as the coefficient of determination) for each genotype from the genotypic variance-covariance matrix and the prediction error variance (PEV) matrix of the genotype BLUPs.

Usage

```
H2_Reliability_parameters(G_g, C22_g)
```

Arguments

G_g	Genotypic variance-covariance matrix.
C22_g	Prediction error variance matrix associated with the genotype effects.

Details

The reliability of the i th genotype is

$$r_i^2 = 1 - \frac{\text{var}(\hat{g}_i^{BLUP})}{\text{var}(g_i)}$$

where:

- $\text{var}(\hat{g}_i^{BLUP})$ is the i th diagonal element of the PEV matrix $C_{22(g)}$
- $\text{var}(g_i)$ is the i th diagonal element of the genotypic variance-covariance matrix $G_{(g)}$

As only the diagonal elements are used, r_i^2 does not account for the off-diagonal elements (i.e. covariances) of either matrix. The overall reliability is obtained as the mean across genotypes, $\bar{r}^2 = \frac{1}{n_g} \sum_{i=1}^{n_g} r_i^2$.

Genotypes whose genotypic variance (the corresponding diagonal element of $G_{(g)}$) is not strictly positive yield an undefined reliability and are returned as NA (with a warning) rather than Inf/NaN.

Value

A named numeric vector of per-genotype reliabilities. Entries for genotypes with a non-positive genotypic variance are NA.

References

- Schmidt, P., Hartung, J., Bennewitz, J., & Piepho, H.-P. (2019). Heritability in Plant Breeding on a Genotype-Difference Basis. *Genetics*, 212(4), 991–1008. <https://doi.org/10.1534/genetics.119.302134>
- Mrode, R. A. (2014). *Linear Models for the Prediction of Animal Breeding Values* (3rd ed.). CABI.

Examples

```
G_g <- diag(0.15, 3, 3)
C22_g <- matrix(
  c(
    0.08, 0.01, 0.00,
    0.01, 0.07, 0.01,
    0.00, 0.01, 0.09
  ),
  nrow = 3, byrow = TRUE
)
H2_Reliability_parameters(G_g, C22_g)
```

H2_Standard

Calculate standard heritability from model object

Description

Compute standard heritability using the classic ratio method of genotypic and phenotypic variance. See Falconer & Mackay (1996)

Usage

```
h2_Standard(model,
            target,
            options = NULL,
            marginal = TRUE,
            stratification = NULL,
            vc = NULL,
            ...)
H2_Standard(model,
            target,
            options = NULL,
            marginal = TRUE,
            stratification = NULL,
            vc = NULL,
            ...)
```

Arguments

model	Model object of class lmerMod/merMod or asreml
target	The name of the random effect for which heritability is to be calculated.
options	NULL by default, for internal checking of model object before calculations
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
vc	A list of precomputed variance components. Should be in the same structure as the output of <code>var_comp()</code>
...	Additional arguments that specify heritability calculation when interactions with genotype effects are modelled

Details

The equation used to calculate standard heritability (broad-sense) is:

$$H_{Standard}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{1}{n_g} \sum_{i=1}^{n_g} \sigma_p^2 / n_{gi}}$$

where:

- n_g is the number of genotypes
- n_{gi} is the number of replicate for a given genotype i
- σ_g is the variance attributed to genotype differences
- σ_p is the variance attributed to phenotypic differences

The equation used to calculate standard heritability (narrow-sense) is:

$$h_{Standard}^2 = \frac{\text{Var}(g_i - g_j)}{\text{Var}(y_{i..} - y_{j..})}$$

where:

- g_i is the random effect of the i^{th} genotype
- $y_{i..}$ is the sample average of the i^{th} genotype

Value

Numeric value

References

Falconer, D. S., & Mackay, T. F. C. (1996). Introduction to quantitative genetics (4th ed.). Longman.

See Also

[H2_Standard\(\)](#), [h2_Standard\(\)](#)

Examples

```
# lme4 model
lettuce_subset <- lettuce_phenotypes |> subset(loc == "L2")
lettuce_lme4 <- lme4::lmer(y ~ rep + (1 | gen), data = lettuce_subset)
H2_Standard(lettuce_lme4, target = "gen")

# asreml model (Requires license)
## Not run:
lettuce_asreml <- asreml::asreml(fixed = y ~ rep,
                                random = ~ gen,
                                data = lettuce_subset,
                                trace = FALSE
                                )

H2_Standard(lettuce_asreml, target = "gen")

## End(Not run)
```

H2_Standard_parameters

Calculate Standard heritability using variance parameters

Description

Compute Standard heritability for genotype means using the variance components of genotype and residuals.

Usage

```
H2_Standard_parameters(vc_g, vc_e, n_r = 1)
```

Arguments

vc_g	Numeric. Genotype variance component
vc_e	Numeric. Residuals variance component
n_r	A numeric vector of size n_g, the number of genotype replicates.

Details

The equation for Standard heritability is as follows:

$$H_{Standard}^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{1}{n_g} \sum_{i=1}^{n_g} \sigma_p^2 / n_{gi}}$$

where:

- n_g is the number of genotypes
- n_{gi} is the number of replicate for a given genotype i
- σ_g is the variance attributed to genotype differences
- σ_p is the variance attributed to phenotypic differences

Value

Numeric value

References

Falconer, D. S., & Mackay, T. F. C. (1996). Introduction to quantitative genetics (4th ed.). Longman.

Examples

```
H2_Standard_parameters(vc_g = 0.25, vc_e = 0.8)
```

lettuce_markers	<i>Molecular marker data and genomic relatedness matrix of 89 lettuce varieties</i>
-----------------	---

Description

Molecular marker data and genomic relatedness matrix of 89 lettuce varieties

Usage

```
lettuce_markers
```

```
lettuce_GRM
```

Format

lettuce_markers:

A data frame with 89 rows and 301 columns:

- gen genotype identifier
- 300 genetic markers scored as -1, 0, 1 (see Details)

lettuce_GRM:

A matrix array with 89 rows and 89 columns where each row/column represents a genotype

Details

The varieties were genotyped with a total of 300 markers (i.e. 95 single nucleotide polymorphisms and 205 amplified fragment length polymorphism markers, see Hayes et al. (2014) for more details of marker matrix. The biallelic marker M_{iw} for the i th genotype and the w th marker with alleles A_1 (i.e. the reference allele) and A_2 was coded as:

- 1 for $A_1 A_1$,
- -1 for $A_2 A_2$
- 0 for $A_1 A_2$ and $A_2 A_1$

Source

https://figshare.com/articles/dataset/Lettuce_trial_phenotypic_and_marker_data_/8299493

References

Hadasch, S., Simko, I., Hayes, R.J., Ogutu, J.O. and Piepho, H.-P. (2016), Comparing the Predictive Abilities of Phenotypic and Marker-Assisted Selection Methods in a Biparental Lettuce Population. The Plant Genome, 9: plantgenome2015.03.0014. doi:10.3835/plantgenome2015.03.0014

Hayes, R. J., Galeano, C. H., Luo, Y., Antonise, R., & Simko, I. (2014). Inheritance of Decay of Fresh-cut Lettuce in a Recombinant Inbred Line Population from ‘Salinas 88’ × ‘La Brillante’. Journal of the American Society for Horticultural Science, 139(4), 388–398. doi:10.21273/JASHS.139.4.388

lettuce_phenotypes	<i>Phenotypic data of 89 lettuce varieties</i>
--------------------	--

Description

89 lettuce varieties tested at three environments, each laid out as a randomized complete block design. The measured trait was resistance to downy mildew scored on a scale ranging from 0 to 5.

Usage

lettuce_phenotypes

Format

lettuce_phenotypes:
A data frame with 703 rows and 4 columns:

- loc environment identifier
- gen genotype identifier
- rep replicate identifier
- y resistance to downy mildew scored on a scale ranging from 0 to 5

Source

https://figshare.com/articles/dataset/Lettuce_trial_phenotypic_and_marker_data_/8299493

References

Hadasch, S., Simko, I., Hayes, R.J., Ogutu, J.O. and Piepho, H.-P. (2016), Comparing the Predictive Abilities of Phenotypic and Marker-Assisted Selection Methods in a Biparental Lettuce Population. The Plant Genome, 9: plantgenome2015.03.0014. doi:10.3835/plantgenome2015.03.0014

Hayes, R. J., Galeano, C. H., Luo, Y., Antonise, R., & Simko, I. (2014). Inheritance of Decay of Fresh-cut Lettuce in a Recombinant Inbred Line Population from ‘Salinas 88’ × ‘La Brillante’. Journal of the American Society for Horticultural Science, 139(4), 388–398. doi:10.21273/JASHS.139.4.388

lizard_markers	<i>Molecular markers data and genomic relatedness matrix of Australian lizards</i>
----------------	--

Description

Molecular markers data and genomic relatedness matrix of Australian lizards

Usage

lizard_markers

lizard_GRM

Format

lizard_markers:

A data frame with 261 rows and 8438 columns:

- gen individual identifier, equivalent to liz_id in lizard_phenotypes
- 8437 genetic markers scored as 0, 2, 1 (see Details)

lizard_GRM:

A matrix array with 261 rows and 261 columns where each row/column represents a genotype

Details

See `?snpReady::G.matrix` for how GRM was computed. The biallelic marker M_{iw} for the i th genotype and the w th marker with alleles A_1 (i.e. the reference allele) and A_2 was coded as:

- 0 for $A_1 A_1$,
- 1 for $A_1 A_2$ and $A_2 A_1$
- 2 for $A_2 A_2$

Source

https://osf.io/hjkxd/?view_only=12a6b6010567474fac9fec54472aa3d

References

Kar, F., Nakagawa, S. and Noble, D.W.A. (2024) “Heritability and developmental plasticity of growth in an oviparous lizard,” *Heredity*, 132(2), pp. 67–76. Available at: <https://doi.org/10.1038/s41437-023-00660-3>.

lizard_phenotypes

Phenotypic data of Australian lizards

Description

Phenotypic data for Australian lizards (*L. delicata*). Lizard eggs were incubated at two different incubation treatment temperatures. Lizards were weighed to investigate differences in growth between treatments.

Usage

lizard_phenotypes

Format

lizard_phenotypes:

A data frame with 3928 rows and 9 columns:

- liz_id individual identifier, equivalent to gen in lizard_markers 261 individuals
- treatment temperature (degrees celcius) at which lizard eggs were incubated
- dam_id dam identifier
- sire_id sire identifier
- mass mass of lizard in
- ln_mass natural log mass
- days_since_hatch days since hatching (age)
- z_days_since_hatch scaled and centered days_since_hatch see ?scale()
- z_days_since_hatch_i2 squared z_days_since_hatch see Kar et al 2024 to see details on their analysis

Source

https://osf.io/hjkxd/?view_only=12a6b6010567474fac9fec54472aa3d

References

Kar, F., Nakagawa, S. and Noble, D.W.A. (2024) “Heritability and developmental plasticity of growth in an oviparous lizard,” *Heredity*, 132(2), pp. 67–76. Available at: <https://doi.org/10.1038/s41437-023-00660-3>.

var_comp

*Extract variance components***Description**

This function provides the variance matrix quantities needed to evaluate heritability with respect to a target random-effect term in a fitted linear mixed model.

Usage

```
var_comp(
  model,
  target,
  calc_C22 = TRUE,
  calc_V = TRUE,
  calc_C11 = TRUE,
  marginal = TRUE,
  stratification = NULL,
  solver = c("direct", "LMM"),
  ...
)
```

Arguments

model	Model object of class lmerMod/merMod or asreml
target	The name of the random effect for which heritability is to be calculated.
calc_C22	Logical; whether to compute the prediction error variance (PEV) matrix for the transformed target effect.
calc_V	Logical; whether to retain the marginal variance matrix of the response and supporting quantities (V, G, Z, X, idx, and m) in the output.
calc_C11	Logical; whether to compute the variance matrix of the fixed-effect counterpart estimator for the transformed target effect.
marginal	Logical; if TRUE, construct marginal (strata-averaged) mappings so that each genotype receives a single averaged effect per term. If FALSE, mappings will only consider the main genotype effect and ignore the interacting terms.
stratification	A one-row data frame defining the stratum in which genotype effects should be evaluated. The columns must correspond to model terms that interact with target.
solver	A string specifying the solver for the PEV matrix. Can be either "direct" (directly invert V) or "LMM" (Solve the LMM equation).
...	Additional arguments passed to downstream helper functions.

Value

A named list with the following elements:

`n_g` Number of transformed genetic coefficients after applying the mapping matrix `m`.

`gnames` Names of the transformed genetic coefficients.

`G_g` Variance matrix of the transformed target genetic effect.

`C22_g` Prediction error variance matrix of the transformed target effect, if `calc_C22 = TRUE`; otherwise `NULL`.

`G_g_tilde` Variance matrix of the fixed-effect counterpart estimator for the transformed target effect, if `calc_C11 = TRUE`; otherwise `NULL`.

`G_g_tilde_no_cov` Variance matrix of the fixed-effect counterpart estimator for the transformed target effect, without considering target covariance, if `calc_C11 = TRUE`; otherwise `NULL`.

`C11_g` Estimation error variance matrix of the fixed-effect counterpart estimator for the transformed target effect, if `calc_C11 = TRUE`; otherwise `NULL`.

`V` Marginal covariance matrix of the response, if `calc_V = TRUE`; otherwise `NULL`.

`G` Variance matrix of all random effects, if `calc_V = TRUE`; otherwise `NULL`.

`Z` Random-effect design matrix, if `calc_V = TRUE`; otherwise `NULL`.

`X` Fixed-effect design matrix, if `calc_V = TRUE`; otherwise `NULL`.

`idx` Indices of the random-effect coefficients associated with the target term, if `calc_V = TRUE`; otherwise `NULL`.

`W` Linear mapping from the original target coefficients to the transformed target effect, if `calc_V = TRUE`; otherwise `NULL`.

`marginal` Logical scalar indicating whether the returned quantities correspond to a marginal definition of the target effect.

`stratification` The user-supplied stratification object, if any.

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