Package: Ritable (via r-universe)

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Title Pedigree-Based Heritability Estimation for Family Cohort Studies

Version 0.1.0

Description Provides profile-likelihood variance-components estimation of narrow-sense heritability (h2) for quantitative traits in family cohort studies. Additive genetic relationship matrices are built from pedigrees via 'kinship2'. Phenotypes are inverse-normal transformed internally. Likelihood-ratio tests use a one-sided chi-squared boundary correction equivalent to SOLAR Eclipse. Ninety-five percent confidence intervals are derived from the profile likelihood rather than Wald approximations. Batch estimation over many traits returns tidy data frames ready for downstream visualisation (forest plots, heatmaps).

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URL https://r-itable.circadia-lab.uk, https://github.com/circadia-bio/R-itable

BugReports https://github.com/circadia-bio/R-itable/issues

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Imports kinship2, stats, utils, rlang, cli

Suggests ggplot2, scales, pkgdown, testthat (>= 3.0.0), knitr, rmarkdown

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Contents

`build_grm` *Build an additive genetic relationship matrix from a pedigree*

Description

Constructs the additive genetic relationship matrix **A** (= 2 x kinship matrix) for a set of study subjects, using a pedigree that may include additional founder parents not in the study sample.

Usage

```
build_grm(
  ped_df,
  study_ids = NULL,
  id_col = "id",
  pat_col = "pat",
  mom_col = "mom",
  sex_col = "sex"
)
```

Arguments

`ped_df`	A data frame with at least the columns `id`, `pat`, `mom`, and `sex`. Missing parents should be `NA` or `0`. `sex` should be numeric: `1` = male, `2` = female (any other value is recoded to `1` with a warning).
`study_ids`	Character or integer vector of IDs for the study subjects whose sub-matrix should be extracted. Defaults to all IDs in `ped_df`.
`id_col`, `pat_col`, `mom_col`, `sex_col`	Column names for the four required pedigree fields. Defaults are `"id"`, `"pat"`, `"mom"`, `"sex"`.

Details

The function calls `kinship2::kinship()` on the full pedigree (including founders), then multiplies by 2 to obtain the additive relationship matrix, and finally subsets to `study_ids`. Including founders in the pedigree ensures that kinship coefficients between study subjects connected only through founders are estimated correctly.

Value

A symmetric numeric matrix of dimension `length(study_ids) x length(study_ids)`, with diagonal entries equal to 1 for non-inbred individuals and row/column names matching `study_ids`.

Examples

```
# Minimal two-generation pedigree: two couples, four offspring
ped <- data.frame(
  id  = 1:8,
  pat = c(0, 0, 0, 0, 1, 1, 3, 3),
  mom = c(0, 0, 0, 0, 2, 2, 4, 4),
  sex = c(1, 2, 1, 2, 1, 2, 1, 2)
)
A <- build_grm(ped, study_ids = 5:8)
round(A, 3)
```

---

herit_batch *Batch heritability estimation over multiple traits*

Description

A convenience wrapper around `herit_vc()` that iterates over a vector of trait names, optionally across multiple covariate models, and returns a tidy data frame.

Usage

```
herit_batch(
  traits,
  grm,
  data,
  covs_list = NULL,
  id_col = "IID",
  min_n = 80L,
  ci_level = 0.95,
  .progress = TRUE
)
```

Arguments

`traits`	Character vector of trait column names in `data`.
`grm`	Numeric matrix: additive genetic relationship matrix as returned by `build_grm()`.
`data`	Data frame containing ID, trait, and covariate columns.
`covs_list`	A named list of covariate vectors, where each element defines one covariate model. If `NULL`, a single unadjusted model is run. Example: `list(unadj = NULL, cov1 = c("age", "sex"), cov2 = c("age", "sex", "age2"))`.

id_col	Name of the individual ID column. Default "IID".
min_n	Minimum sample size to attempt estimation. Default 80.
ci_level	Profile-likelihood CI level. Default 0.95.
.progress	Logical. Show a cli progress bar. Default TRUE.

Value

A data frame (tibble-compatible) with one row per successfully fitted model and columns: label, trait, covariates, n, h2, se, ci_lo, ci_hi, pval, sigma2_a, sigma2_e. Failed / skipped models are silently omitted.

See Also

herit_vc(), build_grm(), plot_forest()

Examples

```
## Not run:
A    <- build_grm(my_pedigree, study_ids = my_data$IID)

res  <- herit_batch(
  traits     = c("bmi", "systolic_bp", "hdl"),
  grm        = A,
  data       = my_data,
  covs_list  = list(
    unadj = NULL,
    cov1  = c("age", "sex"),
    cov2  = c("age", "sex", "age2")
  )
)

# Significant adjusted models
subset(res, grepl("cov2", label) & pval < 0.05)

## End(Not run)
```

---

herit_vc *Profile-likelihood variance-components heritability estimation*

Description

Estimates narrow-sense heritability (h^2) for a single quantitative trait using a profile-likelihood variance-components approach equivalent to SOLAR Eclipse. The phenotype is inverse-normal transformed internally.

Usage

```
herit_vc(
  trait,
  grm,
  data,
  covs = NULL,
  id_col = "IID",
  label = NULL,
  min_n = 80L,
  ci_level = 0.95,
  verbose = TRUE
)
```

Arguments

trait	Character string: name of the trait column in data.
grm	Numeric matrix: the additive genetic relationship matrix for all individuals in data, as returned by build_grm(). Row and column names must match the ID column of data.
data	Data frame containing id_col, trait, and any covariate columns.
covs	Character vector of covariate column names, or NULL for an intercept-only model. Covariates are mean-centred and scaled to unit variance before fitting.
id_col	Name of the individual ID column in data. Default "IID".
label	Optional string label for this model (used in batch output). If NULL, defaults to "<trait>_adj" or "<trait>_unadj".
min_n	Minimum number of complete observations required to attempt estimation. Models with fewer observations return NULL silently. Default 80.
ci_level	Confidence level for the profile-likelihood interval. Default 0.95.
verbose	Logical. Print progress to the console. Default TRUE.

Details

Model: Omega = sigma2_p [h2 A + (1 - h2) I_n]

Optimisation: eigendecomposition of A followed by 1-D profile-likelihood optimisation over h2 in (0, 1) using a coarse grid to seed stats::optimize().

LRT: one-sided chi-squared(1) boundary correction – the null is on the boundary of the parameter space (h2 = 0), so the p-value is halved relative to a standard chi-squared test. This matches the SOLAR Eclipse convention.

CIs: derived by uniroot() on the profile log-likelihood, falling back to a Wald interval if the root-finding fails.

Value

A named list with elements:

label Model label.

`trait` Trait name.

`covariates` Covariate names joined by `"+"`, or `""`.

`n` Sample size after dropping missing values.

`h2` MLE of narrow-sense heritability.

`se` Standard error from profile-likelihood curvature (Wald).

`ci_lo`, `ci_hi` Profile-likelihood confidence interval bounds.

`pval` One-sided LRT p-value with chi-squared(1) boundary correction.

`var_covariates` Proportion of phenotypic variance explained by fixed-effect covariates (R^2 on INT-transformed phenotype). `NA` for unadjusted models. Corresponds to the "variance explained" column in Leocadio-Miguel et al. (2025).

`sigma2_a` Additive genetic variance (σ^2_g in SOLAR notation).

`sigma2_e` Residual environmental variance (σ^2_e).

Returns `NULL` if `n` < `min_n` or if the GRM subset is degenerate.

See Also

`build_grm()`, `herit_batch()`, `int_transform()`

Examples

```
## Not run:
# Build GRM then estimate heritability
A   <- build_grm(my_pedigree, study_ids = my_data$IID)
res <- herit_vc("bmi", grm = A, data = my_data,
                covs = c("age", "sex", "age2"))
str(res)

## End(Not run)
```

`int_transform` *Inverse-normal (rank-based) transformation*

Description

Applies a rank-based inverse-normal transformation (INT) to a numeric vector, placing empirical quantiles onto a standard normal scale.

Usage

```
int_transform(x, ties = "average")
```

Arguments

`x`	Numeric vector. `NA`s are preserved.
`ties`	Method passed to `base::rank()`. Default `"average"`.

Details

The Blom-style formula used is:

$$\Phi^{-1}\left(\frac{r_i - 0.5}{n}\right)$$

where r_i is the rank of observation i and n is the number of non-missing observations. This is the standard transformation used in SOLAR Eclipse and most variance-components heritability software.

Value

A numeric vector of the same length as `x`, with `NA`s in the same positions and non-missing values transformed to approximate normality.

Examples

```
set.seed(1)
x <- rexp(200, rate = 0.5)   # right-skewed
hist(x,              main = "Raw")
hist(int_transform(x), main = "INT")
```

---

plot_forest *Forest plot of heritability estimates*

Description

Produces a ggplot2 forest plot from the output of `herit_batch()` or a list of `herit_vc()` results coerced to a data frame.

Usage

```
plot_forest(
  results,
  model_filter = NULL,
  colour_by = "trait",
  sig_threshold = 0.05,
  title = NULL,
  x_limits = c(0, 1)
)
```

Arguments

`results`	Data frame as returned by `herit_batch()`, containing at least columns `label`, `trait`, `h2`, `ci_lo`, `ci_hi`, `pval`.
`model_filter`	Optional character vector of model name substrings to keep (matched against `label`). E.g. `"cov2"` to show only the age + sex + age-squared model.

colour_by	Column to colour points by. Default "trait". Set to NULL for a monochrome plot.
sig_threshold	Numeric. Traits with pval below this threshold are shown with a filled point; others with an open point. Default 0.05.
title	Optional plot title string.
x_limits	Numeric vector of length 2 for the x-axis range. Default c(0, 1).

Details

Requires **ggplot2** (listed in Suggests). An informative error is thrown if it is not installed.

Value

A ggplot2::ggplot object. Colours follow the Ritable_colours palette by default (pink #FE9EC7 and blue #44ACFF as the primary pair).

See Also

herit_batch(), Ritable_colours

Examples

```
## Not run:
res <- herit_batch(c("bmi", "hdl", "systolic_bp"),
                   grm = A, data = my_data,
                   covs_list = list(unadj = NULL,
                                    cov2  = c("age", "sex", "age2")))

plot_forest(res, model_filter = "cov2", title = "Adjusted heritability")

## End(Not run)
```

Ritable_colours *R-itable colour palette*

Description

A named character vector of the four brand colours used throughout R-itable figures and documentation.

Usage

```
Ritable_colours
```

Format

An object of class character of length 4.

Details

`pink #FE9EC7` – primary accent; significant traits, sex effect

`blue #44ACFF` – primary brand colour; estimates, CI lines

`sky #89D4FF` – secondary blue; muted elements, CI shading

`cream #F9F6C4` – soft highlight; code backgrounds

Examples

```
Ritable_colours
```

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