Package ‘pegs’

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Type Package

Title Pseudo-Expectation Gauss-Seidel

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Description A lightweight, dependency-free, and simplified implementation of the Pseudo-Expectation Gauss-Seidel (PEGS) algorithm. It fits the multivariate ridge regression model for genomic prediction Xavier and Habier (2022) <doi:10.1186/s12711-022-00730-w> and Xavier et al. (2025) <doi:10.1093/genetics/iyae179>, providing heritability estimates, genetic correlations, breeding values, and regression coefficient estimates for prediction. This package provides an alternative to the 'bWGR' package by Xavier et al. (2019) <doi:10.1093/bioinformatics/btz794> by using 'LAPACK' for its algebraic operations.

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`pegs-package` *Pseudo-Expectation Gauss-Seidel*

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Author(s)

Alencar Xavier

Examples

```
# Load simulated data
data(test);

# Fit multivariate ridge regression
fit = pegs(Y,X);

# Heritability
print(fit$h2);

# Genetic correlations
print(fit$GC);

# Accuracy
print(mean(diag(cor(fit$hat,simu$tbv))));
```

`pegs` *Pseudo-Expectation Gauss-Seidel for Multi-Trait Models*

Description

This function implements the Pseudo-Expectation Gauss-Seidel (PEGS) algorithm for multi-trait genomic prediction models. It supports fitting one or more random effects and can apply factor-analytic approximations to the genetic covariance structure.

Usage

```
pegs(Y, X, maxit = 100, logtol = -4, NNC = FALSE,
     covbend = 1.1, covMinEv = 10e-4, XFA = -1)
```

Arguments

`Y`	A numeric matrix (n x k) of dependent variables, where n is the number of observations and k is the number of response variables. Missing values should be NA.
`X`	A numeric matrix (n x p) of predictors (i.e., markers) for a single random effect, or a named list of such matrices for multiple random effects.
`maxit`	An integer specifying the maximum number of iterations.
`logtol`	A numeric value for the convergence tolerance on a log10 scale. The algorithm stops when the log10 of the sum of squared changes in coefficients is less than this value.
`NNC`	A logical value. If TRUE, imposes a constraint of non-negative correlations on the genetic covariance matrix.
`covbend`	A numeric bending factor used to inflate the diagonal of the covariance matrix if it is not positive semi-definite. The bending amount is calculated as `abs(min_eigenvalue) * covbend`.
`covMinEv`	The minimum allowable eigenvalue for the genetic covariance matrix. If the smallest eigenvalue falls below this threshold, the matrix is "bent" (diagonally inflated) to make it positive semi-definite.
`XFA`	An integer specifying the number of factors (principal components) to use in the factor-analytic approximation of the genetic covariance matrix. • `XFA = -1` (Default): Fits a full-rank model (no approximation). • `XFA = 0`: Fits a diagonal model, assuming independent genetic effects among traits. • `XFA > 0`: Fits a reduced-rank model using the specified number of factors.

Value

A list containing the following components:

mu Vector of intercepts for each response variable.

b A matrix of regression coefficients (p x k) if a single `X` matrix is provided, or a named list of such matrices if a list is provided for `X`.

hat Matrix of predicted values (n x k).

h2 Vector of heritability estimates for each trait.

GC The genetic correlation matrix (k x k) if a single `X` matrix is provided, or a named list of such matrices for each random effect.

bend The inflation factor added to the diagonal of the genetic variance matrix. This will be a single value if one random effect is fit, or a named vector if multiple effects are fit.

numit The number of iterations until convergence.

cnv The final convergence value.

Examples

```
# Load simulated data with one random effect
data(test)

# Fit a standard multi-trait model
fit <- pegs(Y, X)

# Heritability
print(fit$h2)

# Genetic correlations
print(fit$GC)

# Accuracy
print(mean(diag(cor(fit$hat, simu$tbv))))
```

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