

# Package: pegs (via r-universe)

May 13, 2026

**Type** Package

**Title** Pseudo-Expectation Gauss-Seidel

**Version** 0.2

**Date** 2025-12-07

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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.

**License** GPL-3

**Depends** R (>= 2.10)

**NeedsCompilation** yes

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**Repository** <https://alencxav.r-universe.dev>

**Date/Publication** 2025-12-12 21:33:13 UTC

**RemoteUrl** <https://github.com/cran/pegs>

**RemoteRef** HEAD

**RemoteSha** 25a60499b799aea4603404d6b656407a3ac08746

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 pegs-package

*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.

### 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))));
```

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 pegs

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


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### 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**

<b>Y</b>	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.
<b>X</b>	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.
<b>maxit</b>	An integer specifying the maximum number of iterations.
<b>logtol</b>	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.
<b>NNC</b>	A logical value. If TRUE, imposes a constraint of non-negative correlations on the genetic covariance matrix.
<b>covbend</b>	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 $\text{abs}(\text{min\_eigenvalue}) * \text{covbend}$ .
<b>covMinEv</b>	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.
<b>XFA</b>	An integer specifying the number of factors (principal components) to use in the factor-analytic approximation of the genetic covariance matrix. <ul style="list-style-type: none"> <li>• XFA = -1 (Default): Fits a full-rank model (no approximation).</li> <li>• XFA = 0: Fits a diagonal model, assuming independent genetic effects among traits.</li> <li>• XFA &gt; 0: Fits a reduced-rank model using the specified number of factors.</li> </ul>

**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 <- pegas(Y, X)

# Heritability
print(fit$h2)

# Genetic correlations
print(fit$GC)

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

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