

Package: GINAX (via r-universe)

May 13, 2026

Type Package

Title Performs Genome-wide iterative fine-mapping for non-Gaussian data using GINA-X

Version 0.1.0

Description Implements GINA-X, a genome-wide iterative fine-mapping method designed for non-Gaussian traits. It supports the identification of credible sets of genetic variants.

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Encoding UTF-8

LazyData false

biocViews Software, StatisticalMethod, VariantAnnotation

Imports GA (>= 3.2), caret (>= 6.0-86), memoise (>= 1.1.0), Matrix (>= 1.2-18), stats (>= 4.2.2)

Depends R (>= 4.2.0)

Suggests knitr, rmarkdown, formatR, rrBLUP, testthat (>= 3.0.0)

RoxygenNote 7.3.2

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs libicu-dev

Repository <https://xss55.r-universe.dev>

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RemoteRef HEAD

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GINAX	<i>Performs GINA-X as described in the manuscript, Xu, Williams, Tegge, and Ferreira Genome-wide iterative fine-mapping for non-Gaussian data, Nature Genetics, Submitted.</i>
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Description

Performs GINA-X as described in the manuscript, Xu, Williams, Tegge, and Ferreira Genome-wide iterative fine-mapping for non-Gaussian data, Nature Genetics, Submitted.

Usage

```
GINAX(
  Y,
  Covariance,
  SNPs,
  family,
  Z = NULL,
  offset = NULL,
  FDR_Nominal = 0.05,
  maxiterations = 2000,
  runs_til_stop = 400
)
```

Arguments

Y	The observed phenotypes, count or binary.
Covariance	A list of covariance matrices that are the covariance matrices of the random effects. This matches the list of design matrices in Z.
SNPs	The SNP matrix, where each column represents a single SNP encoded as the numeric coding 0, 1, 2. This is entered as a matrix object.
family	Specify if the response is count ("poisson") or binary ("bernoulli").
Z	A list of matrices specifying the design matrix of each random effect of interest.
offset	If family = "poisson", the offset of each ecotype, can be a vector or a number if the number of offset is the same for each ecotype. If family = "binomial", offset = NULL.
FDR_Nominal	The nominal false discovery rate for which SNPs are selected from in the screening step.
maxiterations	The maximum iterations the genetic algorithm in the model selection step iterates for, defaulted at 2000
runs_til_stop	The number of iterations at the same best model before the genetic algorithm in the model selection step converges, defaulted at 400

Value

The column indices of SNPs that were in the best model identified by GINAX

Examples

```
data("Y_binary");data("SNPs");data("kinship")
n <- length(Y_binary)
covariance <- list()
covariance[[1]] <- kinship

output_binary <- GINAX(Y=Y_binary, SNPs=SNPs,
                      Covariance=covariance, Z=NULL, family="bernoulli",
                      offset=NULL, FDR_Nominal = 0.05,
                      maxiterations = 1000, runs_til_stop = 200)
```

kinship	<i>Example Dataset1: kinship</i>
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Description

This dataset contains kinship matrix.

Usage

```
data(kinship)
```

Format

A matrix for kinship

Source

Generated for package example

SNPs	<i>Example Dataset4: SNPs</i>
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Description

This dataset contains all SNPs.

Usage

```
data(SNPs)
```

Format

A data frame with 328 rows and 9000 variables

Source

Generated for package example

Y_binary

Example Dataset3: Y_binary

Description

This dataset contains response variable (binary data).

Usage

```
data(Y_binary)
```

Format

A vector for binary data

Source

Generated for package example

Y_poisson

Example Dataset2: Y_poisson

Description

This dataset contains response variable (count data).

Usage

```
data(Y_poisson)
```

Format

A vector for poisson data

Source

Generated for package example

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