Package 'GINAX'

October 14, 2025

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.

License GPL-3

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

NeedsCompilation no

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Contents

`GINAX` *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.*

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
## Not run:
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)

## End(Not run)
```

`kinship` *Example Dataset1: kinship*

Description

This dataset contains kinship matrix.

Usage

```
data(kinship)
```

Format

A matrix for kinship

Source

Generated for package example

`SNPs` *Example Dataset4: SNPs*

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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