

Package ‘emBALVI’

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Title EM Bayesian Adaptive LASSO Variational Inference Based GWAS

Version 0.1.0

Description Performs Genome-Wide Association Study (GWAS) analysis using Expectation-Maximization Bayesian Adaptive LASSO with Variational Inference (emBALVI). Includes genotype preprocessing, genomic relationship matrix construction, GWAS analysis, Manhattan and QQ plotting.s.

Depends R (>= 4.0)

Imports ggplot2, RColorBrewer

Suggests rmarkdown, testthat (>= 3.0.0), roxygen2

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Encoding UTF-8

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RoxygenNote 7.3.3

NeedsCompilation no

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buildGRM	<i>Build VanRaden Genomic Relationship Matrix</i>
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Description

Build VanRaden Genomic Relationship Matrix

Usage

```
buildGRM(X)
```

Arguments

X Numeric genotype matrix

Value

GRM matrix

convert_to_dosage	<i>Convert HMP Genotype to Dosage</i>
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Description

Convert HMP Genotype to Dosage

Usage

```
convert_to_dosage(snp_matrix)
```

Arguments

snp_matrix SNP matrix

Value

Numeric dosage matrix

 emBALVI

EM-BALVI GWAS

Description

Performs genome-wide association using expectation-maximization Bayesian adaptive LASSO with variational inference.

Usage

```
emBALVI(Y, X, B, G, max_iter = 20, tol = 1e-06)
```

Arguments

Y	Phenotype vector
X	Genotype matrix (numeric dosage)
B	Fixed effect design matrix
G	Genomic relationship matrix
max_iter	Maximum iterations
tol	Convergence tolerance

Value

Data frame of marker effects and p-values

 phenotypes_potatoyield

Potato Yield Phenotype Dataset

Description

Phenotypic data used for GWAS analysis in emBALVI.

Usage

```
phenotypes_potatoyield
```

Format

A data frame with genotype IDs and yield phenotype.

Source

Real potato yield experiment dataset

plot_manhattan	<i>Manhattan Plot for emBALVI</i>
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Description

Manhattan Plot for emBALVI

Usage

```
plot_manhattan(results)
```

Arguments

results	GWAS result data frame
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Value

A ggplot object

plot_qq	<i>QQ Plot for emBALVI GWAS Results</i>
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Description

Generates a Quantile-Quantile (QQ) plot for GWAS p-values.

Usage

```
plot_qq(results)
```

Arguments

results	GWAS result data frame (must contain column 'p')
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Value

A ggplot object

snp_NN_10_hmp

SNP Genotype Dataset (HMP Format)

Description

Raw SNP genotype matrix in HapMap-like format.

Usage

snp_NN_10_hmp

Format

A data frame containing SNP markers and genotype calls.

Source

Real SNP dataset used for EM-BALVI GWAS

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