Package 'predhy.GUI'

May 9, 2026

Type Package

Title Genomic Prediction of Hybrid Performance with Graphical User Interface

Version 2.1.1

Description Performs genomic prediction of hybrid performance using eight GS methods including GBLUP, BayesB, RKHS, PLS, LASSO, Elastic net, XGBoost and LightGBM.
GBLUP: genomic best liner unbiased prediction, RKHS: reproducing kernel Hilbert space, PLS: partial least squares regression, LASSO: least absolute shrinkage and selection operator, XGBoost: extreme gradient boosting, LightGBM: light gradient boosting machine.
It also provides fast cross-validation and mating design scheme for training population (Xu S et al (2016) <doi:10.1111/tpj.13242>; Xu S (2017) <doi:10.1534/g3.116.038059>).
A complete manual for this package is provided in the manual folder of the package installation directory.
You can locate the manual by running the following command in R: system.file(``manual'', package = ``predhy.GUI'').

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

Depends R (>= 4.1.0)

Imports shiny, data.table, DT, predhy(>= 2.1.2), BGLR, pls, glmnet, xgboost, lightgbm, foreach, doParallel, parallel, htmltools

NeedsCompilation no

Repository CRAN

Date/Publication 2025-11-03 16:10:02 UTC

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Contents

`hybrid_phe` *Phenotypic data of hybrids*

Description

This dataset contains phenotypic data of 410 hybrids for grain yield in maize.

Usage

```
hybrid_phe
```

Format

A data frame with 410 rows and 3 variables:

`M` The names of male parents.

`F` The names of female parents.

`GY` The grain yield of hybrids.

`input_geno` *Genotype in Hapmap Format*

Description

Genotypic data of 348 maize inbred lines in Hapmap format with double bit.

Usage

```
input_geno
```

Format

A data frame with 4979 rows and 359 columns.

input_geno1 *Genotype in Numeric Format*

Description

Genotypic data of 50 rice inbred lines with 1000 SNPs.

Usage

```
input_geno1
```

Format

A data frame with 1000 rows and 50 variables.

predhy.GUI *Graphical User Interface for R package predhy*

Description

Graphical User Interface for cross validation, genotype conversion and hybrid performance prediction.

Usage

```
predhy.GUI()
```

Value

No return value, called for Graphical User Interface

Examples

```
{
predhy.GUI()}
```

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