

User manual for

predhy.GUI

Performs Genomic Prediction of Hybrid Performance

With

Graphical User Interface

(Vision 2.1)

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Last updated on October, 2025

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1. Getting started

The software package `predhy.GUI` runs only in the R software environment and can be freely downloaded from the R website (<https://cran.r-project.org>).

1.1 installation

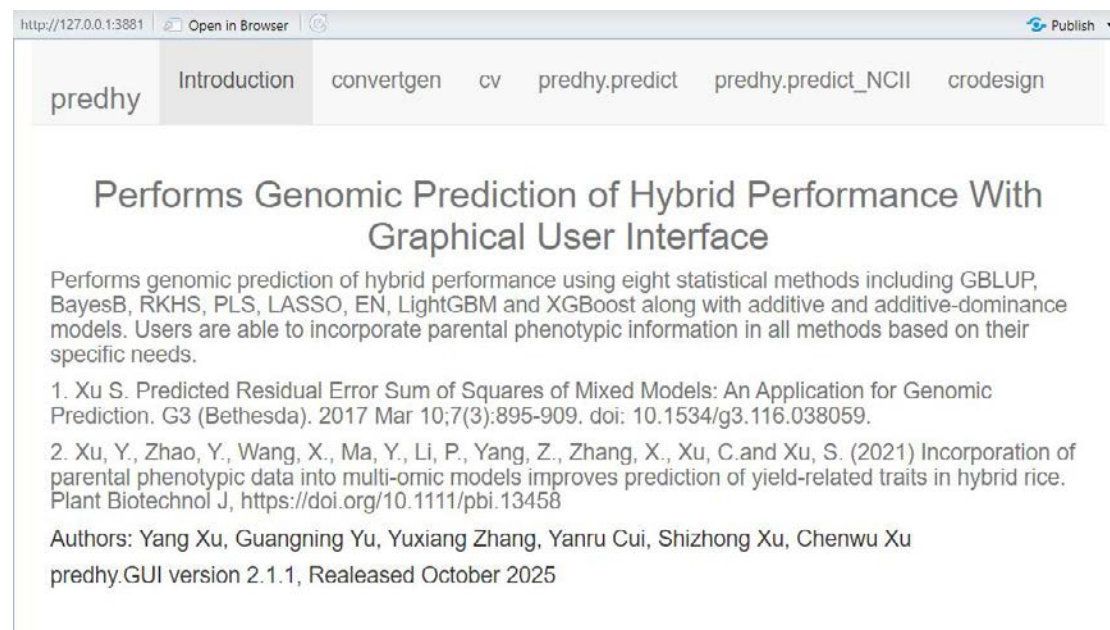
Within R environment, the `predhy.GUI` software can be installed online using the below command:

```
install.packages("predhy.GUI")
```

1.2 Run `predhy.GUI`

Once the software `predhy.GUI` is installed, users may run the software using two commands:

```
library("predhy.GUI")  
predhy.GUI()
```



The screenshot shows a web browser window with the URL `http://127.0.0.1:3881`. The browser has a tab labeled "Open in Browser" and a "Publish" button. The web page has a navigation bar with the following links: `predhy`, `Introduction`, `convertgen`, `cv`, `predhy.predict`, `predhy.predict_NCII`, and `crodesign`. The main content area has the title "Performs Genomic Prediction of Hybrid Performance With Graphical User Interface". Below the title, there is a paragraph describing the software: "Performs genomic prediction of hybrid performance using eight statistical methods including GBLUP, BayesB, RKHS, PLS, LASSO, EN, LightGBM and XGBoost along with additive and additive-dominance models. Users are able to incorporate parental phenotypic information in all methods based on their specific needs." There are two references listed: 1. Xu S. Predicted Residual Error Sum of Squares of Mixed Models: An Application for Genomic Prediction. G3 (Bethesda). 2017 Mar 10;7(3):895-909. doi: 10.1534/g3.116.038059. 2. Xu, Y., Zhao, Y., Wang, X., Ma, Y., Li, P., Yang, Z., Zhang, X., Xu, C. and Xu, S. (2021) Incorporation of parental phenotypic data into multi-omic models improves prediction of yield-related traits in hybrid rice. Plant Biotechnol J, <https://doi.org/10.1111/pbi.13458>. The authors are listed as: Yang Xu, Guangning Yu, Yuxiang Zhang, Yanru Cui, Shizhong Xu, Chenwu Xu. The version is `predhy.GUI` version 2.1.1, Released October 2025.

2. Dataset input

2.1 Genotype datasets

2.1.1 Input_genotype dataset

Numeric format for Genotypic dataset (*.csv format file)

The first column stands for marker ID. Among the remaining columns, each column lists all the genotypes for one individual while the first row shows the individual names. For each marker, homozygous genotypes are expressed by 1 and -1, respectively, and the heterozygous genotypes are indicated by zero, missing values are indicated by NA.

| | R001 | R002 | R003 | R004 | R005 | R006 | R007 | R008 |
|-------|------|------|------|------|------|------|------|------|
| SNP1 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP2 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP3 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP4 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP5 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP6 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP7 | -1 | 1 | 1 | NA | -1 | 1 | -1 | -1 |
| SNP8 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP9 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |
| SNP10 | -1 | 1 | 1 | 1 | -1 | 1 | -1 | -1 |

Hapmap format for Genotypic dataset (*.txt format file)

Please see the TASSEL software in details. Here we introduce simply. The first eleven columns describe the specific information of markers and individuals, and their column names must be "rs#", "alleles", "chrom", "pos", "strand", "assembly#", "center", "protLSID", "assayLSID", "panel" and "QCcode".

The values for marker genotypes should be character, such as AA, TT, CC, GG, NN, AC and AG, where the "NN" indicates missing or unknown genotypes. In the 2 and 5 to 11 columns, "NA" indicates **no information** available. All the individual genotypic information will be showed from the 12 to last columns. In each column, individual name is listed in the first row, i.e., "A002", and the others are the genotypes (character).

| rs | alleles | chrom | pos | strand | assembly | center | protLSID | assayLSID | panel | QCcode | A002 | A003 | A004 | A005 | A006 |
|---------------|---------|-------|---------|--------|----------|--------|----------|-----------|-------|--------|------|------|------|------|------|
| SNP_1_14068 | T/C | 1 | 14068 | NA | NA | NA | NA | NA | NA | NA | NA | TT | TT | NA | TT |
| SNP_1_338176 | G/T | 1 | 338176 | NA | NA | NA | NA | NA | NA | NA | NA | GG | GG | NA | GG |
| SNP_1_703171 | G/A | 1 | 703171 | NA | NA | NA | NA | NA | NA | NA | GG | GA | GG | GA | GA |
| SNP_1_1033512 | C/T | 1 | 1033512 | NA | NA | NA | NA | NA | NA | NA | TT | TT | CC | NA | TT |
| SNP_1_1401306 | A/C | 1 | 1401306 | NA | NA | NA | NA | NA | NA | NA | CC | CC | CC | NA | CC |
| SNP_1_1465404 | C/T | 1 | 1465404 | NA | NA | NA | NA | NA | NA | NA | CC | CC | CC | CC | CT |
| SNP_1_1725463 | C/T | 1 | 1725463 | NA | NA | NA | NA | NA | NA | NA | CT | CT | CC | CT | CT |
| SNP_1_1866006 | C/T | 1 | 1866006 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| SNP_1_2045326 | G/A | 1 | 2045326 | NA | NA | NA | NA | NA | NA | NA | GG | AA | AA | GG | GG |
| SNP_1_2670571 | A/G | 1 | 2670571 | NA | NA | NA | NA | NA | NA | NA | AA | AA | AA | AA | AA |
| SNP_1_2950255 | G/C | 1 | 2950255 | NA | NA | NA | NA | NA | NA | NA | GG | GG | GG | GG | GG |
| SNP_1_3818861 | A/T | 1 | 3818861 | NA | NA | NA | NA | NA | NA | NA | AA | AA | AA | AA | AA |
| SNP_1_4185501 | C/G | 1 | 4185501 | NA | NA | NA | NA | NA | NA | NA | GG | CC | CC | CC | CC |
| SNP_1_4616639 | G/T | 1 | 4616639 | NA | NA | NA | NA | NA | NA | NA | GG | GG | GG | GT | GT |
| SNP_1_5036129 | G/A | 1 | 5036129 | NA | NA | NA | NA | NA | NA | NA | GG | GG | GG | GG | GG |

2.1.2 Inbred_gene dataset (*.csv format file)

A matrix for genotypes of parental lines in numeric format, coded as 1, 0 and -1. The first columns indicates the names of inbred lines, which must be provided. Among the remaining columns, each column lists all the genotypes for a SNP while the first row shows the SNP names.

It can be obtained from the original genotype using convertgen function.

| | SNP_1_14068 | SNP_1_338176 | SNP_1_703171 | SNP_1_1033512 | SNP_1_1401306 | SNP_1_1465404 | SNP_1_1725463 | SNP_1_1866006 |
|------|-------------|--------------|--------------|---------------|---------------|---------------|---------------|---------------|
| A002 | 0.521126761 | 0.800711744 | 1 | -1 | -1 | 1 | 0 | 0.580952381 |
| A003 | 1 | 0.800711744 | 0 | -1 | -1 | 1 | 0 | 0.580952381 |
| A004 | 1 | 1 | 1 | 1 | -1 | 1 | 1 | 0.580952381 |
| A005 | 0.521126761 | 0.800711744 | 0 | -0.239875389 | -0.865319865 | 1 | 0 | 0.580952381 |
| A006 | 1 | 1 | 0 | -1 | -1 | 0 | 0 | 0.580952381 |
| A007 | 0 | -1 | 1 | -1 | -1 | 1 | 0 | -1 |
| A008 | 1 | 1 | 0 | -1 | -1 | 1 | 0 | -1 |
| A010 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0.580952381 |
| A011 | 1 | 1 | 0 | -1 | -1 | 1 | 0 | -1 |
| A012 | 1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 |
| A013 | 1 | 1 | 0 | -1 | -1 | 1 | 0 | 0.580952381 |
| A014 | 1 | 1 | 1 | -1 | -0.865319865 | 0 | 0 | -1 |
| A015 | -1 | 0.800711744 | 0 | -0.239875389 | -0.865319865 | 1 | 0 | 1 |
| A016 | 0 | 0 | 1 | -1 | -1 | 1 | 0 | -1 |
| A017 | -1 | 0 | 1 | -1 | -1 | 1 | 0 | 1 |
| A018 | 1 | 0 | 1 | -1 | -1 | 1 | 0 | 1 |
| A020 | 0.521126761 | 1 | 1 | 1 | 1 | 1 | 0 | 1 |
| A021 | -1 | 1 | 1 | -1 | -1 | 1 | 0 | 1 |
| A022 | 1 | 0.800711744 | 1 | -1 | -1 | 1 | 0 | -1 |
| A023 | 1 | 1 | 1 | 1 | -1 | 1 | 0 | 1 |

2.2 Phenotype datasets (*.csv format file)

2.2.1 Hybrid phenotype

A data frame with three columns. The first column and the second column are the names of male and female parents of the corresponding hybrids, respectively; the third column is the phenotypic values of hybrids. The names of male and female parents must match the rownames of inbred_gen. Missing (NA) values are not allowed.

| M | F | Trait1 |
|------|------|----------|
| A002 | A017 | 1433.745 |
| A003 | A393 | 1451.795 |
| A003 | A256 | 952.38 |
| A003 | A187 | 522.58 |
| A003 | A071 | 1457.775 |
| A003 | A439 | 1320.1 |
| A005 | A429 | 1638.91 |
| A005 | A430 | 1592.485 |
| A006 | A017 | 2050.12 |
| A006 | A021 | 1948.125 |
| A006 | A304 | 1474.83 |

2.2.2 Parent phenotype

A matrix of phenotypic values of parent. The names of the matrix must match the rownames of inbred_gen.

| | parent_phe |
|------|------------|
| A002 | 1 |
| A003 | 1 |
| A004 | 1 |
| A005 | 1 |
| A006 | 2 |
| A007 | 1 |
| A008 | 1 |
| A010 | 1 |
| A011 | 1 |
| A012 | 1 |

2.3 Parent names dataset(*.csv format file)

male_name: a data frame with only one column, of the names of male parents, with “M” in the first row.

female_name: a data frame with only one column, of the names of female parents, with “F” in the first row.

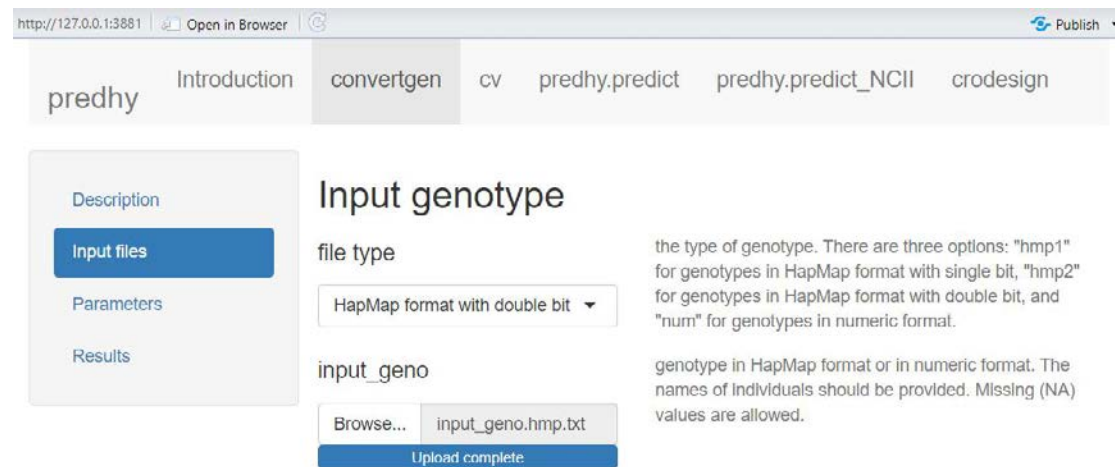
| M | F |
|------|------|
| A002 | A008 |
| A003 | A008 |
| A003 | A008 |
| A003 | A008 |
| A003 | A010 |
| A003 | A010 |
| A005 | A010 |
| A005 | A010 |
| A006 | A010 |
| A006 | A010 |
| A006 | A011 |
| A006 | A011 |
| A006 | A011 |
| A006 | A011 |
| A007 | A012 |

3. Operation process

3.1 convertgen

Dataset Input

Users must first click the drop-down menu to select the genotype file type, which includes “HapMap format with single bit”, “HapMap format with double bit”, “numeric format”. Then users can click the file input box to upload their data.



The screenshot shows a web browser window with the URL `http://127.0.0.1:3881`. The page has a navigation bar with links: `predhy`, `Introduction`, `convertgen` (active), `cv`, `predhy.predict`, `predhy.predict_NCII`, and `crodesign`. On the left, a sidebar contains links: `Description`, `Input files` (active), `Parameters`, and `Results`. The main content area is titled `Input genotype` and contains a `file type` dropdown menu set to `HapMap format with double bit`. Below this is an `input_geno` section with a `Browse...` button and a text input field containing `input_geno.hmp.txt`. An `Upload complete` button is at the bottom. To the right of the `input_geno` field, there is explanatory text: "the type of genotype. There are three options: 'hmp1' for genotypes in HapMap format with single bit, 'hmp2' for genotypes in HapMap format with double bit, and 'num' for genotypes in numeric format." and "genotype in HapMap format or in numeric format. The names of Individuals should be provided. Missing (NA) values are allowed."

Method select & Parameter setting

missingrate: max missing percentage for each SNP, users are allowed to choose one by sliding the bottom on the sliderInput.

maf: minor allele frequency for each SNP, users are allowed to choose one by sliding the bottom on the sliderInput.

Impute: users can click on the checkbox to decide whether to impute *NA* SNP or not.

http://127.0.0.1:3881 Open in Browser Publish

predhy Introduction **convertgen** cv predhy.predict predhy.predict_NCII crodesign

Description
Input files
Parameters
Results

Parameters for SNPs

missingrate max missing percentage for each SNP, default is 0.2.

0 0.2 0.3
0 0.0306 0.12 0.18 0.24 0.3

maf minor allele frequency for each SNP, default is 0.05.

0 0.05 0.2
0 0.0204 0.08 0.12 0.16 0.2

☒ Impute

logical. If TRUE, Imputation. Default is TRUE.

Run the software

After uploading all the needed files and setting the parameters, users can run the Software simply by clicking “Start calculation”. When calculation is down, the result will be given in the datatable below the panel, user may download the full data by clicking at “Download Genotype” bottom.

http://127.0.0.1:3881 Open in Browser Publish

predhy Introduction **convertgen** cv predhy.predict predhy.predict_NCII crodesign

Description
Input files
Parameters
Results

Converted genotype

▶ Start calculation

Show 10 entries Search:

| | SNP_1_14068 | SNP_1_338176 | SNP_1_703171 | SNP_1_1033512 |
|------|--------------------|-------------------|--------------|---------------------|
| A002 | 0.5211267605633803 | 0.800711743772242 | 1 | -1 |
| A003 | 1 | 0.800711743772242 | 0 | -1 |
| A004 | 1 | 1 | 1 | 1 |
| A005 | 0.5211267605633803 | 0.800711743772242 | 0 | -0.2398753894080997 |
| A006 | 1 | 1 | 0 | -1 |
| A007 | 0 | -1 | 1 | -1 |
| A008 | 1 | 1 | 0 | -1 |
| A010 | 1 | 0 | 1 | 1 |
| A011 | 1 | 1 | 0 | -1 |
| A012 | 1 | 1 | 1 | -1 |

Showing 1 to 10 of 348 entries

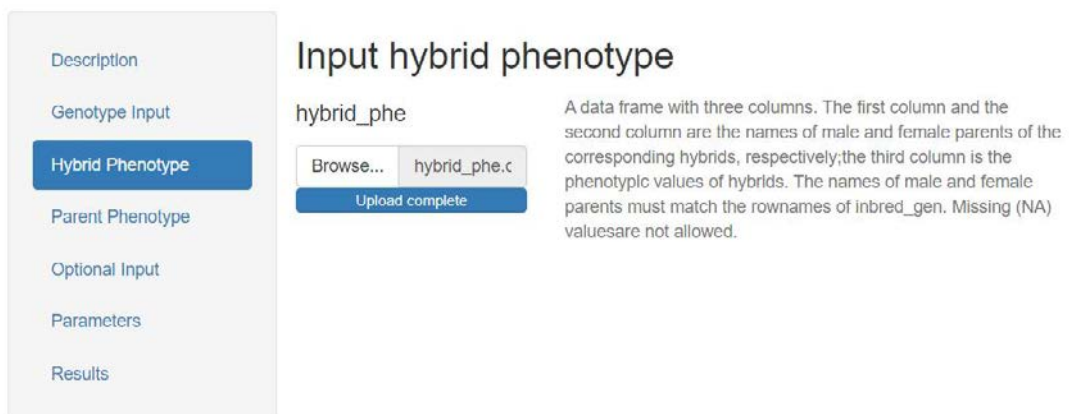
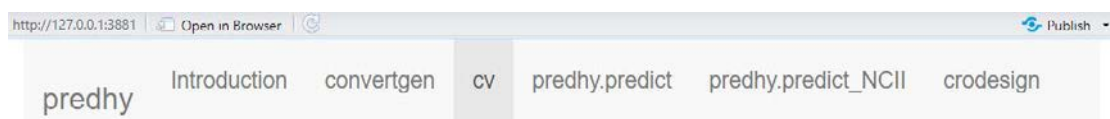
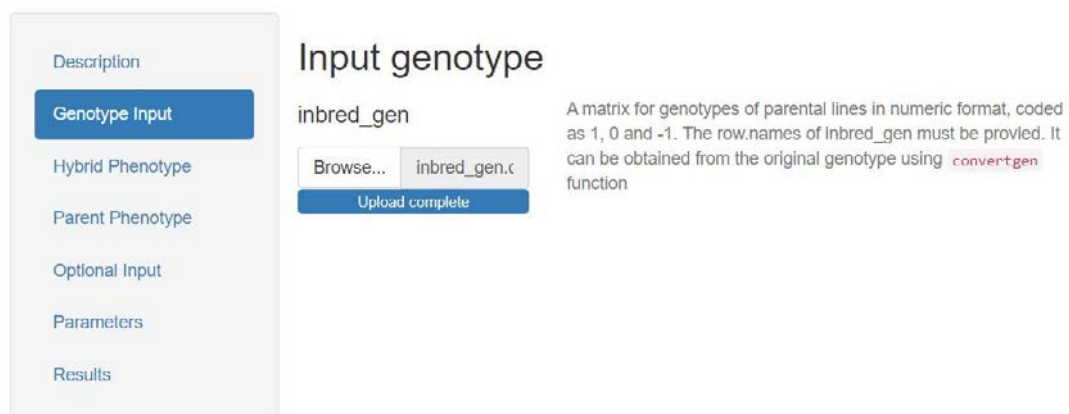
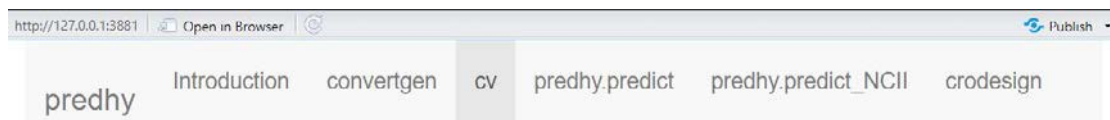
Previous 1 2 3 4 5 ... 35 Next

[Download Genotype](#)

3.2 cv

Dataset Input

Users must upload the `inbred_gen` and hybrid phenotype files, while the design matrix and the parental phenotype are optional. In design matrix module, users should upload the design matrix if you select “**Input a design matrix**”; In parent phenotype module, users should upload the parent phenotype if you select “**Input parent phenotype**”; users don’t need to upload those file, which will be ignored, if you select “**Not included**”. The dominance genotype is also optional, in dominance genotype module, if you select “**Include dominance genotypes**”; users don’t need to upload this file and the dominance genotype will be calculated automatically; if you select “**Not included**”, it will be ignored.



http://127.0.0.1:3881 | Open in Browser | Publish

predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description

Genotype Input

Hybrid Phenotype

Parent Phenotype

Optional Input

Parameters

Results

Input parent phenotype

A matrix of a phenotypic values of parent (Optional)

Parent Phenotype

Browse... parent_phe.csv

Upload complete

☐ Not included
☒ Input parent phenotype

http://127.0.0.1:3881 | Open in Browser | Publish

predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description

Genotype Input

Hybrid Phenotype

Parent Phenotype

Optional Input

Parameters

Results

Input design matrix of the fixed effects & dominance genotypes

design matrix of the fixed effects(Optional)

☒ Not included
☐ Input a design matrix

dominance genotypes(Optional)

☒ Not included
☐ Include dominance genotypes

Method select & Parameter setting

Method: There are eight GS methods in the predhy.GUI, including "GBLUP", "BayesB", "RKHS", "PLS", "LASSO", "EN", "XGBoost", "LightGBM". Users may select one of those methods or all of them simultaneously with "ALL".

Number of folds: The k for k-fold cross validation.

Replicates: Repeat number of independent replicates for the cross-validation.

The random number: The random number.

CPU: the number of CPU for parallel calculation.

http://127.0.0.1:3881 | Open in Browser | Publish

predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description
Genotype Input
Hybrid Phenotype
Parent Phenotype
Optional Input
Parameters
Results

Select models & other parameters

GS methods
GBLUP

the number of folds
5

replicates
1

the random number
133

the number of CPU
1

Run the software

After uploading all the needed files and setting the parameters, users can run the Software simply by clicking “Start calculation”. The result will be print on the panel if a single method is selected. If you chose “ALL” in method, a plot of cross validation result for eight methods will be given.

predhy

Introduction

convertgen

cv

predhy.predict

predhy.predict_NCII

crodesign

Description

Genotype Input

Hybrid Phenotype

Parent Phenotype

Optional Input

Parameters

Results

Trait predictability (R_Square)

► Start calculation

GBLUP R_Square = 0.2251

predhy

Introduction

convertgen

cv

predhy.predict

predhy.predict_NCII

crodesign

Description

Genotype Input

Hybrid Phenotype

Parent Phenotype

Optional Input

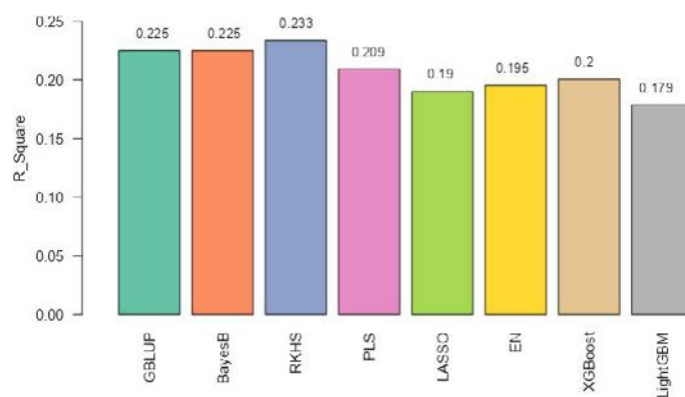
Parameters

Results

Trait predictability (R_Square)

► Start calculation

Trait predictability of 8 methods



3.3 predhy.predict

This function was designed to predict all potential crosses of a given set of parents using a subset of crosses as the training sample.

Dataset Input

Users must upload the `inbred_gen` and `hybrid` phenotype files, while the parent phenotype is optional.

The screenshot shows the web interface for the `predhy.predict` function. The browser address bar shows `http://127.0.0.1:3881`. The navigation bar includes links for `predhy`, `Introduction`, `convertgen`, `cv`, `predhy.predict` (active), `predhy.predict_NCII`, and `crodesign`. On the left, a sidebar contains links for `Description`, `Input files` (highlighted), `Methods & Models`, `Selection`, and `Phenotypic values`. The main content area is titled 'Input genotype & phenotype'. It contains two file upload sections: `inbred_gen` and `hybrid_phe`. Each section has a 'Browse...' button, a text input field with the filename (e.g., `inbred_gen.c`), and an 'Upload complete' button. To the right of these sections, descriptive text explains the format of the files. Below these sections, there is a label 'A matrix of a phenotypic values of parent (Optional)' and two radio buttons: 'Not included' (selected) and 'Input parent phenotype'.

http://127.0.0.1:3881 Open in Browser Publish

predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description
Input files
Methods & Models
Selection
Phenotypic values

Input genotype & phenotype

inbred_gen
Browse... inbred_gen.c
Upload complete

A matrix for genotypes of parental lines in numeric format, coded as 1, 0 and -1. The row.names of `inbred_gen` must be provided. It can be obtained from the original genotype using `convertgen` function

hybrid_phe
Browse... hybrid_phe.c
Upload complete

A data frame with three columns. The first column and the second column are the names of male and female parents of the corresponding hybrids, respectively; the third column is the phenotypic values of hybrids. The names of male and female parents must match the rownames of `inbred_gen`. Missing (NA) values are not allowed.

A matrix of a phenotypic values of parent (Optional)

☒ Not included
☐ Input parent phenotype

Method select & Parameter setting

Method: There are eight GS methods in the `predhy`.GUI for hybrid performance predicting, including "GBLUP", "BayesB", "RKHS", "PLS", "LASSO", "EN", "XGBoost", "LightGBM". Users should select one of those methods.

Prediction model: There are four options: the additive model, the additive-dominance model, the additive-phenotypic model, the additive-dominance-phenotypic model, user can choose one by select one of the choices.

The screenshot shows the 'predhy.predict' web interface. The browser address bar displays 'http://127.0.0.1:3881'. The navigation bar includes links for 'predhy', 'Introduction', 'convertgen', 'cv', 'predhy.predict' (active), 'predhy.predict_NCII', and 'crodesign'. A 'Publish' button is in the top right. On the left, a sidebar contains links for 'Description', 'Input files', 'Methods & Models' (highlighted in blue), 'Selection', and 'Phenotypic values'. The main content area is titled 'Select methods & models'. It features two dropdown menus: 'GS methods' with 'GBLUP' selected, and 'GS models' with 'the additive model' selected.

Select hybrids: Selection of hybrids based on the prediction results. There are three options: select = "all", which selects all potential crosses. select = "top", which selects the top n crosses. select = "bottom", which selects the bottom n crosses. User can decide number hybrids to select when select = "top" or select = "bottom".

This screenshot shows the 'predhy.predict' web interface with the 'Selection' tab selected in the sidebar. The main content area is titled 'Select hybrids'. It includes a descriptive text: 'the selection of hybrids based on the prediction results'. Below this is a dropdown menu with 'the top n crosses' selected. Further down, another descriptive text reads: 'the number of selected top or bottom hybrids, only when select = "top" or select = "bottom"'. At the bottom, there is a text input field containing the number '100'.

Run the software

After uploading all the needed files and setting the parameters, users can run the Software simply by clicking “Start calculation”. When calculation is down, the result will be given in the datatable below the panel, user may download the full data by clicking at “Download Results” bottom.

http://127.0.0.1:3881 Open in Browser Publish

predhy Introduction convertgen cv **predhy.predict** predhy.predict_NCII crodesign

Description
Input files
Methods & Models
Selection
Phenotypic values

Phenotypic values of the predicted hybrids

[Start calculation](#)

[Download Results](#)

Show entries Search:

| | top_100 |
|-----------|-------------------|
| A062/A291 | 1926.446905224698 |
| A169/A291 | 1923.3362122002 |
| A133/A291 | 1920.018562590968 |
| A027/A291 | 1919.059207234987 |
| A017/A291 | 1916.779254205353 |
| A038/A291 | 1916.639470265751 |
| A062/A169 | 1905.340900313774 |
| A052/A291 | 1904.015803388827 |
| A062/A133 | 1902.023250704543 |
| A291/A398 | 1901.883709023961 |

Showing 1 to 10 of 100 entries

Previous 2 3 4 5 ... 10 Next

3.4 predhy.predict_NCII

This function was designed to predict all potential crosses of a given set of parents (usually between different heterotic groups) using a subset of crosses as the training sample, following the North Carolina mating design II.

Dataset Input

Users must upload the inbred_gen and phenotype files, along with the Heterotic group dataset (two files, one contains male_names, the other contains female_names), while the parent phenotype is optional.

http://127.0.0.1:3881 | Open in Browser | Publish

predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description

Input files

Parent names

Methods & Models

Selection

Phenotypic values

Input genotype & phenotype

inbred_gen A matrix for genotypes of parental lines in numeric format, coded as 1, 0 and -1. The row.names of inbred_gen must be provided. It can be obtained from the original genotype using `convertgen` function

Browse... inbred_gen.c

Upload complete

hybrid_phe A data frame with three columns. The first column and the second column are the names of male and female parents of the corresponding hybrids, respectively; the third column is the phenotypic values of hybrids. The names of male and female parents must match the rownames of inbred_gen. Missing (NA) values are not allowed.

Browse... hybrid_phe.c

Upload complete

A matrix of a phenotypic values of parent (Optional)

☒ Not included

☐ Input parent phenotype

http://127.0.0.1:3881 | Open in Browser | Publish

predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description

Input files

Parent names

Methods & Models

Selection

Phenotypic values

Input names of parents

male_name a vector of the names of male parents.

Browse... male_name.csv

Upload complete

female_name a vector of the names of female parents.

Browse... female_name.csv

Upload complete

Method select & Parameter setting

Method: There are eight GS methods in the predhy.GUI for hybrid performance predicting, including "GBLUP", "BayesB", "RKHS", "PLS", "LASSO", "EN", "XGBoost", "LightGBM". Users should select one of those methods.

Prediction model: There are four options: the additive model, the additive-dominance model, the additive-phenotypic model, the additive-dominance-phenotypic model, user can choose one by select one of the choices.

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predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description

Input files

Parent names

Methods & Models

Selection

Phenotypic values

Select methods & models

GS methods

PLS

GS models

the additive model

Select hybrids: Selection of hybrids based on the prediction results. There are three options: select = "all", which selects all potential crosses. select = "top", which selects the top n crosses. select = "bottom", which selects the bottom n crosses. User can decide number hybrids to select when select = "top" or select = "bottom".

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predhy Introduction convertgen cv predhy.predict predhy.predict_NCII crodesign

Description

Input files

Parent names

Methods & Models

Selection

Phenotypic values

Select hybrids

the selection of hybrids based on the prediction results

the top n crosses

the number of selected top or bottom hybrids, only when select = "top" or select = "bottom".

100

Run the software

After uploading all the needed files and setting the parameters, users can run the Software simply by clicking "Start calculation". When calculation is down, the result will be given in the datatable below the panel, user may download the full data by clicking at "Download Results" bottom.

predhy

[Introduction](#)

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Phenotypic values of the predicted hybrids

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Show entries

Search:

top_100

| | |
|-----------|-------------------|
| A014/A014 | 2171.048111502145 |
| A014/A038 | 2168.236895244563 |
| A038/A014 | 2168.236895244563 |
| A038/A038 | 2165.425678986982 |
| A014/A358 | 2156.81104166041 |
| A358/A014 | 2156.81104166041 |
| A038/A358 | 2153.999825402828 |
| A358/A038 | 2153.999825402828 |
| A358/A358 | 2142.573971818676 |
| A014/A253 | 2107.792308368091 |

Showing 1 to 10 of 100 entries

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3.5 crodesign

This function was designed to generate a mating design for a subset of crosses based on a balanced random partial rectangle cross-design (BRPRCD) (Xu et al. 2016).

Dataset Input

Users need to upload the Parent names dataset (two files, one contains male_names, the other contains female_names).

The screenshot shows the 'crodesign' web application interface. At the top, there is a navigation bar with links: 'predhy', 'Introduction', 'convertgen', 'cv', 'predhy.predict', 'predhy.predict_NCII', and 'crodesign'. The 'crodesign' link is highlighted. On the left side, there is a sidebar with a 'Description' section and a list of options: 'Parent names' (highlighted in blue), 'Input parameters', and 'Results'. The main content area is titled 'Input parent names'. It contains two sections: 'male parent name' and 'female parent name'. Each section has a description: 'a table containing names of male parents' and 'a table containing names of female parents' respectively. Below each description, there is a 'Browse...' button, a text input field (containing 'male_name.' and 'female_nam' respectively), and an 'Upload complete' button.

Method selection & Parameter setting

percentage: User can decide the percentage of all potential hybrids to be evaluated in the field by clicking the numericInput.

seed: The random number.

The screenshot shows the 'crodesign' web application interface. At the top, there is a navigation bar with links: 'predhy', 'Introduction', 'convertgen', 'cv', 'predhy.predict', 'predhy.predict_NCII', and 'crodesign'. The 'crodesign' link is highlighted. On the left side, there is a sidebar with a 'Description' section and a list of options: 'Parent names', 'Input parameters' (highlighted in blue), and 'Results'. The main content area is titled 'Parameters'. It contains two sections: 'percentage' and 'seed'. The 'percentage' section has a description: 'an Integer denoting 1/d percentage of crosses to be evaluated in the field.' and a numeric input field with the value '50'. The 'seed' section has a description: 'the random number' and a numeric input field with the value '123'.

Run the software

After uploading all the needed files and setting the parameters, users can run the Software simply by clicking “Start calculation”. When calculation is down, the result will be given in the datatable below the panel, user may download the full data by clicking at “Download crodesign” bottom.

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Publish

predhy

Introduction

convertgen

cv

predhy.predict

predhy.predict_NCII

crodesign

Description

Parent names

Input parameters

Results

Results

▶ Start calculation

Download crodesign

Show 10 entries

Search:

| | crossID | male_Name | female_Name |
|----|---------|-----------|-------------|
| 1 | 1 | A008 | A007 |
| 2 | 2 | A054 | A007 |
| 3 | 3 | A156 | A007 |
| 4 | 4 | A005 | A007 |
| 5 | 5 | A335 | A007 |
| 6 | 6 | A426 | A007 |
| 7 | 7 | A025 | A007 |
| 8 | 8 | A011 | A007 |
| 9 | 9 | A186 | A007 |
| 10 | 10 | A092 | A030 |

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