Package: gpcp (via r-universe)

October 25, 2026

Type Package

Title Genomic Prediction of Cross Performance

Version 0.1.0

Maintainer Christine Nyaga <cmn92@cornell.edu>

Description This function performs genomic prediction of cross performance using genotype and phenotype data. It processes data in several steps including loading necessary software, converting genotype data, processing phenotype data, fitting mixed models, and predicting cross performance based on weighted marker effects. For more information, see Labroo et al. (2023) <doi:10.1007/s00122-023-04377-z>.

License GPL (>= 3)

Encoding UTF-8

LazyData true

LinkingTo Rcpp, RcppArmadillo

Imports BiocManager, Rcpp, dplyr, sommer, AGHmatrix, snpStats, VariantAnnotation, tools, magrittr, methods

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

Depends R (>= 2.10)

NeedsCompilation yes

Author Marlee Labroo [aut], Christine Nyaga [cre, aut], Lukas Mueller [aut]

Config/pak/sysreqs libbz2-dev liblzma-dev libssl-dev xz-utils zlib1g-dev

Repository https://cran.r-universe.dev

Date/Publication 2024-11-06 15:50:02 UTC

RemoteUrl https://github.com/cran/gpcp

RemoteRef HEAD

RemoteSha 18d39d679053ca803b351aa6e8835d70a815ca14

Contents

phenotypeFile 2
runGPCP 3

Index **5**

`phenotypeFile` *Example Phenotype Data*

Description

This is a sample phenotype dataset used for genomic prediction.

Usage

```
phenotypeFile
```

Format

A data frame with 24 columns:

ATW Description of ATW
AUDPC_YAD Area Under Disease Progress Curve for YAD
AUDPC_YMV Area Under Disease Progress Curve for YMV
Accession Genotype IDs for each individual
Block Block information
DMC Dry Matter Content values
Design Experimental design
LOC Location of the trials
NPH Number of Plants Harvested
OXBI Oxidation Index
Oxint180Minutes Oxidation intensity after 180 minutes
PLOT Plot number
REP Replication number
Settweight Weight of the planting setts
TTNPL Total Tuber Number per Plant
TTWPL Total Tuber Weight per Plant
Trial Trial name or ID
Vigor Plant vigor score
YIELD Yield values
Year Year of the experiment
Yield.per.plot..kg. Yield per plot in kilograms
Yield_udj Unadjusted Yield
rAUDPC_YAD Relative AUDPC for YAD
rAUDPC_YMV Relative AUDPC for YMV

Source

Generated for the gpcp package example

Examples

```
data(phenotypeFile)
head(phenotypeFile)
```

`runGPCP` *Genomic Prediction of Cross Performance This function performs genomic prediction of cross performance using genotype and phenotype data.*

Description

Genomic Prediction of Cross Performance This function performs genomic prediction of cross performance using genotype and phenotype data.

Usage

```
runGPCP(
  phenotypeFile,
  genotypeFile,
  genotypes,
  traits,
  weights = NA,
  userSexes = "",
  userFixed = NA,
  userRandom = NA,
  Ploidy = NA,
  NCrosses = NA
)
```

Arguments

`phenotypeFile`	A data frame containing phenotypic data, typically read from a CSV file.
`genotypeFile`	Path to the genotypic data, either in VCF or HapMap format.
`genotypes`	A character string representing the column name in the phenotype file for the genotype IDs.
`traits`	A string of comma-separated trait names from the phenotype file.
`weights`	A numeric vector specifying weights for the traits.
`userSexes`	A string representing the column name corresponding to the individuals' sexes.
`userFixed`	A string of comma-separated fixed effect variables.
`userRandom`	A string of comma-separated random effect variables.
`Ploidy`	An integer representing the ploidy level of the organism.
`NCrosses`	An integer specifying the number of top crosses to output.

Value

A data frame containing predicted cross performance.

Examples

```
# Load phenotype data from CSV
phenotypeFile <- read.csv(system.file("extdata", "phenotypeFile.csv", package = "gpcp"))
genotypeFile <- system.file("extdata", "genotypeFile_Chr9and11.vcf", package = "gpcp")
finalcrosses <- runGPCP(
    phenotypeFile = phenotypeFile,
    genotypeFile = genotypeFile,
    genotypes = "Accession",
    traits = "YIELD,DMC",
    weights = c(3, 1),
    userFixed = "LOC,REP",
    Ploidy = 2,
    NCrosses = 150
)
print(finalcrosses)
```

Index

∗ **datasets**
phenotypeFile, 2

phenotypeFile, 2

runGPCP, 3