

# Package: gpcp (via r-universe)

November 7, 2024

**Type** Package

**Title** Genomic Prediction of Cross Performance

**Version** 0.1.0

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**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](https://doi.org/10.1007/s00122-023-04377-z)>.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**LinkingTo** Rcpp, RcppArmadillo

**Imports** BioeManager, 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

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**Repository** CRAN

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**Config/pak/sysreqs** make libpng-dev libxml2-dev libssl-dev

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phenotypeFile	<i>Example Phenotype Data</i>
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### 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)
```

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

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\* **datasets**

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