



# Package ‘GWASP’

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**Type** Package

**Title** GWAS with PCA

**Version** 0.1.0

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**Description** Perform GWAS using GLM incorporating PCs and additional covariates.  
User-supplied covariate data and a user-specified number of non-linear dependent PCs  
are incorporated into a general linear model to better account of population structure.

**URL** Tutorials: <https://wcrump.github.io/GWASP/Tutorials/GWASP.Tutorial.html>  
FAQ: <https://wcrump.github.io/GWASP/FAQ/FAQ.html>

**License** What license is it under?

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

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check.name	<i>Check first column of data frame for names</i>
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## Description

If values in first column of data frame are not integers or numerics, the first column will be erased.

**Usage**

```
check.name(df)
```

**Arguments**

df                      A data frame

**Value**

A data frame (with first column removed if values were not integers or numerics)

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filter.pca	<i>Filter PCs</i>
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**Description**

Filter out PCs colinear with other covariates.

**Usage**

```
filter.pca(PCA, covs = NULL, threshold = 0.2)
```

**Arguments**

PCA                      The output list from the prcomp() function.

covs                     A matrix/data frame of covariates (rows = individuals, columns = covariates)

threshold                A numerical value (0-1) indicating the maximum allowed correlation between any one covariate and any one PC

**Value**

A prcomp() list output with PCs filtered

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G2P	<i>Simulate a phenotype</i>
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**Description**

Simulate a phenotypic data from genotypic data.

**Usage**

```
G2P(X = NULL, h2 = 0.5, alpha = 1, NQTN = 10, distribution = "normal", a2 = 0)
```

**Arguments**

x	A genotype matrix (rows = taxa, columns = markers).
h2	The heritability of the simulated trait.
alpha	The p parameter in an approximated geometric distribution
NQTN	The number markers contributing to the phenotype (if known)
a2	The proportion of non-additive interactive variance

**Value**

A list of the marker effects (1\*NQTN), the phenotype (n\*1), the combined additive effects (n\*1), the residual effects (n\*1), the additive marker indices (1\*m), and the interaction marker positions (1\*nint)

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GLM.func	<i>GWAS by GLM</i>
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**Description**

Perform GWAS using a general linear model method incorporating principle components and additional covariates if present.

**Usage**

```
GLM.func(X = NULL, y = NULL, C = NULL, PCs = 1, r = 0.2)
```

**Arguments**

x	A matrix of genotype data with dimensions n x m
y	A matrix of phenotype data with dimensions n x 1
C	A matrix of covariate data with dimensions n x t
PCs	A matrix of principle components with dimensions n x ? (variable number of PCs)
r	A numeric (0-1) indicating the correlation value of any PC-covariate pair at which the PC will be excluded from model

**Value**

A matrix of p values with dimensions 1 x m

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GWASbyCor	<i>Perform GWAS by Correlation</i>
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**Description**

Perform GWAS by Correlation

**Usage**

```
GWASbyCor(X, y)
```

**Arguments**

X	A genotype matrix with dimensions n x m (rows = taxa, columns = markers).
y	A phenotype vector of length n

**Value**

A vector of p-values of length m

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manhattan_plot	<i>Generate a Manhattan Plot of a GWAS result</i>
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**Description**

Generate a Manhattan Plot of a GWAS result

**Usage**

```
manhattan_plot(marker_map, pvals, QTN_index = c(), trait = "unknown")
```

**Arguments**

marker_map	A data.frame containing marker 'rs', 'chr', and 'pos' (should be in the same order as the GWAS results)
pvals	The untransformed p-values from a GWAS test
QTN_index	The indices of any known QTNs
trait	The name of the trait

**Value**

A ggplot object Manhattan plot

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qq\_plot*Generate a Quantile-Quantile Plot of a GWAS result*

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**Description**

Generate a Quantile-Quantile Plot of a GWAS result

**Usage**

```
qq_plot(marker_map, pvals, QTN_index, trait = "unknown")
```

**Arguments**

marker_map	A data.frame containing marker 'rs', 'chr', and 'pos' (should be in the same order as the GWAS results)
pvals	The untransformed p-values from a GWAS test
QTN_index	The indices of any known QTNs
trait	The name of the trait

**Value**

A ggplot object quantile-quantile plot

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