Package 'HaploVar'

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Type Package

Title Defining Local Haplotype Variants for Use in Trait Association and Trait Prediction Analyses

Version 0.1.1

Description A local haplotyping tool for use in trait association and trait prediction analyses pipelines. 'HaploVar' enables users take single nucleotide polymorphisms (SNPs) (in VCF format) and a linkage disequilibrium (LD) matrix, calculate local haplotypes and format the output to be compatible with a wide range of trait association and trait prediction tools. The local haplotypes are calculated from the LD matrix using a clustering algorithm called density-based spatial clustering of applications with noise ('DBSCAN') (Ester et al., 1996) <ISBN: 1577350049>.

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Encoding UTF-8

RoxygenNote 7.3.2

Imports dplyr, tidyr, tibble, magrittr, dbscan

Depends R (>= 4.00)

LazyData true

LazyDataCompression xz

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Contents

`collate_define_haplotypes` *Collate define_haplotypes Lists*

Description

This function collates a list of output files from define_haplotypes.

Usage

```
collate_define_haplotypes(haplotype_list)
```

Arguments

`haplotype_list` A list of the lists created by the define_haplotypes function.

Value

A collated list of all haplotype tables.

`collate_haplotype_variants` *Collate haplotype_variants Tables*

Description

This function collates a list of output files from haplotype_variants.

Usage

```
collate_haplotype_variants(haplotype_variants_list, format = 1)
```

Arguments

haplotype_variants_list	A list of the tables created by the define_haplotypes function.
format	The format you want the output table to be in. This should be the same number you used when running define_haplotypes.

Value

A collated table of haplotype variants.

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define_haplotypes *Define Haplotypes*

Description

This function requires a VCF and an LD matrix. It will then define local haplotypes and return a list of tables. Each table within the list represents one haplotype. These haplotype tables display the SNP genotypes within the haplotype.

Usage

```
define_haplotypes(
  vcf,
  LD,
  epsilon = 0.6,
  MGmin = 30,
  hetmiss_as = "allele",
  keep_outliers = FALSE
)
```

Arguments

vcf	A VCF file.
LD	A LD matrix file.
epsilon	Affects haplotype size. It is a parameter of the DBSCAN clustering tool. The default is 0.6.
MGmin	The minimum number of SNPs within a cluster for it to be defined as a haplotype.The default is 30.
hetmiss_as	Affects how missing data is handled for all instances where one allele in a genotype is missing.If hetmiss_as = "allele" the genotype is assumed to be heterozygous. If hetmiss_as = "miss" the genotype is treated as NA.
keep_outliers	If FALSE, removes SNPs that are determined to be outliers.

Value

A list of haplotype tables.

`define_haplotypes_globally` *Define Haplotypes Globally*

Description

This function requires a list of VCF files and an LD matrices. The list of VCF files and LD matrices must be the same length. It will then define local haplotypes for each pair of files (VCF and LD matrix) and return a list of tables. Each table within the list represents one haplotype. These haplotype tables display the SNP genotypes within the haplotype.

Usage

```
define_haplotypes_globally(
  vcf_list,
  LD_list,
  epsilon = NULL,
  MGmin = 30,
  hetmiss_as = "allele",
  keep_outliers = FALSE
)
```

Arguments

`vcf_list`	A list of VCF files.
`LD_list`	A list LD matrix files.
`epsilon`	A list of epsilon values the same length as the list of VCF files. The epsilon affects haplotype size. It is a parameter of the DBSCAN clustering tool. The default is 0.6.
`MGmin`	The minimum number of SNPs within a cluster for it to be defined as a haplotype.The default is 30.
`hetmiss_as`	Affects how missing data is handled for all instances where one allele in a genotype is missing.If hetmiss_as = "allele" the genotype is assumed to be heterozygous. If hetmiss_as = "miss" the genotype is treated as NA.
`keep_outliers`	If FALSE, removes SNPs that are determined to be outliers.

Value

A collated list of haplotype tables for all VCF files provided.

haplotype_variants *Identify Haplotype Variants*

Description

This function requires a VCF and an LD matrix. It will then define local haplotypes and identify the variants for each haplotype. The output can be formatted in six ways, to be compatible with a wide range of GWAS and genomic selection tools.

Usage

```
haplotype_variants(
  vcf,
  LD,
  epsilon = 0.6,
  MGmin = 30,
  minFreq = 2,
  hetmiss_as = "allele",
  keep_outliers = FALSE,
  format = 1
)
```

Arguments

vcf	A VCF file.
LD	A LD matrix file.
epsilon	Affects haplotype size. It is a parameter of the DBSCAN clustering tool. The default is 0.6.
MGmin	The minimum number of SNPs within a cluster for it to be defined as a haplotype.The default is 30.
minFreq	The minimum number of individuals a haplotype variant must be present in to be considered a valid haplotype variant. The default is 2.
hetmiss_as	Affects how missing data is handled for all instances where one allele in a genotype is missing.If hetmiss_as = "allele" the genotype is assumed to be heterozygous. If hetmiss_as = "miss" the genotype is treated as NA.
keep_outliers	If FALSE removes SNPs, that are determined to be outliers.
format	The output format. There are six different output formats (1,2,3,4,5,6).

Value

A table of haplotype genotypes in your chosen format.

haplotype_variants_global
Identify Haplotype Variants Globally

Description

This function requires a list of VCF files and an LD matrices. It will then define local haplotypes and identify the variants for each haplotype. The output can be formatted in six ways, to be compatible with a wide range of GWAS and genomic selection tools.

Usage

```
haplotype_variants_global(
  vcf_list,
  LD_list,
  epsilon = NULL,
  MGmin = 30,
  minFreq = 2,
  hetmiss_as = "allele",
  keep_outliers = FALSE,
  format = 1
)
```

Arguments

vcf_list	A list of VCF files.
LD_list	A list of LD matrix files.
epsilon	A list of epsilon values the same length as the list of VCF files. The epsilon affects haplotype size. It is a parameter of the DBSCAN clustering tool. The default is 0.6.
MGmin	The minimum number of SNPs within a cluster for it to be defined as a haplotype.The default is 30.
minFreq	The minimum number of individuals a haplotype variant must be present in to be considered a valid haplotype variant. The default is 2.
hetmiss_as	Affects how missing data is handled for all instances where one allele in a genotype is missing.If hetmiss_as = "allele" the genotype is assumed to be heterozygous. If hetmiss_as = "miss" the genotype is treated as NA.
keep_outliers	If FALSE removes SNPs, that are determined to be outliers.
format	The output format. There are six different output formats (1,2,3,4,5,6).

Value

A table of haplotype genotypes in your chosen format.

LD *Linkage Disequilibrium Matrix*

Description

Pairwise R^2 values for 490 Brassica napus single nucleotide polymorphisms (SNPs).

Usage

```
LD
```

Format

An object of class `data.frame` with 490 rows and 490 columns.

Source

Wu, D., Liang, Z., Yan, T., Xu, Y., Xuan, L., Tang, J., Zhou, G., Lohwasser, U., Hua, S., Wang, H., Chen, X., Wang, Q., Zhu, L., Maodzeka, A., Hussain, N., Li, Z., Li, X., Shamsi, I. H., Jilani, G., ... Jiang, L. (2019). Whole-Genome Resequencing of a Worldwide Collection of Rapeseed Accessions Reveals the Genetic Basis of Ecotype Divergence. Molecular Plant, 12(1), 30–43. https://doi.org/10.1016/j.molp.2018.11.007

vcf *Brassica napus genotype data in VCF format*

Description

A subset of Brassica napus genotype data for chromosome C01. The genotype data reports single nucleotide polymorphism (SNP) data. The variables are as follows:

Usage

```
vcf
```

Format

A data frame with 490 rows and 1000 variables:

#CHROM The chromsome where the SNP is located

POS The reference position of the SNP (bp)

ID The name/ID of the SNP

REF Reference base

ALT Alternate base

QUAL Phred-scaled quality score of the alternate base

FILTER PASS if the SNP has passed all filters

INFO Additional information

FORMAT The data type of the genotype

R4155_R4155 Genotypes for sample R4155_R4155

R4156_R4156 Genotypes for sample R4156_R4156

R4157_R4157 Genotypes for sample R4157_R4157

R4158_R4158 Genotypes for sample R4158_R4158

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