

Package: haployper (via r-universe)

August 24, 2024

Type Package

Title Tool for Clustering Genotypes in Haplotypes

Version 0.1

Date 2016-03-28

Author Sebastian Simondi <sebastian.simondi@gmail.com> and Gaston Quero, with contributions from Victoria Bonnecarrere and Lucia Gutierrez

Maintainer Gaston Quero <gastonquero@gmail.com>

Description Function to identify haplotypes within QTL (Quantitative Trait Loci). One haplotype is a combination of SNP (Single Nucleotide Polymorphisms) within the QTL. This function groups together all individuals of a population with the same haplotype. Each group contains individual with the same allele in each SNP, whether or not missing data. Thus, haployper groups individuals, that to be imputed, have a non-zero probability of having the same alleles in the entire sequence of SNP's. Moreover, haployper calculates such probability from relative frequencies.

Depends R (>= 2.10)

License GPL-3

LazyData TRUE

RoxygenNote 5.0.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Imports graphics, utils

NeedsCompilation no

Date/Publication 2016-04-06 17:23:47

Repository <https://gastonquero.r-universe.dev>

RemoteUrl <https://github.com/cran/haployper>

RemoteRef HEAD

RemoteSha 9537d5ab5f33d18d503909fb60d6e5ae1d222ead

Contents

haplotyper	2
rice_qtl	3
sim_qtl	3
Index	4

haplotyper

haplotyper function identifies haplotypes within QTL.

Description

This function groups together all individuals of a population with the same haplotype.

Usage

```
haplotyper(x, Print = FALSE)
```

Arguments

- x a data.frame that should be loaded with read.table function. Each row represents the individuals while each column represents the markers. The first column contains the names of the genotypes.
- Print option for print the haplotyper result. The default is FALSE

Details

Each group contains individual with the same allele in each SNP, whether or not missing data.

Value

a matrix with the haplotypes

Author(s)

Sebastian Simondi, Victoria Bonnecarrere, Lucia Gutierrez, Gaston Quero

See Also

read.table function

Examples

```
## Not run:
data(rice_qtl)
haplotyper(rice_qtl)

## End(Not run)
```

`rice_qtl` *Real experimental data*

Description

The data is a QTL for rice Grain Quality

Usage

`rice_qtl`

Format

A data frame 326 rows (individual) and 38 variables (SNPs)

Source

Uruguayan Rice Breeding GWAS (URiB)

`sim_qtl` *simple QTL simulated*

Description

A dataset containing the marcadores

Usage

`sim_qtl`

Format

A data frame 5 rows (individuals) and 7 variables (snps)

Source

simulated data

Index

* datasets

[rice_qtl, 3](#)
[sim_qtl, 3](#)

[haplotyper, 2](#)

[rice_qtl, 3](#)

[sim_qtl, 3](#)