

Package ‘clusterhap’

October 12, 2022

Type Package

Title Clustering Genotypes in Haplotypes

Version 0.1

Date 2016-05-13

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

Maintainer Gaston Quero <gastonquero@gmail.com>

Description One haplotype is a combination of SNP (Single Nucleotide Polymorphisms) within the QTL (Quantitative Trait Loci). clusterhap 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, clusterhap groups individuals, that to be imputed, have a non-zero probability of having the same alleles in the entire sequence of SNP's. Moreover, clusterhap 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

Repository CRAN

Date/Publication 2016-05-16 14:37:36

R topics documented:

clusterhap	2
rice_qtl	3
sim_qtl	3

clusterhap	<i>clusterhap function identifies haplotypes within QTL.</i>
------------	--

Description

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

Usage

```
clusterhap(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 clusterhap 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)

Gaston Quero, Sebastian Simondi, Victoria Bonnacarrere, Lucia Gutierrez.

See Also

read.table function

Examples

```
#### Simple simulated data
data("sim_qtl")
clusterhap(sim_qtl, Print=TRUE)

### Real experimental data

## Not run:
data(rice_qtl)
clusterhap(rice_qtl)

## End(Not run)
```

rice_qtl	<i>Real experimental data</i>
----------	-------------------------------

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	<i>simple QTL simulated</i>
---------	-----------------------------

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

clusterhap, 2

rice_qtl, 3

sim_qtl, 3