Package ‘clusterhap’

October 12, 2022

Type Package
Title Clustering Genotypes in Haplotypes
Version 0.1
Date 2016-05-13
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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

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clusterhap

clusterhap function identifies haplotypes within QTL.

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

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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**

**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)

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**sim_qtl**

**Description**
A dataset containing the marcadores

**Usage**
sim_qtl

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

**Source**
simulated data
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