Package 'rehh.data'

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Version 1.0.0

License GPL (>= 2)

Title Data Only: Searching for Footprints of Selection using Haplotype
Homozygosity Based Tests

Description Contains example data for the 'rehh' package.

Depends R (>= 2.10)

NeedsCompilation no

Repository CRAN

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R topics documented:

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rehh.data-package   *Data Only: Searching for Footprints of Selection using Haplotype Homozygosity Based Tests Description: Contains example data for the 'rehh' package.*

Description

Contains example data for the package rehh.

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Details

Package:	rehh.data
Version:	1.0.0
License:	GPL(>=2)

Index:

References

Gautier M., Klassmann A., and Vitalis R. (2016). rehh: An R package to detect footprints of selection in genome-wide SNP data from haplotype structure. *Molecular Ecology Resources*, submitted

Gautier M. and Vitalis R. (2012). rehh: An R package to detect footprints of selection in genome-wide SNP data from haplotype structure. *Bioinformatics*, **28**(8), 1176–1177.

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128–3143.

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wgscan.cgu   *Whole genome scan results for the CGU (Creole from Guadeloupe island)*

Description

A dataframe object with of 44,057 rows (SNPs) and 7 columns: i) chromosome name (CHR), ii) position of the SNP in bp (POSITION), iii) Ancestral allele frequency (freq_A), iv) iHH for the ancestral allele (iHH_A), v) iHH for the derived allele (iHH_D), vi) iES using the estimator by Tang et al. (2007) (iES_Tang_et_al_2007), vii) iES using the estimator by Sabeti et al. (2007) (iES_Sabeti_et_al_2007).

Usage

```
data(wgscan.cgu)
```

References

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128–3143.

| wgscan.eut | *Whole genome scan results for a pool of European taurine cattle* |

Description

A dataframe object with 44,057 rows (SNPs) and 7 columns: i) chromosome name (CHR), ii) position of the SNP in bp (POSITION), iii) Ancestral allele frequency (freq_A), iv) iHH for the ancestral allele (iHH_A), v) iHH for the derived allele (iHH_D), vi) iES using the estimator by Tang et al. (2007) (iES_Tang_et_al_2007), vii) iES using the estimator by Sabeti et al. (2007) (iES_Sabeti_et_al_2007).

Usage

```
data(wgscan.eut)
```

References

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128–3143.

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