

Package: rehh.data (via r-universe)

August 24, 2024

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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

Date/Publication 2016-11-08 11:10:29

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

Contains example data for the package rehh.

Details

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

Index:

wgscan.cgu	Whole genome scan results for the CGU (Creole from Guadeloupe island)
wgscan.eut	Whole genome scan results for a pool of European taurine cattle

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.

wgscan.cgu	<i>Whole genome scan results for the CGU (Creole from Guadeloupe island)</i>
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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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