Package: rehh.data (via r-universe)

June 4, 2026

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

Version 1.0.1

Description Contains example data for the 'rehh' package.

License GPL (>= 2)

Depends R (>= 2.10)

Encoding UTF-8

LazyData true

NeedsCompilation no

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Repository https://mgautierinra.r-universe.dev

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RemoteUrl https://github.com/cran/rehh.data

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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.

Details

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

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```
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. (2017). rehh 2.0: a reimplementation of the R package rehh to detect positive selection from haplotype structure. *Molecular Ecology Resources*, **17**, 78–90.

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` *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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