Package 'SNPhoodData'

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Title Additional and more complex example data for the SNPhood package
Version 1.36.0
Author Christian Arnold, Judith Zaugg
Maintainer Christian Arnold <christian.arnold@embl.de></christian.arnold@embl.de>
Description This companion package for SNPhood provides some example datasets of a larger size than allowed for the SNPhood package. They include full and real-world examples for performing analyses with the SNPhood package.
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BugReports christian.arnold@embl.de
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Description

This companion package for SNPhood provides some example datasets of a larger size than allowed for the SNPhood package. They include full and real-world examples for performing analyses with SNPhood.

Details

For a list of files that the package provides, type

```
list.files(pattern = "*", system.file("extdata", package = "SNPhoodData"),full.names
= TRUE)
```

See also the package vignette (browseVignettes("SNPhoodData")).

Data

For an even more detailed overview of the data that the SNPhoodData package provides, see the vignette. Briefly, the example dataset consists of the following files:

- 14,000 previously identified H3K27ac QTLs for individuals from the YRI population [1,2] (file cisQ.H3K27AC.chr21.txt)
- H3K27ac ChIP-Seq data in BAM format for two individuals (GM10847, GM12890) obtained from Kasowski et al [2] from the CEU population (two replicates each, files SNYDER_HG19_*). The reads have previously been mapped to the personalized phased genomes of these individuals [2].
- Corresponding genotypes for the SNPs were obtained from the *1000 Genomes Project* [3] (file genotypes.vcf.gz)

For the references, see the corresponding package vignette by typing browseVignettes("SNPhoodData").

Usage

You may use the example files to run a full SNPhood analysis. For a full example, see the workflow vignette in the SNPhood package (browseVignettes("SNPhood"))

Contact Information

We value all the feedback that we receive and will try to reply in a timely manner. Please report any bug that you encounter as well as any feature request that you may have to <SNPhood@gmail.com>.

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