# Package 'SNPhoodData'

May 15, 2025

Title Additional and more complex example data for the SNPhood package	
<b>Version</b> 1.38.0	
Author Christian Arnold, Judith Zaugg	
Maintainer Christian Arnold <christian.arnold@embl.de></christian.arnold@embl.de>	
<b>Description</b> 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.	
VignetteBuilder knitr	
Suggests BiocStyle,knitr,rmarkdown	
<b>Depends</b> R (>= $3.2$ )	
biocViews ExperimentData	
License LGPL (>= 3)	
LazyData true	
BugReports christian.arnold@embl.de	
NeedsCompilation no	
git_url https://git.bioconductor.org/packages/SNPhoodData	
git_branch RELEASE_3_21	
git_last_commit 14607c2	
git_last_commit_date 2025-04-15	
Repository Bioconductor 3.21	
Date/Publication 2025-05-15	
Contents	
SNPhoodData	2
Index	3

2 SNPhoodData

SNPhood package	SNPhoodData	SNPhoodData: Additional and more complex example data for the SNPhood package
-----------------	-------------	---

## 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>.

# **Index**

```
* SNPhood-Data,

SNPhoodData, 2

* SNPhoodData,

SNPhoodData-package

SNPhoodData, 2

SNPhoodData, 2

SNPhoodData, 2

SNPhoodData-package (SNPhoodData), 2
```