

# Package ‘SNPhoodData’

September 11, 2025

**Title** Additional and more complex example data for the SNPhood package

**Version** 1.39.0

**Author** Christian Arnold, Judith Zaugg

**Maintainer** Christian Arnold <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.

**VignetteBuilder** knitr

**Suggests** BiocStyle,knitr,rmarkdown

**Depends** 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** devel

**git\_last\_commit** 60c6f41

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-09-11

## Contents

|                       |   |
|-----------------------|---|
| SNPhoodData . . . . . | 2 |
| Index                 | 3 |

---

|             |                                                                                      |
|-------------|--------------------------------------------------------------------------------------|
| SNPhoodData | <i>SNPhoodData: Additional and more complex example data for the SNPhood package</i> |
|-------------|--------------------------------------------------------------------------------------|

---

## 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, [2](#)
  - \* **SNPhoodData-package**  
    SNPhoodData, [2](#)
- SNPhoodData, [2](#)  
SNPhoodData-package (SNPhoodData), [2](#)