

Example data for breakpointR

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August 8, 2018

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1 Data description

This package provides data for demonstration purposes in package `breakpointR`. It contains five example BAM files to illustrate functionalities of `breakpointR` package, as well as corresponding results stored in 'BreakPoint' objects in order to demonstrate plotting options. The following example data are present inside the package `strandseqExampleData`:

```
library(strandseqExampleData)
?example_bams
?example_results
```

Example data can be loaded in the following way:

```
## Example BAM files
path <- system.file("extdata", "example_bams", package="strandseqExampleData")
files <- list.files(path, full.names=TRUE, pattern=".bam$")
```

```
files

## [1] "/extdata/example_bams/example_lib1.bam" "/extdata/example_bams/example_lib2.bam"
## [3] "/extdata/example_bams/example_lib3.bam" "/extdata/example_bams/example_lib4.bam"
## [5] "/extdata/example_bams/example_lib5.bam"
```

```
## Example results
path <- system.file("extdata", "example_results", package="strandseqExampleData")
files <- list.files(path, full.names=TRUE)
```

```
files

## [1] "/extdata/example_results/example_lib1.RData"
## [2] "/extdata/example_results/example_lib2.RData"
## [3] "/extdata/example_results/example_lib3.RData"
## [4] "/extdata/example_results/example_lib4.RData"
## [5] "/extdata/example_results/example_lib5.RData"
```

2 Session Info

```
toLatex(sessionInfo())
```

- R version 3.4.4 (2018-03-15), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=en_US.UTF-8, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Debian GNU/Linux 9 (stretch)
- Matrix products: default
- BLAS: /usr/lib/atlas-base/atlas/libblas.so.3.0
- LAPACK: /usr/lib/atlas-base/atlas/liblapack.so.3.0
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, stats4, utils
- Other packages: BiocGenerics 0.24.0, cowplot 0.9.3, devtools 1.13.4, GenomInfoDb 1.14.0, GenomicRanges 1.30.3, ggplot2 3.0.0, IRanges 2.12.0, knitr 1.20, S4Vectors 0.16.0, strandseqExampleData 0.99.0
- Loaded via a namespace (and not attached): assertthat 0.2.0, backports 1.1.2, bindr 0.1.1, bindrcpp 0.2.2, Biobase 2.38.0, BiocInstaller 1.28.0, BiocParallel 1.12.0, BiocStyle 2.6.1, Biostrings 2.46.0, bitops 1.0-6, codetools 0.2-15, colorspace 1.3-2, commonmark 1.5, compiler 3.4.4, crayon 1.3.4, DelayedArray 0.4.1, desc 1.2.0, digest 0.6.15, doParallel 1.0.11, dplyr 0.7.6, evaluate 0.10.1, foreach 1.4.4, GenomInfoDbData 1.0.0, GenomicAlignments 1.14.2, git2r 0.19.0, glue 1.3.0, grid 3.4.4, gtable 0.2.0, gtools 3.8.1, highr 0.6, htmltools 0.3.6, iterators 1.0.9, lattice 0.20-35, lazyeval 0.2.1, magrittr 1.5, Matrix 1.2-12, matrixStats 0.54.0, memoise 1.1.0, munsell 0.4.3, pillar 1.2.2, pkgconfig 2.0.1, plyr 1.8.4, purrr 0.2.5, R6 2.2.2, Rcpp 0.12.17, RCurl 1.95-4.10, rlang 0.2.1, rmarkdown 1.9, roxygen2 6.0.1, rprojroot 1.3-2, Rsamtools 1.30.0, rstudioapi 0.7, scales 0.5.0, stringi 1.2.2, stringr 1.3.1, SummarizedExperiment 1.8.1, testthat 2.0.0, tibble 1.4.2, tidyselect 0.2.4, tinytex 0.5, tools 3.4.4, withr 2.1.2, xml2 1.2.0, XVector 0.18.0, yaml 2.1.19, zlibbioc 1.24.0