Package 'MutSeqRData'

November 10, 2026

Title Experimental Data for MutSeqR Examples

Version 1.0.0

Description Experimental data for use with the MutSeqR vignette and examples. This dataset is taken from LeBlanc et al., 2022. 24 MutaMouse animals were exposed to one of three doses of benzo[a]pyrene or a vehicle control for 28 days by oral gavage. 28 days after the end of the exposure, bone marrow of the femurs was harvested from euthanized animals. DNA extraction was conducted via DNeasy Blood and Tissue kit. DNA samples were sequenced using TwinStrand's Duplex Sequencing on the Mouse Mutagenesis Panel at > 10,000 depth. The Mouse Mutagenesis Panel comprises 20 2.4kb genomic targets with one located on each mouse autosome (two on chromosome 1). Pre-processing of sequence reads was redone since publication using an updated version of TwinStrand's Mutagenesis App (v. 3.20.1) which produced tabular mutation data files for each sample. Data contained herein are only those required for running MutSeqR examples and vignette.

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Depends R (>= 3.5.0)

Encoding UTF-8

LazyData false

biocViews ExperimentHub, Mus_musculus_Data, Genome, Somatic, SequencingData

Suggests BiocStyle, knitr, rmarkdown

RoxygenNote 7.3.1

VignetteBuilder knitr

BugReports https://github.com/EHSRB-BSRSE-Bioinformatics/MutSeqRData/issues

URL https://github.com/EHSRB-BSRSE-Bioinformatics/MutSeqRData/

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Contents

MutSeqRData 2

Index **4**

`MutSeqRData` *Supporting data for MutSeqR package*

Description

Package: MutSeqRData provides example data for MutSeqR. It includes the following objects:

Example import_mut_data: Data frame object containing list of sequenced sites for sample dna00996.1. Used as an example for importing tabular datasets with MutSeqR.

Example import_mut_data using Custom column names: Data frame object containing list of sequenced sites for sample dna00996.1. Used as an example for importing tabular datasets with MutSeqR when dataset has custom column names.

Example import_vcf_data: Block compressed VCF file containing list of sequenced sites for sample dna00996.1. Used as an example for importing VCF datasets with MutSeqR.

Example mutation data: Data frame object containing list of sequenced sites for 24 samples. Unfiltered. Used as an example for filtering mutation data with MutSeqR.

Example mutation data filtered: Data frame object containing the filtered list of sequenced sites for 24 samples. Used as an example for downstream MutSeqR functions.

Precalculated Depth at Base 6 Resolution: Data frame object containing the pre-calculated total depth values for each sample at 6-base subtype resolution. Used as an example in calculate_mf()

Precalculated Depth at Base 12 Resolution: Data frame object containing the pre-calculated total depth values for each sample at 12-base subtype resolution. Used as a reference for users.

Precalculated Depth at Base 96 Resolution: Data frame object containing the pre-calculated total depth values for each sample at 96-base subtype resolution. Used as a reference for users.

Precalculated Depth at Base 192 Resolution: Data frame object containing the pre-calculated total depth values for each sample at 192-base subtype resolution. Used as a reference for users.

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Index

∗ **utilities**
MutSeqRData, 2

MutSeqRData, 2
MutSeqRData-package *(*MutSeqRData*)*, 2