Package ‘MUGAExampleData’

January 22, 2026

Type Package

Title Example {M}ouse {U}niversal {G}enotyping {A}rray data for genome reconstruction and quantitative trait locus mapping.

Version 1.31.0

Date 2013-10-02

Author Daniel Gatti <`Dan.Gatti@jax.org`>

Maintainer Daniel Gatti <`Dan.Gatti@jax.org`>

Description This package contains example data for the MUGA array that is used by the R package DOQTL.

biocViews ExperimentData, Mus_musculus_Data

Depends R (>= 2.10.0)

License GPL-3

git_url https://git.bioconductor.org/packages/MUGAExampleData

git_branch devel

git_last_commit 4ad6682

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2026-01-22

Contents

`call.rate.batch` *Call rates and batch information for Svenson et.al samples.*

Description

The allele call rate and batch information for each sample in the data set.

Usage

```
data(call.rate.batch)
```

Format

Data.frame with three columns. sample: contains the sample ID. call.rate: contains the allele call rate. batch: contains the batch ID, which is the source directory where the raw files for this batch were stored.

Details

This is the summary of the allele call rate and batch from each of the raw data files (FinalReport1 and FinalReport2).

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(call.rate.batch)
```

`FinalReport1` *Allele call and intensity data for the first set of MUGA samples.*

Description

Allele call and intensity data for the first set of MUGA samples.

Usage

```
data(FinalReport1)
```

Format

Text with tab delimeters.

Details

This is the *_FinalReport.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(FinalReport1)
```

`FinalReport2` *Allele call and intensity data for the second set of MUGA samples.*

Description

Allele call and intensity data for the second set of MUGA samples.

Usage

```
data(FinalReport2)
```

Format

Text with tab delimeters.

Details

This is the *_FinalReport.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(FinalReport2)
```

`geno` *Allele calls for Svenson et.al samples.*

Description

The allele calls for each sample in the data set.

Usage

```
data(geno)
```

Format

Character matrix containing the allele calls coded as "A", "C", "G", "T", "H" or "-". num.samples x num.snps. Sample names in rownames and SNP IDs in colnames.

Details

This is the summary of the allele calls from each of the raw data files (FinalReport1 and FinalReport2).

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(geno)
```

`model.probs` *Founder haplotype probabilities for the Svenson et.al. data.*

Description

A 3D array containing the eight founder haplotype contributions from each sample at each marker on the array.

Usage

```
data(model.probs)
```

Format

Numeric 3D array containing founder haplotype probabilities. num.samples x num.founders x num.snps. Sample names in dimnames[[1]], founder letter codes in dimnames[[2]] and SNP IDs in dimnames[[3]].

Details

These are reconstructed founder haplotype probabilities for the DO samples in this data set. They were reconstructed using a hidden Markov model based on the MUGA intensities.

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(model.probs)
```

`MUGAExampleData` *Example Mouse Universal Genotyping Array data for genome reconstruction and quantitative trait locus mapping.*

Description

Example MUGA data for a set of ~150 samples from Svenson et.al., Genetics, 2012.

Details

Package:	MUGAExampleData
Type:	Package
Version:	1.0
Date:	2013-10-02
License:	What license is it under?

Author(s)

Daniel Gatti <Dan.Gatti@jax.org>

References

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(FinalReport1)
data(Samples1)
```

`pheno` *Phenotype data for Svenson et.al samples.*

Description

The clinical phenotypes for each mouse in the Svenson et.al. data set.

Usage

`data(pheno)`

Format

Data.frame containing sample IDs, sex, diet and measured clinical phenotypes for 149 DO mice.

Details

The clinical phenotypes for each mouse in the Svenson et.al. data set.

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(pheno)
```

`Samples1` *Sample list for the first MUGA data set.*

Description

List of samples that correspond to the samples in FinalReport1.

Usage

`data(Samples1)`

Format

Table with tab delimiters.

Details

This is the Sample_Map.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(Samples1)
```

`Samples2` *Sample list for the second MUGA data set.*

Description

List of samples that correspond to the samples in FinalReport2.

Usage

```
data(Samples2)
```

Format

Table with tab delimiters.

Details

This is the Sample_Map.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(Samples2)
```

`x` *X allele intensities for Svenson et.al samples.*

Description

Matrix of allele intensities from the MUGA for each of the Svenson et.al. samples at each marker.

Usage

```
data(x)
```

Format

X allele intensities for each sample at each marker. num.samples x num.snps. Sample names in rownames and SNP IDs in colnames.

Details

This is the summary of the X allele intensities from each of the raw data files (FinalReport1 and FinalReport2).

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(x)
```

`y` *Y allele intensities for Svenson et.al samples.*

Description

Matrix of allele intensities from the MUGA for each of the Svenson et.al. samples at each marker.

Usage

```
data(y)
```

Format

Y allele intensities for each sample at each marker. num.samples x num.snps. Sample names in rownames and SNP IDs in colnames.

Details

This is the summary of the Y allele intensities from each of the raw data files (FinalReport1 and FinalReport2).

Source

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

Examples

```
data(y)
```

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