Package ‘marinerData’

August 29, 2024

Title ExperimentHub data for the mariner package

Version 1.4.0

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Description Subsampled Hi-C in HEK cells expressing the NHA9 fusion with an F to S mutated IDR (``FS'') or without any mutations to the IDR (``Wildtype'' or ``WT''). These files are used for testing mariner functions and some examples.

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BugReports https://support.bioconductor.org/t/marinerData

Imports utils, ExperimentHub

Suggests knitr, rmarkdown, ExperimentHubData, testthat (>= 3.0.0)

biocViews ExperimentHub, ExperimentData, SequencingData

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Config/testthat/edition 3

VignetteBuilder knitr

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Contents

`FS_5kbLoops.txt` *Example NHA9 (FS) Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from HEK cells expressing an NHA9 fusion with an F to S mutated IDR.

Value

Downloads and caches a `.txt` file in BEDPE format.

Examples

```
bedpeFile <- FS_5kbLoops.txt()
bedpeFile
```

`LEUK_HEK_PJA27_inter_30.hic`
Example NHA9 (FS) Hi-C data

Description

Subsampled Hi-C in HEK cells expressing the NHA9 fusion with an F to S mutated IDR.

Value

Downloads and caches a `.hic` file.

Examples

```
hicFile <- LEUK_HEK_PJA27_inter_30.hic()
hicFile
```

LEUK_HEK_PJA30_inter_30.hic *Example NHA9 (WT) Hi-C data*

Description

Subsampled Hi-C in HEK cells expressing the NHA9 fusion with a Wildtype IDR.

Value

Downloads and caches a `.hic` file.

Examples

```
hicFile <- LEUK_HEK_PJA30_inter_30.hic()
hicFile
```

LIMA_0000.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 0 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_0000.bedpe()
bedpeFile
```

LIMA_0030.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 30 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_0030.bedpe()
bedpeFile
```

LIMA_0060.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 60 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_0060.bedpe()
bedpeFile
```

LIMA_0090.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 90 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_0090.bedpe()
bedpeFile
```

LIMA_0120.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 120 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_0120.bedpe()
bedpeFile
```

LIMA_0240.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 240 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_0240.bedpe()
bedpeFile
```

LIMA_0360.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 360 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_0360.bedpe()
bedpeFile
```

LIMA_1440.bedpe *Example Timecourse Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 1440 minutes.

Value

Downloads and caches a `.bedpe` file in BEDPE format.

Examples

```
bedpeFile <- LIMA_1440.bedpe()
bedpeFile
```

marinerData *ExperimentHub datasets for the mariner package*

Description

Subsampled Hi-C in HEK cells expressing the NHA9 fusion with an F to S mutated IDR ("FS") or without any mutations to the IDR ("Wildtype" or "WT"). Accompanying loop calls identified using SIP (https://github.com/PouletAxel/SIP) are also provided. For more information or full datasets, see https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE143465.

Also included are loop calls identified using SIP (https://github.com/PouletAxel/SIP) from a THP-1 activation timecourse after stimulation with LPS & IF-G for 0, 30, 60, 80, 120, 2440, 360, or 1440 minutes. For more information or full datasets, see https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE201353.

These files are used for testing mariner functions and some examples.

Value

Downloads and caches `.hic` or BEDPE-formatted `.txt` files.

Author(s)

Eric S. Davis

`WT_5kbLoops.txt` *Example NHA9 (WT) Loops*

Description

Loops called with SIP (https://github.com/PouletAxel/SIP) using Hi-C data from HEK cells expressing an NHA9 fusion with a Wildtype IDR.

Value

Downloads and caches a `.txt` file in BEDPE format.

Examples

```
bedpeFile <- WT_5kbLoops.txt()
bedpeFile
```

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