Package ‘QDNAseq.mm10’

February 1, 2017

Type Package
Title Bin annotation mm10
Version 1.4.0
Date 2015-09-30
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Description This package provides QDNAseq bin annotations for the mouse genome build mm10.
Depends R (>= 3.2.1), QDNAseq
biocViews ExperimentData, OrganismData, Mus_musculus_Data
License GPL
URL https://github.com/tgac-vumc/QDNAseq.mm10
BugReports https://github.com/tgac-vumc/QDNAseq.mm10/issues
NeedsCompilation no

R topics documented:

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Description

This package provides QDNAseq binannotations for the mouse genome build mm10 for bin sizes 1, 5, 10, 15, 30, 50, 100, 500 and 1000 kbp (kilobasepair).

The datasets are named as follows:

- mm10.1kbp.SR50
- mm10.5kbp.SR50
- mm10.10kbp.SR50
- mm10.15kbp.SR50
- mm10.30kbp.SR50
- mm10.50kbp.SR50
- mm10.100kbp.SR50
- mm10.500kbp.SR50
- mm10.1000kbp.SR50

License

This package is licensed under GPL.

Author(s)

Daoud Sie

Examples

data("mm10.30kbp.SR50")
assign("bins", get("mm10.30kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

# or

bins <- getBinAnnotations(binSize=30, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

Mm10 1000kbp bin annotations

Description

Bin annotations are calculated for non-overlapping 1000kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
• bases: Percentage of non-N nucleotides (of full bin size),
• gc: Percentage of C and G nucleotides (of non-N nucleotides),
• mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
• blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
• residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gnerre et al. (see references),
• use: Whether the bin should be used in subsequent analysis steps,

Value

Returns an AnnotatedDataFrame object.

Author(s)

Daoud Sie

References


Examples

data("mm10.1000kbp.SR50")
assign("bins", get("mm10.1000kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

# or

bins <- getBinAnnotations(binSize=1000, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")
**Description**

Bin annotations are calculated for non-overlapping 100kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
- bases: Percentage of non-N nucleotides (of full bin size),
- gc: Percentage of C and G nucleotides (of non-N nucleotides),
- mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
- blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
- residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gnerre et al. (see references),
- use: Whether the bin should be used in subsequent analysis steps,

**Value**

Returns an AnnotatedDataFrame object.

**Author(s)**

Daoud Sie

**References**


**Examples**

```r
data("mm10.100kbp.SR50")
assign("bins", get("mm10.100kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="/bam")

# or

bins <- getBinAnnotations(binSize=100, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="/bam")
```

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**mm10.10kbp.SR50**

**Mm10 10kbp bin annotations**

**Description**

Bin annotations are calculated for non-overlapping 10kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
- bases: Percentage of non-N nucleotides (of full bin size),
- gc: Percentage of C and G nucleotides (of non-N nucleotides),
- mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
- blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
- residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gnerre et al. (see references),
- use: Whether the bin should be used in subsequent analysis steps,

**Value**

Returns an `AnnotatedDataFrame` object.

**Author(s)**

Daoud Sie

**References**


### Examples

```r
data("mm10.10kbp.SR50")
assign("bins", get("mm10.10kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

# or

bins <- getBinAnnotations(binSize=10, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")
```

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#### mm10.15kbp.SR50

**Mm10 15kbp bin annotations**

### Description

Bin annotations are calculated for non-overlapping 15kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
- bases: Percentage of non-N nucleotides (of full bin size),
- gc: Percentage of C and G nucleotides (of non-N nucleotides),
- mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
- blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
- residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gn-erre et al. (see references),
- use: Whether the bin should be used in subsequent analysis steps,

### Value

Returns an AnnotatedDataFrame object.

### Author(s)

Daoud Sie
**References**


**Examples**

```r
data("mm10.15kbp.SR50")
assign("bins", get("mm10.15kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

# or

bins <- getBinAnnotations(binSize=15, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")
```

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**mm10.1kbp.SR50**  
*Mm10 1kbp bin annotations*

**Description**

Bin annotations are calculated for non-overlapping 1kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
- bases: Percentage of non-N nucleotides (of full bin size),
- gc: Percentage of C and G nucleotides (of non-N nucleotides),
- mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
- blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
- residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gnirre et al. (see references),
- use: Whether the bin should be used in subsequent analysis steps,

**Value**

Returns an `AnnotatedDataFrame` object.
mm10.30kbp.SR50

Author(s)
Daoud Sie

References


Examples
data("mm10.1kbp.SR50")
assign("bins", get("mm10.1kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")
#

# or

bins <- getBinAnnotations(binSize=1, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

mm10.30kbp.SR50

Mm10 30kb bin annotations

Description
Bin annotations are calculated for non-overlapping 30kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
- bases: Percentage of non-N nucleotides (of full bin size),
- gc: Percentage of C and G nucleotides (of non-N nucleotides),
- mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
- blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
- residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gnirre et al. (see references),
- use: Whether the bin should be used in subsequent analysis steps,
Value

Returns an AnnotatedDataFrame object.

Author(s)

Daoud Sie

References


Examples

data("mm10.30kbp.SR50")
assign("bins", get("mm10.30kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

# or

bins <- getBinAnnotations(binSize=30, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

mm10.500kbp.SR50

Mm10 500kbp bin annotations

Description

Bin annotations are calculated for non overlapping 500kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

• chromosome: Chromosome name,
• start: Base pair start position,
• end: Base pair end position,
• bases: Percentage of non-N nucleotides (of full bin size),
• gc: Percentage of C and G nucleotides (of non-N nucleotides),
• mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
• blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
mm10.50kbp.SR50

- residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gnerre et al. (see references),
- use: Whether the bin should be used in subsequent analysis steps,

**Value**

Returns an `AnnotatedDataFrame` object.

**Author(s)**

Daoud Sie

**References**


**Examples**

```r
data("mm10.500kbp.SR50")
assign("bins", get("mm10.500kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")

# or

bins <- getBinAnnotations(binSize=500, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")
```

**Description**

Bin annotations are calculated for non-overlapping 50kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
- bases: Percentage of non-N nucleotides (of full bin size),
- **gc**: Percentage of C and G nucleotides (of non-N nucleotides),
- **mappability**: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
- **blacklist**: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
- **residual**: Median loess residual calculated from normal C57BL/6J mouse samples from Gnerré et al. (see references),
- **use**: Whether the bin should be used in subsequent analysis steps,

**Value**

Returns an `AnnotatedDataFrame` object.

**Author(s)**

Daoud Sie

**References**


**Examples**

```r
data("mm10.50kbp.SR50")
assign("bins", get("mm10.50kbp.SR50"))
```

```
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")
```

```
# or

bins <- getBinAnnotations(binSize=50, genome="mm10")
```

```
## Not run: readCounts <- binReadCounts(bins=bins, path="./bam")
```
Description

Bin annotations are calculated for non-overlapping 5kbp bins generated as described in Scheinin et al. (see references). The annotated data frame contains:

- chromosome: Chromosome name,
- start: Base pair start position,
- end: Base pair end position,
- bases: Percentage of non-N nucleotides (of full bin size),
- gc: Percentage of C and G nucleotides (of non-N nucleotides),
- mappability: Average mappability of 50mers with a maximum of 2 mismatches as described in by Derrien et al. (see references),
- blacklist: Percent overlap with ENCODE blacklisted regions (unused, ENCODE blacklist data is not available for mouse),
- residual: Median loess residual calculated from normal C57BL/6J mouse samples from Gn erre et al. (see references),
- use: Whether the bin should be used in subsequent analysis steps,

Value

Returns an AnnotatedDataFrame object.

Author(s)

Daoud Sie

References


Examples

data("mm10.5kbp.SR50")
assign("bins", get("mm10.5kbp.SR50"))
## Not run: readCounts <- binReadCounts(bins=bins, path="/bam")

# or

bins <- getBinAnnotations(binSize=5, genome="mm10")
## Not run: readCounts <- binReadCounts(bins=bins, path="/bam")
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