Package ‘QDNAseq.mm10’

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Type Package
Title Bin annotation mm10
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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

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This package provides QDNAseq bin annotations 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
```r
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")
```

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 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**

```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")
```

---

**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 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("mm10.15kbp.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")

---

mm10.1kbp.SR50 Mm10 1kb 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 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("mm10.1kbp.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 30kbp 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**

```r
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")
```

**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

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")

---

**mm10.50kbp.SR50**  **Mm10 50kbp bin annotations**

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 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("mm10.50kbp.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 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("mm10.5kbp.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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