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

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`QDNAseq.mm10-package` *Package QDNAseq.mm10*

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.SR50` *Mm10 1000kbp bin annotations*

Description

Bin annotations are caclulated 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

Fast Computation and Applications of Genome Mappability. Derrien T, Estelle J, Sola S, Knowles D, Raineri E, Guigo R, Ribeca P January 19, 2012 *PLOS ONE* doi: 10.1371/journal.pone.0030377

High-quality draft assemblies of mammalian genomes from massively parallel sequence data. Gnerre S, Maccallum I, Przybylski D, Ribeiro F, Burton J, Walker B, Sharpe T, Hall G, Shea T, Sykes S, Berlin A, Aird D, Costello M, Daza R, Williams L, Nicol R, Gnirke A, Nusbaum C, Lander E, Jaffe D 2011 *Proceedings of the National Academy of Sciences of the United States of America* vol: **108 no. 4** 1512–1518 doi: 10.1073/pnas.1017351108

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")
```

`mm10.100kbp.SR50` *Mm10 100kbp bin annotations*

Description

Bin annotations are caclulated 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

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Examples

```
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")
```

`mm10.10kbp.SR50` *Mm10 10kbp bin annotations*

Description

Bin annotations are caclulated 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

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Examples

```
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")
```

---

mm10.15kbp.SR50 *Mm10 15kbp bin annotations*

Description

Bin annotations are caclulated 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 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

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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 1kbp bin annotations*

Description

Bin annotations are caclulated 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

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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 caclulated 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 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

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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 caclulated 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),
- 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

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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 caclulated 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

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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")
```

`mm10.5kbp.SR50` *Mm10 5kbp bin annotations*

Description

Bin annotations are caclulated 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

DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Scheinin I, Sie D, Bengtsson H, van de Wiel M, Olshen A, van Thuijl H, van Essen H, Eijk P, Rustenburg F, Meijer G, Reijneveld J, Wesseling P, Pinkel D, Albertson D, Ylstra B 2014 *Genome Research* vol: **24 (12)** pp: 1–11

Fast Computation and Applications of Genome Mappability. Derrien T, Estelle J, Sola S, Knowles D, Raineri E, Guigo R, Ribeca P January 19, 2012 *PLOS ONE* doi: 10.1371/journal.pone.0030377

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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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