

Package ‘seqCNA.annot’

February 29, 2024

Type Package

Title Annotation for the copy number analysis of deep sequencing cancer data with seqCNA

Version 1.38.0

Date 2013-03-27

Author David Mosen-Ansorena

Maintainer David Mosen-Ansorena <dmosen.gn@cicbiogune.es>

Import

Depends R (>= 2.10)

Description

Provides annotation on GC content, mappability and genomic features for various genomes

License GPL-3

biocViews Genome, CopyNumberVariationData

git_url <https://git.bioconductor.org/packages/seqCNA.annot>

git_branch RELEASE_3_18

git_last_commit d8179ef

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-02-29

R topics documented:

seqCNA.annot-package	2
hg18	2
hg18_len	3
hg19	3
hg19_len	4
supported.builds	5

Index	6
--------------	----------

seqCNA.annot-package *Annotation for the copy number analysis of deep sequencing cancer data with seqCNA*

Description

Provides annotation on GC content, mappability and genomic features for various genomes

Details

Package: seqCNA.annot
Type: Package
Version: 0.99.0
Date: 2013-03-27
License: GPL-3

Author(s)

David Mosen-Ansorena

Maintainer: David Mosen-Ansorena <dmosen.gn@cicbiogune.es>

hg18 *A table with GC content, mappability and presence of common CNVs for the hg18 human genome build.*

Description

GC content can be used for read count correction, while mappability and CNV information can be used for window filtering.

Usage

```
data(hg18)
```

Format

A data frame with 2881044 observations on the following 3 variables.

GC A numeric vector with the proportion of G and C bases per 1000bp window over the total of non-N bases.

Mapp A numeric vector with the mean mappability of 35-mers within each 1000bp window.

CNV A numeric vector with the proportion of each window affected by the presence of a common CNV (frequency > 0.01).

References

Integrating common and rare genetic variation in diverse human populations. Altshuler DM, Gibbs RA, Brooks LD, McEwen JE. Nature. 2010 Sep 2; 467:52-8

Examples

```
data(hg18)
```

hg18_len	<i>A table with information on chromosome lengths for the hg18 human genome build.</i>
----------	--

Description

The table is used to create genomic windows for the whole chromosome lengths.

Usage

```
data(hg18_len)
```

Format

A data frame with 24 observations on the following 2 variables.

chr A factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8 9 X Y.

length A numeric vector.

Examples

```
data(hg18_len)
```

hg19	<i>A table with GC content, mappability and presence of common CNVs for the hg19 human genome build.</i>
------	--

Description

GC content can be used for read count correction, while mappability and CNV information can be used for window filtering.

Usage

```
data(hg19)
```

Format

A data frame with 2881044 observations on the following 3 variables.

GC A numeric vector with the proportion of G and C bases per 1000bp window over the total of non-N bases.

Mapp A numeric vector with the mean mappability of 35-mers within each 1000bp window.

CNV A numeric vector with the proportion of each window affected by the presence of a common CNV (frequency > 0.01).

References

Integrating common and rare genetic variation in diverse human populations. Altshuler DM, Gibbs RA, Brooks LD, McEwen JE. Nature. 2010 Sep 2; 467:52-8

Examples

```
data(hg19)
```

hg19_len	<i>A table with information on chromosome lengths for the hg19 human genome build.</i>
----------	--

Description

The table is used to create genomic windows for the whole chromosome lengths.

Usage

```
data(hg19_len)
```

Format

A data frame with 24 observations on the following 2 variables.

chr A factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8 9 X Y.

length A numeric vector.

Examples

```
data(hg19_len)
```

<code>supported.builds</code>	<i>Names of the genome builds for which the package contains annotation.</i>
-------------------------------	--

Description

A vector with the names of the genome builds with annotation in the package.

Usage

```
supported.builds()
```

Value

A vector with the names of the genome builds with annotation in the package.

Author(s)

David Mosen-Ansorena

Examples

```
supported.builds()
```

Index

* **Information**

supported.builds, [5](#)

* **datasets**

hg18, [2](#)

hg18_len, [3](#)

hg19, [3](#)

hg19_len, [4](#)

hg18, [2](#)

hg18_len, [3](#)

hg19, [3](#)

hg19_len, [4](#)

seqCNA.annot (seqCNA.annot-package), [2](#)

seqCNA.annot-package, [2](#)

supported.builds, [5](#)