

# Package ‘conumee’

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**Title** Enhanced copy-number variation analysis using Illumina DNA methylation arrays

**Version** 1.10.0

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**Description** This package contains a set of processing and plotting methods for performing copy-number variation (CNV) analysis using Illumina 450k or EPIC methylation arrays.

**Imports** methods, stats, DNACopy, rtracklayer, GenomicRanges, IRanges, GenomeInfoDb

**Depends** R (>= 3.0), minfi,  
IlluminaHumanMethylation450kanno.ilmn12.hg19,  
IlluminaHumanMethylation450kmanifest,  
IlluminaHumanMethylationEPICanno.ilm10b2.hg19,  
IlluminaHumanMethylationEPICmanifest

**Suggests** BiocStyle, knitr, rmarkdown, minfiData, RCurl

**License** GPL (>= 2)

**LazyData** false

**Collate** classes.R annotation.R load.R process.R output.R data.R

**biocViews** CopyNumberVariation, DNAMethylation, MethylationArray, Microarray, Normalization, Preprocessing, QualityControl, Software

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1

**NeedsCompilation** no

## R topics documented:

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|                    |                           |
|--------------------|---------------------------|
| CNV.analysis-class | <i>CNV.analysis class</i> |
|--------------------|---------------------------|

---

## Description

CNV analysis data of a single sample is stored in this class

## Usage

```
## S4 method for signature 'CNV.analysis'
show(object)

## S4 method for signature 'CNV.analysis'
names(x)

## S4 replacement method for signature 'CNV.analysis'
names(x) <- value

## S4 method for signature 'CNV.analysis'
coef(object)
```

## Arguments

|        |  |
|--------|--|
| object | CNV.analysis object                            |
| x      | CNV.analysis object (defined by show generic). |
| value  | Replacement names.                             |

## Details

Use `CNV.fit` to create. Modified by `CNV.bin`, `CNV.detail` and `CNV.segment`.

**Value**

CNV.analysis class.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
anno <- CNV.create_anno()

# create object
x <- CNV.fit(query = d['GroupB_1'], ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno)

# modify object
x <- CNV.bin(x)
x <- CNV.detail(x)
x <- CNV.segment(x)

# general information
x
show(x)

# coefficients of linear regression
coef(x)

# show or replace sample name
names(x)
names(x) <- 'Sample 1'

# output plots
CNV.genomeplot(x)
CNV.genomeplot(x, chr = 'chr6')
#CNV.detailplot(x, name = 'MYCN')
#CNV.detailplot_wrap(x)
CNV.write(x, what = 'segments')
```

---

CNV.anno-class

*CNV.anno class*

---

**Description**

Annotations required for CNV analysis are stored in this class.

**Usage**

```
## S4 method for signature 'CNV.anno'
show(object)
```

**Arguments**

object            CNV.anno object

**Details**

This class does not contain any sample data. Use `CNV.create_anno` to create.

**Value**

CNV.anno class.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# create object
anno <- CNV.create_anno()

# general information
anno
show(anno)
```

---

CNV.bin

*CNV.bin*

---

**Description**

Combine single probe intensity values into predefined bins.

**Usage**

```
CNV.bin(object, ...)
```

## S4 method for signature 'CNV.analysis'  
CNV.bin(object)

**Arguments**

object            CNV.analysis object.  
...                Additional parameters (CNV.bin generic, currently not used).

**Details**

The median intensity per bin is calculated. Bins are defined using `CNV.create_anno`. A value by which all probe and bin intensity values are shifted in subsequent analysis steps is calculated by minimizing the median absolute deviation from all bins to zero (ideally shifting the copy-neutral state to 0).

**Value**

CNV.analysis object.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create object
x <- CNV.fit(query = d['GroupB_1'], ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno)

# modify object
x <- CNV.bin(x)
#x <- CNV.detail(x)
#x <- CNV.segment(x)

# general information
x
show(x)

# coefficients of linear regression
coef(x)

# show or replace sample name
names(x)
names(x) <- 'Sample 1'
```

---

CNV.check

*CNV.check*

---

**Description**

Check intensity values.

**Usage**

```
CNV.check(object)

## S4 method for signature 'CNV.data'
CNV.check(object)
```

**Arguments**

object            CNV.data object.

**Details**

This method checks if intensities are positive and not NA. If not, they are set to 1. Warnings are given if intensities are abnormally high or low (> 50000 or < 5000, respectively).

**Value**

CNV.data object.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

---

|                 |                        |
|-----------------|------------------------|
| CNV.create_anno | <i>CNV.create_anno</i> |
|-----------------|------------------------|

---

**Description**

Create annotations for CNV analysis.

**Usage**

```
CNV.create_anno(bin_minprobes = 15, bin_minsize = 50000,
  bin_maxsize = 5000000, array_type = "450k", chrXY = FALSE,
  exclude_regions = NULL, detail_regions = NULL)
```

**Arguments**

|                 |  |
|-----------------|--|
| bin_minprobes   | numeric. Minimum number of probes per bin. Bins are iteratively merged with neighboring bin until minimum number is reached. |
| bin_minsize     | numeric. Minimum size of a bin.  |
| bin_maxsize     | numeric. Maximum size of a bin. Merged bins that are larger are filtered out.  |
| array_type      | character. One of 450k, EPIC, or overlap. Defaults to 450k.  |
| chrXY           | logical. Should chromosome X and Y be included in the analysis?  |
| exclude_regions | GRanges object or path to bed file containing genomic regions to be excluded.  |
| detail_regions  | GRanges object or path to bed file containing genomic regions to be examined in detail.                                      |

**Details**

This function collects all annotations required for CNV analysis using Illumina 450k or EPIC arrays. The output CNV.anno object is not editable. Rerun CNV.create\_anno to change parameters.

**Value**

CNV.anno object.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# create annotation object
anno <- CNV.create_anno()
anno
```

---

|                 |                        |
|-----------------|------------------------|
| CNV.create_bins | <i>CNV.create_bins</i> |
|-----------------|------------------------|

---

**Description**

Split genome into bins of defined size.

**Usage**

```
CNV.create_bins(hg19.anno, bin_minsize = 50000, hg19.gap, hg19.exclude)
```

**Arguments**

|              |     |
|--------------|-----|
| hg19.anno    | foo |
| bin_minsize  | foo |
| hg19.gap     | foo |
| hg19.exclude | foo |

**Value**

GRanges object.

---

|                |                       |
|----------------|-----------------------|
| CNV.data-class | <i>CNV.data class</i> |
|----------------|-----------------------|

---

**Description**

Intensities of one or multiple samples are stored in this class.

**Usage**

```
## S4 method for signature 'CNV.data'
show(object)

## S4 method for signature 'CNV.data,ANY,ANY,ANY'
x[i]

## S4 method for signature 'CNV.data'
names(x)

## S4 replacement method for signature 'CNV.data'
names(x) <- value
```

**Arguments**

|        |   |
|--------|---|
| object | CNV.data object                               |
| x      | CNV.data object (defined by Extract generic). |
| i      | index. logical, numeric or character.         |
| value  | Replacement names.                            |

**Details**

Use `CNV.load` to create.

**Value**

`CNV.data` class.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# create object
library(minfiData)
data(MsetEx)

d <- CNV.load(MsetEx)

# general information
d
show(d)

# show or replace sample names
names(d)
names(d) <- toupper(names(d))

# subset samples
d[1:2]
```

---

CNV.detail

*CNV.detail*

---

**Description**

Combine single probe values within detail regions.

**Usage**

```
CNV.detail(object, ...)
```

## S4 method for signature 'CNV.analysis'

```
CNV.detail(object)
```

**Arguments**

`object` CNV.analysis object.

... Additional parameters (`CNV.detail` generic, currently not used).

**Details**

The median intensity per detail region is calculated. Detail regions are defined using `CNV.create_anno(detail_bed=)`



**Value**

CNV.analysis object.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create object
x <- CNV.fit(query = d['GroupB_1'], ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno)

# modify object
x <- CNV.bin(x)
x <- CNV.detail(x)
#x <- CNV.segment(x)

# general information
x
show(x)

# coefficients of linear regression
coef(x)

# show or replace sample name
names(x)
names(x) <- 'Sample 1'
```

---

CNV.detailplot

*CNV.detailplot*

---

**Description**

Create CNV plot for detail region.

**Usage**

```
CNV.detailplot(object, ...)

## S4 method for signature 'CNV.analysis'
CNV.detailplot(object, name, yaxt = "l",
  ylim = c(-1.25, 1.25), set_par = TRUE, cols = c("red", "red",
  "lightgrey", "green", "green"))
```

**Arguments**

|         |   |
|---------|---|
| object  | CNV.analysis object.  |
| ...     | Additional parameters (CNV.detailplot generic, currently not used).   |
| name    | character. Name of detail region to plot.   |
| yaxt    | character. Include y-axis? 'l': left, 'r': right, 'n': no. Defaults to 'l'.   |
| ylim    | numeric vector. The y limits of the plot. Defaults to c(-1.25, 1.25).   |
| set_par | logical. Use recommended graphical parameters for oma and mar? Defaults to TRUE. Original parameters are restored afterwards.                         |
| cols    | character vector. Colors to use for plotting intensity levels of bins. Centered around 0. Defaults to c('red', 'red', 'lightgrey', 'green', 'green'). |

**Details**

This method provides the functionality for generating detail regions CNV plots. Probes are shown as dots, bins are shown as lines. See parameters for more information.

**Value**

NULL.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create/modify object
x <- CNV.segment(CNV.detail(CNV.bin(CNV.fit(query = d['GroupB_1'],
  ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno))))

# output plots
CNV.genomeplot(x)
CNV.genomeplot(x, chr = 'chr6')
CNV.detailplot(x, name = 'PTEN')
CNV.detailplot_wrap(x)

# output text files
CNV.write(x, what = 'segments')
CNV.write(x, what = 'detail')
CNV.write(x, what = 'bins')
CNV.write(x, what = 'probes')
```

---

CNV.detailplot\_wrap    *CNV.detailplot\_wrap*

---

### Description

Create CNV plot for all detail regions.

### Usage

```
CNV.detailplot_wrap(object, ...)

## S4 method for signature 'CNV.analysis'
CNV.detailplot_wrap(object, set_par = TRUE,
  main = NULL, ...)
```

### Arguments

|         |   |
|---------|---|
| object  | CNV.analysis object.  |
| ...     | Additional paramters supplied to CNV.detailplot.  |
| set_par | logical. Use recommended graphical parameters for oma and mar? Defaults to TRUE. Original parameters are restored afterwards. |
| main    | character. Title of the plot. Defaults to sample name.  |

### Details

This method is a wrapper of the CNV.detailplot method to plot all detail regions.

### Value

NULL.

### Author(s)

Volker Hovestadt <conumee@hovestadt.bio>

### Examples

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create/modify object
x <- CNV.segment(CNV.detail(CNV.bin(CNV.fit(query = d['GroupB_1'],
  ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno))))

# output plots
CNV.genomeplot(x)
CNV.genomeplot(x, chr = 'chr6')
CNV.detailplot(x, name = 'PTEN')
```

```

CNV.detailplot_wrap(x)

# output text files
CNV.write(x, what = 'segments')
CNV.write(x, what = 'detail')
CNV.write(x, what = 'bins')
CNV.write(x, what = 'probes')

```

---

CNV.fit

*CNV.fit*


---

### Description

Normalize query sample intensities by fitting intensities to reference set using a linear regression model.

### Usage

```

CNV.fit(query, ref, anno, ...)

## S4 method for signature 'CNV.data,CNV.data,CNV.anno'
CNV.fit(query, ref, anno, name = NULL,
        intercept = TRUE)

```

### Arguments

|           |  |
|-----------|--|
| query     | CNV.data object of query sample (single sample).             |
| ref       | CNV.data object of reference set.                            |
| anno      | CNV.anno object. Use CNV.create_anno do create.              |
| ...       | Additional parameters (CNV.fit generic, currently not used). |
| name      | character. Optional parameter to set query sample name.      |
| intercept | logical. Should intercept be considered? Defaults to TRUE.   |

### Details

The log<sub>2</sub> ratio of query intensities versus a linear combination of reference set intensities that best reflects query intensities is calculated (as determined by linear regression). The annotations provided to CNV.fit are saved within the returned CNV.analysis object and used for subsequent analysis steps.

### Value

CNV.analysis object.

### Author(s)

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```

# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create object
x <- CNV.fit(query = d['GroupB_1'], ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno)

# modify object
#x <- CNV.bin(x)
#x <- CNV.detail(x)
#x <- CNV.segment(x)

# general information
x
show(x)

# coefficients of linear regression
coef(x)

# show or replace sample name
names(x)
names(x) <- 'Sample 1'

```

---

CNV.genomeplot

*CNV.genomeplot*


---

**Description**

Create CNV plot for the whole genome or chromosomes.

**Usage**

```
CNV.genomeplot(object, ...)
```

```

## S4 method for signature 'CNV.analysis'
CNV.genomeplot(object, chr = "all", chrX = TRUE,
  chrY = TRUE, centromere = TRUE, detail = TRUE, main = NULL,
  ylim = c(-1.25, 1.25), set_par = TRUE, cols = c("red", "red",
  "lightgrey", "green", "green"))

```

**Arguments**

|        |  |
|--------|--|
| object | CNV.analysis object.   |
| ...    | Additional parameters (CNV.detailplot generic, currently not used).  |
| chr    | character vector. Which chromosomes to plot. Defaults to 'all'.  |
| chrX   | logical. Plot values for chrX? Defaults to TRUE. Set CNV.create_anno(chrXY = FALSE) if chrX and Y should not be included at all. |
| chrY   | logical. Plot values for chrY? Defaults to TRUE.   |

|            |   |
|------------|---|
| centromere | logical. Show dashed lines at centromeres? Defaults to TRUE.  |
| detail     | logical. If available, include labels of detail regions? Defaults to TRUE.  |
| main       | character. Title of the plot. Defaults to sample name.  |
| ylim       | numeric vector. The y limits of the plot. Defaults to c(-1.25, 1.25).   |
| set_par    | logical. Use recommended graphical parameters for oma and mar? Defaults to TRUE. Original parameters are restored afterwards.                         |
| cols       | character vector. Colors to use for plotting intensity levels of bins. Centered around 0. Defaults to c('red', 'red', 'lightgrey', 'green', 'green'). |

### Details

This method provides the functionality for generating CNV plots for the whole genome or defined chromosomes. Bins are shown as dots, segments are shown as lines. See parameters for more information.

### Value

NULL.

### Author(s)

Volker Hovestadt <conumee@hovestadt.bio>

### Examples

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create/modify object
x <- CNV.segment(CNV.detail(CNV.bin(CNV.fit(query = d['GroupB_1'],
  ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno))))

# output plots
CNV.genomeplot(x)
CNV.genomeplot(x, chr = 'chr6')
CNV.detailplot(x, name = 'PTEN')
CNV.detailplot_wrap(x)

# output text files
CNV.write(x, what = 'segments')
CNV.write(x, what = 'detail')
CNV.write(x, what = 'bins')
CNV.write(x, what = 'probes')
```

---

`CNV.load`*CNV.load*

---

**Description**

Prepare combined intensities from various input objects.

**Usage**

```
CNV.load(input, ...)  
  
## S4 method for signature 'GenomicRatioSet'  
CNV.load(input, names = NULL)  
  
## S4 method for signature 'MethylSet'  
CNV.load(input, names = NULL)  
  
## S4 method for signature 'data.frame'  
CNV.load(input, names = NULL)  
  
## S4 method for signature 'matrix'  
CNV.load(input, names = NULL)  
  
## S4 method for signature 'numeric'  
CNV.load(input, names = NULL)
```

**Arguments**

|                    |   |
|--------------------|---|
| <code>input</code> | Object of <code>MethylSet</code> class (minfi package), <code>data.frame</code> class, <code>matrix</code> class or <code>numeric</code> class.   |
| <code>...</code>   | Additional parameters ( <code>CNV.load</code> generic, currently not used).   |
| <code>names</code> | Vector specifying sample names. If not supplied, <code>colnames</code> are used. For <code>MethylSet</code> input, the first column of <code>pData(input)</code> matching <code>'name'</code> (grep) is used. |

**Details**

This method gathers combined intensities of the Methylated and Unmethylated signals for all supplied probes. Probe IDs must be supplied as row names or in a separate column named `'ID_REF'` or `'TargetID'`. If column names match `'intensity'`, only those columns are used. Else, if column names match `'signal'` or `'methylated'`, only those columns are used. Otherwise, all columns are used.

**Value**

`CNV` data object.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
library(minfiData)
d <- CNV.load(MsetEx)
d
```

---

|                |                       |
|----------------|-----------------------|
| CNV.merge_bins | <i>CNV.merge_bins</i> |
|----------------|-----------------------|

---

**Description**

Merge bins containing less than the defined number probes with neighboring bin containing fewer probes.

**Usage**

```
CNV.merge_bins(hg19.anno, hg19.tile, bin_minprobes = 20, hg19.probes,
  bin_maxsize = 5e+06, verbose = FALSE)
```

**Arguments**

|               |     |
|---------------|-----|
| hg19.anno     | foo |
| hg19.tile     | foo |
| bin_minprobes | foo |
| hg19.probes   | foo |
| bin_maxsize   | foo |
| verbose       | foo |

**Value**

GRanges object.

---

|             |                    |
|-------------|--------------------|
| CNV.process | <i>CNV.process</i> |
|-------------|--------------------|

---

**Description**

Given a case index, control indices, CNV.data, and CNV.anno, along with hints about sex chromosomes, call CN for a sample.

**Usage**

```
CNV.process(case, controls, CNdata, anno)
```

```
## S4 method for signature 'integer,integer,CNV.data,CNV.anno'
CNV.process(case, controls,
  CNdata, anno)
```



**Arguments**

|          |                                      |
|----------|--------------------------------------|
| case     | index of the case to process CN for. |
| controls | indices of the control samples.      |
| CNdata   | CNV.data object.                     |
| anno     | CNV.anno object.                     |

**Details**

This method wraps most of conumee, and tries to call sex chromosomes properly using chrX/chrY information derived from the source GenomicRatioSet. For female subjects, chrY is dropped.

**Value**

CNV.analysis object.

**Author(s)**

Tim Triche, Jr. <tim.triche@gmail.com>

---

CNV.segment

*CNV.segment*

---

**Description**

Segment bin values (wrapper of DNACopy package).

**Usage**

```
CNV.segment(object, ...)

## S4 method for signature 'CNV.analysis'
CNV.segment(object, alpha = 0.001, nperm = 50000,
  min.width = 5, undo.splits = "sdundo", undo.SD = 2.2, verbose = 0,
  ...)
```

**Arguments**

|             |  |
|-------------|--|
| object      | CNV.analysis object.   |
| ...         | Additional parameters supplied to the segment method of the DNACopy package. |
| alpha       | See details. Defaults to 0.001.  |
| nperm       | See details. Defaults to 50000.  |
| min.width   | See details. Defaults to 5.  |
| undo.splits | See details. Defaults to 'sdundo'.   |
| undo.SD     | See details. Defaults to 2.2.  |
| verbose     | See details. Defaults to 0.  |

**Details**

This method is a wrapper of the CNA, segment, segments.summary and segments.p methods of the DNACopy package. Please refer to the respective man pages for more detailed information. The default parameters of CNV.segment override some of the default parameters of segment and are optimized for 450k data CNV analysis.

**Value**

CNV.analysis object.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create object
x <- CNV.fit(query = d['GroupB_1'], ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno)

# modify object
x <- CNV.bin(x)
x <- CNV.detail(x)
x <- CNV.segment(x)

# general information
x
show(x)

# coefficients of linear regression
coef(x)

# show or replace sample name
names(x)
names(x) <- 'Sample 1'
```

---

CNV.write

*CNV.write*

---

**Description**

Output CNV analysis results as table.

**Usage**

```
CNV.write(object, ...)
```

```
## S4 method for signature 'CNV.analysis'
CNV.write(object, file = NULL, what = "segments")
```

**Arguments**

|        |   |
|--------|---|
| object | CNV.analysis object.  |
| ...    | Additional parameters (CNV.write generic, currently not used).  |
| file   | Path where output file should be written to. Defaults to NULL: No file is written, table is returned as data.frame object.          |
| what   | character. This should be (an unambiguous abbreviation of) one of 'probes', 'bins', 'detail' or 'segments'. Defaults to 'segments'. |

**Value**

if parameter file is not supplied, the table is returned as a data.frame object.

**Examples**

```
# prepare
library(minfiData)
data(MsetEx)
d <- CNV.load(MsetEx)
data(detail_regions)
anno <- CNV.create_anno(detail_regions = detail_regions)

# create/modify object
x <- CNV.segment(CNV.detail(CNV.bin(CNV.fit(query = d['GroupB_1'],
  ref = d[c('GroupA_1', 'GroupA_2', 'GroupA_3')], anno))))

# output plots
CNV.genomeplot(x)
CNV.genomeplot(x, chr = 'chr6')
CNV.detailplot(x, name = 'PTEN')
CNV.detailplot_wrap(x)

# output text files
CNV.write(x, what = 'segments')
CNV.write(x, what = 'detail')
CNV.write(x, what = 'bins')
CNV.write(x, what = 'probes')
```

---

|                |                       |
|----------------|-----------------------|
| detail_regions | <i>detail_regions</i> |
|----------------|-----------------------|

---

**Description**

Example of genomic regions to be analyzed in detail (e.g. candidate oncogenes/TSGs).

**Details**

Imported using rtracklayer. Raw data stored in inst/extdata/detail\_regions.bed.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

---

|                 |                        |
|-----------------|------------------------|
| exclude_regions | <i>exclude_regions</i> |
|-----------------|------------------------|

---

**Description**

Example of genomic regions to exclude (e.g. known polymorphic regions).

**Details**

Imported using `rtracklayer`. Raw data stored in `inst/extdata/exclude_regions.bed`.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

---

|               |                      |
|---------------|----------------------|
| read.450k.url | <i>read.450k.url</i> |
|---------------|----------------------|

---

**Description**

Read IDAT files from the web.

**Usage**

```
read.450k.url(url = NULL, idat = NULL)
```

**Arguments**

|                   |   |
|-------------------|---|
| <code>url</code>  | URL of the directory in which the IDAT files are located.   |
| <code>idat</code> | Vector of IDAT names. <code>url</code> and <code>idat</code> default to the TCGA example described in the vignette. |

**Details**

This method downloads the provided list of IDAT files to a temporary folder (using the `Rcurl` package). It then uses the `'read.450k.exp'` method of the `'minfi'` package.

**Value**

`RGChannelSet` object.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

**Examples**

```
RGsetTCGA <- read.450k.url()
```

---

`tbl_ucsc``tbl_ucsc`

---

**Description**

UCSC tables required for creating annotation object.

**Details**

Imported using `rtracklayer::browserSession('UCSC'): chromInfo, gap, cytoBand`.

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

---

`tcgaBRCA.sentrinx2name` *tcgaBRCA.sentrinx2name*

---

**Description**

Named vector for Sentrinx ID to TCGA ID conversion of breast cancer example data (see README).

**Details**

Based on [https://tcga-data.nci.nih.gov/tcgafiles/ftp\\_auth/distro\\_ftpusers/anonymous/tumor/brca/cg](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/brca/cg)

**Author(s)**

Volker Hovestadt <conumee@hovestadt.bio>

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