

# Package ‘PREDA’

March 30, 2021

**Version** 1.36.0

**Title** Position Related Data Analysis

**Author** Francesco Ferrari <francesco.ferrari@ifom.eu>

**Maintainer** Francesco Ferrari <francesco.ferrari@ifom.eu>

**License** GPL-2

**Depends** R (>= 2.9.0), Biobase, lokern (>= 1.0.9), multtest, stats, methods, annotate

**Suggests** quantsmooth, qvalue, limma, caTools, affy, PREDAsampledata

**Enhances** Rmpi, rsprng

**Description** Package for the position related analysis of quantitative functional genomics data.

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**biocViews** Software, CopyNumberVariation, GeneExpression, Genetics

**git\_url** <https://git.bioconductor.org/packages/PREDA>

**git\_branch** RELEASE\_3\_12

**git\_last\_commit** bf51167

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2021-03-29

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analysesNames

*Get the names of the analyses in the from PREDA objects***Description**

Get the names of the analyses in the from StatisticsForPREDA objects, PREDAResults objects and objects from classes extending these classes.

**Usage**

```
analysesNames(.Object)
```

**Arguments**

`.Object` an object of class `StatisticsForPREDA`, `PREDAResults` or any other class extending these classes

**Value**

Character vector of `analysesNames`

**Author(s)**

Francesco Ferrari

**See Also**

["StatisticsForPREDA"](#), ["PREDAResults"](#)

**Examples**

```
require(PREDAsampledata)
data(SODEGIRGEanalysisResults)
analysesNames(SODEGIRGEanalysisResults)
```

---

```
computeDatasetSignature
```

*Function to compute dataset signature for recurrent significant genomic regions*

---

**Description**

Function to compute dataset signature for recurrent significant genomic regions

**Usage**

```
# computeDatasetSignature(.Object, genomicRegionsList=genomicRegionsList,
# multTestCorrection="fdr", signature_qval_threshold=0.05,
# returnRegions=TRUE, use.referencePositions=TRUE)

computeDatasetSignature(.Object, ...)
```

**Arguments**

`.Object` Object of class `GenomicAnnotationsForPREDA`

`...` See below

**genomicRegionsList:** List of `genomicRegions` objects for which the recurrent overlapping regions will be evaluated

**multTestCorrection:** Multiple testing correction that will be adopted to correct the statistic p-values. Possible values are "fdr", for benjamini and Hochberg multiple testing correction and "qvalue" for p-values correction performed with qvalue package.

**signature\_qual\_threshold:** Threshold used to select significant regions resulting from the dataset signature statistic

**returnRegions:** Logical, if TRUE (default) the genomic regions constituting the dataset signature are returned, otherwise a PREDAResults object containing dataset signature statistics is returned.

**use.referencePositions:** Logical, if TRUE the input reference positions used for PREDA analysis will be used to identify significant genomic regions boundaries as well.

## Details

The function adopts a binomial test to identify significant recurrence of genomic regions across multiple dataset samples.

## Value

A GenomicRegions object (if returnRegions = TRUE) or a PREDAResults object containing dataset signature statistics (if returnRegions = FALSE)

## Author(s)

Francesco Ferrari

## See Also

[GenomicRegions](#), [PREDAResults](#)

## Examples

```
## Not run:

require(PREDAsampledData)
data(SODEGIRCNanalysisResults)
data(GEDataForPREDA)

SODEGIR_CN_GAIN<-PREDAResults2GenomicRegions(
SODEGIRCNanalysisResults, qual.threshold=0.01,
smoothStatistic.tail="upper", smoothStatistic.threshold=0.1)

CNgain_signature<-computeDatasetSignature(GEDataForPREDA,
genomicRegionsList=SODEGIR_CN_GAIN)

## End(Not run)
```

---

DataForPREDA-class	<i>Class "DataForPREDA" is used to manage all of the data required as input for PREDA analysis</i>
--------------------	--

---

### Description

This class is used to manage all of the data required as input for PREDA analysis: it is usually created by merging a GenomicAnnotationsForPREDA and a StatisticsForPREDA classes

### Objects from the Class

Objects can be created by calls of the form `new("DataForPREDA", ids, chr, start, end, strand, chromosomesNumbers`

### Slots

**position:** Object of class "integer" ~~

**ids:** Object of class "character" a character vector of unique identifiers for the genomic features under investigation

**chr:** Object of class "integer" a numeric vector representing the chromosome where each ids is mapped. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromsosomees X and Y will be converted to chromosomes 23 and 24 respectively. User defined options will allow this conversion during GenomicAnnotations objects initialization.

**start:** Object of class "integer" a numeric vector of start genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).

**end:** Object of class "integer" a numeric vector of end genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).

**strand:** Object of class "numeric" a numeric vector of strand genomic position for each genomic feature under investigation: value 1 is used for "plus" (forward) strand and value -1 for "minus" (reverse) strand. User defined options will allow the conversion to this format during GenomicAnnotations objects initialization.

**chromosomesNumbers:** Object of class "numeric" a numeric vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in increasing order. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromsosomees X and Y will be converted to chromosomes 23 and 24 respectively.

**chromosomesLabels:** Object of class "character" a character vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in the same order as reported in chromosomesNumbers slot. This slot is actually used just to provide a label for each associated chromosome number, in case that some non numeric chromosome is used (e.g. to preserve the correspondence between chr 23 and the actual chr X in Human)

**optionalAnnotations:** Object of class "matrix" optional annotations associated to the genomic features can be managed along with genomic positions annotations. E.g. GeneSymbol or EntrezGene ids can be associated to gene related GenomicAnnotaitons objects. These additional annotations are not mandatory (the default value for this slot is NULL) The additional annotations must be provided as a matrix of character, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "optionalAnnotationsHeaders" slot.

**optionalAnnotationsHeaders:** Object of class "character" character vector containing the names associated to optional annotations. Please avoid using spaces in annotations names.

**statistic:** Object of class "matrix" a numeric matrix containing gene-centered statistics (or statistics on genomic data centered on other genomic features under investigation). The statistics must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.

**analysesNames:** Object of class "character" a character vector of unique names associated to each column of statistic matrix. This is just a name that will be used to identify each analysis.

**testedTail:** Object of class "character" a character describing what tail of the statistic distribution will be analyzed during PREDA analysis. Possible values are "upper", "lower" or "both". Anyway we strongly recommend using PREDA analysis only for statistics on genomic data with a symmetric distribution around zero.

## Extends

Class "[GenomicAnnotationsForPREDA](#)", directly. Class "[StatisticsForPREDA](#)", directly. Class "[GenomicAnnotations](#)", by class "[GenomicAnnotationsForPREDA](#)", distance 2.

## Methods

**DataForPREDA2dataframe** signature(.Object = "DataForPREDA"): extract data and annotations as a dataframe with probeids as rownames

**DataForPREDA2GenomicAnnotationsForPREDA** signature(.Object = "DataForPREDA"): extract a [GenomicAnnotationsForPREDA](#) object from a data [DataForPREDA](#) object

**DataForPREDA2StatisticsForPREDA** signature(.Object = "DataForPREDA"): extract a [StatisticsForPREDA](#) object from a data [DataForPREDA](#) object

**GenomicAnnotationsFilter\_neg** signature(.Object = "DataForPREDA"): filter annotations to remove selected chromosomes

**GenomicAnnotationsFilter\_pos** signature(.Object = "DataForPREDA"): filter annotations to keep selected chromosomes

**GenomicAnnotationsSortAndCleanNA** signature(.Object = "DataForPREDA"): sort annotations according to selected chromosomes and to remove genes containing any NA annotation field

**initialize** signature(.Object = "DataForPREDA"): initialize method for [DataForPREDA](#) objects

**StatisticsForPREDAFilterColumns\_neg** signature(.Object = "DataForPREDA"): filter statistics to remove selected analyses

**StatisticsForPREDAFilterColumns\_pos** signature(.Object = "DataForPREDA"): filter statistics to keep selected analyses

## Note

This class is better described in the package vignette

## Author(s)

Francesco Ferrari

## See Also

["GenomicAnnotations"](#), ["GenomicAnnotationsForPREDA"](#), ["StatisticsForPREDA"](#), [DataForPREDA2dataframe](#), [DataForPREDA2GenomicAnnotationsForPREDA](#), [DataForPREDA2StatisticsForPREDA](#), [GenomicAnnotationsFilter\\_neg](#), [GenomicAnnotationsFilter\\_pos](#), [GenomicAnnotationsSortAndCleanNA](#), [StatisticsForPREDAFilterColumns\\_neg](#), [StatisticsForPREDAFilterColumns\\_pos](#)

**Examples**

```
showClass("DataForPREDA")
```

---

```
DataForPREDA2dataframe
```

*extract data and annotations as a dataframe*

---

**Description**

extract data and annotations as a dataframe with probeids as rownames

**Usage**

```
DataForPREDA2dataframe(.Object)
```

**Arguments**

.Object            An object of class DataForPREDA

**Details**

extract data and annotations as a dataframe with probeids as rownames

**Value**

a dataframe with probeids as rownames

---

```
DataForPREDA2GenomicAnnotationsForPREDA
```

*extract a GenomicAnnotationsForPREDA object from a data DataForPREDA object*

---

**Description**

extract a GenomicAnnotationsForPREDA object from a data DataForPREDA object

**Usage**

```
DataForPREDA2GenomicAnnotationsForPREDA(.Object)
```

**Arguments**

.Object            an object of class DataForPREDA

**Details**

extract a GenomicAnnotationsForPREDA object from a data DataForPREDA object

**Value**

a GenomicAnnotationsForPREDA object



---

DataForPREDA2StatisticsForPREDA

*extract a StatisticsForPREDA object from a data DataForPREDA object*

---

**Description**

extract a StatisticsForPREDA object from a data DataForPREDA object

**Usage**

DataForPREDA2StatisticsForPREDA(.Object)

**Arguments**

.Object            a data DataForPREDA object

**Details**

extract a StatisticsForPREDA object from a data DataForPREDA object

**Value**

a StatisticsForPREDA object

---

DataForPREDAMedianCenter

*Function to scale median value of DataForPREDA statistics to zero*

---

**Description**

Function to scale median value of DataForPREDA statistics to zero

**Usage**

DataForPREDAMedianCenter(.Object, ...)

**Arguments**

.Object            a DataForPREDA object  
...

**Details**

Scale median value of DataForPREDA statistics to zero

**Value**

a DataForPREDA object

---

eset2GenomicAnnotations

*Function building a GenomicAnnotations object on an ExpressionSet object*

---

## Description

Function building a GenomicAnnotations object on an ExpressionSet object

## Usage

```
# eset2GenomicAnnotations(.Object, retain.chrs,  
# optionalAnnotations)
```

```
eset2GenomicAnnotations(.Object, ...)
```

## Arguments

`.Object` ExpressionSet object. The associated annotation library will be used to build a GenomicAnnotations object.

`...` See below

**retain.chrs:** Numeric vector, containing the list of chromosomes selected for the output GenomicAnnotations object. E.g. set `retain.chrs=1:22` to limit the GenomicAnnotations object to chromosomes from 1 to 22. This might be useful to limit GenomicAnnotations objects to autosomic chromosomes.

**optionalAnnotations:** Character vector to select additional annotations fields to be included into the GenomicAnnotations object.

## Value

An object of class "[GenomicAnnotations](#)"

## Author(s)

Francesco Ferrari

## See Also

["GenomicAnnotations"](#)

## Examples

```
## Not run:  
require("PREDAsampledData")  
data(ExpressionSetRCC)  
  
GEGenomicAnnotations<-eset2GenomicAnnotations(ExpressionSetRCC,  
retain.chrs=1:22)  
  
## End(Not run)
```

genomePlot

*draw a genome plot***Description**

draw a genome plot with user defined genomic regions

**Usage**

```
# genomePlot(.Object, genomicRegions=NULL, draw.blocks=TRUE,
# parallel.plot=TRUE, grouping=NULL, custom.labels=NULL,
# scale.positions=NULL, qval.threshold=0.05,
# use.referencePositions=FALSE, smoothStatistic.tail=NULL,
# smoothStatistic.threshold=NULL, region.colors=NULL,
# limitChrs=NULL)

genomePlot(.Object, ...)
```

**Arguments**

.Object	Object of class GenomicAnnotationsForPREDA, or any other class extending this one.
...	See below

**genomicRegions:** A list of GenomicRegions object containing the genomic regions to be highlighted in the plot.

**draw.blocks:** If TRUE genomic regions are plotted as blocks. Otherwise they are plotted as coloured ticks. Currently only draw.blocks=TRUE is implemented.

**parallel.plot:** Logical, if TRUE multiple copies of each chromosome are drawn.  
In particular a number of copies equal to length(grouping), if grouping is not null, or a number of copies equal to the number of GenomicRegions objects provided as input.

**grouping:** Vector specifying how input GenomicRegions objects will be grouped on chromosomes.

**custom.labels:** A character to specify user defined labels for vertical axis

**scale.positions:** Parameter to set the scale for chromosomal positions (horizontal axis). Possible values are "Mb" or "Kb"

**qval.threshold:** If genomicRegions is NULL, and a PREDAResults or PREDADataAndResults is provided as input, the function PREDAResults2GenomicRegions is applied with this parameter to extract significant GenomicRegions.

**use.referencePositions:** If genomicRegions is NULL, and a PREDAResults or PREDADataAndResults is provided as input, the function PREDAResults2GenomicRegions is applied with this parameter to extract significant GenomicRegions.

**smoothStatistic.tail:** If genomicRegions is NULL, and a PREDAResults or PREDADataAndResults is provided as input, the function PREDAResults2GenomicRegions is applied with this parameter to extract significant GenomicRegions.

**smoothStatistic.threshold:** If genomicRegions is NULL, and a PREDAResults or PREDADataAndResults is provided as input, the function PREDAResults2GenomicRegions is applied with this parameter to extract significant GenomicRegions.

**region.colors:** Character vector specifying the list of colors to be used for drawing each set of GenomicRegions. Must be of length equal to the number of GenomicRegions objects provided as input.

**limitChrs:** Numeric vector, that can be used to limit the plot to a subset of chromosomes.

## Details

See also the PREDA tutorial vignette for more details and sample usage

## Value

A plot of the genome with significant GenomicRegions

## Author(s)

Francesco Ferrari

## See Also

[PREDAResults2GenomicRegions](#), [PREDAResults](#), [PREDADataAndResults](#), [GenomicAnnotationsForPREDA](#)

## Examples

```
## See PREDA tutorial vignette for some examples
```

---

GenomicAnnotations-class

*Class "GenomicAnnotations" to manage information about genomic features*

---

## Description

This class is used to manage information about genomic features under investigation: i.e. genomic genes, SNP or others, with particular focus on the genomic coordinates of each of them. Other additional annotations associated to each element can be stored in a GenomicAnnotations object in the optionalAnnotations slots

## Objects from the Class

Objects can be created by calls of the form `new("GenomicAnnotations", ids, chr, start, end, strand, chromosomesN`

**Slots**

ids: Object of class "character" ~~  
 chr: Object of class "integer" ~~  
 start: Object of class "integer" ~~  
 end: Object of class "integer" ~~  
 strand: Object of class "numeric" ~~  
 chromosomesNumbers: Object of class "numeric" ~~  
 chromosomesLabels: Object of class "character" ~~  
 optionalAnnotations: Object of class "matrix" ~~  
 optionalAnnotationsHeaders: Object of class "character" ~~

**Methods**

**GenomicAnnotations2dataframe** signature(.Object = "GenomicAnnotations"): extracts annotations as a dataframe with probeids as rownames

**GenomicAnnotations2GenomicAnnotationsForPREDA** signature(.Object = "GenomicAnnotations"): generate a new GenomicAnnotationsForPREDA object from a GenomicAnnotations object

**GenomicAnnotations2reference\_positions** signature(.Object = "GenomicAnnotations"): extract from the GenomicAnnotations object a vector containing a vector with reference positions

**GenomicAnnotationsExtract** signature(.Object = "GenomicAnnotations"): extract optional annotations for a specific region

**GenomicAnnotationsFilter\_neg** signature(.Object = "GenomicAnnotations"): filter annotations to remove selected chromosomes

**GenomicAnnotationsFilter\_pos** signature(.Object = "GenomicAnnotations"): filter annotations to keep selected chromosomes

**GenomicAnnotationsSortAndCleanNA** signature(.Object = "GenomicAnnotations"): sort annotations according to selected chromosomes and to remove genes containing any NA annotation field

**GenomicRegionsAnnotate** signature(.Object1 = "GenomicRegions", .Object2 = "GenomicAnnotations"): extract annotations from a GenomicAnnotations object for a set of regions specified as a GenomicRegions object

**initialize** signature(.Object = "GenomicAnnotations"): initialize method for GenomicAnnotations objects

**Note**

This class is better described in the package vignette

**Author(s)**

Francesco Ferrari

**See Also**

[GenomicAnnotations2dataframe](#), [GenomicAnnotations2GenomicAnnotationsForPREDA](#), [GenomicAnnotations2reference\\_positions](#), [GenomicAnnotationsFilter\\_neg](#), [GenomicAnnotationsFilter\\_pos](#), [GenomicAnnotationsSortAndCleanNA](#), [GenomicRegionsAnnotate](#)

**Examples**

```
showClass("GenomicAnnotations")
```

---

```
GenomicAnnotations2dataframe
      extracts annotations as a dataframe
```

---

**Description**

extracts annotations as a dataframe with probeids as rownames

**Usage**

```
GenomicAnnotations2dataframe(.Object)
```

**Arguments**

.Object            A GenomicAnnotations object

**Details**

extract annotations as a dataframe with probeids as rownames

**Value**

a dataframe with probeids as rownames

---

```
GenomicAnnotations2GenomicAnnotationsForPREDA
      generate a GenomicAnnotationsForPREDA object from a Genomi-
      cAnnotations object
```

---

**Description**

generate a new GenomicAnnotationsForPREDA object from a GenomicAnnotations object

**Usage**

```
# GenomicAnnotations2GenomicAnnotationsForPREDA(.Object,
# positions=NULL, reference_position_type=NULL)
```

```
GenomicAnnotations2GenomicAnnotationsForPREDA(.Object,
... )
```

**Arguments**

.Object      An object of class GenomicAnnotations  
 ...          See below  
**positions:** Vector to specify reference positions for GenomicAnnotationsForPREDA object if not specified with reference\_position\_type parameter  
**reference\_position\_type:** Specify which genomic coordinate must be used as reference position for PREDA analysis. Possible values are "start", "end", "median", "strand.start" or "strand.end".  
 "strand.start" is strand specific start: i.e. start on positive strand but end on negative strand. "strand.end" is strand specific end.

**Value**

A GenomicAnnotationsForPREDA object

**Author(s)**

Francesco Ferrari

**See Also**

[GenomicAnnotationsForPREDA](#)

**Examples**

```
## Not run:

GEGenomicAnnotations<-GenomicAnnotationsFromLibrary(annotLibrary
= "org.Hs.eg.db", retain.chrs=1:22)

GEGenomicAnnotationsForPREDA<-
GenomicAnnotations2GenomicAnnotationsForPREDA(
GEGenomicAnnotations, reference_position_type="median")

## End(Not run)
```

---

GenomicAnnotations2reference\_positions

*extract reference positions from the GenomicAnnotations*

---

**Description**

extract from the GenomicAnnotations object a vector containing a vector with reference positions

**Usage**

```
# GenomicAnnotations2reference_positions(.Object,
# reference_position_type=c("start", "end", "median", "strand.start", "strand.end"),
# withnames=TRUE)

GenomicAnnotations2reference_positions(.Object, ...)
```

**Arguments**

.Object      Object of class GenomicAnnotations  
 ...          See below

**reference\_position\_type:** Specify which genomic coordinate must be used as reference position for PREDA analysis. Possible values are "start", "end", "median", "strand.start" or "strand.end".  
 "strand.start" is strand specific start: i.e. start on positive strand but end on negative strand. "strand.end" is strand specific end.

**withnames:** Logical, if TRUE the "ids" slot content is used as names for the output vector

**Value**

A numeric vector with the selected reference positions.

---

GenomicAnnotationsExtract

*extract optional annotations for a specific region*

---

**Description**

extract optional annotations for a specific region

**Usage**

```
# GenomicAnnotationsExtract(.Object, chr, start, end,
# AnnotationsHeader=NULL, sep.character="; ",
# complete.inclusion=FALSE, skipSorting=FALSE,
# annotationAsRange=FALSE, getJustFeaturesNumber=FALSE)
```

```
GenomicAnnotationsExtract(.Object, ...)
```

**Arguments**

.Object      An object of class GenomicAnnotations  
 ...          See below

**chr:** Coordinate for the selected genomic region  
**start:** Coordinate for the selected genomic region  
**end:** Coordinate for the selected genomic region  
**AnnotationsHeader:** Character or numeric vector to select the annotations columns to be considered  
**sep.character:** Character used to separate annotated features in the output  
**complete.inclusion:** Logical, if TRUE only annotated features completely included in the region are reported. If FALSE (default), every overlapping the feature is considered.  
**skipSorting:** Logical, if TRUE, annotation sorting is skipped before processing output (to save computational time, e.g. in a long loop)  
**annotationAsRange:** If TRUE, then only the first and last annotated element in the region are reported  
**getJustFeaturesNumber:** Logical: if TRUE, just the number of annotated features in the region is returned



**Details**

Extract annotations associated to a specific genomic region from a GenomiAnnotations object. Only annotations from the specified columns are returned.

**Value**

A character vector is returned

**See Also**

["GenomicAnnotations"](#)

---

GenomicAnnotationsFilter\_neg

*filter annotations to remove selected chromosomes*

---

**Description**

filter annotations to remove selected chromosomes

**Usage**

```
# GenomicAnnotationsFilter_neg(.Object, chrToRemove, chrAsLabels=FALSE)
```

```
GenomicAnnotationsFilter_neg(.Object, ...)
```

**Arguments**

`.Object` An object of class `GenomicAnnotations` or classes inheriting from `GenomicAnnotations`

`...` See below

**chrToRemove:** List of chromosomes to be removed from the annotations object.

**chrAsLabels:** Logical, TRUE if chromosomes are listed as their character labels, instead of using the numeric indexes

---

GenomicAnnotationsFilter\_pos

*filter annotations to keep selected chromosomes*

---

**Description**

filter annotations to keep selected chromosomes

**Usage**

```
# GenomicAnnotationsFilter_pos(.Object, chrToRetain, chrAsLabels=FALSE)
```

```
GenomicAnnotationsFilter_pos(.Object, ...)
```

**Arguments**

- .Object      An object of class GenomicAnnotations or classes inheriting from GenomicAnnotations
- ...          See below
- chrToRetain:** List of chromosomes to be maintained after removing the annotations for all the other chromosomes.
- chrAsLabels:** Logical, TRUE if chromosomes are listed as their character labels, instead of using the numeric indexes

---

**GenomicAnnotationsForPREDA-class**

*Class "GenomicAnnotationsForPREDA" GenomicAnnotations class with additional slot specifying the reference position for PREDA analysis*

---

**Description**

This class is equivalent to the GenomicAnnotations class but includes an additional slot specifying the reference position that will be used for PREDA smoothing of data: this is included in the "position" slot. A unique reference position is required for PREDA analysis because this position is used for smoothing data along chromosomal coordinates. This reference position usually is the start, the end, or the median position of each considered genomic feature, nevertheless other user defined positions could be used as well.

**Objects from the Class**

Objects can be created by calls of the form `new("GenomicAnnotationsForPREDA", ids, chr, start, end, strand, chromo`

**Slots**

- position:** Object of class "integer" a numeric vector of reference genomic positions that will be associated and used for each genomic feature under investigation for smoothing data during PREDA analysis.
- ids:** Object of class "character" a character vector of unique identifiers for the genomic features under investigation
- chr:** Object of class "integer" a numeric vector representing the chromosome where each ids is mapped. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromosomes X and Y will be converted to chromosomes 23 and 24 respectively. User defined options will allow this conversion during GenomicAnnotations objects initialization.
- start:** Object of class "integer" a numeric vector of start genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).
- end:** Object of class "integer" a numeric vector of end genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).
- strand:** Object of class "numeric" a numeric vector of strand genomic position for each genomic feature under investigation: value 1 is used for "plus" (forward) strand and value -1 for "minus" (reverse) strand. User defined options will allow the conversion to this format during GenomicAnnotations objects initialization.

**chromosomesNumbers:** Object of class "numeric" a numeric vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in increasing order. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromosomes X and Y will be converted to chromosomes 23 and 24 respectively.

**chromosomesLabels:** Object of class "character" a character vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in the same order as reported in chromosomesNumbers slot. This slot is actually used just to provide a label for each associated chromosome number, in case that some non numeric chromosome is used (e.g. to preserve the correspondence between chr 23 and the actual chr X in Human)

**optionalAnnotations:** Object of class "matrix" optional annotations associated to the genomic features can be managed along with genomic positions annotations. E.g. GeneSymbol or EntrezGene ids can be associated to gene related GenomicAnnotations objects. These additional annotations are not mandatory (the default value for this slot is NULL) The additional annotations must be provided as a matrix of character, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "optionalAnnotationsHeaders" slot.

**optionalAnnotationsHeaders:** Object of class "character" character vector containing the names associated to optional annotations. Please avoid using spaces in annotations names.

## Extends

Class "[GenomicAnnotations](#)", directly.

## Methods

**genomePlot** signature(.Object = "GenomicAnnotationsForPREDA"): draw a genome plot

**GenomicAnnotations2dataframe** signature(.Object = "GenomicAnnotationsForPREDA"): extract annotations as a dataframe with probeids as rownames

**GenomicAnnotationsFilter\_neg** signature(.Object = "GenomicAnnotationsForPREDA"): filter annotations to remove selected chromosomes

**GenomicAnnotationsFilter\_pos** signature(.Object = "GenomicAnnotationsForPREDA"): filter annotations to keep selected chromosomes

**GenomicAnnotationsForPREDA2dataframe** signature(.Object = "GenomicAnnotationsForPREDA"): extract annotations as a dataframe with probeids as rownames

**GenomicAnnotationsForPREDA2GenomicAnnotations** signature(.Object = "GenomicAnnotationsForPREDA"): extract the GenomicAnnotations object from the GenomicAnnotationsForPREDA object

**GenomicAnnotationsForPREDA2PREDAResults** signature(.Object = "GenomicAnnotationsForPREDA"): add PREDA results information to genomic annotations creating a PREDAResults object

**GenomicAnnotationsSortAndCleanNA** signature(.Object = "GenomicAnnotationsForPREDA"): sort annotations according to selected chromosomes and to remove genes containing any NA annotation field

**initialize** signature(.Object = "GenomicAnnotationsForPREDA"): initialize method for GenomicAnnotationsForPREDA objects

## Note

This class is better described in the package vignette

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicAnnotations"](#), [GenomicAnnotationsSortAndCleanNA](#), [GenomicAnnotationsForPREDA2PREDAResults](#), [GenomicAnnotationsForPREDA2dataframe](#), [GenomicAnnotationsFilter\\_pos](#), [GenomicAnnotationsFilter\\_neg](#), [GenomicAnnotationsFilter\\_pos\\_neg](#)

**Examples**

```
showClass("GenomicAnnotationsForPREDA")
```

---

```
GenomicAnnotationsForPREDA2dataframe
      extract annotations as a dataframe
```

---

**Description**

extract annotations as a dataframe with probeids as rownames

**Usage**

```
GenomicAnnotationsForPREDA2dataframe(.Object)
```

**Arguments**

`.Object` an object of class `GenomicAnnotationsForPREDA`

**Details**

extract annotations from an object of class `GenomicAnnotationsForPREDA` as a dataframe with probeids as rownames

**Value**

a dataframe with probeids as rownames

---

```
GenomicAnnotationsForPREDA2GenomicAnnotations
      extract the GenomicAnnotations object from the GenomicAnnotations-
      ForPREDA object
```

---

**Description**

extract the `GenomicAnnotations` object from the `GenomicAnnotationsForPREDA` object

**Usage**

```
GenomicAnnotationsForPREDA2GenomicAnnotations(.Object)
```

**Arguments**

`.Object` an object of class `GenomicAnnotationsForPREDA`

---

```
GenomicAnnotationsForPREDA2PREDAResults
    add PREDA results information to genomic annotations creating a
    PREDAResults object
```

---

### Description

add PREDA results information to genomic annotations creating a PREDAResults object

### Usage

```
# GenomicAnnotationsForPREDA2PREDAResults(.Object, analysesNames, testedTail, smoothStatistic, pvalue)
GenomicAnnotationsForPREDA2PREDAResults(.Object, ...)
```

### Arguments

.Object	An object of class GenomicAnnotationsForPREDA
...	See below
	<b>analysesNames:</b> analysesNames as in PREDAResults object
	<b>testedTail:</b> testedTail as in PREDAResults object
	<b>smoothStatistic:</b> smoothStatistic as in PREDAResults object
	<b>pvalue:</b> pvalue as in PREDAResults object
	<b>qvalue:</b> qvalue as in PREDAResults object

---

```
GenomicAnnotationsForPREDAFromFile
    Function to create a GenomicAnnotationsForPREDA object from a txt
    file
```

---

### Description

Function to create a GenomicAnnotationsForPREDA object from a txt file

### Usage

```
GenomicAnnotationsForPREDAFromFile(file, ids_column, chr_column,
start_column, end_column, strand_column, chromosomesNumbers =
NULL, chromosomesLabels = NULL, chromosomesLabelsInput = NULL,
MinusStrandString = "-", PlusStrandString = "+",
optionalAnnotationsColumns = NULL, reference_position_type =
"median", ...)
```

**Arguments**

<code>file</code>	Path to the input txt file containing genomic annotations
<code>ids_column</code>	Specify the column from the input txt file with gene (or other genomic features) ids. Can be specified using column index (numeric) or column name (character).
<code>chr_column</code>	Specify the column from the input txt file with chromosome annotations fields for each ids. Can be specified using column index (numeric) or column name (character).
<code>start_column</code>	Specify the column from the input txt file with genomic start position for each genomic element. Can be specified using column index (numeric) or column name (character).
<code>end_column</code>	Specify the column from the input txt file with genomic end position for each genomic element. Can be specified using column index (numeric) or column name (character).
<code>strand_column</code>	Specify the column from the input txt file with genomic strand mapping for each genomic element. Can be specified using column index (numeric) or column name (character).
<code>chromosomesNumbers</code>	Numeric vector to specify the list of numeric values to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
<code>chromosomesLabels</code>	Character vector to specify the list of character labels to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
<code>chromosomesLabelsInput</code>	Character vector to specify the list of character labels associated to each chromosome in the input file. Particularly useful when non numeric character strings are associated to each chromosome in the input file: e.g. "chr3" for chromosome "3".
<code>MinusStrandString</code>	Character string used to identify minus strand in the input text file
<code>PlusStrandString</code>	Character string used to identify plus strand in the input text file
<code>optionalAnnotationsColumns</code>	Character vector of columns headers or numeric vector of columns indices to specify columns of the input file containing additional annotation fields
<code>reference_position_type</code>	Character string to specify which genomic coordinate must be used as reference position for PREDA analysis. See also " <a href="#">GenomicAnnotations2GenomicAnnotationsForPREDA</a> "
<code>...</code>	any other parameter for read.table function that could be useful for parsing the input file, such as "sep", "quote", "header", "na.strings" and other parameters.

**Value**

An object of class "[GenomicAnnotationsForPREDA](#)"

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicAnnotationsForPREDA"](#)

**Examples**

```
## Not run:

data(PREDAsampledata)
CNdataPath <- system.file("sampledata", "CopyNumber", package =
"PREDAsampledata")
CNannotationFile <- file.path(CNdataPath , "SNPAnnot100k.csv")

CNGenomicsAnnotations<-GenomicAnnotationsForPREDAFromfile(
  file=CNannotationFile,
  ids_column=1,
  chr_column="Chromosome",
  start_column=4,
  end_column=4,
  strand_column="Strand",
  chromosomesLabelsInput=1:22,
  MinusStrandString="-", PlusStrandString="+",
  optionalAnnotationsColumns=c("Cytoband", "Entrez_gene"),
  header=TRUE, sep=",", quote="\\"", na.strings = c("NA", "",
"---"))

## End(Not run)
```

---

GenomicAnnotationsFromdataframe

*Function to create a GenomiAnnotations object from a dataframe*

---

**Description**

Function to create a GenomiAnnotations object from a dataframe

**Usage**

```
GenomicAnnotationsFromdataframe(GenomicAnnotations_dataframe, ids_column, chr_column,
start_column, end_column, strand_column, chromosomesNumbers =
NULL, chromosomesLabels = NULL, chromosomesLabelsInput = NULL,
MinusStrandString = "-", PlusStrandString =
"+", optionalAnnotationsColumns = NULL)
```

**Arguments**

**GenomicAnnotations\_dataframe**  
Dataframe object containing genomic annotations.

**ids\_column**  
Specify the column from the input txt file with gene (or other genomic features) ids. Can be specified using column index (numeric) or column name (character).

chr_column	Specify the column from the input txt file with chromosome annotations fields for each ids. Can be specified using column index (numeric) or column name (character).
start_column	Specify the column from the input txt file with genomic start position for each genomic element. Can be specified using column index (numeric) or column name (character).
end_column	Specify the column from the input txt file with genomic end position for each genomic element. Can be specified using column index (numeric) or column name (character).
strand_column	Specify the column from the input txt file with genomic strand mapping for each genomic element. Can be specified using column index (numeric) or column name (character).
chromosomesNumbers	Numeric vector to specify the list of numeric values to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabels	Character vector to specify the list of character labels to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabelsInput	Character vector to specify the list of character labels associated to each chromosome in the input file. Particularly useful when non numeric character strings are associated to each chromosome in the input file: e.g. "chr3" for chromosome "3".
MinusStrandString	Character string used to identify minus strand in the input text file
PlusStrandString	Character string used to identify plus strand in the input text file
optionalAnnotationsColumns	Character vector of columns headers or numeric vector of columns indices to specify columns of the input file containing additional annotation fields

**Value**

An object of class "[GenomicAnnotations](#)"

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicAnnotations"](#)



---

 GenomicAnnotationsFromFile

*Function to create a GenomiAnnotations object from a text file*


---

## Description

Function to create a GenomiAnnotations object from a text file

## Usage

```
GenomicAnnotationsFromFile(file, ids_column, chr_column,
  start_column, end_column, strand_column, chromosomesNumbers =
  NULL, chromosomesLabels = NULL, chromosomesLabelsInput = NULL,
  MinusStrandString = "-", PlusStrandString =
  "+", optionalAnnotationsColumns = NULL, ...)
```

## Arguments

file	Path to the input txt file containing genomic annotations
ids_column	Specify the column from the input txt file with gene (or other genomic features) ids. Can be specified using column index (numeric) or column name (character).
chr_column	Specify the column from the input txt file with chromosome annotations fields for each ids. Can be specified using column index (numeric) or column name (character).
start_column	Specify the column from the input txt file with genomic start position for each genomic element. Can be specified using column index (numeric) or column name (character).
end_column	Specify the column from the input txt file with genomic end position for each genomic element. Can be specified using column index (numeric) or column name (character).
strand_column	Specify the column from the input txt file with genomic strand mapping for each genomic element. Can be specified using column index (numeric) or column name (character).
chromosomesNumbers	Numeric vector to specify the list of numeric values to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabels	Character vector to specify the list of character labels to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabelsInput	Character vector to specify the list of character labels associated to each chromosome in the input file. Particularly useful when non numeric character strings are associated to each chromosome in the input file: e.g. "chr3" for chromosome "3".
MinusStrandString	Character string used to identify minus strand in the input text file

PlusStrandString  
 Character string used to identify plus strand in the input text file

optionalAnnotationsColumns  
 Character vector of columns headers or numeric vector of columns indices to specify columns of the input file containing additional annotation fields

...  
 any other parameter for read.table function that could be useful for parsing the input file, such as "sep", "quote", "header", "na.strings" and other parameters.

**Value**

An object of class "[GenomicAnnotations](#)"

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicAnnotations"](#)

**Examples**

```
## Not run:

data(PREDAsampledata)
CNdataPath <- system.file("sampledata", "CopyNumber", package =
"PREDAsampledata")
CNannotationFile <- file.path(CNdataPath , "SNPAnnot100k.csv")

CNGenomicsAnnotations<-GenomicAnnotationsForPREDAFromfile(
  file=CNannotationFile,
  ids_column=1,
  chr_column="Chromosome",
  start_column=4,
  end_column=4,
  strand_column="Strand",
  chromosomesLabelsInput=1:22,
  MinusStrandString="-", PlusStrandString="+",
  optionalAnnotationsColumns=c("Cytoband", "Entrez_gene"),
  header=TRUE, sep=",", quote="\"", na.strings = c("NA", "",
"---"))

## End(Not run)
```

---

GenomicAnnotationsFromLibrary

*Function extracting a GenomicAnnotations object from a Bioconductor annotation library*

---

**Description**

Function extracting a GenomicAnnotations object from a Bioconductor annotation library

**Usage**

```
GenomicAnnotationsFromLibrary(annotLibrary, probeIDs = NULL,  
retain.chrs = NULL, optionalAnnotations = NULL)
```

**Arguments**

annotLibrary	Character string containing the name of the annotations library to be used for building the GenomicAnnotations object
probeIDs	Optional: list of reference id from the selected annotLibrary to be used for building the GenomicAnnotations object
retain.chrs	Numeric vector, containing the list of chromosomes selected for the output GenomicAnnotations object. E.g. set retain.chrs=1:22 to limit the GenomicAnnotations object to chromosomes from 1 to 22. This might be useful to limit GenomicAnnotations objects to autosomic chromosomes.
optionalAnnotations	Character vector to select additional annotations fields to be included into the GenomicAnnotations object.

**Value**

An object of class "[GenomicAnnotations](#)"

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicAnnotations"](#)

**Examples**

```
## Not run:  
  
GEGenomicAnnotations<-GenomicAnnotationsFromLibrary(annotLibrary=  
"org.Hs.eg.db", retain.chrs=1:22)  
  
# with optional annotations Genesymbols and EntrezGeneIDs  
GEGenomicAnnotations<-GenomicAnnotationsFromLibrary(annotLibrary=  
"hgu133plus2.db", retain.chrs=1:22,  
optionalAnnotations=c("SYMBOL", "ENTREZID"))  
  
## End(Not run)
```

---

GenomicAnnotationsSortAndCleanNA

*sort annotations according to selected chromosomes and to remove genes containing any NA annotation field*

---

### Description

sort annotations according to selected chromosomes and to remove genes containing any NA annotation field

### Usage

```
# GenomicAnnotationsSortAndCleanNA(.Object, sorting_position_column="start")
```

```
GenomicAnnotationsSortAndCleanNA(.Object, ...)
```

### Arguments

`.Object` An object of class `GenomicAnnotations` or any object inheriting from `GenomicAnnotations`

`...` See below

**sorting\_position\_column:** Annotations slot used to sort data within each chromosome. Possible values include "start", "end" or "position" (the last one for `GenomicAnnotationsForPREDA` objects)

---

GenomicRegions-class *Class "GenomicRegions" is used to manage information about genomic regions*

---

### Description

This class is used to manage genomic regions information that can be derived from PREDA analysis results or from other sources: e.g. relevant genomic regions from literature reports can be imported into a `GenomicRegions` object and compared with PREDA analysis results

### Objects from the Class

Objects can be created by calls of the form `new("GenomicRegions", chr, start, end, chromosomesNumbers, chromosomes)`

### Slots

**chr:** Object of class "integer" a numeric vector representing the chromosome where each genomic region is located. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromosomes X and Y will be converted to chromosomes 23 and 24 respectively. User defined options will allow this conversion during `GenomicAnnotations` objects initialization.

**start:** Object of class "integer" a numeric vector of start genomic position for each genomic region. This vector must have the same length of "chr" slot.

- end:** Object of class "integer" a numeric vector of end genomic position for each genomic region. This vector must have the same length of "chr" slot.
- chromosomesNumbers:** Object of class "numeric" a numeric vector containing the list of chromosomes associated to genomic regions in the GenomicRegions object. Each chromosome is represented just once in increasing order. Please note that chromosomes usually not represented with a number will be converted to a number as well. e.g. for Human, chromosomes X and Y will be converted to chromosomes 23 and 24 respectively.
- chromosomesLabels:** Object of class "character" a character vector containing the list of chromosomes associated to genomic regions in the GenomicRegions object. Each chromosome is represented just once in the same order as reported in chromosomesNumbers slot. This slot is actually used just to provide a label for each associated chromosome number, in case that some non numeric chromosome is used (e.g. to preserve the correspondence between chr 23 and the actual chr X in Human)
- optionalAnnotations:** Object of class "matrix" optional annotations associated to the genomic regions can be managed along with GenomicRegions objects. E.g. the list of GeneSymbol or EntrezGene ids associated to each genomic region can be provided as optional annotation. These additional annotations are not mandatory (the default value for this slot is NULL) The additional annotations must be provided as a matrix of character, with a number of rows equal to the length of "chr", "start" and "end" slots and a number of columns equal to the length of "optionalAnnotationsHeaders" slot.
- optionalAnnotationsHeaders:** Object of class "character" the list of names associated to optional annotations. Please avoid using spaces in annotations names.
- ids:** Object of class "character" a character vector of unique identifiers associated to each genomic regions. This is just an optional element of GenomicRegions objects: the default value is NULL.

## Methods

- GenomicRegions2dataframe** signature(.Object = "GenomicRegions"): extract genomic regions information as a dataframe object
- GenomicRegionsAnnotate** signature(.Object1 = "GenomicRegions", .Object2 = "GenomicAnnotations"): extract annotations from a GenomicAnnotations object for a set of regions specified as a GenomicRegions object
- GenomicRegionsChrNumber** signature(.Object = "GenomicRegions"): determine the number of chromosomes with genomic regions
- GenomicRegionsComparison** signature(.Object1 = "GenomicRegions", .Object2 = "GenomicRegions"): compare GenomicRegions objects to identify overlaps
- GenomicRegionsCreateRegionsIds** signature(.Object = "GenomicRegions"): generate unique ids for GenomicRegions objects
- GenomicRegionsFilter\_neg** signature(.Object = "GenomicRegions"): filter genomic regions to remove selected chromosomes
- GenomicRegionsFilter\_pos** signature(.Object = "GenomicRegions"): filter genomic regions to keep selected chromosomes
- GenomicRegionsNumber** signature(.Object = "GenomicRegions"): determine the number of genomic regions
- GenomicRegionsSpan** signature(.Object = "GenomicRegions"): determine the span of each genomic region
- GenomicRegionsTotalSpan** signature(.Object = "GenomicRegions"): determine the total span of genomic regions

**initialize** signature(.Object = "GenomicRegions"): initialize method for GenomicRegions objects

**Note**

This class is better described in the package vignette

**Author(s)**

Francesco Ferrari

**See Also**

[GenomicAnnotationsSortAndCleanNA,PREDDataAndResults2dataframe](#)

**Examples**

```
showClass("GenomicRegions")
```

---

GenomicRegions2dataframe

*extract genomic regions information as a dataframe object*

---

**Description**

extract genomic regions information as a dataframe object

**Usage**

```
GenomicRegions2dataframe(GenomicRegionsObject)
```

**Arguments**

GenomicRegionsObject  
Object of class genomic regions

**Details**

Extract genomic regions information as a dataframe object

**Value**

A dataframe object

**Author(s)**

Francesco Ferrari

**Examples**

```
## Not run:
require(PREDAsampledata)

data(GEanalysisResults)

genomic_regions_UP<-PREDAResults2GenomicRegions(GEanalysisResults
, qval.threshold=0.05, smoothStatistic.tail="upper",
smoothStatistic.threshold=0.5)

dataframe_UPregions<-GenomicRegions2dataframe(
genomic_regions_UP[[1]])

## End(Not run)
```

---

**GenomicRegionsAnnotate**

*extract annotations from a GenomicAnnotations object for a set of regions specified as a GenomicRegions object*

---

**Description**

extract annotations from a GenomicAnnotations object for a set of regions specified as a GenomicRegions object

**Usage**

```
# GenomicRegionsAnnotate(.Object1, .Object2,
# AnnotationsHeaders=NULL, sep.character=";",
# complete.inclusion=FALSE, annotationAsRange=FALSE,
# getJustFeaturesNumber=FALSE)

GenomicRegionsAnnotate(.Object1, .Object2, ...)
```

**Arguments**

.Object1	An object of class GenomicRegions
.Object2	An object of class GenomicAnnotations
...	See below

**AnnotationsHeaders:** Names of optional annotations fields from GenomicAnnotations object that are used to annotate the GenomicRegions object. Multiple annotation fields can be used

**sep.character:** Character sequence used to separate annotation features

**complete.inclusion:** Logical, if TRUE only annotations features entirely covered by one of the genomic regions are considered. (e.g. a gene completely included in the genomic regions from start to end) If FALSE also partial overlapping annotation features are used

**annotationAsRange:** Logical, if TRUE only the first and last annotation features associated to each the genomic region are returned

**getJustFeaturesNumber:** Logical, if TRUE only the numbers of annotation features overlapping the genomic regions are returned. If TRUE, only the first element specified with AnnotationsHeaders parameter is considered.

### Details

The annotation features overlapping the input genomic regions are used to add optional annotations field to the GenomicRegions object.

If previous optional annotations fields are present, they are preserved as well in the output object

### Value

A GenomicRegions object with optionalAnnotations

---

GenomicRegionsChrNumber

*determine the number of chromosomes with genomic regions*

---

### Description

determine the number of chromosomes with genomic regions

### Usage

```
GenomicRegionsChrNumber(.Object)
```

### Arguments

.Object            An object of class GenomicRegions

---

GenomicRegionsComparison

*compare GenomicRegions objects to identify overlaps and differences*

---

### Description

compare GenomicRegions objects to identify overlaps and differences

### Usage

```
GenomicRegionsComparison(.Object1, .Object2)
```

### Arguments

.Object1            An object of Class GenomicRegions

.Object2            An object of Class GenomicRegions



**Details**

Compare GenomicRegions objects to identify overlaps and differences

**Value**

A list containing:

overlapping.regions

GenomicRegions object describing the overlapping regions between input object1 and object2

difference.1.2 GenomicRegions object describing the regions from input object1 not overlapping regions from object2

difference.2.1 GenomicRegions object describing the regions from input object2 not overlapping regions from object1

GenomicRegions1.number

Number of genomic regions in input object1

GenomicRegions2.number

Number of genomic regions in input object2

overlapping.number

Number of overlapping genomic regions between input object1 and object2

GenomicRegions1.totalspan

Total span of genomic regions in input object1

GenomicRegions2.totalspan

Total span of genomic regions in input object2

overlapping.totalspan

Total span of overlapping genomic regions between input object1 and object2

overlap.VS.GenomicRegions1.ratio

Ratio between overlapping regions and regions from input object1

overlap.VS.GenomicRegions2.ratio

Ratio between overlapping regions and regions from input object2

**Author(s)**

Francesco Ferrari

**See Also**

[GenomicRegionsFindOverlap](#), [GenomicRegions](#)

---

GenomicRegionsCreateRegionsIds

*generate unique ids for GenomicRegions objects*

---

**Description**

generate unique ids for GenomicRegions objects

**Usage**

GenomicRegionsCreateRegionsIds(.Object, ...)

**Arguments**

.Object            An object of class GenomicRegions  
 ...

---

GenomicRegionsFilter\_neg

*filter genomic regions to remove selected chromosomes*

---

**Description**

filter genomic regions to remove selected chromosomes

**Usage**

```
# GenomicRegionsFilter_neg(.Object, chrToRemove, chrAsLabels=FALSE, quiet=FALSE)
```

```
GenomicRegionsFilter_neg(.Object, ...)
```

**Arguments**

.Object            An object of class GenomicRegions  
 ...                See below

**chrToRemove:** List of chromosomes to be removed from the genomic regions object.

**chrAsLabels:** Logical, TRUE if chromosomes are listed as their character labels, instead of using the numeric indexes

**quiet:** Logical, if FALSE a message is printed to warn of empty (NULL) result of the filtering selection.

---

GenomicRegionsFilter\_pos

*filter genomic regions to keep selected chromosomes*

---

**Description**

filter genomic regions to keep selected chromosomes

**Usage**

```
# GenomicRegionsFilter_pos(.Object, chrToRetain, chrAsLabels=FALSE, quiet=FALSE)
```

```
GenomicRegionsFilter_pos(.Object, ...)
```

**Arguments**

.Object	An object of class GenomicRegions
...	See below
	<b>chrToRetain:</b> List of chromosomes to be maintained after removing the genomic regions for all the other chromosomes.
	<b>chrAsLabels:</b> Logical, TRUE if chromosomes are listed as their character labels, instead of using the numeric indexes
	<b>quiet:</b> Logical, if FALSE a message is printed to warn of empty (NULL) result of the filtering selection.

---

 GenomicRegionsFindOverlap

*Function to find overlap between GenomicRegions objects*


---

**Description**

Function to find overlap between GenomicRegions objects

**Usage**

```
GenomicRegionsFindOverlap(GenomicRegions1, GenomicRegions2 = NULL)
```

**Arguments**

GenomicRegions1	Either a GenomicRegions object or a list of GenomicRegions objects
GenomicRegions2	Optional with default value NULL. Either a GenomicRegions object or a list of GenomicRegions objects.

**Details**

Input genomic regions object are compared to select overlapping genomic regions that are returned as GenomicRegions objects.

If two single GenomicRegions object are provided, just one comparison is performed and one single GenomicRegions object is returned.

If one single list of GenomicRegions objects is provided as input, then the included GenomicRegions objects are compared to select overlapping GenomicRegions across all of the elements.

If two lists of GenomicRegions objects are provided as input, they must have the same number of elements, because element by element comparison will be performed to identify overlapping GenomicRegions across all of the elements.

**Value**

Either a single GenomicRegions object or a list of GenomicRegions objects.

**Author(s)**

Francesco Ferrari

**See Also**

[GenomicRegionsComparison](#), [GenomicRegions](#)

**Examples**

```
## Not run:
require(PREDAsampledata)
data(SODEGIRCNanalysisResults)
data(SODEGIRGEanalysisResults)

SODEGIR_GE_UP<-PREDAResults2GenomicRegions(
SODEGIRGEanalysisResults, qval.threshold=0.05,
smoothStatistic.tail="upper", smoothStatistic.threshold=0.5)

SODEGIR_CN_GAIN<-PREDAResults2GenomicRegions(
SODEGIRCNanalysisResults, qval.threshold=0.01,
smoothStatistic.tail="upper", smoothStatistic.threshold=0.1)

SODEGIR_AMPLIFIED<-GenomicRegionsFindOverlap(SODEGIR_GE_UP,
SODEGIR_CN_GAIN)

## End(Not run)
```

---

GenomicRegionsFromdataframe

*Function to create a GenomiRegions object from a dataframe*

---

**Description**

Function to create a GenomiRegions object from a dataframe

**Usage**

```
GenomicRegionsFromdataframe(GenomicRegions_dataframe, ids_column=NULL, chr_column,
start_column, end_column, chromosomesNumbers=NULL,
chromosomesLabels=NULL, chromosomesLabelsInput=NULL)
```

**Arguments**

GenomicRegions_dataframe	Dataframe object containing the annotations for genomic regions
ids_column	Specify the column from the input dataframe with (optional) ids for genomic regions. Can be specified using column index (numeric) or column name (character).
chr_column	Specify the column from the input dataframe with chromosome annotations fields. Can be specified using column index (numeric) or column name (character).
start_column	Specify the column from the input dataframe with genomic start position for each genomic region. Can be specified using column index (numeric) or column name (character).

end_column	Specify the column from the input dataframe with genomic end position for each genomic region. Can be specified using column index (numeric) or column name (character).
chromosomesNumbers	Numeric vector to specify the list of numeric values to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabels	Character vector to specify the list of character labels to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabelsInput	Character vector to specify the list of character labels associated to each chromosome in the input. Particularly useful when non numeric character strings are associated to each chromosome in the input file: e.g. "chr3" for chromosome "3".

**Value**

An object of class "[GenomicRegions](#)"

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicRegions"](#)

---

GenomicRegionsFromFile

*Function to create a GenomiRegions object from a text file*

---

**Description**

Function to create a GenomiRegions object from a text file

**Usage**

```
GenomicRegionsFromFile(file, ids_column=NULL, chr_column,
start_column, end_column, chromosomesNumbers=NULL,
chromosomesLabels=NULL, chromosomesLabelsInput=NULL, ...)
```

**Arguments**

file	Path to the input txt file containing genomic regions annotations
ids_column	Specify the column from the input txt file with (optional) ids for genomic regions. Can be specified using column index (numeric) or column name (character).
chr_column	Specify the column from the input txt file with chromosome annotations fields. Can be specified using column index (numeric) or column name (character).

start_column	Specify the column from the input txt file with genomic start position for each genomic region. Can be specified using column index (numeric) or column name (character).
end_column	Specify the column from the input txt file with genomic end position for each genomic region. Can be specified using column index (numeric) or column name (character).
chromosomesNumbers	Numeric vector to specify the list of numeric values to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabels	Character vector to specify the list of character labels to be associated to each chromosome (especially useful for chromosomes not associated to a number such as chr X or Y)
chromosomesLabelsInput	Character vector to specify the list of character labels associated to each chromosome in the input file. Particularly useful when non numeric character strings are associated to each chromosome in the input file: e.g. "chr3" for chromosome "3".
...	any other parameter for read.table function that could be useful for parsing the input file, such as "sep", "quote", "header", "na.strings" and other parameters.

**Value**

An object of class "[GenomicRegions](#)"

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicRegions"](#)

---

GenomicRegionsNumber *determine the number of genomic regions*

---

**Description**

determine the number of genomic regions

**Usage**

```
GenomicRegionsNumber(.Object)
```

**Arguments**

.Object      An object of class GenomicRegions

---

GenomicRegionsSpan     *determine the span of each genomic region*

---

**Description**

determine the span of each genomic region

**Usage**

```
GenomicRegionsSpan(.Object, ...)
```

**Arguments**

.Object     An object of class GenomicRegions  
...

---

GenomicRegionsTotalSpan  
*determine the total span of genomic regions*

---

**Description**

determine the total span of genomic regions

**Usage**

```
GenomicRegionsTotalSpan(.Object, ...)
```

**Arguments**

.Object     Object of Class GenomicRegions  
...

---

getStatisticByName     *extract data for individual analyses using the analysis name*

---

**Description**

extract data for individual analyses using the analysis name

**Usage**

```
# getStatisticByName(.Object, analysisName)  
getStatisticByName(.Object, ...)
```

**Arguments**

- .Object            An object of class StatisticsForPREDA
- ...                See below
- analysisName:** Character name of the analysis to be returned

---

MergeStatisticAnnotations2DataForPREDA

*Merge a StatisticsForPREDA and a GenomicAnnotationsForPREDA object into a DataForPREDA object.*

---

**Description**

This function merges a StatisticsForPREDA and a GenomicAnnotationsForPREDA object into a DataForPREDA object

**Usage**

```
MergeStatisticAnnotations2DataForPREDA(StatisticsForPREDAObject,
GenomicAnnotationsForPREDAObject, sortAndCleanNA = FALSE, quiet =
FALSE, MedianCenter = FALSE)
```

**Arguments**

- StatisticsForPREDAObject  
An object of class StatisticsForPREDA
- GenomicAnnotationsForPREDAObject  
An object of class GenomicAnnotationsForPREDA
- sortAndCleanNA Logical, if TRUE, genomic annotations are sorted for chromosome and genomic position then ids with NA positional annotations are removed
- quiet            Logical, if TRUE messages reporting the number of unmatched ids are suppressed.
- MedianCenter   Logical, if TRUE data are normalized per median sample.

**Value**

An object of class DataForPREDA

**Author(s)**

Francesco Ferrari



---

PREDADataAndResults-class

*Class "PREDADataAndResults" is used to manage the PREDA analysis output*

---

## Description

This class is used to manage the PREDA analysis output along with corresponding input data

## Objects from the Class

Objects can be created by calls of the form `new("PREDADataAndResults", ids, chr, start, end, strand, chromosomes)`

## Slots

**analysesNames:** Object of class "character" a character vector of unique names associated to each column of smoothStatistic, pvalue and qvalue matrices. This is just a name that is used to identify each analysis.

**testedTail:** Object of class "character" a character describing what tail of the statistic distribution will be analyzed during PREDA analysis. Possible values are "upper", "lower" or "both". Anyway we strongly recommend using PREDA analysis only

**smoothStatistic:** Object of class "matrix" a numeric matrix containing smoothed observed statistics as obtained from PREDA analysis. The smoothed statistics must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.

**pvalue:** Object of class "matrix" a numeric matrix containing unadjusted gene-centered pvalues as obtained from PREDA analysis. The pvalue matrix must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.

**qvalue:** Object of class "matrix" a numeric matrix containing adjusted gene-centered pvalues as obtained from PREDA analysis: i.e. usually FDR adjusted pvalues, but other multiple testing methods could be adopted as well The qvalue matrix must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.

**position:** Object of class "integer" a numeric vector of reference genomic positions that will be associated and used for each genomic feature under investigation for smoothing data during PREDA analysis.

**ids:** Object of class "character" a character vector of unique identifiers for the genomic features under investigation

**chr:** Object of class "integer" a numeric vector representing the chromosome where each ids is mapped. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromosomes X and Y will be converted to chromosomes 23 and 24 respectively. User defined options will allow this conversion during GenomicAnnotations objects initialization.

**start:** Object of class "integer" a numeric vector of start genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).

**end:** Object of class "integer" a numeric vector of end genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).

**strand:** Object of class "numeric" a numeric vector of strand genomic position for each genomic feature under investigation: value 1 is used for "plus" (forward) strand and value -1 for "minus" (reverse) strand. User defined options will allow the conversion to this format during GenomicAnnotations objects initialization.

**chromosomesNumbers:** Object of class "numeric" a numeric vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in increasing order. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromsosomees X and Y will be converted to chromsomes 23 and 24 respectively.

**chromosomesLabels:** Object of class "character" a character vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in the same order as reported in chromosomesNumbers slot. This slot is actually used just to provide a label for each associated chromosome number, in case that some non numeric chromosome is used (e.g. to preserve the correspondence between chr 23 and the actual chr X in Human)

**optionalAnnotations:** Object of class "matrix" optional annotations associated to the genomic features can be managed along with genomic positions annotations. E.g. GeneSymbol or EntrezGene ids can be associated to gene related GenomicAnnotations objects. These additional annotations are not mandatory (the default value for this slot is NULL) The additional annotations must be provided as a matrix of character, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "optionalAnnotationsHeaders" slot.

**optionalAnnotationsHeaders:** Object of class "character" character vector containing the names associated to optional annotations. Please avoid using spaces in annotations names.

**statistic:** Object of class "matrix" a numeric matrix containing gene-centered statistics (or statistics on genomic data centered on other genomic features under investigation). The statistics must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.

## Extends

Class "PREDAResults", directly. Class "DataForPREDA", directly. Class "GenomicAnnotationsForPREDA", by class "PREDAResults", distance 2. Class "StatisticsForPREDA", by class "DataForPREDA", distance 2. Class "GenomicAnnotations", by class "PREDAResults", distance 3.

## Methods

**GenomicAnnotationsSortAndCleanNA** signature(.Object = "PREDADataAndResults"): sort annotations according to selected chromosomes and to remove genes containing any NA annotation field

**initialize** signature(.Object = "PREDADataAndResults"): initialize method for PREDADataAndResults objects

**PREDADataAndResults2dataframe** signature(.Object = "PREDADataAndResults"): extract data and annotations as a dataframe with probeids as rownames

## Note

This class is better described in the package vignette

## Author(s)

Francesco Ferrari

**See Also**

["GenomicAnnotations"](#), ["GenomicAnnotationsForPREDA"](#), ["StatisticsForPREDA"](#), ["DataForPREDA"](#), ["PREDAResults"](#), [GenomicAnnotationsSortAndCleanNA](#), [PREDADataAndResults2dataframe](#)

**Examples**

```
showClass("PREDADataAndResults")
```

PREDADataAndResults2dataframe

*extract data and annotations as a dataframe with probeids as rownames*

**Description**

extract data and annotations as a dataframe with probeids as rownames

**Usage**

```
PREDADataAndResults2dataframe(.Object)
```

**Arguments**

.Object            An object of class PREDADataAndResults

PREDAResults-class

*Class "PREDAResults" ~is used to manage the PREDA analysis output*

**Description**

this class is used to manage the basic PREDA analysis output including smoothened statistic, pvalues and qvalues.

**Objects from the Class**

Objects can be created by calls of the form `new("PREDAResults", ids, chr, start, end, strand, chromosomesNumbers`

**Slots**

**analysesNames:** Object of class "character" a character vector of unique names associated to each column of smoothStatistic, pvalue and qvalue matrices. This is just a name that is used to identify each analysis.

**testedTail:** Object of class "character" a character describing what tail of the statistic distribution will be analyzed during PREDA analysis. Possible values are "upper", "lower" or "both". Anyway we strongly recommend using PREDA analysis only

**smoothStatistic:** Object of class "matrix" a numeric matrix containing smoothed observed statistics as obtained from PREDA analysis. The smoothed statistics must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.

- pvalue:** Object of class "matrix" a numeric matrix containing unadjusted gene-centered pvalues as obtained from PREDA analysis. The pvalue matrix must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.
- qvalue:** Object of class "matrix" a numeric matrix containing adjusted gene-centered pvalues as obtained from PREDA analysis: i.e. usually FDR adjusted pvalues, but other multiple testing methods could be adopted as well. The qvalue matrix must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.
- position:** Object of class "integer" a numeric vector of reference genomic positions that will be associated and used for each genomic feature under investigation for smoothing data during PREDA analysis.
- ids:** Object of class "character" a character vector of unique identifiers for the genomic features under investigation
- chr:** Object of class "integer" a numeric vector representing the chromosome where each ids is mapped. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromosomes X and Y will be converted to chromosomes 23 and 24 respectively. User defined options will allow this conversion during GenomicAnnotations objects initialization.
- start:** Object of class "integer" a numeric vector of start genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).
- end:** Object of class "integer" a numeric vector of end genomic position for each genomic feature under investigation (i.e. gene, transcript, SNP or other elements).
- strand:** Object of class "numeric" a numeric vector of strand genomic position for each genomic feature under investigation: value 1 is used for "plus" (forward) strand and value -1 for "minus" (reverse) strand. User defined options will allow the conversion to this format during GenomicAnnotations objects initialization.
- chromosomesNumbers:** Object of class "numeric" a numeric vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in increasing order. Please note that chromosome usually not represented with a number must will be converted to a number as well. e.g. for Human, chromosomes X and Y will be converted to chromosomes 23 and 24 respectively.
- chromosomesLabels:** Object of class "character" a character vector containing the list of chromosomes for which genomic annotations are provided in the GenomicAnnotations object. Each chromosome is represented just once in the same order as reported in chromosomesNumbers slot. This slot is actually used just to provide a label for each associated chromosome number, in case that some non numeric chromosome is used (e.g. to preserve the correspondence between chr 23 and the actual chr X in Human)
- optionalAnnotations:** Object of class "matrix" optional annotations associated to the genomic features can be managed along with genomic positions annotations. E.g. GeneSymbol or EntrezGene ids can be associated to gene related GenomicAnnotations objects. These additional annotations are not mandatory (the default value for this slot is NULL) The additional annotations must be provided as a matrix of character, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "optionalAnnotationsHeaders" slot.
- optionalAnnotationsHeaders:** Object of class "character" character vector containing the names associated to optional annotations. Please avoid using spaces in annotations names.

## Extends

Class "[GenomicAnnotationsForPREDA](#)", directly. Class "[GenomicAnnotations](#)", by class "[GenomicAnnotationsForPREDA](#)", distance 2.

**Methods**

- GenomicAnnotationsSortAndCleanNA** signature(.Object = "PREDAResults"): sort annotations according to selected chromosomes and to remove genes containing any NA annotation field
- initialize** signature(.Object = "PREDAResults"): initialize method for PREDAResults objects
- PREDAResults2dataframe** signature(.Object = "PREDAResults"): extract preda results statistics as a data frame object
- PREDAResults2GenomicRegions** signature(.Object = "PREDAResults"): identify significant genomic regions from a PREDAResults object
- PREDAResults2GenomicRegionsSingle** signature(.Object = "PREDAResults"): identify significant genomic regions from a single analysis in a PREDAResults object
- PREDAResults2PREDADDataAndResults** signature(.Object = "PREDAResults"): merge PREDAResults and input statistics to create a PREDADDataAndResults object
- PREDAResultsGetObservedFlags** signature(.Object = "PREDAResults"): extract genomic positions with significant alterations as a matrix of flags from a PREDAResults object

**Note**

This class is better described in the package vignette

**Author(s)**

Francesco Ferrari

**See Also**

["GenomicAnnotations"](#), ["GenomicAnnotationsForPREDA"](#), [GenomicAnnotationsSortAndCleanNA](#), [PREDAResults2dataframe](#), [PREDAResults2GenomicRegions](#), [PREDAResults2GenomicRegionsSingle](#), [PREDAResults2PREDADDataAndResults](#), [PREDAResultsGetObservedFlags](#)

**Examples**

```
showClass("PREDAResults")
```

---

PREDAResults2dataframe

*extract preda results statistics as a data frame object*

---

**Description**

extract preda results statistics as a data frame object

**Usage**

```
PREDAResults2dataframe(.Object)
```

**Arguments**

.Object            An object of class PREDAResults

---

```
PREDAResults2GenomicRegions
```

*identify significant genomic regions from a PREDAResults object*

---

## Description

identify significant genomic regions from a PREDAResults object

## Usage

```
# PREDAResults2GenomicRegions(.Object, qual.threshold=0.05,
# use.referencePositions=TRUE, smoothStatistic.tail=NULL,
# smoothStatistic.threshold=NULL)
```

```
PREDAResults2GenomicRegions(.Object, ...)
```

## Arguments

`.Object` Object of class PREDAResults or PREDADataAndResults

`...` See below

**qual.threshold:** q-value threshold used to identify significant genomic regions

**use.referencePositions:** Logical, if TRUE the input reference positions used for PREDA analysis will be used to identify significant genomic regions boundaries as well.

**smoothStatistic.tail:** Possible values are "upper" or "lower". This parameter specify if only one tail of the smoothed statistic distribution must be considered. If it is NULL, both tails are used and smoothStatistic.threshold is ignored.

**smoothStatistic.threshold:** Threshold on smoothStatistic values to select significant genomic regions.

## Details

A list of genomic regions objects is returned: one GenomicRegions object for each analysis in the input PREDAresults.

A NULL element is included in the output list whenever no significant regions are identified.

## Value

A list of genomic regions objects

## Author(s)

Francesco Ferrari

### Examples

```
## Not run:
require(PREDAsampledata)

data(GEanalysisResults)

genomic_regions_UP<-PREDAResults2GenomicRegions(GEanalysisResults
, qval.threshold=0.05, smoothStatistic.tail="upper",
smoothStatistic.threshold=0.5)

## End(Not run)
```

---

PREDAResults2GenomicRegionsSingle

*identify significant genomic regions from a single analysis in a  
PREDAResults object*

---

### Description

identify significant genomic regions from a single analysis in a PREDAResults object

### Usage

```
# PREDAResults2GenomicRegionsSingle(.Object,
# qval.threshold=0.05, analysisName=NULL,
# use.referencePositions=TRUE, smoothStatistic.tail=NULL,
# smoothStatistic.threshold=NULL)

PREDAResults2GenomicRegionsSingle(.Object, ...)
```

### Arguments

.Object	Object of class PREDAResults or PREDADataAndResults
...	See below

**qval.threshold:** q-value threshold used to identify significant genomic regions  
**analysisName:** name of the analysis to be considered  
**use.referencePositions:** Logical, if TRUE the input reference positions used for PREDA analysis will be used to identify significant genomic regions boundaries as well.  
**smoothStatistic.tail:** Possible values are "upper" or "lower". This parameter specify if only one tail of the smoothed statistic distribution must be considered. If it is NULL, both tails are used and smoothStatistic.threshold is ignored.  
**smoothStatistic.threshold:** Threshold on smoothStatistic values to select significant genomic regions.

---

```
PREDAResults2PREDADDataAndResults
```

*merge PREDAResults and input statistics to create a PREDADDataAndResults object*

---

### Description

merge PREDAResults and input statistics to create a PREDADDataAndResults object

### Usage

```
# PREDAResults2PREDADDataAndResults(.Object, statistic)
```

```
PREDAResults2PREDADDataAndResults(.Object, ...)
```

### Arguments

.Object	An object of class PREDAResults
...	See below
	<b>statistic:</b> A matrix containing input statistics

---

```
PREDAResultsGetObservedFlags
```

*extract genomic positions with significant alterations as a matrix of flags from a PREDAResults object*

---

### Description

extract genomic positions with significant alterations as a matrix of flags from a PREDAResults object

### Usage

```
# PREDAResultsGetObservedFlags(.Object, qval.threshold=0.05,  
# smoothStatistic.tail=NULL, smoothStatistic.threshold=NULL,  
# null.value=0, significant.value=1)
```

```
PREDAResultsGetObservedFlags(.Object, ...)
```

### Arguments

.Object	An object of class PREDAResults or PREDADDataAndResults
...	See below
	<b>qval.threshold:</b> q-value threshold used to identify significant genomic positions
	<b>smoothStatistic.tail:</b> Possible values are "upper" or "lower". This parameter specify if only one tail of the smoothed statististic distribution must be considered. If it is NULL, both tails are used and smoothStatistic.threshold is ignored.



**smoothStatistic.threshold:** Threshold on smoothStatistic values to select significant genomic regions.

**null.value:** Value (flag) assigned to not significant positions

**significant.value:** Value (flag) assigned to significant positions

---

PREDA\_main

*function performing the core of PREDA analysis*

---

## Description

function performing the core of PREDA analysis

## Usage

```
PREDA_main(inputDataForPREDA, outputGenomicAnnotationsForPREDA
=NULL, nperms = 10000, verbose = TRUE, parallelComputations =
FALSE, multTestCorrection = "fdr", permutePerChromosome = FALSE,
blocksize = 10, permuteStatisticSign = FALSE, smoothMethod =
"lokern_scaledBandwidth_repeated", force = FALSE,
lokern_scaledBandwidthFactor = 2, limit.analysis = NULL)
```

## Arguments

inputDataForPREDA	A Data for PREDA object
outputGenomicAnnotationsForPREDA	A GenomicAnnotationsForPREDA object. If NULL, GenomicsAnnotations for output data are obtained from inputDataForPREDA
nperms	Number of permutations performed in PREDA analysis.
verbose	Logical, if TRUE some messages are printed concerning the advancement of the analysis.
parallelComputations	Logical, if TRUE Rmpi is used to spawn slave processes, thus using parallel computing to speedup the analysis.
multTestCorrection	Multiple testing correction that will be adopted to correct the statistic p-values. Possible values are "fdr", for benjamini and Hochberg multiple testing correction and "qvalue" for p-values correction performed with qvalue package.
permutePerChromosome	Logical, if TRUE data permutations are perfored separatedly for each chromosome. In most cases the default value (FALSE) is preferable to avoid biases related to specific chromosomes extreme alterations.
blocksize	A parameter used to tune parallel computations if parallelComputations is TRUE. This is actually the number of permutations performed on each slave process before every communication with master process. This is useful to reduce the numebr of network communications when slow communicatinos are established among slave processes.

<code>permuteStatisticSign</code>	Logical, if TRUE statistics signs are permuted instead of permuting data along chromosomal position.
<code>smoothMethod</code>	The default smoothing method used in the <code>PREDA_main</code> function is <code>lokern</code> smoothing with scaled bandwidth, using a scaling factor equal to 2. Possible values are "lokern", for standard lokern smoothing, "quantsmooth", "spline" and "runningmean.x", where x is a user defined value for the number of adjacent data points using for running mean smoothing.
<code>force</code>	Logical, if TRUE force skipping quantsmooth control on number of data points. Since quantsmooth is very slow with a high number of input data, a check stopping computation with more than 2000 data points in one or more chromosome was introduced. This parameter allow skipping this security check.
<code>lokern_scaledBandwidthFactor</code>	Factor of scaling for lokern estimated bandwidths
<code>limit.analysis</code>	Vector (numeric or character representing analyses names) to limit the output of preda analysis to a subset of input analyses.

**Details**

See supplementary material about PREDA method

**Value**

If `outputGenomicAnnotationsForPREDA` is NULL, a `PREDADataAndResults` object is returned. Otherwise a `PREDAResults` object is returned instead

**Author(s)**

Francesco Ferrari

**See Also**

Supplementary information about PREDA method

**Examples**

```
#See examples in PREDA tutorial
```

---

```
preprocessingGE
```

*Wrapper function for gene expression data preprocessing for differential expression analysis with PREDA*

---

**Description**

Wrapper function for gene expression data preprocessing for differential expression analysis with PREDA

**Usage**

```
preprocessingGE(SampleInfoFile = NULL, CELfiles_dir = NULL,
AffyBatchInput = NULL, custom_cdfname, arrayNameColumn = NULL,
sampleNameColumn = NULL, classColumn,
referenceGroupLabel, statisticType, optionalAnnotations = NULL,
retain.chrs = NULL, reference_position_type = "median",
testedTail = "both")
```

**Arguments**

SampleInfoFile	Path to sample info file
CELfiles_dir	Path to directory containing raw CEL data files for Affymetrix arrays
AffyBatchInput	Alternatively input raw data can be provided as an AffyBatch object. In this case sample classes will be inferred from phenodata contained in AffyBatch object. In particular classColumn parameter will refer to the column in pData(AffyBatchInput) object.
custom_cdfname	Specify the cdf library to be used for data preprocessing
arrayNameColumn	Column of sampleinfo file containing the name of raw data (CEL) files
sampleNameColumn	Column of sampleinfo file containing the name to be used for samples labels
classColumn	Column of sampleinfo file containing the label of sample classes. If input raw data are provided as an AffyBatch object, this parameter refers instead to the column in pData(AffyBatchInput) object.
referenceGroupLabel	Specify which class label is used for the reference sample used in computing statistics for differential expression.
statisticType	Statistic for differential expression that is computed on input data. Possible values are "tstatistic", "FC" (Fold Change), "FCmedian" (fold change computed on medians)
optionalAnnotations	Character vector to select additional annotations fields to be included into the GenomicAnnotations object.
retain.chrs	Numeric vector, containing the list of chromosomes selected for the output GenomicAnnotations object. E.g. set retain.chrs=1:22 to limit the GenomicAnnotations object to chromosomes from 1 to 22. This might be useful to limit GenomicAnnotations objects to autosomic chromosomes.
reference_position_type	Specify which genomic coordinate must be used as reference position for PREDA analysis. Possible values are "start", "end", "median", "strand.start" or "strand.end".
testedTail	Specify what tail of the distribution will be tested for significantly extreme values in PREDA analysis. Possible values are "both", "upper" or "lower".

**Details**

Preprocess raw (CEL) files for Affymetrix gene expression arrays using user defined CDF libraries and RMA normalization. Then statistics for differential expression are computed. Then annotations are retrieved from the corresponding annotation library.

Please note this function is a user-friendly preprocessing function for Affy gene expression microarrays. Step by step preprocessing functions can be used with any other platform.

**Value**

A DataForPREDA object is returned.

**Author(s)**

Francesco Ferrari

**See Also**

[DataForPREDA](#)

**Examples**

```
## Not run:

require("PREDAsampledata")
CELfilesPath <- system.file("sampledata", "GeneExpression",
package = "PREDAsampledata")
infofile <- file.path(CELfilesPath , "sampleinfoGE_PREDA.txt")
sampleinfo<-read.table(infofile, sep="\t", header=TRUE)

GEDataForPREDA<-preprocessingGE(SampleInfoFile=infofile,
CELfiles_dir=CELfilesPath,
custom_cdfname="hgu133plus2",
arrayNameColumn=1,
sampleNameColumn=2,
classColumn="Class",
referenceGroupLabel="normal",
statisticType="tstatistic",
optionalAnnotations=c("SYMBOL", "ENTREZID"),
retain.chrs=1:22
)

## End(Not run)
```

---

SODEGIRpreprocessingGE

*Wrapper function for gene expression data preprocessing for SODEGIR analysis*

---

**Description**

Wrapper function for gene expression data preprocessing for SODEGIR analysis

**Usage**

```
SODEGIRpreprocessingGE(SampleInfoFile = NULL, CELfiles_dir = NULL,
AffyBatchInput = NULL, custom_cdfname, arrayNameColumn = NULL,
sampleNameColumn = NULL, classColumn,
referenceGroupLabel, statisticType, optionalAnnotations = NULL,
```

```
retain.chrs = NULL, reference_position_type = "median",
testedTail = "both", singleSampleOutput = TRUE,
varianceAll=FALSE)
```

### Arguments

**SampleInfoFile** Path to sample info file

**CELfiles\_dir** Path to directory containing raw CEL data files for Affymetrix arrays

**AffyBatchInput** Alternatively input raw data can be provided as an AffyBatch object. In this case sample classes will be inferred from phenodata contained in AffyBatch object. In particular classColumn parameter will refer to the column in pData(AffyBatchInput) object.

**custom\_cdfname** Specify the cdf library to be used for data preprocessing

**arrayNameColumn**  
Column of sampleinfo file containing the name of raw data (CEL) files

**sampleNameColumn**  
Column of sampleinfo file containing the name to be used for samples labels

**classColumn** Column of sampleinfo file containing the label of sample classes. If input raw data are provided as an AffyBatch object, this parameter refers instead to the column in pData(AffyBatchInput) object.

**referenceGroupLabel**  
Specify which class label is used for the reference sample used in computing statistics for differential expression.

**statisticType** Statistic for differential expression that is computed on input data. Possible values are "tstatistic", "FC" (Fold Change), "FCmedian" (fold change computed on medians)

**optionalAnnotations**  
Character vector to select additional annotations fields to be included into the GenomicAnnotations object.

**retain.chrs** Numeric vector, containing the list of chromosomes selected for the output GenomicAnnotations object. E.g. set retain.chrs=1:22 to limit the GenomicAnnotations object to chromosomes from 1 to 22. This might be useful to limit GenomicAnnotations objects to autosomic chromosomes.

**reference\_position\_type**  
Specify which genomic coordinate must be used as reference position for PREDA analysis. Possible values are "start", "end", "median", "strand.start" or "strand.end". "strand.start" is strand specific start: i.e. start on positive strand but end on negative strand. "strand.end" is strand specific end.

**testedTail** Specify what tail of the distribution will be tested for significantly extreme values in PREDA analysis. Possible values are "both", "upper" or "lower".

**singleSampleOutput**  
Logical, if TRUE a statistic comparing each sample with the reference group is computed.

**varianceAll** This parameter affect the computation only when singleSampleOutput is TRUE. varianceAll is itself a logical parameter. If TRUE, all pathological (e.g. tumor) samples and all normal (reference) samples are used to estimate variance in the comparison of individual pathological samples to the normal reference, as described in the original SODEGIR paper by Bicciato et al. (Nucleic Acids Res. 2009).

The original SODEGIR statistic for Gene Expression was based on the SAM score. However, since July 2018 the original samr package is no more available in CRAN. Therefore in the current PREDA version the `varianceAll=TRUE` and `singleSampleOutput=TREU` can't be used with SAM. When `singleSampleOutput` is `TRUE` and a different `statisticType` is used, the variance is actually computed using only the normal (reference) samples.

If `FALSE` (default value), the computation of statistics for single sample VS reference comparisons only take into account the variance in the reference group of samples.

### Details

Preprocess raw (CEL) files for Affymetrix gene expression arrays using user defined CDF libraries and RMA normalization.

Then statistics for differential expression are computed comparing each sample with the reference group.

Then annotations are retrieved from the corresponding annotation library.

Please note this function is a user-friendly preprocessing function for Affy gene expression microarrays. Step by step preprocessing functions can be used with any other platform.

### Value

A `DataForPREDA` object is returned.

### Author(s)

Francesco Ferrari

### References

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

### See Also

[preprocessingGE](#), [DataForPREDA](#)

### Examples

```
## Not run:
require(PREDAsampledata)

CELfilesPath <- system.file("sampledata", "GeneExpression",
package = "PREDAsampledata")

infofile <- file.path(CELfilesPath , "sampleinfoGE_PREDA.txt")

SODEGIRGEDataForPREDA<-SODEGIRpreprocessingGE(SampleInfoFile=
infofile,
CELfiles_dir=CELfilesPath,
custom_cdfname="hgu133plus2",
arrayNameColumn=1,
```

```

sampleNameColumn=2,
classColumn="Class",
referenceGroupLabel="normal",
statisticType="tstatistic",
optionalAnnotations=c("SYMBOL", "ENTREZID"),
retain.chrs=1:22
)

## End(Not run)

```

---

SODEGIR\_GEstatistics    *Wrapper function for gene expression statistics preprocessing for SODEGIR analysis*

---

### Description

Wrapper function for gene expression statistics preprocessing for SODEGIR analysis.

### Usage

```

# SODEGIR_GEstatistics(.Object, pData_classColumn=NULL,
# referenceGroupLabel=NULL,
# statisticType=c("tstatistic", "FC", "FCmedian", "eBayes"),
# singleSampleOutput=TRUE, varianceAll=FALSE)

SODEGIR_GEstatistics(.Object, ...)

```

### Arguments

.Object	An object of class ExpressionSet containing gene expression input data
...	See below
	<b>pData_classColumn:</b> Column of phenoData slot from the ExpressionSet object, containing the label of sample classes
	<b>referenceGroupLabel:</b> Specify which class label is used for the reference sample used in computing statistics for differential expression.
	<b>statisticType:</b> Statistic for differential expression that is computed on input data. Possible values are "tstatistic", "FC" (Fold Change), "FCmedian" (fold change computed on medians)
	<b>singleSampleOutput:</b> Logical, if TRUE a statistic comparing each sample with the reference group is computed.
	<b>varianceAll:</b> This parameter affect the computation only when singleSampleOutput is TRUE. varianceAll is itself a logical parameter. If TRUE, all pathological (e.g. tumor) samples and all normal (reference) samples are used to estimate variance in the comparison of individual pathological samples to the normal reference, as described in the original SODEGIR apper by Bicciato et al. (Nucleic Acids Res. 2009).

The original SODEGIR statistic for Gene Expression was based on the SAM score. However, since July 2018 the samr package is no more available in CRAN. Therefore in the current PREDA version the varianceAll=TRUE parameter can't be used as SAM is not available. When singleSampleOutput is TRUE and a different statisticType is used, the variance is actually computed using only the normal (reference) samples. If FALSE (default value), the computation of statistics for single sample VS reference comparisons only take into account the variance in the reference group of samples.

### Details

Using an ExpressionSet object as input, statistics for differential expression are computed comparing each sample with the reference group.

### Value

The output is returned as a matrix.

### Author(s)

Francesco Ferrari

### References

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

### See Also

[preprocessingGE](#), [SODEGIRpreprocessingGE](#), [ExpressionSet](#)

---

StatisticsForPREDA-class

*Class "StatisticsForPREDA" is used to manage the datamatrix containing statistics for PREDA analyses*

---

### Description

This class is used to manage the datamatrix containing statistics for PREDA analyses: i.e. the gene (or other genomic feature) centered statistics accounting for differential expression (or for the other type of variation under investigation)

### Objects from the Class

Objects can be created by calls of the form `new("StatisticsForPREDA", ids, statistic, analysesNames, testedTai`



**Slots**

- ids:** Object of class "character" a character vector of unique identifiers for the genomic features under investigation
- statistic:** Object of class "matrix" a numeric matrix containing gene-centered statistics (or statistics on genomic data centered on other genomic features under investigation). The statistics must be provided as a matrix of numeric values, with a number of rows equal to the length of "ids" slot and a number of columns equal to the length of "analysesNames" slot.
- analysesNames:** Object of class "character" a character vector of unique names associated to each column of statistic matrix. This is just a name that will be used to identify each analysis.
- testedTail:** Object of class "character" a character describing what tail of the statistic distribution will be analyzed during PREDA analysis. Possible values are "upper", "lower" or "both". Anyway we strongly recommend using PREDA analysis only for statistics on genomic data with a symmetric distribution around zero.

**Methods**

- analysesNames** signature(.Object = "StatisticsForPREDA"): get the names of the analyses in the StatisticsForPREDA object
- getStatisticByName** signature(.Object = "StatisticsForPREDA"): extract data for individual analyses using the analysis name
- initialize** signature(.Object = "StatisticsForPREDA"): initialize method for StatisticsForPREDA objects
- StatisticsForPREDA2dataframe** signature(.Object = "StatisticsForPREDA"): extract data as a dataframe with probeids as rownames
- StatisticsForPREDAFilterColumns\_neg** signature(.Object = "StatisticsForPREDA"): filter statistics to remove selected analyses
- StatisticsForPREDAFilterColumns\_pos** signature(.Object = "StatisticsForPREDA"): filter statistics to keep selected analyses

**Note**

This class is better described in the package vignette

**Author(s)**

Francesco Ferrari

**See Also**

["DataForPREDA"](#), [analysesNames](#), [getStatisticByName](#) [StatisticsForPREDA2dataframe](#), [StatisticsForPREDAFilterColumns\\_neg](#), [StatisticsForPREDAFilterColumns\\_pos](#)

**Examples**

```
showClass("StatisticsForPREDA")
```

---

StatisticsForPREDA2dataframe

*extract data as a dataframe with probeids as rownames*

---

### Description

extract data as a dataframe with probeids as rownames

### Usage

```
StatisticsForPREDA2dataframe(.Object)
```

### Arguments

.Object            An object of class StatisticsForPREDA

---

StatisticsForPREDAFilterColumns\_neg

*filter statistics to remove selected analyses*

---

### Description

filter statistics to remove selected analyses

### Usage

```
# StatisticsForPREDAFilterColumns_neg(.Object, analysesToRemove,
# analysesAsNames=FALSE)
```

```
StatisticsForPREDAFilterColumns_neg(.Object, ...)
```

### Arguments

.Object            An object of class StatisticsForPREDA

...                See below

**analysesToRemove:** Analysis statistics columns to be removed after filtering

**analysesAsNames:** Logical, if TRUE analyses are listed as their character names.  
If FALSE they can be listed as numeric indexes.

---

StatisticsForPREDAFilterColumns\_pos  
*filter statistics to keep selected analyses*

---

**Description**

filter statistics to keep selected analyses

**Usage**

```
# StatisticsForPREDAFilterColumns_pos(.Object, analysesToRetain,
# analysesAsNames=FALSE)

StatisticsForPREDAFilterColumns_pos(.Object, ...)
```

**Arguments**

.Object	An object of class StatisticsForPREDA
...	See below
	<b>analysesToRetain:</b> Analysis statistics columns to be retained after filtering
	<b>analysesAsNames:</b> Logical, if TRUE analyses are listed as their character names. If FALSE they can be listed as numeric indexes.

---

StatisticsForPREDAFromdataframe  
*Function to create a StatisticsForPREDA objet from a dataframe*

---

**Description**

Function to create a StatisticsForPREDA objet from a dataframe

**Usage**

```
StatisticsForPREDAFromdataframe(StatisticsForPREDA_dataframe, ids_column = NULL,
statistic_columns = NULL, analysesNames = NULL, testedTail =
c("upper", "lower", "both"))
```

**Arguments**

StatisticsForPREDA_dataframe	Input dataframe containing statistics on genomics data.
ids_column	Specify the column from the input dataframe with gene (or other genomic features) ids. Can be specified using column index (numeric) or column name (character).
statistic_columns	Specify the column (or columns) from the input dataframe with gsta.enomic data statistics that will be included in the statisticsForPREDA object. Can be specified using column index (numeric) or column name (character). If NULL (default), all columns excluding ids_column will be considered as input statistics

analysesNames	Names (labels) to be associated to each input statistic. If NULL the column names for statistics_columns will be used.
testedTail	Specify what tail of the distribution will be tested for significantly extreme values in PREDA analysis. Possible values are "both", "upper" or "lower".
...	any other parameter for read.table function that could be useful for parsing the input file, such as "sep", "quote", "header", "na.strings" and other parameters.

### Details

A dataframe is parsed and a statisticsForPREDA object is built using contained data.

### Value

A statisticsForPREDA object

### Author(s)

Francesco Ferrari

### See Also

[StatisticsForPREDA](#)

### Examples

```
## Not run:
require(PREDAsampledata)

CNdataPath <- system.file("sampledata", "CopyNumber", package =
"PREDAsampledata")

CNdataFile <- file.path(CNdataPath , "CNAG_data_PREDA.txt")

CNnotationFile <- file.path(CNdataPath , "SNPAnnot100k.csv")

CNStatisticsForPREDA<-StatisticsForPREDAFromdataframe(file=CNdataFile,
ids_column="AffymetrixSNPsID", testedTail="both", sep="\t",
header=TRUE)

## End(Not run)
```

---

```
statisticsForPREDAfromEset
```

*function to compute a statisticsForPREDA object from an Expression-Set object*

---

### Description

function to compute a statisticsForPREDA object from an ExpressionSet object

**Usage**

```
# statisticsForPREDAfromEset(.Object, pData_classColumn=NULL,
# statisticType=NULL, logged=TRUE, referenceGroupLabel=NULL,
# classVector=NULL, testedTail="both")

statisticsForPREDAfromEset(.Object, ...)
```

**Arguments**

.Object            Object of class ExpressionSet  
 ...                See below

**pData\_classColumn:** Column from pData(.Object) containing the labels for different samples classes.

**statisticType:** Statistic for differential expression that is computed on input data. Possible values are "tstatistic", "FC" (Fold Change), "FCmedian" (fold change computed on medians)

**logged:** Logical value (default TRUE) to specify if the input data are logged (Log2). This parameter will influence the computation of statistics.

**referenceGroupLabel:** Specify which class label is used for the reference sample used in computing statistics for differential expression.

**classVector:** If pData\_classColumn is NULL then a vector specifying the sample classes is required and can be provided with classVector parameter

**testedTail:** Specify what tail of the distribution will be tested for significantly extreme values in PREDA analysis. Possible values are "both", "upper" or "lower". Default value is "both".

**Details**

An object of class ExpressionSet is used as input and gene centered statistics for differential expression are computed on the contained data. The computed statistics are used to build a StatisticsForPREDA object

**Value**

An object of class StatisticsForPREDA

**Author(s)**

Francesco Ferrari

**See Also**

["StatisticsForPREDA"](#)

**Examples**

```
## Not run:

require(PREDAsampledata)

data(ExpressionSetRCC)
```

```
GStatisticsForPREDA<-statisticsForPREDAfromEset(
ExpressionSetRCC, statisticType="tstatistic",
referenceGroupLabel="normal", classVector=sampleinfo["Class"])

## End(Not run)
```

---

StatisticsForPREDAFromfile

*Function to create a StatisticsForPREDA objet from a txt file*

---

## Description

Function to create a StatisticsForPREDA objet from a txt file

## Usage

```
StatisticsForPREDAFromfile(file, ids_column = NULL,
statistic_columns = NULL, analysesNames = NULL, testedTail =
c("upper", "lower", "both"), ...)
```

## Arguments

<code>file</code>	Path to the input txt file containing statistics on genomics data
<code>ids_column</code>	Specify the column from the input txt file with gene (or other genomic features) ids. Can be specified using column index (numeric) or column name (character).
<code>statistic_columns</code>	Specify the column (or columns) from the input txt file with gsta.enomic data statistics that will be included in the statisticsForPREDA object. Can be specified using column index (numeric) or column name (character). If NULL (default), all columns excluding <code>ids_column</code> will be considered as input statistics
<code>analysesNames</code>	Names (labels) to be associated to each input statistic. If NULL the column names for <code>statistic_columns</code> will be used.
<code>testedTail</code>	Specify what tail of the distribution will be tested for significantly extreme values in PREDA analysis. Possible values are "both", "upper" or "lower".
<code>...</code>	any other parameter for <code>read.table</code> function that could be useful for parsing the input file, such as "sep", "quote", "header", "na.strings" and other parameters.

## Details

A txt file is parsed and a statisticsForPREDA object is built using contained data.

## Value

A statisticsForPREDA object

## Author(s)

Francesco Ferrari

**See Also**[StatisticsForPREDA](#)**Examples**

```
## Not run:
require(PREDAsampledata)

CNdataPath <- system.file("sampledata", "CopyNumber", package =
"PREDAsampledata")

CNdataFile <- file.path(CNdataPath , "CNAG_data_PREDA.txt")

CNannotationFile <- file.path(CNdataPath , "SNPAnnot100k.csv")

CNStatisticsForPREDA<-StatisticsForPREDAFromfile(file=CNdataFile,
ids_column="AffymetrixSNPsID", testedTail="both", sep="\t",
header=TRUE)

## End(Not run)
```

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