

# Package ‘ChIPexoQual’

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**Type** Package

**Title** ChIPexoQual

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**Description** Package with a quality control pipeline for ChIP-exo/nexus data.

**URL** <https://github.com/keleslab/ChIPexoQual>

**BugReports** <https://github.com/welch16/ChIPexoQual/issues>

**License** GPL (>=2)

**Depends** R (>= 3.4.0), GenomicAlignments (>= 1.0.1)

**Imports** methods, utils, GenomeInfoDb, stats, BiocParallel, GenomicRanges (>= 1.14.4), ggplot2 (>= 1.0), data.table (>= 1.9.6), Rsamtools (>= 1.16.1), IRanges (>= 1.6), S4Vectors (>= 0.8), biovizBase (>= 1.18), broom (>= 0.4), RColorBrewer (>= 1.1), dplyr (>= 0.5), scales (>= 0.4.0), viridis (>= 0.3), hexbin (>= 1.27), rmarkdown

**Suggests** ChIPexoQualExample (>= 0.99.1), knitr (>= 1.10), BiocStyle, gridExtra (>= 2.2), testthat

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 ARCvURCplot

*ARCvURCplot*


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**Description**

ARCvURCplot returns a ggplot object with the ARC vs URC plot to analyze enrichment and library complexity in ChIP-exo data.

**Usage**

```
ARCvURCplot(..., names.input = NULL, both.strand = FALSE)
```

**Arguments**

...	a list of ExoData objects, or several ExoData objects by themselves.
names.input	a character vector with the names to use in the plot. If it is empty ARCvURCplot is going to create the names as the names of the list when they are available or is going to name them as Sample: 1 ,... , Sample: k.
both.strand	A logical value indicating if the DataFrame contains only regions with reads aligned to both strand or all. The default value is FALSE.

**Value**

A ggplot2 object with the ARC vs URC plot.

**Examples**

```
data(exoExample)
ARCvURCplot(exoExample)
```

---

beta1

*beta1 methods*

---

**Description**

beta1 returns a vector with all the estimated values of the  $d_i = \beta_1 u_i + \beta_2 w_i + \epsilon_i$  models fitted by ChIPexoQual

**Usage**

```
beta1(object)

## S4 method for signature 'ExoData'
beta1(object)
```

**Arguments**

object            a ExoData object.

**Value**

A numeric vector with estimated values for  $\beta_1$ .

**Examples**

```
data(exoExample)
beta1(exoExample)
```

---

beta2

*beta2 methods*

---

**Description**

beta2 returns a vector with all the estimated values of the  $d_i = \beta_1 u_i + \beta_2 w_i + \epsilon_i$  models fitted by ChIPexoQual

**Usage**

```
beta2(object)

## S4 method for signature 'ExoData'
beta2(object)
```

**Arguments**

object            a ExoData object.

**Value**

A numeric vector with estimated values for  $\beta_2$ .

**Examples**

```
data(exoExample)
beta2(exoExample)
```

---

blacklists	<i>list of GRanges objects with the blacklists generated by the ENCODE and modENCODE projects.</i>
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---

**Description**

list of GRanges objects with the blacklists generated by the ENCODE and modENCODE projects.

**Usage**

```
data(blacklists)
```

**Format**

list of GRanges objects.

**Value**

A list with the blacklists listed in <https://sites.google.com/site/anshulkundaje/projects/blacklists>.

---

calculateParamDist	<i>calculateParamDist calculateParamDist calculates the quality parameters of one iteration. This function samples nregions rows from the stat matrix and fits the linear model <math>\text{lm}(d \sim \theta + u + w)</math></i>
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**Description**

calculateParamDist

calculateParamDist calculates the quality parameters of one iteration. This function samples nregions rows from the stat matrix and fits the linear model  $\text{lm}(d \sim \theta + u + w)$

**Usage**

```
calculateParamDist(i, stats, nregions)
```

**Arguments**

<code>i</code>	a numeric value indicating the current iteration.
<code>stats</code>	a <code>data.table</code> object with the response and covariates for the model
<code>nregions</code>	a numeric value indicating the number of regions sampled.

**Value**

a `data.table` with both parameters and some extra info

**Examples**

```
data("exoExample")
DT <- formatRegions(exoExample)
calculateParamDist(1,DT,100)
```

---

ExoData-class	<i>ExoData object and constructors</i>
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---

**Description**

ExoData is a subclass of `GenomicRanges`, used to asses the quality of ChIP-exo/nexus sample.

**Usage**

```
ExoData(file = NULL, reads = NULL, height = 1,
        mc.cores = getOption("mc.cores", 2L), save.reads = FALSE,
        nregions = 1000, ntimes = 100, verbose = TRUE)
```

**Arguments**

<code>file</code>	a character value with location of the bam file with the aligned reads.
<code>reads</code>	a <code>GAlignments</code> object with the aligned reads of a ChIP-exo sample. It is meant to be used instead of <code>file</code> .
<code>height</code>	a numeric value indicating the value used to slice the coverage of the experiment into a set of regions.
<code>mc.cores</code>	a numeric value with the number of cores to use, i.e. at most how many child processes will be run simultaneously.
<code>save.reads</code>	a logical value to indicate if the reads are stored in the <code>ExoData</code> object. The default value is <code>FALSE</code> .
<code>nregions</code>	a numeric value indicating the number of regions sampled to estimate the quality parameter distributions. The default value is <code>1e3</code> .
<code>ntimes</code>	a numeric value indicating the number of times that regions are sampled to estimate the quality parameter distributions. The default value is <code>1e2</code> .
<code>verbose</code>	a logical value indicating if the user want to receive progress details. The default value is <code>FALSE</code> .

**Value**

It returns an ExoData object with the regions obtained after partitioning the genome and the summary statistics for each region. If the `save.reads` parameter is TRUE then it contains a GRanges object with the reads of the ChIP-exo experiment.

**Examples**

```
files <- list.files(system.file("extdata", package = "ChIPexoQualExample"),
  full.names = TRUE)
ExoData(files[5], mc.cores = 2L)
```

---

ExoDataBlacklist	<i>ExoDataBlacklist</i>
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---

**Description**

ExoDataBlacklist separates the regions in an ExoData object by overlapping them with a set of blacklisted regions and calculates the quality parameters in both collections of islands.

**Usage**

```
ExoDataBlacklist(exo, blacklist, which.param = "beta1", nregions = NULL,
  ntimes = NULL)
```

**Arguments**

<code>exo</code>	a ExoData object.
<code>blacklist</code>	a GRanges object with the blacklisted regions or a character indicating which of the blacklist included in ChIPexoQual to use.
<code>which.param</code>	a character value with either "beta1" or "beta2" that determines which parameters in the model $\text{depth}_i \sim \text{uniquePos}_i + \text{width}_i$ to plot. The default value is "beta1".
<code>nregions</code>	a numeric value indicating the number of regions sampled to estimate the quality parameter distributions. The default value is extracted from <code>exo</code> .
<code>ntimes</code>	a numeric value indicating the number of times that regions are sampled to estimate the quality parameter distributions. The default value is extracted from object.

**Value**

A ggplot object with a boxplot that compares the quality scores distribution when the regions overlap a pre-defined collection of blacklists.

**Examples**

```
data(exoExample)
data(blacklists)
ExoDataBlacklist(exoExample,blacklists[["mm9"]],ntimes = 10,nregions = 500)
```

---

ExoDataSubsampling      *ExoDataSubsampling*

---

**Description**

ExoDataSubsampling samples `sample.reads` from the ChIP-exo experiment and creates a list of ExoData objects

**Usage**

```
ExoDataSubsampling(file = NULL, reads = NULL, sample.depth = NULL,
  height = 1, nregions = 1000, ntimes = 1000, verbose = TRUE,
  save.reads = FALSE, mc.cores = getOption("mc.cores", 2L))
```

**Arguments**

<code>file</code>	a character value with location of the bam file with the aligned reads.
<code>reads</code>	a GAlignments object with the aligned reads of a ChIP-exo sample. It is meant to be used instead of <code>file</code> .
<code>sample.depth</code>	a numeric vector with the number of reads to be sampled.
<code>height</code>	a numeric value indicating the value used to slice the coverage of the experiment into a set of regions.
<code>nregions</code>	a numeric value indicating the number of regions sampled to estimate the quality parameter distributions. The default value is 1e3.
<code>ntimes</code>	a numeric value indicating the number of times that regions are sampled to estimate the quality parameter distributions. The default value is 1e2.
<code>verbose</code>	a logical value indicating if the user want to receive progress details. The default value is FALSE.
<code>save.reads</code>	a logical value to indicate if the reads are stored in the ExoData object. The default value is FALSE.
<code>mc.cores</code>	a numeric value with the number of cores to use, i.e. at most how many child processes will be run simultaneously.

**Value**

It returns an ExoData object with the regions obtained after partitioning the genome and the summary statistics for each region. If the `save.reads` parameter is TRUE then it contains a GRanges object with the reads of the ChIP-exo experiment.

**Examples**

```
files <- list.files(system.file("extdata",package = "ChIPexoQualExample"),
  full.names = TRUE)
sample.depth <- seq(1e5,2e5,5e4)
ExoDataSubsampling(file = files[5],sample.depth = sample.depth)
```

---

exoExample	ExoData <i>results for FoxA1 ChIP-exo experiment</i>
------------	--

---

**Description**

ExoData object, generated with ChIPexoQual and the file:

**Usage**

```
data(exoExample)
```

**Format**

ExoData object, which are GRanges with additional columns.

**Details**

- ChIPexo\_carroll\_FoxA1\_mouse\_rep3\_chr1.bam

**Value**

An ExoData object with the 3rd replicate of the FoxA1 experiment from ChIPexoQualExample.

---

formatRegions	<i>formatRegions separates the width, depth and uniquePos summary statistics from the ExoData object to calculate the quality parameters/</i>
---------------	---

---

**Description**

formatRegions

formatRegions separates the width, depth and uniquePos summary statistics from the ExoData object to calculate the quality parameters/

**Usage**

```
formatRegions(exo)
```



**Arguments**

exo                    a ExoData object

**Value**

a data.table with the width, depth and uniquePos of the regions in exo.

**Examples**

```
data("exoExample")
formatRegions(exoExample)
```

---

FSRDistplot

*FSRDistplot*

---

**Description**

FSRDistplot returns a ggplot object with the Forward Strand Ratio distribution plot to analyze strand imbalance in ChIP-exo data.

**Usage**

```
FSRDistplot(..., names.input = NULL, quantiles = c(0, 0.25, 0.5, 0.75, 1),
  depth.values = seq_len(30), both.strand = FALSE)
```

**Arguments**

...                    a list of ExoData objects, or several ExoData objects by themselves.

names.input           a character vector with the names to use in the plot. If it is empty FSRDistplot is going to create the names as the names of the list when they are available or is going to name them as Sample: 1 ,... , Sample: k.

quantiles            a numeric vector with the quantiles used to estimate the FSR distribution at a given depth. The default value is c(0, .25, .5, .75, 1))

depth.values         a numeric vector indicating the regions with depth less or equal to, that are going to be filtered out. The defaulta values are seq\_len(50).

both.strand          a logical value indicating if the DataFrame contains only regions with reads aligned to both strand or all. The default value is FALSE.

**Value**

A ggplot2 object with the FSR distribution plot.

**Examples**

```
data(exoExample)
FSRDistplot(exoExample)
```

---

MAplot

*MAplot*


---

**Description**

MAplot returns a ggplot object with the MA plot to analyze the strand imbalance in ChIP-exo data.

**Usage**

```
MAplot(..., names.input = NULL)
```

**Arguments**

`...` a list of ExoData objects, or several ExoData objects by themselves.

`names.input` a character vector with the names to use in the plot. If it is empty MAplot is going to create the names as the names of the list when they are available or is going to name them as Sample: 1 ,... , Sample: k.

**Value**

A ggplot2 object with the MA plot.

**Examples**

```
data(exoExample)
MAplot(exoExample)
```

---

nreads

*nreads methods*


---

**Description**

nreads returns the number of reads in the object.

**Usage**

```
nreads(object)

## S4 method for signature 'ExoData'
nreads(object)
```

**Arguments**

`object` A ExoData object.

**Value**

The number of reads in the ExoData object.

**Examples**

```
data(exoExample)
nreads(exoExample)
```

---

paramDist                    *paramDist methods*

---

**Description**

paramDist returns a DataFrame with all the estimated coefficients in the  $d_i = \beta_1 u_i + \beta_2 w_i + \epsilon_i$  models fitted by ChIPexoQual

**Usage**

```
paramDist(object)

## S4 method for signature 'ExoData'
paramDist(object = "ExoData")
```

**Arguments**

object                    a ExoData object.

**Value**

A DataFrame with the fitted values of  $\beta_1$  and  $\beta_2$ .

**Examples**

```
data(exoExample)
paramDist(exoExample)
```

---

paramDistBoxplot      *paramDistBoxplot*

---

### Description

paramDistBoxplot returns a ggplot object with a boxplot comparing the ntimes estimations of the chosen parameter.

### Usage

```
paramDistBoxplot(..., names.input = NULL, which.param = "beta1",
  sort.as.numeric = FALSE)
```

### Arguments

`...`            a list of ExoData objects, or several ExoData objects by themselves.

`names.input`    a character vector with the names to use in the plot. If it is empty paramDistBoxplot is going to create the names as the names of the list when they are available or is going to name them as Sample: 1 ,... , Sample: k.

`which.param`    a character value with either "beta1" or "beta2" that determines which parameters in the model  $depth_i \sim uniquePos_i + width_i$  to plot. The default value is "beta1".

`sort.as.numeric` a logical value indicating if the values of `names.input` are meant to be interpreted as numeric and sorted accordingly.

### Value

A ggplot2 object with the boxplot of the chosen parameter

### Examples

```
data(exoExample)
paramDistBoxplot(exoExample)
```

---

regionCompplot      *regionCompplot*

---

### Description

regionCompplot returns a ggplot object with the Region Composition plot to analyze strand imbalance in ChIP-exo data.

### Usage

```
regionCompplot(..., names.input = NULL, depth.values = seq_len(15))
```

**Arguments**

- `...` a list of `ExoData` objects, or several `ExoData` objects by themselves.
- `names.input` a character vector with the names to use in the plot. If it is empty `regionCompplot` is going to create the names as the names of the list when they are available or is going to name them as `Sample: 1 ,... , Sample: k`.
- `depth.values` a numeric vector indicating the regions with depth less or equal to, that are going to be filtered out. The default values are `seq_len(50)`.

**Value**

A `ggplot2` object with the Region Composition plot.

**Examples**

```
data(exoExample)
regionCompplot(exoExample)
```

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