Package 'deltaCaptureC'

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Title This Package Discovers Meso-scale Chromatin Remodeling from 3C Data

Version 1.26.0

Description This package discovers meso-scale chromatin remodelling from 3C data. 3C data is local in nature. It givens interaction counts between restriction enzyme digestion fragments and a preferred 'viewpoint' region. By binning this data and using permutation testing, this package can test whether there are statistically significant changes in the interaction counts between the data from two cell types or two treatments.

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.getRunsAndTotals *A helper function for getRunTotals*

Description

This takes a GRanges object for binneed data and a column name designating where to find the relevant data in the mcols and returns a GRanges giving the consecutive runs of constant sign and their run totals. It is not exported.

Usage

```
.getRunsAndTotals(gr, colName)
```

Arguments

gr	a GRanges object whose mcols gives the relevant binned data
colName	This designates the column in mcols with the relevant data

Value

a GRanges object giving the contiguous regions and their respective sums.

bigBinSize *Big bin size*

Description

The deltaCaptureC package depends on rebinning mean normalized capture C data from a small bin size to a large bin size. This gives the size of the latter. This is used in package documentation.

Usage

```
bigBinSize
```

Format

a numeric scalar

binnedDeltaPlot *Plot of Binned Delta Counts*

Description

The data plotted here are the difference between mean normalized counts for captures in two replicates each of EScells and Neurons. The data here is binned to 1000bp and is shown in a region of 500kb up- and down-stream of the Paupar viewpoint. It is used here to illustrate functioning of the deltaCaptureC package.

Usage

```
binnedDeltaPlot
```

Format

A ggplot object

binnedDeltaSE *Binned difference of mean capture-C counts between EScells and Neurons*

Description

A smaller deltaSE restriction to a region of interest around the viewpoint, here binned to the bigBinSize, 10kb.

Usage

```
binnedDeltaSE
```

Format

A RangedSummarizedExperiment with 1909 rows.

binnedSummarizedExperiment

Binned Capture-C counts of EScells and Neurons

Description

Capture-C counts of EScells and Neurons restricted to a region of interest around the Paupar viewpoint. The data have been binned to smallBins, i.e., bins of size 1000. Used in package documentation.

Usage

```
binnedSummarizedExperiment
```

Format

A RangedSummarizedExperiment.

binSummarizedExperiment

Bin a Summarized experiment into a set of bins given by a GRanges object

Description

This function takes a set of bins given by a GRanges object and a RangedSummarizedExperiment and produces a new RangedSummarizedExperiment with the bins as its rowRanges

Usage

```
binSummarizedExperiment(bins, se, checkDisjoint = FALSE)
```

Arguments

bins	a GRanges object whose ranges should be disjoint
se	a RangedSummarizedExperiment
checkDisjoint	= FALSE if set to true will check that the bins are disjoint

Value

a RangedSummarizedExperiment

Examples

```
binnedSummarizedExperiment = binSummarizedExperiment(smallSetOfSmallBins,smallerDeltaSE)
```

deltaSE *Difference of mean capture-C counts between EScells and Neurons*

Description

This gives the difference in mean normalized capture C counts between two replicates each of EScells and Neurons. It is the underlying kind of data on which deltaCaptureC operates and is here to support documentation.

Usage

```
deltaSE
```

Format

A RangedSummarizedExperiment with 5709 rows.

downshiftDFtoMatrix *Downshift from DF to matrix*

Description

This function takes a data.frame with chr, start, end and numerical data and turns it into a matrix with row names chr:start-end

Usage

```
downshiftDFtoMatrix(df)
```

Arguments

df	This is a data frame whose first three columns are chr, start and end and whose remaining columns are numerical data

Value

A matrix of numerical data

Examples

```
m = downshiftDFtoMatrix(miniSEDF)
```

generatePermutation *Generate permutation for permutation testing*

Description

This function takes a set of row ranges and an inner region and generates a permutation which is symmetric on the inner region and arbitrary on the remainder

Usage

```
generatePermutation(gr, innerRegion)
```

Arguments

gr	a GRanges object which should be ordered
innerRegion	a GRanges object which should be a single interval

Value

a permutation of 1:length(gr)

Examples

```
permutations = generatePermutation(smallBins,viewpointRegion)
```

getDeltaSE *Make delta summarized experiment:*

Description

This function takes a SummarizedExperiment with count data and produces a SummarizedExperiment of the delta track. There should exactly two values for treatment, i.e., byTreatment

Usage

```
getDeltaSE(countsSE, byTreatment = "treatment")
```

Arguments

countsSE	A summarized experiment with assay counts and optionally assay normalized counts
byTreatment	= 'treatment' Allows for specifying some other condition than 'treatment'

Value

A summarized experiment with a single assay consisting of a single column, the delta mean normalized counts.

Examples

```
aSmallDeltaSE = getDeltaSE(miniSE)
```

`getLopsidedness` *Get the lopsidedness statistic*

Description

This function looks at the sidedness around the viewpoint and returns the absolute value of the difference between the sum of the values before and after the viewpoint inside the viewpoint region.

Usage

```
getLopsidedness(se, viewpointRegion, colName = "delta")
```

Arguments

`se`	a SummerizedExperiment giving the delta or permuted delta
`viewpointRegion`	the region around the viewpoint in which to investigate lopsidedness
`colName`	defaults to 'delta'

Value

the lopsidedness around the viewpointMid in the viewpointRegion

Examples

```
lopsidedness = getLopsidedness(binnedDeltaSE,viewpointRegion)
```

`getMeanNormalizedCountsSE` *Make mean treatment summarized experiment:*

Description

Get the mean normalized counts for each treatment

Usage

```
getMeanNormalizedCountsSE(countsSE, byTreatment = "treatment")
```

Arguments

countsSE	A SummarizedExperiment containing an assay 'counts' and optionally an assay 'normalizedCounts'
byTreatment	= 'treatment' This gives the column of colData to use for taking averages

Details

This function takes a SummarizedExperiment. It looks for an assay called normalizedCounts. If this assay is missing, it creates it by normalizing using the size factors. By default, it takes the mean for each value of colData$treatment

Value

A SummarizedExperiment giving mean normalized counts for each value of byTreatment

Examples

```
meanNormalizedCountSE = getMeanNormalizedCountsSE(miniSE)
```

---

getNormalizedCountsSE *Get normalized counts*

Description

This function takes a SummarizedExperiment giving the the counts for each replicate of the two treatments and computes and affixes an assay giving the normalized version of these counts.

Usage

```
getNormalizedCountsSE(se)
```

Arguments

se	A SummarizedExperiment with an assay called counts giving the raw counts for each replicate of the two treatments.

Value

A SummarizedExperiment including a an assay of the normalized counts called normalizedCounts.

Examples

```
miniSENormalized = getNormalizedCountsSE(miniSE)
```

getOverlapWeights *Get the binning factors for one set of GRanges into another*

Description

This function takes two GRanges, one representing a set of bins and the other representing data to be pro-rated over those bins and returns a data frame giving the overlaps, various widths and the fractions for pro-rating scores

Usage

```
getOverlapWeights(bins, gr, checkDisjoint = FALSE)
```

Arguments

bins	a set of GRanges to be used for binning data.
gr	the GRanges of the data to be binned
checkDisjoint	= FALSE if this is TRUE it will check to see that the ranges in each of bins and gr are disjoint

Value

A data frame giving index pairs for the intersections, widths of the intersections and the fraction of each gr range meeting each bin

Examples

```
overlapWeights = getOverlapWeights(weightsExampleBins,weightsExampleGr)
```

getPValueCutoff *This function returns the significance levels for min, max, "abs" and lopsidedness.*

Description

Given an Nx4 matrix with columns 'min','max','abs' and 'lopsidededness', this function returns the cutoff levels for a given pValue.

Usage

```
getPValueCutoff(runStats, p = 0.05)
```

Arguments

runStats	a matrix with columns 'min','max','abs' and 'lopsidededness'
p	=.05 the desired p-value

Value

a vector with cutoff values

Examples

```
dimnames = list(c(),c('min','max','abs','lopsidedness'))
m = 10 * (matrix(runif(400),ncol=4,dimnames=dimnames) - 0.5)
cutoffs = getPValueCutoff(m,.05)
```

---

getRunAndLopsidednessStatistics

Get the distribution of run and lopsidedness statistics

Description

Get the distribution of run and lopsidedness statistics

Usage

```
getRunAndLopsidednessStatistics(
  scrambledDeltas,
  viewpointRegion,
  colName = "delta"
)
```

Arguments

scrambledDeltas	a list of rebinned (i.e., to large bin size) of scrambled deltas
viewpointRegion	a GRanges object giving the region that is reserved for lopsidedness
colName	= 'delta'

Value

a Nx4 matrix giving the min, max, max(abs(min),abs(max)) and lopsidedness for the run totals in the list of scrambled deltas.

`getRunStatistics` *This function is called by getRunsStatisticsDist on the individual elements of a list of scrambled runs.*

Description

This is a helper function. Currently not exported.

Usage

```
getRunStatistics(runTotals)
```

Arguments

`runTotals`	is a GRanges object giving the consecutive runs and their totals.

Value

a vector of the min, max and absolute value of the min and max for the run totals.

`getRunStatisticsDist` *This takes a list of (scrambled) runs and returns their run statistics*

Description

This function takes a list of (scrambled) runs and extracts their run totals as a matrix with colnames 'min','max' and 'abs', the latter being the max of the absolute values of the previous two

Usage

```
getRunStatisticsDist(runTotalsList)
```

Arguments

`runTotalsList`	this is a list whose members are GRanges objects giving the consecutive runs and their totals

Value

a Nx3 matrix giving the min, max and max(abs(min),abs(max)) run totals

getRunTotals *Get the runs and their values*

Description

This function finds the runs of consecutive ranges in which the sign of the data does not change. It returns a GRanges object containing the contiguous ranges and the weighted sum of data in each.

Usage

```
getRunTotals(se, innerRegion, colName = "delta")
```

Arguments

se	a SummarizedExperiment whose first assay has a column named colName. Typically this will be a one-column matrix with delta.
innerRegion	a Granges object defining the region surrounding the viewpoint to be excluded from run total calculations
colName	defaults to 'delta'

Value

a GRanges object giving the contiguous regions and their respective sums

Examples

```
runTotals = getRunTotals(binnedDeltaSE,viewpointRegion)
```

getSignificantRegions *Get ths significant regions from delta data*

Description

This function takes delta data as a SummarizedExperiment and required ancillary data and returns a GenomicRanges object whose mcols indicate the significant regions.

Usage

```
getSignificantRegions(
  deltaSE,
  regionOfInterest,
  viewpointRegion,
  smallBinSize,
  bigBinSize,
  numPermutations = 1000,
  pValue = 0.05
)
```

Arguments

deltaSE	a ranged summarized experiment with a one-column assay giving the delta mean count
regionOfInterest	a GenomicRanges object specifying the region of interest
viewpointRegion	the region withheld from arbitrary permutation
smallBinSize	size to bin original data to for permutation
bigBinSize	size to bin data to for significance testing. Must be a multiple of smallBinSize
numPermutations	= 1000 the number of permutations to be used for permutation testing
pValue	the desired significance level

Value

a GRanges object giving the bigBin binning of region of interest whose mcols gives the values of delta and logicals telling whether the bin is in the viewpoint regsion and whether it rises to statistical significance

---

getSizeFactorsDF *Get the size factors for count normalization*

Description

This function takes a data frame giving chr, start, end and count for experimental replicates and returns the size factors for each of the replicates for use in normalization

Usage

```
getSizeFactorsDF(countsDF)
```

Arguments

countsDF	A data frame whose first three columns are chr, start and end, and whose remaining columns are count data for experimental replicates

Value

The size factors for the columns of countsDF

Examples

```
sf = getSizeFactorsDF(miniSEDF)
```

getSizeFactorsSE *Get the size factors for SummarizedExperiment*

Description

This function takes a SummarizedExperiment with an assay counts and returns this object with a column sizeFactors added to its colData

Usage

```
getSizeFactorsSE(se)
```

Arguments

se	A SummarizedExperiment with an assay counts

Value

The same SummarizedExperiment with an additional column in its colData giving the size factors for counts

Examples

```
miniSEWithSizeFactors = getSizeFactorsSE(miniSE)
```

miniDeltaSE *Difference of mean capture-C counts between EScells and Neurons*

Description

A smaller deltaSE restriction to a region of interest around the viewpoint.

Usage

```
miniDeltaSE
```

Format

A RangedSummarizedExperiment with 1909 rows.

miniSE *Capture-C counts of EScells and Neurons*

Description

Capture-C counts of EScells and Neurons restricted to a region of interest around the Paupar viewpoint. Used in package documentation.

Usage

```
miniSE
```

Format

A RangedSummarizedExperiment with 1909 rows.

miniSEDF *Capture-C counts of EScells and Neurons*

Description

Capture-C counts of EScells and Neurons restricted to a region of interest around the Paupar viewpoint. This contains the same information as miniSE, but here packaged as a data frame. Used in package documentation.

Usage

```
miniSEDF
```

Format

A data frame with 1909 rows.

numPermutations *Number of permutations used in example permutation testing.*

Description

Number of permutations used in example permutation testing in the example in the documentation.

Usage

```
numPermutations
```

Format

A numeric scalar

`plotSignificantRegions` *This produces a plot of the region of interest showing regions of significance.*

Description

This function takes a input the GRanges object produced by getSignificant regions and produces a ggplot of significant features

Usage

```
plotSignificantRegions(
  significantRegions,
  significanceType = "abs",
  title = "Significant Regions",
  xLabel = "viewpoint",
  legend = TRUE
)
```

Arguments

`significantRegions`	a GRanges object as produced by getSignificantRegions
`significanceType`	= 'abs' a variable indicating whether to plot significance according to min, max or abs.
`title`	a title for the plot
`xLabel`	= 'viewpoint' supplies an xlabel
`legend`	= TRUE whether or not to show the legend

Value

a ggplot object

Examples

```
plotOfSignificantRegions = plotSignificantRegions(significantRegions)
```

plotTitle *Title for delta capture-C plot*

Description

A title for the illustrative plot in the documentation

Usage

```
plotTitle
```

Format

A character scalar

pValue *P-value*

Description

P-value used in the illustrative example of discovering statistically significant chromatin remodeling. Used in package documentation.

Usage

```
pValue
```

Format

A numeric scalar

rebinToMultiple *Rebin a SummarizedExperiment to a multiple of its bin width*

Description

This is a faster way of rebinning when the old bins are consecutive and constant width and the new bins are to be a multiple of that width

Usage

```
rebinToMultiple(se, multiple, deleteShort = FALSE)
```

Arguments

se	a RangedSummarizedExperiment to be rebinned
multiple	the factor by which to fatten the bins
deleteShort	= FALSE when set to true if the final bin is short it will be deleted

Value

a RangedSummarizedExperiment

Examples

```
rebinnedSummarizedExperiment = rebinToMultiple(binnedSummarizedExperiment,10)
```

---

regionOfInterest *Region of interest surrounding the viewpoint*

Description

This is the region 500kb up- and down-stream of the Paupar viewpoint, and defines the region on which we will look for statistically significan chromatin remodeling. This is used in package documentation.

Usage

```
regionOfInterest
```

Format

A GRanges object with one segment.

---

significanceType *Type for testing significance*

Description

Significance testing can be carried out by maximum, minimum or maximum absolute value. This has the value abs thus choosing the last of these. This is used in package documentation.

Usage

```
significanceType
```

Format

A scalar character

significantRegions *Regions of significant remodeling in example data*

Description

A GRanges object giving the value of delta in each bin and the significance or lack thereof according to the various statistical tests. This is used in package documentation.

Usage

```
significantRegions
```

Format

A GRanges object

significantRegionsPlot *A plot of the significant regions in the sample data.*

Description

A ggplot object show the values of delta in the region of interest and the significant sub-regions. This is used for documentation purposes.

Usage

```
significantRegionsPlot
```

Format

a ggplot object

smallBins *Small Bins*

Description

The deltaCaptureC package depends on rebinning mean normalized capture C data from a small bin size to a large bin size. These are the small bins. They have a bin size of 1000 bp, i.e., smallBinSize, and span the region of interest. This is used in package documentation.

Usage

```
smallBins
```

Format

a GRanges object

smallBinSize *Small Bin Size*

Description

The deltaCaptureC package depends on rebinning mean normalized capture C data from a small bin size to a large bin size. This gives the size of the former. This is used in package documentation.

Usage

```
smallBinSize
```

Format

a numeric scalar

smallerDeltaSE *A subset of miniDeltaSE.*

Description

This is a subset of miniDeltaSE. It's here so that the example for binSummarizedExperiment will run more quickly.

Usage

```
smallerDeltaSE
```

Format

A RangedSummarizedExperiment.

smallSetOfSmallBins *Small Bins*

Description

This is a subset of the bins in smallBins and is here so that the example for binSummarizedExperiment will run more quickly.

Usage

```
smallSetOfSmallBins
```

Format

a GRanges object

viewpointRegion *Region surrounding the viewpoint*

Description

This is the region 50kb up- and down-stream of the Paupar viewpoint. This is the region in which counts strongly depend on distance from the viewpoint and will be treated distinctly from the region of interest.

Usage

```
viewpointRegion
```

Format

A GRanges object with one segment.

`weightsExampleBins` *Weights example bins*

Description

This GRanges object is here to support the example for the function getOverlapWeights().

Usage

```
weightsExampleBins
```

Format

a GRanges object

`weightsExampleGr` *Weights example*

Description

This GRanges object is here to support the example for the function getOverlapWeights().

Usage

```
weightsExampleGr
```

Format

a GRanges object

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