Package ‘EDASeq’

December 21, 2016

Version 2.8.0

Title Exploratory Data Analysis and Normalization for RNA-Seq

Description Numerical and graphical summaries of RNA-Seq read data. Within-lane normalization procedures to adjust for GC-content effect (or other gene-level effects) on read counts: loess robust local regression, global-scaling, and full-quantile normalization (Risso et al., 2011). Between-lane normalization procedures to adjust for distributional differences between lanes (e.g., sequencing depth): global-scaling and full-quantile normalization (Bullard et al., 2010).

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Date 08-30-2011

Depends Biobase (>= 2.15.1), ShortRead (>= 1.11.42)

Imports methods, graphics, BiocGenerics, IRanges (>= 1.13.9), DESeq, aroma.light, Rsamtools (>= 1.5.75), biomaRt, Biostrings, AnnotationDbi, GenomicFeatures, GenomicRanges

Suggests BiocStyle, knitr, yeastRNASeq, leeBamViews, edgeR, KernSmooth

VignetteBuilder knitr

License Artistic-2.0

LazyLoad yes

biocViews Sequencing, RNASeq, Preprocessing, QualityControl, DifferentialExpression

URL https://github.com/drisso/EDASeq

BugReports https://github.com/drisso/EDASeq/issues

NeedsCompilation no

R topics documented:

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EDASeq-package

Exploratory Data Analysis and Normalization for RNA-Seq data

Description

Numerical summaries and graphical representations of some key features of the data along with implementations of both within-lane normalization methods for GC content bias and between-lane normalization methods to adjust for sequencing depth and possibly other differences in distribution.

Details

The SeqExpressionSet class is used to store gene-level counts along with sample information. It extends the virtual class eSet. See the help page of the class for details.

"Read-level" information is managed via the FastqFileList and BamFileList classes of Rsamtools. Most used graphic tools for the FastqFileList and BamFileList objects are: 'barplot', 'plotQuality', 'plotNtFrequency'. For SeqExpressionSet objects are: 'biasPlot', 'meanVarPlot', 'MDPlot'. To perform gene-level normalization use the functions 'withinLaneNormalization' and 'betweenLaneNormalization'.

An 'As' method exists to coerce SeqExpressionSet objects to CountDataSet objects (DESeq package).

See the package vignette for a typical Exploratory Data Analysis example.

Author(s)

Davide Risso and Sandrine Dudoit. Maintainer: Davide Risso <risso.davide@gmail.com>

References


Description

High-level functions to produce barplots of some complex objects.

Methods

signature(height = "BamFile") Usage: barplot(height, strata = c("rname", "strand")) It produces a barplot of the total number of reads in each chromosome (if "rname") or strand.

signature(height = "BamFileList") It produces a barplot of the total number of reads in each object in height. If unique=TRUE is specified, it stratified the total by uniquely/non-uniquely mapped reads.

signature(height = "FastqFileList") It produces a barplot of the total number of reads in each object in height.

Description

Between-lane normalization for sequencing depth and possibly other distributional differences between lanes.

Usage

betweenLaneNormalization(x, which = c("median", "upper", "full"), offset = FALSE, round = TRUE)

Arguments

x A numeric matrix representing the counts or a SeqExpressionSet object.
which Method used to normalized. See the details section and the reference below for details.
offset Should the normalized value be returned as an offset leaving the original counts unchanged?
round If TRUE the normalization returns rounded values (pseudo-counts). Ignored if offset=TRUE.

Details

This method implements three normalizations described in Bullard et al. (2010). The methods are:
median: a scaling normalization that forces the median of each lane to be the same.
upper: the same but with the upper quartile.
full: a non linear full quantile normalization, in the spirit of the one used in microarrays.
Methods

signature(x = "matrix") It returns a matrix with the normalized counts if offset=FALSE or with the offset if offset=TRUE.

signature(x = "SeqExpressionSet") It returns a linkS4class(SeqExpressionSet) with the normalized counts in the normalizedCounts slot and with the offset in the offset slot (if offset=TRUE).

Author(s)
Davide Risso.

References


Examples

library(yeastRNASeq)
data(geneLevelData)
data(yeastGC)

sub <- intersect(rownames(geneLevelData), names(yeastGC))

mat <- as.matrix(geneLevelData[sub, ])

data <- newSeqExpressionSet(mat,
    phenoData=AnnotatedDataFrame(
        data.frame(conditions=factor(c("mut", "mut", "wt", "wt")),
            row.names=colnames(geneLevelData)),
        featureData=AnnotatedDataFrame(data.frame(gc=yeastGC[sub])))

norm <- betweenLaneNormalization(data, which="full", offset=FALSE)
Arguments

x  A numeric vector with the quantity of interest (e.g. gene counts, log-fold-changes, ...)

y  A numeric vector with the covariate of interest (e.g. gene length, GC-content, ...)

num.bins  A numeric value specifying the number of bins in which to stratify y. Default to 10.

...  See par

Methods

signature(x = "numeric", y = "numeric", num.bins = "numeric") It plots a line representing the regression of every column of the matrix x on the numeric covariate y. One can pass the usual graphical parameters as additional arguments (see par).

Examples

library(yeastRNASeq)
data(geneLevelData)
data(yeastGC)

sub <- intersect(rownames(geneLevelData), names(yeastGC))

mat <- as.matrix(geneLevelData[sub,])
data <- newSeqExpressionSet(mat,
  phenoData = AnnotatedDataFrame(data.frame(conditions = factor(c("mut", "mut", "wt", "wt")),
                                  row.names = colnames(geneLevelData))),
  featureData = AnnotatedDataFrame(data.frame(gc = yeastGC[sub])))

lfc <- log(geneLevelData[sub, 3] + 1) - log(geneLevelData[sub, 1] + 1)
biasBoxplot(lfc, yeastGC[sub], las=2, cex.axis=.7)
signature(x = "SeqExpressionSet", y = "character") It plots a line representing the regression of every lane in x on the covariate specified by y. y must be one of the column of the featureData slot of the x object. One can pass the usual graphical parameters as additional arguments (see par). The parameter color_code (optional) must be a number specifying the column of phenoData to be used for color-coding. By default it is color-coded according to the first column of phenoData. If legend=TRUE and col is not specified a legend with the information stored in phenoData is added.

Examples

library(yeastRNASeq)
data(geneLevelData)
data(yeastGC)

sub <- intersect(rownames(geneLevelData), names(yeastGC))
mat <- as.matrix(geneLevelData[sub,])
data <- newSeqExpressionSet(mat, 
    phenoData=AnnotatedDataFrame(
        data.frame(conditions=factor(c("mut", "mut", "wt", "wt")),
            row.names=colnames(geneLevelData))),
    featureData=AnnotatedDataFrame(data.frame(gc=yeastGC[sub])))

biasPlot(data,"gc",ylim=c(0,5),log=TRUE)

boxplot-methods

Methods for Function boxplot in Package EDASeq

Description
High-level functions to produce boxplots of some complex objects.

Methods

signature(x = "FastqQuality") It plots the distribution of the quality per read position.
signature(x = "SeqExpressionSet") It plots the distribution of the log counts in each lane of x.

geneLengthAndGCContent

Get gene length and GC-content

Description
Automatically retrieves gene length and GC-content information from Biomart or org.db packages.

Usage
geneLengthAndGCContent(id, org, mode=c("biomart", "org.db"))
Arguments

id  Character vector of one or more ENSEMBL or ENTREZ gene IDs.

org  Organism three letter code, e.g. 'hsa' for 'Homo sapiens'. See also: http://www.genome.jp/kegg/catalog/org_list.html;
     In org.db mode, this can be also a specific genome assembly, e.g. 'hg38' or 'sac-Cer3'.

mode  Mode to retrieve the information. Defaults to 'biomart'. See Details.

Details

The 'biomart' mode is based on functionality from the biomaRt package and retrieves the required
information from the BioMart database. This is available for all ENSEMBL organisms and is
typically most current, but can be time-consuming when querying several thousand genes at a time.

The 'org.db' mode uses organism-based annotation packages from Bioconductor. This is much
faster than the 'biomart' mode, but is only available for selected model organism currently supported
by BioC annotation functionality.

Results for the same gene ID(s) can differ between both modes as they are based on different sources
for the underlying genome assembly. While the 'biomart' mode uses the latest ENSEMBL version,
the 'org.db' mode uses BioC annotation packages typically built from UCSC.

Value

A numeric matrix with two columns: gene length and GC-content.

Author(s)

Ludwig Geistlinger <Ludwig.Geistlinger@bio.ifi.lmu.de>

See Also

getSequence to retrieve a genomic sequence from BioMart, genes to extract genomic coordinates
from a TxDb object, getSeq to extract genomic sequences from a BSgenome object, alphabetFrequency
to calculate nucleotide frequencies.

Examples

geneLengthAndGCContent("ENSG0000012048", "hsa")

MDPlot-methods  

Methods for Function MDPlot in Package EDASeq

Description

MDPlot produces a mean-difference smooth scatterplot of two lanes in an experiment.

Usage

MDPlot(x, y, ...)
Arguments

\(x\) Either a numeric matrix or a `SeqExpressionSet` object containing the gene expression.

\(y\) A numeric vector specifying the lanes to be compared.

... See `par`

Details

The mean-difference (MD) plot is a useful plot to visualize difference in two lanes of an experiment. From a MDPlot one can see if normalization is needed and if a linear scaling is sufficient or nonlinear normalization is more effective.

The MDPlot also plots a lowess fit (in red) underlying a possible trend in the bias related to the mean expression.

Methods

```r
signature(x = "matrix", y = "numeric")
signature(x = "SeqExpressionSet", y = "numeric")
```

Examples

```r
library(yeastRNASeq)
data(geneLevelData)
data(yeastGC)

sub <- intersect(rownames(geneLevelData), names(yeastGC))
mat <- as.matrix(geneLevelData[sub,])
data <- newSeqExpressionSet(mat,
    phenoData=AnnotatedDataFrame(
    data.frame(conditions=factor(c("mut", "mut", "wt", "wt")),
             row.names=colnames(geneLevelData))),
    featureData=AnnotatedDataFrame(data.frame(gc=yeastGC[sub])))

MDPlot(data,c(1,3))
```

Description

`meanVarPlot` produces a `smoothScatter` plot of the mean variance relation.

Methods

```r
signature(x = "SeqExpressionSet") It takes as additional argument log, which if true consider the logarithm of the counts before computing mean and variance. To avoid missing values, we consider the maximum between 0 and the log of the counts. Along with the scatter plot the function plots a line representing the `lowess` fit.
```
newSeqExpressionSet

Function to create a new SeqExpressionSet object.

Description

User-level function to create new objects of the class SeqExpressionSet.

Usage

newSeqExpressionSet(counts,
                      normalizedCounts = matrix(data=NA, nrow=nrow(counts), ncol=ncol(counts), dimnames=dimnames(counts),
                      offset = matrix(data=0, nrow=nrow(counts), ncol=ncol(counts), dimnames=dimnames(counts),
                      phenoData = annotatedDataFrameFrom(counts, FALSE),
                      featureData = annotatedDataFrameFrom(counts, TRUE),
                      ...)
                      )

Arguments

- counts: A matrix containing the counts for an RNA-Seq experiment. One column for each lane and one row for each gene.
- normalizedCounts: A matrix with the same dimensions of counts with the normalized counts.
- offset: A matrix with the same dimensions of counts defining the offset (usually useful for normalization purposes). See the package vignette for a discussion on the offset.
- phenoData: A data.frame or AnnotatedDataFrame with sample information, such as biological condition, library preparation protocol, flow-cell,...
- featureData: A data.frame or AnnotatedDataFrame with feature information, such as gene length, GC-content, ...

... Other arguments will be passed to the constructor inherited from eSet.

Value

An object of class SeqExpressionSet.

Author(s)

Davide Risso

See Also

SeqExpressionSet

Examples

counts <- matrix(data=0, nrow=100, ncol=4)
for(i in 1:4) {
counts[, i] <- rpois(100, lambda=50)
}
cond <- c(rep("A", 2), rep("B", 2))
plotPCA-methods

Methods for Function plot in Package EDASeq

Description
High-level function to produce plots given one BamFileList object and one FastqFileList object.

Methods
signature(x = "BamFileList", y = "FastqFileList") It produces a barplot of the percentage of mapped reads. If strata=TRUE it stratifies the bars according to the unique/non-unique mapped reads. To be meaningful, x should be a set of aligned reads and y a set of raw reads on the same samples.

plotNtFrequency-methods

Methods for Function plotNtFrequency in Package EDASeq

Description
Plots the nucleotide frequencies per position.

Methods
signature(x = "ShortRead")
signature(x = "BamFile")
It plots the nucleotide frequencies per position, averaging all the reads in x.

plotPCA-methods

Methods for Function plotPCA in Package EDASeq

Description
plotPCA produces a Principal Component Analysis (PCA) plot of the counts in object.

Usage
## S4 method for signature 'matrix'
plotPCA(object, k=2, labels=TRUE, isLog=FALSE, ...)
## S4 method for signature 'SeqExpressionSet'
plotPCA(object, k=2, labels=TRUE, ...)
Arguments

- **object**: Either a numeric matrix or a `SeqExpressionSet` object containing the gene expression.
- **k**: The number of principal components to be plotted.
- **labels**: Logical. If TRUE, and k=2, it plots the colnames of object as point labels.
- **isLog**: Logical. Set to TRUE if the data are already on the log scale.
- **...**: See `par`

Details

The Principal Component Analysis (PCA) plot is a useful diagnostic plot to highlight differences in the distribution of replicate samples, by projecting the samples into a lower dimensional space. If there is strong differential expression between two classes, one expects the samples to cluster by class in the first few Principal Components (PCs) (usually 2 or 3 components are enough). This plot also highlights possible batch effects and/or outlying samples.

Methods

signature(x = "matrix")
signature(x = "SeqExpressionSet")

Examples

```r
library(yeastRNASeq)
data(geneLevelData)

mat <- as.matrix(geneLevelData)
data <- newSeqExpressionSet(mat,
    phenoData=AnnotatedDataFrame(
        data.frame(conditions=factor(c("mut", "mut", "wt", "wt")),
        row.names=colnames(geneLevelData))))

plotPCA(data, col=rep(1:2, each=2))
```

Description

`plotQuality` produces a plot of the quality of the reads.

Methods

signature(x = "BamFileList") It produces a plot that summarizes the per-base mean quality of the reads of each BAM file in x.

signature(x = "BamFile") It produces a boxplot of the per-base distribution of the quality scores of the reads in x.

signature(x = "FastqFileList") It produces a plot that summarizes the per-base mean quality of the reads of each FASTQ file in x.
plotRLE-methods

Details
Since FASTQ files can be very long, it can be very expensive to process a whole file. One way to avoid this, is to consider a subset of the file and then plot the quality of the subset. As long as one assumes that the subset is random, this is a good approximation. The function `FastqSampler` of `ShortRead` can be used for this. See its help page for an example.

Description
`plotRLE` produces a Relative Log Expression (RLE) plot of the counts in `x`.

Usage
`plotRLE(x, ...)`

Arguments
- `x`: Either a numeric matrix or a `SeqExpressionSet` object containing the gene expression.
- `...`: See `par`.

Details
The Relative Log Expression (RLE) plot is a useful diagnostic plot to visualize the differences between the distributions of read counts across samples. It shows the boxplots of the log-ratios of the gene-level read counts of each sample to those of a reference sample (defined as the median across the samples). Ideally, the distributions should be centered around the zero line and as tight as possible. Clear deviations indicate the need for normalization and/or the presence of outlying samples.

Methods
- `signature(x = "matrix")`
- `signature(x = "SeqExpressionSet")`

Examples
```R
library(yeastRNASeq)
data(geneLevelData)
mat <- as.matrix(geneLevelData)
data <- newSeqExpressionSet(mat, phenoData=AnnotatedDataFrame(
    data.frame(conditions=factor(c("mut", "mut", "wt", "wt")),
                row.names=colnames(geneLevelData))))

plotRLE(data, col=rep(2:3, each=2))
```
**SeqExpressionSet-class**

"SeqExpressionSet" class for collections of short reads

---

**Description**

This class represents a collection of digital expression data (usually counts from RNA-Seq technology) along with sample information.

**Objects from the Class**

Objects of this class can be created from a call to the `newSeqExpressionSet` constructor.

**Extends**

Class `eSet`, directly. Class `VersionedBiobase`, by class `eSet`, distance 2. Class `Versioned`, by class `eSet`, distance 3.

**Slots**

Inherited from `eSet`:

- **assayData** Contains matrices with equal dimensions, and with column number equal to `nrow(phenoData)`. `assayData` must contain a matrix `counts` with rows representing features (e.g., genes) and columns representing samples. The optional matrices `normalizedCounts` and `offset` can be added to represent a normalization in terms of pseudo-counts or offset, respectively, to be used for subsequent analyses. See the vignette for details. Class: `AssayData-class`.

- **phenoData** Sample information. For compatibility with DESeq, there should be at least the column `conditions`. See `eSet` for details.

- **featureData** Feature information. It is recommended to include at least length and GC-content information. This slot is used for `withinLaneNormalization`. See `eSet` for details.

- **experimentData** See `eSet`

- **annotation** See `eSet`

- **protocolData** See `link{eSet}`

**Methods**

See `eSet` for inherited methods. Additional methods:

- **counts** signature(object="SeqExpressionSet") : returns the counts matrix.

- **counts<-** signature(object = "SeqExpressionSet") : method to replace the counts matrix.

- **normCounts** signature(object="SeqExpressionSet") : returns the normalizedCounts matrix.

- **normCounts<-** signature(object = "SeqExpressionSet") : method to replace the normalizedCounts matrix.

- **offst** signature(object = "SeqExpressionSet") : returns the offset matrix.

- **offst<-** signature(object = "SeqExpressionSet") : method to replace the offset slot.

- **boxplot** signature(x = "SeqExpressionSet") : produces a boxplot of the log counts.

---
### meanVarPlot signature

```r
signature(x = "SeqExpressionSet"): produces a smoothScatter plot of the mean variance relation. See meanVarPlot for details.
```

### biasPlot signature

```r
signature(x = "SeqExpressionSet", y = "character"): produces a plot of the 
lowess regression of the counts on some covariate of interest (usually GC-content or length). See biasPlot for details.
```

### wihtinLaneNormalization signature

```r
signature(x = "SeqExpressionSet", y = "missing"): within lane normalization for GC-content (or other lane specific) bias. See withinLaneNormalization for details.
```

### betweenLaneNormalization signature

```r
signature(x = "SeqExpressionSet"): between lane normalization for sequencing depth and possibly other distributional differences between lanes. See betweenLaneNormalization for details.
```

### coerce signature

```r
signature(from = "SeqExpressionSet", to = "CountDataSet"): coercion to DESeq class CountDataSet for compatibility with downstream analysis.
```

### Author(s)

Davide Risso <risso.davide@gmail.com>

### See Also

eSet, newSeqExpressionSet, biasPlot, withinLaneNormalization, betweenLaneNormalization

### Examples

```r
showMethods(class="SeqExpressionSet", where=getNamespace("EDASeq"))

counts <- matrix(data=0, nrow=100, ncol=4)
for(i in 1:4) {
  counts[,i] <- rpois(100,lambda=50)
}
cond <- c(rep("A", 2), rep("B", 2))
data <- newSeqExpressionSet(counts, phenoData=AnnotatedDataFrame(data.frame(conditions=cond)))

head(counts(data))
boxplot(data, col=as.numeric(pData(data)[,1])+1)
```
Arguments

- **x**: A numeric matrix representing the counts or a `SeqExpressionSet` object.
- **y**: A numeric vector representing the covariate to normalize for (if `x` is a matrix) or a character vector with the name of the covariate (if `x` is a `SeqExpressionSet` object). Usually it is the GC-content.
- **which**: Method used to normalize. See the details section and the reference below for details.
- **offset**: Should the normalized value be returned as an offset leaving the original counts unchanged?
- **num.bins**: The number of bins used to stratify the covariate for `median`, `upper` and `full` methods. Ignored if `loess`. See the reference for a discussion on the number of bins.
- **round**: If TRUE the normalization returns rounded values (pseudo-counts). Ignored if `offset=TRUE`.

Details

This method implements four normalizations described in Risso et al. (2011).

The **loess** normalization transforms the data by regressing the counts on `y` and subtracting the loess fit from the counts to remove the dependence.

The **median**, **upper** and **full** normalizations are based on the stratification of the genes based on `y`. Once the genes are stratified in `num.bins` strata, the methods work as follows.

- **median**: scales the data to have the same median in each bin.
- **upper**: the same but with the upper quartile.
- **full**: forces the distribution of each stratum to be the same using a non linear full quantile normalization, in the spirit of the one used in microarrays.

Methods

- `signature(x = "matrix", y = "numeric")` It returns a matrix with the normalized counts if `offset=FALSE` or with the offset if `offset=TRUE`.
- `signature(x = "SeqExpressionSet", y = "character")` It returns a `SeqExpressionSet` with the normalized counts in the `normalizedCounts` slot and with the offset in the `offset` slot (if `offset=TRUE`).

Author(s)

Davide Risso.

References

Examples

```r
library(yeastRNASeq)
data(geneLevelData)
data(yeastGC)

sub <- intersect(rownames(geneLevelData), names(yeastGC))
mat <- as.matrix(geneLevelData[sub, ])
data <- newSeqExpressionSet(mat,
phenoData=AnnotatedDataFrame(
data.frame(conditions=factor(c("mut", "mut", "wt", "wt")),
row.names=colnames(geneLevelData))),
featureData=AnnotatedDataFrame(data.frame(gc=yeastGC[sub])))
norm <- withinLaneNormalization(data, "gc", which="full", offset=FALSE)
```

---

**yeastGC**  
*GC-content of S. Cerevisiae genes*

**Description**

This data set gives the GC-content (proportion of G and C) of the genes of *S. Cerevisiae*, from SGD release 64 annotation.

**Usage**

`yeastGC`

**Format**

A vector containing 6717 observations.

**Source**

SGD release 64: [http://www.yeastgenome.org](http://www.yeastgenome.org)

---

**yeastLength**  
*Length of S. Cerevisiae genes*

**Description**

This data set gives the length (in base pairs) of the genes of *S. Cerevisiae*, from SGD release 64 annotation.

**Usage**

`yeastLength`
**yeastLength**

**Format**

A vector containing 6717 observations.

**Source**

SGD release 64: [http://www.yeastgenome.org](http://www.yeastgenome.org)
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