Package ‘samExploreR’

April 26, 2017

Type Package

Title samExploreR package: high-performance read summarisation to count vectors with availability of sequencing depth reduction simulation

Version 1.0.0

Depends ggplot2, Rsubread, RNAseqData, HNRNPC.bam.chr14, edgeR, R (>= 3.4.0)

Author Alexey Stupnikov, Shailesh Tripathi and Frank Emmert-Streib

Maintainer shailesh.tripathy@gmail.com

Description This R package is designed for subsampling procedure to simulate sequencing experiments with reduced sequencing depth. This package can be used to anlayze data generated from all major sequencing platforms such as Illumina GA, HiSeq, MiSeq, Roche GS-FLX, ABI SOLiD and LifeTech Ion PGM Proton sequencers. It supports multiple operating systems including Linux, Mac OS X, FreeBSD and Solaris. Was developed with usage of Rsubread.

Imports grDevices, stats, graphics

License GPL-3

LazyLoad yes

Suggests BiocStyle, RUnit, BiocGenerics, Matrix

biocViews Sequencing, SequenceMatching, RNASeq, ChIPSeq, DNaseq, WholeGenome, GeneTarget, Alignment, GeneExpression, GeneticVariability, GeneRegulation, Preprocessing, GenomeAnnotation, Software

NeedsCompilation no

R topics documented:

df_intersect .................................................. 2
df_sole .......................................................... 2
exploreRep ..................................................... 3
exploreRob ..................................................... 4
plotsamExplorer ............................................. 6
samExplore .................................................... 7

Index 9
Description

Example data for plotting output of samExplore function. Dataframe consists three columns, first column contains names of new Genes or exons, second column provides sequence depth and third column provide total counts for the corresponding sequence coverage.

Usage

data("df_intersect")

Format

A data frame with 1125 observations on the following 3 variables.

Label  a character vector
Variable a numeric vector
Value   a numeric vector

Details

Example data for plotting output of samExplore function. Dataframe consists three columns, first column contains names of new Genes or exons, second column provides sequence depth and third column provide total counts for the corresponding sequence coverage.

Value

Example data for plotting results.

Examples

data(df_intersect)

Description

Example data for plotting output of samExplore function. Dataframe consists three columns, first column contains names of new Genes or exons, second column provides sequence depth and third column provide total counts for the corresponding sequence coverage.

Usage

data("df_sole")
exploreRep

Format
A data frame with 1125 observations on the following 3 variables.

Label a character vector
Variable a numeric vector
Value a numeric vector

Details
Example data for plotting output of samExplore function. Dataframe consists three columns, first column contains names of new Genes or exons, second column provides sequence depth and third column provide total counts for the corresponding sequence coverage.

Value
Example data for plotting results.

Examples
data(df_sole)

exploreRep

exploreRep: function to explore the reproducibility

Description
This function explores the reproducibility of analysis with annotation altering

Usage
exploreRep(df_d, lbl_vect, f)

Arguments
df_d a dataframe containing the dataset to explore with 3 columns: label, f ratio, value to compare (e.g. number of differentially expressed genes)
lbl_vect a vector of character strings specifying the labels for which the analysis should be run
f A numeric value of f for which the analysis should be run

Details
exploreRep function to explore the reproducibility of the analysis with altering of annotation. It runs ANOVA test for values to compare (e.g. number of differentially expressed genes) corresponding to different Annotation labels (i.e. analysis’ run for different annotation types).

This function takes as input a dataframe containing the dataset to explore.

Here is the example of the dataframe
AnnotA 0.1  13
AnnotB 0.1 101
AnnotC 0.1  36
AnnotA 0.1  13
AnnotB 0.1 101
AnnotC 0.1  36
AnnotA 0.4  40
AnnotB 0.4 153
AnnotC 0.4  62
AnnotA 0.8  71
AnnotB 0.8 203
AnnotC 0.8 160

exploreRob Third column gives the values to compare (here number of differentially expressed genes).
exploreRep function subsets the dataset to consider only values for one f and runs ANOVA test for groups corresponding to annotations of interest.

Value
An output of aov function

Author(s)
Alexey Stupnikov and Shailesh Tripathi

Examples

#library(samExploreR)
data("df_sole")
#run ANOVA for annotation types labeled 'New, Gene' and 'New, Exon' and
#f value 0.9
exploreRep(df_sole, lbl_vect = c('New, Gene', 'Old, Gene'), f = 0.9)

#run ANOVA for annotation type labeled 'Old' and 'New' and f value 0.5
exploreRep(df_sole, lbl_vect = c('New, Gene', 'Old, Gene'), f = 0.5)

---

exploreRob: function to explore the robustness

Description
This function explores the robustness of analysis with sequencing depth altering

Usage
exploreRob(df_d, lbl, f_vect)
Arguments

df_d  a dataframe containing the dataset to explore with 3 columns: label, f ratio, value to compare (e.g. number of differentially expressed genes)

lbl  a character string specifying the label for which the analysis should be run

f_vect  A numeric vector containing the values of f for which the analysis should be run

Details

exploreRob function to explore the robustness of the analysis with altering of sequencing depth.
It runs ANOVA test for values to compare (e.g. number of differentially expressed genes) corresponding to different f ratio values (i.e. values of sequencing depth)

This function takes as input a dataframe containing the dataset to explore.

Here is the example of the dataframe

...  
AnnotA 0.1 13  
AnnotB 0.1 101  
AnnotC 0.1 36  
AnnotA 0.1 13  
AnnotB 0.1 101  
AnnotC 0.1 36  
AnnotA 0.4 40  
AnnotB 0.4 153  
AnnotC 0.4 62  
AnnotA 0.8 71  
AnnotB 0.8 203  
AnnotC 0.8 160  
...

exploreRob function subsets the dataset to consider only values for one type of annotation and runs ANOVA test for groups corresponding to f values of interest.

Value
  An output of aov function

Author(s)
  Alexey Stupnikov and Shailesh Tripathi

Examples

#library(samExploreR)  
data("df_sole")  
#run ANOVA for annotation type labeled 'New, Gene' and f values 0.9, 0.95  
exploreRob(df_sole, lbl = "New, Gene", f_vect = c(0.9, 0.95))

#run ANOVA for annotation type labeled 'Old' and f values 0.5, 0.95  
exploreRob(df_sole, lbl = "Old", f_vect = c(0.5, 0.95))
plotsamExplorer

Plots the results of output dataframe object.

Description
Boxplot results between sequence-depth and number of differentially expressed genes.

Usage

plotsamExplorer(dat, save = FALSE, filename = NULL, p.depth = 0.9, font.size = 3.5, anova = TRUE, x.lab=NULL, y.lab=NULL, leg.lab=NULL)

Arguments
- **dat**: is a dataframe object, which consists three columns strictly labelled as: "Label", "Variable" and "Value".
- **save**: is a logical value to save plot as a pdf.
- **filename**: is a character to assign filename, if a user want to save the plot.
- **p.depth**: is a numeric value for anova test to be performed for number differentially expressed genes of different sequence-depths.
- **font.size**: is a numeric value to set font size of the plot.
- **anova**: is a logical value for anova test to be performed for number differentially expressed genes of different sequence-depths.
- **x.lab**: is a string value to assign a label for x-axis.
- **y.lab**: is a string value to assign a label for y-axis.
- **leg.lab**: is a string vector assigns lables for legends in the plot.

Value
Generates a plot in a pdf format.

Author(s)
Frank-Emmert Streib, Shailesh Tripathi, Aleksei sputnikov

Examples

```r
 data("df_sole")
data("df_intersect")

plotsamExplorer(df_sole, save=TRUE, filename="ss",p.depth=.9, font.size=4, anova=TRUE)
plotsamExplorer(df_intersect, save=TRUE, filename="ss",p.depth=.9, font.size=4, anova=FALSE)
```
**Description**

samExplore: This function assigns mapped sequencing reads to genomic features and simulates a sample with reduced sequencing depth.

**Usage**

```r
```

**Arguments**

- `...` These are the same arguments of `featureCounts` function of `Rsubread` package, for more details check `featureCounts` function.
- `subsample_d` numeric value which describes fraction of reads to be remained in subsampling.
- `N_boot` integer value for number of resample procedures to be run.
- `countboot` is a character vector which contains following options: `all`, `Assigned`, `Unassigned_Ambiguity`, `Unassigned_MultiMapping`, `Unassigned_NoFeatures`, `Unassigned_Unmapped`, `Unassigned_MappingQuality`, `Unassigned_FragmentLength`, `Unassigned_Chimera`, `Unassigned_Secondary`, `Unassigned_Nonjunction`, `Unassigned_Duplicate`. A user can select any of these options for resampling if user selects `all` then the resampling procedure will consider all assigned and unassigned reads. If a user selects `Assigned` option then resampling procedure will consider `Assigned` reads only for resampling. If a user selects any other option it will consider those unmapped reads along with `Assigned` reads. A user can select more than one choices and input as a vector.

**Details**

samExplore See `featureCounts` for details. Output is a list objects which has three components.

1) "bootres": is a list object of size of input files, each list object contains a resampling matrix of features.
2) "target.size": it is a numeric vector contains total feature counts of a certain sequence depth for each input file.
3) "feature main": returns a list object which is the output of `featureCounts` function of Rsubread package.

**Value**

returns a list object.
Examples

# Simulate a sample with sequencing depth 80% of initial for SAM format
# single-end reads using built-in RefSeq annotation for hg19:
#### Consider all mapped and unmapped reads for resampling#
inpf <- RNAseqData.HNRNPC.bam.chr14_BAMFILES
res1 <- samExplore(files=inpf, annot.inbuilt="hg19", subsample_d = 0.8)
#### Consider Assigned and Unassigned Unmapped reads for resampling#
res2 <- samExplore(inpf, N.boot=10, subsample_d=.8,
                   countboot=c("Assigned","Unassigned_Unmapped"))
#### Consider only Assigned reads for resampling#
res3 <- samExplore(inpf, N.boot=10, subsample_d=.8,
                   countboot="Assigned")
Index

*Topic datasets
  df_intersect, 2
  df_sole, 2
  df_intersect, 2
  df_sole, 2
  exploreRep, 3
  exploreRob, 4
  plotsamExplorer, 6
  samExplore, 7