

Package ‘APalyzer’

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Type Package

Title A toolkit for APA analysis using RNA-seq data

Version 1.2.0

Description Perform 3'UTR APA, Intronic APA and gene expression analysis using RNA-seq data.

biocViews Sequencing, RNASeq, DifferentialExpression, GeneExpression, GeneRegulation, Annotation, DataImport, Software

Imports GenomicRanges, GenomicFeatures, GenomicAlignments, DESeq, ggrepel, SummarizedExperiment, Rsubread, stats, ggplot2, methods, rtracklayer, ensemblDb, VariantAnnotation, dplyr, tidyr, repmis

Suggests knitr, rmarkdown, BiocStyle, org.Mm.eg.db, AnnotationDbi, TBX20BamSubset, Rsamtools, testthat

URL <https://github.com/RJWANGbioinfo/APalyzer/>

BugReports <https://github.com/RJWANGbioinfo/APalyzer/issues>

VignetteBuilder knitr

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APABox	<i>APABox, APA RED Box plotting</i>
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Description

APA RED Box plotting

Usage

```
APABox(df, xlab = "APAre", ylab = "RED",
        plot_title = NULL)
```

Arguments

df	a dataframe of APAdiff output
xlab	lable of x-axis, default is 'APAre'
ylab	lable of y-axis, default is 'RED'
plot_title	Main title of plot

Value

The function APABox return a Box plot.

Author(s)

Ruijia Wang

Examples

```
library("TBX20BamSubset")
library("Rsamtools")
flsall = getBamFileList()
extpath = system.file("extdata",
  "mm9_TBX20.APAout.RData", package="APALyzer")
load(extpath)
sampleTable1 = data.frame(samplename = c(names(flsall)),
  condition = c(rep("NT",3),rep("KD",3)))
sampleTable2 = data.frame(samplename = c("SRR316184","SRR316187"),
  condition = c("NT","KD"))
## 3'UTR APA plot
test_3UTRmuti=APAdiff(sampleTable1,DFUTRraw,
  conKET='NT',trtKEY='KD',PAS='3UTR',CUTreads=0)
UTR_APA_PLOTBOX=APABox(test_3UTRmuti, plot_title='3UTR APA')
```

```
## IPA plot
test_IPAmuti=APAdiff(sampleTable1,IPA_OUTraw,
  conKET='NT',trtKEY='KD',PAS='IPA',CUTreads=0)
IPA_PLOTBOX=APABox(test_IPAmuti, plot_title='IPA')
```

APAdiff	<i>APAdiff, calculate delta relative expression (RED) and statistics significance between two sample groups</i>
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Description

Calculate delta relative expression (RED) and statistics significance between two sample groups.

Usage

```
APAdiff(sampleTable,mutiraw, conKET='NT',
  trtKEY='KD',PAS='3UTR',CUTreads=0,p_adjust_methods="fdr")
```

Arguments

sampleTable	a dataframe of sample table containing 8 colmun for Intronic PASs: 'sample-name','condition'
mutiraw	a dataframe output obtained using either PASEXP_3UTR or PASEXP_IPA
conKET	the name of control in the samplatable, default is 'NT'
trtKEY	the name of control in the samplatable, default is 'KD'
PAS	type of PAS analyzed, either '3UTR' or 'IPA', default is '3UTR'
CUTreads	reads cutoff used for the analysis, default is 0
p_adjust_methods	p value correction method, the method can be "holm", "hochberg", "hommel", "bonferroni", "BH", "BY","fdr", "none", default is "fdr"

Value

The function APAdiff return a dataframe containing RED, pvalue and regulation pattern (UP, DN or NC) for either each gene (3'UTR APA) or each PAS (IPA).

Author(s)

Ruijia Wang

Examples

```
library("TBX20BamSubset")
library("Rsamtools")
flsall = getBamFileList()
extpath = system.file("extdata",
  "mm9_TBX20.APAout.RData", package="APalyzer")
load(extpath)
```

```

sampleTable1 = data.frame(samplename = c(names(flsall)),
  condition = c(rep("NT",3),rep("KD",3)))
sampleTable2 = data.frame(samplename = c("SRR316184","SRR316187"),
  condition = c("NT","KD"))
## Analysis 3'UTR APA between KD and NT group using muti-replicates
test_3UTRmuti=APAdiff(sampleTable1,DFUTRraw,
  conKET='NT',trtKEY='KD',PAS='3UTR',CUTreads=0,p_adjust_methods="fdr")

## Analysis 3'UTR APA between KD and NT group without replicates
test_3UTRsing=APAdiff(sampleTable2,DFUTRraw,
  conKET='NT',trtKEY='KD',PAS='3UTR',CUTreads=0,p_adjust_methods="fdr")

## Analysis IPA between KD and NT group
test_IPAmuti=APAdiff(sampleTable1,IPA_OUTraw,
  conKET='NT',trtKEY='KD',PAS='IPA',CUTreads=0,p_adjust_methods="fdr")

## Analysis IPA between KD and NT group without replicates
test_IPAsing=APAdiff(sampleTable2,IPA_OUTraw,
  conKET='NT',trtKEY='KD',PAS='IPA',CUTreads=0,p_adjust_methods="fdr")

```

APAVolcano

APAVolcano, APA Volcano plotting

Description

APA Volcano plotting

Usage

```

APAVolcano (df, Pcol = "pvalue",PAS='3UTR',
  top = -1, markergenes = NULL,
  y_cutoff = 0.05,xlab = "RED", ylab = "-Log10(P-value)",
  PAScolor = c("gray80", "red", "blue"),
  alpha = 0.75, plot_title = NULL,
  width = 4, height = 2.5)

```

Arguments

df	a dataframe of APAdiff output
Pcol	p-value column used to for y-axis of volcano plot, default is 'pvalue'
top	number of genes/IPA to label in the plot, default is -1, which don't lable top genes, user can set it >0, e.g., top = 5
markergenes	a set of genes to label in the plot
PAS	type of PAS analyzed, either '3UTR' or 'IPA', default is '3UTR'
y_cutoff	y cutoff line, default is 0.05
xlab	lable of x-axis, default is 'RED'
ylab	lable of y-axis, default is '-Log10(P-value)'
PAScolor	dot color for 'NC','UP' and 'DN' gene/IPAs, default is "gray80", "red", and "blue"

alpha	alpha of the dot, default is 0.75
plot_title	Main title of plot
width	width of the dot, default is 4
height	height of the dot, default is 2.5

Value

The function APAVolcano return a Volcano plot.

Author(s)

Ruijia Wang

Examples

```
library("TBX20BamSubset")
library("Rsamtools")
flsall = getBamFileList()
extpath = system.file("extdata",
"mm9_TBX20.APAout.RData", package="APALyzer")
load(extpath)
sampleTable1 = data.frame(samplename = c(names(flsall)),
condition = c(rep("NT",3),rep("KD",3)))
sampleTable2 = data.frame(samplename = c("SRR316184","SRR316187"),
condition = c("NT","KD"))
## 3'UTR APA plot
test_3UTRmuti=APAdiff(sampleTable1,DFUTRraw,
conKET='NT',trtKEY='KD',PAS='3UTR',CUTreads=0)
UTR_APA_PLOT=APAVolcano(test_3UTRmuti, PAS='3UTR', Pcol = "pvalue", top=5, plot_title='3UTR APA')

## IPA plot
test_IPAmuti=APAdiff(sampleTable1,IPA_OUTraw,
conKET='NT',trtKEY='KD',PAS='IPA',CUTreads=0)
IPA_PLOT=APAVolcano(test_IPAmuti, PAS='IPA', Pcol = "pvalue", top=5, plot_title='IPA')
```

download_testbam

download_testbam, download bam files of mouse testis and heart

Description

download bam files of mouse testis and heart

Usage

```
download_testbam()
```

Value

The function download_testbam download test data bam files.

Author(s)

Ruijia Wang

Examples

```
download_testbam()
```

 GENEXP_CDS

GENEXP_CDS, count reads mapped to CDS regions and calculate TPM for coding gene

Description

Map reads to CDS regions and calculate TPM for each gene.

Usage

```
GENEXP_CDS(CDSbygene, fls, Strandtype="NONE")
```

Arguments

CDSbygene	a genomic ranges of CDS regions for each coding gene
fls	bamfile lists containing the file and path of bam files
Strandtype	strand type of the bam file; "forward" is forward sequencing, "invert" is reverse sequencing and "NONE" is non-strand specific, Default is "NONE".

Value

The function GENEXP_CDS() return a dataframe containing reads count, TPM for each gene

Author(s)

Ruijia Wang

Examples

```
## count reads mapped to CDS regions and calculate TPM for each gene
## using forward sequencing
library("TBX20BamSubset")
library("Rsamtools")
library("GenomicAlignments")
library("GenomicFeatures")
library("org.Mm.eg.db")
flsall = getBamFileList()
extpath = system.file("extdata", "mm9.chr19.refGene.R.DB", package="APALyzer")
txdb = loadDb(extpath, packageName='GenomicFeatures')
IDDB = org.Mm.eg.db
CDSdbraw = REFCDS(txdb,IDDB)
DFGENERaw = GENEXP_CDS(CDSdbraw, flsall, Strandtype="forward")
```

PAS2GEF	<i>PAS2GEF, build reference regions for 3'UTR PASs</i>
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Description

Build 3'UTR PAS and IPA (IPA and LE) Reference using GTF file.

Usage

```
PAS2GEF(GTFfile)
```

Arguments

GTFfile	GTF file of gene annotation
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Value

The function PAS2GEF() returns 3 input tables of PAS references: PASREF\$refUTRraw is for 3'UTR PAS, PASREF\$dfIPA and PASREF\$dfLE are for IPA references.

Author(s)

Ruijia Wang

Examples

```
## build Reference ranges for 3'UTR PASs in mouse
download.file(url='ftp://ftp.ensembl.org/pub/release-99/gtf/mus_musculus/Mus_musculus.GRCm38.99.gtf.gz',
             destfile='Mus_musculus.GRCm38.99.gtf.gz')
GTFfile="Mus_musculus.GRCm38.99.gtf.gz"

PASREF=PAS2GEF(GTFfile)
refUTRraw=PASREF$refUTRraw
dfIPA=PASREF$dfIPA
dfLE=PASREF$dfLE
```

PASEXP_3UTR	<i>PASEXP_3UTR, calculate relative expression of aUTR and cUTR regions</i>
-------------	--

Description

Map reads to 3'UTR APA regions and calculate relative expression of aUTR and cUTR regions.

Usage

```
PASEXP_3UTR(UTRdb, f1S, Strandtype="NONE")
```

Arguments

UTRdb	a genomic ranges of aUTR(pPAS to dPAS) and cUTR(cdsend to pPAS) regions for each gene
f1s	bamfile lists containing the file and path of bam files
Strandtype	strand type of the bam file; "forward" is forward sequencing, "invert" is reverse sequencing and "NONE" is non-strand specific, Default is "NONE".

Value

The function PASEXP_3UTR() return a dataframe containing reads count, RPKM and relative expression of aUTR and cUTR for each gene

Author(s)

Ruijia Wang

Examples

```
## count reads mapped to 3'UTR APA regions and
## calculate relative expression of aUTR and cUTR regions
## using forward sequencing
library("TBX20BamSubset")
library("Rsamtools")
library("GenomicAlignments")
library("repmis")
flsall = getBamFileList()
URL="https://github.com/RJWANGbioinfo/PAS_reference_RData/blob/master/"
file="mm9_REF.RData"
source_data(paste0(URL,file,"?raw=True"))
refUTRraw = refUTRraw[which(refUTRraw$Chrom=='chr19'),]
UTRdbraw = REF3UTR(refUTRraw)
DFUTRraw = PASEXP_3UTR(UTRdbraw, flsall, Strandtype="forward")
```

PASEXP_IPA

PASEXP_IPA, calculate relative expression of IPA regions

Description

Map reads to IPA regions and calculate relative expression of aUTR and cUTR regions.

Usage

```
PASEXP_IPA(dfIPAraw, dfLEraw, f1s, Strandtype="NONE", nts=1, minMQS=0)
```

Arguments

dfIPAraw	a dataframe containing 8 columns for Intronic PASs: 'PASid', 'gene_symbol', 'Chrom', 'Strand', 'Pos', 'upstreamSS', 'downstreamSS'. 'upstreamSS' means closest 5'/3' splice site to IPA, 'downstreamSS' means closest 3' splice site
dfLEraw	a dataframe containing 5 columns for 3' least exon: 'gene_symbol', 'Chrom', 'Strand', 'LEstart', 'TES'. 'LEstart' means the start position of last 3' exon.

f1s	bamfile lists containing the file and path of bam files
Strandtype	strand type of the bam file; "forward" is forward sequencing, "invert" is reverse sequencing and "NONE" is non-strand specific, Default is "NONE".
nts	number of threads used for computing, parameter used by featureCounts , nthread option, Default is 1
minMQS	minimum mapping quality score of counted reads, parameter used by featureCounts , minMQS option, Default is 0

Value

The function PASEXP_IPA() return a dataframe containing reads count, RPKM and relative expression of aUTR and cUTR for each gene

Author(s)

Ruijia Wang

Examples

```
## count reads mapped to IPA regions and
## calculate relative expression of aUTR and cUTR regions
## using forward sequencing
library("TBX20BamSubset")
library("Rsamtools")
library("GenomicAlignments")
library("repmis")
f1sall = getBamFileList()
URL="https://github.com/RJWANGbioinfo/PAS_reference_RData/blob/master/"
file="mm9_REF.RData"
source_data(paste0(URL,file,"?raw=True"))
IPA_OUTraw=PASEXP_IPA(dfIPA, dfLE, f1sall, Strandtype="forward", nts=1)
```

REF3UTR

REF3UTR, build reference regions for 3'UTR PASs

Description

Build 3'UTR PAS Reference for distal and proximal PAS.

Usage

```
REF3UTR(refUTR)
```

Arguments

refUTR	a dataframe containing 6 columns for 3'UTR PASs: 'gene_symbol', 'Chrom', 'Strand', 'Proximal', 'Distal', 'cdsend'
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Value

The function REF3UTR() returns a genomic ranges of aUTR(pPAS to dPAS) and cUTR(cdsend to pPAS) regions for each gene

Author(s)

Ruijia Wang

Examples

```
## build Reference ranges for 3'UTR PASs in mouse
library(repmis)
URL="https://github.com/RJWANGbioinfo/PAS_reference_RData/blob/master/"
file="mm9_REF.RData"
source_data(paste0(URL, file, "?raw=True"))
refUTRraw=refUTRraw[which(refUTRraw$Chrom=='chr19'),]
UTRdbraw=REF3UTR(refUTRraw)
```

REF4PAS

REF4PAS, build reference regions for 3'UTR and Intronic PAS using dataframe formatted input

Description

build reference regions for 3'UTR and Intronic PAS using dataframe formatted input

Usage

```
REF4PAS(refUTRraw, dfIPArw, dfLEraw)
```

Arguments

refUTRraw	a dataframe containing 6 colmuns for 3'UTR PASs: 'gene_symbol', 'Chrom', 'Strand', 'Proximal', 'Distal', 'cdsend'
dfIPArw	a dataframe containing 8 colmuns for Intronic PASs: 'PASid', 'gene_symbol', 'Chrom', 'Strand', 'Pos', 'upstreamSS', 'downstreamSS'. 'upstreamSS' means closest 5'/3' splice site to IPA, 'downstreamSS' means closest 3' splice site
dfLEraw	a dataframe containing 5 colmuns for 3' least exon: 'gene_symbol', 'Chrom', 'Strand', 'LEstart', 'TES'. 'LEstart' means the start position of last 3' exon.

Value

The function REF4PAS() returns list a genomic ranges of 3'UTR, Intronic PAS and last 3'exon regions for each gene

Author(s)

Ruijia Wang

Examples

```
## build Reference ranges for 3'UTR and Intronic PAS in mouse (mm9)
library(repmis)
URL="https://github.com/RJWANGbioinfo/PAS_reference_RData/blob/master/"
file="mm9_REF.RData"
source_data(paste0(URL, file, "?raw=True"))
refUTRraw=refUTRraw[which(refUTRraw$Chrom=='chr19'),]
dfIPAraw=dfIPA[which(dfIPA$Chrom=='chr19'),]
dfLEraw=dfLE[which(dfLE$Chrom=='chr19'),]
PASREF=REF4PAS(refUTRraw,dfIPAraw,dfLEraw)
UTRdbraw=PASREF$UTRdbraw
dfIPA=PASREF$dfIPA
dfLE=PASREF$dfLE
```

REFCDS

*REFCDS, build reference regions for CDS of protein coding genes***Description**

Build CDS reference for protein coding genes.

Usage

```
REFCDS(txdb, IDDB)
```

Arguments

txdb	a TranscriptDb generate using GenomicFeatures
IDDB	Genome annotation of the corresponding species, e.g., "org.Hs.eg.db"

Value

The function REFCDS() returns a genomic ranges of CDS regions for each coding gene

Author(s)

Ruijia Wang

Examples

```
## build Reference ranges for CDS in mouse coding genes
library("GenomicFeatures")
library("org.Mm.eg.db")
extpath = system.file("extdata", "mm9.chr19.refGene.R.DB", package="APalyzer")
txdb = loadDb(extpath, packageName='GenomicFeatures')
IDDB = org.Mm.eg.db
CDSdbraw = REFCDS(txdb, IDDB)
```

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