Package ‘IVAS’

April 4, 2024

**Type** Package

**Title** Identification of genetic Variants affecting Alternative Splicing

**Version** 2.22.0

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**Description** Identification of genetic variants affecting alternative splicing.

**License** GPL-2

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**R topics documented:**

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>IVAS-package</td>
<td>2</td>
</tr>
<tr>
<td>ASdb-class</td>
<td>2</td>
</tr>
<tr>
<td>calSignificant</td>
<td>3</td>
</tr>
<tr>
<td>CalSigSNP</td>
<td>3</td>
</tr>
<tr>
<td>chrseparate</td>
<td>4</td>
</tr>
</tbody>
</table>
DESCRIPTION

The tool is to detect genomic variants affecting the alternative splicing using genotypic and gene expression data (RNA-seq).

INDEX

IVAS-package

IVAS: Identification of genomic variants affecting Alternative Splicing

DESCRIPTION

This class is the main object for storing results of the present package.

NOTE

An ASdb object stores information of alternative splicing patterns, expression ratios between transcripts with and without alternative target exons, and significant sQTLs from the functions of the present package. This ASdb object can be populated further slots during the analysis using functions for the analysis. Typically, an ASdb object can be created when the function Splicingfinder completes to define alternative splicing patterns. After creation, the ASdb contains the slot labeled as "SplicingModel", and the slot includes a list object named by "ES", "ASS", and "IR" (alternative splicing exons are saved separately in each element of the list based on their splicing pattern types; "ES": Exon skipping, "ASS": Alternative splice site, and "IR": Intron retention). In the next analysis step, further result slots can be added. The function RatioFromFPKM can add the "Ratio" slot containing expression ratio for each alternative splicing pattern based on the "SplicingModel" slot of the present class and for each individual from a matrix of FPKM values. Then, the result of the sQTLsFinder function can be saved by adding the "sQTLs" slot including significance of association between the expression ratios, which is stored in the "Ratio" slot of the present class, and SNPs for each alternative splicing exon.
calSignificant

See Also
Splicingfinder, RatioFromFPKM, sQTLsFinder

Examples

```r
sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
sample.Txdb <- loadDb(sampleDB)
data(sampleexp)
data(samplesnp)
data(samplesnplocus)
ASdb <- Splicingfinder(sample.Txdb)
ASdb <- RatioFromFPKM(sample.Txdb, ASdb, sampleexp)
ASdb <- sQTLsFinder(ASdb, samplesnp, samplesnplocus, method="lm")
ASdb
```

calSignificant  Deprecated

Description
This function is deprecated and will be made defunct. Instead, use Splicingfinder.

CalSigSNP  Calculate significance SNPs

Description
This function performs linear regression test to identify significance associations between expression ratio and genotypes using the lm function.

Usage

```r
CalSigSNP(ratio.mat=NULL, snp.mat=NULL, overlapsnp=NULL,
each.snplocus=NULL, chr, each.gene=NULL, GroupSam=NULL, method="lm")
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ratio.mat</td>
<td>A data frame consisting of expression ratio of an alternatively spliced exon.</td>
</tr>
<tr>
<td>snp.mat</td>
<td>A data frame of genotype data.</td>
</tr>
<tr>
<td>overlapsnp</td>
<td>A data frame containing SNPs which is within an alternatively spliced exon and its flanking introns.</td>
</tr>
<tr>
<td>each.snplocus</td>
<td>A data frame consisting of locus information of SNP markers in the snpdata.</td>
</tr>
<tr>
<td>chr</td>
<td>The chromosome number that you would like to test in this function.</td>
</tr>
<tr>
<td>each.gene</td>
<td>The gene name that you would like to test in this function.</td>
</tr>
</tbody>
</table>
chrseparate

GroupSam

method

A list object of a group of each sample.
The option for statistical models and boxplot. ("lm" : analysis using linear regression model, "glm" : analysis using generalized linear mixed model, "both" : "lm" and "glm", and "boxplot" : for writing boxplot).

Value

The lm or glm method returns matrix including: SNP marker IDs, P values, information of differential median values of expression ratio among genotypes ("sig" if differential median > 0.1 and "not sig" otherwise), gene names, and methods ("lm" or "glm"). The boxplot method returns matrix with relative ratio values and genotypes of samples.

Author(s)

Seonggyun Han, Sangsoo Kim

References


See Also

lm, glmer

Examples

```r
sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
sample.Txdb <- loadDb(sampleDB)
data(sampleexp)
data(samplesnp)
data(samplesnplocus)
ASdb <- Splicingfinder(sample.Txdb)
ASdb <- RatioFromFPKM(sample.Txdb,ASdb,sampleexp,CalIndex="ASS7")
ratio.mat <- slot(ASdb,"Ratio")$ASS
ratio.mat <- rbind(ratio.mat[,grep("NA",colnames(ratio.mat))])
each.snp <- rbind(samplesnp[rownames(samplesnp) == "rs3810232",])
each.snplocus <- rbind(samplesnplocus[samplesnplocus[,"SNP"] == "rs3810232",])
overlapsnp <- rbind(c(snp="rs3810232",locus="54704760"))
CalSigSNP(ratio.mat,as.matrix(each.snp),overlapsnp,each.snplocus,"19","ENSG00000170889",method="lm")
```

chrseparate

Separate a TxDb object based on a chromosome.

Description

With the isActiveSeq method in GenomicFeatures package, this function filters the TxDb object in the GenomicFeatures package based on a single chromosome.
**findAlternative**

**Usage**

```r
chrseparate(GTFdb = NULL, chrname = NULL)
```

**Arguments**

- `GTFdb` The TxDb object in the `GenomicFeatures` package.
- `chrname` The chromosome number you would like to select from TxDb

**Value**

This function returns the TxDb limited to the chromosome number that you want.

**Author(s)**

Seonggyun Han, Sangsoo Kim

**References**


**See Also**

`isActiveSeq`, `seqinfo`

**Examples**

```r
sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
sample.Txdb <- loadDb(sampleDB)
filtered.txdb <- chrseparate(sample.Txdb, 19)
```

---

**findAlternative**

*Find alternative exons of a gene.*

**Description**

Search alternative exons among transcript isoforms from a single gene.

**Usage**

```r
findAlternative(geneid = NULL, txTable = NULL, totalExrange = NULL, totalInrange = NULL, one.chr = NULL)
```
Arguments

geneid Ensembl gene name.
txTable The matrix of transcripts including transcript IDs, Ensembl gene names, Ensembl transcript names, transcript start sites, and transcript end sites.
totalExrange A list of GRanges objects including total exon ranges in each transcript resulted from the `exonsBy` function in GenomicFeatures.
totalInrange A list of GRanges objects including total intron ranges in each transcript resulted from the `intronsByTranscript` function in GenomicFeatures.
one.chr The chromosome number that you would like to test

Value

alterIntron A GRanges object with flanking introns of alternative exons
tableBygene An information table of transcripts including transcript IDs, Ensembl gene names, Ensembl transcript names, transcript start sites, and transcript end sites.
exonRange All exons locus of a gene
intronRange All intron locus of a gene

Author(s)

Seonggyun Han, Sangsoo Kim

References


See Also

GRanges, IRanges

Examples

```r
sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
sample.Txdb <- loadDb(sampleDB)
filtered.txdb <- chrseparate(sample.Txdb,19)
trans.exon.range <- exonsBy(filtered.txdb,by="tx")
trans.intron.range <- intronsByTranscript(filtered.txdb)
txTable <- select(filtered.txdb, keys=names(trans.exon.range), columns=c("TXID","TXNAME","GENEID","TXSTART","TXEND"), keytype="TXID")
txTable <- select(filtered.txdb, keys=names(trans.exon.range), columns=c("TXID","TXNAME","GENEID","TXSTART","TXEND"), keytype="TXID")
Altvalue <- findAlternative("ENSG00000170889", txTable, trans.exon.range, trans.intron.range, 19)
```
findOversnp  

**Description**

Find SNPs which belong to alternative exons and flanking introns of them.

**Usage**

```r
findOversnp(altInvalue = NULL, snprange = NULL)
```

**Arguments**

- `altInvalue`: A list data set from the `findAlternative` function.
- `snprange`: A matrix of SNP ranges.

**Value**

This function returns a matrix with SNPs which are located in alternative exons and flanking introns and ranges of those SNPs.

**Author(s)**

Seonggyun Han, Sangsoo Kim

**See Also**

`findOverlaps`

**Examples**

```r
code
```
### Deprecated functions in package ‘IVAS’

**Description**

These functions are provided for compatibility with older versions of ‘IVAS’ only, and will be defunct at the next release.

**Details**

The following functions are deprecated and will be made defunct; use the replacement indicated below:

- MsqtlFinder: `sQTLsFinder`
- sqtlfinder: `sQTLsFinder`
- calSignificant: `Splicingfinder`

### MsqtlFinder

**Deprecated**

**Description**

This function is deprecated and will be made defunct. Instead, use `sQTLsFinder`.

### RatioFromFPKM

**Estimate relative expression ratio.**

**Description**

With the FPKM expression data set of transcripts, this function estimates relative expression ratio between transcripts with and without alternatively spliced exons based on splicing models of the ASdb object.

**Usage**

```r
RatioFromFPKM(GTFdb = NULL, ASdb = NULL,
              Total.expdata = NULL, CalIndex = NULL, Ncor = 1, out.dir = NULL)
```
**RatioFromFPKM**

**Arguments**

- **GTFdb**: A TxDb object in the GenomicFeatures package.
- **ASdb**: A ASdb object including "SplicingModel" slot from the Splicingfinder function.
- **Total.expdata**: A data frame of expression data.
- **CalIndex**: An index number in the ASdb object which will be tested in this function.
- **Ncor**: The number of cores for multi-threads function.
- **out.dir**: An output directory.

**Value**

ASdb with the slot (labeled by "Ratio") containing results from the the RatioFromFPKM function. The "Ratio" slot contains a list object and each element of the list object returns the results assigned to three elements, which is of each alternative splicing type (i.e. Exon skipping, Alternative splice site, Intron retention). Three elements are as follows:

- **ES**: A data frame for the result of Exon skipping, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), 1stEX (alternatively spliced target exon), 2ndEX (second alternatively spliced target exon which is the other one of the mutually exclusive spliced exons), DownEX (downstream exon range), UpEX (upstream exon range), Types (splicing type), and names of individuals.

- **ASS**: A data frame for the result of Alternative splice sites, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), ShortEX (shorter spliced target exon), LongEX (longer spliced target exon), NeighborEX (neighboring down or upstream exons), Types (splicing type), and names of individuals.

- **IR**: A data frame for the result of Intron retention, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), RetainEX (retained intron exon), DownEX (downstream exon range), UpEX (upstream exon range), Types (splicing type), and names of individuals.

**Author(s)**

Seonggyun Han, Sangsoo Kim

**See Also**

isActiveSeq, seqinfo, Splicingfinder

**Examples**

```r
sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
sample.Txdb <- loadDb(sampleDB)
data(sampleexp)
ASdb <- Splicingfinder(sample.Txdb)
ASdb <- RatioFromFPKM(sample.Txdb,ASdb,sampleexp)
```
sampleexp  

**Description**  
CEU expression data including 78 individuals

**Usage**  
data("sampleexp")

**Format**  
A data frame with 64 transcript expressions on the 78 individuals

**Value**  
A data frame with 64 transcript expressions on the 78 individuals

**Source**  
The data was generated by GEUVADIS (Genetic European Variation in Health and Disease, A European Medical Sequencing Consortium) RNA sequencing project for 1000 Genomes samples (http://www.geuvadis.org/web/geuvadis/RNAseq-project).

**References**  

**Examples**  
data(sampleexp)

samplesnp  

**Description**  
CEU genotype data including 78 individuals

**Usage**  
data("samplesnp")
**samplesnplocus**

**Format**
A data frame with 11 SNPs on the 78 individuals

**Value**
A data frame with 11 SNPs on the 78 individuals

**Source**
The data has 1000 genomes Phages 1 dataset and was imputed by GEUVADIS (Genetic European Variation in Health and Disease, A European Medical Sequencing Consortium) RNA sequencing project for 1000 Genomes samples (http://www.geuvadis.org/web/geuvadis/RNAsseq-project).

**References**

**Examples**

data(samplesnp)

---

<table>
<thead>
<tr>
<th>samplesnplocus</th>
<th>snplocus</th>
</tr>
</thead>
</table>

**Description**
snplocus

**Usage**
data("samplesnplocus")

**Format**
A data frame with 11 SNPs and locus of them

**Value**
A data frame with 11 SNPs and locus of them

**Examples**
data(samplesnplocus)
saveBplot  

Description
Save boxplots

Usage
saveBplot(ASdb=ASdb,Total.snpdata=NULL,Total.snplocus=NULL,CalIndex=NULL,out.dir=NULL)

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ASdb</td>
<td>A ASdb object including &quot;sQTLs&quot; slot from the sQTLsFinder function.</td>
</tr>
<tr>
<td>Total.snpdata</td>
<td>A data frame of genotype data.</td>
</tr>
<tr>
<td>Total.snplocus</td>
<td>A data frame containing locus information of SNP markers in the snpdata.</td>
</tr>
<tr>
<td>CalIndex</td>
<td>An index number in the ASdb object which will be tested in this function.</td>
</tr>
<tr>
<td>out.dir</td>
<td>An output directory.</td>
</tr>
</tbody>
</table>

Value
This function draws the boxplot

Author(s)
Seonggyun Han, Sangsoo Kim

See Also
boxplot

Examples
```r
sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
sample.Txdb <- loadDb(sampleDB)
data(sampleexp)
data(samplesnp)
data(samplesnplocus)
ASdb <- Splicingfinder(sample.Txdb)
ASdb <- RatioFromFPKM(sample.Txdb,ASdb,sampleexp)
ASdb <- sQTLsFinder(ASdb,samplesnp,samplesnplocus,method="lm")
saveBplot(ASdb=ASdb,Total.snpdata=samplesnp,Total.snplocus=samplesnplocus,CalIndex="ASS7",out.dir="./result"")
```
Description

Find alternatively spliced exons based on GTF reference transcript models.

Usage

Splicingfinder(GTFdb = NULL , txTable = NULL , calGene = NULL , Ncor = 1 , out.dir = NULL)

Arguments

- **GTFdb**: A TxDb object in the GenomicFeatures package.
- **txTable**: A matrix of transcripts including transcript IDs, gene names, transcript names, transcript start sites, and transcript end sites based on a GTF reference transcript model file.
- **calGene**: An interest of a gene that will be tested. If calGene is inputted by a single gene, the splicing pattern for the only gene is tested. If not, the splicing patterns for total of genes are tested.
- **Ncor**: The number of cores for multi-threads.
- **out.dir**: An output directory.

Value

ASdb with the slot (labeled by "SplicingModel") containing results from the Splicingfinder function. The "Splicingfinder" slot contains a list object and each element of the list object returns the results assigned to three elements, which is of each alternative splicing type (i.e. Exon skipping, Alternative splice site, Intron retention). Three elements are as follows;

- **ES**: A data frame for the result of Exon skipping, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), 1stEX (alternatively spliced target exon), 2ndEX (second alternatively spliced target exon which is the other one of the mutually exclusive spliced exons), DownEX (downstream exon range), UpEX (upstream exon range), 1st_des (shorter spliced target exons in a representative exon), 2nd_des (second alternatively spliced target exons in a representative exon), Do_des (downstream exons in a representative exon), Up_des (upstream exons in a representative exon), and Types (splicing type).

- **ASS**: A data frame for the result of Alternative splice site, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), ShortEX (shorter spliced target exon), LongEX (longer spliced target exon), NeighborEX (neighboring downstream or upstream exons), Short_des (shorter spliced target exons in a representative exon), Long_des (longer spliced target exons in a representative exon), Neighbor_des (neighboring downstream or upstream exons in a representative exon), and Types (splicing type).
### Description

This function is deprecated and will be made defunct. Instead, use `sQTLsFinder`.

<table>
<thead>
<tr>
<th>sqtlfinder</th>
<th>Deprecated</th>
</tr>
</thead>
</table>

### sQTLsFinder

Find SQTLS.

<table>
<thead>
<tr>
<th>sQTLsFinder</th>
<th>Find SQTLS.</th>
</tr>
</thead>
</table>

### Description

Find significant SNPs using the calSignificant function.

#### Usage

```r
sQTLsFinder(ASdb, Total.snpdata = NULL, Total.snplocus = NULL,
            GroupSam = NULL, method = "lm", CalIndex = NULL, Ncor = 1, out.dir = NULL)
```
sQTLsFinder

Arguments

ASdb A ASdb object including "SplicingModel" and "Ratio" slots from the Splicingfinder and RatioFromFPKM functions, respectively.

Total.snpdata A data frame of genotype data.

Total.snplocus A data frame containing locus information of SNP markers in the snpdata.

GroupSam A list object of a conditions for each individual. If GroupSam is not NULL, the odds ratio and its confidence intervals between conditions are calculated.


CalIndex An index number in the ASdb object which will be tested in this function.

Ncor The number of cores for multi-threads function.

out.dir An output directory.

Value

ASdb with the slot (labeled by "sQTLs") containing results from the sQTLsFinder function. The "Splicingfinder" slot contains a list object and each element of the list object returns the results assigned to three elements, which is of each alternative splicing type (i.e. Exon skipping, Alternative splice site, Intron retention). Three elements are as follows;

ES A data frame for the result of Exon skipping, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), 1stEX (alternatively spliced target exon), 2ndEX (second alternatively spliced target exon which is the other one of the mutually exclusive spliced exons), DownEX (downstream exon range), UpEX (upstream exon range), Types (splicing type), pByGeno (P-values of "lm" or "glm" test for association PSI values and genotypes), FdrByGeno (pByGeno), diff ("diff" if differential median > 0.1 and "Nondiff" otherwise), pByGroups (P-values of chi-square test for association between genotypes of two groups), fdrByGroups (FDR values for the pByGroups column), OR (odds ratio), lowCI (low confidence interval), highCI (high confidence interval), and methods ("lm" or "glm").

ASS A data frame for the result of Alternative splice sites, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), ShortEX (shorter spliced target exon), LongEX (longer spliced target exon), NeighborEX (neighboring down or upstream exons), Types (splicing type), pByGeno (P-values of "lm" or "glm" test for association PSI values and genotypes), FdrByGeno (pByGeno), diff ("diff" if differential median > 0.1 and "Nondiff" otherwise), pByGroups (P-values of chi-square test for association between genotypes of two groups), fdrByGroups (FDR values for the pByGroups column), OR (odds ratio), lowCI (low confidence interval), highCI (high confidence interval), and methods ("lm" or "glm").

IR A data frame for the result of Intron retention, consisting of the columns named as follows; Index (index number), EnsID (gene name), Nchr (chromosome name), RetainEX (retained intron exon), DownEX (downstream exon range), UpEX (upstream exon range), Types (splicing type), pByGeno (P-values of "lm" or
"glm" test for association PSI values and genotypes), FdrByGeno (pByGeno),
diff ("diff" if differential median > 0.1 and "Nondiff" otherwise), pByGroups (P-
values of chi-square test for association between genotypes of two groups), fdr-
ByGroups (FDR values for the pByGroups column), OR (odds ratio), lowCI(low
confidence interval), highCI(high confidence interval), and methods ("lm" or
"glm").

The boxplot method returns matrix data with relative ratio values and genotypes of samples.

Author(s)
Seonggyun Han, Sangsoo Kim

References

See Also
lm, glmer

Examples
sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
sample.Txdb <- loadDb(sampleDB)
data(sampleexp)
data(samplesnp)
data(samplesnplocus)
ASdb <- Splicingfinder(sample.Txdb)
ASdb <- RatioFromFPKM(sample.Txdb,ASdb,sampleexp)
ASdb <- sQTLsFinder(ASdb,samplesnp,samplesnplocus,method="lm")
Index

* datasets
  sampleexp, 10
  samplesnp, 10
  samplesnplocus, 11

* package
  IVAS-package, 2
  ASdb-class, 2
  boxplot, 12
  calSignificant, 3
  CalSigSNP, 3
  chrseparate, 4
  exonsBy, 6
  findAlternative, 5, 7
  findOverlaps, 7
  findOversnp, 7
  glmer, 4, 16
  GRanges, 6
  intronsByTranscript, 6
  IRanges, 6
  isActiveSeq, 4, 5, 9, 14
  IVAS (IVAS-package), 2
  IVAS-deprecated, 8
  IVAS-package, 2

lm, 3, 4, 16
MsqtlFinder, 8
RatioFromFPKM, 2, 3, 8, 9, 15

sampleexp, 10
samplesnp, 10
samplesnplocus, 11
saveBplot, 12
seqinfo, 5, 9, 14

Splicingfinder, 2, 3, 8, 9, 13, 15
sqtlfinder, 14
sQTLsFinder, 2, 3, 8, 12, 14, 14, 15