

Package ‘splicegear’

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Title splicegear

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Description A set of tools to work with alternative splicing

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R topics documented:

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as.data.frame.SpliceExprSet
SpliceExprSet object to data.frame converter

Description

Converts a SpliceExprSet object to a data.frame.

Usage

```
## S3 method for class 'SpliceSites'  
as.data.frame(x, row.names = NA, optional = NA, ...)  
  
## S3 method for class 'SpliceExprSet'  
as.data.frame(x, row.names = NA, optional = NA, ...)
```

Arguments

x	object SpliceSites-class or SpliceExprSet-class .
row.names	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
optional	logical. If TRUE, setting row names is optional.
...	currently ignored.

Details

Data are traditionally stored in objects of class `data.frame`. This function links the object-oriented design of the package with the large amount of functions working on `data.frames`.

Value

A `data.frame`. For both functions the first column names are `begin`, `end`, `isintypeI`, `isintypeII`, `exprs` and `genenames`. In the case of `as.data.frame.SpliceExprSet`, the next variable names will be the ones in the [AnnotatedDataFrame-class](#) attribute of the [ExpressionSet-class](#) object belonging to the [SpliceExprSet-class](#). The last variable names will be the ones in the slot `info` of the [Probes-class](#) object.

Author(s)

Laurent Gautier

Examples

```

data(spliceset)

dataf <- as.data.frame(spliceset)

lm.panel <- function(x, y, ...) {
  points(x,y,...)
  p.lm <- lm(y~x); abline(p.lm)
}

## probe intensity values conditioned by the position of the probes on
## the mRNA
coplot(log(exprs) ~ Material | begin, data=dataf, panel=lm.panel)

```

barplot.SpliceSites *barplot for SpliceSites*

Description

Displays a barplot of the associated AnnotatedDataFrame.

Usage

```

## S3 method for class 'SpliceSites'
barplot(height, type.as = c("typeI", "typeII", "all"),
        info = "tissue", ...)

```

Arguments

height	object of class SpliceSites-class .
type.as	the type of alternative splicing (see SpliceSites-class for further details).
info	the name of the covariate in the AnnotatedDataFrame (see details).
...	optional parameters to be passed to the underlying function barplot .

Details

When the objects are built from the XML format we propose as an exchange, the parameter info can at least take the values "tissue" and "histology". One can refer to the slots `spsiteIpos.pData` and `spsiteIIpos.pData` to know what are the possible choices.

Value

See the value returned by the function [barplot](#).

See Also

[SpliceSites-class](#), [barplot](#)

Examples

```
data(spsites)
barplot(spsites)
```

<code>buildSpliceSites</code>	<i>Functions to query PALSdb</i>
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Description

Functions to make a query on PALSdb, and build objects from the result of a query.

Usage

```
queryPALSdb(query, disp = c("data", "browser"),
            field = c("keyword", "ug.id", "gb.id", "human.cytoband", "mouse.cytoband", "cluster_count"),
            species = c("human", "mouse"),
            e.value = "1e-1",
            ident.threshold = c("90% 50b", "95% 50b", "90% 45b"))

getPALSdbURL(query, disp = c("data", "browser"),
            field = c("keyword", "ug.id", "gb.id", "human.cytoband", "mouse.cytoband", "cluster_count"),
            species = c("human", "mouse"),
            e.value = "1e-1",
            ident.threshold = c("90% 50b", "95% 50b", "90% 45b"))

buildSpliceSites(xml, verbose=TRUE)
```

Arguments

<code>query</code>	query string
<code>xml</code>	an object of class XML (as returned by xmlTreeParse)
<code>disp</code>	(idem genbank and pubmed)
<code>field</code>	The field on which the query will be based
<code>species</code>	the specie to work with
<code>e.value</code>	E-value
<code>ident.threshold</code>	threshold for matching sequences
<code>verbose</code>	verbose output.

Details

`queryPALSdb` returns an an object of class XML when `disp = "data"`.

The function `buildSpliceSites` constructs `SpliceSites` objects from the XML data. The variables in the slots `spsiteIpos.pData` and `spsiteIIpos.pData` are at least tissue (tissue information), histology and site (site numbering).

Value

An object of class XML for queryPALSdb, an URL for getPALSdbURL or a list of objects of class SpliceSites.

Author(s)

laurent@cbs.dtu.dk

References

"Standardized output for putative alternative splicing: application to the study of splice variants with microarrays", Gautier L. et al., 2003, manuscript in preparation.

See Also

[queryPALSdb](#)

Examples

```
library(XML)

filename <- system.file("extdata", "example.xml", package="splicegear")

xml <- xmlTreeParse(filename, asTree=TRUE)

spsites <- buildSpliceSites(xml)
```

getRelSignStrength *functions to perform SPLICE*

Description

Implementations of the SPLICE algorithm

Usage

```
getRelSignStrength(x, tissue = as.factor(1:ncol(x)), fun = mean, nipt = 30, nitt = 30, ...)

getFinalRatio(x, tissue=as.factor(1:ncol(x)), fun=mean, ...)
```

Arguments

x	a matrix. One probe per line, one column per sample. Typically this would be the slot exprs of an instance of class ExprSet.
tissue	a covariate (factor) about the samples.
fun	a function to obtain a summary value (mean by default)

nipt see reference.
nitt see reference.
... optional parameters for the function fun

Details

getFinalRatio will call getRelSignStrength. The values are log-transformed. It is probably a good idea to avoid feeding function with values that are already on log scale.

Value

A matrix of the same dimension than the input x, holding 'RSS' (Relative Signal Strength) or 'final ratios' respectively, as described in the reference. Two attributes nip and nit are attached the returned matrix.

Author(s)

laurent@cbs.dtu.dk

References

Genome Research (2001), Hu et. al., vol. 11, p.1244

Examples

```
data(spliceset)

## The intensity values in the example are log-transformed.
## Undo by taking the exponential
exprs(spliceset) <- exp(exprs(spliceset))

## Re-order the rows of different slots to have the probes sorted by
## position
spliceset <- sort.SpliceExprSet(spliceset)
## extract the expression matrix
expr.m <- exprs(spliceset)
fr <- getFinalRatio(expr.m, tissue=pData(spliceset@eset)[[1]])
```

Description

Convenience function to use the package grid

Usage

```
grid.expand.gp(n, parlist = list())
grid.make.numeric2npc(x, xlim=NULL, lower.blank=0, upper.blank=0)
```

Arguments

n	number of parameters
parlist	list of parameters
x	numeric value
xlim	range for Xs
lower.blank, upper.blank	size for margins

Details

call the function gpar on the list of parameters.

Value

Function used for its side effect.

See Also

[lattice](#)

grid.plot.Probes	<i>Plot splicegear objects</i>
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Description

Plot objects defined in the package splicegear

Usage

```
grid.plot.Probes(x, col = "black", add = FALSE, probepos.yscale = NULL,
                xlim = NULL, vp = NULL, ...)

grid.plot.SpliceSites(x, col.typeI = "orange", col.typeI.window = "yellow",
                    col.typeII = "red", add = FALSE, ylim = NULL, vp = NULL,
                    ...)

grid.plot.SpliceExprSet(x, probes.opt = list(), expr.opt = list(col = NA, lty = 1:6),
                      fig.xratio = c(2, 1), fig.yratio = c(2, 1), probepos.yscale = NULL,
                      ylim = NULL, ...)
```

Arguments

x	object of Probes-class , SpliceSites-class or SpliceExprSet-class
add	add to an existing plot
col	color(s) for the probes (recycled if necessary).
col.typeI	color(s) for the type I spliced out exons
col.typeI.window	background color for the type I spliced out ‘windows’
col.typeII	color for the type II splicing events
expr.opt	list of options to plot expression values
probepos.yscale	specify coordinates on the y-axis for the probes.
probes.opt	options to plot the probes
fig.xratio	ratio for the left and right parts of the plot
fig.yratio	ratio for the upper and lower parts of the plot
vp	a viewport (grid package stuff)
xlim	range for the x-axis (see plot).
ylim	range for the y-axis
...	optional parameters

Details

The ‘type I’/‘type II’ thing is described in the references found in the help files for [plot.SpliceSites](#).

Value

These functions are mainly used for their side effects. `grid.plot.SpliceSites` returns the range for the y-axis when needed.

See Also

`plot.SpliceSites`, `plot.Probes`

Examples

```
## plot splice sites
data(spsites)
grid.plot(spsites)

## plot probes
data(probes)
grid.plot(probes)

## combined plot
grid.plot(probes, spsites)
```

isProbeOnSpliceSite *Check the presence of probes on certain exons*

Description

Return whether the probes are located on exons involved in (putative) alternative splicing or not.

Usage

```
isProbeOnSpliceSite(probes, spSites)
## isSpliceSiteOnProbe is not yet implemented
```

Arguments

probes	object of class Probes
spSites	object of class spliceSites

Value

The returned value in a list of two vectors of mode logical of the same length:

isintypeI	whether the probes are in a 'type I' region or not.
isintypeII	whether the probe are in a 'type II' region or not.

Author(s)

Laurent

References

For details about 'type I' and 'type II', please refer to Huang Y.-H and Chen Y.-T and Lai J.-J. and Yang S.-T. and Yang U.-C., PALSdb: Putative Alternative Splicing database, Nucleic Acids Research, 2002, pages 186-190

matchprobes2Probes *create Probes object from matchprobes results*

Description

Create Probes object from results the results of the function matchprobes (in the package 'match-probes').

Usage

```
matchprobes2Probes(mpo, probes.length, names = NULL)
```

Arguments

mpo	Probes-class object
probes.length	Length for the probes (see details).
names	names for the elements in the list returned.

Details

Currently only probes of unique length are assumed. In the case of Affymetrix chips, 25 base pairs is the value you probably want.

Value

A list of Probes-class objects.

References

<http://www.cbs.dtu.dk/laurent/download/splicegear/>

See Also

[Probes-class](#), the package `matchprobes`

plot.SpliceExprSet *plot a SpliceExprSet*

Description

Plot a object of class `SpliceExprSet`

Usage

```
## S3 method for class 'SpliceExprSet'
plot(x,
      probes.opt = list(), expr.opt = list(col = NA, lty = 1:6),
      fig.xratio = c(2, 1), fig.yratio = c(2, 1),
      probepos.yscale = NULL, ylim,
      ...)
```

Arguments

x	a SpliceExprSet-class
probes.opt	optional parameters to be passed for the plotting of the Probes-class
expr.opt	optional parameters to be passed for the plotting of the ExpressionSet-class
fig.xratio	ratio between the left and right parts of the plot
fig.yratio	ratio between the upper and lower parts of the plot

probepos.yscale enforce 'y' positions for the probes.
 ylim range for the y-axis
 ... optional parameters to be passed to the function plot

Details

The argument `probepos.yscale` can be used to scale probes according to their position on the reference sequence, as shown in the last example below.

Value

function used for its side-effect(s).

Author(s)

laurent

See Also

[SpliceExprSet-class](#)

Examples

```

data(spliceset)

levels(pData(spliceset@eset)$Material)
## Liver, Mix and SNB19
cl.mat <- c("red", "yellow", "blue")[as.integer(pData(spliceset@eset)$Material)]
## colored in red, yellow and blue respectively
plot(spliceset, expr.opt = list(col = cl.mat, log = "x"))

## sort
spliceset <- sort.SpliceExprSet(spliceset)
begin.pos <- spliceset@probes@pos[, 1]
plot(spliceset, expr.opt = list(col=cl.mat), probepos.yscale = begin.pos)

```

plot.SpliceSites *plot a SpliceSites object*

Description

plot objects.

Usage

```
## S3 method for class 'Probes'
plot(x, col="black",
      xlab = "sequence", ylab = "probes",
      add=FALSE, probepos.yscale=NULL, xlim=NULL,
      ...)
## S3 method for class 'SpliceSites'
plot(x, col.typeI = "orange",
      col.typeI.window = "yellow",
      col.typeII = "red",
      add=FALSE, ylim=NULL, ...)
```

Arguments

<code>x</code>	object of class <code>Probes</code> or <code>SpliceSites</code> .
<code>col</code>	color argument for the probes.
<code>col.typeI</code>	color argument for the type I splice sites
<code>col.typeI.window</code>	color argument for the type I ‘window’
<code>col.typeII</code>	color argument for the type II splice sites
<code>add</code>	add the plot to an existing plot. Make a new plot if ‘FALSE’
<code>probepos.yscale</code>	scaling argument
<code>xlim, ylim</code>	range of plotting window
<code>xlab, ylab</code>	labels for the axis
<code>...</code>	optional parameters to be passed to the function <code>plot</code> .

Details

If the parameter `main` is not specified, the function tries to extract the attribute ‘name’ from `x`.

The two functions can be combined to display both objects on the same plot.

Value

The range for the y-axis is returned whenever needed (see `invisible`).

Author(s)

Laurent

References

"Standardized output for putative alternative splicing; a R package as an application to combine them with microarray data", Gautier L. Dao C. and Yang U.C., 2003, submitted.

See Also[SpliceSites-class](#)**Examples**

```
data(spsites)

plot(spsites, main=attr(spsites, "name"))

sp.pData <- spsites@spsiteIpos.pData

##col <- as.integer(factor(sp.pData$tissue))

##plot(spsites, col.typeI=col, main=attr("name", spsites))
```

`plot.SpliceSitesGenomic`*Function to plot SpliceSitesGenomic objects*

Description

Function to plot SpliceSitesGenomic objects.

Usage

```
## S3 method for class 'SpliceSitesGenomic'
plot(x, col.variant = par("col"), col.exon = "white",
      split = FALSE, main = names(x@variants), ...)
```

Arguments

<code>x</code>	SpliceSitesGenomic-class
<code>col.variant</code>	a vector of colors for the different variants. The colors are recycled as necessary.
<code>col.exon</code>	a vector of colors for the exons. The colors are recycled as necessary.
<code>split</code>	split the plot of the variants in individual plots
<code>main</code>	character to use as a title. Recycled as necessary.
<code>...</code>	optional graphical parameters

Value

This function is used for its side-effect.

Author(s)

Laurent

See Also

[SpliceSitesGenomic-class](#)

Examples

```
## a 10 bp window
seq.length <- as.integer(10)
## positions of the exons
spsiteIpos <- matrix(c(1, 3.5, 5, 9, 3, 4, 8, 10), nc=2)
## known variants
variants <- list(a=c(1,2,3,4), b=c(1,2,3), c=c(1,3,4))
##
n.exons <- nrow(spsiteIpos)

spvar <- new("SpliceSitesGenomic", spsiteIpos=spsiteIpos,
            variants=variants, seq.length=seq.length)

par(mfrow = c(3,1), mar = c(3.1, 2.1, 2.1, 1.1))

plot(spvar, split=TRUE, col.exon=rainbow(n.exons))
```

Probes-class

Class "Probes"

Description

Information about a set of probes

Objects from the Class

Objects can be created by calls of the form `new("Probes", pos)` or `new("Probes", pos, info)`. The object are primarily storing the location of the probe on a matching sequence sequence. Optional information can be stored in the slot `info` (a `data.frame`).

Slots

pos: Object of class `"matrix"`. It expects one row per probe. The first column should give the start position while the second column should give the end position

info: Object of class `"data.frame"`. Optional information one wishes to carry around can be stored here.

Methods

initialize signature(`.Object` = `"Probes"`): ...

show signature(`object`): show minimal information

plot signature(`x` = `"Probes"`, `y` = `"missing"`): plot the position of the probes. (see [plot.Probes](#))

plot signature(x = "Probes", y = "SpliceSites"): plot the positions of the probes and the positions of the splice sites

See Also

[SpliceSites-class](#), [SpliceExprSet-class](#),

Examples

```
data(probes)
```

```
plot(probes)
```

sort.SpliceExprSet *A function to sort a SpliceExprSet*

Description

Sort the probes in a SpliceExprSet (and reflect this in all the relevant places).

Usage

```
## S3 method for class 'SpliceExprSet'  
sort(x, decreasing, fun = function(x) order(x@probes@pos[, 1]), reverse = FALSE, ...)
```

Arguments

x	a SpliceExprSet.
decreasing	currently ignored
fun	a function to do the sorting
reverse	return the reverse of the sorting order
...	currently ignored

Value

An object of class SpliceExprSet

Author(s)

Laurent

See Also

[SpliceExprSet-class](#)

Examples

```
data(spliceset)

s.spliceset <- sort.SpliceExprSet(spliceset)
```

SpliceExprSet-class *Class "SpliceExprSet"*

Description

A class to store probe expression values with alternative splicing information

Objects from the Class

Objects can be created by calls of the form `new("SpliceExprSet", ...)`.

Slots

spliceSites: Object of class "SpliceSites". The probes and splice site information.

probes: Object of class "Probes". The matching expression values.

eset: Object of class "ExpressionSet". The matching expression values.

Methods

grid.plot signature(x = "SpliceExprSet", y = "missing"): ...

plot signature(x = "SpliceExprSet", y = "missing"): a plotting method.

show signature(object = "SpliceExprSet"): a printing method.

spliceSites signature(object = "SpliceExprSet"): accessor.

Author(s)

laurent@cbs.dtu.dk

References

a manuscript in preparation

See Also

[as.data.frame.SpliceExprSet](#), [sort.SpliceExprSet](#) and [SpliceSites-class](#)

Examples

```
data(eset, package="splicegear")
data(probes, package="splicegear")
data(spsites, package="splicegear")

spliceset <- new("SpliceExprSet", eset=eset,
                probes=probes, spliceSites=spsites)

plot(spliceset)
```

spliceset	<i>Example data for splicegear</i>
-----------	------------------------------------

Description

The putative splice variants for a reference sequence, the matching probes from the Affymetrix chip 'HG-U95A' and probe intensities from the 'dilution' dataset.

Usage

```
#data(eset, package="splicegear")
#data(probes, package="splicegear")
#data(spsites, package="splicegear")
#data(spliceset, package="splicegear")
```

Format

The formats are objects of class [ExpressionSet-class](#), [Probes-class](#), [SpliceSites-class](#) and [SpliceExprSet-class](#) respectively.

Details

The attribute "name" is set to the ID of the Unigene cluster from which the reference sequence is taken.

References

"PALSdb", ref. GeneLogic's dilution dataset.

Examples

```
data(spliceset, package="splicegear")

plot(spliceset, main=attr(spliceset, "name"))
```

SpliceSites-class *Class "SpliceSites"*

Description

A class to store (putative) splice sites

Objects from the Class

Objects can be created by calls of the form `new("SpliceSites", ...)`.

Slots

seq: Object of class "character". The reference sequence.

seq.length: Object of class "integer". The length for the reference sequence (used when the slot `seq` is set to "").

spsiteIpos: Object of class "matrix". A two-columns matrix to store the begin and end positions of type I splice variant.

spsiteIIpos: Object of class "integer". A vector to store the positions for type II splice variants.

spsiteIIIpos: Object of class "matrix". Idem `spsiteIpos`, but for type III splice variants.

spsiteIpos.pData: Object of class [AnnotatedDataFrame](#). Used to store covariate information related to the splice variants.

spsiteIIpos.pData: Object of class [AnnotatedDataFrame](#).

spsiteIIIpos.pData: Object of class [AnnotatedDataFrame](#).

Methods

show signature(object = "SpliceSites"): A printing method.

plot signature(x = "SpliceSites", y = "missing"): A plotting method

Author(s)

laurent@cbs.dtu.dk

References

"Plenty of splicin' or 'can regular Affymetrix chips be used to observe alternative splicing ?'", Gautier L. et al., 2003, manuscript in preparation (and the title might have to chang. . .).

See Also

[isSpliceSiteOnProbe](#), [isProbeOnSpliceSite](#), [plot.SpliceSites](#), [spliceset](#).

Examples

```

data(spliceset)

print(spliceset)

par(mfrow=c(1,2))

plot(spliceset, main=attr(spliceset, "name"))

## filter out supporting matches with unique positions
filter.typeI <- function(x) {unique(x[duplicated(x), , drop=FALSE])}
spliceset.filter <- spliceset
sSites <- spliceset.filter@spliceSites
sSites@spsiteIpos <- filter.typeI(sSites@spsiteIpos)
spliceset.filter@spliceSites <- sSites
## plot the resulting new object
plot(spliceset.filter)

```

SpliceSitesGenomic-class

Class "SpliceSitesGenomic"

Description

A class to store alternative splicing information on a genomic point of view.

Objects from the Class

Objects can be created by calls of the form `new("SpliceSitesGenomic", seq, seq.length, spsiteIpos, spsiteIIpos`

Slots

variants: Object of class "list". There is one element per splice variant. Each element in the list should be a vector of integers. Each integer refers to an exon. The sequence of integers determines the sequence of exons in the splice variant.

seq: Object of class "character", from class "SpliceSites".

seq.length: Object of class "integer", from class "SpliceSites".

spsiteIpos: Object of class "matrix", from class "SpliceSites".

spsiteIIpos: Object of class "integer", from class "SpliceSites". This should not have any practical use in this class.

spsiteIIIpos: Object of class "matrix", from class "SpliceSites". This should not have any practical use in this class.

spsiteIpos.pData: Object of class "AnnotatedDataFrame", from class "SpliceSites".

spsiteIIpos.pData: Object of class "AnnotatedDataFrame", from class "SpliceSites". This should not have any practical use in this class.

spsiteIIIpos.pData: Object of class "AnnotatedDataFrame", from class "SpliceSites". This should not have any practical use in this class.

Extends

Class "SpliceSites", directly.

Methods

plot signature(x = "SpliceSitesGenomic", y = "missing"): a plotting method for demonstration purposes.

See Also

[SpliceSites-class](#) and [plot.SpliceSitesGenomic](#).

Examples

```
## a 10 bp window
seq.length <- as.integer(10)
## positions of the exons
spsiteIpos <- matrix(c(1, 3.5, 5, 9, 3, 4, 8, 10), nc=2)
## known variants
variants <- list(a=c(1,2,3,4), b=c(1,2,3), c=c(1,3,4))

spvar <- new("SpliceSitesGenomic", spsiteIpos=spsiteIpos,
            variants=variants, seq.length=seq.length)

plot(spvar)
```

split.SpliceSites	<i>split an instance of SpliceSites</i>
-------------------	---

Description

Split an instance of SpliceSites into several instances of SpliceSites

Usage

```
## S3 method for class 'SpliceSites'
split(x, f = list(typeI = NA, typeII = NA), drop=NULL, ...)
```

Arguments

x	an instance of class SpliceSites-class .
f	a list of two factors (see details).
drop	not used (here to keep R CMD check happy)
...	see drop above.

Details

The split usually is performed on a factor. Two factors are required because of the two categories of splicing events (type I (deletion of a fragment of the reference sequence) and type II (insertion of an element of the reference sequence)). A character can be used instead of a factor. In this case the covariates with the given name, in the slots `spsiteIpos.pData` and `spsiteIIpos.pData` respectively, are used to make the split. When equal to NA, the covariate named `site` will be used.

Value

A list of objects of class `SpliceSites`

See Also

[SpliceSites-class](#)

Examples

```
data(spsites)
split(spsites)
```

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