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 objects 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
```r
data(probes)
plot(probes)
```
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
```r
data(ezet, package="splicegear")
data(probes, package="splicegear")
data(spsites, package="splicegear")

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

plot(spliceset)
```
**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**

- `probepos`: Object of class "matrix". A two-columns matrix to store the begin and end positions of probes (one row per probe).
- `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**

- `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`. 
SpliceSitesGenomic-class

Examples

```r
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, spsiteIIIpos, spsiteIpos.pData, spsiteIIpos.pData,  
s SITEIIIpos.pData, ...).

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.
as.data.frame.SpliceExprSet

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)

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 will be the ones in the `AnnotatedDataFrame-class` attribute of the `ExpressionSet-class` object belonging 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

```r
## 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`.

---

`barplot.SpliceSites`
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)

__buildSpliceSites\__  
Functions to query PALSdb

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"),
    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"),
    species = c("human", "mouse"),
    e.value = "1e-1",
    ident.threshold = c("90% 50b", "95% 50b", "90% 45b"))

buildSpliceSites(xml, verbose=TRUE)

Arguments

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

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


See Also

queryPALSdb

Examples

library(XML)

filename <- system.file("data", "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, ...)
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 prob-
ably 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]])
grid.expand.gp is a convenience function for grid.

### Description

Convenience function to use the package grid

### Usage

```r
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 is used to plot splicegear objects.

### 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

```r
## 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

```r
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

**matchprobes2Probes**

*create Probes object from matchprobes results*

**Description**

Create Probes object from results the results of the function matchprobes (in the package ’matchprobes’).

**Usage**

```r
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**

```r
## 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),
probe.pos.yscale = NULL, ylim,
...)
```
### plot.SpliceExprSet

**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**

```r
data(spliceset)

levels(pData(spliceset@eset)$Material)
## Liver, Mix and SNB19
c1.mat <- c("red", "yellow","blue")[as.integer(pData(spliceset@eset)$Material)]
## colored in red, yellow and blue respectively
plot(spliceset, expr.opt = list(col = c1.mat, log = "x"))

## sort
spliceset <- sort.SpliceExprSet(spliceset)
begin.pos <- spliceset@probes@pos[, 1]
plot(spliceset, expr.opt = list(col=c1.mat), probepos.yscale = begin.pos)
```
plot.SpliceSites

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

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

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
plot.SpliceSitesGenomic

References


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

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

Value

This function is used for its side-effect.

Author(s)

Laurent
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)

spliceset Example data for splicegear

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"))
Description

Split an instance of SpliceSites into several instances of SpliceSites

Usage

```r
## 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

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