

# 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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**License** LGPL

**Depends** R (>= 2.6.0), methods, Biobase(>= 2.5.5)

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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 <a href="#">SpliceSites-class</a> or <a href="#">SpliceExprSet-class</a> .
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 <a href="#">SpliceSites-class</a> .
type.as	the type of alternative splicing (see <a href="#">SpliceSites-class</a> for further details).
info	the name of the covariate in the AnnotatedDataFrame (see details).
...	optional parameters to be passed to the underlying function <a href="#">barplot</a> .

**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", "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**

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

---

**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**

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

**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      *split an instance of SpliceSites*

---

**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 <a href="#">SpliceSites-class</a> .
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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