# Package: SpliceWiz (via r-universe)

November 1, 2026

**Title** interactive analysis and visualization of alternative splicing in R

**Version** 1.14.0

**Date** 2025-03-13

**Description** The analysis and visualization of alternative splicing (AS) events from RNA sequencing data remains challenging. SpliceWiz is a user-friendly and performance-optimized R package for AS analysis, by processing alignment BAM files to quantify read counts across splice junctions, IRFinder-based intron retention quantitation, and supports novel splicing event identification. We introduce a novel visualization for AS using normalized coverage, thereby allowing visualization of differential AS across conditions. SpliceWiz features a shiny-based GUI facilitating interactive data exploration of results including gene ontology enrichment. It is performance optimized with multi-threaded processing of BAM files and a new COV file format for fast recall of sequencing coverage. Overall, SpliceWiz streamlines AS analysis, enabling reliable identification of functionally relevant AS events for further characterization.

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**Depends** NxtIRFdata

**Imports** ompBAM, methods, stats, utils, tools, parallel, scales, magrittr, Rcpp (>= 1.0.5), data.table, fst, ggplot2, AnnotationHub, RSQLite, BiocFileCache, BiocGenerics, BiocParallel, Biostrings, BSgenome, DelayedArray, DelayedMatrixStats, genefilter, GenomeInfoDb, GenomicRanges, HDF5Array, h5mread, htmltools, IRanges, patchwork, pheatmap, progress, plotly, R.utils, rhdf5, rtracklayer, SummarizedExperiment, S4Vectors, shiny, shinyFiles, shinyWidgets, shinydashboard, stringi, rhandsontable, DT, grDevices, heatmaply, matrixStats, RColorBrewer, rvest, httr

**Suggests** knitr, rmarkdown, crayon, splines, testthat (>= 3.0.0), DESeq2, limma, DoubleExpSeq, edgeR, DBI, GO.db, AnnotationDbi, fgsea, Rsubread

**LinkingTo** ompBAM, Rcpp, RcppProgress

**SystemRequirements** C++11, GNU make

**Collate** AllImports.R RcppExports.R zzz.R AllClasses.R AllGenerics.R ASEFilter-methods.R NxtSE-methods.R globals.R ggplot_themes.R example_data.R wrappers.R make_plot_data.R Coverage.R covPlotly-methods.R covDataObject-methods.R covPlotObject-methods.R plotCoverage.R utils.R File_finders.R BuildRef_GO.R BuildRef.R ViewRef.R STAR_utils.R Mappability.R ProcessBAM_docs.R ProcessBAM.R CollateData.R MakeSE.R Filters.R ASE-methods.R ASE-GLM-edgeR.R dash_filterModules.R dash_globals.R dash_settings.R dash_ref_new_ui.R dash_ref_new_server.R dash_expr_ui.R dash_expr_server.R dash_QC.R dash_filters.R dash_DE_ui.R dash_DE_server.R dash_vis_ui.R dash_vis_server.R dash_cov_ui.R dash_cov_server.R dash_GO_ui.R dash_GO_server.R dash_ui.R dash_server.R dash.R SpliceWiz-package.R

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**VignetteBuilder** knitr

**biocViews** Software, Transcriptomics, RNASeq, AlternativeSplicing, Coverage, DifferentialSplicing, DifferentialExpression, GUI, Sequencing

**URL** https://github.com/alexchwong/SpliceWiz

**BugReports** https://support.bioconductor.org/

**Config/testthat/edition** 3

**Config/pak/sysreqs** cmake make libmagick++-dev gsfonts libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

**Repository** Bioconductor 3.23

**Date/Publication** 2026-04-28 12:58:37 UTC

**RemoteUrl** https://github.com/bioc/SpliceWiz

**RemoteRef** RELEASE_3_23

**RemoteSha** 1f1fc5742057d338f4583e3a039978b70cfa8bea

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`SpliceWiz-package` *SpliceWiz: efficient and precise alternative splicing analysis in R*

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## Description

SpliceWiz is a computationally efficient and user friendly workflow that analyses aligned short-read RNA sequencing for differential intron retention and alternative splicing.

## Details

SpliceWiz uses isoform-specific alignments to quantify percent-spliced-in ratios (i.e. ratio of the "included" isoform, as a proportion of "included" and "excluded" isoforms). For intron retention (IR), the abundance of the intron-retaining transcript (included isoform) is quantified using the trimmed-mean depth of intron coverage with reads, whereas the spliced transcript (excluded isoform) is measured as the splicing of the intron as well as that of overlapping introns (since splicing of any overlapping intron implies the intron of interest is not retained). For other forms of alternative splicing, junction reads (reads aligned across splice junctions) are used to quantify included and excluded isoforms.

SpliceWiz processes BAM files (aligned RNA sequencing) using ompBAM::ompBAM-package. ompBAM is a C++ library that allows R packages (via the Rcpp framework) to efficiently read BAM files using OpenMP-based multi-threading. SpliceWiz processes BAM files via the processBAM function, using a splicing and intron reference built from any given genome / gene annotation resource using the buildRef function. processBAM generates two outputs per BAM file: a `txt.gz`

file which is a gzip-compressed text file with multiple tables, containing information including junction read counts and intron retention metrics. This output is very similar to that of IRFinder, as the analysis steps of SpliceWiz's BAM processing was built on an improved version of IRFinder's source code (version 1.3.1). Additionally, processBAM outputs a COV file, which is a binary bgzf-compressed file that contains strand-specific coverage data.

Once individual files have been analysed, SpliceWiz compiles a dataset using these individual outputs, using collateData. This function unifies junctions detected across the dataset, and generates included / excluded counts of all putative IR events and annotated alternative splicing events (ASEs). This dataset is exported as a collection of files including an H5 database. The data is later imported into the R session using the makeSE function, as a NxtSE object.

The NxtSE object is a specialized SummarizedExperiment object tailored for use in SpliceWiz. Annotation of rows provide information about ASEs via rowData, while columns allows users to provide annotations via colData.

SpliceWiz offers several novel filters via the ASEFilter class. See ASEFilter for details.

Once the NxtSE is annotated and filtered, differential analysis is performed, using limma, DoubleExpSeq (DES), edgeR and DESeq2 wrappers. These wrappers model isoform counts as log-normal (limma), beta-binomial (DES) and negative-binomial (edgeR and DESeq2) distributions. See ASE-methods for details.

Finally, SpliceWiz provides visualisation tools to illustrate alternative splicing using coverage plots, including a novel method to normalise RNA-seq coverage grouped by experimental condition. This approach accounts for variations introduced by sequenced library size and gene expression. SpliceWiz efficiently computes and visualises means and variations in per-nucleotide coverage depth across alternate exons in genomic loci.

The main functions are:

- Build-Reference-methods - Prepares genome and gene annotation references from FASTA and GTF files and synthesizes the SpliceWiz reference for processing BAM files, collating the NxtSE object.
- STAR-methods - (Optional) Provides wrapper functions to build the STAR genome reference and alignment of short-read FASTQ raw sequencing files. This functionality is only available on systems with STAR installed.
- processBAM - OpenMP/C++ based algorithm to analyse single or multiple BAM files.
- collateData - Collates an experiment based on multiple IRFinder outputs for individual samples, into one unified H5-based data structure.
- makeSE - Constructs a NxtSE (H5-based SummarizedExperiment) object, specialised to house measurements of retained introns and junction counts of alternative splice events.
- applyFilters - Use default or custom filters to remove alternative splicing or IR events pertaining to low-abundance genes and transcripts.
- ASE-methods - one-step method to perform differential alternate splice event (ASE) analysis on a NxtSE object using limma or DESeq2.
- make_plot_data: Functions that compile individual and group-mean percent spliced in (PSI) values of IR and alternative splice events; useful to produce scatter plots or heatmaps.
- Coverage: methods that retrieve coverage data from COV files.
- getCoverageData / getPlotObject / plotView: Functions for plotting SpliceWiz's novel coverage plots.

See the SpliceWiz Quick-Start for worked examples on how to use SpliceWiz SpliceWiz Cookbook for real-life usage examples

## Author(s)

Alex Wong

## References

Wong ACH, Wong JJ-L, Rasko JEJ, Schmitz U. SpliceWiz: interactive analysis and visualization of alternative splicing in R. Briefings in Bioinformatics, Volume 25, Issue 1, January 2024, bbad468. https://doi.org/10.1093/bib/bbad468

## See Also

Useful links:

- https://github.com/alexchwong/SpliceWiz
- Report bugs at https://support.bioconductor.org/

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`ASE-GLM-edgeR` *Using Generalised linear models (GLMs) to analyse differential ASEs using edgeR*

---

## Description

These functions allow users to fit custom GLMs included/excluded counts using edgeR for differential Alternative Splice Events (ASEs)

## Usage

```
fitASE_edgeR(
  se,
  strModelFormula,
  strASEFormula,
  useQL = TRUE,
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
  filter_antinear = FALSE
)

fitASE_edgeR_custom(
  se,
  model_IncExc,
  model_ASE,
  useQL = TRUE,
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
```

```
  filter_antinear = FALSE
)

testASE_edgeR(
  se,
  fit,
  coef_IncExc = ncol(fit[["model_IncExc"]]),
  contrast_IncExc = NULL,
  coef_ASE = ncol(fit[["model_ASE"]]),
  contrast_ASE = NULL
)

addPSI_edgeR(results, se, condition, conditionList)
```

## Arguments

| | |
|---|---|
| se | The NxtSE object created by `makeSE()`. To reduce runtime and avoid excessive multiple testing, consider filtering the object using applyFilters |
| strModelFormula | A string specifying the model formula to fit isoform counts to assess differential expression in isolation. Should take the form of `"~0 + batch1 + batch2 + test_factor"`, where `batch1` and `batch2` are batch factors (if any), and `test_factor` is the variate of interest. |
| strASEFormula | A string specifying the model formula to fit PSIs (isoform ratios). The variate of interest should be specified as an interactiion term with `ASE`. For example, following the above example, the ASE formula should be `"~0 + batch1 + batch2 + test_factor + test_factor:ASE"` |
| useQL | (default `TRUE`) Whether to use edgeR's quasi-likelihood method to help reduce false positives from near-zero junction / intron counts. NB: edgeR's quasi-likelihood method is run with legacy method (Lun and Smyth (2017)). |
| IRmode | (default `all`) Choose the approach to quantify IR events. Default `all` considers all introns as potentially retained, and calculates IR-ratio based on total splicing across the intron using the "SpliceOver" or "SpliceMax" approach (see collateData). Other options include `annotated` which calculates IR-ratios for annotated introns only, and `annotated_binary` which calculates PSI considering the "included" isoform as the IR-transcript, and the "excluded" transcript is quantified from splice counts only across the exact intron (but not that of overlapping introns). IR-ratio are denoted as "IR" events, whereas PSIs calculated using IR and intron-spliced binary alternatives are denoted as "RI" events. |
| filter_antiover, filter_antinear | Whether to remove novel IR events that overlap over or near anti-sense genes. Default will exclude antiover but not antinear introns. These are ignored if strand-specific RNA-seq protocols are used. |
| model_IncExc | A model matrix in which to model differential expression of isoform counts in isolation. The number of rows must equal that of the number of samples in `se` |
| model_ASE | A model matrix in which to model differential PSIs. The number of rows must be twice that of the number of samples in `se`, the first half are for included counts, and the second half are for excluded counts. See example below. |

`fit` The output returned by the `fitASE_edgeR` and `fitASE_edgeR_custom` functions.

`coef_IncExc, coef_ASE`
model coefficients to be dropped for LRT test between full and reduced models. Directly parsed onto `edgeR::glmQLFTest`. See `?edgeR::glmQLFTest` for details

`contrast_IncExc, contrast_ASE`
numeric vector specifying one or more #' contrasts of the linear model coefficients to be tested. Directly parsed onto `edgeR::glmQLFTest`. See `?edgeR::glmQLFTest` for details

`results` The return value of `testASE_edgeR()`, to be used as input to append mean and delta PSI values onto.

`condition` The name of the column containing the condition values in `colData(se)`

`conditionList` A list (or vector) of condition values of which to calculate mean PSIs

## Details

**edgeR** accounts appropriately for zero-counts which are often problematic as PSI approaches zero or one, leading to false positives. The following functions allow users to define model formulas to test relative expressions of included / excluded counts (to assess whether isoforms are differentially regulated, in isolation), as well as together as an interaction (the latter provides results of differential ASE analysis)

See the examples section for a brief explanation of how to use these functions.

See also ASE-methods for further explanations of results output.

## Value

`fitASE_edgeR` and `fitASE_edgeR_custom` returns a named list containing the following:

- `IncExc` and `ASE` are `DGEGLM` objects containing the fitted models for isoform counts and PSIs, respectively
- `model_IncExc` and `model_ASE` are model matrices of the above fitted models.

`testASE_edgeR()` returns a data.table containing the following:

- EventName: The name of the ASE event. This identifies each ASE in downstream functions including makeMeanPSI, makeMatrix, and plotCoverage
- EventType: The type of event. See details section above.
- EventRegion: The genomic coordinates the event occupies. This spans the most upstream and most downstream splice junction involved in the ASE, and is use to guide the plotCoverage function.
- flags: Indicates which isoforms are NMD substrates and/or which are formed by novel splicing only.

**edgeR specific output** equivalent to statistics returned by `edgeR::topTags()`:

- logFC, logCPM, F, PValue, FDR: log fold change, log counts per million, F statistic, p value and (Benjamini Hochberg) adjusted p values of the differential PSIs for the contrasts or coefficients tested.

- inc/exc_(...): edgeR statistics corresponding to differential expression testing for raw included / excluded counts in isolation (not of the PSIs).

`addPSI_edgeR()` appends the following columns to the above output

- AvgPSI_X: the average percent spliced in / percent IR levels for condition X. Note this is a geometric mean, based on the arithmetic mean of logit PSI values.
- deltaPSI: The difference in PSI between the mean values of the two conditions.
- abs_deltaPSI: The absolute value of difference in PSI between the mean values of the two conditions.

## Functions

- `fitASE_edgeR()`: Use edgeR to fit counts and ASE models with a given design formula
- `fitASE_edgeR_custom()`: Use edgeR to fit counts and ASE models with a given design formula
- `testASE_edgeR()`: Use edgeR to return differential ASE results. coef and contrast are parsed onto edgeR's glmQLFTest function
- `addPSI_edgeR()`: Adds average and delta PSIs of conditions of interest onto results produced by testASE_edgeR(). Note this is done automatically for other methods described in `ASE-methods`.

## References

Lun A, Smyth G (2017). 'No counts, no variance: allowing for loss of degrees of freedom when assessing biological variability from RNA-seq data' Stat Appl Genet Mol Biol, 017 Apr 25;16(2):83-93. https://doi.org/10.1515/sagmb-2017-0010

## Examples

```
# Load the NxtSE object and set up the annotations
# - see ?makeSE on example code of generating this NxtSE object
se <- SpliceWiz_example_NxtSE()

colData(se)$treatment <- rep(c("A", "B"), each = 3)
colData(se)$replicate <- rep(c("P","Q","R"), 2)
require("edgeR")

fit <- fitASE_edgeR(
    se,
    strModelFormula = "~0 + replicate + treatment",
    strASEFormula = "~0 + replicate + treatment + treatment:ASE"
)

# Get coefficient terms of Included / Excluded counts isolated model
colnames(fit$model_IncExc)
# [1] "replicateP" "replicateQ" "replicateR" "treatmentB"

# Get coefficient terms of PSI model
colnames(fit$model_ASE)
```

```
# [1] "replicateP" "replicateQ" "replicateR" "treatmentB"
# [5] "treatmentA:ASEIncluded" "treatmentB:ASEIncluded"

# Contrast between treatment "B" against treatment "A"
res <- testASE_edgeR(se, fit,
    contrast_IncExc = c(0,0,0,1),
    contrast_ASE = c(0,0,0,0,-1,1)
)

### # Add mean PSI values to results:
res_withPSI <- addPSI_edgeR(res, se, "treatment", c("B", "A"))


### Using custom model matrices to model counts
#   - the equivalent analysis can be performed as follows:

# Sample annotations for isoform count expressions
colData <- as.data.frame(colData(se))

# Sample annotations for isoform count PSI analysis
colData_ASE <- rbind(colData, colData)
colData_ASE$ASE <- rep(c("Included", "Excluded"), each = nrow(colData))
rownames(colData_ASE) <- c(
    paste0(rownames(colData), ".Included"),
    paste0(rownames(colData), ".Excluded")
)

model_IncExc <- model.matrix(
    ~0 + replicate + treatment,
    data = colData
)

model_ASE <- model.matrix(
    ~0 + replicate + treatment + treatment:ASE,
    data = colData_ASE
)

fit <- fitASE_edgeR_custom(se, model_IncExc, model_ASE)

res_customModel <- testASE_edgeR(se, fit,
    contrast_IncExc = c(0,0,0,1),
    contrast_ASE = c(0,0,0,0,-1,1)
)

# Check this produces identical results:
identical(res_customModel, res)

### Time series examples using edgeR and splines
# - similar to section 4.8 in the edgeR vignette

colData(se)$timepoint <- rep(c(1,2,3), each = 2)
colData(se)$batch <- rep(c("1", "2"), 3)
```

```
# First, we set up a polynomial spline with 2 degrees of freedom:
Time <- poly(colData(se)$timepoint, df = 2)

# Next, we define the batch factor:
Batch <- factor(colData(se)$batch)

# Finally, we construct the same factors for ASE analysis. Note that
#   each factor must be repeated twice

Time_ASE <- rbind(Time, Time)
Batch_ASE <- c(Batch, Batch)
ASE <- factor(
    rep(c("Included", "Excluded"), each = nrow(colData(se)))
)

# Now, we set up the model matrices for isoform and PSI count modelling
model_IncExc <- model.matrix(~0 + Batch + Time)
model_ASE <- model.matrix(~0 + Batch_ASE + Time_ASE + Time_ASE:ASE)

fit <- fitASE_edgeR_custom(se, model_IncExc, model_ASE)

# Note the coefficients of interest in the constructed models:

colnames(model_IncExc)
# [1] "Batch1" "Batch2" "Time1"  "Time2"

colnames(model_ASE)
# [1] "Batch_ASE1" "Batch_ASE2" "Time_ASE1" "Time_ASE2"
# [5] "Time_ASE1:ASEIncluded" "Time_ASE2:ASEIncluded"

# We are interested in a model in which `Time` is excluded, thus:

res <- testASE_edgeR(se, fit,
    coef_IncExc = 3:4,
    coef_ASE = 5:6
)

# Finally, add PSI values for each time point:

res_withPSI <- addPSI_edgeR(res, se, "timepoint", c(1, 2, 3))
```

---

ASE-methods *Differential Alternative Splicing Event analysis*

---

## Description

Use Limma, DESeq2, DoubleExpSeq, and edgeR wrapper functions to test for differential Alternative Splice Events (ASEs)

## Usage

```
ASE_limma(
  se,
  test_factor,
  test_nom,
  test_denom,
  batch1 = "",
  batch2 = "",
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
  filter_antinear = FALSE
)

ASE_edgeR(
  se,
  test_factor,
  test_nom,
  test_denom,
  batch1 = "",
  batch2 = "",
  useQL = TRUE,
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
  filter_antinear = FALSE
)

ASE_limma_timeseries(
  se,
  test_factor,
  batch1 = "",
  batch2 = "",
  degrees_of_freedom = 1,
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
  filter_antinear = FALSE
)

ASE_edgeR_timeseries(
  se,
  test_factor,
  batch1 = "",
  batch2 = "",
  degrees_of_freedom = 1,
  useQL = TRUE,
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
  filter_antinear = FALSE
)
```

```
ASE_DESeq(
  se,
  test_factor,
  test_nom,
  test_denom,
  batch1 = "",
  batch2 = "",
  n_threads = 1,
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
  filter_antinear = FALSE
)

ASE_DoubleExpSeq(
  se,
  test_factor,
  test_nom,
  test_denom,
  IRmode = c("all", "annotated", "annotated_binary"),
  filter_antiover = TRUE,
  filter_antinear = FALSE
)
```

## Arguments

| | |
|---|---|
| se | The NxtSE object created by `makeSE()`. To reduce runtime and avoid excessive multiple testing, consider filtering the object using applyFilters |
| test_factor | The column name in the sample annotation `colData(se)` that contains the desired variables to be contrasted. For `ASE_limma_timeseries()` and `ASE_DESeq()` (when `test_nom` and `test_denom` parameters are left blank), `test_factor` must contain numerical values representing the time variable. |
| test_nom | The nominator condition to test for differential ASE. Usually the "treatment" condition |
| test_denom | The denominator condition to test against for differential ASE. Usually the "control" condition |
| batch1, batch2 | (Optional, limma and DESeq2 only) One or two condition types containing batch information to account for. |
| IRmode | (default `all`) Choose the approach to quantify IR events. Default `all` considers all introns as potentially retained, and calculates IR-ratio based on total splicing across the intron using the "SpliceOver" or "SpliceMax" approach (see collateData). Other options include `annotated` which calculates IR-ratios for annotated introns only, and `annotated_binary` which calculates PSI considering the "included" isoform as the IR-transcript, and the "excluded" transcript is quantified from splice counts only across the exact intron (but not that of overlapping introns). IR-ratio are denoted as "IR" events, whereas PSIs calculated using IR and intron-spliced binary alternatives are denoted as "RI" events. |

`filter_antiover`, `filter_antinear`
: Whether to remove novel IR events that overlap over or near anti-sense genes. Default will exclude antiover but not antinear introns. These are ignored if strand-specific RNA-seq protocols are used.

`useQL`
: (default `TRUE`) Whether to use edgeR's quasi-likelihood method to help reduce false positives from near-zero junction / intron counts. NB: edgeR's quasi-likelihood method is run with legacy method (Lun and Smyth (2017)).

`degrees_of_freedom`
: (default `1`) The complexity of time series trends modeled by `ASE_limma_timeseries` and `ASE_edgeR_timeseries`. E.g., `1` will only model linear trends, `2` extends the capacity for quadratic trends, and `3` for cubic trends, etc.

`n_threads`
: (DESeq2 only) How many threads to use for DESeq2 based analysis.

## Details

Using **limma**, SpliceWiz models included and excluded counts as log-normal distributed, whereas using **DESeq2**, SpliceWiz models included and excluded counts as negative binomial distributed with dispersion shrinkage according to their mean count expressions. For **limma** and **DESeq2**, differential ASE are considered as the "interaction" between included and excluded splice counts for each sample. See this vignette for an explanation of how this is done.

SpliceWiz's **limma** wrapper implements an additional filter where ASEs with an average cpm values of either Included or Excluded counts are less than 1. **DESeq2** has its own method for handling outliers, which seems to work well for handling situations where PSI ~= 0 or PSI ~= 1.

Time series are supported by SpliceWiz to a limited extent. Time series analysis can be performed via limma or DESeq2. For limma time-series analysis, use `ASE_limma_timeseries()`, specifying the `test_factor` as the column of numeric values containing time series data. For DESeq, time series differential analysis can be activated using the `ASE_DESeq()` function, again specifying `test_factor` as the column containing time series data (and leaving `test_nom` and `test_denom` parameters blank). See examples below.

**edgeR** models counts using a negative binomial model. It accounts appropriately for zero-counts which are often problematic as PSI approaches zero or one, leading to false positives. The edgeR-based option produces differential ASEs that are less biased towards low counts. Our preliminary analysis shows it to be more accurate than limma or DoubleExpSeq based methods.

For time series analysis using edgeR, `ASE_edgeR_timeseries()` can be used interchangeably with its counterpart limma-based function. For complex models, please see ASE-GLM-edgeR to build your own GLM models.

Using **DoubleExpSeq**, included and excluded counts are modeled using the generalized beta prime distribution, using empirical Bayes shrinkage to estimate dispersion.

**EventType** are as follow:

- `IR` = intron retention (IR-ratio) - all introns are considered
- `MXE` = mutually exclusive exons
- `SE` = skipped exons
- `AFE` = alternate first exon
- `ALE` = alternate last exon

- `A5SS` = alternate 5'-splice site
- `A3SS` = alternate 3'-splice site
- `RI` = (known / annotated) intron retention (PSI).

NB: SpliceWiz measures intron retention events using two different approaches, the choice of which is left to the user - see ASE-methods:

- **IR** (intron retention) events: considers all introns to be potentially retained. Given in most scenarios there may be uncertainty as to which of the many mutually-overlapping introns are spliced to produce the major isoform, SpliceWiz adopts the IRFinder approach by using the IR-ratio. The "included" isoform is the relative abundance of the IR-transcript, as approximated by the trimmed-mean depth of coverage across the intron (excluding outliers including exons of other transcripts, intronic elements such as snoRNAs, etc). The "excluded isoform" includes **all** spliced transcripts that contain an overlapping intron, as estimated via SpliceWiz's `SpliceOver` and IRFinder's `SpliceMax` methods - see collateData.
- **RI** (annotated retained introns) considers only annotated retained introns, i.e., those annotated within the given reference. These are quantified using PSI, considering the included (IR-transcript) and excluded (splicing of the exact intron) as binary alternatives.

SpliceWiz considers "included" counts as those that represent abundance of the "included" isoform, whereas "excluded" counts represent the abundance of the "excluded" isoform. To allow comparison between modalities, SpliceWiz applies a convention whereby the "included" transcript is one where its splice junctions are by definition shorter than those of "excluded" transcripts. Specifically, this means the included / excluded isoforms are as follows:

| EventType | Included | Excluded |
|---|---|---|
| IR or RI | Intron Retention | Spliced Intron |
| MXE | Upstream exon inclusion | Downstream exon inclusion |
| SE | Exon inclusion | Exon skipping |
| AFE | Downstream exon usage | Upstream exon usage |
| ALE | Upstream exon usage | Downstream exon usage |
| A5SS | Downstream 5'-SS | Upstream 5'-SS |
| A3SS | Upstream 3'-SS | Downstream 3'-SS |

## Value

For all methods, a data.table containing the following:

- EventName: The name of the ASE event. This identifies each ASE in downstream functions including makeMeanPSI, makeMatrix, and plotCoverage
- EventType: The type of event. See details section above.
- EventRegion: The genomic coordinates the event occupies. This spans the most upstream and most downstream splice junction involved in the ASE, and is use to guide the plotCoverage function.
- flags: Indicates which isoforms are NMD substrates and/or which are formed by novel splicing only.

- AvgPSI_nom, Avg_PSI_denom: the average percent spliced in / percent IR levels for the two conditions being contrasted. `nom` and `denom` in column names are replaced with the condition names. Note this is a geometric mean, based on the arithmetic mean of logit PSI values.
- deltaPSI: The difference in PSI between the mean values of the two conditions.
- abs_deltaPSI: The absolute value of difference in PSI between the mean values of the two conditions.

**limma specific output**

- logFC, AveExpr, t, P.Value, adj.P.Val, B: limma topTable columns of differential ASE. See limma::topTable for details.
- inc/exc_(logFC, AveExpr, t, P.Value, adj.P.Val, B): limma results for differential testing for raw included / excluded counts only

**edgeR specific output** equivalent to statistics returned by edgeR::topTags:

- logFC, logCPM, F, PValue, FDR: log fold change, log counts per million, F statistic, p value and (Benjamini Hochberg) adjusted p values.
- inc/exc_(...): edgeR statistics corresponding to differential expression testing for raw included / excluded counts in isolation

**DESeq2 specific output**

- baseMean, log2FoldChange, lfcSE, stat, pvalue, padj: DESeq2 results columns for differential ASE; see DESeq2::results for details.
- inc/exc_(baseMean, log2FoldChange, lfcSE, stat, pvalue, padj): DESeq2 results for differential testing for raw included / excluded counts only

**DoubleExp specific output**

- MLE_nom, MLE_denom: Maximum likelihood expectation of PSI values for the `denom` in column names are replaced with the condition names
- MLE_LFC: Log2-fold change of the MLE
- P.Value, adj.P.Val: Nominal and BH-adjusted P values
- n_eff: Number of effective samples (i.e. non-zero or non-unity PSI)
- mDepth: Mean Depth of splice coverage in each of the two groups.
- Dispersion_Reduced, Dispersion_Full: Dispersion values for reduced and full models. See DoubleExpSeq::DBGLM1 for details.

## Functions

- `ASE_limma()`: Use limma to perform differential ASE analysis of a filtered NxtSE object
- `ASE_edgeR()`: Use edgeR to perform differential ASE analysis of a filtered NxtSE object
- `ASE_limma_timeseries()`: Use limma to perform differential ASE analysis of a filtered NxtSE object (time series)
- `ASE_edgeR_timeseries()`: Use edgeR to perform differential time series of a filtered NxtSE object

- `ASE_DESeq()`: Use DESeq2 to perform differential ASE analysis of a filtered NxtSE object
- `ASE_DoubleExpSeq()`: Use DoubleExpSeq to perform differential ASE analysis of a filtered NxtSE object (uses double exponential beta-binomial model) to estimate group dispersions, followed by LRT

## References

Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK (2015). 'limma powers differential expression analyses for RNA-sequencing and microarray studies.' Nucleic Acids Research, 43(7), e47. https://doi.org/10.1093/nar/gkv007

Love MI, Huber W, Anders S (2014). 'Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2.' Genome Biology, 15, 550. https://doi.org/10.1186/s13059-014-0550-8

Ruddy S, Johnson M, Purdom E (2016). 'Shrinkage of dispersion parameters in the binomial family, with application to differential exon skipping.' Ann. Appl. Stat. 10(2): 690-725. https://doi.org/10.1214/15-AOAS871

Gilis J, Vitting-Seerup K, Van den Berge K, Clement L (2021). 'Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications.' F1000Research 2021, 10:374. https://doi.org/10.12688/f1000research.51749.1

Lun A, Smyth G (2017). 'No counts, no variance: allowing for loss of degrees of freedom when assessing biological variability from RNA-seq data' Stat Appl Genet Mol Biol, 017 Apr 25;16(2):83-93. https://doi.org/10.1515/sagmb-2017-0010

## Examples

```
# Load the NxtSE object and set up the annotations
# - see ?makeSE on example code of generating this NxtSE object
se <- SpliceWiz_example_NxtSE(novelSplicing = TRUE)

colData(se)$treatment <- rep(c("A", "B"), each = 3)
colData(se)$replicate <- rep(c("P","Q","R"), 2)

# Limma analysis (counts modeled using log-normal distribution)

require("limma")
res_limma <- ASE_limma(se, "treatment", "A", "B")

# edgeR analysis (counts modeled using negative binomial distribution)
# - QL: whether quasi-likelihood method was used

require("edgeR")
res_edgeR <- ASE_edgeR(se, "treatment", "A", "B", useQL = FALSE)
res_edgeR_QL <- ASE_edgeR(se, "treatment", "A", "B", useQL = TRUE)

# DoubleExpSeq analysis (counts modeled using beta binomial distribution)

require("DoubleExpSeq")
res_DES <- ASE_DoubleExpSeq(se, "treatment", "A", "B")

# DESeq2 analysis (counts modeled using negative binomial distribution)
```

```
require("DESeq2")
res_DESeq <- ASE_DESeq(se, "treatment", "A", "B")

# Time series examples

colData(se)$timepoint <- rep(c(1,2,3), each = 2)
colData(se)$batch <- rep(c("1", "2"), 3)

res_limma_timeseries <- ASE_limma_timeseries(se, "timepoint")
res_edgeR_timeseries <- ASE_edgeR_timeseries(se, "timepoint")
res_DESeq_timeseries <- ASE_DESeq(se, "timepoint")
```

---

`ASEFilter-class` *SpliceWiz filters to remove low-confidence alternative splicing and intron retention events*

---

## Description

SpliceWiz implements a number of novel filters designed to exclude alternative splicing events (ASEs) that yield low-confidence estimates.

## Usage

```
ASEFilter(
  filterClass = c("Data", "Annotation"),
 filterType = c("Depth", "Participation", "Consistency", "Modality", "Protein_Coding",
    "NMD", "TSL", "Terminus", "ExclusiveMXE", "StrictAltSS"),
  pcTRUE = 100,
  minimum = 20,
  maximum = 1,
  minDepth = 5,
  condition = "",
  minCond = -1,
  EventTypes = c("IR", "MXE", "SE", "A3SS", "A5SS", "AFE", "ALE", "RI")
)
```

## Arguments

| | |
|---|---|
| `filterClass` | Must be either `"Data"` or `"Annotation"`. See details |
| `filterType` | Must be a valid `"Data"` or `"Annotation"` filter. See details |
| `pcTRUE` | If conditions are set, what percentage of all samples in each of the condition must satisfy the filter for the event to pass the filter check. Must be between 0 and 100 (default 100) |
| `minimum` | Filter-dependent argument. See details |
| `maximum` | Filter-dependent argument. See details |
| `minDepth` | Filter-dependent argument. See details |

`condition` (default "") If set, must match the name of an experimental condition in the NxtSE object to be filtered, i.e. a column name in `colData(se)`. Leave blank to disable filtering by condition

`minCond` (default -1) If condition is set, how many minimum number of conditions must pass the filter criteria. For example, if condition = "Batch", and batches are "A", "B", or "C", setting `minCond = 2` with `pcTRUE = 100` means that all samples belonging to two of the three types of `Batch` must pass the filter criteria. Setting `-1` means all elements of `condition` must pass criteria. Set to `-1` when the number of elements in the experimental condition is unknown. Ignored if `condition` is left blank.

`EventTypes` What types of events are considered for filtering. Must be one or more of `c("IR", "MXE", "SE", "A3SS", "A5SS", "AFE", "ALE", "RI")`. Events not specified in `EventTypes` are not filtered (i.e. they will pass the filter without checks)

## Details

### Annotation Filters

- **Modality**: Filters for specific modalities of ASEs. All events belonging to the specified `EventTypes` are removed. No additional parameters required.
- **Protein_Coding**: Filters for alternative splicing or IR events involving protein-coding transcripts. No additional parameters required.
- **NMD**: Filters for events in which one isoform is a predicted NMD substrate.
- **TSL**: filters for events in which both isoforms have a TSL level below or equal to `minimum`
- **Terminus**: In alternate first exons, the splice junction must not be shared with another transcript for which it is not its first intron. For alternative last exons, the splice junction must not be shared with another transcript for which it is not its last intron
- **ExclusiveMXE**: For MXE events, the two alternate casette exons must not overlap in their genomic regions
- **StrictAltSS**: For A5SS / A3SS events, the two alternate splice sites must not be interupted by detected introns

### Data Filters

- **Depth**: Filters IR or alternative splicing events of transcripts that are "expressed" with adequate `Depth` as calculated by the sum of all splicing and IR reads spanning the event. Events with `Depth` below `minimum` are filtered out
- **Participation**: Participation means different things to IR and alternative splicing.

  For **IR**, Participation refers to the percentage of the measured intron covered with reads. Only introns of samples with a depth of intron coverage (intron depth) above `minDepth` are assessed, where introns with coverage percentage below `minimum` are filtered out.

  For **non-IR ASEs**, Participation refers to the percentage of all splicing events observed across the genomic region (SpliceOver metric) that is compatible with either the included or excluded event. This prevents SpliceWiz from doing differential analysis between two minor isoforms.

Instead of IntronDepth, in AS events SpliceWiz considers events where the SpliceOver metric exceed `minDepth`. Then, events with a SpliceOver metric below `minimum` are excluded.

We recommend testing IR events for > 70% coverage and AS events for > 40% coverage as given in the default filters which can be accessed using getDefaultFilters

- **Consistency**: Skipped exons (SE) and mutually exclusive exons (MXE) comprise reads aligned to two contiguous splice junctions. Most algorithms take the average counts from both junctions. This will inadvertently include transcripts that share one but not both splice events. To check that this is not happening, we require both splice junctions to have comparable counts. This filter checks whether reads from each splice junction comprises a reasonable proportion of the sum of these reads.

  Events are excluded if either of the upstream or downstream event is lower than total splicing events by a log-2 magnitude above `maximum`. For example, if `maximum = 2`, we require both upstream and downstream events to represent at least 1/(2^2) = 1/4 of the sum of upstream and downstream event. If `maximum = 3`, then each junction must be at least 1/8 of total, etc. This is considered for each isoform of each event, and is NOT tested when total (upstream+downstream) counts belonging to each isoform is below `minDepth`.

  IR-events are also checked. For IR events, the upstream and downstream exon-intron spanning reads must comprise a reasonable proportion of total exon-intron spanning reads.

We highly recommend using the default filters, which can be acquired using getDefaultFilters

## Value

An ASEFilter object with the specified parameters

## Functions

- `ASEFilter()`: Constructs a ASEFilter object

## See Also

Run_SpliceWiz_Filters

## Examples

```
# Create a ASEFilter that filters for protein-coding ASE
f1 <- ASEFilter(filterClass = "Annotation", filterType = "Protein_Coding")

# Create a ASEFilter that filters for Depth >= 20 in IR events
f2 <- ASEFilter(
    filterClass = "Data", filterType = "Depth",
    minimum = 20, EventTypes = c("IR", "RI")
)

# Create a ASEFilter that filters for Participation > 60% in splice events
```

```
# that must be satisfied in at least 2 categories of condition "Genotype"
f3 <- ASEFilter(
    filterClass = "Data", filterType = "Participation",
    minimum = 60, EventTypes = c("MXE", "SE", "AFE", "ALE", "A3SS", "A5SS"),
    condition = "Genotype", minCond = 2
)

# Create a ASEFilter that filters for Depth > 10 in all events
# that must be satisfied in at least 50% of each gender
f4 <- ASEFilter(
    filterClass = "Data", filterType = "Depth",
    minimum = 10, condition = "gender", pcTRUE = 50
)

# Get a description of what these filters do:
f1
f2
f3
f4
```

---

Build-Reference-methods

*Builds reference files used by SpliceWiz*

---

## Description

These function builds the reference required by the SpliceWiz engine, as well as alternative splicing annotation data for SpliceWiz. See examples below for guides to making the SpliceWiz reference.

## Usage

```
getResources(
  reference_path = "./Reference",
  fasta = "",
  gtf = "",
  overwrite = FALSE,
  force_download = FALSE,
  verbose = TRUE
)

buildRef(
  reference_path = "./Reference",
  fasta = "",
  gtf = "",
  overwrite = FALSE,
  force_download = FALSE,
  chromosome_aliases = NULL,
```

```
  genome_type = "",
  nonPolyARef = "",
  MappabilityRef = "",
  BlacklistRef = "",
  ontologySpecies = "",
  useExtendedTranscripts = TRUE,
  lowMemoryMode = TRUE,
  verbose = TRUE
)

buildFullRef(
  reference_path = "./Reference",
  fasta = "",
  gtf = "",
  use_STAR_mappability = FALSE,
  overwrite = FALSE,
  force_download = FALSE,
  chromosome_aliases = NULL,
  genome_type = "",
  nonPolyARef = "",
  MappabilityRef = "",
  BlacklistRef = "",
  ontologySpecies = "",
  useExtendedTranscripts = TRUE,
  verbose = TRUE,
  n_threads = 4,
  ...
)

getNonPolyARef(genome_type)

getAvailableGO(localHub = FALSE, ah = AnnotationHub(localHub = localHub))
```

## Arguments

| | |
|---|---|
| reference_path | (REQUIRED) The directory path to store the generated reference files |
| fasta | The file path or web link to the user-supplied genome FASTA file. Alternatively, the name of the AnnotationHub record containing the genome resource. May be omitted if getResources() has already been run using the same reference_path. |
| gtf | The file path or web link to the user-supplied transcript GTF file (or gzipped GTF file). Alternatively, the name of the AnnotationHub record containing the transcript GTF file. May be omitted if getResources() has already been run using the same reference_path. |
| overwrite | (default FALSE) For getResources(): if the genome FASTA and gene annotation GTF files already exist in the resource subdirectory, it will not be overwritten. For buildRef() and buildFullRef(): the SpliceWiz reference will not be overwritten if one already exist. A reference is considered to exist if the file SpliceWiz.ref.gz is present inside reference_path. |

force_download (default FALSE) When online resources are retrieved, a local copy is stored in the SpliceWiz BiocFileCache. Subsequent calls to the web resource will fetch the local copy. Set force_download to TRUE will force the resource to be downloaded from the web. Set this to TRUE only if the web resource has been updated since the last retrieval.

verbose (default TRUE) If FALSE, will silence progress messages

chromosome_aliases (Highly optional) A 2-column data frame containing chromosome name conversions. If this is set, allows processBAM to parse BAM alignments to a genome whose chromosomes are named differently to the reference genome. The most common scenario is where Ensembl genome typically use chromosomes "1", "2", ..., "X", "Y", whereas UCSC/Gencode genome use "chr1", "chr2", ..., "chrX", "chrY". See example below. Refer to https://github.com/dpryan79/ChromosomeMappings for a list of chromosome alias resources.

genome_type Allows buildRef() to select default nonPolyARef and MappabilityRef for selected genomes. Allowed options are: hg38, hg19, mm10, and mm9.

nonPolyARef (Optional) A BED file of regions defining known non-polyadenylated transcripts. This file is used for QC analysis to measure Poly-A enrichment quality of samples. An RDS file (openable using readRDS()) of a GRanges object is acceptable. If omitted, and genome_type is defined, the default for the specified genome will be used.

MappabilityRef (Optional) A BED file of low mappability regions due to repeat elements in the genome. If omitted, the file generated by calculateMappability() will be used where available, and if this is not, the default file for the specified genome_type will be used. If genome_type is not specified, MappabilityRef is not used. An RDS file (openable using readRDS()) of a GRanges object is acceptable. See details.

BlacklistRef A BED file of regions to be otherwise excluded from IR analysis. If omitted, a blacklist is not used (this is the default). An RDS file (openable using readRDS()) of a GRanges object is acceptable.

ontologySpecies (default "") The species for which gene ontology classifications should be fetched from AnnotationHub. Ignored if genome_type is set (as human or mouse GO will be used instead).

useExtendedTranscripts (default TRUE) Should non-protein-coding transcripts such as anti-sense and lincRNA transcripts be included in searching for IR / AS events? Setting FALSE (vanilla IRFinder) will exclude transcripts other than protein_coding and processed_transcript transcripts from IR analysis.

lowMemoryMode (default TRUE) By default, SpliceWiz converts FASTA files to TwoBit, then uses the TwoBit file to fetch genome sequences. In most cases, this method uses less memory and is faster, but can be very slow on some systems. Set this option to FALSE (which will convert the TwoBit file back to FASTA) if you experience very slow genome fetching (e.g. when annotating splice motifs).

use_STAR_mappability (default FALSE) In buildFullRef(), whether to run STAR_mappability to calculate low-mappability regions. We recommend setting this to FALSE for the

| | |
|---|---|
| | common genomes (human and mouse), and to TRUE for genomes not supported by genome_type. When set to false, the MappabilityExclusion default file corresponding to genome_type will automatically be used. |
| n_threads | The number of threads used to generate the STAR reference and mappability calculations. Multi-threading is not used for SpliceWiz reference generation (but multiple cores are utilised in data-table and fst file processing automatically, where available). See STAR-methods |
| ... | For buildFullRef(), additional parameters to be parsed into STAR_buildRef which buildFullRef() runs internally. See STAR_buildRef |
| localHub | (default FALSE) For getAvailableGO(), whether to use offline mode for AnnotationHub resources. If TRUE, offline mode will be used. |
| ah | For getAvailableGO(), the AnnotationHub object. Leave as default to use the entirety of AnnotationHub resources. |

## Details

getResources() processes the files, downloads resources from web links or from AnnotationHub(), and saves a local copy in the "resource" subdirectory within the given reference_path. Resources are retrieved via either:

1. User-supplied FASTA and GTF file. This can be a file path, or a web link (e.g. 'http://', 'https://' or 'ftp://'). Use fasta and gtf to specify the files or web paths to use.
2. AnnotationHub genome and gene annotation (Ensembl): supply the names of the genome sequence and gene annotations to fasta and gtf.

buildRef() will first run getResources() if resources are not yet saved locally (i.e. getResources() is not already run). Then, it creates the SpliceWiz references. Typical run-times are 5 to 10 minutes for human and mouse genomes (after resources are downloaded).

NB: the parameters fasta and gtf can be omitted in buildRef() if getResources() is already run.

buildFullRef() builds the STAR aligner reference alongside the SpliceWiz reference. The STAR reference will be located in the STAR subdirectory of the specified reference path. If use_STAR_mappability is set to TRUE this function will empirically compute regions of low mappability. This function requires STAR to be installed on the system (which only runs on linux-based systems).

getNonPolyARef() returns the path of the non-polyA reference file for the human and mouse genomes.

Typical usage involves running buildRef() for human and mouse genomes and specifying the genome_type to use the default MappabilityRef and nonPolyARef files for the specified genome. For non-human non-mouse genomes, use one of the following alternatives:

- Create the SpliceWiz reference without using Mappability Exclusion regions. To do this, simply run buildRef() and omit MappabilityRef. This is acceptable assuming the introns assessed are short and do not contain intronic repeats
- Calculating Mappability Exclusion regions using the STAR aligner, and building the SpliceWiz reference. This can be done using the buildFullRef() function, on systems where STAR is installed

- Instead of using the STAR aligner, any genome splice-aware aligner could be used. See Mappability-methods for an example workflow using the Rsubread aligner. After producing the `MappabilityExclusion.bed.gz` file (in the `Mappability` subfolder), run `buildRef()` using this file (or simply leave it blank).

BED files are tab-separated text files containing 3 unnamed columns specifying chromosome, start and end coordinates. To view an example BED file, open the file specified in the path returned by `getNonPolyARef("hg38")`

If `MappabilityRef`, `nonPolyARef` and `BlacklistRef` are left blank, the following will be used (by priority):

1. The previously used Mappability, non-polyA and/or Blacklist file resource from a previous run, if available,
2. The resource implied by the `genome_type` parameter, if specified,
3. No resource is used.

**To rebuild a SpliceWiz reference using existing resources** This is typically run when updating an old resource to a new SpliceWiz version. Simply run buildRef(), specifying the existing reference directory, leave the `fasta` and `gtf` parameters blank, and set `overwrite = TRUE`. SpliceWiz will use the previously-used resources to re-create the reference.

See examples below for common use cases.

## Value

For `getResources`: creates the following local resources:

- `reference_path/resource/genome.2bit`: Local copy of the genome sequences as a TwoBitFile.
- `reference_path/resource/transcripts.gtf.gz`: Local copy of the gene annotation as a gzip-compressed file.

For `buildRef()` and `buildFullRef()`: creates a SpliceWiz reference which is written to the given directory specified by `reference_path`. Files created includes:

- `reference_path/settings.Rds`: An RDS file containing parameters used to generate the SpliceWiz reference
- `reference_path/SpliceWiz.ref.gz`: A gzipped text file containing collated SpliceWiz reference files. This file is used by processBAM
- `reference_path/fst/`: Contains fst files for subsequent easy access to SpliceWiz generated references
- `reference_path/cov_data.Rds`: An RDS file containing data required to visualise genome / transcript tracks.

`buildFullRef()` also creates a `STAR` reference located in the `STAR` subdirectory inside the designated `reference_path`

For `getNonPolyARef()`: Returns the file path to the BED file for the nonPolyA loci for the specified genome.

For `getAvailableGO()`: Returns a vector containing names of species with supported gene ontology annotations.

## Functions

- `getResources()`: Processes / downloads a copy of the genome and gene annotations and stores this in the "resource" subdirectory of the given reference path
- `buildRef()`: First calls `getResources()` (if required). Afterwards creates the SpliceWiz reference in the given reference path
- `buildFullRef()`: One-step function that fetches resources, creates a STAR reference (including mappability calculations), then creates the SpliceWiz reference
- `getNonPolyARef()`: Returns the path to the BED file containing coordinates of known non-polyadenylated transcripts for genomes `hg38`, `hg19`, `mm10` and `mm9`,
- `getAvailableGO()`: Returns available species on Bioconductor's AnnotationHub. Currently, only Bioconductor's OrgDb/Ensembl gene ontology annotations are supported.

## See Also

Mappability-methods for methods to calculate low mappability regions

STAR-methods for a list of STAR wrapper functions

AnnotationHub

https://github.com/alexchwong/SpliceWizResources for RDS files of Mappability Exclusion GRanges objects (for hg38, hg19, mm10 and mm9) that can be use as input files for `MappabilityRef` in `buildRef()`. These resources are intended for SpliceWiz users on older Bioconductor versions (3.13 or earlier)

## Examples

```
# Quick runnable example: generate a reference using SpliceWiz's example genome

example_ref <- file.path(tempdir(), "Reference")
getResources(
    reference_path = example_ref,
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)
buildRef(
    reference_path = example_ref
)

# NB: the above is equivalent to:

example_ref <- file.path(tempdir(), "Reference")
buildRef(
    reference_path = example_ref,
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)

# Get the path to the Non-PolyA BED file for hg19
```

```
getNonPolyARef("hg19")

# View available species for AnnotationHub's Ensembl/orgDB-based GO resources

availSpecies <- getAvailableGO()

# Build example reference with `Homo sapiens` Ens/orgDB gene ontology

ont_ref <- file.path(tempdir(), "Reference_withGO")
buildRef(
    reference_path = ont_ref,
    fasta = chrZ_genome(),
    gtf = chrZ_gtf(),
    ontologySpecies = "Homo sapiens"
)

## Not run:

### Long examples ###

# Generate a SpliceWiz reference from user supplied FASTA and GTF files for a
# hg38-based genome:

buildRef(
    reference_path = "./Reference_user",
    fasta = "genome.fa", gtf = "transcripts.gtf",
    genome_type = "hg38"
)

# NB: Setting `genome_type = hg38`, will automatically use default
# nonPolyARef and MappabilityRef for `hg38`

# Reference generation from Ensembl's FTP links:

FTP <- "ftp://ftp.ensembl.org/pub/release-94/"
buildRef(
    reference_path = "./Reference_FTP",
    fasta = paste0(FTP, "fasta/homo_sapiens/dna/",
        "Homo_sapiens.GRCh38.dna.primary_assembly.fa.gz"),
    gtf = paste0(FTP, "gtf/homo_sapiens/",
        "Homo_sapiens.GRCh38.94.chr.gtf.gz"),
    genome_type = "hg38"
)

# Get AnnotationHub record names for Ensembl release-94:

# First, search for the relevant AnnotationHub record names:

ah <- AnnotationHub::AnnotationHub()
AnnotationHub::query(ah, c("Homo Sapiens", "release-94"))

buildRef(
```

```
    reference_path = "./Reference_AH",
    fasta = "AH65745",
    gtf = "AH64631",
    genome_type = "hg38"
)

# Build a SpliceWiz reference, setting chromosome aliases to allow
# this reference to process BAM files aligned to UCSC-style genomes:

chrom.df <- GenomeInfoDb::genomeStyles()$Homo_sapiens

buildRef(
    reference_path = "./Reference_UCSC",
    fasta = "AH65745",
    gtf = "AH64631",
    genome_type = "hg38",
    chromosome_aliases = chrom.df[, c("Ensembl", "UCSC")]
)

# One-step generation of SpliceWiz and STAR references, using 4 threads.
# NB1: requires a linux-based system with STAR installed.
# NB2: A STAR reference genome will be generated in the `STAR` subfolder
#      inside the given `reference_path`.
# NB3: A custom Mappability Exclusion file will be calculated using STAR
#      and will be used to generate the SpliceWiz reference.

buildFullRef(
    reference_path = "./Reference_with_STAR",
    fasta = "genome.fa", gtf = "transcripts.gtf",
    genome_type = "hg38",
    use_STAR_mappability = TRUE,
    n_threads = 4
)

# NB: the above is equivalent to running the following in sequence:

getResources(
    reference_path = "./Reference_with_STAR",
    fasta = "genome.fa", gtf = "transcripts.gtf"
)
STAR_buildRef(
    reference_path = reference_path,
    also_generate_mappability = TRUE,
    n_threads = 4
)
buildRef(
    reference_path = "./Reference_with_STAR",
    genome_type = ""
)

## End(Not run)
```

collateData *Collates a dataset from (processBAM) output files of individual samples*

## Description

collateData() creates a dataset from a collection of processBAM output files belonging to an experiment.

## Usage

```
collateData(
  Experiment,
  reference_path,
  output_path,
  IRMode = c("SpliceOver", "SpliceMax"),
  packageCOVfiles = FALSE,
  novelSplicing = FALSE,
  forceStrandAgnostic = FALSE,
  novelSplicing_minSamples = 3,
  novelSplicing_countThreshold = 10,
  novelSplicing_minSamplesAboveThreshold = 1,
  novelSplicing_requireOneAnnotatedSJ = TRUE,
  novelSplicing_useTJ = TRUE,
  overwrite = FALSE,
  n_threads = 1,
  lowMemoryMode = TRUE
)
```

## Arguments

| | |
|---|---|
| Experiment | (Required) A 2 or 3 column data frame, ideally generated by findSpliceWizOutput or findSamples. The first column designate the sample names, and the 2nd column contains the path to the processBAM output file (of type sample.txt.gz). (Optionally) a 3rd column contains the coverage files (of type sample.cov) of the corresponding samples. NB: all other columns are ignored. |
| reference_path | (Required) The path to the reference generated by Build-Reference-methods |
| output_path | (Required) The path to contain the output files for the collated dataset |
| IRMode | (default SpliceOver) The algorithm to calculate 'splice abundance' in IR quantification. Valid options are SpliceOver and SpliceMax. See details |
| packageCOVfiles | (default FALSE) Whether COV files should be copied over to the NxtSE object. This is useful if one wishes to transfer the NxtSE folder to a collaborator, who can then open the NxtSE object with valid COV file paths. |

`novelSplicing` (default FALSE) Whether collateData will use novel junction reads detected in samples to infer novel splice variants. All tandem split reads (those bridging two consecutive splice junctions) are used, as well as novel split reads that satisfy abundance criteria (see `novelSplicing_minSamples`, `novelSplicing_minSamplesAboveThreshold`, and `novelSplicing_countThreshold`) are used to synthesise a dataset-specific SpliceWiz reference. See details.

`forceStrandAgnostic`
(default `FALSE`) In poorly-prepared stranded libraries, it may be better to quantify in unstranded mode. Set this to `TRUE` if your stranded libraries may be contaminated with unstranded reads

`novelSplicing_minSamples`
(default 3) Novel junctions are included in building of novel reference if number samples with non-zero counts exceeds this number.

`novelSplicing_countThreshold`
(default 10) Threshold of split-reads across novel junctions; used in conjunction with `novelSplicing_minSamplesAboveThreshold`

`novelSplicing_minSamplesAboveThreshold`
(default 1) Novel junctions are included in building of novel reference if novel junction reads are above a pre-defined threshold exceeds this number

`novelSplicing_requireOneAnnotatedSJ`
(default `TRUE`) The default requires novel junctions to have one annotated splice site. If this is disabled, collateData will include novel junctions where neither splice site is annotated.

`novelSplicing_useTJ`
(default `TRUE`) For novel splicing, should SpliceWiz use reads with 2 or more junctions to find novel exons? Ignored if novelSplicing is set to `FALSE`.

`overwrite` (default `FALSE`) If `collateData()` has previously been run using the same set of samples, it will not be overwritten unless this is set to `TRUE`.

`n_threads` (default 1) The number of threads to use. If you run out of memory, try lowering the number of threads

`lowMemoryMode` (default `TRUE`) `collateData()` will perform optimizations to conserve memory if this is set to `TRUE`. Otherwise, will prioritise performance.

## Details

In Windows, collateData runs using only 1 thread, as BiocParallel's MulticoreParam is not supported.

It is assumed that all sample processBAM outputs were generated using the same reference.

The combination of junction counts and IR quantification from processBAM is used to calculate percentage spliced in (PSI) of alternative splice events, and intron retention ratios (IR-ratio) of retained introns. Also, QC information is collated. Data is organised in a H5file and FST files for memory and processor efficient downstream access using makeSE.

The original IRFinder algorithm, see the following wiki, uses `SpliceMax` to estimate abundance of spliced transcripts. This calculates the number of mapped splice events that share the boundary coordinate of either the left or right flanking exon `SpliceLeft,SpliceRight`, estimating splice abundance as the larger of the two values.

SpliceWiz proposes a new algorithm, `SpliceOver`, to account for the possibility that the major isoform shares neither boundary, but arises from either of the flanking exon clusters. Exon clusters are contiguous regions covered by exons from any transcript (except those designated as `retained_intron` or `sense_intronic`), and are separated by obligate intronic regions (genomic regions that are introns for all transcripts). For introns that are internal to a single exon cluster (i.e. akin to "known-exon" introns from IRFinder), `SpliceOver` uses GenomicRanges::findOverlaps to sum all splice reads that overlap the same genomic region as the intron of interest.

Detection of novel ASEs: When `novelSplicing` is set to `TRUE`, novel junctions (split reads across unannotated junctions from samples of the dataset being collated) are used in conjunction with the reference to compile a list of novel ASEs. To avoid being overwhelmed by a large number of false positive novel junctions (often due to mis-alignments), a simple filtering strategy is used. This involves including novel junctions only if it occurs in a minimum number of samples (default 3), or if the number of split reads of a novel junction is above a pre-defined threshold (default 10) in a certain number of samples (default 1). These parameters can be set using `novelSplicing_minSamples`, `novelSplicing_countThreshold` and `novelSplicing_minSamplesAboveThreshold` respectively.

## Value

`collateData()` writes to the directory given by `output_path`. This output directory is portable (i.e. it can be moved to a different location after running `collateData()` before running makeSE), but individual files within the output folder should not be moved.

Also, the processBAM and collateData output folders should be copied to the same destination and their relative paths preserved. Otherwise, the locations of the "COV" files will not be recorded in the collated data and will have to be re-assigned using `covfile(se)<-`. See makeSE

## See Also

processBAM, makeSE

## Examples

```
buildRef(
    reference_path = file.path(tempdir(), "Reference"),
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)

bams <- SpliceWiz_example_bams()
processBAM(bams$path, bams$sample,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "SpliceWiz_Output")
)

expr <- findSpliceWizOutput(file.path(tempdir(), "SpliceWiz_Output"))
collateData(expr,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "Collated_output")
)
```

```
# Enable novel splicing:

collateData(expr,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "Collated_output"),
  novelSplicing = TRUE
)
```

---

coord2GR *Converts genomic coordinates into a GRanges object*

---

## Description

This function takes a string vector of genomic coordinates and converts it into a GRanges object.

## Usage

```
coord2GR(coordinates)
```

## Arguments

| | |
|---|---|
| coordinates | A string vector of one or more genomic coordinates to be converted |

## Details

Genomic coordinates can take one of the following syntax:

- `seqnames:start`
- `seqnames:start-end`
- `seqnames:start-end/strand`

The following examples are considered valid genomic coordinates:

- "chr1:21535"
- "chr3:10550-10730"
- "X:51231-51330/-"
- "chrM:2134-5232/+"

## Value

A GRanges object that corresponds to the given coordinates

## Examples

```
se <- SpliceWiz_example_NxtSE()

coordinates <- rowData(se)$EventRegion

gr <- coord2GR(coordinates)
```

`covDataObject-class` *Container to hold raw data for SpliceWiz coverage plots*

## Description

This object is generated using getCoverageData or getGenomeData methods, and is used as input for generating coverage plots.

## Usage

```
## S4 method for signature 'covDataObject'
showEvents(object)

getCoverageData(
  se,
  Event,
  Gene,
  seqname,
  start,
  end,
  coordinates,
  strand = c("*", "+", "-"),
  zoom_factor = 0.2,
  bases_flanking = 100,
  tracks,
  condition,
  ...
)

getGenomeData(
  reference_path,
  Gene,
  seqname,
  start,
  end,
  coordinates,
  zoom_factor = 0.2,
  bases_flanking = 100,
  ...
)

plotAnnoTrack(
  object,
  Event,
  view_start,
  view_end,
  reverseGenomeCoords = FALSE,
```

```
  condensed = FALSE,
  selected_transcripts = "",
  plot_key_isoforms = FALSE,
  usePlotly = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| object | For plotAnnoTrack(), the covDataObject created by getCoverageData() or getGenomeData() |
| se | A NxtSE object, created by makeSE. COV files must be linked to the NxtSE object. To do this, see the example in makeSE. Required by plotCoverage. Not required by plotGenome if reference_path is supplied. |
| Event | The EventName of the IR / alternative splicing event to be displayed. Use rownames(se) to display a list of valid events. |
| Gene | Whether to use the range for the given Gene. If given, overrides Event (but Event or norm_event will be used to normalise by condition). Valid Gene entries include gene_id (Ensembl ID) or gene_name (Gene Symbol). |
| seqname, start, end | The chromosome (string) and genomic start/end coordinates (numeric) of the region to display. If present, overrides both Event and Gene. E.g. for a given region of chr1:10000-11000, use the parameters: seqname = "chr1", start = 10000, end = 11000 |
| coordinates | A string specifying genomic coordinates can be given instead of seqname,start,end. Must be of the format "chr:start-end", e.g. "chr1:10000-11000" |
| strand | Whether to show coverage of both strands "*" (default), or from the "+" or "-" strand only. |
| zoom_factor | Zoom out from event. Each level of zoom zooms out by a factor of 3. E.g. for a query region of chr1:10000-11000, if a zoom_factor of 1.0 is given, chr1:99000-12000 will be displayed. |
| bases_flanking | (Default = 100) How many bases flanking the zoomed window. Useful when used in conjunction with zoom_factor == 0. E.g. for a given region of chr1:10000-11000, if zoom_factor = 0 and bases_flanking = 100, the region chr1:9900-11100 will be displayed. |
| tracks | The names of individual samples, or the names of the different conditions to be plotted. For the latter, set condition to the specified condition category. |
| condition | To display normalised coverage per condition, set this to the condition category. If omitted, tracks are assumed to refer to the names of individual samples. |
| ... | Ignored / not used |
| reference_path | The path of the reference generated by Build-Reference-methods. Required by plotGenome if a NxtSE object is not specified. |
| view_start, view_end | Start and end coordinates of plotting function. Note that plot coordinates may be different from retrieval coordinates and is useful for zooming in. |

`reverseGenomeCoords`
: Whether the genomic axis should be reversed to make it more convenient to plot reverse-stranded genes

`condensed`
: (default 'FALSE) Whether the genomic track should be condensed to plot whole genes, rather than transcripts. Preferred if multiple genes are plotted on a zoomed-out plot

`selected_transcripts`
: (default `""`) One or more transcript names or ID's to be displayed on the annotation track.

`plot_key_isoforms`
: (default `FALSE`) If `TRUE`, plots only transcripts involved in the given splicing `Event`.

`usePlotly`
: (default `FALSE`) Whether to return a plotly or ggplot object.

## Value

For getCoverageData(): A covDataObject containing required data used to generate downstream
For plotAnnoTrack(): A ggplot or plotly object

## Functions

- `showEvents(covDataObject)`: Returns the EventNames for which events can be normalized using the given covDataObject
- `getCoverageData()`: Get coverage / genome data for plotting coverage plots
- `getGenomeData()`: Get coverage / genome data for plotting coverage plots
- `plotAnnoTrack()`: Directly plots the annotation from a covDataObject.

## See Also

covPlotObject

## Examples

```
se <- SpliceWiz_example_NxtSE(novelSplicing = TRUE)

# Assign annotation of the experimental conditions
colData(se)$treatment <- rep(c("A", "B"), each = 3)

dataObj <- getCoverageData(
    se,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
    tracks = colnames(se)
)

# Show `EventName`s of supported splicing events
# contained within covDataObject

showEvents(dataObj)
```

```
# A limited covDataObject containing only the reference can be generated
# from the SpliceWiz reference

buildRef(
    reference_path = file.path(tempdir(), "Reference"),
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)

genomeObj <- getGenomeData(
    reference_path = file.path(tempdir(), "Reference"),
    Gene = "SRSF3"
)

# Plot reference track directly from the covDataObject

# NB: Event plotting is not supported for reference-derived `covDataObject`s
plotAnnoTrack(genomeObj)

plotAnnoTrack(dataObj, Event = "SE:SRSF3-203-exon4;SRSF3-202-int3")
```

---

`Coverage` *Calls SpliceWiz's C++ function to retrieve coverage from a COV file*

---

## Description

This function returns an RLE / RLEList or data.frame containing coverage data from the given COV file

COV files are generated by SpliceWiz's processBAM and BAM2COV functions. It records alignment coverage for each nucleotide in the given BAM file. It stores this data in "COV" format, which is an indexed BGZF-compressed format specialised for the storage of unstranded and stranded alignment coverage in RNA sequencing.

Unlike BigWig files, COV files store coverage for both positive and negative strands.

These functions retrieves coverage data from the specified COV file. They are computationally efficient as they utilise random-access to rapidly search for the requested data from the COV file.

## Usage

```
getCoverage(file, seqname = "", start = 0, end = 0, strand = c("*", "+", "-"))

getCoverage_DF(
  file,
  seqname = "",
```

```
  start = 0,
  end = 0,
  strand = c("*", "+", "-")
)

getCoverageRegions(
  file,
  regions,
  strandMode = c("unstranded", "forward", "reverse")
)

getCoverageBins(
  file,
  region,
  bins = 2000,
  strandMode = c("unstranded", "forward", "reverse"),
  bin_size
)
```

## Arguments

| | |
|---|---|
| `file` | (Required) The file name of the COV file |
| `seqname` | (Required for `getCoverage_DF`) A string denoting the chromosome name. If left blank in `getCoverage`, retrieves RLEList containing coverage of the entire file. |
| `start`, `end` | 1-based genomic coordinates. If `start = 0` and `end = 0`, will retrieve RLE of specified chromosome. |
| `strand` | Either "*", "+", or "-" |
| `regions` | A GRanges object for a set of regions to obtain mean / total coverage from the given COV file. |
| `strandMode` | The stranded-ness of the RNA-seq experiment. "unstranded" means that an unstranded protocol was used. Stranded protocols can be either "forward", where the first read is the same strand as the expressed transcript, or "reverse" where the second strand is the same strand as the expressed transcript. |
| `region` | In `getCoverageBins`, a single query region as a GRanges object |
| `bins` | In `getCoverageBins`, the number of bins to divide the given `region`. If `bin_size` is given, overrides this parameter |
| `bin_size` | In `getCoverageBins`, the number of nucleotides per bin |

## Value

For `getCoverage`: If seqname is left as "", returns an RLEList of the whole BAM file, with each RLE in the list containing coverage data for one chromosome. Otherwise, returns an RLE containing coverage data for the requested genomic region

For `getCoverage_DF`: Returns a two-column data frame, with the first column `coordinate` denoting genomic coordinate, and the second column `value` containing the coverage depth for each coordinate nucleotide.

For `getCoverageRegions`: Returns a GRanges object with an extra metacolumn: `cov_mean`, which gives the mean coverage of each of the given ranges.

For `getCoverageBins`: Returns a GRanges object which spans the given `region`, divided by the number of `bins` or by width as given by `bin_size`. Mean coverage in each bin is calculated (returned by the `cov_mean` metadata column). This function is useful for retrieving coverage of a large region for visualisation, especially when the size of the region vastly exceeds the width of the figure.

## Functions

- `getCoverage()`: Retrieves alignment coverage as an RLE or RLElist
- `getCoverage_DF()`: Retrieves alignment coverage as a data.frame
- `getCoverageRegions()`: Retrieves total and mean coverage of a GRanges object from a COV file
- `getCoverageBins()`: Retrieves coverage of a single region from a COV file, binned by the given number of bins or bin_size

## Examples

```
se <- SpliceWiz_example_NxtSE()

cov_file <- covfile(se)[1]

# Retrieve Coverage as RLE

cov <- getCoverage(cov_file, seqname = "chrZ",
  start = 10000, end = 20000,
  strand = "*"
)

# Retrieve Coverage as data.frame

cov.df <- getCoverage_DF(cov_file, seqname = "chrZ",
  start = 10000, end = 20000,
  strand = "*"
)

# Retrieve mean coverage of 100-nt window regions as defined
# in a GRanges object:

gr <- GenomicRanges::GRanges(
    seqnames = "chrZ",
    ranges = IRanges::IRanges(
        start = seq(1, 99901, by = 100),
        end = seq(100, 100000, by = 100)
    ), strand = "-"
)

gr.unstranded <- getCoverageRegions(cov_file,
    regions = gr,
    strandMode = "unstranded"
```

```
)

gr.stranded <- getCoverageRegions(cov_file,
    regions = gr,
    strandMode = "reverse"
)

# Retrieve binned coverage of a large region

gr.fetch <- getCoverageBins(
    cov_file,
    region = GenomicRanges::GRanges(seqnames = "chrZ",
        ranges = IRanges::IRanges(start = 100, end = 100000),
        strand = "*"
    ),
    bins = 2000
)

# Plot coverage using ggplot:

require(ggplot2)

ggplot(cov.df, aes(x = coordinate, y = value)) +
    geom_line() + theme_white

ggplot(as.data.frame(gr.unstranded),
    aes(x = (start + end) / 2, y = cov_mean)) +
    geom_line() + theme_white

ggplot(as.data.frame(gr.fetch),
    aes(x = (start + end)/2, y = cov_mean)) +
    geom_line() + theme_white

# Export COV data as BigWig

cov_whole <- getCoverage(cov_file)
bw_file <- file.path(tempdir(), "sample.bw")
rtracklayer::export(cov_whole, bw_file, "bw")
```

---

`covPlotly-class` *Container for plotly-based coverage plots*

---

## Description

A `covPlotly` object is created when plotView is called using a `covPlotObject` as input. It stores metadata alongside the plotly object, which allows it to be drawn at various resolutions. Smaller resolutions lead to faster draws at expense of more jagged plots.

## Usage

```
## S4 method for signature 'covPlotly'
getExonRanges(object)

## S4 method for signature 'covPlotly'
setResolution(object, resolution)

## S4 method for signature 'covPlotly'
showExons(object)
```

## Arguments

| | |
|---|---|
| `object` | A covPlotly object |
| `resolution` | How many horizontal pixels of resolution should be shown in the final plotly object. Set to `0` to disable. |

## Value

For `show()`: A plotly object synthesised by `plotView()` For `getExonRanges()`: A named GRanges object containing exon ranges For `showExons()`: A named GRanges object containing exon ranges, and additionally "shows" the plotly coverage plot with annotation replaced by named exons For `setResolution()` Returns the `covPlotly` object with addition of resolution set by the corresponding parameter. When `show()` is called, the plotly object with the new coverage resolution will be displayed.

## Functions

- `getExonRanges(covPlotly)`: Returns a named GRanges object containing exon ranges, without showing the associated plotly object
- `setResolution(covPlotly)`: Returns a covPlotly object after setting the output resolution of the plotly-based coverage plots.
- `showExons(covPlotly)`: Returns a named GRanges object containing exon ranges, and shows the plotly object with the annotation track showing the named exons

## See Also

plotView

## Examples

```
se <- SpliceWiz_example_NxtSE(novelSplicing = TRUE)

# Assign annotation of the experimental conditions
colData(se)$treatment <- rep(c("A", "B"), each = 3)

# Retrieve coverage data for all samples for the gene "SRSF3" (and surrounds)

dataObj <- getCoverageData(
    se,
```

```
    Gene = "SRSF3",
    tracks = colnames(se)
)

plotObj_samples <- getPlotObject(
    dataObj,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3"
)

if(interactive()) {

    # Create covPlotly object by setting `usePlotly = TRUE`
    p <- plotView(plotObj_samples, usePlotly = TRUE)

    # Display plotly plot
    show(p)

    # Set resolution to 2000; display new plot
    p <- setResolution(p, resolution = 2000)
    show(p)

    # Display exon annotation along with generated plot;
    # - also returns GRanges object
    gr <- showExons(p)
}
```

---

`covPlotObject-class` *Versatile coverage plots for SpliceWiz*

---

## Description

Here, we implement fast and versatile ggplot and plotly based coverage and sashimi plots. Users can plot with unlimited number of individual, individual-normalized, or group-normalized tracks. Also implemented is user-defined group-comparison differential plots (including t-test plots). Additionally, users can generate ggplots subsetted by exon groups. See details below.

## Usage

```
getPlotObject(object, Event, strand = c("*", "+", "-"), tracks, condition, ...)

## S4 method for signature 'covPlotObject'
tracks(object)

## S4 method for signature 'covPlotObject'
condition(object)

plotView(
  object,
```

```
  view_start,
  view_end,
  oldP = covPlotly(),
  centerByEvent = FALSE,
  EventZoomFactor = 0.2,
  EventBasesFlanking = 100,
  resolution = 5000,
  trackList = list(),
  diff_stat = c("t-test", "none"),
  diffList = list(),
  reverseGenomeCoords = FALSE,
  ribbon_mode = c("sd", "sem", "ci", "none"),
  normalizeCoverage = FALSE,
  plotAnnotations = TRUE,
  plotAnnoSubTrack = TRUE,
  showExonRanges = FALSE,
  verticalLayout = c(4, 1, 1, 2),
  horizontalLayout = c(),
  filterByTranscripts = "",
  filterByEventTranscripts = FALSE,
  filterByExpressedTranscripts = TRUE,
  condenseTranscripts = FALSE,
  plotJunctions = TRUE,
  plotJuncPSI = FALSE,
  junctionThreshold = 0.01,
  plotRanges = GRanges(),
  rangesBasesFlanking = 100,
  usePlotly = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| `object` | For `getPlotObject()`, a `covDataObject` created using `getCoverageData`. For `plotView()`, a `covPlotObject` created using `getPlotObject()`. |
| `Event` | The EventName of the alternative splicing event which will be highlighted and used for normalization |
| `strand` | The strand for coverage / junction plotting. Options are `"+"`, `"-"`, or `"*"` (unstranded - default) |
| `tracks` | Sample names or condition categories |
| `condition` | For condition-based group plots, the name of the condition. |
| `...` | Ignored / not used |
| `view_start, view_end` | The start and end coordinates for plotting |
| `oldP` | (Optional) If plotting the same tracks and track-widths, supplying the old `covPlotly` object (returned from a previous call to `plotView()`) results in faster run-time (as plotly::subplot is a time- consuming function) |

centerByEvent (default FALSE) If true, centers the view to the specified Event

EventZoomFactor
: If centerByEvent = TRUE, the zoom-out factor to plot the view. Zooms out in exponents of 3 (i.e., zoom of 1 means 3x, 2 means 9x, and 0 means 1x)

EventBasesFlanking
: (default 100) If centerByEvent = TRUE, includes how many bases flanking the event.

resolution The number of horizontal "pixels" or data-points to plot. This is calculated per sub-plot. Smaller numbers lead to lower resolution but faster plots. Default is 5000

trackList A list, with each element being a vector of 1 or more track names or indices to plot. If a vector is supplied it will be coerced to a list

diff_stat (default "t-test") Which statistical method to perform differential comparisons.

diffList A list, with each element being a vector of size 2, containing names or indices of which tracks to contrast.

reverseGenomeCoords
: If TRUE, the genomic coordinate axis will be reversed to plot negative stranded genes

ribbon_mode The statistic to represent variance. Options are "sd" - standard deviation, "sem" - standard error of the mean, "ci" - 95% confidence interval, or "none"

normalizeCoverage
: If TRUE, coverages and junctions of individual samples will be normalized by the given Event.

plotAnnotations
: Whether the main annotation track should be plotted

plotAnnoSubTrack
: If plotting by exon ranges (using plotRanges), whether a separate sub-track showing zoomed-in exons should be shown above the main annotation track (and below the coverage plots)

showExonRanges (only applies if usePlotly = FALSE) Whether the main annotation track should be replaced by labeled exon names. If TRUE the returned value of plotView() is a named GRanges object containing the exon ranges

verticalLayout A vector (of length 4) containing relative heights of the following elements: (1) main block of coverage tracks, (2) differential track, (3) annotation sub-track, and (4) main annotation track. Default c(4,1,1,2)

horizontalLayout
: A vector containing relative widths of coverage tracks. Only used alongside plotRanges with more than 1 range to plot. If omitted, plotView will attempt to scale widths to the widths of the exon ranges.

filterByTranscripts
: (default "") One or more named transcripts to filter the annotation track.

filterByEventTranscripts
: (default FALSE) If TRUE, only transcripts involved in the given Event will be plotted, if any

`filterByExpressedTranscripts`
: (default `TRUE`) Only transcripts with supported junctions will be plotted on the annotation axis. An expressed junction is that which contains more than the minimum `junctionThreshold` in at least 1 track

`condenseTranscripts`
: Whether to plot by genes `TRUE` or transcripts `FALSE`

`plotJunctions`
: Whether to plot junction counts as numbered arcs. Plots normalized junctions if `normalizeCoverage = TRUE`.

`plotJuncPSI`
: If plotting group coverage plots, whether to plot mean +/- sd of normalized junction counts `FALSE`, or estimated junction PSI based on SpliceOver metric applied to each junction `TRUE`.

`junctionThreshold`
: (default `0.01`) Junctions with expressions below this threshold will not be plotted. For raw counts, this is a fraction of maximum coverage value of the track.

`plotRanges`
: A GRanges object containing one or more exon ranges to plot. If given, `view_start` and `view_end` will be ignored. Typical use is to use the output of the `plotView(..., usePlotly = FALSE)`, which returns a named GRanges object, then subset this output by exon name.

`rangesBasesFlanking`
: (default `100`) How many flanking bases to add to each of `plotRanges`. Ignored if only 1 range given (or using `view_start` and `view_end`)

`usePlotly`
: If `TRUE`, returns a `covPlotly` object containing the plotly-based interactive plot. If `FALSE`, returns a ggplot object.

## Details

The typical pipeline for plotting versatile coverage plots is as follows:

- A `covDataObject` is generated by calling `getCoverageData()` using an input `NxtSE` object. This step retrieves coverage, junction counts and normalization data for the relevant genomic region being queried. A new `covDataObject` is necessary when querying a new genomic region.
- A `covPlotObject` is generated by calling `getPlotObject()` using an input `covDataObject`. This step retrieves alternative splicing event specific data, such as normalized coverages, or group combined coverages. A new `covPlotObject` is required when changing `condition`, `Event`, `strand`, or when querying using a different set of `tracks`.
- Plots can be generated by calling `plotView()` using a `covPlotObject`. Interactive plotly plots can be generated by setting `usePlotly = TRUE`, otherwise, static plots are generated. For interactive plots, a `covPlotly` object is returned, which contains raw data which is downsampled by pixel resolution prior to plotting for performance reasons. A new `covPlotly` is required unless one only wishes to downsample the resolution
  - see setResolution for `covPlotly` objects.

Tracks are now versatile (unlimited). Samples are retrieved by individual sample names at `getCoverageData()`. If `condition` is set in `getPlotObject()`, track names are defined by their condition categorical names; otherwise, tracks are named by individual samples when retrieved using `getPlotObject()`.

- When calling `plotView()`, `trackList` by default displays all tracks as ordered in the `covPlotObject`. Users can supply a vector containing either the track names (or numbers, as ordered in the `covPlotObject`). Alternatively, multiple traces can be stacked in a single track by using a list, e.g. `trackList = list(A = c(1,2,3), B = c(4,5,6))`.
- For differential comparisons, `diffList` takes a list of pairs of samples. For example, if `trackList = list("A", "B")`, then setting `diffList = list(c("A", "B"))` will compare groups "A" and "B". This is only activated by setting `diff_stat` to anything other than `none`. For now, only `t-test` is supported.

`plotView()` supports plotting by exon ranges, for which only static plots are currently supported. The workflow for generating such a plot is as follows:

- A GRanges object is returned by the `plotView()` function and setting `showExonRanges = TRUE`. `plotView()` will simultaneously show an annotation plot of exons labelled by their "exon names", which is the transcript name appended with "-E" followed by the exon number.
- If `plotView()` is called and `usePlotly = TRUE` is set, a `covPlotly` object is returned. Calling `showExons()` on this object will display a plotly plot showing exon names, and returning a GRanges object of exon ranges.
- Exon ranges can be supplied to the `plotView()` function by setting the `plotRanges` parameter as a GRanges object. This will generate a static plot showing coverage plots segmented by exons.

## Value

For `getPlotObject()`: A `covPlotObject` object containing Event-based data to create coverage plots using `plotView()`.

For `plotView()`:

- If `usePlotly = TRUE`, returns a `covPlotly` object containing plotly-based interactive plot
- If `usePlotly = FALSE`, returns a patchwork-assembled static plot, unless `showExonRanges = TRUE` in which it shows the plot and returns a named GRanges object containing exon ranges.

## Functions

- `getPlotObject()`: Generates a covPlotObject object from a covDataObject. Allows users to change parameters such as viewing window, conditions, tracks, and other parameters, for customizing plot parameters
- `tracks(covPlotObject)`: Returns the tracks contained in the covPlotObject object
- `condition(covPlotObject)`: Returns the condition value set in the covPlotObject object
- `plotView()`: Creates a coverage plot using the stored data in the covPlotObject

## See Also

getCoverageData covPlotly

## Examples

```
se <- SpliceWiz_example_NxtSE(novelSplicing = TRUE)

# Assign annotation of the experimental conditions
colData(se)$treatment <- rep(c("A", "B"), each = 3)

# Retrieve coverage data for all samples for the gene "SRSF3" (and surrounds)

dataObj <- getCoverageData(
    se,
    Gene = "SRSF3",
    tracks = colnames(se)
)

# Retrieves raw / normalized coverage / junction data for the
# specified SRSF3 skipped exon event:

plotObj_samples <- getPlotObject(
    dataObj,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3"
)

# Retrieves data for samples grouped by the specified condition

plotObj_group <- getPlotObject(
    dataObj,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
    condition = "treatment",
    tracks = c("A", "B")
)

# Display tracks and conditions of covPlotObject

tracks(plotObj_group)
condition(plotObj_group)

# Show static ggplots

plotView(plotObj_samples)

plotView(plotObj_group, centerByEvent = TRUE)

# Plot junctions using PSI estimates based on individual junction SpliceOver
# metrics

plotView(plotObj_group, centerByEvent = TRUE, plotJuncPSI = TRUE)


# Show normalized coverages, individual samples stacked in grouped tracks

plotView(
    plotObj_samples,
```

```
    normalizeCoverage = TRUE,
    trackList = list(A = c(1,2,3), B = c(4,5,6))
)

# Show stacked group comparisons with t-test

plotView(
    plotObj_group,
    trackList = list(c(1,2)),
    diffList = list(c("A", "B")),
    diff_stat = "t-test"
)

# Show interactive plotly:

if(interactive()) {
    p <- plotView(plotObj_samples, usePlotly = TRUE)
    show(p)
}

# Show exons with coverage plot

# static:
gr <- plotView(plotObj_samples, showExonRanges = TRUE)

# interactive:
if(interactive()) {
    p <- plotView(plotObj_samples, usePlotly = TRUE)
    gr <- showExons(p)
}

# Plot coverage by exons

p <- plotView(plotObj_samples,
    plotRanges = gr[c("SRSF3-203-E3", "SRSF3-203-E4", "SRSF3-203-E5")],
    horizontalLayout = c(1,1,1)
)
```

---

`example-SpliceWiz-data` *SpliceWiz Example BAMs and NxtSE Experiment Object*

---

## Description

`SpliceWiz_example_bams()` is a wrapper function to obtain and make a local copy of 6 example files provided by the NxtIRFdata companion package to demonstrate the use of SpliceWiz. See NxtIRFdata::example_bams for a description of the provided BAM files.

`SpliceWiz_example_NxtSE()` retrieves a ready-made functioning NxtSE object. The steps to reproduce this object is shown in the example code in makeSE

## Usage

```
SpliceWiz_example_bams()

SpliceWiz_example_NxtSE(novelSplicing = FALSE)
```

## Arguments

| | |
|---|---|
| novelSplicing | Whether to import an example NxtSE with novel splice event discovery. |

## Value

In SpliceWiz_example_bams(): returns a 2-column data frame containing sample names and BAM paths of the example dataset.

In SpliceWiz_example_NxtSE(): returns a NxtSE object.

## Functions

- SpliceWiz_example_bams(): Returns a 2-column data frame, containing sample names and sample paths (in tempdir()) of example BAM files
- SpliceWiz_example_NxtSE(): Returns a (in-memory / realized) NxtSE object that was pre-generated using the SpliceWiz example reference and example BAM files

## References

Generation of the mappability files was performed using SpliceWiz using a method analogous to that described in:

Middleton R, Gao D, Thomas A, Singh B, Au A, Wong JJ, Bomane A, Cosson B, Eyras E, Rasko JE, Ritchie W. IRFinder: assessing the impact of intron retention on mammalian gene expression. Genome Biol. 2017 Mar 15;18(1):51. doi:10.1186/s1305901711844

## See Also

makeSE

## Examples

```
# returns a data frame with the first column as sample names, and the
# second column as BAM paths

SpliceWiz_example_bams()

# Returns a NxtSE object created by the example bams aligned to the
# mock NxtSE reference

se <- SpliceWiz_example_NxtSE()
```

`findSamples` *Convenience Function to (recursively) find all files in a folder.*

## Description

Often, files e.g. raw sequencing FASTQ files, alignment BAM files, or processBAM output files, are stored in a single folder under some directory structure. They can be grouped by being in common directory or having common names. Often, their sample names can be gleaned by these common names or the names of the folders in which they are contained. This function (recursively) finds all files and extracts sample names assuming either the files are named by sample names (`level = 0`), or that their names can be derived from the parent folder (`level = 1`). Higher `level` also work (e.g. `level = 2`) mean the parent folder of the parent folder of the file is named by sample names. See details section below.

## Usage

```
findSamples(sample_path, suffix = ".txt.gz", level = 0)

findFASTQ(
  sample_path,
  paired = TRUE,
  fastq_suffix = c(".fastq", ".fq", ".fastq.gz", ".fq.gz"),
  level = 0
)

findBAMS(sample_path, level = 0)

findSpliceWizOutput(sample_path, level = 0)
```

## Arguments

| | |
|---|---|
| `sample_path` | The path in which to recursively search for files that match the given `suffix` |
| `suffix` | A vector of or or more strings that specifies the file suffix (e.g. '.bam' denotes BAM files, whereas ".txt.gz" denotes gzipped txt files). |
| `level` | Whether sample names can be found in the file names themselves (level = 0), or their parent directory (level = 1). Potentially parent of parent directory (level = 2). Support max level <= 3 (for sanity). |
| `paired` | Whether to expect single FASTQ files (of the format "sample.fastq"), or paired files (of the format "sample_1.fastq", "sample_2.fastq") |
| `fastq_suffix` | The name of the FASTQ suffix. Options are: ".fastq", ".fastq.gz", ".fq", or ".fq.gz" |

## Details

Paired FASTQ files are assumed to be named using the suffix `_1` and `_2` after their common names; e.g. `sample_1.fastq`, `sample_2.fastq`. Alternate FASTQ suffixes for `findFASTQ()` include ".fq", ".fastq.gz", and ".fq.gz".

In BAM files, often the parent directory denotes their sample names. In this case, use `level = 1` to automatically annotate the sample names using `findBAMS()`.

processBAM outputs two files per BAM processed. These are named by the given sample names. The text output is named "sample1.txt.gz", and the COV file is named "sample1.cov", where `sample1` is the name of the sample. These files can be organised / tabulated using the function `findSpliceWizOutput`. The generic function `findSamples` will organise the processBAM text output files but exclude the COV files. Use the latter as the `Experiment` in collateData if one decides to collate an experiment without linked COV files, for portability reasons.

## Value

A multi-column data frame with the first column containing the sample name, and subsequent columns being the file paths with suffix as determined by `suffix`.

## Functions

- `findSamples()`: Finds all files with the given suffix pattern. Annotates sample names based on file or parent folder names.
- `findFASTQ()`: Use findSamples() to return all FASTQ files in a given folder
- `findBAMS()`: Use findSamples() to return all BAM files in a given folder
- `findSpliceWizOutput()`: Use findSamples() to return all processBAM output files in a given folder, including COV files

## Examples

```
# Retrieve all BAM files in a given folder, named by sample names
bam_path <- tempdir()
example_bams(path = bam_path)
df.bams <- findSamples(sample_path = bam_path,
  suffix = ".bam", level = 0)
# equivalent to:
df.bams <- findBAMS(bam_path, level = 0)

# Retrieve all processBAM() output files in a given folder,
# named by sample names

expr <- findSpliceWizOutput(file.path(tempdir(), "SpliceWiz_Output"))
## Not run:

# Find FASTQ files in a directory, named by sample names
# where files are in the form:
# - "./sample_folder/sample1.fastq"
# - "./sample_folder/sample2.fastq"

findFASTQ("./sample_folder", paired = FALSE, fastq_suffix = ".fastq")

# Find paired gzipped FASTQ files in a directory, named by parent directory
# where files are in the form:
# - "./sample_folder/sample1/raw_1.fq.gz"
# - "./sample_folder/sample1/raw_2.fq.gz"
```

```
# - "./sample_folder/sample2/raw_1.fq.gz"
# - "./sample_folder/sample2/raw_2.fq.gz"

findFASTQ("./sample_folder", paired = TRUE, fastq_suffix = ".fq.gz")

## End(Not run)
```

---

`Gene-ontology-methods` *Gene ontology (over-representation) analysis using enriched genes of top alternative splicing events*

---

## Description

Genes containing differential alternative splicing events (ASEs) may be enriched in key functional pathways. This can be identified using a simple over-representation analysis. Biologists can identify key pathways of interest in order to focus on studying ASEs belonging to genes of functional interest.

## Usage

```
goASE(
  enrichedEventNames,
  universeEventNames = NULL,
  se,
  ontologyType = c("BP", "MF", "CC"),
 pAdjustMethod = c("BH", "holm", "hochberg", "hommel", "bonferroni", "BY", "fdr",
    "none"),
  ontologyRef = NULL,
  ...
)

goGenes(
  enrichedGenes,
  universeGenes = NULL,
  ontologyRef,
  ontologyType = c("BP", "MF", "CC"),
 pAdjustMethod = c("BH", "holm", "hochberg", "hommel", "bonferroni", "BY", "fdr",
    "none"),
  ...
)

extract_gene_ids_for_GO(enrichedEventNames, universeEventNames = NULL, se)

subset_EventNames_by_GO(EventNames, go_id, se)

plotGO(
```

```
  res_go = NULL,
  plot_x = c("log10FDR", "foldEnrichment", "nGenes"),
  plot_size = c("nGenes", "foldEnrichment", "log10FDR"),
  plot_color = c("foldEnrichment", "nGenes", "log10FDR"),
  filter_n_terms = 20,
  filter_padj = 1,
  filter_pvalue = 1,
  trim_go_term = 50
)
```

## Arguments

| | |
|---|---|
| enrichedEventNames | A vector of EventNames. This is typically one or more EventNames of differential ASEs |
| universeEventNames | A vector of EventNames, typically the EventNames of all ASEs that were tested. If left as NULL, all genes are considered background genes. |
| se | The NxtSE object containing the GO reference and the EventNames |
| ontologyType | One of either "BP" - biological pathways, "MF" - molecular function, or "CC" - cellular component. |
| pAdjustMethod | The method for p-value adjustment for FDR. See ?p.adjust |
| ontologyRef | A valid gene ontology reference. This can be generated either using viewGO(reference_path) or ref(se)$ontology. This field is required for goGenes() and optional for goASE(). See details. |
| ... | Additional arguments to be passed to fgsea::fora() |
| enrichedGenes | A vector of gene_id representing the list of enriched genes. To generate a list of valid gene_id, see viewGenes |
| universeGenes | (default NULL) A vector of gene_id representing the list of background genes. |
| EventNames, go_id | In subset_EventNames_by_GO(), a vector of ASE EventNames to subset against the given go_id. |
| res_go | For plotGO, the gene ontology results data object returned by the goASE() function. |
| plot_x, plot_size, plot_color | What parameters should be plotted on the x-axis, bubble-size, or bubble-color? Valid options are c("log10FDR", "foldEnrichment", "nGenes"). Defaults are "log10FDR", "nGenes", "foldEnrichment"‘ for x-axis, bubble size/color, respectively |
| filter_n_terms | (default 20) How many top terms to plot. |
| filter_padj, filter_pvalue | Whether given GO results should be filtered by adjusted p value (FDR) or nominal p value, respectively, prior to plot |
| trim_go_term | (default 50) For long GO terms, description will be trimmed by first n characters, where trim_go_term = n |

## Details

Users can perform GO analysis using either the GO annotation compiled via building the SpliceWiz reference using `buildRef()` , or via a custom-supplied gene ontology annotation. This is done by supplying their own GO annotations as an argument to `ontologyRef`. This should be coerceable to a `data.frame` containing the following columns:

- `gene_id` Gene ID's matching that used by the SpliceWiz reference
- `go_id` Gene ontology ID terms, of the form `GO:XXXXXXX`

## Value

For `goASE()` and `goGenes()`, a data table containing the following:

- go_id: Gene ontology ID
- go_term: Gene ontology term
- pval: Raw p values
- padj: Adjusted p values
- overlap: Number of enriched genes (of enriched ASEs)
- size: Number of background genes (of background ASEs)
- overlapGenes: A list of `gene_id`'s from genes of enriched ASEs
- expected: The number of overlap genes expected by random

For `extract_gene_ids_for_GO()`, a list containing the following:

- genes: A vector of enriched `gene_ids`
- universe: A vector of background `gene_ids`

For `subset_EventNames_by_GO()`, a vector of all ASE `EventNames` belonging to the given gene ontology `go_id`

## Functions

- `goASE()`: Performs over-representation gene ontology analysis using a given list of enriched / background ASEs
- `goGenes()`: Performs GO analysis given the set of enriched and (optionally) the background (universe) genes.
- `extract_gene_ids_for_GO()`: Produces a list containing enriched and universe `gene_ids` of given enriched and background ASE `EventNames`
- `subset_EventNames_by_GO()`: Returns a list of ASEs enriched in a given gene ontology category
- `plotGO()`: Produces a lollipop plot based on the given gene ontology results object

## See Also

Build-Reference-methods on how to generate gene ontology annotations

## Examples

```
# Generate example reference with `Homo sapiens` gene ontology

ref_path <- file.path(tempdir(), "Reference_withGO")
buildRef(
    reference_path = ref_path,
    fasta = chrZ_genome(),
    gtf = chrZ_gtf(),
    ontologySpecies = "Homo sapiens"
)

# Perform GO analysis using first 1000 genes
ontology <- viewGO(ref_path)
allGenes <- sort(unique(ontology$gene_id))

exampleGeneID <- allGenes[1:1000]
exampleBkgdID <- allGenes

go_df <- goGenes(
    enrichedGenes = exampleGeneID,
    universeGenes = exampleBkgdID,
    ontologyRef = ontology
)

# Plots the top 12 GO terms

plotGO(go_df, filter_n_terms = 12)

# Below example code of how to use output of differential ASEs for GO analysis
# It will not work with the example dataset because the reference must be
# either human / mouse, or a  valid `ontologySpecies` given to buildRef()
# We hope the example code is simple enough to understand for users to adapt
# to their own workflows.

## Not run:

se <- SpliceWiz_example_NxtSE(novelSplicing = TRUE)

colData(se)$treatment <- rep(c("A", "B"), each = 3)

require("limma")
res_limma <- ASE_limma(se, "treatment", "A", "B")

# Perform gene ontology analysis of the first 10 differential ASEs

go_df <- goASE(
  enrichedEventNames = res_limma$EventName[1:10],
  universeEventNames = res_limma$EventName,
  se = se
)

# Return a list of all ASEs belonging to the top enriched category
```

```
GOsubset_EventName <- subset_EventNames_by_GO(
  EventNames = res_limma$EventName,
  go_id = go_df$go_id[1],
  se = se
)

# Return a list of all ASEs belonging to the top enriched category.
# - typically used if one wishes to export `gene_id` for use in other gene
#   ontology tools

gene_id_list <- extract_gene_ids_for_GO(
  enrichedEventNames = res_limma$EventName[1:10],
  universeEventNames = res_limma$EventName,
  se = se
)


## End(Not run)
```

---

`Graphics-User-Interface` *Launches the SpliceWiz Graphics User Interface (GUI) using Shiny Dashboard*

---

## Description

This function launches the SpliceWiz interactive app using Shiny Dashboard This is (by default) a dialog window within the RStudio application with the resolution specified by the `res` parameter. Alternatively, setting `mode = "browser"` will launch a resizable browser window (using the default internet browser). The demo mode can be launched by setting `demo = TRUE`. See the SpliceWiz Quick-Start for a guide to using the SpliceWiz GUI.

## Usage

```
spliceWiz(
  mode = c("dialog", "browser"),
  res = c("1080p", "720p", "960p", "1440p"),
  demo = FALSE
)
```

## Arguments

| | |
|---|---|
| `mode` | (default `"dialog"`) `"dialog"` displays SpliceWiz in a dialog box with specified width and height. `"browser"` opens SpliceWiz in a browser-like resizable window. |
| `res` | (default "1080p") Sets width and height of the app to pre-defined dimensions. Possible options are "720p, "960p", "1080p", "1440p", which specifies the height of the app. All are displayed in aspect ratio 16x9 |

demo (default FALSE) If set to TRUE, SpliceWiz will place demo reference and BAM files into the temporary directory.

## Value

Runs an interactive shinydashboard SpliceWiz app with the specified mode.

## Functions

- spliceWiz(): Launches the SpliceWiz GUI

## Examples

```
if(interactive()) {

# Launches interactive ShinyDashboard SpliceWiz app as fixed-size dialog box
# 1080p = 1920 x 1080 pixels
    spliceWiz(mode = "dialog", res = "1080p")

# Launches interactive ShinyDashboard SpliceWiz app as browser window
    spliceWiz(mode = "browser")

}
```

---

# isCOV *Validates the given file as a valid COV file*

---

## Description

This function takes the path of a possible COV file and checks whether its format complies with that of the COV format defined by this package.

## Usage

```
isCOV(coverage_files)
```

## Arguments

coverage_files A vector containing the file names of files to be checked

## Details

COV files are BGZF-compressed files. The first 4 bytes of the file must always be 'COV\1', distinguishing it from BAM or other files in BGZF format. This function checks whether the given file complies with this.

## Value

TRUE if all files are valid COV files. FALSE otherwise

## See Also

processBAM collateData

## Examples

```
se <- SpliceWiz_example_NxtSE()

cov_files <- covfile(se)

isCOV(cov_files) # returns true if these are true COV files
```

---

`make_plot_data` *Construct data of percent-spliced-in (PSI) matrices and group-average PSIs*

---

## Description

`makeMatrix()` constructs a matrix of PSI values of the given alternative splicing events (ASEs).

`makeMeanPSI()` constructs a table of "average" PSI values, with samples grouped by a number of given conditions (e.g. "group A" and "group B") of a given condition category (e.g. condition "treatment"). See details below.

## Usage

```
makeMatrix(
  se,
  event_list,
  sample_list = colnames(se),
  method = c("PSI", "logit", "Z-score"),
  depth_threshold = 10,
  logit_max = 5,
  na.percent.max = 0.1
)

makeMeanPSI(
  se,
  event_list = rownames(se),
  condition,
  conditionList,
  depth_threshold = 10,
  logit_max = 10
)
```

## Arguments

| | |
|---|---|
| se | (Required) A NxtSE object generated by makeSE |
| event_list | A character vector containing the names of ASE events (as given by the EventName column of differential ASE results table generated by one of the ASE-methods, or the rownames of the NxtSE object) |
| sample_list | (default = colnames(se)) In makeMatrix(), a list of sample names in the given experiment to be included in the returned matrix |
| method | In makeMatrix(), rhe values to be returned (default = "PSI"). It can alternately be "logit" which returns logit-transformed PSI values, or "Z-score" which returns Z-score-transformed PSI values |
| depth_threshold | (default = 10) Samples with the number of reads supporting either included or excluded isoforms below this values are excluded |
| logit_max | PSI values close to 0 or 1 are rounded up/down to plogis(-logit_max) and plogis(logit_max), respectively. See details. |
| na.percent.max | (default = 0.1) The maximum proportion of values in the given dataset that were transformed to NA because of low splicing depth. ASE events where there are a higher proportion (default 10%) NA values will be excluded from the final matrix. Most heatmap functions will spring an error if there are too many NA values in any given row. This option caps the number of NA values to avoid returning this error. |
| condition | The name of the column containing the condition values in colData(se) |
| conditionList | A list (or vector) of condition values of which to calculate mean PSIs |

## Details

Note that this function takes the geometric mean of PSI, by first converting all values to logit(PSI), taking the average logit(PSI) values of each condition, and then converting back to PSI using inverse logit.

Samples with low splicing coverage (either due to insufficient sequencing depth or low gene expression) are excluded from calculation of mean PSIs. The threshold can be set using depth_threshold. Excluding these samples is appropriate because the uncertainty of PSI is high when the total included / excluded count is low. Note that events where all samples in a condition is excluded will return a value of NaN.

Using logit-transformed PSI values is appropriate because PSI values are bound to the (0,1) interval, and are often thought to be beta-distributed. The link function often used with beta-distributed models is the logit function, which is defined as logit(x) = function(x) log(x / (1 - x)), and is equivalent to stats::qlogis. Its inverse is equivalent to stats::plogis.

Users wishing to calculate arithmetic means of PSI are advised to use makeMatrix, followed by rowMeans on subsetted sample columns.

## Value

For makeMatrix: A matrix of PSI (or alternate) values, with columns as samples and rows as ASE events.

For makeMeanPSI: A 3 column data frame, with the first column containing event_list list of ASE events, and the last 2 columns containing the average PSI values of the nominator and denominator conditions.

## Functions

- makeMatrix(): constructs a matrix of PSI values of the given alternative splicing events (ASEs)
- makeMeanPSI(): constructs a table of "average" PSI values

## Examples

```
se <- SpliceWiz_example_NxtSE()

colData(se)$treatment <- rep(c("A", "B"), each = 3)

event_list <- rowData(se)$EventName

mat <- makeMatrix(se, event_list[1:10])

diag_values <- makeMeanPSI(se, event_list,
  condition = "treatment",
  conditionList = list("A", "B")
)
```

---

# makeSE *Imports a collated dataset into the R session as an NxtSE object*

---

## Description

Creates a NxtSE object from the data (that was collated using collateData). This object is used for downstream differential analysis of IR and alternative splicing events using ASE-methods, data generation for visualization of scatter plots and heatmaps via make_plot_data methods, and coverage visualisation using plotCoverage

## Usage

```
makeSE(
  collate_path,
  colData,
  RemoveOverlapping = TRUE,
  realize = FALSE,
  verbose = TRUE
)
```

## Arguments

| | |
|---|---|
| collate_path | (Required) The output path of collateData pointing to the collated data |
| colData | (Optional) A data frame containing the sample annotation information. The first column must contain the sample names. Omit colData to generate a NxtSE object of the whole dataset without any assigned annotations. Alternatively, if the names of only a subset of samples are given, then makeSE() will construct the NxtSE object based only on the samples given. The colData can be set later using colData |
| RemoveOverlapping | (default = TRUE) Whether to filter out overlapping IR events belonging to minor isoforms. See details. |
| realize | (default = FALSE) Whether to load all assay data into memory. See details |
| verbose | (default = TRUE) Whether loading messages are displayed |

## Details

makeSE retrieves the data collated by collateData, and initialises a NxtSE object. It references the required on-disk assay data using DelayedArrays, thereby utilising 'on-disk' memory to conserve memory usage.

For extremely large datasets, loading the entire data into memory may consume too much memory. In such cases, make a subset of the NxtSE object (e.g. subset by samples) before loading the data into memory (RAM) using realize_NxtSE. Alternatively supply a data frame to the colData parameter of the makeSE() function. Only samples listed in the first column of the colData data frame will be imported into the NxtSE object.

It should be noted that downstream applications of SpliceWiz, including ASE-methods, plotCoverage, are much faster if the NxtSE is realized. It is recommended to realize the NxtSE object before extensive usage.

If COV files assigned via collateData have been moved relative to the collate_path, the created NxtSE object will not be linked to any COV files and plotCoverage cannot be used. To reassign these files, a vector of file paths corresponding to all the COV files of the data set can be assigned using covfile(se) <- vector_of_cov_files. See the example below for details.

If RemoveOverlapping = TRUE, makeSE will remove introns that overlap other introns with higher junction read counts in the dataset. This means that SpliceWiz will assess a set of non-overlapping introns which belong to likely major isoforms, ensuring that overlapping IR events are not 'double-counted'.

NB: Since version 1.3.4, SpliceWiz has improved the algorithm of generating the set of non-overlapping introns (prior versions appear to generate sets of introns that still overlap). To use the prior algorithm for compatibility with prior analysis, set RemoveOverlapping = FALSE.

## Value

A NxtSE object containing the compiled data in DelayedArrays (or as matrices if realize = TRUE), pointing to the assay data contained in the given collate_path

## Examples

```
# The following code can be used to reproduce the NxtSE object
# that can be fetched with SpliceWiz_example_NxtSE()

buildRef(
    reference_path = file.path(tempdir(), "Reference"),
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)

bams <- SpliceWiz_example_bams()
processBAM(bams$path, bams$sample,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "SpliceWiz_Output")
)

expr <- findSpliceWizOutput(file.path(tempdir(), "SpliceWiz_Output"))
collateData(expr,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "Collated_output")
)

se <- makeSE(collate_path = file.path(tempdir(), "Collated_output"))

# "Realize" NxtSE object to load all H5 assays into memory:

se <- realize_NxtSE(se)

# If COV files have been removed since the last call to collateData()
# reassign them to the NxtSE object, for example:

covfile_path <- system.file("extdata", package = "SpliceWiz")
covfile_df <- findSamples(covfile_path, ".cov")

covfile(se) <- covfile_df$path
```

---

# Mappability-methods *Calculate low mappability genomic regions*

---

## Description

These functions empirically calculate low-mappability (Mappability Exclusion) regions using the given reference. A splice-aware alignment software capable of aligning reads to the genome is required. See details and examples below.

## Usage

```
generateSyntheticReads(
```

```
  reference_path,
  read_len = 70,
  read_stride = 10,
  error_pos = 35,
  verbose = TRUE,
  alt_fasta_file
)

calculateMappability(
  reference_path,
  aligned_bam = file.path(reference_path, "Mappability", "Aligned.out.bam"),
  threshold = 4,
  n_threads = 1
)
```

## Arguments

| | |
|---|---|
| reference_path | The directory of the reference prepared by getResources |
| read_len | The nucleotide length of the synthetic reads |
| read_stride | The nucleotide distance between adjacent synthetic reads |
| error_pos | The position of the procedurally-generated nucleotide error from the start of each synthetic reads |
| verbose | Whether additional status messages are shown |
| alt_fasta_file | (Optional) The path to the user-supplied genome fasta file, if different to that found inside the resource subdirectory of the reference_path. If getResources has already been run, this parameter should be omitted. |
| aligned_bam | The BAM file of alignment of the synthetic reads generated by generateSyntheticReads(). Users should use a genome splice-aware aligner, preferably the same aligner used to align the samples in their experiment. |
| threshold | Genomic regions with this alignment read depth (or below) in the aligned synthetic read BAM are defined as low mappability regions. |
| n_threads | The number of threads used to calculate mappability exclusion regions from aligned bam file of synthetic reads. |

## Details

Creating a Mappability Exclusion BED file is a three-step process.

- First, using generateSyntheticReads(), synthetic reads are systematically generated using the given genome contained within reference_path, prepared via getResources. Alternatively, use alt_fasta_file to set the genome sequence if this is different to that prepared by getResources or if getResources is not yet run.
- Second, an aligner such as STAR (preferably the same aligner used for the subsequent RNA-seq experiment) is required to align these reads to the source genome. Poorly mapped regions of the genome will be reflected by regions of low coverage depth.

- Finally, the BAM file containing the aligned reads is analysed using `calculateMappability()`, to identify low-mappability regions to compile the Mappability Exclusion BED file.

It is recommended to leave all parameters to their default settings. Regular users should only specify `reference_path`, `aligned_bam` and `n_threads`, as required.

NB: STAR_mappability runs all 3 steps required, using the `STAR` aligner. This only works in systems where `STAR` is installed.

NB2: buildFullRef builds the STAR reference, then calculates mappability. It then uses the calculated mappability regions to build the SpliceWiz reference.

NB3: In systems where `STAR` is not available, consider using HISAT2 or Rsubread. A working example using Rsubread is shown below.

## Value

- For `generateSyntheticReads`: writes `Reads.fa` to the `Mappability` subdirectory inside the given `reference_path`.
- For `calculateMappability`: writes a gzipped BED file named `MappabilityExclusion.bed.gz` to the `Mappability` subdirectory inside `reference_path`. This BED file is automatically used by buildRef if its `MappabilityRef` parameter is not specified.

## Functions

- `generateSyntheticReads()`: Generates synthetic reads from a genome FASTA file, for mappability calculations.
- `calculateMappability()`: Generate a BED file defining low mappability regions, using reads generated by `generateSyntheticReads()`, aligned to the genome.

## See Also

Build-Reference-methods

## Examples

```
# (1a) Creates genome resource files

ref_path <- file.path(tempdir(), "refWithMapExcl")

getResources(
    reference_path = ref_path,
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)

# (1b) Systematically generate reads based on the example genome:

generateSyntheticReads(
    reference_path = ref_path
)
## Not run:
```

```
# (2) Align the generated reads using Rsubread:

# (2a) Build the Rsubread genome index:

subreadIndexPath <- file.path(ref_path, "Rsubread")
if(!dir.exists(subreadIndexPath)) dir.create(subreadIndexPath)
Rsubread::buildindex(
    basename = file.path(subreadIndexPath, "reference_index"),
    reference = chrZ_genome()
)

# (2b) Align the synthetic reads using Rsubread::subjunc()

Rsubread::subjunc(
    index = file.path(subreadIndexPath, "reference_index"),
    readfile1 = file.path(ref_path, "Mappability", "Reads.fa"),
    output_file = file.path(ref_path, "Mappability", "AlignedReads.bam"),
    useAnnotation = TRUE,
    annot.ext = chrZ_gtf(),
    isGTF = TRUE
)

# (3) Analyse the aligned reads in the BAM file for low-mappability regions:

calculateMappability(
    reference_path = ref_path,
    aligned_bam = file.path(ref_path, "Mappability", "AlignedReads.bam")
)

# (4) Build the example reference using the calculated Mappability Exclusions

buildRef(ref_path)

# NB the default is to search for the BED file generated by
# `calculateMappability()` in the given reference_path

## End(Not run)
```

---

NxtSE-class *The NxtSE class*

---

## Description

The NxtSE class inherits from the SummarizedExperiment class and is constructed using makeSE. NxtSE extends SummarizedExperiment by housing additional assays pertaining to IR and splice junction counts.

## Usage

```
NxtSE(...)
```

```
## S4 method for signature 'NxtSE'
up_inc(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
down_inc(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
up_exc(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
down_exc(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
covfile(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
sampleQC(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
sourcePath(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
row_gr(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
ref(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
junc_PSI(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
junc_counts(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
junc_counts_uns(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
junc_gr(x, withDimnames = TRUE, ...)

## S4 method for signature 'NxtSE'
update_NxtSE(x, ...)

## S4 method for signature 'NxtSE'
realize_NxtSE(x, includeJunctions = FALSE, withDimnames = TRUE, ...)

## S4 replacement method for signature 'NxtSE'
up_inc(x, withDimnames = TRUE) <- value
```

```
## S4 replacement method for signature 'NxtSE'
down_inc(x, withDimnames = TRUE) <- value

## S4 replacement method for signature 'NxtSE'
up_exc(x, withDimnames = TRUE) <- value

## S4 replacement method for signature 'NxtSE'
down_exc(x, withDimnames = TRUE) <- value

## S4 replacement method for signature 'NxtSE'
covfile(x, withDimnames = TRUE) <- value

## S4 replacement method for signature 'NxtSE'
sampleQC(x, withDimnames = TRUE) <- value

## S4 method for signature 'NxtSE,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 replacement method for signature 'NxtSE,ANY,ANY,NxtSE'
x[i, j, ...] <- value

## S4 method for signature 'NxtSE'
cbind(..., deparse.level = 1)

## S4 method for signature 'NxtSE'
rbind(..., deparse.level = 1)
```

## Arguments

| | |
|---|---|
| `...` | In NxtSE(), additional arguments to be passed onto SummarizedExperiment() |
| `x` | A NxtSE object |
| `withDimnames` | (default TRUE) Whether exported assays should be supplied with row and column names of the NxtSE object. See SummarizedExperiment |
| `includeJunctions` | When realizing a NxtSE object, include whether junction counts and PSIs should be realized into memory. Not recommended for general use, as they are only used for coverage plots. |
| `value` | The value to replace. Must be a matrix for the up_inc<-, down_inc<-, up_exc<- and down_exc<- replacers, and a character vector for covfile<- |
| `i, j` | Row and column subscripts to subset a NxtSE object. |
| `drop` | A logical(1), ignored by these methods. |
| `deparse.level` | See base::cbind for a description of this argument. |

## Value

See Functions section (below) for details

**Functions**

- `NxtSE()`: Constructor function for NxtSE; akin to SummarizedExperiment(...)
- `up_inc(NxtSE)`: Gets upstream included events (SE/MXE), or upstream exon-intron spanning reads (IR)
- `down_inc(NxtSE)`: Gets downstream included events (SE/MXE), or downstream exon-intron spanning reads (IR)
- `up_exc(NxtSE)`: Gets upstream excluded events (MXE only)
- `down_exc(NxtSE)`: Gets downstream excluded events (MXE only)
- `covfile(NxtSE)`: Gets a named vector with the paths to the corresponding COV files
- `sampleQC(NxtSE)`: Gets a data frame with the QC parameters of the samples
- `sourcePath(NxtSE)`: Retrieves the directory path containing the source data for this NxtSE object.
- `row_gr(NxtSE)`: Retrieves a GRanges object representing the genomic spans of the ASEs (EventRegion as GRanges)
- `ref(NxtSE)`: Retrieves a list of annotation data associated with this NxtSE object; primarily used in plotCoverage()
- `junc_PSI(NxtSE)`: Getter for junction PSI DelayedMatrix; primarily used in plotCoverage()
- `junc_counts(NxtSE)`: Getter for junction counts DelayedMatrix; primarily used in plotCoverage()
- `junc_counts_uns(NxtSE)`: Getter for (unstranded) junction counts DelayedMatrix; primarily used in plotCoverage()
- `junc_gr(NxtSE)`: Getter for junction GenomicRanges coordinates; primarily used in plotCoverage()
- `update_NxtSE(NxtSE)`: Updates NxtSE object to the latest version.
- `realize_NxtSE(NxtSE)`: Converts all DelayedMatrix assays as matrices (i.e. performs all delayed calculation and loads resulting object to RAM)
- `up_inc(NxtSE) <- value`: Sets upstream included events (SE/MXE), or upstream exon-intron spanning reads (IR)
- `down_inc(NxtSE) <- value`: Sets downstream included events (SE/MXE), or downstream exon-intron spanning reads (IR)
- `up_exc(NxtSE) <- value`: Sets upstream excluded events (MXE only)
- `down_exc(NxtSE) <- value`: Sets downstream excluded events (MXE only)
- `covfile(NxtSE) <- value`: Sets the paths to the corresponding COV files
- `sampleQC(NxtSE) <- value`: Sets the values in the data frame containing sample QC
- `x[i`: Subsets a NxtSE object
- `` `[`(x = NxtSE, i = ANY, j = ANY) <- value ``: Sets a subsetted NxtSE object
- `cbind(NxtSE)`: Combines two NxtSE objects (by samples - columns)
- `rbind(NxtSE)`: Combines two NxtSE objects (by AS/IR events - rows)

## Examples

```
# Run the full pipeline to generate a NxtSE object:

buildRef(
    reference_path = file.path(tempdir(), "Reference"),
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)

bams <- SpliceWiz_example_bams()
processBAM(bams$path, bams$sample,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "SpliceWiz_Output")
)

expr <- findSpliceWizOutput(file.path(tempdir(), "SpliceWiz_Output"))
collateData(expr,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "Collated_output")
)

se <- makeSE(collate_path = file.path(tempdir(), "Collated_output"))

# Coerce NxtSE -> SummarizedExperiment
se_raw <- as(se, "SummarizedExperiment")

# Coerce SummarizedExperiment -> NxtSE
se_NxtSE <- as(se_raw, "NxtSE")
identical(se, se_NxtSE) # Returns TRUE

# Update NxtSE object to the latest version
# - useful if an NxtSE object made with old SpliceWiz version
# - was stored as an RDS obejct

se <- update_NxtSE(se)

# Get directory path of NxtSE (i.e., collate_path)
sourcePath(se)

# Get Main Assay Counts
assay(se, "Included") # Junction (or IR depth) counts for included isoform
assay(se, "Excluded") # Junction (or IR depth) counts for excluded isoform

# Get Auxiliary Counts (for filter use only)
assay(se, "Coverage") # Participation ratio (intron coverage for IR/RI)
assay(se, "minDepth") # SpliceOver junction counts (Intron Depths for IR/RI)
assay(se, "Depth")    # Sum of intron depth and SpliceOver (used for
                      # coverage normalization factor

# Get Junction reads of SE / MXE and spans-reads of IR events
up_inc(se)   # Upstream included junction counts (IR/MXE/SE/RI)
down_inc(se) # Downstream included junction counts (IR/MXE/SE/RI)
```

```
up_exc(se)   # Upstream excluded junction counts (MXE only)
down_exc(se) # Downstream excluded junction counts (MXE only)

# Get Junction counts
junc_counts(se) # stranded (if RNA-seq is auto-detected as stranded)
junc_counts_uns(se) # unstranded (sum of junction reads from both strand)
junc_PSI(se) # PSI of junction (as proportion of SpliceOver metric)

# Get Junction GRanges object
junc_gr(se)

# Get EventRegion as GRanges object
row_gr(se)

# Get list of available coverage files
covfile(se)

# Get sample QC information
sampleQC(se)

# Get resource data (used internally for plotCoverage())
cov_data <- ref(se)
names(cov_data)

# Subset functions
se_by_samples <- se[,1:3]
se_by_events <- se[1:10,]
se_by_rowData <- subset(se, EventType == "IR")

# Cbind (bind event_identical NxtSE by samples)
se_by_samples_1 <- se[,1:3]
se_by_samples_2 <- se[,4:6]
se_cbind <- cbind(se_by_samples_1, se_by_samples_2)
identical(se, se_cbind) # should return TRUE

# Rbind (bind sample_identical NxtSE by events)
se_IR <- subset(se, EventType == "IR")
se_SE <- subset(se, EventType == "SE")
se_IRSE <- rbind(se_IR, se_SE)
identical(se_IRSE, subset(se, EventType %in% c("IR", "SE"))) # TRUE

# Convert HDF5-based NxtSE to in-memory se
# makeSE() creates a HDF5-based NxtSE object where all assay data is stored
# as an h5 file instead of in-memory. All operations are performed as
# delayed operations as per DelayedArray package.
# To realize the NxtSE object as an in-memory object, use:

se_real <- realize_NxtSE(se)
identical(se, se_real) # should return FALSE

# To check the difference, run:
class(up_inc(se))
class(up_inc(se_real))
```

plotCoverage *RNA-seq Coverage Plots and Genome Tracks*

## Description

Generate plotly / ggplot RNA-seq genome and coverage plots from command line. Note that these are legacy functions. More expansive functionality is available using getCoverageData / getPlotObject / plotView functions.

## Usage

```
plotCoverage(
  se,
  Event,
  Gene,
  seqname,
  start,
  end,
  coordinates,
  strand = c("*", "+", "-"),
  zoom_factor = 0.2,
  bases_flanking = 100,
  tracks,
  track_names = tracks,
  condition,
  ribbon_mode = c("sd", "ci", "sem", "none"),
  selected_transcripts = "",
  reverseGenomeCoords = FALSE,
  plotJunctions = FALSE,
  junctionThreshold = 0.01,
  plot_key_isoforms = FALSE,
  condense_tracks = FALSE,
  stack_tracks = FALSE,
  t_test = FALSE,
  norm_event,
  usePlotly = FALSE
)

plotGenome(
  se,
  reference_path,
  Event,
  Gene,
  seqname,
  start,
```

```
  end,
  coordinates,
  zoom_factor = 0.2,
  bases_flanking = 100,
  reverseGenomeCoords = FALSE,
  condense_tracks = FALSE,
  selected_transcripts = "",
  plot_key_isoforms = FALSE,
  usePlotly = FALSE
)
```

## Arguments

| | |
|---|---|
| se | A NxtSE object, created by makeSE. COV files must be linked to the NxtSE object. To do this, see the example in makeSE. Required by plotCoverage. Not required by plotGenome if reference_path is supplied. |
| Event | The EventName of the IR / alternative splicing event to be displayed. Use rownames(se) to display a list of valid events. |
| Gene | Whether to use the range for the given Gene. If given, overrides Event (but Event or norm_event will be used to normalise by condition). Valid Gene entries include gene_id (Ensembl ID) or gene_name (Gene Symbol). |
| seqname, start, end | The chromosome (string) and genomic start/end coordinates (numeric) of the region to display. If present, overrides both Event and Gene. E.g. for a given region of chr1:10000-11000, use the parameters: seqname = "chr1", start = 10000, end = 11000 |
| coordinates | A string specifying genomic coordinates can be given instead of seqname,start,end. Must be of the format "chr:start-end", e.g. "chr1:10000-11000" |
| strand | Whether to show coverage of both strands "*" (default), or from the "+" or "-" strand only. |
| zoom_factor | Zoom out from event. Each level of zoom zooms out by a factor of 3. E.g. for a query region of chr1:10000-11000, if a zoom_factor of 1.0 is given, chr1:99000-12000 will be displayed. |
| bases_flanking | (Default = 100) How many bases flanking the zoomed window. Useful when used in conjunction with zoom_factor == 0. E.g. for a given region of chr1:10000-11000, if zoom_factor = 0 and bases_flanking = 100, the region chr1:9900-11100 will be displayed. |
| tracks | The names of individual samples, or the names of the different conditions to be plotted. For the latter, set condition to the specified condition category. |
| track_names | The names of the tracks to be displayed. If omitted, the track_names will default to the input in tracks |
| condition | To display normalised coverage per condition, set this to the condition category. If omitted, tracks are assumed to refer to the names of individual samples. |
| ribbon_mode | (default "sd") Whether coverage ribbons signify standard deviation "sd", 95% confidence interval "ci", standard error of the mean "sem", or none "none". Only applicable when condition is set. |

`selected_transcripts`
: (Optional) A vector containing transcript ID or transcript names of transcripts to be displayed on the gene annotation track. Useful to remove minor isoforms that are not relevant to the samples being displayed.

`reverseGenomeCoords`
: (default `FALSE`) Whether to reverse the genomic coordinates - helpful for intuitive plotting of negative-strand genes

`plotJunctions`
: (default `FALSE`) If `TRUE`, sashimi plot junction arcs are plotted. Currently only implemented for plots of individual samples.

`junctionThreshold`
: (default `0.01`) The threshold expression of junction reads below which junction arcs will be omitted. This removes cluttering of junction arcs from lowly-expressed (rare) junctions. For individual tracks, this is the fraction of coverage height. For by-condition tracks, this is a PSI threshold.

`plot_key_isoforms`
: (default `FALSE`) If `TRUE`, only transcripts involved in the selected `Event` or pair of `Events` will be displayed.

`condense_tracks`
: (default `FALSE`) Whether to collapse the transcript track annotations by gene.

`stack_tracks`
: (default `FALSE`) Whether to graph all the conditions on a single coverage track. If set to `TRUE`, each condition will be displayed in a different colour on the same track. Ignored if `condition` is not set.

`t_test`
: (default `FALSE`) Whether to perform a pair-wise T-test. Only used if there are TWO condition tracks.

`norm_event`
: Whether to normalise by an event different to that given in "Event". The difference between this and Event is that the genomic coordinates can be centered around a different `Event`, `Gene` or region as given in `seqname/start/end`. If `norm_event` is different to `Event`, `norm_event` will be used for normalisation and `Event` will be used to define the genomic coordinates of the viewing window. `norm_event` is required if `Event` is not set and `condition` is set.

`usePlotly`
: If `TRUE`, returns a `covPlotly` object containing the plotly-based interactive plot. If `FALSE`, returns a ggplot object.

`reference_path`
: The path of the reference generated by Build-Reference-methods. Required by `plotGenome` if a NxtSE object is not specified.

## Details

In RNA sequencing, alignments to spliced transcripts will "skip" over genomic regions of introns. This can be illustrated in a plot using a horizontal genomic axis, with the vertical axis representing the number of alignments covering each nucleotide. As a result, the coverage "hills" represent the expression of exons, and "valleys" to introns.

Different alternatively-spliced isoforms thus produce different coverage patterns. The change in the coverage across an alternate exon relative to its constitutively-included flanking exons, for example, represents its alternative inclusion or skipping. Similarly, elevation of intron valleys represent increased intron retention.

With multiple replicates per sample, coverage is dependent on library size and gene expression. To compare alternative splicing ratios, normalisation of the coverage of the alternate exon (or alternatively retained intron) relative to their constitutive flanking exons, is required. There is no established method for this normalisation, and can be confounded in situations where flanking elements are themselves alternatively spliced.

SpliceWiz performs this coverage normalisation using the same method as its estimate of spliced / intronic transcript abundance using the `SpliceOver` method (see details section in collateData). This normalisation can be applied to correct for library size and gene expression differences between samples of the same experimental condition. After normalisation, mean and variance of coverage can be computed as ratios relative to total transcript abundance. This method can visualise alternatively included genomic regions including casette exons, alternate splice site usage, and intron retention.

`plotCoverage` generates plots showing depth of alignments to the genomic axis. Plots can be generated for individual samples or samples grouped by experimental conditions. In the latter, mean and 95% confidence intervals are shown.

`plotGenome` generates genome transcript tracks only. Protein-coding regions are denoted by thick rectangles, whereas non-protein coding transcripts or untranslated regions are denoted with thin rectangles. Introns are denoted as lines.

## Value

For `plotCoverage` and `plotGenome`:

- If `usePlotly = FALSE` returns a patchwork-assembled static plot
- If `usePlotly = TRUE` returns a covPlotly object, which generates a plotly interactive plot when shown using `show()`

## Functions

- `plotCoverage()`: Legacy function - works by internally calling getCoverageData(), getPlotObject(), then plotView()
- `plotGenome()`: Legacy function - works by internally calling getGenomeData(), followed by plotAnnoTrack()

## Examples

```
se <- SpliceWiz_example_NxtSE(novelSplicing = TRUE)

# Assign annotation of the experimental conditions
colData(se)$treatment <- rep(c("A", "B"), each = 3)

# Verify that the COV files are linked to the NxtSE object:
covfile(se)

# Plot the genome track only, with specified gene:
plotGenome(se, Gene = "SRSF3")

# View the genome track, specifying a genomic region via coordinates:
plotGenome(se, coordinates = "chrZ:10000-20000")
```

```
# Return a list of ggplot and plotly objects, also plotting junction counts
plotCoverage(
    se = se,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
    tracks = colnames(se)[1:4], plotJunctions = TRUE
)

# Plot the same, but as a plotly interactive plot

if(interactive()) {
    p <- plotCoverage(
        se = se,
        Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
        tracks = colnames(se)[1:4], plotJunctions = TRUE,
        usePlotly = TRUE
    )
    show(p)
}

# Plot by condition "treatment", including provisional PSIs
plotCoverage(
    se = se,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
    tracks = c("A", "B"), condition = "treatment", plotJunctions = TRUE
)

# As above, but stack all traces into the same track
# - NB: plotJunctions is disabled when `stack_tracks = TRUE`
plotCoverage(
    se = se,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
    tracks = c("A", "B"), condition = "treatment", stack_tracks = TRUE
)

# Plot the above, but unstancked, and with t-test track
# - NB: plotJunctions is disabled when `stack_tracks = TRUE`
plotCoverage(
    se = se,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
    tracks = c("A", "B"), condition = "treatment", t_test = TRUE
)

# Select only transcripts involved in the selected alternative splicing event
plotCoverage(
    se = se,
    Event = "SE:SRSF3-203-exon4;SRSF3-202-int3",
    tracks = colnames(se)[1:4],
    plot_key_isoforms = TRUE
)
```

processBAM *Runs the OpenMP/C++ based SpliceWiz algorithm*

## Description

These function calls the SpliceWiz C++ routine on one or more BAM files.

The routine is an improved version over the original IRFinder, with OpenMP-based multi-threading and the production of compact "COV" files to record alignment coverage. A SpliceWiz reference built using Build-Reference-methods is required.

After `processBAM()` is run, users should call collateData to collate individual outputs into an experiment / dataset.

BAM2COV creates COV files from BAM files without running `processBAM()`.

See details for performance info.

## Usage

```
BAM2COV(
  bamfiles = "./Unsorted.bam",
  sample_names = "sample1",
  output_path = "./cov_folder",
  n_threads = 1,
  useOpenMP = TRUE,
  overwrite = FALSE,
  verbose = FALSE,
  multiRead = FALSE
)

processBAM(
  bamfiles = "./Unsorted.bam",
  sample_names = "sample1",
  reference_path = "./Reference",
  output_path = "./SpliceWiz_Output",
  n_threads = 1,
  useOpenMP = TRUE,
  overwrite = FALSE,
  run_featureCounts = FALSE,
  verbose = FALSE,
  skipCOVfiles = FALSE,
  multiRead = FALSE
)
```

## Arguments

| | |
|---|---|
| `bamfiles` | A vector containing file paths of 1 or more BAM files |

| | |
|---|---|
| sample_names | The sample names of the given BAM files. Must be a vector of the same length as bamfiles |
| output_path | The output directory of this function |
| n_threads | (default 1) The number of threads to use. See details. |
| useOpenMP | (default TRUE) Whether to use OpenMP. If set to FALSE, BiocParallel will be used if n_threads is set |
| overwrite | (default FALSE) If output files already exist, will not attempt to re-run. If run_featureCounts is TRUE, will not overwrite gene counts of previous run unless overwrite is TRUE. |
| verbose | (default FALSE) Set to TRUE to allow processBAM() to output progress bars and messages |
| multiRead | (default FALSE) Whether SpliceWiz/ompBAM should use one (set to FALSE) or all available threads (set to TRUE) to read BAM files from the storage drive. In SSD drives or high performance computing clusters, setting to TRUE may slightly improve performance, whereas if reading from disk is the speed bottleneck, the default setting FALSE should result in higher performance. |
| reference_path | The directory containing the SpliceWiz reference |
| run_featureCounts | (default FALSE) Whether this function will run Rsubread::featureCounts on the BAM files after counting spliced reads. If so, the output will be saved to "main.FC.Rds in the output_path directory as a list object. |
| skipCOVfiles | (default FALSE) Whether processBAM should skip the production of COV files (containing coverage data). Default is to create COV files unless this is set to TRUE. COV files can be generated separately using BAM2COV |

## Details

Typical run-times for a 100-million paired-end alignment BAM file takes 10 minutes using a single core. Using 8 threads, the runtime is approximately 2-5 minutes, depending on your system's file input / output speeds. Approximately 10 Gb of RAM is used when OpenMP is used. If OpenMP is not used (see below), this memory usage is multiplied across the number of processor threads (i.e. 40 Gb if n_threads = 4).

OpenMP is natively available to Linux / Windows compilers, and OpenMP will be used if useOpenMP is set to TRUE, using multiple threads to process each BAM file. On Macs, if OpenMP is not available at compilation, BiocParallel will be used, processing BAM files simultaneously, with one BAM file per thread.

## Value

Output will be saved to output_path. Output files will be named using the given sample_names. For processBAM():

- sample.txt.gz: The main output file containing the quantitation of IR and splice junctions, as well as QC information

- sample.cov: Contains coverage information in compressed binary. See getCoverage
- main.FC.Rds: A single file containing gene counts for the whole dataset (only if `run_featureCounts == TRUE`)

For `BAM2COV()`:

- sample.cov: Contains coverage information in compressed binary. See getCoverage

## Functions

- `BAM2COV()`: Converts BAM files to COV files without running `processBAM()`
- `processBAM()`: Processes BAM files. Requires a SpliceWiz reference generated by buildRef()

## See Also

Build-Reference-methods collateData isCOV

## Examples

```
# Run BAM2COV, which only produces COV files but does not run `processBAM()`:

bams <- SpliceWiz_example_bams()

BAM2COV(bams$path, bams$sample,
  output_path = file.path(tempdir(), "SpliceWiz_Output"),
  n_threads = 2, overwrite = TRUE
)

# Run processBAM(), which produces:
# - text output of intron coverage and spliced read counts
# - COV files which record read coverages

example_ref <- file.path(tempdir(), "Reference")

buildRef(
    reference_path = example_ref,
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)

bams <- SpliceWiz_example_bams()

processBAM(bams$path, bams$sample,
  reference_path = file.path(tempdir(), "Reference"),
  output_path = file.path(tempdir(), "SpliceWiz_Output"),
  n_threads = 2
)
```

`Run_SpliceWiz_Filters` *Filtering for IR and Alternative Splicing Events*

## Description

These function implements filtering of alternative splicing events, based on customisable criteria. See ASEFilter for details on how to construct SpliceWiz filters

## Usage

```
getDefaultFilters()

applyFilters(se, filters = getDefaultFilters())

runFilter(se, filterObj)
```

## Arguments

| | |
|---|---|
| `se` | the NxtSE object to filter |
| `filters` | A vector or list of one or more ASEFilter objects. If left blank, the SpliceWiz default filters will be used. |
| `filterObj` | A single ASEFilter object. |

## Details

We highly recommend using the default filters, which are as follows:

- (1) Depth filter of 20,
- (2) Participation filter requiring 70% coverage in IR events.
- (3) Participation filter requiring 40% coverage in MXE, SE, A5SS and A3SS events (i.e. Included + Excluded isoforms must cover at least 40% of all junction events across the given region)
- (4) Consistency filter requring log difference of 2 (for skipped exon and mutually exclusive exon events, each junction must comprise at least 1/(2^2) = 1/4 of all reads associated with each isoform). For retained introns, the exon-intron overhangs must not differ by 1/4
- (5) Terminus filter: In alternate first exons, the splice junction must not be shared with another transcript for which it is not its first intron. For alternative last exons, the splice junction must not be shared with another transcript for which it is not its last intron
- (6) ExclusiveMXE filter: For MXE events, the two alternate casette exons must not overlap in their genomic regions
- (7) StrictAltSS filter: For A5SS / A3SS events, the two alternate splice sites must not be interrupted by an intron

In all data-based filters, we require at least 80% samples (`pcTRUE = 80`) to pass this filters from the entire dataset (`minCond = -1`).

Threshold depths for Participation filters:

For IR/RI, Participation filter is only applied for IR events for which the intron depth is above a certain threshold (set by `minDepth`). This avoids the filters running on samples for which there is no IR.

For non-IR ASEs, Participation is only run on events with splice depth (SpliceOver metric) higher than `minDepth`. This avoids filters running on events with low total participation (i.e., (Inc+Exc)/SpliceOver)

Threshold depths for Consistency filters: Consistency filters are only applied for events where the sum of upstream and downstream junction counts surpass a given threshold `minDepth`. This is applied on both included and excluded counts (the latter only applies to MXE). This avoids consistency filters running on events with insufficient junction counts (leading to high variance between up/downstream values).

For an explanation of the various parameters mentioned here, see ASEFilter

## Value

For `runFilter` and `applyFilters`: a vector of type `logical`, representing the rows of NxtSE that should be kept.

For `getDefaultFilters`: returns a list of default recommended filters that should be parsed into `applyFilters`.

## Functions

- `getDefaultFilters()`: Returns a vector of recommended default SpliceWiz filters
- `applyFilters()`: Run a vector or list of ASEFilter objects on a NxtSE object
- `runFilter()`: Run a single filter on a NxtSE object

## See Also

ASEFilter for details describing how to create and assign settings to ASEFilter objects.

## Examples

```
# see ?makeSE on example code of how this object was generated

se <- SpliceWiz_example_NxtSE()

# Get the list of SpliceWiz recommended filters

filters <- getDefaultFilters()

# View a description of what these filters do:

filters

# Filter the NxtSE using the first default filter ("Depth")
```

```
se.depthfilter <- se[runFilter(se, filters[[1]]), ]

# Filter the NxtSE using all four default filters

se.defaultFiltered <- se[applyFilters(se, getDefaultFilters()), ]
```

---

`setSWthreads` *Sets the number of threads used by SpliceWiz*

---

## Description

SpliceWiz uses the computationally efficient packages `fst` and `data.table` to compute file and data operations, respectively. Both packages make use of parallelisation. If excessive number of threads are allocated, it may impact the running of other operations on your system. Use this function to manually allocate the desired number of threads

## Usage

```
setSWthreads(threads = 0)
```

## Arguments

| | |
|---|---|
| `threads` | (default `0`) The number of threads for SpliceWiz to use. Set as `0` to use the recommended number of threads appropriate for the system (approximately half the available threads) |

## Value

Nothing.

## Examples

```
setSWthreads(0)
```

---

`STAR-methods` *STAR wrappers for building reference for STAR, and aligning RNA-sequencing*

---

## Description

These STAR helper / wrapper functions allow users to (1) create a STAR genome reference (with or without GTF), (2) align one or more RNA-seq samples, and (3) calculate regions of low mappability. STAR references can be created using one-step (genome and GTF), or two-step (genome first, then on-the-fly with injected GTF) approaches.

## Usage

```
STAR_version()

STAR_buildRef(
  reference_path,
  STAR_ref_path = file.path(reference_path, "STAR"),
  n_threads = 4,
  overwrite = FALSE,
  sjdbOverhang = 100,
  sparsity = 1,
  also_generate_mappability = FALSE,
  map_depth_threshold = 4,
  additional_args = NULL,
  ...
)

STAR_alignExperiment(
  Experiment,
  STAR_ref_path,
  BAM_output_path,
  n_threads = 4,
  overwrite = FALSE,
  two_pass = FALSE,
  trim_adaptor = "AGATCGGAAG",
  additional_args = NULL
)

STAR_alignReads(
  fastq_1 = c("./sample_1.fastq"),
  fastq_2 = NULL,
  STAR_ref_path,
  BAM_output_path,
  n_threads = 4,
  overwrite = FALSE,
  two_pass = FALSE,
  trim_adaptor = "AGATCGGAAG",
  memory_mode = "NoSharedMemory",
  additional_args = NULL
)

STAR_buildGenome(
  reference_path,
  STAR_ref_path = file.path(reference_path, "STAR"),
  n_threads = 4,
  overwrite = FALSE,
  sparsity = 1,
  also_generate_mappability = FALSE,
  map_depth_threshold = 4,
```

```
  additional_args = NULL,
  ...
)

STAR_loadGenomeGTF(
  reference_path,
  STAR_ref_path,
  STARgenome_output = file.path(tempdir(), "STAR"),
  n_threads = 4,
  overwrite = FALSE,
  sjdbOverhang = 100,
  extraFASTA = "",
  additional_args = NULL
)

STAR_mappability(
  reference_path,
  STAR_ref_path = file.path(reference_path, "STAR"),
  map_depth_threshold = 4,
  n_threads = 4,
  ...
)
```

## Arguments

| | |
|---|---|
| reference_path | The path to the reference. getResources must first be run using this path as its reference_path |
| STAR_ref_path | (Default - the "STAR" subdirectory under reference_path) The directory containing the STAR reference to be used or to contain the newly-generated STAR reference |
| n_threads | The number of threads to run the STAR aligner. |
| overwrite | (default FALSE) For STAR_buildRef, STAR_buildGenome and STAR_loadGenomeGTF - if STAR genome already exists, should it be overwritten. For STAR_alignExperiment and STAR_alignReads - if BAM file already exists, should it be overwritten. |
| sjdbOverhang | (Default = 100) A STAR setting indicating the length of the donor / acceptor sequence on each side of the junctions. Ideally equal to (mate_length - 1). See the STAR aligner manual for details. |
| sparsity | (default 1) Sets STAR's --genomeSAsparseD option. For human (and mouse) genomes, set this to 2 to allow STAR to perform genome generation and mapping using < 16 Gb of RAM, albeit with slightly lower mapping rate (~ 0.1% lower, according to STAR's author). Setting this to higher values is experimental (and not tested) |
| also_generate_mappability | Whether STAR_buildRef() and STAR_buildGenome() also calculate Mappability Exclusion regions. |
| map_depth_threshold | (Default 4) The depth of mapped reads threshold at or below which Mappability |

exclusion regions are defined. See Mappability-methods. Ignored if `also_generate_mappability = FALSE`

`additional_args`
: A character vector of additional arguments to be parsed into STAR. See examples below.

`...`
: Additional arguments to be parsed into `generateSyntheticReads()`. See Mappability-methods.

`Experiment`
: A two or three-column data frame with the columns denoting sample names, forward-FASTQ and reverse-FASTQ files. This can be conveniently generated using findFASTQ

`BAM_output_path`
: The path under which STAR outputs the aligned BAM files. In `STAR_alignExperiment()`, STAR will output aligned BAMS inside subdirectories of this folder, named by sample names. In `STAR_alignReads()`, STAR will output directly into this path.

`two_pass`
: Whether to use two-pass mapping. In `STAR_alignExperiment()`, STAR first-pass will align every sample to generate a list of splice junctions but not BAM files. The junctions are then given to STAR to generate a temporary genome containing information about novel junctions, thereby improving novel junction detection. In `STAR_alignReads()`, STAR will use `--twopassMode Basic`

`trim_adaptor`
: The sequence of the Illumina adaptor to trim via STAR's `--clip3pAdapterSeq` option

`fastq_1`, `fastq_2`
: In STAR_alignReads: character vectors giving the path(s) of one or more FASTQ (or FASTA) files to be aligned. If single reads are to be aligned, omit `fastq_2`

`memory_mode`
: The parameter to be parsed to `--genomeLoad`; either `NoSharedMemory` or `LoadAndKeep` are used.

`STARgenome_output`
: The output path of the created on-the-fly genome

`extraFASTA`
: (default `""`) One or more FASTA files containing spike-in genome sequences (e.g. ERCC, Sequins), as required.

## Details

### Pre-requisites

`STAR_buildRef()` and `STAR_buildGenome()` require prepared genome and gene annotation reference retrieved using getResources, which is run internally by buildRef

`STAR_loadGenomeGTF()` requires the above, and additionally a STAR genome created using `STAR_buildGenome()`

`STAR_alignExperiment()`, `STAR_alignReads()`, and `STAR_mappability()`: requires a `STAR` genome, which can be built using `STAR_buildRef()` or `STAR_buildGenome()` followed by `STAR_loadGenomeGTF()`

### Function Description

For `STAR_buildRef`: this function will create a `STAR` genome reference using the same genome FASTA and gene annotation GTF used to create the SpliceWiz reference. Optionally, it will run `STAR_mappability` if `also_generate_mappability` is set to `TRUE`

For STAR_alignExperiment: aligns a set of FASTQ or paired FASTQ files using the given STAR genome using the STAR aligner. A data.frame specifying sample names and corresponding FASTQ files are required

For STAR_alignReads: aligns a single or pair of FASTQ files to the given STAR genome using the STAR aligner.

For STAR_buildGenome: Creates a STAR genome reference, using ONLY the FASTA file used to create the SpliceWiz reference. This allows users to create a single STAR reference for use with multiple transcriptome (GTF) references (on different occasions). Optionally, it will run STAR_mappability if also_generate_mappability is set to TRUE

For STAR_loadGenomeGTF: Creates an "on-the-fly" STAR genome, injecting GTF from the given SpliceWiz reference_path, setting sjdbOverhang setting, and (optionally) any spike-ins via the extraFASTA parameter. This allows users to create a single STAR reference for use with multiple transcriptome (GTF) references, with different sjdbOverhang settings, and/or spike-ins (on different occasions or for different projects).

For STAR_mappability: this function will first will run generateSyntheticReads, then use the given STAR genome to align the synthetic reads using STAR. The aligned BAM file will then be processed using calculateMappability to calculate the lowly-mappable genomic regions, producing the MappabilityExclusion.bed.gz output file.

## Value

For STAR_version(): The STAR version

For STAR_buildRef(): None

For STAR_alignExperiment(): None

For STAR_alignReads(): None

For STAR_buildGenome(): None

For STAR_loadGenomeGTF(): The path of the on-the-fly STAR genome, typically in the subdirectory "_STARgenome" within the given STARgenome_output directory

For STAR_mappability(): None

## Functions

- STAR_version(): Checks whether STAR is installed, and its version
- STAR_buildRef(): Creates a STAR genome reference, using both FASTA and GTF files used to create the SpliceWiz reference
- STAR_alignExperiment(): Aligns multiple sets of FASTQ files, belonging to multiple samples
- STAR_alignReads(): Aligns a single sample (with single or paired FASTQ or FASTA files)
- STAR_buildGenome(): Creates a STAR genome reference, using ONLY the FASTA file used to create the SpliceWiz reference
- STAR_loadGenomeGTF(): Creates an "on-the-fly" STAR genome, injecting GTF from the given SpliceWiz reference_path, setting sjdbOverhang setting, and (optionally) any spike-ins as extraFASTA
- STAR_mappability(): Calculates lowly-mappable genomic regions using STAR

## See Also

Build-Reference-methods findSamples Mappability-methods

The latest STAR documentation

## Examples

```
# 0) Check that STAR is installed and compatible with SpliceWiz

STAR_version()
## Not run:

# The below workflow illustrates
# 1) Getting the reference resource
# 2) Building the STAR Reference, including Mappability Exclusion calculation
# 3) Building the SpliceWiz Reference, using the Mappability Exclusion file
# 4) Aligning (a) one or (b) multiple raw sequencing samples.


# 1) Reference generation from Ensembl's FTP links

FTP <- "ftp://ftp.ensembl.org/pub/release-94/"

getResources(
    reference_path = "Reference_FTP",
    fasta = paste0(FTP, "fasta/homo_sapiens/dna/",
        "Homo_sapiens.GRCh38.dna.primary_assembly.fa.gz"),
    gtf = paste0(FTP, "gtf/homo_sapiens/",
        "Homo_sapiens.GRCh38.94.chr.gtf.gz")
)

# 2) Generates STAR genome within the SpliceWiz reference. Also generates
# mappability exclusion gzipped BED file inside the "Mappability/" sub-folder

STAR_buildRef(
    reference_path = "Reference_FTP",
    STAR_ref_path = file.path("Reference_FTP", "STAR"),
    n_threads = 8,
    also_generate_mappability = TRUE
)

# 2a) Generates STAR genome of the example SpliceWiz genome.
#     This demonstrates using custom STAR parameters, as the example
#     SpliceWiz genome is ~100k in length,
#     so --genomeSAindexNbases needs to be
#     adjusted to be min(14, log2(GenomeLength)/2 - 1)

getResources(
    reference_path = "Reference_chrZ",
    fasta = chrZ_genome(),
    gtf = chrZ_gtf()
)
```

```
STAR_buildRef(
    reference_path = "Reference_chrZ",
    STAR_ref_path = file.path("Reference_chrZ", "STAR"),
    n_threads = 8,
    additional_args = c("--genomeSAindexNbases", "7"),
    also_generate_mappability = TRUE
)

# 3) Build SpliceWiz reference using the newly-generated
#    Mappability exclusions

#' NB: also specifies to use the hg38 nonPolyA resource

buildRef(reference_path = "Reference_FTP", genome_type = "hg38")

# 4a) Align a single sample using the STAR reference

STAR_alignReads(
    fastq_1 = "sample1_1.fastq", fastq_2 = "sample1_2.fastq",
    STAR_ref_path = file.path("Reference_FTP", "STAR"),
    BAM_output_path = "./bams/sample1",
    n_threads = 8
)

# 4b) Align multiple samples, using two-pass alignment

Experiment <- data.frame(
    sample = c("sample_A", "sample_B"),
    forward = file.path("raw_data", c("sample_A", "sample_B"),
        c("sample_A_1.fastq", "sample_B_1.fastq")),
    reverse = file.path("raw_data", c("sample_A", "sample_B"),
        c("sample_A_2.fastq", "sample_B_2.fastq"))
)

STAR_alignExperiment(
    Experiment = Experiment,
    STAR_ref_path = file.path("Reference_FTP", "STAR"),
    BAM_output_path = "./bams",
    n_threads = 8,
    two_pass = TRUE
)

# - Building a STAR genome (only) reference, and injecting GTF as a
#   subsequent step
#
#   This is useful for users who want to create a single STAR genome, for
#   experimentation with different GTF files.
#   It is important to note that the chromosome names of the genome (FASTA)
#   file and the GTF file needs to be identical. Thus, Ensembl and Gencode
#   GTF files should not be mixed (unless the chromosome GTF names have
#   been fixed)
```

```
# - also set sparsity = 2 to build human genome so that it will fit in
#   16 Gb RAM. NB: this step's RAM usage can be set using the
#   `--limitGenomeGenerateRAM` parameter

STAR_buildGenome(
    reference_path = "Reference_FTP",
    STAR_ref_path = file.path("Reference_FTP", "STAR_genomeOnly"),
    n_threads = 8, sparsity = 2,
    additional_args = c("--limitGenomeGenerateRAM", "16000000000")
)

# - Injecting a GTF into a genome-only STAR reference
#
#   This creates an on-the-fly STAR genome, using a GTF file
#   (derived from a SpliceWiz reference) into a new location.
#   This allows a single STAR reference to use multiple GTFs
#   on different occasions.

STAR_new_ref <- STAR_loadGenomeGTF(
    reference_path = "Reference_FTP",
    STAR_ref_path = file.path("Reference_FTP", "STAR_genomeOnly"),
    STARgenome_output = file.path(tempdir(), "STAR"),
    n_threads = 4,
    sjdbOverhang = 100
)

# This new reference can then be used to align your experiment:

STAR_alignExperiment(
    Experiment = Experiment,
    STAR_ref_path = STAR_new_ref,
    BAM_output_path = "./bams",
    n_threads = 8,
    two_pass = TRUE
)

# Typically, one should `clean up` the on-the-fly STAR reference (as it is
#   large!). If it is in a temporary directory, it will be cleaned up
#   when the current R session ends; otherwise this needs to be done manually:

unlink(file.path(tempdir(), "STAR"), recursive = TRUE)


## End(Not run)
```

---

`theme_white` *ggplot2 themes*

---

## Description

A ggplot theme object for white background figures +/- a legend

## Usage

```
theme_white

theme_white_legend

theme_white_legend_plot_track
```

## Format

An object of class theme (inherits from gg) of length 10.

An object of class theme (inherits from gg) of length 9.

An object of class theme (inherits from gg) of length 10.

## Functions

- theme_white: White theme without figure legend
- theme_white_legend: White theme but with a figure legend (if applicable)
- theme_white_legend_plot_track: White theme with figure legend but without horizontal grid lines. Used internally in PlotGenome

## See Also

plotCoverage

## Examples

```
library(ggplot2)
df <- data.frame(
  gp = factor(rep(letters[1:3], each = 10)),
  y = rnorm(30))
ggplot(df, aes(gp, y)) +
  geom_point() +
  theme_white
```

---

# View-Reference-methods

*View SpliceWiz Reference in read-able data frames*

---

## Description

These functions allow users to construct tables containing SpliceWiz's reference of alternate splicing events, intron retention events, and other relevant data

## Usage

```
viewASE(reference_path)

viewIR(reference_path, directional = TRUE)

viewIntrons(reference_path)

viewIR_NMD(reference_path)

viewExons(reference_path)

viewGenes(reference_path)

viewGO(reference_path)

viewProteins(reference_path)

viewTranscripts(reference_path)
```

## Arguments

| | |
|---|---|
| `reference_path` | The directory containing the SpliceWiz reference |
| `directional` | (default `TRUE`) Whether to view IR events for stranded RNAseq `TRUE` or unstranded protocol `FALSE` |

## Value

A data frame containing the relevant info. See details

## Functions

- `viewASE()`: Outputs summary of alternative splicing events constructed by SpliceWiz
- `viewIR()`: Outputs summary of assessed IRFinde-like IR events, constructed by SpliceWiz
- `viewIntrons()`: Outputs summary of all introns from the annotation, constructed by SpliceWiz
- `viewIR_NMD()`: Outputs information for every intron - whether retention of the intron will convert the transcript to an NMD substrate
- `viewExons()`: Outputs information for every exon from the annotation.
- `viewGenes()`: Outputs information for every gene from the annotation.
- `viewGO()`: Outputs information for every gene from the annotation.
- `viewProteins()`: Outputs information for every protein-coding exon from the annotation.
- `viewTranscripts()`: Outputs information for every transcript from the annotation.

## See Also

Build-Reference-methods

## Examples

```
ref_path <- file.path(tempdir(), "Reference_withGO")
buildRef(
    reference_path = ref_path,
    fasta = chrZ_genome(),
    gtf = chrZ_gtf(),
    ontologySpecies = "Homo sapiens"
)

df <- viewASE(ref_path)

df <- viewIR(ref_path, directional = TRUE)

df <- viewIntrons(ref_path)

df <- viewIR_NMD(ref_path)

df <- viewExons(ref_path)

df <- viewGenes(ref_path)

df <- viewProteins(ref_path)

df <- viewTranscripts(ref_path)

df <- viewGO(ref_path)
```

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