

Package ‘crisprDesign’

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Title Comprehensive design of CRISPR gRNAs for nucleases and base editors

Version 1.15.0

Description Provides a comprehensive suite of functions to design and annotate CRISPR guide RNA (gRNAs) sequences. This includes on- and off-target search, on-target efficiency scoring, off-target scoring, full gene and TSS contextual annotations, and SNP annotation (human only). It currently supports five types of CRISPR modalities (modes of perturbations): CRISPR knockout, CRISPR activation, CRISPR inhibition, CRISPR base editing, and CRISPR knockdown. All types of CRISPR nucleases are supported, including DNA- and RNA-target nucleases such as Cas9, Cas12a, and Cas13d. All types of base editors are also supported. gRNA design can be performed on reference genomes, transcriptomes, and custom DNA and RNA sequences. Both unpaired and paired gRNA designs are enabled.

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Contents

| | |
|---------------------------------------|----|
| addCompositeScores | 3 |
| addConservationScores | 4 |
| addDistanceToTss | 6 |
| addEditedAlleles | 7 |
| addEditingSites | 8 |
| addExonTable | 9 |
| addGeneAnnotation | 10 |
| addIsoformAnnotation | 13 |
| addNtcs | 14 |
| addOffTargetScores | 15 |
| addOnTargetScores | 16 |
| addOpsBarcodes | 18 |
| addPamScores | 18 |
| addPfamDomains | 19 |
| addReinitiationFlag | 20 |
| addRepeats | 21 |
| addRestrictionEnzymes | 22 |
| addSequenceFeatures | 24 |
| addSNPAnnotation | 25 |
| addSpacerAlignments | 27 |
| addTssAnnotation | 32 |
| addTxTable | 33 |
| completeSpacers | 34 |
| convertToMinMaxGRanges | 36 |
| convertToProtospacerGRanges | 37 |
| crisprNuclease | 37 |
| designCompleteAnnotation | 43 |
| designOpsLibrary | 45 |
| findSpacerPairs | 46 |
| findSpacers | 48 |
| flattenGuideSet | 50 |
| getBarcodeDistanceMatrix | 51 |
| getConsensusIsoform | 52 |
| getMrnaSequences | 53 |
| getPreMrnaSequences | 53 |
| getTssObjectFromTxObject | 54 |
| getTxDb | 55 |
| getTxInfoDataFrame | 56 |
| grListExample | 57 |

| | |
|---|-----------|
| grRepeatsExample | 57 |
| GuideSet2DataFrames | 58 |
| guideSetExample | 59 |
| guideSetExampleFullAnnotation | 59 |
| guideSetExampleWithAlignments | 60 |
| pamOrientation | 60 |
| preparePfamTable | 62 |
| queryTss | 63 |
| queryTxObject | 64 |
| rankSpacers | 65 |
| reexports | 66 |
| removeRepeats | 66 |
| removeSpacersWithSecondaryTargets | 67 |
| snpObjectExample | 68 |
| tssObjectExample | 69 |
| TxDB2GRangesList | 69 |
| updateOpsLibrary | 70 |
| validateOpsLibrary | 71 |
| Index | 73 |

addCompositeScores *Add on-target composite score to a [GuideSet](#) object.*

Description

Add on-target composite score to a [GuideSet](#) object.

Usage

```
addCompositeScores(object, ...)
```

```
## S4 method for signature 'GuideSet'
```

```
addCompositeScores(
  object,
  methods = c("ruleset1", "ruleset3", "lindel", "deephf", "enpamgb", "casrxrf",
             "crisprater", "crisprscan"),
  scoreName = "score_composite"
)
```

```
## S4 method for signature 'PairedGuideSet'
```

```
addCompositeScores(
  object,
  methods = c("ruleset1", "ruleset3", "lindel", "deephf", "enpamgb", "crisprater",
             "crisprscan", "casrxrf"),
  scoreName = "score_composite"
)
```

```
## S4 method for signature 'NULL'
```

```
addCompositeScores(object)
```

Arguments

| | |
|-----------|---|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| methods | Character vector specifying method names for on-target efficiency prediction algorithms to be used to create the composite score. Note that the specified scores must be added first to the object using <code>addOnTargetScores</code> . |
| scoreName | String specifying the name of the composite score to be used as a column name. Users can choose whatever they like. Default is "score_composite". |

Details

The function creates a composite score across a specified list of on-target scores by first transforming each individual score into a rank, and then taking the average rank across all specified methods. This can improve on-target activity prediction robustness. A higher score indicates higher on-target activity.

Value

guideSet with column specified by scoreName appended in `mcols(guideSet)`.

Author(s)

Jean-Philippe Fortin

See Also

[addOnTargetScores](#) to add on-target scores.

Examples

```
gs <- findSpacers("CCAACATAGTGAAACCACGTCTCTATAAAGAATAAAAAATTAGCCGGGTTA")
gs <- addOnTargetScores(gs, methods=c("ruleset1", "crisprater"))
gs <- addCompositeScores(gs, methods=c("ruleset1", "crisprater"))
```

`addConservationScores` *Add on-target composite score to a [GuideSet](#) object.*

Description

Add on-target composite score to a [GuideSet](#) object.

Usage

```
addConservationScores(object, ...)

## S4 method for signature 'GuideSet'
addConservationScores(
  object,
  conservationFile,
  nucExtension = 9,
```

```
    fun = c("mean", "max"),
    scoreName = "score_conservation"
)

## S4 method for signature 'PairedGuideSet'
addConservationScores(
  object,
  conservationFile,
  nucExtension = 9,
  fun = c("mean", "max"),
  scoreName = "score_conservation"
)

## S4 method for signature 'NULL'
addConservationScores(object)
```

Arguments

| | |
|------------------|---|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| conservationFile | String specifying the BigWig file containing conservation scores. |
| nucExtension | Number of nucleotides to include on each side of the cut site to calculate the conservation score. 9 by default. The region will have $(2 * \text{nucExtension} + 1)$ nucleotides in total. |
| fun | String specifying the function to use to calculate the final conservation score in the targeted region. Must be either "mean" (default) or "max". |
| scoreName | String specifying the name of the conservation score to be used as a column name. Users can choose whatever they like. Default is "score_conservation". |

Details

The function creates a conservation score for each gRNA by using the max, or average, conservation score in the genomic region where the cut occurs. A BigWig file storing conservation scores must be provided. Such files can be downloaded from the UCSC genome browser. See vignette for more information.

Value

guideSet with column specified by scoreName appended in `mcols(guideSet)`.

Author(s)

Jean-Philippe Fortin

addDistanceToTss *Add distance to TSS for a specified TSS id*

Description

Add distance to TSS for a specified TSS id.

Usage

```
addDistanceToTss(object, ...)  
  
## S4 method for signature 'GuideSet'  
addDistanceToTss(object, tss_id)  
  
## S4 method for signature 'PairedGuideSet'  
addDistanceToTss(object, tss_id)
```

Arguments

| | |
|--------|--|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| tss_id | String specifying TSS id to calculate the distance. The column <code>tssAnnotation(object)\$tss_id</code> will be used to search for the TSS id. |

Value

A [GuideSet](#) object or a [PairedGuideSet](#) object with an additional metadata column called `distance_to_tss` reporting the distance (in nucleotides) between the TSS position of the TSS specified by `tss_id` and the protospacer position. The `pam_site` coordinate is used as the representative position of protospacer sequences.

Note that a TSS annotation must be available in the object. A TSS annotation can be added using `addTssAnnotation`.

Author(s)

Jean-Philippe Fortin

See Also

[addTssAnnotation](#) to add TSS annotation.

Examples

```
data(guideSetExampleFullAnnotation)  
tss_id <- "ENSG00000120645_P1"  
gs <- guideSetExampleFullAnnotation  
gs <- addDistanceToTss(gs, tss_id)
```

addEditedAlleles *To add edited alleles for a CRISPR base editing GuideSet*

Description

To add edited alleles for a CRISPR base editing GuideSet.

Usage

```
addEditedAlleles(
  guideSet,
  baseEditor,
  editingWindow = NULL,
  substitutions = NULL,
  nMaxAlleles = 100,
  minEditingWeight = 0,
  minMutationScore = 0.3,
  addFunctionalConsequence = TRUE,
  addSummary = TRUE,
  txTable = NULL,
  verbose = TRUE
)
```

Arguments

| | |
|--------------------------|--|
| guideSet | A GuideSet object. |
| baseEditor | A BaseEditor object. |
| editingWindow | A numeric vector of length 2 specifying start and end positions of the editing window with respect to the PAM site. If NULL (default), the editing window of the BaseEditor object will be considered. |
| substitutions | A character vector indicating the substitutions to be considered in predicting the edited alleles. If NULL (default), all substitutions are considered. |
| nMaxAlleles | Maximum number of edited alleles to report for each gRNA. Alleles from high to low scores. 100 by default. |
| minEditingWeight | Numeric value indicating the minimum editing weight required for an edited allele to be listed. Default of 0. |
| minMutationScore | Numeric value indicating the minimum editing score that an allele must have to call a mutation. Default of "0.3". |
| addFunctionalConsequence | Should variant classification of the edited alleles be added? TRUE by default. If TRUE, txTable must be provided. |
| addSummary | Should a summary of the variant classification be added to the metadata columns of the guideSet object? TRUE by default. |
| txTable | Table of transcript-level nucleotide and amino acid information needed for variant classification. Usually returned by getTxInfoDataFrame . |
| verbose | Should messages be printed to console? TRUE by default. |

Value

The original guideSet object with an additional metadata column (editedAlleles) storing the annotated edited alleles. The edited alleles are always reported from 5' to 3' direction on the strand corresponding to the gRNA strand.

Author(s)

Jean-Philippe Fortin

Examples

```
data(BE4max, package="crisprBase")
data(grListExample, package="crisprDesign")
library(BSgenome.Hsapiens.UCSC.hg38)
bsgenome <- BSgenome.Hsapiens.UCSC.hg38
gr <- queryTxObject(grListExample,
                    featureType="cds",
                    queryColumn="gene_symbol",
                    queryValue="IQSEC3")
gs <- findSpacers(gr[1],
                 crisprNuclease=BE4max,
                 bsgenome=bsgenome)
gs <- unique(gs)
gs <- gs[1:2] # For the sake of time

# Getting transcript info:
txid="ENST00000538872"
txTable <- getTxInfoDataFrame(tx_id=txid,
                              txObject=grListExample,
                              bsgenome=bsgenome)

#Adding alleles:
editingWindow <- c(-20,-8)
gs <- addEditedAlleles(gs,
                      baseEditor=BE4max,
                      txTable=txTable,
                      editingWindow=editingWindow,
                      substitutions="C2T")
```

addEditingSites

Add optimal editing site for base editing gRNAs.

Description

Add optimal editing site for base editing gRNAs.

Usage

```
addEditingSites(object, ...)

## S4 method for signature 'GuideSet'
addEditingSites(object, substitution)
```

```
## S4 method for signature 'PairedGuideSet'
addEditingSites(object, substitution)
```

```
## S4 method for signature 'NULL'
addEditingSites(object)
```

Arguments

| | |
|--------------|---|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| substitution | String indicating which substitution should be used to estimate the optimal editing position. E.g. "C2T" will return the optimal editing position for C to T editing. |

Value

An updated object with a column `editing_site` added to `mcols(object)`.

Author(s)

Jean-Philippe Fortin

| | |
|--------------|---|
| addExonTable | <i>Add a gene-specific exon table to a GuideSet object.</i> |
|--------------|---|

Description

Add a gene-specific exon table to a [GuideSet](#) object.
 Add a gene-specific exon table to a [GuideSet](#) object.

Usage

```
addExonTable(
  guideSet,
  gene_id,
  txObject,
  valueColumn = "percentCDS",
  useConsensusIsoform = FALSE
)
```

Arguments

| | |
|---------------------|--|
| guideSet | A GuideSet object or a PairedGuideSet object. |
| gene_id | String specifying gene ID. |
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList to provide a gene model annotation. |
| valueColumn | String specifying column in <code>geneAnnotation(guideSet)</code> to use as values in the output exon table. |
| useConsensusIsoform | Should a consensus isoform be used to annotate exons? FALSE by default. If TRUE, the isoform constructed by <code>getConsensusIsoform</code> will be used. |

Value

A [GuideSet](#) object with a "exonTable" DataFrame stored in `mcols(guideSet)`. The entries in the DataFrame correspond to the values specified by `valueColumn`. Rows correspond to gRNAs in the `GuideSet`, columns correspond to all exons found in `txObject` for gene specified by `gene_id`.

Author(s)

Jean-Philippe Fortin

See Also

[addGeneAnnotation](#) to add gene annotation and [addTxTable](#) to add a transcript table.

Examples

```
if (interactive()){
  data(guideSetExample, package="crisprDesign")
  data(grListExample, package="crisprDesign")
  guideSet <- addGeneAnnotation(guideSetExample,
                               txObject=grListExample)
  guideSet <- addExonTable(guideSet,
                           gene_id="ENSG00000120645",
                           txObject=grListExample)

  guideSet$exonTable
}
```

`addGeneAnnotation` *Add gene context annotation to a [GuideSet](#) object*

Description

Add gene context annotation to spacer sequence stored in a [GuideSet](#) object

Usage

```
addGeneAnnotation(object, ...)
```

```
## S4 method for signature 'GuideSet'
addGeneAnnotation(
  object,
  txObject,
  anchor = c("cut_site", "pam_site", "editing_site"),
  ignore_introns = TRUE,
  ignore_strand = TRUE,
  addPfam = FALSE,
  mart_dataset = NULL
)
```

```
## S4 method for signature 'PairedGuideSet'
addGeneAnnotation(
```

```

object,
txObject,
anchor = c("cut_site", "pam_site", "editing_site"),
ignore_introns = TRUE,
ignore.strand = TRUE,
addPfam = FALSE,
mart_dataset = NULL
)

```

Arguments

| | |
|----------------|---|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList to provide a gene model annotation. |
| anchor | String specifying which relative coordinate of gRNAs should be used to locate gRNAs within gene. Must be either "cut_site", "pam_site" or "editing_site". |
| ignore_introns | Should gene introns be ignored when annotating? TRUE by default. |
| ignore.strand | Should gene strand be ignored when annotating? TRUE by default. |
| addPfam | Should Pfam domains annotation be added? FALSE by default. If set to TRUE, biomaRt must be installed. |
| mart_dataset | String specifying dataset to be used by biomaRt for Pfam domains annotation . E.g. "hsapiens_gene_ensembl". |

Details

For DNA-targeting nucleases, the different columns stored in `mcols(guideSet)[["geneAnnotation"]]` are:

- tx_id Transcript ID.
- gene_symbol Gene symbol.
- gene_id Gene ID.
- protein_id Protein ID.
- ID gRNA ID.
- pam_site gRNA PAM site coordinate.
- cut_site gRNA cut site coordinate.
- chr gRNA chromosome name.
- strand gRNA strand.
- cut_cds Is the gRNA cut site located within the coding sequence (CDS) of the targeted isoform?
- cut_fiveUTRs Is the gRNA cut site located within the 5'UTR of the targeted isoform?
- cut_threeUTRs Is the gRNA cut site located within the 3'UTR of the targeted isoform?
- cut_introns Is the gRNA cut site located within an intron of the targeted isoform?
- percentCDS Numeric value to indicate the relative position of the cut site with respect to the start of the CDS sequence when cut_cds is TRUE. The relative position is expressed as a percentage from the total length of the CDS.

- **percentTx** Numeric value to indicate the relative position of the cut site with respect to the start of the mRNA sequence (therefore including 5' UTR). The relative position is expressed as a percentage from the total length of the mRNA sequence.
- **aminoAcidIndex** If `cut_cds` is TRUE, integer value indicating the amino acid index with respect to the start of the protein.
- **downstreamATG** Number of potential reinitiation sites (ATG codons) downstream of the gRNA cut site, within 85 amino acids.
- **nIsoforms** Numeric value indicating the number of isoforms targeted by the gRNA.
- **totalIsoforms** Numeric value indicating the total number of isoforms existing for the gene targeted by the gRNA and specified in `gene_id`.
- **percentIsoforms** Numeric value indicating the percentage of isoforms for the gene specified in `gene_id` targeted by the gRNA. Equivalent to $nIsoforms/totalIsoforms*100$.
- **isCommonExon** Logical value to indicate whether or not the gRNA is targeting an exon common to all isoforms.
- **nCodingIsoforms** Numeric value indicating the number of coding isoforms targeted by the gRNA. 5' UTRs and 3' UTRs are excluded.
- **totalCodingIsoforms** Numeric value indicating the total number of coding isoforms existing for the gene targeted by the gRNA and specified in `gene_id`.
- **percentCodingIsoforms** Numeric value indicating the percentage of coding isoforms for the gene specified in `gene_id` targeted by the gRNA. Equivalent to $nCodingIsoforms/totalCodingIsoforms*100$. 5' UTRs and 3' UTRs are excluded.
- **isCommonCodingExon** Logical value to indicate whether or not the gRNA is targeting an exon common to all coding isoforms.

Value

A [GuideSet](#) object with a "geneAnnotation" list column stored in `mcols(guideSet)`. See details section for a description of the different gene annotation columns.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

See Also

[addTssAnnotation](#) to add TSS annotation, and [geneAnnotation](#) to retrieve an existing gene annotation.

Examples

```
data(guideSetExample, package="crisprDesign")
data(grListExample, package="crisprDesign")
guideSet <- addGeneAnnotation(guideSetExample[1:6],
                             txObject=grListExample)

# To access a gene annotation already added:
ann <- geneAnnotation(guideSet)
```

addIsoformAnnotation *Add isoform-specific annotation to a [GuideSet](#) object*

Description

Add isoform-specific annotation to a [GuideSet](#) object.

Usage

```
addIsoformAnnotation(object, ...)  
  
## S4 method for signature 'NULL'  
addDistanceToTss(object)  
  
## S4 method for signature 'GuideSet'  
addIsoformAnnotation(object, tx_id)  
  
## S4 method for signature 'PairedGuideSet'  
addIsoformAnnotation(object, tx_id)  
  
## S4 method for signature 'NULL'  
addIsoformAnnotation(object)
```

Arguments

| | |
|--------|--|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| tx_id | String specifying Ensembl ID for the isoform transcript of interested. E.g. "ENST00000311936". |

Value

A [GuideSet](#) object or a [PairedGuideSet](#) object with the following added columns: percentCDS, percentCodingIsoforms, and isCommonCodingExon. The column values are specific to the transcript specified by tx_id. The percentCDS column indicates at what percentage of the coding sequence the gRNA is cutting. The column percentCodingIsoforms indicates the percentage of coding isoforms that are targeted by the gRNA. The column isCommonCodingExon indicates whether or not the exon targeted by the gRNA is common to all isoforms for the gene.

Author(s)

Jean-Philippe Fortin

Examples

```
data(guideSetExampleFullAnnotation)  
tx_id <- "ENST00000538872"  
gs <- guideSetExampleFullAnnotation  
gs <- addIsoformAnnotation(gs, tx_id)
```

addNtcs *Add non-targeting control (NTC) sequences to [GuideSet](#)*

Description

Add non-targeting control (NTC) sequences to a [GuideSet](#) object.

Usage

```
addNtcs(object, ...)

## S4 method for signature 'GuideSet'
addNtcs(object, ntcs)

## S4 method for signature 'PairedGuideSet'
addNtcs(object, ntcs)

## S4 method for signature 'NULL'
addNtcs(object, ...)
```

Arguments

| | |
|--------|---|
| object | A GuideSet or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| ntcs | A named character vector of NTC sequences. Sequences must consist of appropriate DNA or RNA bases, and have the same spacer length as spacers in object. Vector names are assigned as IDs and seqlevels, and must be unique and distinct from IDs and seqnames present in object. |

Details

NTC sequences are appended as spacers to the [GuideSet](#) object. Each NTC sequence is assigned to its own "chromosome" in the `ntc` genome, as reflected in the [Seqinfo](#) of the resulting [GuideSet](#) object. As placeholder values, NTC ranges are set to \emptyset and strands set to $*$.

All annotation for NTC spacers appended to object are set to NA or empty list elements. To annotate NTC spacers, you must call the appropriate function after adding NTCs to the [GuideSet](#) object.

Value

The original object with appended `ntcs` spacers. Pre-existing annotation in object will be set to NA or empty list elements for appended NTC spacers.

Examples

```
set.seed(1000)
data(guideSetExample, package="crisprDesign")
ntcs <- vapply(1:4, function(x){
  seq <- sample(c("A", "C", "G", "T"), 20, replace=TRUE)
  paste0(seq, collapse="")
}, FUN.VALUE=character(1))
names(ntcs) <- paste0("ntc_", 1:4)
```

```
gs <- addNtcs(guideSetExample, ntcs)
gs
```

addOffTargetScores *Add CFD and MIT scores to a [GuideSet](#) object.*

Description

Add CFD and MIT off-target scores to a [GuideSet](#) object. Both the CFD and MIT methods are available for the SpCas9 nuclease. The CFD method is also available for the CasRx nuclease. Other nucleases are currently not supported.

Usage

```
addOffTargetScores(object, ...)

## S4 method for signature 'GuideSet'
addOffTargetScores(object, max_mm = 2, includeDistance = TRUE, offset = 0)

## S4 method for signature 'PairedGuideSet'
addOffTargetScores(object, max_mm = 2, includeDistance = TRUE, offset = 0)

## S4 method for signature 'NULL'
addOffTargetScores(object)
```

Arguments

| | |
|-----------------|--|
| object | A GuideSet object or a PairedGuideSet object. <code>crisprNuclease(object)</code> must be either using SpCas9 or CasRx. |
| ... | Additional arguments, currently ignored. |
| max_mm | The maximum number of mismatches between the spacer sequence and the protospacer off-target sequence to be considered in the off-target score calculations. Off-targets with a number of mismatches greater than <code>max_mm</code> will be excluded; this is useful if one wants to avoid the aggregated off-target scores to be driven by a large number of off-targets that have low probability of cutting. |
| includeDistance | Should a distance penalty for the MIT score be included? TRUE by default. |
| offset | Numeric value specifying an offset to add to the denominator when calculating the aggregated score (inverse summation formula). 0 by default. |

Details

See the [crisprScore](#) package for a description of the different off-target scoring methods.

Value

A [GuideSet](#) or a [PairedGuideSet](#) object with added scores. The alignments annotation returned by `alignments(object)` will have additional column storing off-target scores. Those scores representing the off-target score for each gRNA and off-target pair. For SpCas9, a column containing an aggregated specificity off-target score for each scoring method is added to the metadata columns obtained by `mcols(object)`.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

See Also

link{addOnTargetScores} to add on-target scores.

Examples

```
data(guideSetExampleWithAlignments, package="crisprDesign")
gs <- guideSetExampleWithAlignments
gs <- addOffTargetScores(gs)
```

addOnTargetScores *Add on-target scores to a [GuideSet](#) object.*

Description

Add on-target scores to a [GuideSet](#) object for all methods available in the **crisprScore** package for a given CRISPR nuclease. Requires **crisprScore** package to be installed.

Usage

```
addOnTargetScores(object, ...)

## S4 method for signature 'GuideSet'
addOnTargetScores(
  object,
  enzyme = c("WT", "ESP", "HF"),
  promoter = c("U6", "T7"),
  tracrRNA = c("Hsu2013", "Chen2013"),
  directRepeat = "aaccctaccaactggtcggggtttgaaac",
  binaries = NULL,
  methods = c("ruleset1", "ruleset3", "lindel", "deephf", "enpamgb", "casrxrf",
    "crisprater", "crisprscan"),
  condaEnv = NULL
)

## S4 method for signature 'PairedGuideSet'
addOnTargetScores(
  object,
  enzyme = c("WT", "ESP", "HF"),
  promoter = c("U6", "T7"),
  tracrRNA = c("Hsu2013", "Chen2013"),
  directRepeat = "aaccctaccaactggtcggggtttgaaac",
  binaries = NULL,
  methods = c("ruleset1", "ruleset3", "lindel", "deephf", "enpamgb", "crisprater",
    "crisprscan", "casrxrf"),
  condaEnv = NULL
)
```

```
## S4 method for signature 'NULL'
addOnTargetScores(object)
```

Arguments

| | |
|--------------|--|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| enzyme | Character string specifying the Cas9 variant to be used for DeepHF scoring. Wildtype Cas9 (WT) by default. See details below. |
| promoter | Character string specifying promoter used for expressing sgRNAs for wildtype Cas9 (must be either "U6" or "T7") for DeepHF scoring. "U6" by default. |
| tracrRNA | String specifying which tracrRNA is used for SpCas9. Must be either "Hsu2013" (default) or "Chen2013". Only used for the RuleSet3 method. |
| directRepeat | String specifying the direct repeat used in the CasRx construct. |
| binaries | Named list of paths for binaries needed for CasRx-RF. Names of the list must be "RNAfold", "RNAhybrid", and "RNAplfold". Each list element is a string specifying the path of the binary. If NULL (default), binaries must be available on the PATH. |
| methods | Character vector specifying method names for on-target efficiency prediction algorithms. |
| condaEnv | String specifying the path of the conda environment needed to run the scoring calculations. See the crisprScore vignette for instructions on how to build the environment. |

Details

See [crisprScore](#) package for a description of each score.

Value

guideSet with columns of on-target scores appended in `mcols(guideSet)`.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

See Also

[addOffTargetScores](#) to add off-target scores.

Examples

```
if (interactive()){
  gs <- findSpacers("CCAACATAGTGAAACCACGTCTCTATAAAGAATAAAAAATTAGCCGGGTTA")
  gs <- addOnTargetScores(gs)
}
```

addOpsBarcodes *Add optical pooled screening (OPS) barcodes*

Description

Add optical pooled screening (OPS) barcodes.

Usage

```
addOpsBarcodes(guideSet, n_cycles = 9, rt_direction = c("5prime", "3prime"))
```

Arguments

| | |
|--------------|--|
| guideSet | A GuideSet object. |
| n_cycles | Integer specifying the number of sequencing cycles used in the in situ sequencing. This effectively determines the length of the barcodes to be used for sequencing. |
| rt_direction | String specifying from which direction the reverse transcription of the gRNA spacer sequence will occur. Must be either "5prime" or "3prime". "5prime" by default. |

Value

The original guideSet object with an additional column opsBarcode stored in mcols(guideSet). The column is a DNAStrngSet storing the OPS barcode.

Author(s)

Jean-Philippe Fortin

Examples

```
data(guideSetExample, package="crisprDesign")
guideSetExample <- addOpsBarcodes(guideSetExample)
```

addPamScores *Add PAM scores to a [GuideSet](#) object.*

Description

Add PAM scores to a [GuideSet](#) object based on the [CrisprNuclease](#) object stored in the [GuideSet](#) object. PAM scores indicate nuclease affinity (recognition) to different PAM sequences. A score of 1 indicates a PAM sequence that is fully recognized by the nuclease.

Usage

```
addPamScores(object, ...)

## S4 method for signature 'GuideSet'
addPamScores(object)

## S4 method for signature 'PairedGuideSet'
addPamScores(object)

## S4 method for signature 'NULL'
addPamScores(object)
```

Arguments

```
object      A GuideSet or a PairedGuideSet object.
...         Additional arguments, currently ignored.
```

Value

guideSet with an appended score_pam column in mcols(guideSet).

Author(s)

Jean-Philippe Fortin

Examples

```
# Using character vector as input:
data(enAsCas12a, package="crisprBase")
gs <- findSpacers("CCAACATAGTGAAACCACGTCTCTATAAAGAATACAAAAAATTAGCCGGGTGTTA",
                 canonical=FALSE,
                 crisprNuclease=enAsCas12a)
gs <- addPamScores(gs)
```

| | |
|----------------|---|
| addPfamDomains | <i>Add Pfam domains annotation to GuideSet object</i> |
|----------------|---|

Description

Add Pfam domains annotation to [GuideSet](#) object.

Usage

```
addPfamDomains(object, ...)

## S4 method for signature 'GuideSet'
addPfamDomains(object, pfamTable)

## S4 method for signature 'PairedGuideSet'
addPfamDomains(object, pfamTable)
```

```
## S4 method for signature 'NULL'
addPfamDomains(object)
```

Arguments

object A [GuideSet](#) object or a [PairedGuideSet](#) object.
 ... Additional arguments, currently ignored.
 pfamTable A [DataFrame](#) obtained using [preparePfamTable](#).

Details

In order to call this function, the object must contain a gene annotation by calling first [addGeneAnnotation](#).

Value

An updated object with a column pfam added to `geneAnnotation(object)`.

Author(s)

Jean-Philippe Fortin

See Also

See [preparePfamTable](#) to prepare the Pfam domain DataFrame object, and see [addGeneAnnotation](#) to add a gene annotation to the object.

addReinitiationFlag *Add a logical flag for gRNAs leading to potential reinitiation*

Description

Add a logical flag for gRNAs leading to potential reinitiation.

Usage

```
addReinitiationFlag(
  guideSet,
  tx_id,
  grnaLocationUpperLimit = 150,
  cdsCutoff = 0.2
)
```

Arguments

guideSet A [GuideSet](#) object.
 tx_id String specifying Ensembl ID for the isoform transcript of interested. E.g. "ENST00000311936".
 grnaLocationUpperLimit
 Integer value specifying the number of nucleotides upstream of the start of the CDS in which to search for problematic gRNAs. Default value is 150. gRNAs beyond this value will not be flagged.

cdsCutoff Numeric value between 0 and 1 to specify the percentage of the CDS in which to search for problematic gRNAs. Default is 0.20. gRNAs beyond this value will not be flagged.

Value

The original object with an appended column `reinitiationFlag` with logical values. A TRUE value indicates a gRNA in proximity of a potential reinitiation site, and therefore should be avoided.

Author(s)

Jean-Philippe Fortin

addRepeats *Annotate a [GuideSet](#) object with repeat elements*

Description

Add an annotation column to a [GuideSet](#) object that identifies spacer sequences overlapping repeat elements.

Usage

```
addRepeats(object, ...)

## S4 method for signature 'GuideSet'
addRepeats(object, gr.repeats = NULL, ignore.strand = TRUE)

## S4 method for signature 'PairedGuideSet'
addRepeats(object, gr.repeats = NULL, ignore.strand = TRUE)

## S4 method for signature 'NULL'
addRepeats(object)
```

Arguments

`object` A [GuideSet](#) object or a [PairedGuideSet](#) object.
`...` Additional arguments, currently ignored.
`gr.repeats` A [GRanges](#) object containing repeat elements regions.
`ignore.strand` Should gene strand be ignored when annotating? TRUE by default.

Value

`guideSet` with an `inRepeats` column appended in `mcols(guideSet)` that signifies whether the spacer sequence overlaps a repeat element.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

See Also

link{removeRepeats}.

Examples

```
data(guideSetExample, package="crisprDesign")
data(grRepeatsExample, package="crisprDesign")
guideSet <- addRepeats(guideSetExample,
                      gr.repeats=grRepeatsExample)
```

addRestrictionEnzymes *Restriction enzyme recognition sites in spacer sequences*

Description

Add restriction site enzymes annotation.

Usage

```
addRestrictionEnzymes(object, ...)

## S4 method for signature 'GuideSet'
addRestrictionEnzymes(
  object,
  enzymeNames = NULL,
  patterns = NULL,
  includeDefault = TRUE,
  flanking5 = "ACCG",
  flanking3 = "GTTT"
)

## S4 method for signature 'PairedGuideSet'
addRestrictionEnzymes(
  object,
  enzymeNames = NULL,
  patterns = NULL,
  includeDefault = TRUE,
  flanking5 = "ACCG",
  flanking3 = "GTTT"
)

## S4 method for signature 'NULL'
addRestrictionEnzymes(object)
```

Arguments

| | |
|-------------|--|
| object | A GuideSet or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| enzymeNames | Character vector of enzyme names. |

addSequenceFeatures *Add spacer sequence feature annotation columns to a [GuideSet](#) object*

Description

Add spacer sequence feature annotation columns, such as GC content, homopolymers, and hairpin predictions, to a [GuideSet](#) object.

Usage

```
addSequenceFeatures(object, ...)

## S4 method for signature 'GuideSet'
addSequenceFeatures(
  object,
  addHairpin = FALSE,
  backbone = "AGGCTAGTCCGT",
  tp53 = TRUE,
  ...
)

## S4 method for signature 'PairedGuideSet'
addSequenceFeatures(
  object,
  addHairpin = FALSE,
  backbone = "AGGCTAGTCCGT",
  tp53 = TRUE,
  ...
)

## S4 method for signature 'NULL'
addSequenceFeatures(object, ...)
```

Arguments

| | |
|------------|---|
| object | A GuideSet or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| addHairpin | Whether to include predicted hairpin formation via sequence complementarity. FALSE by default. See details. |
| backbone | Backbone sequence in the guide RNA that is susceptible to hairpin formation with a complementary region in the spacer sequence. |
| tp53 | Should TP53-related toxicity features be added? TRUE by default. See details. |

Details

The addHairpin argument set to TRUE will indicate which spacers are predicted to form internal hairpins. Such hairpins can happen when there is a palindromic sequence within the spacer having arms of ≥ 4 nt and $\geq 50\%$ GC content, and are separated by a loop of ≥ 4 nt. Backbone hairpin formation is predicted when the spacer and backbone share a complementary sequence of ≥ 5 nt and

$\geq 50\%$ GC content. The argument backbone allows users to specify the vector backbone sequence directly downstream of the spacer sequence.

The tp53 argument set to TRUE will add sequence-based features that have been reported to make SpCas9 gRNAs toxic for cells with wildtype TP53 (see <https://doi.org/10.1038/s41467-022-32285-1>). Currently, only one feature is reported and consists of the extended NNGG PAM sequence (1 nucleotide + PAM sequence) for SpCas9. gRNAs with extended CNGG PAM sequences, and in particular CCGG, should be avoided.

Value

The original object with the following columns appended to `mcols(object)`:

- `percentGC` — percent GC content
- `polyA`, `polyC`, `polyG`, `polyT` — presence of homopolymers of 4nt or longer
- `selfHairpin` — prediction of hairpin formation within the spacer sequence via self-complementarity if `addHairpin` is TRUE.
- `backboneHairpin` — prediction of hairpin formation with the backbone sequence via complementarity if `addHairpin` is TRUE.
- `NNGG` — extended PAM sequence for SpCas9 if `tp53` is TRUE corresponding to one nucleotide upstream of the PAM sequence followed by the PAM sequence itself.

Examples

```
custom_seq <- c("ATTTCGGAGGCGGAGAGGCGGGAGGAGCG")
data(SpCas9, package="crisprBase")
guideSet <- findSpacers(custom_seq, crisprNuclease=SpCas9)
guideSet <- addSequenceFeatures(guideSet)
```

| | |
|------------------|--|
| addSNPAnnotation | <i>Add SNP annotation to a GuideSet object</i> |
|------------------|--|

Description

Add SNP annotation to a [GuideSet](#) object. Only available for sgRNAs designed for human genome.

Usage

```
addSNPAnnotation(object, ...)

## S4 method for signature 'NULL'
addGeneAnnotation(object)

## S4 method for signature 'GuideSet'
addSNPAnnotation(object, snpObject, maf = 0.01)

## S4 method for signature 'PairedGuideSet'
addSNPAnnotation(object, snpObject, maf = 0.01)

## S4 method for signature 'NULL'
addSNPAnnotation(object)
```

Arguments

| | |
|-----------|--|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| snpObject | Either a character string specifying a path to a VCF file or a GRanges object. |
| maf | Minimum minor allele frequency to report (for a least one source among 1000Genomes and TOPMED). Must be between 0 and 1 (exclusive). |

Details

The different columns stored in `mcols(guideSet)[["snps"]]` are:

- ID sgRNA ID.
- rs Reference SNP cluster ID (e.g. rs17852242)
- rs_site Genomic coordinate of the SNP.
- rs_site_rel Position of SNP relative to the PAM site.
- allele_ref DNASTring specifying the SNP reference allele.
- allele_minor DNASTring specifying the SNP minor allele.
- MAF_1000G Minor allele frequency in the 1000 Genomes project.
- MAF_TOPMED Minor allele frequency in the TOPMed project.
- type Type of SNP ("ins": insertion, "del": deletion).
- length Length of SNP in nucleotides.

Value

`guideSet` appended with `hasSNP` column and `snps` list-column, both stored in `mcols{guideSet}`.

See Also

`link{snps}` to retrieve an existing SNP annotation stored in a [GuideSet](#) object. See details section for a description of the different columns.

Examples

```
vcf <- system.file("extdata",
                  file="common_snps_dbsnp151_example.vcf.gz",
                  package="crisprDesign")
data(guideSetExample, package="crisprDesign")
guideSet <- addSNPAnnotation(guideSetExample, snpObject=vcf)
```

addSpacerAlignments *Functions for finding and characterizing on- and off-targets of spacer sequences.*

Description

Functions for finding and characterizing on- and off-targets of spacer sequences.

Usage

```
addSpacerAlignments(object, ...)
```

```
addSpacerAlignmentsIterative(object, ...)
```

```
## S4 method for signature 'GuideSet'
```

```
addSpacerAlignmentsIterative(  
  object,  
  aligner = c("bowtie", "bwa", "biostrings"),  
  colname = "alignments",  
  addSummary = TRUE,  
  txObject = NULL,  
  tssObject = NULL,  
  custom_seq = NULL,  
  aligner_index = NULL,  
  bsgenome = NULL,  
  n_mismatches = 0,  
  all_alignments = FALSE,  
  canonical = TRUE,  
  standard_chr_only = FALSE,  
  both_strands = TRUE,  
  anchor = c("cut_site", "pam_site"),  
  annotationType = c("gene_symbol", "gene_id"),  
  tss_window = NULL,  
  alignmentThresholds = c(n0 = 5, n1 = 100, n2 = 100, n3 = 1000, n4 = 1000)  
)
```

```
## S4 method for signature 'PairedGuideSet'
```

```
addSpacerAlignmentsIterative(  
  object,  
  aligner = c("bowtie", "bwa", "biostrings"),  
  colname = "alignments",  
  addSummary = TRUE,  
  txObject = NULL,  
  tssObject = NULL,  
  custom_seq = NULL,  
  aligner_index = NULL,  
  bsgenome = NULL,  
  n_mismatches = 0,  
  all_alignments = FALSE,  
  canonical = TRUE,  
  standard_chr_only = FALSE,
```

```
both_strands = TRUE,  
anchor = c("cut_site", "pam_site"),  
annotationType = c("gene_symbol", "gene_id"),  
tss_window = NULL,  
alignmentThresholds = c(n0 = 5, n1 = 100, n2 = 100, n3 = 1000, n4 = 1000)  
)
```

```
## S4 method for signature 'NULL'  
addSpacerAlignmentsIterative(object)
```

```
## S4 method for signature 'GuideSet'  
addSpacerAlignments(  
  object,  
  aligner = c("bowtie", "bwa", "biostrings"),  
  colname = "alignments",  
  addSummary = TRUE,  
  txObject = NULL,  
  tssObject = NULL,  
  custom_seq = NULL,  
  aligner_index = NULL,  
  bsgenome = NULL,  
  n_mismatches = 0,  
  n_max_alignments = 1000,  
  all_alignments = TRUE,  
  canonical = TRUE,  
  standard_chr_only = FALSE,  
  both_strands = TRUE,  
  anchor = c("cut_site", "pam_site"),  
  annotationType = c("gene_symbol", "gene_id"),  
  tss_window = NULL  
)
```

```
## S4 method for signature 'PairedGuideSet'  
addSpacerAlignments(  
  object,  
  aligner = c("bowtie", "bwa", "biostrings"),  
  colname = "alignments",  
  addSummary = TRUE,  
  txObject = NULL,  
  tssObject = NULL,  
  custom_seq = NULL,  
  aligner_index = NULL,  
  bsgenome = NULL,  
  n_mismatches = 0,  
  n_max_alignments = 1000,  
  all_alignments = FALSE,  
  canonical = TRUE,  
  standard_chr_only = FALSE,  
  both_strands = TRUE,  
  anchor = c("cut_site", "pam_site"),  
  annotationType = c("gene_symbol", "gene_id"),  
  tss_window = NULL
```

```

)

## S4 method for signature 'NULL'
addSpacerAlignments(object)

getSpacerAlignments(
  spacers,
  aligner = c("bowtie", "bwa", "biostrings"),
  custom_seq = NULL,
  aligner_index = NULL,
  bsgenome = NULL,
  n_mismatches = 0,
  n_max_alignments = 1000,
  all_alignments = TRUE,
  crisprNuclease = NULL,
  canonical = TRUE,
  standard_chr_only = FALSE,
  both_strands = TRUE
)

```

Arguments

| | |
|-------------------|---|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| aligner | Which genomic alignment method should be used? Must be one of "bowtie", "bwa", and "biostrings". "bowtie" by default. Note that "bwa" is not available for Windows machines. |
| colname | String specifying the column name storing the alignments in <code>mcols(guideSet)</code> . "alignments" by default. |
| addSummary | Should summary columns be added to <code>guideSet</code> ? TRUE by default. |
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList for annotating on-target and off-target alignments using gene annotation. |
| tssObject | A GRanges object specifying TSS coordinates. |
| custom_seq | Optional string specifying the target DNA sequence for the search space. This will limit the off-target search to the specified custom sequence. |
| aligner_index | String specifying bowtie or BWA index. Must be provided when aligner is either "bowtie" or "bwa". |
| bsgenome | A BSgenome object from which to extract sequences if a GRanges object is provided as input. |
| n_mismatches | Maximum number of mismatches permitted between guide RNA and genomic DNA. |
| all_alignments | Should all all possible alignments be returned? FALSE by default. |
| canonical | TRUE returns only those alignments having canonical PAM sequences; FALSE returns alignments having canonical or noncanonical PAM sequences; NA returns all alignments regardless of their PAM sequence. |
| standard_chr_only | Should only standard chromosomes be considered? If TRUE, the function will attempt to remove scaffold sequences automatically. FALSE by default. |

| | |
|---------------------|--|
| both_strands | When custom_seq is specified, should both strands be considered? TRUE by default. |
| anchor | The position within the protospacer as determined by CrisprNuclease to use when annotating with overlapping gene regions. |
| annotationType | Gene identifier to return when annotating alignments with gene and/or promoter overlaps. Corresponding txObject or tssObject argument must have mcol column name for selected type. |
| tss_window | Window size of promoters upstream of gene TSS to search for overlap with spacer sequence. Must be a numeric vector of length 2: upstream limit and downstream limit. Default is c(-500, 500), which includes 500bp upstream and downstream of the TSS. |
| alignmentThresholds | Named numeric vector of the maximum on-target alignments tolerated for addSpacerAlignments . Thresholds not provided will take default values. |
| n_max_alignments | Maximum number of alignments to report by bowtie for each spacer. Effectively set to Inf when allPossible is TRUE. |
| spacers | Character vector of gRNA spacer sequences. All sequences must be equal in length. |
| crisprNuclease | A CrisprNuclease object. |

Details

The columns stored in `mcols(guideSet)[["alignments"]]` are:

- spacer Spacer sequence of the query gRNA.
- protospacer Protospacer sequence in the target DNA.
- pam PAM sequence.
- pam_site PAM site of the found protospacer.
- n_mismatches Integer value specifying the number of nucleotide mismatches between the gRNA spacer sequence and the protospacer sequence found in the genome or custom sequence.
- canonical Whether the PAM sequence of the found protospacer sequence is canonical.
- cute_site Cut site of the found protospacer.

The following columns are also stored when a txObject is provided:

- cds Character vector specifying gene names of CDS overlapping the found protospacer sequence.
- fiveUTRs Character vector specifying gene names of 5'UTRs overlapping the found protospacer sequence.
- threeUTRs Character vector specifying gene names of 3'UTRs overlapping the found protospacer sequence.
- exons Character vector specifying gene names of exons overlapping the found protospacer sequence.
- introns Character vector specifying gene names of introns overlapping the found protospacer sequence.
- intergenic Character vector specifying the nearest gene when the found protospacer sequence is not located in a gene.

addTssAnnotation *Add TSS context annotation to a [GuideSet](#) object*

Description

Add transcription start site (TSS) context annotation to spacer sequences stored in a [GuideSet](#) object.

Usage

```
addTssAnnotation(object, ...)

## S4 method for signature 'GuideSet'
addTssAnnotation(
  object,
  tssObject,
  anchor = c("cut_site", "pam_site"),
  tss_window = NULL,
  ignore.strand = TRUE
)

## S4 method for signature 'PairedGuideSet'
addTssAnnotation(
  object,
  tssObject,
  anchor = c("cut_site", "pam_site"),
  tss_window = NULL,
  ignore.strand = TRUE
)

## S4 method for signature 'NULL'
addTssAnnotation(object)
```

Arguments

| | |
|---------------|---|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| tssObject | A GRanges object containing TSS coordinates and annotation. |
| anchor | A character string specifying which gRNA-specific coordinate to use (cut_site or pam_site) when searching for overlapping TSS regions. "cut_site" by default. |
| tss_window | A numeric vector of length 2 establishing the window size of the genomic region around the TSS to include as the "TSS region". The values set the upstream and downstream limits, respectively. The default is c(-500, 500), which includes 500bp upstream (note the negative value) and downstream of the TSS. |
| ignore.strand | If TRUE (default), includes annotation for gRNAs irrespective of their target strand. Otherwise, only gRNAs targeting the gene strand will be annotated. |

Details

`mcols(guideSet)[["tssAnnotation"]]` includes all columns from `mcols(tssObject)` in addition to the columns described below.

- `chr` — gRNA chromosome name.
- `anchor_site` — Genomic coordinate used to search for overlapping TSS regions.
- `strand` — Strand the gRNA is located on.
- `tss_id` — The ID for the TSS in `tssObject`, if present.
- `tss_strand` — Strand the TSS is located on, as provided in `tssObject`
- `tss_pos` — Genomic coordinate of the TSS, as provided in `tssObject`.
- `dist_to_tss` — Distance (in nucleotides) between the gRNA `anchor_site` and `tss_pos`. Negative values indicate gRNA targets upstream of the TSS.

Value

A [GuideSet](#) object with a `tssAnnotation` list column stored in `mcols(guideSet)`. See details section for descriptions of TSS annotation columns.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

See Also

[addGeneAnnotation](#) to add gene annotation, and [tssAnnotation](#) to retrieve an existing TSS annotation.

Examples

```
data(guideSetExample, package="crisprDesign")
data(tssObjectExample, package="crisprDesign")
guideSet <- addTssAnnotation(guideSetExample,
                             tssObject=tssObjectExample)

# To access TSS annotation:
ann <- tssAnnotation(guideSet)
```

`addTxTable`

Add a gene-specific transcript table to a [GuideSet](#) object.

Description

Add a gene-specific transcript table to a [GuideSet](#) object.

Add a gene-specific transcript table to a [GuideSet](#) object.

Usage

```
addTxTable(guideSet, gene_id, txObject, valueColumn = "percentCDS")
```

Arguments

| | |
|-------------|---|
| guideSet | A GuideSet object or a PairedGuideSet object. |
| gene_id | String specifying gene ID. |
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList to provide a gene model annotation. |
| valueColumn | String specifying column in <code>geneAnnotation(guideSet)</code> to use as values in the output transcript table. |

Value

A [GuideSet](#) object with a "txTable" `DataFrame` stored in `mcols(guideSet)`. The entries in the `DataFrame` correspond to the values specified by `valueColumn`. Rows correspond to gRNAs in the `GuideSet`, columns correspond to all transcripts found in `txObject` for gene specified by `gene_id`.

Author(s)

Jean-Philippe Fortin

See Also

[addGeneAnnotation](#) to add gene annotation.

Examples

```
if (interactive()){
  data(guideSetExample, package="crisprDesign")
  data(grListExample, package="crisprDesign")
  guideSet <- addGeneAnnotation(guideSetExample,
                               txObject=grListExample)
  guideSet <- addTxTable(guideSet,
                        gene_id="ENSG00000120645",
                        txObject=grListExample)

  guideSet$txTable
}
```

completeSpacers

Get complete spacer information

Description

These functions serve to "fill-in-the-blank" for spacers lacking information.

Usage

```
getPAMSequence(chr, pam_site, strand, crisprNuclease = NULL, bsgenome = NULL)

getSpacerSequence(
  chr,
  pam_site,
```

```

    strand,
    crisprNuclease = NULL,
    bsgenome = NULL,
    spacerLen = NULL
  )

getPAMSiteFromStartAndEnd(
  start = NULL,
  end = NULL,
  strand,
  crisprNuclease = NULL,
  spacerLen = NULL
)

```

Arguments

| | |
|----------------|---|
| chr | The chromosome in which the protospacer sequence is located. |
| pam_site | Coordinate of the first nucleotide of the PAM sequence. |
| strand | Either "+" or "-". |
| crisprNuclease | A CrisprNuclease object. |
| bsgenome | A BSgenome object. |
| spacerLen | Spacer sequence length. If NULL, the information is obtained from <code>crisprNuclease</code> . |
| start | Coordinate of the first nucleotide of the spacer sequences. Must be always less than end. |
| end | Coordinate of the last nucleotide of the spacer sequence. Must be always greater than start. |

Details

Functions that return coordinates (`getPAMSite`, `getCutSite`, `getSpacerRanges`) do not check whether coordinates exceed chromosomal lengths.

The start and end coordinates of a genomic range is strand-independent, and always obeys `start <= end`.

Value

A numeric or character vector, depending on the function.

`getPAMSequence` returns a character vector of PAM sequences.

`getSpacerSequence` returns a character vector of spacer sequences.

Examples

```

if (requireNamespace("BSgenome.Hsapiens.UCSC.hg38")){
  library(BSgenome.Hsapiens.UCSC.hg38)
  bsgenome <- BSgenome.Hsapiens.UCSC.hg38
  dat <- data.frame(chr='chr4', start=1642343, strand='+')
  dat$pam_site <- getPAMSiteFromStartAndEnd(start=dat$start,
                                           strand=dat$strand)
  dat$pam <- getPAMSequence(chr=dat$chr,
                           pam_site=dat$pam_site,
                           strand=dat$strand,

```

```

                                bsgenome=bsgenome)
dat$spacer <- getSpacerSequence(chr=dat$chr,
                                pam_site=dat$pam_site,
                                strand=dat$strand,
                                bsgenome=bsgenome)
}

```

convertToMinMaxGRanges

Convert a GuideSet object into a GRanges containing the range of all targeting gRNAs.

Description

Convert a GuideSet object into a GRanges object containing the minimum and maximum coordinates for all targeting gRNAs.

Usage

```
convertToMinMaxGRanges(guideSet, anchor = c("cut_site", "pam_site"))
```

Arguments

| | |
|----------|--|
| guideSet | A GuideSet object. |
| anchor | A character string specifying which gRNA-specific coordinate to use (cut_site or pam_site) when defining the min and max coordinates of GuideSet object. |

Value

A GRanges object with start and end coordinates corresponding to the minimum and maximum coordinates of the GuideSet object sites defined by anchor.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

Examples

```

data(guideSetExample, package="crisprDesign")
gr <- convertToMinMaxGRanges(guideSetExample)

```

`convertToProtospacerGRanges`*Convert PAM site coordinates to protospacer start and end coordinates*

Description

Convert PAM site coordinates to protospacer start and end coordinates.

Usage

```
convertToProtospacerGRanges(guideSet)
```

Arguments

`guideSet` A [GuideSet](#) object.

Value

A [GuideSet](#) object with start and end coordinates corresponding to the start and end coordinates of the protospacer sequences.

Author(s)

Jean-Philippe Fortin

Examples

```
data(guideSetExample, package="crisprDesign")
gr <- convertToProtospacerGRanges(guideSetExample)
```

`crisprNuclease`*An S4 class to store CRISPR gRNA sequences with modular annotations.*

Description

An S4 class to store CRISPR gRNA sequences with modular annotations.

Usage

```
crisprNuclease(object, ...)
```

```
targetOrigin(object, ...)
```

```
customSequences(object, ...)
```

```
bsgenome(object, ...)
```

```
spacers(object, ...)
```

```
protospacers(object, ...)  
pamSites(object, ...)  
snps(object, ...)  
alignments(object, ...)  
onTargets(object, ...)  
offTargets(object, ...)  
geneAnnotation(object, ...)  
tssAnnotation(object, ...)  
enzymeAnnotation(object, ...)  
editedAlleles(object, ...)  
txTable(object, ...)  
exonTable(object, ...)  
tssAnnotation(object) <- value  
geneAnnotation(object) <- value  
enzymeAnnotation(object) <- value  
snps(object) <- value  
alignments(object) <- value  
addCutSites(object, ...)  
  
GuideSet(  
  ids = NA_character_,  
  protospacers = NA_character_,  
  pams = NULL,  
  seqnames = NA_character_,  
  pam_site = 0L,  
  strand = "*",  
  CrisprNuclease = NULL,  
  targetOrigin = c("bsgenome", "customSequences"),  
  bsgenome = NULL,  
  customSequences = NULL,  
  ...,  
  seqinfo = NULL,  
  seqlengths = NULL  
)
```

```
## S4 method for signature 'GuideSet'
targetOrigin(object)

## S4 method for signature 'GuideSet'
customSequences(object)

## S4 method for signature 'GuideSet'
bsgenome(object)

## S4 method for signature 'GuideSet'
crisprNuclease(object)

## S4 method for signature 'GuideSet'
spacers(object, as.character = FALSE, returnAsRna = FALSE)

## S4 method for signature 'GuideSet'
pams(object, as.character = FALSE, returnAsRna = FALSE)

## S4 method for signature 'GuideSet'
pamSites(object)

## S4 method for signature 'GuideSet'
cutSites(object)

## S4 method for signature 'GuideSet'
addCutSites(object)

## S4 method for signature 'GuideSet'
protospacers(
  object,
  as.character = FALSE,
  include.pam = FALSE,
  returnAsRna = FALSE
)

## S4 method for signature 'GuideSet'
spacerLength(object)

## S4 method for signature 'GuideSet'
prototypeSequence(object)

## S4 method for signature 'GuideSet'
pamLength(object)

## S4 method for signature 'GuideSet'
pamSide(object)

## S4 method for signature 'GuideSet'
snps(object, unlist = TRUE, use.names = TRUE)

## S4 method for signature 'GuideSet'
```

```
alignments(object, columnName = "alignments", unlist = TRUE, use.names = TRUE)

## S4 method for signature 'GuideSet'
onTargets(object, columnName = "alignments", unlist = TRUE, use.names = TRUE)

## S4 method for signature 'GuideSet'
offTargets(
  object,
  columnName = "alignments",
  max_mismatches = Inf,
  unlist = TRUE,
  use.names = TRUE
)

## S4 replacement method for signature 'GuideSet'
alignments(object) <- value

## S4 replacement method for signature 'GuideSet'
geneAnnotation(object) <- value

## S4 replacement method for signature 'GuideSet'
tssAnnotation(object) <- value

## S4 replacement method for signature 'GuideSet'
enzymeAnnotation(object) <- value

## S4 replacement method for signature 'GuideSet'
snps(object) <- value

## S4 method for signature 'GuideSet'
geneAnnotation(
  object,
  unlist = TRUE,
  gene_id = NULL,
  tx_id = NULL,
  gene_symbol = NULL,
  use.names = TRUE
)

## S4 method for signature 'GuideSet'
editedAlleles(object, unlist = TRUE, use.names = TRUE)

## S4 method for signature 'GuideSet'
tssAnnotation(
  object,
  unlist = TRUE,
  gene_id = NULL,
  gene_symbol = NULL,
  use.names = TRUE
)

## S4 method for signature 'GuideSet'
```

```
enzymeAnnotation(object, unlist = TRUE, use.names = TRUE)
```

```
## S4 method for signature 'GuideSet'
txTable(object, unlist = TRUE, use.names = TRUE)
```

```
## S4 method for signature 'GuideSet'
exonTable(object, unlist = TRUE, use.names = TRUE)
```

Arguments

| | |
|-----------------|---|
| object | GuideSet object. |
| ... | Additional arguments for class-specific methods |
| value | Object to replace with |
| ids | Character vector of unique gRNA ids. The ids can be anything, as long as they are unique. |
| protospacers | Character vector of protospacers sequences. |
| pams | Character vector of PAM sequences. |
| seqnames | Character vector of chromosome names. |
| pam_site | Integer vector of PAM site coordinates. |
| strand | Character vector of gRNA strand. Only accepted values are "+" and "-". |
| CrisprNuclease | CrisprNuclease object. |
| targetOrigin | String specifying the origin of the DNA target. Must be either 'bsgenome' or 'customSequences'. |
| bsgenome | BSgenome object or string specifying BSgenome package name. Must be specified when targetOrigin is set to "bsgenome". |
| customSequences | DNAStrngSet object. Must be specified when targetOrigin is set to "custom-Sequences". |
| seqinfo | A Seqinfo object containing information about the set of genomic sequences present in the target genome. |
| seqlengths | NULL, or an integer vector named with levels(seqnames) and containing the lengths (or NA) for each level in levels(seqnames). |
| as.character | Should sequences be returned as a character vector? FALSE by default, in which case sequences are returned as a DNAStrngSet . |
| returnAsRna | Should the sequences be returned as RNA instead of DNA? FALSE by default. |
| include.pam | Should PAM sequences be included? FALSE by default. |
| unlist | Should the annotation be returned as one table instead of a list? TRUE by default. |
| use.names | Whether to include spacer IDs as (row)names (TRUE), or as a separate column (FALSE). |
| columnName | Name of the column storing the alignments annotation to be retrieved. |
| max_mismatches | What should be the maximum number of mismatches considered for off-targets? Inf by default. |
| gene_id | Character vector of Ensembl gene IDs to subset gene annotation data by. If NULL (default), all genes are considered. |
| tx_id | Character vector of Ensembl transcript IDs to subset gene annotation data by. If NULL (default), all transcript are considered. |
| gene_symbol | Character vector of gene symbols to subset gene annotation data by. If NULL (default), all genes are considered. |

Value

A GuideSet object.

Functions

- GuideSet(): Create a [GuideSet](#) object

Constructors

Use the constructor `link{GuideSet}` to create a GuideSet object.

Accessors

`crisprNuclease`: To get [CrisprNuclease](#) object used to design gRNAs.

`spacers`: To get spacer sequences.

`protospacers`: To get protospacer sequences.

`spacerLength`: To get spacer length.

`pams`: To get PAM sequences.

`pamSites`: To get PAM site coordinates.

`pamLength`: To get PAM length.

`pamSide`: To return the side of the PAM sequence with respect to the protospacer sequence.

`prototypeSequence`: To get a prototype protospacer sequence.

`cutSites`: To get cut sites.

`alignments`: To get genomic alignments annotation.

`onTargets`: To get on-target alignments annotation

`offTargets`: To get off-target alignments annotation

`snps`: To get SNP annotation.

`geneAnnotation`: To get gene annotation.

`tssAnnotation`: To get TSS annotation.

`enzymeAnnotation`: To get restriction enzymes annotation.

`editedAlleles`: To get edited alleles annotation.

Examples

```
protospacers <- c("AGGTCGTGTGTGGGGGGGG",
                 "AGGTCGTGTGTGGGGGGGG")
pams <- c("AGG", "CGG")
pam_site=c(10,11)
seqnames="chr7"
data(SpCas9, package="crisprBase")
CrisprNuclease <- SpCas9
strand=c("+", "-")
ids <- paste0("grna_", seq_along(protospacers))
gr <- GuideSet(ids=ids,
               protospacers=protospacers,
               pams=pams,
               seqnames=seqnames,
               CrisprNuclease=CrisprNuclease,
               pam_site=pam_site,
```

```
strand=strand,
targetOrigin="customSequences",
customSequences=protospacers)
```

designCompleteAnnotation

One-step gRNA design and annotation function

Description

One-step gRNA design and annotation function to facilitate the design and generation of genome-wide gRNA databases for a combination of parameters such as nuclease, organism, and CRISPR modality.

Usage

```
designCompleteAnnotation(
  queryValue = NULL,
  queryColumn = "gene_id",
  featureType = "cds",
  modality = c("CRISPRko", "CRISPRa", "CRISPRi", "CRISPRkd"),
  bsgenome = NULL,
  bowtie_index = NULL,
  vcf = NULL,
  crisprNuclease = NULL,
  tssObject = NULL,
  txObject = NULL,
  grRepeats = NULL,
  scoring_methods = NULL,
  tss_window = NULL,
  n_mismatches = 3,
  max_mm = 2,
  canonical_ontarget = TRUE,
  canonical_offtarget = FALSE,
  all_alignments = TRUE,
  conservationFile = NULL,
  nucExtension = 9,
  binaries = NULL,
  canonicalIsoforms = NULL,
  pfamTable = NULL,
  verbose = TRUE
)
```

Arguments

| | |
|-------------|--|
| queryValue | Vector specifying the value(s) to search for in txObject[[featureType]][[queryColumn]]. |
| queryColumn | Character string specifying the column in txObject[[featureType]] to search for queryValue(s). |

| | |
|---------------------|---|
| featureType | For CRISPRko, string specifying the type of genomic feature to use to design gRNAs. Must be of the following: "transcripts", "exons", "cds", "fiveUTRs", "threeUTRs" or "introns". The default is "cds". |
| modality | String specifying the CRISPR modality. Must be one of the following: "CRISPRko", "CRISPRa", "CRISPRi" or "CRISPRkd". CRISPRkd is reserved for DNA-targeting nucleases only such as CasRx. |
| bsgenome | A BSgenome object from which to extract sequences if a GRanges object is provided as input. |
| bowtie_index | String specifying path to a bowtie index. |
| vcf | Either a character string specifying a path to a VCF file or connection, or a VCF object. |
| crisprNuclease | A CrisprNuclease object. |
| tssObject | A GRanges object specifying TSS coordinates. |
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList for annotating on-target and off-target alignments using gene annotation. |
| grRepeats | A GRanges object containing repeat elements regions. |
| scoring_methods | Character vector to specify which on-target scoring methods should be calculated. See crisprScore package to obtain available methods. |
| tss_window | Vector of length 2 specifying the start and coordinates of the CRISPRa/CRISPRi target region with respect to the TSS position. |
| n_mismatches | Maximum number of mismatches permitted between guide RNA and genomic DNA. |
| max_mm | The maximum number of mismatches between a spacer and an off-target to be accepted when calculating aggregate off-target scores. 2 by default. |
| canonical_ontarget | Should only canonical PAM sequences be searched for designing gRNAs? TRUE by default. |
| canonical_offtarget | Should only canonical PAM sequences be searched during the off-target search? TRUE by default. |
| all_alignments | Should all possible alignments be returned? TRUE by default. |
| conservationFile | String specifying the BigWig file containing conservation scores. |
| nucExtension | Number of nucleotides to include on each side of the cut site to calculate the conservation score. 9 by default. The region will have (2*nucExtension + 1) nucleotides in total. |
| binaries | Named list of paths for binaries needed for CasRx-RF. Names of the list must be "RNAfold", "RNAhybrid", and "RNAlfold". Each list element is a string specifying the path of the binary. If NULL (default), binaries must be available on the PATH. |
| canonicalIsoforms | Optional data.frame with 2 columns detailing Ensembl canonical isoforms. First column must be named "tx_id", and second column must be named "gene_id", corresponding to Ensembl transcript and gene ids, respectively. |
| pfamTable | A DataFrame obtained using preparePfamTable . |
| verbose | Should messages be printed? |

Value

A GuideSet object.

Author(s)

Jean-Philippe Fortin

designOpsLibrary *Design gRNA library for optical pooled screening*

Description

Design gRNA library for optical pooled screening

Usage

```
designOpsLibrary(
  df,
  n_guides = 4,
  gene_field = "gene",
  min_dist_edit = 2,
  dist_method = c("hamming", "levenshtein"),
  splitByChunks = FALSE
)
```

Arguments

| | |
|---------------|--|
| df | data.frame containing information about candidate gRNAs from which to build the OPS library. See details. |
| n_guides | Integer specifying how many gRNAs per gene should be selected. 4 by default. |
| gene_field | String specifying the column in df specifying gene names. |
| min_dist_edit | Integer specifying the minimum distance edit required for barcodes to be considered dissimilar. Barcodes that have edit distances less than the min_dist_edit will not be included in the library. 2 by default. |
| dist_method | String specifying distance method. Must be either "hamming" (default) or "levenshtein". |
| splitByChunks | Should distances be calculated in a chunk-wise manner? FALSE by default. Highly recommended when the set of query barcodes is large to reduce memory footprint. |

Value

A subset of the df containing the gRNAs selected for the OPS library.

Author(s)

Jean-Philippe Fortin

Examples

```

data(guideSetExample, package="crisprDesign")
guideSet <- unique(guideSetExample)
guideSet <- addOpsBarcodes(guideSet)
guideSet <- guideSet[1:200]

df <- data.frame(ID=names(guideSet),
                 spacer=spacers(guideSet, as.character=TRUE),
                 opsBarcode=as.character(guideSet$opsBarcode))

# Creating mock gene:
df$gene <- rep(paste0("gene",1:10),each=20)
df$rank <- rep(1:20,10)
opsLib <- designOpsLibrary(df)

```

| | |
|-----------------|--|
| findSpacerPairs | <i>Find pairs of CRISPR gRNA spacers from a pair of genomic regions.</i> |
|-----------------|--|

Description

Returns all possible, valid gRNA sequences for a given CRISPR nuclease from either a [GRanges](#) object or a set of sequence(s) contained in either a [DNAStringSet](#), [DNAString](#) or character vector of genomic sequences.

Usage

```

findSpacerPairs(
  x1,
  x2,
  sortWithinPair = TRUE,
  pamOrientation = c("all", "out", "in"),
  minCutLength = NULL,
  maxCutLength = NULL,
  crisprNuclease = NULL,
  bsgenome = NULL,
  canonical = TRUE,
  both_strands = TRUE,
  spacer_len = NULL,
  strict_overlap = TRUE,
  remove_ambiguities = TRUE
)

```

Arguments

- | | |
|----|--|
| x1 | Either a GRanges , a DNAStringSet , or a DNAString object, or a character vector of genomic sequences. This specifies the sequence space from which gRNAs in position 1 of the pairs will be designed. Alternatively, a GuideSet object can be provided. |
| x2 | Either a GRanges , a DNAStringSet , or a DNAString object, or a character vector of genomic sequences. This specifies the sequence space from which gRNAs in position 2 of the pairs will be designed. Alternatively, a GuideSet object can be provided. |

| | |
|--------------------|---|
| sortWithinPair | Should gRNAs be sorted by chr and position within a pair? TRUE by default. |
| pamOrientation | String specifying a constraint on the PAM orientation of the pairs. Should be either "all" (default), "out" (for the so-called PAM-out orientation) or "in" (for PAM-in orientation). |
| minCutLength | Integer specifying the minimum cut length allowed (distance between the two cuts) induced by the gRNA pair. If NULL (default), the argument is ignored. Note that this parameter is only applicable for pairs of gRNAs targeting the same chromosome. |
| maxCutLength | Integer specifying the maximum cut length allowed (distance between the two cuts) induced by the gRNA pair. If NULL (default), the argument is ignored. Note that this parameter is only applicable for pairs of gRNAs targeting the same chromosome. |
| crisprNuclease | A CrisprNuclease object. |
| bsgenome | A BSgenome object from which to extract sequences if x is a GRanges object. |
| canonical | Whether to return only guide sequences having canonical PAM sequences. If TRUE (default), only PAM sequences with the highest weights stored in the crisprNuclease object will be considered. |
| both_strands | Whether to consider both strands in search for protospacer sequences. TRUE by default. |
| spacer_len | Length of spacers to return, if different from the default length specified by crisprNuclease . |
| strict_overlap | Whether to only include gRNAs that cut in the input range, as given by <code>cut_site</code> (TRUE) or to include all gRNAs that share any overlap with the input range (FALSE). TRUE by default. Ignored when x is not a GRanges object. |
| remove_ambiguities | Whether to remove spacer sequences that contain ambiguous nucleotides (not explicitly A, C, G, or T). TRUE by default. |

Details

This function returns a [PairedGuideSet](#) object that stores gRNA pairs targeting the two genomic regions provided as input. The gRNAs in position 1 target the first genomic region, and the gRNAs in position 2 target the second genomic region.

This function can be used for the following scenarios:

1. Designing pairs of gRNAs targeting different genes, for instance for dual-promoter Cas9 systems, or polycistronic Cas12a constructs. This can also be used to target a given gene with multiple gRNAs for improved efficacy (for instance CRISPRa and CRISPRi)
2. Designing pairs of gRNAs for double nicking systems such as Cas9 D10A.

See vignette for more examples.

Value

A [PairedGuideSet](#) object.

Author(s)

Jean-Philippe Fortin

See Also

[findSpacers](#) to find unpaired spacer sequences, and the [PairedGuideSet](#) object documentation to understand the output of `findSpacerPairs`.

Examples

```
library(GenomicRanges)
library(BSgenome.Hsapiens.UCSC.hg38)
library(crisprBase)
bsgenome <- BSgenome.Hsapiens.UCSC.hg38

# Region 1:
gr1 <- GRanges(c("chr12"),
               IRanges(start=22224014, end=22225007))

# Region 2:
gr2 <- GRanges(c("chr13"),
               IRanges(start=23224014, end=23225007))

# Pairs targeting the same region:
pairs <- findSpacerPairs(gr1, gr1, bsgenome=bsgenome)

# Pairs targeting two regions:
# The gRNA in position targets gr1
# and the gRNA in position 2 targets gr2
pairs <- findSpacerPairs(gr1, gr2, bsgenome=bsgenome)
```

findSpacers

Find CRISPR gRNA spacer sequences from a set of DNA sequences.

Description

Returns all possible, valid gRNA sequences for a given CRISPR nuclease from either a [GRanges](#) object or a set of sequence(s) contained in either a [DNAStringSet](#), [DNAString](#) or character vector of genomic sequences.

Usage

```
findSpacers(
  x,
  crisprNuclease = NULL,
  bsgenome = NULL,
  canonical = TRUE,
  both_strands = TRUE,
  spacer_len = NULL,
  strict_overlap = TRUE,
  remove_ambiguities = TRUE,
  remove_duplicates = TRUE
)
```

Arguments

| | |
|--------------------|---|
| x | Either a GRanges , a DNAStringSet , or a DNAString object, or a character vector of genomic sequences. See details. |
| crisprNuclease | A CrisprNuclease object. |
| bsgenome | A BSgenome object from which to extract sequences if x is a GRanges object. |
| canonical | Whether to return only guide sequences having canonical PAM sequences. If TRUE (default), only PAM sequences with the highest weights stored in the crisprNuclease object will be considered. |
| both_strands | Whether to consider both strands in search for protospacer sequences. TRUE by default. |
| spacer_len | Length of spacers to return, if different from the default length specified by crisprNuclease . |
| strict_overlap | Whether to only include gRNAs that cut in the input range, as given by <code>cut_site</code> (TRUE) or to include all gRNAs that share any overlap with the input range (FALSE). TRUE by default. Ignored when x is not a GRanges object. |
| remove_ambiguities | Whether to remove spacer sequences that contain ambiguous nucleotides (not explicitly A, C, G, or T). TRUE by default. |
| remove_duplicates | Whether to remove duplicated protospacer sequences originating from overlapping genomic ranges. TRUE by default. |

Details

If x is a [GRanges](#) object then a [BSgenome](#) must be supplied to `bsgenome`, from which the genomic sequence is obtained, unless the `bsgenome` can be inferred from `genome(x)`, for example, "hg38". Otherwise, all supplied sequences are treated as the "+" strands of chromosomes in a "custom" genome.

Ranges or sequences in x may contain names where permitted. These names are stored in `region` in the `mcols` of the output, and as `seqnames` of the output if x is not a [GRanges](#) object. If not NULL, `names(x)` must be unique, otherwise ranges or sequences are enumerated with the "region_" prefix.

When x is a [GRanges](#), the * strand is interpreted as both strands. Consequently, the `both_strands` argument has no effect on such ranges.

Value

A [GuideSet](#) object.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

Examples

```
# Using custom sequence as input:
my_seq <- c(my_seq="CCAANAGTGAAACCACGTCTCTATAAAGAATACAAAAAATTAGCCGGGTGTTA")
guides <- findSpacers(my_seq)

# Exon-intro region of human KRAS specified
```

```
# using a GRanges object:
library(GenomicRanges)
library(BSgenome.Hsapiens.UCSC.hg38)
bsgenome <- BSgenome.Hsapiens.UCSC.hg38

gr_input <- GRanges(c("chr12"),
                    IRanges(start=25224014, end=25227007))
guideSet <- findSpacers(gr_input, bsgenome=bsgenome)

# Designing guides for enAsCas12a nuclease:
data(enAsCas12a, package="crisprBase")
guideSet <- findSpacers(gr_input,
                        canonical=FALSE,
                        bsgenome=bsgenome,
                        crisprNuclease=enAsCas12a)
```

| | |
|-----------------|--|
| flattenGuideSet | <i>Create a list of annotation tables from a GuideSet object</i> |
|-----------------|--|

Description

Create a list of annotation tables from a GuideSet object

Usage

```
flattenGuideSet(guideSet, useSpacerCoordinates = TRUE, primaryOnly = FALSE)
```

Arguments

| | |
|----------------------|--|
| guideSet | A GuideSet object |
| useSpacerCoordinates | Should the spacer coordinates be used as start and end coordinates? TRUE by default. If FALSE, the PAM site coordinate is used for both start and end. |
| primaryOnly | Should only the primary table (on-targets) be returned? FALSE by default. |

Value

A simple list of tables containing annotations derived from a GuideSet object. The first table ("primary") is always available, while the other tables will be only available when the annotations were added to the GuideSet object.

- `primary` Primary table containing genomic coordinates and sequence information of the gRNA sequences. Also contains on-target and off-target scores when available.
- `alignments` Table of on- and off-target alignments.
- `geneAnnotation` Gene context annotation table.
- `tssAnnotation` TSS context annotation table.
- `enzymeAnnotation` Boolean table indicating whether or not recognition motifs of restriction enzymes are found.
- `snps` SNP annotation table (human only).

Author(s)

Jean-Philippe Fortin

getBarcodeDistanceMatrix

*Get distance between query and target sets of barcodes***Description**

Get distance between query and target sets of barcodes

Usage

```
getBarcodeDistanceMatrix(
  queryBarcodes,
  targetBarcodes = NULL,
  binnarize = TRUE,
  min_dist_edit = NULL,
  dist_method = c("hamming", "levenshtein"),
  ignore_diagonal = TRUE,
  splitByChunks = FALSE,
  n_chunks = NULL
)
```

Arguments

| | |
|-----------------|---|
| queryBarcodes | Character vector of DNA sequences or DNAStrngSet. |
| targetBarcodes | Optional character vector of DNA sequences or DNAStrngSet. If NULL, distances will be calculated between barcodes provided in queryBarcodes. |
| binnarize | Should the distance matrix be made binnary? TRUE by default. See details section. |
| min_dist_edit | Integer specifying the minimum distance edit required for barcodes to be considered dissimilar when binnarize=TRUE, ignored otherwise. |
| dist_method | String specifying distance method. Must be either "hamming" (default) or "levenshtein". |
| ignore_diagonal | When targetBarcodes=NULL, should the diagonal distances be set to 0 to ignore self distances? TRUE by default. |
| splitByChunks | Should distances be calculated in a chunk-wise manner? FALSE by default. Highly recommended when the set of query barcodes is large to reduce memory footprint. |
| n_chunks | Integer specifying the number of chunks to be used when splitByChunks=TRUE. If NULL (default), number of chunks will be chosen automatically. |

Value

A sparse matrix of class dgMatrix or dsMatrix in which rows correspond to queryBarcodes and columns correspond to targetBarcodes. If binnarize=TRUE, a value of 0 indicates that two barcodes have a distance greater or equal to min_dist_edit, otherwise the value is 1. If binnarize=FALSE, values represent the actual calculated distances between barcodes.

Author(s)

Jean-Philippe Fortin

Examples

```
data(guideSetExample, package="crisprDesign")
guideSetExample <- addOpsBarcodes(guideSetExample)
barcodes <- as.character(guideSetExample$opsBarcode)
dist <- getBarcodeDistanceMatrix(barcodes, min_dist_edit=2)
```

getConsensusIsoform *Get the genomic ranges of a consensus isoform*

Description

Get the genomic ranges of a consensus isoform. The consensus isoform is taken as the union of exons across all isoforms where overlapping exons are merged to produce a simplified set through the reduce method of the GenomicRanges package.

Usage

```
getConsensusIsoform(gene_id, txObject)
```

Arguments

| | |
|----------|---|
| gene_id | String specifying Ensembl ID for the gene of interest. E.g. "ENSG00000049618". ID must be present in txObject\$exons\$gene_id. |
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList to provide a gene model annotation. |

Value

A GRanges object.

Author(s)

Jean-Philippe Fortin

Examples

```
data(grListExample)
gene_id <- "ENSG00000120645"
gr <- getConsensusIsoform(gene_id, grListExample)
```

getMrnaSequences *Retrieve mRNA sequences*

Description

A function for retrieving mRNA sequences of select transcripts.

Usage

```
getMrnaSequences(txids, txObject, bsgenome)
```

Arguments

| | |
|----------|--|
| txids | A character vector of Ensembl transcript IDs. IDs not present in txObject will be silently ignored. |
| txObject | A TxDb object or a GRangesList object obtained from TxDb2GRangesList . Defines genomic ranges for txids. |
| bsgenome | A BSgenome object from which to extract mRNA sequences. |

Value

A [DNAStringSet](#) object of mRNA sequences. Note that sequences are returned as DNA rather than RNA.

Author(s)

Jean-Philippe Fortin

Examples

```
library(BSgenome.Hsapiens.UCSC.hg38)
data(grListExample)
bsgenome <- BSgenome.Hsapiens.UCSC.hg38
txids <- c("ENST00000538872", "ENST00000382841")
out <- getMrnaSequences(txids, grListExample, bsgenome)
```

getPreMrnaSequences *Retrieve pre-mRNA sequences*

Description

A function for retrieving pre-mRNA sequences of select transcripts.

Usage

```
getPreMrnaSequences(txids, txObject, bsgenome)
```

Arguments

| | |
|----------|--|
| txids | A character vector of Ensembl transcript IDs. IDs not present in txObject will be silently ignored. |
| txObject | A TxDb object or a GRangesList object obtained from TxDb2GRangesList . Defines genomic ranges for txids. |
| bsgenome | A BSgenome object from which to extract pre-mRNA sequences. |

Value

A [DNAStringSet](#) object of mRNA sequences. Note that sequences are returned as DNA rather than RNA.

Author(s)

Jean-Philippe Fortin

Examples

```
library(BSgenome.Hsapiens.UCSC.hg38)
data(grListExample)
bsgenome <- BSgenome.Hsapiens.UCSC.hg38
txids <- c("ENST00000538872", "ENST00000382841")
out <- getPreMrnaSequences(txids, grListExample, bsgenome)
```

getTssObjectFromTxObject

Extract TSS coordinates from a gene model object

Description

Extract TSS coordinates from a gene model object.

Usage

```
getTssObjectFromTxObject(txObject)
```

Arguments

| | |
|----------|---|
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList for annotating on-target and off-target alignments using gene annotation. |
|----------|---|

Value

A [GRanges](#) object containing TSS coordinates

Author(s)

Jean-Philippe Fortin

Examples

```
data(grListExample, package="crisprDesign")
tss <- getTssObjectFromTxObject(grListExample)
```

getTxDb

getTxDb

Description

Convenience function for constructing a [TxDb](#) object.

Usage

```
getTxDb(file = NA, organism, release = NA, tx_attrib = "gencode_basic", ...)
```

Arguments

| | |
|-----------|--|
| file | File argument for makeTxDbFromGFF (see help page for makeTxDbFromGFF). If NA (default), function will return a TxDb object from Ensembl using makeTxDbFromEnsembl . |
| organism | String specifying genus and species name (e.g. "Homo sapiens" for human). Required if file is not provided. If file is provided, this value can be set to NA to have organism information as unspecified. |
| release | Ensembl release version; passed to makeTxDbFromEnsembl when file is not specified. See help page for makeTxDbFromEnsembl . |
| tx_attrib | Argument passed to makeTxDbFromEnsembl when file is not specified. See help page for makeTxDbFromEnsembl . |
| ... | Additional arguments passed to either makeTxDbFromGFF (if file is specified) or makeTxDbFromEnsembl if file is NA. |

Value

A [TxDb](#) object.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

Examples

```
if (interactive()){
  # To obtain a TxDb for Homo sapiens from Ensembl:
  txdb <- getTxDb()

  # To obtain a TxDb from a GFF file:
  file='https://www.mirbase.org/ftp/CURRENT/genomes/hsa.gff3'
  txdb <- getTxDb(file=file)
}
```

getTxInfoDataFrame *To obtain a DataFrame of transcript-specific CDS and mRNA coordinates*

Description

To obtain a DataFrame of transcript-specific CDS and mRNA coordinates.

Usage

```
getTxInfoDataFrame(
  tx_id,
  txObject,
  bsgenome,
  extend = 30,
  checkCdsLength = TRUE
)
```

Arguments

| | |
|----------------|---|
| tx_id | String specifying ENSEMBL Transcript id. |
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList . |
| bsgenome | BSgenome object from which to extract sequences if a GRanges object is provided as input. |
| extend | Integer value specifying how many nucleotides in intron regions should be included. |
| checkCdsLength | Should the CDS nucleotide length be a multiple of 3? TRUE by default. |

Value

A DataFrame containing nucleotide and amino acid information. The columns are:

- chr Character specifying chromosome.
- pos Integer value specifying coordinate in reference genome.
- strand Character specifying strand of transcript.
- nuc Character specifying nucleotide on the strand specified by strand.
- aa Character specifying amino acid.
- aa_number Integer specifying amino acid number from 5' end.
- exon Integer specifying exon number.
- pos_plot Integer specifying plot coordinate. Useful for plotting.
- pos_mrna Integer specifying relative mRNA coordinate from the start of the mRNA.
- pos_cds Integer specifying relative CDS coordinate from the start of the CDS.
- region Character specifying gene region: 3UTR, 5UTR, CDS, Intron, Upstream (promoter) or downstream.

Author(s)

Jean-Philippe Fortin

Examples

```
library(BSgenome.Hsapiens.UCSC.hg38)
bsgenome <- BSgenome.Hsapiens.UCSC.hg38
data("grListExample")
tx_id <- "ENST00000538872"
df <- getTxInfoDataFrame(tx_id=tx_id,
  txObject=grListExample,
  bsgenome=bsgenome)
```

grListExample

Example of a TxDb object converted to a GRangesList

Description

Example of a TxDb object converted to a GRangesList object for human gene IQSEC3 (ENSG00000120645).

Usage

```
data(grListExample, package="crisprDesign")
```

Format

Named GRangesList with 7 elements: transcripts, exons, cds, fiveUTRs, threeUTRs, introns and tss.

Details

The full human transcriptome TxDb object was obtained from the Ensembl 104 release using the getTxDb function and converted to a GRangesList object using the TxDb2GRangesList function and subsequently subsetting to only contain the IQSEC3 gene (ENSG00000120645) located at the start of chr12 in the human genome (hg38 build).

grRepeatsExample

Example of a GRanges object containing repeat elements

Description

Example of a GRanges object containing genomic coordinates of repeat elements found in the neighborhood of human gene IQSEC3 (ENSG00000120645).

Usage

```
data(grRepeatsExample, package="crisprDesign")
```

Format

A GRanges object.

GuideSet2DataFrames *Create a list of annotation tables from a GuideSet object*

Description

Create a list of annotation tables from a GuideSet object

Usage

```
GuideSet2DataFrames(guideSet, useSpacerCoordinates = TRUE, primaryOnly = FALSE)
```

Arguments

| | |
|-----------------------------------|--|
| <code>guideSet</code> | A GuideSet object |
| <code>useSpacerCoordinates</code> | Should the spacer coordinates be used as start and end coordinates? TRUE by default. If FALSE, the PAM site coordinate is used for both start and end. |
| <code>primaryOnly</code> | Should only the primary table (on-targets) be returned? FALSE by default. |

Value

A simple list of tables containing annotations derived from a GuideSet object. The first table ("primary") is always available, while the other tables will be only available when the annotations were added to the GuideSet object.

- `primary` Primary table containing genomic coordinates and sequence information of the gRNA sequences. Also contains on-target and off-target scores when available.
- `alignments` Table of on- and off-target alignments.
- `geneAnnotation` Gene context annotation table.
- `tssAnnotation` TSS context annotation table.
- `enzymeAnnotation` Boolean table indicating whether or not recognition motifs of restriction enzymes are found.
- `snps` SNP annotation table (human only).

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

Examples

```
data(guideSetExampleFullAnnotation)
tables <- GuideSet2DataFrames(guideSetExampleFullAnnotation)
```

| | |
|-----------------|--|
| guideSetExample | <i>Example of a GuideSet object storing gRNA sequences targeting the CDS of IQSEC3</i> |
|-----------------|--|

Description

Example of a [GuideSet](#) object storing gRNA sequences targeting the coding sequence of human gene IQSEC3 (ENSG00000120645) for SpCas9 nuclease.

Usage

```
data(guideSetExample, package="crisprDesign")
```

Format

A [GuideSet](#) object.

Details

The object was obtained by calling [findSpacers](#) on the CDS region of human gene IQSEC3. See code in `inst/scripts/generateGuideSet.R`.

| | |
|-------------------------------|--|
| guideSetExampleFullAnnotation | <i>Example of a fully-annotated GuideSet object storing gRNA sequences targeting the CDS of IQSEC3</i> |
|-------------------------------|--|

Description

Example of a fully-annotated [GuideSet](#) object storing gRNA sequences targeting the coding sequence of human gene IQSEC3 (ENSG00000120645) for SpCas9 nuclease.

Usage

```
data(guideSetExampleFullAnnotation, package="crisprDesign")
```

Format

A [GuideSet](#) object.

Details

The object was obtained by applying all available `add*` annotation functions in `crisprDesign` (e.g. `addSequenceFeatures`) to a randomly selected 20-guide subset of `guideSetExample`. See code in `inst/scripts/generateGuideSetFullAnnotation.R`.

guideSetExampleWithAlignments

Example of a [GuideSet](#) object storing gRNA sequences targeting the CDS of IQSEC3 with off-target alignments.

Description

Example of a [GuideSet](#) object storing gRNA sequences targeting the coding sequence of human gene IQSEC3 (ENSG00000120645) for SpCas9 nuclease with off-target alignments.

Usage

```
data(guideSetExampleWithAlignments, package="crisprDesign")
```

Format

A [GuideSet](#) object.

Details

The object was obtained by adding off-target alignments to a randomly selected 20-guide subset of `guideSetExample`. See code in `inst/scripts/generateGuideSetFullAnnotation.R`.

pamOrientation

An S4 class to store pairs of CRISPR gRNA sequences.

Description

An S4 class to store pairs of CRISPR gRNA sequences.

Usage

```
pamOrientation(object, ...)
```

```
pamDistance(object, ...)
```

```
spacerDistance(object, ...)
```

```
cutLength(object, ...)
```

```
PairedGuideSet(GuideSet1 = NULL, GuideSet2 = NULL)
```

```
## S4 method for signature 'PairedGuideSet'
pamOrientation(object)
```

```
## S4 method for signature 'PairedGuideSet'
pamDistance(object)
```

```
## S4 method for signature 'PairedGuideSet'
```

```

spacerDistance(object)

## S4 method for signature 'PairedGuideSet'
cutLength(object)

## S4 method for signature 'PairedGuideSet'
crisprNuclease(object, index = NULL)

## S4 method for signature 'PairedGuideSet'
spacers(object, as.character = FALSE, returnAsRna = FALSE, index = NULL)

## S4 method for signature 'PairedGuideSet'
pams(object, as.character = FALSE, returnAsRna = FALSE, index = NULL)

## S4 method for signature 'PairedGuideSet'
pamSites(object, index = NULL)

## S4 method for signature 'PairedGuideSet'
cutSites(object, index = NULL)

## S4 method for signature 'PairedGuideSet'
protospacers(
  object,
  as.character = FALSE,
  include.pam = FALSE,
  returnAsRna = FALSE,
  index = NULL
)

## S4 method for signature 'PairedGuideSet'
spacerLength(object, index = NULL)

## S4 method for signature 'PairedGuideSet'
pamLength(object, index = NULL)

## S4 method for signature 'PairedGuideSet'
pamSide(object, index = NULL)

```

Arguments

| | |
|--------------|--|
| object | PairedGuideSet object. |
| ... | Additional arguments for class-specific methods |
| GuideSet1 | A GuideSet object containing gRNAs at the first position of the pairs. |
| GuideSet2 | A GuideSet object containing gRNAs at the second position of the pairs. |
| index | Integer value indicating gRNA position. Must be either 1, 2, or NULL (default). If NULL, both positions are returned. |
| as.character | Should sequences be returned as a character vector? FALSE by default, in which case sequences are returned as a DNAStringSet . |
| returnAsRna | Should the sequences be returned as RNA instead of DNA? FALSE by default. |
| include.pam | Should PAM sequences be included? FALSE by default. |

Value

A PairedGuideSet object.

Functions

- PairedGuideSet(): Create a [PairedGuideSet](#) object

Constructors

Use the constructor `link{PairedGuideSet}` to create a PairedGuideSet object.

Examples

```
library(crisprDesign)
data(guideSetExample, package="crisprDesign")
gs <- guideSetExample
gs <- gs[order(BiocGenerics::start(gs))]
gs1 <- gs[1:10]
gs2 <- gs[1:10+10]
pgs <- PairedGuideSet(gs1, gs2)
```

```
preparePfamTable
```

```
Obtain Pfam domains from biomaRt
```

Description

Obtain Pfam domains from biomaRt for all transcripts found in a gene model object.

Usage

```
preparePfamTable(txObject, mart_dataset)
```

Arguments

| | |
|--------------|---|
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList to provide a gene model annotation. |
| mart_dataset | String specifying dataset to be used by biomaRt for Pfam domains annotation . E.g. "hsapiens_gene_ensembl". |

Value

A [DataFrame](#) object with the following columns:

- `ensembl_transcript_id` Ensembl transcript ID.
- `pfam` Pfam domain name.
- `pfam_start` Start amino acid coordinate of the Pfam domain.
- `pfam_end` End amino acid coordinate of the Pfam domain.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

Examples

```
data(grListExample, package="crisprDesign")

if (interactive()){
  pfamTable <- preparePfamTable(grListExample,
                                mart_dataset="hsapiens_gene_ensembl")
}
```

queryTss

Convenience function to search for TSS coordinates.

Description

Convenience function to search for TSS coordinates.

Usage

```
queryTss(tssObject, queryColumn, queryValue, tss_window = NULL)
```

Arguments

| | |
|-------------|---|
| tssObject | A GRanges containing genomic positions of transcription starting sites (TSSs). |
| queryColumn | String specifying which column of <code>mcols(tssObject)</code> should be searched for. |
| queryValue | Character vector specifying the values to search for in <code>tssObject[[queryColumn]]</code> . |
| tss_window | Numeric vector of length 2 establishing the genomic region to return. The value pair sets the 5 prime and 3 prime limits, respectively, of the genomic region with respect to the TSS. Use negative value(s) to set limit(s) upstream of the TSS. Default is <code>c(-500, 500)</code> , which includes 500bp upstream and downstream of the TSS. |

Value

A [GRanges](#) object. Searches yielding no results will return an empty [GRanges](#) object.

Author(s)

Luke Hoberecht, Jean-Philippe Fortin

See Also

[queryTxObject](#) for querying gene annotations.

Examples

```
data(tssObjectExample, package="crisprDesign")
queryTss(tssObjectExample,
         queryColumn="gene_symbol",
         queryValue="IQSEC3")
```

| | |
|---------------|---|
| queryTxObject | <i>Convenience function to search for gene coordinates.</i> |
|---------------|---|

Description

Convenience function to search for gene coordinates.

Usage

```
queryTxObject(
  txObject,
  featureType = c("transcripts", "exons", "cds", "fiveUTRs", "threeUTRs", "introns"),
  queryColumn,
  queryValue
)
```

Arguments

| | |
|-------------|---|
| txObject | A TxDb object or a GRangesList object obtained using TxDb2GRangesList . |
| featureType | The genomic feature in txObject to base your query on. Must be one of the following: "transcripts", "exons", "cds", "fiveUTRs", "threeUTRs" or "introns". |
| queryColumn | Character string specifying the column in txObject[[featureType]] to search for queryValue(s). |
| queryValue | Vector specifying the value(s) to search for in txObject[[featureType]][[queryColumn]]. |

Value

A [GRanges](#) object. Searches yielding no results will return an empty [GRanges](#) object.

Author(s)

Luke Hoberecht, Jean-Philippe Fortin

See Also

[queryTss](#) for querying TSS annotations.

Examples

```
data(grListExample, package="crisprDesign")
queryTxObject(grListExample,
  featureType="cds",
  queryColumn="gene_symbol",
  queryValue="IQSEC3")
```

| | |
|-------------|---------------------------------|
| rankSpacers | <i>Recommended gRNA ranking</i> |
|-------------|---------------------------------|

Description

Function for ranking spacers using recommended crisprDesign criteria. CRISPRko, CRISPRa and CRISPRi modalities are supported.

Usage

```
rankSpacers(
  guideSet,
  tx_id = NULL,
  commonExon = FALSE,
  modality = c("CRISPRko", "CRISPRa", "CRISPRi"),
  useDistanceToTss = TRUE
)
```

Arguments

| | |
|------------------|--|
| guideSet | A GuideSet object. |
| tx_id | Optional string specifying transcript ID to use isoform-specific information for gRNA ranking. |
| commonExon | Should gRNAs targeting common exons by prioritized? FALSE by default. If TRUE, tx_id must be provided. |
| modality | String specifying the CRISPR modality. Should be one of the following: "CRISPRko", "CRISPRa", or "CRISPRi". |
| useDistanceToTss | Should distance to TSS be used to rank gRNAs for CRISPRa and CRISPRi applications? TRUE by default. For SpCas9 and human targets, this should be set to FALSE if addCrispraiScores was used. |

Details

For each nuclease, we rank gRNAs based on several rounds of priority. For SpCas9, gRNAs with unique target sequences and without 1- or 2-mismatch off-targets located in coding regions are placed into the first round. Then, gRNAs with a small number of one- or two-mismatch off-targets (less than 5) are placed into the second round. Remaining gRNAs are placed into the third round. Finally, any gRNAs overlapping a common SNP (human only), containing a polyT stretch, or with extreme GC content (below 20) are placed into the fourth round.

If tx_id is specified, within each round of selection, gRNAs targeting the first 85 percent of the specific transcript are prioritized first. If tx_id is specified, and commonExon is set to TRUE, gRNAs targeting common exons across isoforms are also prioritized. If a conservation score is available, gRNAs targeting conserved regions (phyloP conservation score greater than 0), are also prioritized.

Within each bin, gRNAs are ranked by a composite on-target activity rank to prioritize active gRNAs. The composite on-target activity rank is calculated by taking the average rank across the DeepHF and RuleSet3 scores for CRISPRko. For CRISPRa or CRISPRi, the CRISPRai scores are used if available.

The process is identical for enAsCas12a, with the exception that the enPAMGb method is used as the composite score.

For CasRx, gRNAs targeting all isoforms of a given gene, with no 1- or 2-mismatch off-targets, are placed into the first round. gRNAs targeting at least 50 percent of the isoforms of a given gene, with no 1- or 2-mismatch off-targets, are placed into the second round. Remaining gRNAs are placed into the third round. Within each round of selection, gRNAs are further ranked by the CasRxRF on-target score.

Value

A [GuideSet](#) object ranked from best to worst gRNAs, with a column rank stored in `mcols(guideSet)` indicating gRNA rank.

Author(s)

Luke Hoberecht, Jean-Philippe Fortin

Examples

```
data(guideSetExampleFullAnnotation, package="crisprDesign")
gs <- rankSpacers(guideSetExampleFullAnnotation,
                  tx_id = "ENST00000538872")
gs
```

reexports

Objects exported from other packages

Description

These objects are imported from other packages. Follow the links below to see their documentation.

S4Vectors [mcols](#)

Seqinfo [seqnames](#)

removeRepeats

Remove [GuideSet](#) gRNAs that overlap repeat elements

Description

Remove [GuideSet](#) gRNAs that overlap repeat elements.

Usage

```
removeRepeats(object, ...)

## S4 method for signature 'GuideSet'
removeRepeats(object, gr.repeats = NULL, ignore.strand = TRUE)

## S4 method for signature 'PairedGuideSet'
removeRepeats(object, gr.repeats = NULL, ignore.strand = TRUE)

## S4 method for signature 'NULL'
removeRepeats(object)
```

Arguments

| | |
|---------------|---|
| object | A GuideSet object or a PairedGuideSet object. |
| ... | Additional arguments, currently ignored. |
| gr.repeats | A GRanges object containing repeat elements regions. |
| ignore.strand | Should gene strand be ignored when annotating? TRUE by default. |

Value

object filtered for spacer sequences not overlapping any repeat elements. An `inRepeats` column is also appended in `mcols(object)`.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

See Also

`link{addRepeats}`.

Examples

```
data(guideSetExample, package="crisprDesign")
data(grRepeatsExample, package="crisprDesign")
guideSet <- removeRepeats(guideSetExample,
                          gr.repeats=grRepeatsExample)
```

removeSpacersWithSecondaryTargets

Remove gRNAs targeting secondary targets

Description

Remove gRNAs targeting secondary targets

Usage

```
removeSpacersWithSecondaryTargets(
  guideSet,
  geneID,
  geneColumn = "gene_id",
  ignoreGenesWithoutSymbols = TRUE,
  ignoreReadthroughs = TRUE
)
```

Arguments

guideSet A [GuideSet](#) object.

geneID String specifying gene ID of the main gene target.

geneColumn Column in geneAnnotation(guideSet) specifying gene IDs

ignoreGenesWithoutSymbols
 Should gene without gene symbols be ignored when removing co-targeting gRNAs?

ignoreReadthroughs
 Should readthrough genes be ignored when removing co-targeting gRNAs?

Details

The protospacer target sequence of gRNAs can be located in overlapping genes, and this function allows users to filter out such gRNAs. This ensures remaining gRNAs are targeting only one gene.

Value

A [GuideSet](#) object with gRNAs targeting multiple targets removed.

Author(s)

Jean-Philippe Fortin

snpObjectExample

Example of a [GRanges](#) object containing SNPs

Description

Example of a [GRanges](#) object containing genomic coordinates of SNPs in the neighborhood of human gene IQSEC3 (ENSG00000120645).

Usage

```
data(snpObjectExample, package="crisprDesign")
```

Format

A [GRanges](#) object.

| | |
|------------------|---|
| tssObjectExample | <i>Example of a GRanges object containing TSS coordinates</i> |
|------------------|---|

Description

Example of a [GRanges](#) containing transcription starting site (TSS) coordinates for human gene IQSEC3 (ENSG00000120645).

Usage

```
data(tssObjectExample, package="crisprDesign")
```

Format

[GRanges](#) object of length 2 corresponding to the 2 TSSs of gene IQSEC3.

Details

The TSS coordinates were obtained from the two transcript stored in the `grListExample` object for gene IQSEC3.

| | |
|------------------|---|
| Txdb2GRangesList | <i>Convert a TxDb object into a GRangesList</i> |
|------------------|---|

Description

Convenience function to reformat a [TxDb](#) object into a [GRangesList](#).

Usage

```
Txdb2GRangesList(
  txdb,
  standardChromOnly = TRUE,
  genome = NULL,
  seqlevelsStyle = c("UCSC", "NCBI")
)
```

Arguments

| | |
|-------------------|---|
| txdb | A TxDb object. |
| standardChromOnly | Should only standard chromosomes be kept? TRUE by default. |
| genome | Optional string specifying genome. e.g. "hg38", to be added to <code>genome(txdb)</code> . |
| seqlevelsStyle | String specifying which style should be used for sequence names. "UCSC" by default (including "chr"). "NCBI" will omit "chr" in the sequence names. |

Value

A named [GRangesList](#) of length 7 with the following elements: transcripts, exons, introns, cds, fiveUTRs, threeUTRs and tss.

Author(s)

Jean-Philippe Fortin, Luke Hoberecht

See Also

[getTxDb](#) to obtain a [TxDb](#) object.

Examples

```
if (interactive()){
  # To obtain a TxDb for Homo sapiens from Ensembl:
  txdb <- getTxDb()

  # To convert to a GRanges list:
  txdb <- TxDb2GRangesList(txdb)
}
```

updateOpsLibrary

Update OPS library with additional gRNAs

Description

Update OPS library with additional gRNAs

Usage

```
updateOpsLibrary(
  opsLibrary,
  df,
  n_guides = 4,
  gene_field = "gene",
  min_dist_edit = 2,
  dist_method = c("hamming", "levenshtein"),
  splitByChunks = FALSE
)
```

Arguments

| | |
|---------------|--|
| opsLibrary | data.frame obtained from designOpsLibrary. |
| df | data.frame containing information about additional candidate gRNAs to add to the OPS library. |
| n_guides | Integer specifying how many gRNAs per gene should be selected. 4 by default. |
| gene_field | String specifying the column in df specifying gene names. |
| min_dist_edit | Integer specifying the minimum distance edit required for barcodes to be considered dissimilar. Barcodes that have edit distances less than the min_dist_edit will not be included in the library. 2 by default. |
| dist_method | String specifying distance method. Must be either "hamming" (default) or "levenshtein". |

`splitByChunks` Should distances be calculated in a chunk-wise manner? FALSE by default. Highly recommended when the set of query barcodes is large to reduce memory footprint.

Value

A data.frame containing the original gRNAs from the input opsLibrary data.frame as well as additional gRNAs selected from the input data.frame df.

Author(s)

Jean-Philippe Fortin

Examples

```
data(guideSetExample, package="crisprDesign")
guideSet <- unique(guideSetExample)
guideSet <- addOpsBarcodes(guideSet)
guideSet1 <- guideSet[1:200]
guideSet2 <- guideSet[201:400]

df1 <- data.frame(ID=names(guideSet1),
                  spacer=spacers(guideSet1, as.character=TRUE),
                  opsBarcode=as.character(guideSet1$opsBarcode))
df2 <- data.frame(ID=names(guideSet2),
                  spacer=spacers(guideSet2, as.character=TRUE),
                  opsBarcode=as.character(guideSet2$opsBarcode))

# Creating mock gene:
df1$gene <- rep(paste0("gene",1:10),each=20)
df2$gene <- rep(paste0("gene",1:10+10),each=20)
df1$rank <- rep(1:20,10)
df2$rank <- rep(1:20,10)
opsLib <- designOpsLibrary(df1)
opsLib <- updateOpsLibrary(opsLib, df2)
```

validateOpsLibrary *Validate gRNA library for optical pooled screening*

Description

Validate gRNA library for optical pooled screening

Usage

```
validateOpsLibrary(
  df,
  min_dist_edit = 2,
  dist_method = c("hamming", "levenshtein")
)
```

Arguments

| | |
|----------------------------|---|
| <code>df</code> | data.frame containing information about candidate gRNAs from which to build the OPS library. See details. |
| <code>min_dist_edit</code> | Integer specifying the minimum distance edit required for barcodes to be considered dissimilar. |
| <code>dist_method</code> | String specifying distance method. Must be either "hamming" (default) or "levenshtein". |

Value

The original `df` is all checks pass. Otherwise, a stop error.

Author(s)

Jean-Philippe Fortin

Examples

```
data(guideSetExample, package="crisprDesign")
guideSet <- unique(guideSetExample)
guideSet <- addOpsBarcodes(guideSet)
df <- data.frame(ID=names(guideSet),
                 spacer=spacers(guideSet, as.character=TRUE),
                 opsBarcode=as.character(guideSet$opsBarcode))
df$gene <- rep(paste0("gene",1:40),each=20)
df$rank <- rep(1:20,40)
opsLib <- designOpsLibrary(df)
opsLib <- validateOpsLibrary(opsLib)
```

Index

* datasets

- grListExample, 57
- grRepeatsExample, 57
- guideSetExample, 59
- guideSetExampleFullAnnotation, 59
- guideSetExampleWithAlignments, 60
- snpObjectExample, 68
- tssObjectExample, 69

* internal

- reexports, 66

- addCompositeScores, 3
- addCompositeScores, GuideSet-method
 - (addCompositeScores), 3
- addCompositeScores, NULL-method
 - (addCompositeScores), 3
- addCompositeScores, PairedGuideSet-method
 - (addCompositeScores), 3
- addConservationScores, 4
- addConservationScores, GuideSet-method
 - (addConservationScores), 4
- addConservationScores, NULL-method
 - (addConservationScores), 4
- addConservationScores, PairedGuideSet-method
 - (addConservationScores), 4
- addCutSites (crisprNuclease), 37
- addCutSites, GuideSet-method
 - (crisprNuclease), 37
- addDistanceToTss, 6
- addDistanceToTss, GuideSet-method
 - (addDistanceToTss), 6
- addDistanceToTss, NULL-method
 - (addIsoformAnnotation), 13
- addDistanceToTss, PairedGuideSet-method
 - (addDistanceToTss), 6
- addEditedAlleles, 7
- addEditingSites, 8
- addEditingSites, GuideSet-method
 - (addEditingSites), 8
- addEditingSites, NULL-method
 - (addEditingSites), 8
- addEditingSites, PairedGuideSet-method
 - (addEditingSites), 8
- addExonTable, 9

- addGeneAnnotation, 10, 10, 20, 33, 34
- addGeneAnnotation, GuideSet-method
 - (addGeneAnnotation), 10
- addGeneAnnotation, NULL-method
 - (addSNPAnnotation), 25
- addGeneAnnotation, PairedGuideSet-method
 - (addGeneAnnotation), 10
- addIsoformAnnotation, 13
- addIsoformAnnotation, GuideSet-method
 - (addIsoformAnnotation), 13
- addIsoformAnnotation, NULL-method
 - (addIsoformAnnotation), 13
- addIsoformAnnotation, PairedGuideSet-method
 - (addIsoformAnnotation), 13
- addNtcs, 14
- addNtcs, GuideSet-method (addNtcs), 14
- addNtcs, NULL-method (addNtcs), 14
- addNtcs, PairedGuideSet-method
 - (addNtcs), 14
- addOffTargetScores, 15, 17
- addOffTargetScores, GuideSet-method
 - (addOffTargetScores), 15
- addOffTargetScores, NULL-method
 - (addOffTargetScores), 15
- addOffTargetScores, PairedGuideSet-method
 - (addOffTargetScores), 15
- addOnTargetScores, 4, 16
- addOnTargetScores, GuideSet-method
 - (addOnTargetScores), 16
- addOnTargetScores, NULL-method
 - (addOnTargetScores), 16
- addOnTargetScores, PairedGuideSet-method
 - (addOnTargetScores), 16
- addOpsBarcodes, 18
- addPamScores, 18
- addPamScores, GuideSet-method
 - (addPamScores), 18
- addPamScores, NULL-method
 - (addPamScores), 18
- addPamScores, PairedGuideSet-method
 - (addPamScores), 18
- addPfamDomains, 19
- addPfamDomains, GuideSet-method

- (addPfamDomains), 19
- addPfamDomains, NULL-method
 - (addPfamDomains), 19
- addPfamDomains, PairedGuideSet-method
 - (addPfamDomains), 19
- addReinitiationFlag, 20
- addRepeats, 21
- addRepeats, GuideSet-method
 - (addRepeats), 21
- addRepeats, NULL-method (addRepeats), 21
- addRepeats, PairedGuideSet-method
 - (addRepeats), 21
- addRestrictionEnzymes, 22
- addRestrictionEnzymes, GuideSet-method
 - (addRestrictionEnzymes), 22
- addRestrictionEnzymes, NULL-method
 - (addRestrictionEnzymes), 22
- addRestrictionEnzymes, PairedGuideSet-method
 - (addRestrictionEnzymes), 22
- addSequenceFeatures, 24
- addSequenceFeatures, GuideSet-method
 - (addSequenceFeatures), 24
- addSequenceFeatures, NULL-method
 - (addSequenceFeatures), 24
- addSequenceFeatures, PairedGuideSet-method
 - (addSequenceFeatures), 24
- addSNPAnnotation, 25
- addSNPAnnotation, GuideSet-method
 - (addSNPAnnotation), 25
- addSNPAnnotation, NULL-method
 - (addSNPAnnotation), 25
- addSNPAnnotation, PairedGuideSet-method
 - (addSNPAnnotation), 25
- addSpacerAlignments, 27, 31
- addSpacerAlignments, GuideSet-method
 - (addSpacerAlignments), 27
- addSpacerAlignments, NULL-method
 - (addSpacerAlignments), 27
- addSpacerAlignments, PairedGuideSet-method
 - (addSpacerAlignments), 27
- addSpacerAlignmentsIterative, 30, 31
- addSpacerAlignmentsIterative
 - (addSpacerAlignments), 27
- addSpacerAlignmentsIterative, GuideSet-method
 - (addSpacerAlignments), 27
- addSpacerAlignmentsIterative, NULL-method
 - (addSpacerAlignments), 27
- addSpacerAlignmentsIterative, PairedGuideSet-method
 - (addSpacerAlignments), 27
- addTssAnnotation, 6, 12, 32
- addTssAnnotation, GuideSet-method
 - (addTssAnnotation), 32
- addTssAnnotation, NULL-method
 - (addTssAnnotation), 32
- addTssAnnotation, PairedGuideSet-method
 - (addTssAnnotation), 32
- addTxTable, 10, 33
- alignments (crisprNuclease), 37
- alignments, GuideSet-method
 - (crisprNuclease), 37
- alignments<- (crisprNuclease), 37
- alignments<-, GuideSet-method
 - (crisprNuclease), 37
- BaseEditor, 7
- BSgenome, 29, 35, 41, 44, 47, 49, 53, 54, 56
- bsgenome (crisprNuclease), 37
- bsgenome, GuideSet-method
 - (crisprNuclease), 37
- completeSpacers, 34
- convertToMinMaxGRanges, 36
- convertToProtospacerGRanges, 37
- CrisprNuclease, 18, 30, 35, 41, 42, 44, 47, 49
- crisprNuclease, 37
- crisprNuclease, GuideSet-method
 - (crisprNuclease), 37
- crisprNuclease, PairedGuideSet-method
 - (pamOrientation), 60
- customSequences (crisprNuclease), 37
- customSequences, GuideSet-method
 - (crisprNuclease), 37
- cutLength (pamOrientation), 60
- cutLength, PairedGuideSet-method
 - (pamOrientation), 60
- cutSites, GuideSet-method
 - (crisprNuclease), 37
- cutSites, PairedGuideSet-method
 - (pamOrientation), 60
- DataFrame, 20, 44, 62
- designCompleteAnnotation, 43
- designOpsLibrary, 45
- DNAStrng, 46, 48, 49
- DNAStrngSet, 41, 46, 48, 49, 53, 54, 61
- editedAlleles (crisprNuclease), 37
- editedAlleles, GuideSet-method
 - (crisprNuclease), 37
- enzymeAnnotation, 23
- enzymeAnnotation (crisprNuclease), 37
- enzymeAnnotation, GuideSet-method
 - (crisprNuclease), 37
- enzymeAnnotation<- (crisprNuclease), 37
- enzymeAnnotation<-, GuideSet-method
 - (crisprNuclease), 37

- exonTable (crisprNuclease), 37
- exonTable, GuideSet-method (crisprNuclease), 37
- findSpacerPairs, 46
- findSpacers, 48, 48, 59
- flattenGuideSet, 50
- geneAnnotation, 12
- geneAnnotation (crisprNuclease), 37
- geneAnnotation, GuideSet-method (crisprNuclease), 37
- geneAnnotation<- (crisprNuclease), 37
- geneAnnotation<-, GuideSet-method (crisprNuclease), 37
- getBarcodeDistanceMatrix, 51
- getConsensusIsoform, 52
- getMrnaSequences, 53
- getPAMSequence (completeSpacers), 34
- getPAMSiteFromStartAndEnd (completeSpacers), 34
- getPreMrnaSequences, 53
- getSpacerAlignments, 31
- getSpacerAlignments (addSpacerAlignments), 27
- getSpacerSequence (completeSpacers), 34
- getTssObjectFromTxObject, 54
- getTxDb, 55, 57, 70
- getTxInfoDataFrame, 7, 56
- GRanges, 21, 29, 31, 32, 44, 46–49, 56, 57, 63, 64, 67–69
- GRangesList, 9, 11, 29, 34, 44, 52–54, 56, 57, 62, 64, 69
- grListExample, 57
- grRepeatsExample, 57
- GuideSet, 3–7, 9–26, 29, 32–34, 36, 37, 41, 42, 46, 49, 59–61, 65–68
- GuideSet (crisprNuclease), 37
- GuideSet-class (crisprNuclease), 37
- GuideSet2DataFrames, 58
- guideSetExample, 59
- guideSetExampleFullAnnotation, 59
- guideSetExampleWithAlignments, 60
- makeTxDbFromEnsembl, 55
- makeTxDbFromGFF, 55
- mcols, 66
- mcols (reexports), 66
- offTargets (crisprNuclease), 37
- offTargets, GuideSet-method (crisprNuclease), 37
- onTargets (crisprNuclease), 37
- onTargets, GuideSet-method (crisprNuclease), 37
- PairedGuideSet, 4–6, 9, 11, 13–15, 17, 19–22, 24, 26, 29, 32, 34, 47, 61, 62, 67
- PairedGuideSet (pamOrientation), 60
- PairedGuideSet-class (pamOrientation), 60
- pamDistance (pamOrientation), 60
- pamDistance, PairedGuideSet-method (pamOrientation), 60
- pamLength, GuideSet-method (crisprNuclease), 37
- pamLength, PairedGuideSet-method (pamOrientation), 60
- pamOrientation, 60
- pamOrientation, PairedGuideSet-method (pamOrientation), 60
- pams, GuideSet-method (crisprNuclease), 37
- pams, PairedGuideSet-method (pamOrientation), 60
- pamSide, GuideSet-method (crisprNuclease), 37
- pamSide, PairedGuideSet-method (pamOrientation), 60
- pamSites (crisprNuclease), 37
- pamSites, GuideSet-method (crisprNuclease), 37
- pamSites, PairedGuideSet-method (pamOrientation), 60
- preparePfamTable, 20, 44, 62
- protospacers (crisprNuclease), 37
- protospacers, GuideSet-method (crisprNuclease), 37
- protospacers, PairedGuideSet-method (pamOrientation), 60
- prototypeSequence, GuideSet-method (crisprNuclease), 37
- queryTss, 63, 64
- queryTxObject, 63, 64
- rankSpacers, 65
- reexports, 66
- removeRepeats, 66
- removeRepeats, GuideSet-method (removeRepeats), 66
- removeRepeats, NULL-method (removeRepeats), 66
- removeRepeats, PairedGuideSet-method (removeRepeats), 66

removeSpacersWithSecondaryTargets, 67

Seqinfo, 14, 41

seqnames, 66

seqnames (reexports), 66

snpObjectExample, 68

snps (crisprNuclease), 37

snps, GuideSet-method (crisprNuclease), 37

snps<- (crisprNuclease), 37

snps<- , GuideSet-method (crisprNuclease), 37

spacerDistance (pamOrientation), 60

spacerDistance, PairedGuideSet-method (pamOrientation), 60

spacerLength, GuideSet-method (crisprNuclease), 37

spacerLength, PairedGuideSet-method (pamOrientation), 60

spacers (crisprNuclease), 37

spacers, GuideSet-method (crisprNuclease), 37

spacers, PairedGuideSet-method (pamOrientation), 60

targetOrigin (crisprNuclease), 37

targetOrigin, GuideSet-method (crisprNuclease), 37

tssAnnotation, 33

tssAnnotation (crisprNuclease), 37

tssAnnotation, GuideSet-method (crisprNuclease), 37

tssAnnotation<- (crisprNuclease), 37

tssAnnotation<- , GuideSet-method (crisprNuclease), 37

tssObjectExample, 69

TxDB, 9, 11, 29, 34, 44, 52–57, 62, 64, 69, 70

TxDB2GRangesList, 9, 11, 29, 34, 44, 52–54, 56, 57, 62, 64, 69

txTable (crisprNuclease), 37

txTable, GuideSet-method (crisprNuclease), 37

updateOpsLibrary, 70

validateOpsLibrary, 71

VCF, 44