

Package ‘crisprScore’

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Title On-Target and Off-Target Scoring Algorithms for CRISPR gRNAs

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Suggests BiocStyle, knitr, rmarkdown, testthat

biocViews CRISPR, FunctionalGenomics, FunctionalPrediction

Description Provides R wrappers of several on-target and off-target scoring methods for CRISPR guide RNAs (gRNAs). The following nucleases are supported: SpCas9, AsCas12a, enAsCas12a, and Rfx-Cas13d (CasRx). The available on-target cutting efficiency scoring methods are RuleSet1, Azimuth, DeepHF, DeepCpf1, enPAM+GB, and CRISPRscan. Both the CFD and MIT scoring methods are available for off-target specificity prediction. The package also provides a Lindel-derived score to predict the probability of a gRNA to produce indels inducing a frameshift for the Cas9 nuclease. Note that DeepHF, DeepCpf1 and enPAM+GB are not available on Windows machines.

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cfd.mm.weights.cas9 *Mismatch position weights for the CFD off-target algorithm (Cas9)*

Description

CFD off-target scoring weights for each nucleotide position and each pair of DNA:RNA mismatches, for 20-mer spacer sequences. Position 20 refers to the spacer position adjacent to the PAM sequence. A higher weight indicates greater mismatch tolerance by the Cas9 nuclease.

Usage

```
cfd.mm.weights.cas9
```

Format

Numeric vector

Source

<https://dx.doi.org/10.1038%2Fnbt.3437>

cf_d.mm.weights.casrx *Mismatch position weights for the CFD off-target algorithm (CasRx)*

Description

CFD off-target scoring weights for each nucleotide position and each pair of DNA:RNA mismatches, for 27-mer spacer sequences. Position 1 refers to the spacer position adjacent to the PAM sequence. A higher weight indicates greater mismatch tolerance by the CasRx nuclease.

Usage

cf_d.mm.weights.casrx

Format

Numeric vector

cf_d.pam.weights.cas9 *PAM sequence weights for the CFD off-target algorithm (Cas9)*

Description

CFD off-target PAM weights for each possible 3-mer Cas9 PAM sequences. A higher weight indicates greater mismatch tolerance by the Cas9 nuclease.

Usage

cf_d.pam.weights.cas9

Format

Numeric vector

Source

<https://dx.doi.org/10.1038%2Fnbt.3437>

`cfp.pam.weights.casrx` *PAM sequence weights for the CFD off-target algorithm (CasRx)*

Description

CFD off-target PAM weights for each possible 1-mer CasRx PAM sequences. A higher weight indicates greater mismatch tolerance by the CasRx nuclease.

Usage

```
cfp.pam.weights.casrx
```

Format

Numeric vector

`getAzimuthScores` *Calculate on-target sgRNA activity scores for Cas9 using Azimuth*

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the Azimuth scoring method. The Azimuth algorithm is an improvement upon the commonly-used 'Rule Set 2', also developed by the Doench lab.

Usage

```
getAzimuthScores(sequences, fork = FALSE)
```

Arguments

<code>sequences</code>	Character vector of 30bp sequences needed for Azimuth scoring, see details below.
<code>fork</code>	Set to TRUE to preserve changes to the R configuration within the session.

Details

The input sequences for Azimuth scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 3 nucleotides downstream of the protospacer sequence, for a total of 30 nucleotides: [4nt][20nt-spacer][NGG][3nt]. Note that a canonical PAM sequence (NGG) is required for Azimuth.

Value

getAzimuthScores returns a data.frame with sequence and score columns. The Azimuth score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References

Doench, J., Fusi, N., Sullender, M. et al. Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. *Nat Biotechnol* 34, 184–191 (2016). <https://doi.org/10.1038/nbt.3437>.

Examples

```
if (interactive()){
  flank5 <- "ACCT" #4bp
  spacer <- "ATCGATGCTGATGCTAGATA" #20bp
  pam <- "AGG" #3bp
  flank3 <- "TTG" #3bp
  input <- paste0(flank5, spacer, pam, flank3)
  results <- getAzimuthScores(input)
}
```

 getCasRxRFScores

Calculate on-target sgRNA activity scores for CasRx using CasRx-RF

Description

Calculate on-target sgRNA activity scores for CasRx (RfxCas13d) using the CasRx-RF algorithm.

Usage

```
getCasRxRFScores(
  mrnaSequence,
  directRepeat = "aaccctaccaactggtcggggtttgaaac",
  binaries = NULL,
  sort = FALSE,
  verbose = TRUE
)
```

Arguments

mrnaSequence	A DNASTringSet representing the mRNA sequence for which to extract spacer sequences and calculate scores.
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.
sort	Should spacers be sorted by score? FALSE by default.
verbose	Should messages be printed to console? TRUE by default.

Details

The function first extracts all 23mer spacer sequences targeting the mRNA sequence, and scores them for on-target activity.

Value

A data.frame with the following columns:

- ID Character vector specifying spacer ID.
- spacer 23-mer spacer sequence.
- pfs_site coordinate of the protospacer flanking sequence (PFS).
- protospacer 23-mer protospacer sequence (reverse complement of the spacer sequence).
- PFS PFS nucleotide.
- score Raw score (not standardized).
- standardizedScore Score standardized between 0 and 1.
- quartile Quartile score (1 to 4, with 4 being the best quartile).

A scores closer to 1 indicates higher predicted on-target activity.

Author(s)

Jean-Philippe Fortin

References

Wessels HH, Méndez-Mancilla A, Guo X, et al. Massively parallel Cas13 screens reveal principles for guide RNA design. *Nat biotechnol.* 2020 Jun;38(6):722-7.

Examples

```
fasta <- file.path(system.file(package="crisprScore"),
  "casxrf/test.fa")
mrnaSequence <- Biostrings::readDNASTringSet(filepath=fasta,
  format="fasta",
  use.names=TRUE)
results <- getCasRxRFScores(mrnaSequence)
```

getCFDScores	<i>Calculate CFD off-target specificity scores</i>
--------------	--

Description

Calculate cutting frequency determination (CFD) off-target specificity scores for CRISPR/Cas9 or CRISPR/CasRX.

Usage

```
getCFDScores(spacers, protospacers, pams, nuclease = c("SpCas9", "CasRx"))
```

Arguments

spacers	Character vector of 20bp spacer sequences. Must be in 5' to 3' direction. For SpCas9, must be of length 20bp. For CasRx, must be at most of length 27bp.
protospacers	Character vector of 20bp protospacer sequences (target sequences). Must be in 5' to 3' direction.
pams	Character vector of PAM sequences.
nuclease	String specifying the nuclease. Either "SpCas9" (default) or "CasRx".

Value

getCFDScores returns a data.frame with spacer, protospacer, and score columns. The CFD score takes on a value between 0 and 1. For a given pair (on-target, off-target), a higher CFD score indicates a higher likelihood for the nuclease to cut at the off-target. Non-canonical PAM sequences are taken into account by the CFD algorithm.

Author(s)

Jean-Philippe Fortin

References

Doench, J., Fusi, N., Sullender, M. et al. Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. *Nat Biotechnol* 34, 184–191 (2016). <https://doi.org/10.1038/nbt.3437>.

Examples

```
# Calculating MIT scores for two off-targets with respect to
# one spacer sequence:
spacer <- "AGGTGTAGTGTGTGATAA"
protospacer1 <- "CGGTGTAGTGTGTGATAA"
protospacer2 <- "CGGTGTCGTGTGTGATAA"
results <- getCFDScores(spacers=spacer,
  protospacers=c(protospacer1, protospacer2),
```

```

    pams=c("AGG", "CGG")
  )

```

getCrispraiScores *Calculate on-target sgRNA activity scores for CRISPRa and CRISPRi*

Description

Use the Weissman lab scoring method (library design v2) to calculate on-target sgRNA activity scores for Cas9-based CRISPR activation (CRISPRa) and CRISPR inactivation (CRISPRi) gene perturbation studies. The algorithm incorporates chromatin features, transcription start site, and sequence to predict gRNA activity scores. Only sgRNAs designed for the human genome (hg38 build) using Cas9 are supported at the moment, and only spacers of length 19 are supported at the moment.

Usage

```

getCrispraiScores(
  tss_df,
  sgrna_df,
  verbose = FALSE,
  modality = c("CRISPRa", "CRISPRi"),
  fastaFile = NULL,
  chromatinFiles = NULL,
  fork = FALSE
)

```

Arguments

tss_df	A data.frame specifying coordinates of transcription start site (TSS) of the targeted promoter regions. Must have the following columns: gene_symbol, promoter, transcripts, position, strand, and chr. See details section below for more information.
sgrna_df	A A data.frame specifying coordinates and spacer sequences of the sgRNAs to score. Must have the following columns: grna_id, tss_id, pam_site, strand, and spacer_19mer. See details section below for more information.
verbose	Should messages be printed to the console? TRUE by default.
modality	Which mode of perturbation is being used? Must be a string specifying either CRISPRa or CRISPRi.
fastaFile	String specifying fasta file of the hg38 genome.
chromatinFiles	Named character vector of length 3 specifying BigWig files containing chromatin accessibility data.
fork	Set to TRUE to preserve changes to the R configuration within the session.

Details

tss_df details: This must be a data.frame that contains the following columns: * gene_symbol: string specifying sHGNC/HUGO gene identifier. * promoter: string specifying promoter ID (e.g. "P1" or "P2"). * transcripts: Ensembl transcript identifier. * position: start position of TSS in hg38 coordinates. * strand: strand of the gene/TSS. Must be either + or -. * chr: string specifying chromosome (e.g. "chr1").

sgrna_df details: This must be a data.frame that contains the following columns: * grna_id: string specifying a unique sgRNA identifier. * tss_id: string specifying name of the TSS. * pam_site: genomic ccoordinate of the N in the NGG PAM sequence. * strand: strand fo the sgRNA. Must be either + or -. * spacer_19mer: string specifying sgRNA 19mer spacer sequence.

Value

getWeissmanScores returns a data.frame with grna_id and score columns. The Weissman score takes on a value between 0 and 1. A higher score indicates higher sgRNA efficiency.

Author(s)

Pirunthan Perampalam, Jean-Philippe Fortin

References

Horlbeck et al. Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation eLife 2016;5:e19760. <https://doi.org/10.7554/eLife.19760>.

Examples

```
## Not run:
results <- getCrispraiScores(tss_df=tssExampleCrispra,
                             sgrna_df=sgrnaExampleCrispra,
                             modality="CRISPRa")

results <- getCrispraiScores(tss_df=tssExampleCrispri,
                             sgrna_df=sgrnaExampleCrispri,
                             modality="CRISPRi")

## End(Not run)
```

getCRISPRscanScores *Calculate on-target sgRNA activity scores for Cas9 using CRISPRscan*

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the CRISPRscan scoring method. The method is also know as the Moreno-Mateos score. The CRISPRscan algorithm was trained using in vitro transcription of sgRNAs using a T7 promoter, and might therefore be suboptimal to predict sgRNA activity when expressed from U6 promoter.

Usage

```
getCRISPRscanScores(sequences)
```

Arguments

sequences Character vector of 35bp sequences needed for CRISPRscan scoring, see details below.

Details

The input sequences for Rule Set 1 scoring require 6 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 6 nucleotides downstream of the protospacer sequence, for a total of 35 nucleotides: [6nt][20nt-spacer][NGG][6nt]. Note that a canonical PAM sequence (NGG) is required for CRISPRscan.

Value

getCRISPRscanScores returns a data.frame with sequence and score columns. The CRISPRscan score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References

Moreno-Mateos MA, et al. CRISPRscan: designing highly efficient sgRNAs for CRISPR-Cas9 targeting in vivo. Nature methods. 2015 Oct;12(10):982-8.

Examples

```
flank5 <- "ACCTGG" #6bp
spacer <- "ATCGATGCTGATGCTAGATA" #20bp
pam <- "AGG" #3bp
flank3 <- "TTGAGC" #6bp
input <- paste0(flank5, spacer, pam, flank3)
results <- getCRISPRscanScores(input)
```

getDeepCpf1Scores *Calculate on-target sgRNA activity scores for Cas12a using DeepCpf1*

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas12a-induced knockout using the Deep-Cpf1 scoring method. Currently not supported on Windows machines.

Usage

```
getDeepCpf1Scores(sequences, convertPAM = TRUE, fork = FALSE)
```

Arguments

sequences	Character vector of 34bp sequences needed for DeepCpf1 scoring, see details below.
convertPAM	Should non-canonical PAM sequences be converted to TTTC? TRUE by default.
fork	Set to TRUE to preserve changes to the R configuration within the session.

Details

The input sequences for DeepCpf1 scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (4bp PAM sequence + 23bp spacer sequence) and 3 nucleotides downstream of the protospacer sequence, for a total of 34 nucleotides. If `convertPAM` is set to TRUE, any non-canonical PAM sequence will be converted to TTTC for scoring purposes.

Value

getDeepCpf1Scores returns a data.frame with sequence and score columns. The DeepCpf1 score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References

Kim, H., Min, S., Song, M. et al. Deep learning improves prediction of CRISPR–Cpf1 guide RNA activity. *Nat Biotechnol* 36, 239–241 (2018). <https://doi.org/10.1038/nbt.4061>.

Examples

```
if (interactive()){
  flank5 <- "ACC" #3bp
  pam    <- "TTTT" #4bp
  spacer <- "AATCGATGCTGATGCTAGATATT" #23bp
  flank3 <- "AAGT" #4bp
  input  <- paste0(flank5, pam, spacer, flank3)
  results <- getDeepCpf1Scores(input)
}
```

getDeepHFScores *Calculate on-target sgRNA activity scores for Cas9 using DeepHF*

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the DeepHF scoring method. Both U6 and T7 promoters are supported. Three different versions of the SpCas9 nuclease are supported: wildtype (WT-SpCas9), high-fidelity Cas9 (SpCas9-HF1) and enhanced Cas9 (eSpCas9). Currently not supported on Windows machines.

Usage

```
getDeepHFScores(  
  sequences,  
  enzyme = c("WT", "ESP", "HF"),  
  promoter = c("U6", "T7"),  
  fork = FALSE  
)
```

Arguments

sequences	Character vector of 23bp protospacer sequences.
enzyme	Character string specifying the Cas9 variant. 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"). "U6" by default.
fork	Set to TRUE to preserve changes to the R configuration within the session.

Details

Input sequences for DeepHF scoring must be 23bp protospacer sequences (20bp spacer sequences + 3bp PAM sequences). Only canonical PAM sequences (NGG) are allowed. Users can specify for which Cas9 they wish to score sgRNAs by using the argument enzyme: "WT" for Wildtype Cas9 (WT-SpCas9), "HF" for high-fidelity Cas9 (SpCas9-HF), or "ESP" for enhanced Cas9 (eSpCas9). For wildtype Cas9, users can also specify the promoter used for expressing sgRNAs using the argument promoter ("U6" by default).

Value

getDeepHFScores returns a data.frame with sequence and score columns. The DeepHF score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References

Wang, D., Zhang, C., Wang, B. et al. Optimized CRISPR guide RNA design for two high-fidelity Cas9 variants by deep learning. Nat Commun 10, 4284 (2019). <https://doi.org/10.1038/s41467-019-12281-8>

Examples

```
if (interactive()){
  spacer <- "ATCGATGCTGATGCTAGATA" #20bp
  pam    <- "AGG" #3bp
  input  <- paste0(spacer, pam)

  # Wiltype Cas9 using U6 promoter:
  results <- getDeepHFScores(input)

  # Wiltype Cas9 using T7 promoter:
  results <- getDeepHFScores(input, promoter="T7")

  #' High-fidelity Cas9:
  results <- getDeepHFScores(input, enzyme="HF")

  #' Enhanced Cas9:
  results <- getDeepHFScores(input, enzyme="ESP")
}
```

getEnPAMGBScores	<i>Calculate on-target sgRNA activity scores for enCas12a using en-PAM+GB</i>
------------------	---

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas12a-induced knockout using the en-PAM+GB scoring method. Currently not supported on Windows machines.

Usage

```
getEnPAMGBScores(sequences, fork = FALSE)
```

Arguments

sequences	Character vector of 34bp sequences needed for enPAM+GB scoring, see details below.
fork	Set to TRUE to preserve changes to the R configuration within the session.

Details

The input sequences for enPAM+GB scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (4bp PAM sequence + 23bp spacer sequence) and 3 nucleotides downstream of the protospacer sequence, for a total of 34 nucleotides. Both canonical and non-canonical PAM sequences can be provided.

Value

getEnPAMGBScores returns a data.frame with sequence and score columns.

Author(s)

Jean-Philippe Fortin

References

DeWeirdt, P.C., Sanson, K.R., Sangree, A.K. et al. Optimization of AsCas12a for combinatorial genetic screens in human cells. Nat Biotechnol 39, 94–104 (2021). <https://doi.org/10.1038/s41587-020-0600-6>.

Examples

```
if (interactive()){
  flank5 <- "CATG" #4bp
  pam    <- "TTTT" #4bp
  spacer <- "TTTGGGAACCAATCGATAATCAC" #23bp
  flank3 <- "ATT" #3bp
  input  <- paste0(flank5, pam, spacer, flank3)
  results <- getEnPAMGBScores(input)
}
```

getLindelScores	<i>Predict frameshift ratios from CRISPR/Cas9 indel prediction using Lindel</i>
-----------------	---

Description

Predict frameshift ratios from CRISPR/Cas9 indel prediction using the Lindel prediction algorithm.

Usage

```
getLindelScores(sequences, fork = FALSE)
```

Arguments

sequences	Character vector of 65bp sequences needed for Lindel scoring, see details below.
fork	Set to TRUE to preserve changes to the R configuration within the session.

Details

The input sequences for Lindel scoring require 13 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 29 nucleotides downstream of the protospacer sequence, for a total of 65 nucleotides. Note that only canonical PAM sequences (NGG) are accepted by Lindel.

Value

A data.frame with predicted frameshift ratio (between 0 and 1). A higher ratio indicates a greater chance of a frameshift indel introduced by CRISPR/Cas9-induced double-strand breaks.

Author(s)

Jean-Philippe Fortin

References

Wei Chen, Aaron McKenna, Jacob Schreiber, Maximilian Haeussler, Yi Yin, Vikram Agarwal, William Stafford Noble, Jay Shendure, Massively parallel profiling and predictive modeling of the outcomes of CRISPR/Cas9-mediated double-strand break repair, *Nucleic Acids Research*, Volume 47, Issue 15, 05 September 2019, Pages 7989–8003, <https://doi.org/10.1093/nar/gkz487>.

Examples

```
if (interactive()){
  flank5 <- "ACCTTTAATCGA" #13bp
  spacer <- "TGCTGATGCTAGATTAAG" #20bp
  pam <- "TGG" #3bp
  flank3 <- "CTTTAATCGATGCTGATGCTAGATATTA" #29bp
  input <- paste0(flank5, spacer, pam, flank3)
  results <- getLindelScores(input)
}
```

getMITScores

Calculate MIT off-target specificity scores for CRISPR/Cas9

Description

Calculate MIT off-target specificity scores for CRISPR/Cas9.

Usage

```
getMITScores(spacers, protospacers, pams, includeDistance = TRUE)
```

Arguments

spacers	Character vector of 20bp spacer sequences.
protospacers	Character vector of 20bp protospacer sequences for off-targets.
pams	Character vector of 3nt PAM sequences.
includeDistance	Should distance between mismatches be considered during scoring? TRUE by default.

Value

getMITScores returns a data.frame with spacer, protospacer, and score columns. The MIT score takes on a value between 0 and 1. For a given pair (on-target, off-target), a higher MIT score indicates a higher likelihood for the Cas9 nuclease to cut at the off-target. Non-canonical PAM sequences are taken into account by the MIT algorithm.

Author(s)

Jean-Philippe Fortin

References

Hsu, P., Scott, D., Weinstein, J. et al. DNA targeting specificity of RNA-guided Cas9 nucleases. *Nat Biotechnol* 31, 827–832 (2013). <https://doi.org/10.1038/nbt.2647>.

Examples

```
# Calculating MIT scores for two off-targets with respect to
# one spacer sequence:
spacer <- "AGGTGTAGTGTGTGATAA"
protospacer1 <- "CGGTGTAGTGTGTGATAA"
protospacer2 <- "CGGTGTCGTGTGTGATAA"
pams <- c("AGG", "CGG")
results <- getMITScores(spacers=spacer,
  protospacers=c(protospacer1, protospacer2),
  pams=pams
)
```

getRuleSet1Scores *Calculate on-target sgRNA activity scores for Cas9 using Rule Set 1*

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the Rule Set 1 scoring method. The Rule Set 1 algorithm was an early on-target efficiency method developed by the Doench lab.

Usage

```
getRuleSet1Scores(sequences)
```

Arguments

sequences Character vector of 30bp sequences needed for Rule Set 1 scoring, see details below.

Details

The input sequences for Rule Set 1 scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 3 nucleotides downstream of the protospacer sequence, for a total of 30 nucleotides: [4nt][20nt-spacer][NGG][3nt]. Note that a canonical PAM sequence (NGG) is required for Rule Set 1.

Value

getRuleSet1Scores returns a data.frame with sequence and score columns. The Rule Set 1 score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References

Doench, John G., et al. Rational design of highly active sgRNAs for CRISPR-Cas9-mediated gene inactivation. Nat Biotech 32, 1262-1267 (2014). <https://doi.org/10.1038/nbt.3026>.

Examples

```
flank5 <- "ACCT" #4bp
spacer <- "ATCGATGCTGATGCTAGATA" #20bp
pam <- "AGG" #3bp
flank3 <- "TTG" #3bp
input <- paste0(flank5, spacer, pam, flank3)
results <- getRuleSet1Scores(input)
```

mit.weights

Mismatch position weights for the MIT off-target algorithm (Cas9)

Description

MIT off-target scoring weights for each nucleotide position, for 20-mer spacer sequences. Position 20 refers to the spacer position adjacent to the PAM sequence. A higher weight indicates greater mismatch tolerance by the Cas9 nuclease.

Usage

```
mit.weights
```

Format

Numeric vector

Source

<https://dx.doi.org/10.1038%2Fnbt.2647>

scoringMethodsInfo *data.frame detailing available scoring methods*

Description

data.frame detailing available scoring methods with information needed to extract nucleotide sequences needed by each scoring algorithm.

Usage

```
data(scoringMethodsInfo)
```

Format

A data frame with 6 columns:

method name of the scoring method

nuclease nuclease compatible with the scoring method

left upstream offset (relative to PAM site) to extract nucleotide sequence needed for scoring

right downstream offset (relative to PAM site) to extract nucleotide sequence needed for scoring

type type of the scoring algorithm (on-target or off-target)

label proper case-sensitive method name for labeling

len length of the nucleotide sequence needed for scoring

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