Package ‘scanMiR’

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Description A set of tools for working with miRNA affinity models (KdModels), efficiently scanning for miRNA binding sites, and predicting target repression. It supports scanning using miRNA seeds, full miRNA sequences (enabling 3' alignment) and KdModels, and includes the prediction of slicing and TDMD sites. Finally, it includes utility and plotting functions (e.g. for the visual representation of miRNA-target alignment).
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## Description

Aggregates miRNA binding sites with log_kd values to predict transcript repression. See the vignette for more detail.

## Usage

```r
aggregateMatches(
  m,
  a = 0.007726,
  b = 0.5735,
  c = 0.181,
  p3 = 0.051,
  coef_utr = 0,
  coef_orf = 0,
  p3.range = c(3L, 8L),
  keepSiteInfo = TRUE,
  toInt = FALSE,
  BP = NULL
)
```
assignKdType

Arguments

- **m**: A GRanges or data.frame of matches as returned by `findSeedMatches`.
- **a**: The relative concentration of unbound AGO-miRNA complexes.
- **b**: Factor specifying the additional repression by a single bound AGO.
- **c**: Penalty for sites that are found within the ORF region.
- **p3**: Factor specifying additional repression due to 3p alignment.
- **coef_utr**: Factor specifying additional repression due to UTR length.
- **coef_orf**: Factor specifying additional repression due to ORF length.
- **p3.range**: Range used for 3p alignment.
- **keepSiteInfo**: Logical; whether to return information about site types (default = TRUE). Ignored if ‘m’ does not contain ‘log_kd’ values.
- **toInt**: Logical; whether to convert repression scores to integers (default = FALSE).
- **BP**: Pass ‘BiocParallel::MulticoreParam(ncores, progressbar=TRUE)’ to enable multithreading. Note that in addition, ‘aggregateMatches’ uses the data.table package, which is often set to use multi-threading by default (which would be multiplied by threads determined by ‘BP’). See `setDTthreads` for more information.

Value

A data.frame containing aggregated repression values and/or information about the numbers and types of matches.

Examples

```r
# we create mock RNA sequences and seeds:
seqs <- getRandomSeq(n=10)

# load sample KdModel
data(SampleKdModel)

# find matches
matches <- findSeedMatches(seqs, SampleKdModel)

# aggregate matches
aggregateMatches(matches)
```

Description

Assigns a log_kd and match type to a set of matched sequences.

Usage

```r
assignKdType(x, mod, mer8 = NULL)
```
Arguments

- **x**: A vector of matched sequences, each of 12 nucleotides
- **mod**: An object of class ‘KdModel’
- **mer8**: The optional set of 8mers included in the model (for internal use; can be reconstructed from the model).

Value

A data.frame with one row for each element of ‘x’, and the columns ‘type’ and ‘log_kd’. To save space, the reported log_kd is multiplied by 1000, rounded and saved as an integer.

Examples

```r
data(SampleKdModel)
assignKdType(c("CTAGCATTAAGT","ACGTACGTACGT"), SampleKdModel)
```

Description

conservation

Usage

`conservation(x)`

Arguments

- **x**: A KdModelList, or a KdModel

Value

A vector of the conservation status for each miRNA

Examples

```r
data(SampleKdModel)
conservation(SampleKdModel)
```
**dummyKdData**

Create dummy log\_kd per 12-mer data

---

**Description**

Create dummy log\_kd per 12-mer data

**Usage**

dummyKdData(mod = NULL)

**Arguments**

mod

Optional model from which to create the dummy data

**Value**

A data.frame with 12-mers and log\_kds

**Examples**

kd <- dummyKdData()

---

**findSeedMatches**

Predicting and characterizing miRNA binding sites

---

**Description**

‘findSeedMatches’ takes a set of sequences and a set of miRNAs (given either as target seeds, mature miRNA sequences, or a KdModelList).

**Usage**

findSeedMatches(
    seqs,
    seeds,
    shadow = 0L,
    onlyCanonical = FALSE,
    maxLogKd = c(-1, -1.5),
    keepMatchSeq = FALSE,
    minDist = 7L,
    p3.extra = FALSE,
    p3.params = list(maxMirLoop = 7L, maxTargetLoop = 9L, maxLoopDiff = 4L, mismatch = TRUE, GUwob = TRUE),
    agg.params = .defaultAggParams(),
    ret = c("GRanges", "data.frame", "aggregated"),
)
Arguments

seqs  A character vector or ‘DNAStringSet’ of DNA sequences in which to look.

seeds A character vector of 7-nt seeds to look for. If RNA, will be reversed and complemented before matching. If DNA, they are assumed to be the target sequence to look for. Alternatively, a list of objects of class ‘KdModel’ or an object of class ‘KdModelList’ can be given.

shadow Integer giving the shadow, i.e. the number of nucleotides hidden at the beginning of the sequence (default 0).

onlyCanonical Logical; whether to restrict the search only to canonical binding sites.

maxLogKd Maximum log_kd value to keep. This has a major impact on the number of sites returned, and hence on the memory requirements. Set to Inf to disable (not recommended when running large scans!).

keepMatchSeq Logical; whether to keep the sequence (including flanking dinucleotides) for each seed match (default FALSE).

minDist Integer specifying the minimum distance between matches of the same miRNA (default 7). Closer matches will be reduced to the highest-affinity. To disable the removal of overlapping features, use ‘minDist=-Inf’.

p3.extra Logical; whether to keep extra information about 3’ alignment. Disable (default) this when running large scans, otherwise you might hit your system’s memory limits.

p3.params Named list of parameters for 3’ alignment with slots ‘maxMirLoop’ (integer, default = 7), ‘maxTargetLoop’ (integer, default = 9), ‘maxLoopDiff’ (integer, default = 4), ‘mismatch’ (logical, default = TRUE) and ‘GUwob’ (logical, default = TRUE).

agg.params A named list with slots ‘a’, ‘b’, ‘c’, ‘p3’, ‘coef_utr’, ‘coef_orf’ and ‘keepSiteInfo’ indicating the parameters for the aggregation. Ignored if ‘ret=”aggregated”’. For further details see documentation of ‘aggregateMatches’.

ret The type of data to return, either "GRanges" (default), "data.frame", or "aggregated" (aggregates affinities/sites for each seed-transcript pair).

BP Pass ‘BiocParallel::MulticoreParam(ncores, progressbar=TRUE)” to enable multithreading.

verbose Logical; whether to print additional progress messages (default on if not multithreading)

n_seeds Integer; the number of seeds that are processed in parallel to avoid memory issues.
get3pAlignment

useTmpFiles Logical; whether to write results for single miRNAs in temporary files (ignored when scanning for a single seed). Alternatively, ‘useTmpFiles’ can be a character vector of length 1 indicating the path to the directory in which to write temporary files.

keepTmpFiles Logical; whether to keep the temporary files at the end of the process; ignored if ‘useTmpFiles=FALSE’. Temporary files are removed only upon successful completion of the function, meaning that they will not be deleted in case of errors.

Value

A GRanges of all matches. If ‘seeds’ is a ‘KdModel’ or ‘KdModelList’, the ‘log_kd’ column will report the ln(Kd) multiplied by 1000, rounded and saved as an integer. If ‘ret!=”GRanges”, returns a data.frame.

Examples

# we create mock RNA sequences and seeds:
seqs <- getRandomSeq(n=10)
seeds <- c("AAACCAC", "AAACCUU")
findSeedMatches(seqs, seeds)
Arguments

seqs A set of sequences in which to look for 3’ matches (i.e. upstream of the seed match)
mirseq The sequence of the mature miRNA
mir3p.start The position in ‘mirseq’ in which to start looking
allow.mismatch Logical; whether to allow mismatches
maxMirLoop Maximum miRNA loop size
maxTargetLoop Maximum target loop size
maxLoopDiff Maximum size difference between miRNA and target loops
TGsub Logical; whether to allow T/G substitutions.
siteType The optional type of seed-complementarity, as returned by getMatchTypes. This is needed to identify slicing/TDMD sites. If given, should be a vector of the same length as ‘seqs’.

Value

A data.frame with one row for each element of ‘seqs’, indicating the size of the miRNA bulge, the size of the target mRNA bulge, the number of mismatches at the 3’ end, and the partial 3’ alignment score (i.e. roughly the number of consecutive matching nucleotides)

Examples

g3pAlignment(seqs="NNAGTGTGCCATNN", mirseq="TGGAGTGTGACAATGGTGTTTG")

description

Returns the minimum and maximum 8-mer log-kd values

Usage

g8merRange(mod)

Arguments

mod A ‘KdModel’

Value

A numeric vector of length two

Examples

data("SampleKdModel")
g8merRange(SampleKdModel)
**getKdModel**

**Description**

getKdModel

**Usage**

getKdModel(kd, mirseq = NULL, name = NULL, conservation = NA_integer_, ...)

**Arguments**

kd

A data.frame containing the log_kd per 12-mer sequence, or the path to a text/csv file containing such a table. Should contain the columns 'log_kd', '12mer' (or 'X12mer'), and eventually 'mirseq' (if the 'mirseq' argument is NULL) and 'mir' (if the 'name' argument is NULL).

mirseq

The miRNA (cDNA) sequence.

name

The name of the miRNA.

conservation

The conservation level of the miRNA. See 'scanMiR:::.conservation_levels()' for possible values.

... Any additional information to be saved with the model.

**Value**

An object of class ‘KdModel’.

**Examples**

kd <- dummyKdData()
mod <- getKdModel(kd=kd, mirseq="TTATGCTAATCGTGATAGGGT", name="my-miRNA")

**getKmers**

**Description**

Returns all combinations of ‘n’ elements of ‘from’

**Usage**

getKmers(n = 4, from = c(“A”, “C”, “G”, “T”))
getMatchTypes

Arguments

- n Number of elements from Letters sampled

Value

A character vector

Examples

getKmers(3)

Description

Given a seed and a set of sequences matching it, returns the type of match.

Usage

getMatchTypes(x, seed, checkWobble = TRUE)

Arguments

- x A character vector of short sequences.
- seed A 7 or 8 nucleotides string indicating the seed (5' to 3' sequence of the target RNA). If of length 7, an "A" will be appended.
- checkWobble Whether to flag wobbled sites

Value

A factor of match types.

Examples

x <- c("AACACTCCAG","GACACTCCGC","GTACTCCAT","ACGTACGTAC")
getMatchTypes(x, seed="ACACTCCA")
**getRandomSeq**

**Description**

Produces a random sequence of the given letters

**Usage**

```r
generateRandomSeq(length = 3000, alphabet = c("A", "C", "G", "T"), n = 1)
```

**Arguments**

- `length`: Length of the sequence
- `alphabet`: Letters from which to sample
- `n`: The number of sequences to generate

**Value**

A character vector of length 1

**Examples**

```r
generateRandomSeq(100)
```

---

**getSeed8mers**

**Description**

Generates all possible 8mers with 4 consecutive and positioned matches to a given seed.

**Usage**

```r
generateSeed8mers(seed, addNs = FALSE)
```

**Arguments**

- `seed`: The miRNA seed (target DNA sequence), a character vector of length 8 (if of length 7, a "A" will be added on the right)
- `addNs`: Logical; whether to include 8mers with one flanking N

**Value**

A vector of 1024 8mers.
Examples

head(getSeed8mers("ACACTCCA"))

Description

Methods for the \code{KdModel} class

Usage

\begin{verbatim}
## S4 method for signature 'KdModel'
show(object)

## S4 method for signature 'KdModel'
summary(object)

## S4 method for signature 'KdModel'
c(x, ...)
\end{verbatim}

Arguments

\code{object, x, ...} An object of class \code{KdModel}

Value

Depends on the method.

See Also

\code{KdModel, KdModelList}

Examples

data(SampleKdModel)
SampleKdModel
summary(SampleKdModel)
**KdModelList-class**

**KdModelList**

**Description**

KdModelList

**Usage**

\[
\texttt{KdModelList(..., description = NULL, makeUnique = FALSE)}
\]

**Arguments**

- `...` Any number of \texttt{KdModel} objects or lists thereof.
- `description` A description for the collection.
- `makeUnique` Logical; whether to rename models if names are duplicated.

**Value**

A KdModelList

**Examples**

```r
data(SampleKdModel)
mods <- KdModelList(SampleKdModel, SampleKdModel, makeUnique = TRUE)
mods
```

---

**KdModelList-methods**

**Methods for the KdModelList classes**

**Description**

Methods for the \texttt{KdModelList} classes

**Usage**

```r
## S4 method for signature 'KdModelList'
summary(object)

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

**Arguments**

- `object, x` An object of class \texttt{KdModelList}
- `i` the index of item(s) to select
- `j, drop, ...` ignored
plotKdModel

Value

Depends on the method.

See Also

KdModel, KdModelList

Examples

# create a KdModelList:
data(SampleKdModel)
kml <- KdModelList( SampleKdModel, SampleKdModel, makeUnique=TRUE )
summary(kml)
kml[[1]] # returns a KdModelList
kml[[2]] # returns a KdModel
conservation(kml)

Description

Plots the summary of an affinity model.

Usage

plotKdModel(mod, what = c("both", "seeds", "logo"), n = 10)

Arguments

mod
  A ‘KdModel’
what
  Either ‘seeds’, ‘logo’, or ‘both’ (default).
n
Details

‘what=’seeds’ ‘ plots the -$log$(K_d) values of the top ‘n’ 7-mers (including both canonical and non-canonical sites), with or without the final "A" vis-a-vis the first miRNA nucleotide. ‘what=’logo’ ‘ plots a ‘seqLogo’ (requires the [seqLogo](https://bioconductor.org/packages/release/bioc/html/seqLogo.html) package) showing the nucleotide-wise information content and preferences for all 12-mers (centered around the seed, oriented in the direction of the target mRNA). ‘what=’both’ ‘ plots both. Note that if the package ‘ggseqlogo’ is installed, this will be used instead to plot the logo, resulting in more detailed plot annotation.

Value

If ‘what=’logo’ ‘, returns nothing and plots a position weight matrix. Otherwise returns a ggplot.
removeOverlappingRanges

Examples

data(SampleKdModel)
plotKdModel(SampleKdModel, what="seeds")

Description

Removes elements from a GRanges that overlap (or are within a given distance of) other elements higher up in the list (i.e. assumes that the ranges are sorted in order of priority). The function handles overlaps between more than two ranges by successively removing those that overlap higher-priority ones.

Usage

removeOverlappingRanges(
  x,
  minDist = 7L,
  retIndices = FALSE,
  ignore.strand = FALSE
)

Arguments

x A GRanges, sorted by (decreasing) importance.
minDist Minimum distance between ranges.
retIndices Logical; whether to return the indices of entries to remove, rather than the filtered GRanges.
ignore.strand Logical. Whether the strand of the input ranges should be ignored or not.

Value

A filtered GRanges, or an integer vector of indices to be removed if ’retIndices==TRUE’.

Examples

calllibrary(GenomicRanges)
gr <- GRanges(seqnames=rep("A",4), IRanges(start=c(10,25,45,35), width=6))
removeOverlappingRanges(gr, minDist=7)
SampleKdModel  

*Example KdModel (hsa-miR-155-5p)*

**Description**


**Value**

a ‘KdModel’ object

**Examples**

data(SampleKdModel)
SampleKdModel

SampleTranscript  

*Example transcript sequence*

**Description**

An artificial transcript sequence used for examples.

**Value**

a named character vector of length 1.

viewTargetAlignment  

*viewTargetAlignment*

**Description**

viewTargetAlignment
viewTargetAlignment

Usage

viewTargetAlignment(
  m,
  miRNA,
  seqs = NULL,
  flagBulgeMatches = FALSE,
  p3.params = list(),
  min3pMatch = 3L,
  hideSingletons = FALSE,
  UGsub = TRUE,
  ...,
  outputType = c("print", "data.frame", "plot", "ggplot")
)

Arguments

m       A GRanges of length 1 giving the information for a given match, as produced by findSeedMatches.
miRNA   A miRNA sequence, or a KdModel object of the miRNA corresponding to the match in 'm'; alternatively, a KdModelList including the model.
seqs    The sequences corresponding to the seqnames of 'm'. Not needed if 'm' contains the target sequences.
flagBulgeMatches Logical; whether to flag matches inside the bulge (default FALSE)
p3.params See findSeedMatches.
min3pMatch The minimum 3' alignment for any to be plotted
hideSingletons Logical; whether to hide isolated single base-pair matches
UGsub    Logical; whether to show U-G matches
...      Passed to 'text' if 'outputType="plot"'.
outputType Either 'print' (default, prints to console), 'data.frame', or 'plot'.

Value

Returns nothing 'outputType="print"'. If 'outputType="data.frame"', returns a data.frame containing the alignment strings; if 'outputType="ggplot"' returns a 'ggplot' object.

Examples

data(SampleKdModel)
seq <- c(seq1="CGACCCCTATCACGTCCGCAGCATTAAAT")
m <- findSeedMatches(seq, SampleKdModel, verbose=FALSE)
viewTargetAlignment(m, miRNA=SampleKdModel, seqs=seq)
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