

Package ‘pqsfinder’

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Type Package

Title Identification of potential quadruplex forming sequences

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Description The main functionality of the this package is to detect DNA sequence patterns that are likely to fold into an intramolecular G-quadruplex (G4). Unlike many other approaches, this package is able to detect sequences responsible for G4s folded from imperfect G-runs containing bulges or mismatches and as such is more sensitive than competing algorithms.

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biocViews MotifDiscovery, SequenceMatching, GeneRegulation

LazyData TRUE

Depends Biostrings

Imports Rcpp (>= 0.12.3), GenomicRanges, IRanges, S4Vectors, methods

Suggests BiocStyle, knitr, Gviz, rtracklayer, biomaRt, BSgenome.Hsapiens.UCSC.hg38

LinkingTo Rcpp, BH, flowCore

SystemRequirements GNU make

VignetteBuilder knitr

RoxygenNote 5.0.1

NeedsCompilation yes

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as.character,PQSViews-method
Coerce to character vector

Description

Coerce to character vector

Usage

```
## S4 method for signature 'PQSViews'
as.character(x)
```

Arguments

x PQSViews object.

Value

Character vector representing PQS.

density,PQSViews-method
Get density vector

Description

Density vector represents numbers of PQS (potential quadruplex forming sequences) overlapping at each position in input sequence.

Usage

```
## S4 method for signature 'PQSViews'
density(x)
```

Arguments

x PQSViews object

Value

Density vector

Examples

```
pqs <- pqsfinder(DNAString("CCCCCGGGTGGGTGGGTGGGAAAA"))
density(pqs)
```

pqsfinder

Identificate potential quadruplex forming sequences.

Description

Function for identification of all potential intramolecular quadruplex patterns (PQS) in DNA sequence.

Usage

```
pqsfinder(subject, strand = "*", max_len = 50L, min_score = 42L,
  run_min_len = 3L, run_max_len = 11L, loop_min_len = 0L,
  loop_max_len = 30L, max_bulges = 3L, max_mismatches = 2L,
  max_defects = 3L, tetrad_bonus = 45L, bulge_penalty = 20L,
  mismatch_penalty = 31L, loop_mean_factor = 1, loop_sd_factor = 1,
  run_re = "G{1,5}.{0,5}G{1,5}", custom_scoring_fn = NULL,
  use_default_scoring = TRUE, verbose = FALSE)
```

Arguments

subject	DNAString object.
strand	Strand specification. Allowed values are "+", "-" or "*", where the last one represents both strands. Implicitly, the input DNAString object is assumed to encode the "+" strand.
max_len	Maximal length of PQS.
min_score	Minimal PQS score.
run_min_len	Minimal length of quadruplex run.
run_max_len	Maximal length of quadruplex run.
loop_min_len	Minimal length of quadruplex loop.
loop_max_len	Maximal length of quadruplex loop.
max_bulges	Maximal number of runs with bulge.
max_mismatches	Maximal number of runs with mismatch.
max_defects	Maximum number of defects in total (max_bulges + max_mismatches).
tetrad_bonus	Score bonus for one complete G tetrad.

bulge_penalty	Penalization for a bulge in quadruplex run.
mismatch_penalty	Penalization for a mismatch in tetrad.
loop_mean_factor	Penalization factor of loop lengths mean.
loop_sd_factor	Penalization factor of loop lengths standard deviation.
run_re	Regular expression specifying one run of quadruplex.
custom_scoring_fn	Custom quadruplex scoring function. It takes the following 10 arguments: subject - Input DNASTring object, score - implicit PQS score, start - PQS start position, width - PQS width, loop_1 - start pos. of loop #1, run_2 - start pos. of run #2, loop_2 - start pos. of loop #2, run_3 - start pos. of run #3, loop_3 - start pos. of loop #3, run_4 - start pos. of run #4. Return value of the function has to be new score represented as a single integer value. Please note that if use_default_scoring is enabled, the custom scoring function is evaluated AFTER the default scoring system but ONLY IF the default scoring system resulted in non-zero score (for performance reasons). On the other hand, when use_default_scoring is disabled, custom scoring function is evaluated on every PQS.
use_default_scoring	Enables default internal scoring system. This option is particularly useful in case you intend to radically change the default behavior and specify your own scoring function. By disabling the default scoring you will get a full control above the underlying detection algorithm.
verbose	Enables detailed output. Turn it on if you want to see all possible PQS found at each positions and not just the best one. It is highly recommended to use this option for debugging custom quadruplex scoring function. Each PQS is reported on separate row in the following format: start cnt pqs_sequence score, where start is the PQS starting position, pqs_sequence shows the PQS sequence structure with each run surrounded by square brackets and score is the score assigned to the particular PQS by all applied scoring functions.

Value

PQSViews object

Examples

```
pv <- pqsfinder(DNASTring("CCCCCGGGTGGGTGGGTGGGAAAA"))
```

PQSViews *PQSViews class constructor.*

Description

User friendly constructor for PQSViews class representing potential quadruplex forming sequences (PQS). PQSViews is a subclass of [XStringViews](#) class and adds one more slot to store PQS density.

Usage

```
PQSViews(subject, start, width, strand, score, density)
```

Arguments

subject	DNAStrng object.
start	Vector of PQS start positions.
width	Vector of PQS lengths.
strand	Vector of PQS strand specifications.
score	Vector of PQS scores.
density	Numbers of PQS overlapping at each position in subject.

Value

PQSViews object

Examples

```
pv <- PQSViews(DNAStrng("CGGGCGGGC"), 1:2, 2:3, "+", 10:11, 1:10)
start(pv)
width(pv)
strand(pv)
score(pv)
density(pv)
```

PQSViews-class *An S4 class to represent potential quadruplex forming sequences.*

Description

Represents potential quadruplex forming sequences found by [pqsfinder](#) function. This is a subclass of [XStringViews-class](#) class and adds one more slot.

Slots

density Numbers of PQS (potential quadruplex forming sequences) overlapping at each position in input sequence.

score,PQSViews-method *Get PQS score vector*

Description

Get PQS score vector

Usage

```
## S4 method for signature 'PQSViews'  
score(x)
```

Arguments

x PQSViews object

Value

Score vector

Examples

```
pqs <- pqsfinder(DNAString("CCCCCGGGTGGGTGGGTGGGAAAA"))  
score(pqs)
```

show,PQSViews-method *Show method*

Description

Show method

Usage

```
## S4 method for signature 'PQSViews'  
show(object)
```

Arguments

object PQSViews object.

Value

PQSViews object printed.

strand,PQSViews-method

Get PQS strand vector

Description

Get PQS strand vector

Usage

```
## S4 method for signature 'PQSViews'  
strand(x)
```

Arguments

x PQSViews object

Value

Strand vector

Examples

```
pqs <- pqsfinder(DNAString("CCCCCGGGTGGGTGGGTGGGAAAA"))  
strand(pqs)
```

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