

Package ‘periodicDNA’

March 30, 2021

Type Package

Title Set of tools to identify periodic occurrences of k-mers in DNA sequences

Version 1.0.0

Date 2020-05-03

Encoding UTF-8

Description This R package helps the user identify k-mers (e.g. di- or tri-nucleotides) present periodically in a set of genomic loci (typically regulatory elements). The functions of this package provide a straightforward approach to find periodic occurrences of k-mers in DNA sequences, such as regulatory elements. It is not aimed at identifying motifs separated by a conserved distance; for this type of analysis, please visit MEME website.

URL <https://github.com/js2264/periodicDNA>

BugReports <https://github.com/js2264/periodicDNA/issues>

RoxygenNote 7.1.0

Depends R (>= 4.0), Biostrings, GenomicRanges, IRanges, BSgenome, BiocParallel

Imports S4Vectors, rtracklayer, stats, GenomeInfoDb, magrittr, zoo, ggplot2, methods, parallel, cowplot

Suggests BSgenome.Scerevisiae.UCSC.sacCer3, BSgenome.Celegans.UCSC.ce11, BSgenome.Dmelanogaster.UCSC.dm6, BSgenome.Drerio.UCSC.danRer10, BSgenome.Hsapiens.UCSC.hg38, BSgenome.Mmusculus.UCSC.mm10, reticulate, testthat, covr, knitr, rmarkdown, pkgdown

VignetteBuilder knitr

biocViews SequenceMatching, MotifDiscovery, MotifAnnotation, Sequencing, Coverage, Alignment, DataImport

License GPL-3 + file LICENSE

git_url <https://git.bioconductor.org/packages/periodicDNA>

git_branch RELEASE_3_12

git_last_commit f4416e8

git_last_commit_date 2020-10-27

Date/Publication 2021-03-29

Author Jacques Serizay [aut, cre] (<<https://orcid.org/0000-0002-4295-0624>>)

Maintainer Jacques Serizay <jacquesserizay@gmail.com>

R topics documented:

ce11_all_REs	2
ce11_ATACseq	3
ce11_proms	3
ce11_proms_seqs	4
ce11_TSSs	5
ce11_WW_10bp	5
getPeriodicity	6
getPeriodicityTrack	8
getPeriodicityWithIterations	9
plotAggregateCoverage	11
plotPeriodicityResults	14
setUpBPPARAM	15
theme_ggplot2	15

Index **18**

ce11_all_REs	<i>ce11_all_REs</i>
--------------	---------------------

Description

Regulatory elements annotated in *C. elegans* (ce11) according to Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv.

Usage

```
data(ce11_all_REs)
```

Format

GRanges

Source

[BiorXiv](#)

References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. ([DOI](#))

Examples

```
data(ce11_all_REs)
table(ce11_all_REs$regulatory_class)
table(ce11_all_REs$which.tissues)
```

`ce11_ATACseq`*ce11_ATACseq*

Description

Sample of ATAC-seq from mixed tissues in *C. elegans* young adults

Usage

```
data(ce11_ATACseq)
```

Format

RleList

Source

[BiorXiv](#)

References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", [BiorXiv](#). (DOI)

Examples

```
data(ce11_ATACseq)
ce11_ATACseq
```

`ce11_proms`*ce11_proms*

Description

Promoters annotated in *C. elegans* (ce11) according to Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", [BiorXiv](#).

Usage

```
data(ce11_proms)
```

Format

GRanges

Source

[BiorXiv](#)

References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. ([DOI](#))

Examples

```
data(ce11_proms)
table(ce11_proms$which.tissues)
```

ce11_proms_seqs	<i>ce11_proms_seqs</i>
-----------------	------------------------

Description

Sample of sequences of promoters annotated in *C. elegans* (ce11) according to Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv.

Usage

```
data(ce11_proms_seqs)
```

Format

DNASTringSet

Source

[BiorXiv](#)

References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. ([DOI](#))

Examples

```
data(ce11_proms_seqs)
head(ce11_proms_seqs)
```

`ce11_TSSs``ce11_TSSs`

Description

Coordinates of promoter TSSs annotated in *C. elegans* (ce11) used in Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv.

Usage

```
data(ce11_TSSs)
```

Format

GRanges

Source

[BiorXiv](#)

References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. ([DOI](#))

Examples

```
data(ce11_TSSs)
lengths(ce11_TSSs)
ce11_TSSs[[1]]
```

`ce11_WW_10bp``ce11_WW_10bp`

Description

Sample of WW 10-bp periodicity track generated by `getPeriodicityTrack()` in `ce11` over annotated accessible sites, with default parameters

Usage

```
data(ce11_WW_10bp)
```

Format

RleList

Source

[BiorXiv](#)

References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. (DOI)

Examples

```
data(ce11_WW_10bp)
ce11_WW_10bp
```

getPeriodicity	<i>A function to compute k-mer periodicity in sequence(s).</i>
----------------	--

Description

This function takes a set of sequences and a k-mer of interest, map a k-mer of interest in these sequences, computes all the pairwise distances (distogram), normalize it for distance decay, and computes the resulting power spectral density of the normalized distogram.

Usage

```
getPeriodicity(x, motif, ...)

## S3 method for class 'DNAStrngSet'
getPeriodicity(
  x,
  motif,
  range_spectrum = seq(1, 200),
  BPPARAM = setUpBPPARAM(1),
  roll = 3,
  verbose = TRUE,
  sample = 0,
  n_shuffling = 0,
  cores_shuffling = 1,
  cores_computing = 1,
  order = 1,
  ...
)

## S3 method for class 'GRanges'
getPeriodicity(x, motif, genome = "BSgenome.Celegans.UCSC.ce11", ...)

## S3 method for class 'DNAStrng'
getPeriodicity(x, motif, ...)
```

Arguments

x	a DNAStrng, DNAStrngSet or GRanges object.
motif	a k-mer of interest
...	Arguments passed to S3 methods

range_spectrum	Numeric vector Range of the distogram to use to run the Fast Fourier Transform on (default: 1:200, i.e. all pairs of k-mers at a maximum of 200 bp from each other).
BPPARAM	split the workload over several processors using BiocParallel
roll	Integer Window to smooth the distribution of pairwise distances (default: 3, to discard the 3-bp periodicity of dinucleotides which can be very strong in vertebrate genomes)
verbose	Boolean
sample	Integer if > 0, will randomly sample this many integers from the dists vector before normalization. This ensures consistency when looking at periodicity in different genomes, since different genomes will have different GC percent
n_shuffling	Integer, how many times should the sequences be shuffled? (default = 0)
cores_shuffling	integer, Number of cores used for shuffling (used if n_shuffling > 0)
cores_computing	integer, split the workload over several processors using BiocParallel (used if n_shuffling > 0)
order	Integer, which order to take into consideration for shuffling (ushuffle python library must be installed for orders > 1) (used if n_shuffling > 0)
genome	genome ID, BSgenome or DNASTringSet object (optional, if x is a GRanges)

Value

A list containing the results of getPeriodicity function.

- The dists vector is the raw vector of all distances between any possible k-mer.
- The hist.data.frame is the distribution of distances over range_spectrum.
- The normalized_hist is the raw hist, normalized for decay over increasing distances.
- The spectra object is the output of the FFT applied over normalized_hist.
- The PSD data frame is the power spectral density scores over given frequencies.
- The motif object is the k-mer being analysed.
- The final periodicity metrics computed by getPeriodicity()

If getPeriodicity() is ran with n_shuffling > 0, the resulting list also contains PSD values computed when iterating through shuffled sequences.

Methods (by class)

- DNASTringSet: S3 method for DNASTringSet
- GRanges: S3 method for GRanges
- DNASTring: S3 method for DNASTring

Examples

```
data(ce11_proms_seqs)
periodicity_result <- getPeriodicity(
  ce11_proms_seqs[1:100],
  motif = 'TT'
)
```

```

head(periodicity_result$PSD)
plotPeriodicityResults(periodicity_result)
#
data(ce11_TSSs)
periodicity_result <- getPeriodicity(
  ce11_TSSs[['Ubiq. ']][1:10],
  motif = 'TT',
  genome = 'BSgenome.Celegans.UCSC.ce11'
)
head(periodicity_result$PSD)
plotPeriodicityResults(periodicity_result)
#
data(ce11_TSSs)
periodicity_result <- getPeriodicity(
  ce11_TSSs[['Ubiq. ']][1:10],
  motif = 'TT',
  genome = 'BSgenome.Celegans.UCSC.ce11',
  n_shuffling = 10
)
head(periodicity_result$PSD)
plotPeriodicityResults(periodicity_result)

```

getPeriodicityTrack *Function to generate a k-mer periodicity track*

Description

This function takes a set of GRanges in a genome, recover the corresponding sequences and divides them using a sliding window. For each sub-sequence, it then computes the PSD value of a k-mer of interest at a chosen period, and generates a linear .bigWig track from these values.

Usage

```

getPeriodicityTrack(
  genome = NULL,
  granges,
  motif = "WW",
  period = 10,
  BPPARAM = setUpBPPARAM(1),
  extension = 1000,
  window_size = 100,
  step_size = 2,
  range_spectrum = seq(5, 50),
  smooth_track = 20,
  bw_file = NULL
)

```

Arguments

genome	DNAStrngSet, BSgenome or genome ID
granges	GRanges object
motif	character, k-mer of interest.

period	Integer, the period of the k-mer to study (default=10).
BPPARAM	split the workload over several processors using BiocParallel
extension	Integer, the width the GRanges are going to be extended to (default 1000).
window_size	Integer, the width of the bins to split the GRanges objects in (default 100).
step_size	Integer, the increment between bins over GRanges (default 2).
range_spectrum	Numeric vector, the distances between nucleotides to take into consideration when performing Fast Fourier Transform (default seq_len(50)).
smooth_track	Integer, smooth the resulting track
bw_file	character, the name of the output bigWig track

Value

Rlelist and a bigWig track in the working directory.

Examples

```
data(ce11_proms)
track <- getPeriodicityTrack(
  genome = 'BSgenome.Celegans.UCSC.ce11',
  ce11_proms[1],
  extension = 200,
  window_size = 100,
  step_size = 10,
  smooth_track = 1,
  motif = 'WW',
  period = 10,
  BPPARAM = setUpBPPARAM(1)
)
track
unlink(
  'BSgenome.Celegans.UCSC.ce11_WW_10-bp-periodicity_g-100^10_smooth-1.bw'
)
```

getPeriodicityWithIterations

A function to compute PSDs with iterations

Description

This function computes PSD values of a given k-mer of interest in a set of input sequences. It also iterates the PSD calculation process over shuffled sequences, if `n_shuffling` is used.

Usage

```
getPeriodicityWithIterations(x, ...)

## S3 method for class 'DNAStringSet'
getPeriodicityWithIterations(
  x,
  motif,
```

```

    n_shuffling = 10,
    cores_shuffling = 1,
    cores_computing = 1,
    order = 1,
    verbose = 1,
    ...
)

## S3 method for class 'GRanges'
getPeriodicityWithIterations(x, genome, ...)

```

Arguments

x	DNASTringSet, sequences of interest
...	Arguments passed to S3 methods
motif	character, k-mer of interest
n_shuffling	integer, Number of shuffling
cores_shuffling	integer, Number of cores used for shuffling
cores_computing	integer, split the workload over several processors using BiocParallel
order	Integer, which order to take into consideration for shuffling (ushuffle python library must be installed for orders > 1)
verbose	integer, Should the function be verbose?
genome	genome ID, BSgenome or DNASTringSet object (optional, if x is a GRanges)

Value

Several metrics

Methods (by class)

- DNASTringSet: S3 method for DNASTring
- GRanges: S3 method for GRanges

Examples

```

data(ce11_proms_seqs)
res <- getPeriodicityWithIterations(
  ce11_proms_seqs[1:10],
  genome = 'BSgenome.Celegans.UCSC.ce11',
  motif = 'TT',
  cores_shuffling = 1
)
res$observed_PSD
res$shuffled_PSD

```

plotAggregateCoverage *A function to plot aggregated signals over sets of GRanges*

Description

This function takes one or several RleList genomic tracks (e.g. imported by rtraklayer::import(..., as = 'Rle')) and one or several GRanges objects. It computes coverage of the GRanges by the genomic tracks and returns an aggregate coverage plot.

Usage

```
plotAggregateCoverage(x, ...)

## S3 method for class 'CompressedRleList'
plotAggregateCoverage(x, granges, ...)

## S3 method for class 'SimpleRleList'
plotAggregateCoverage(
  x,
  granges,
  colors = NULL,
  xlab = "Center of elements",
  ylab = "Score",
  xlim = NULL,
  ylim = NULL,
  quartiles = c(0.025, 0.975),
  verbose = FALSE,
  bin = 1,
  plot_central = TRUE,
  run_in_parallel = FALSE,
  split_by_granges = FALSE,
  norm = "none",
  ...
)

## S3 method for class 'list'
plotAggregateCoverage(
  x,
  granges,
  colors = NULL,
  xlab = "Center of elements",
  ylab = "Score",
  xlim = NULL,
  ylim = NULL,
  quartiles = c(0.025, 0.975),
  verbose = FALSE,
  bin = 1,
  plot_central = TRUE,
  split_by_granges = TRUE,
  split_by_track = FALSE,
  free_scales = FALSE,
```

```

run_in_parallel = FALSE,
norm = "none",
...
)

```

Arguments

x	a single signal track (CompressedRleList or SimpleRleList class), or several signal tracks (SimpleRleList or CompressedRleList class) grouped in a named list
...	additional parameters
granges	a GRanges object or a named list of GRanges
colors	a vector of colors
xlab	x axis label
ylab	y axis label
xlim	y axis limits
ylim	y axis limits
quartiles	Which quantiles to use to determine y scale automatically?
verbose	Boolean
bin	Integer Width of the window to use to smooth values by zoo::rollMean
plot_central	Boolean Draw a vertical line at 0
run_in_parallel	Boolean Should the plots be computed in parallel using mclapply?
split_by_granges	Boolean Facet plots over the sets of GRanges
norm	character Should the signal be normalized ('none', 'zscore' or 'log2')?
split_by_track	Boolean Facet plots by the sets of signal tracks
free_scales	Boolean Should each facet have independent y-axis scales?

Value

An aggregate coverage plot.

Methods (by class)

- CompressedRleList: S3 method for CompressedRleList
- SimpleRleList: S3 method for SimpleRleList
- list: S3 method for list

Examples

```

data(ce11_ATACseq)
data(ce11_WW_10bp)
data(ce11_proms)

p1 <- plotAggregateCoverage(
  ce11_ATACseq,
  resize(ce11_proms[1:100], fix = 'center', width = 1000)
)

```

```

p1

proms <- resize(ce11_proms[1:100], fix = 'center', width = 400)
p2 <- plotAggregateCoverage(
  ce11_ATACseq,
  list(
    'Ubiq & Germline promoters' =
      proms[proms$which.tissues %in% c('Ubiq.', 'Germline')],
    'Other promoters' =
      proms[!(proms$which.tissues %in% c('Ubiq.', 'Germline'))]
  )
)
p2

p3 <- plotAggregateCoverage(
  list(
    'atac' = ce11_ATACseq,
    'WW_10bp' = ce11_WW_10bp
  ),
  proms,
  norm = 'zscore'
)
p3

p4 <- plotAggregateCoverage(
  list(
    'ATAC-seq' = ce11_ATACseq,
    'WW 10-bp periodicity' = ce11_WW_10bp
  ),
  list(
    'Ubiq & Germline promoters' =
      proms[proms$which.tissues %in% c('Ubiq.', 'Germline')],
    'Other promoters' =
      proms[!(proms$which.tissues %in% c('Ubiq.', 'Germline'))]
  ),
  norm = 'zscore'
)
p4

p5 <- plotAggregateCoverage(
  list(
    'ATAC-seq' = ce11_ATACseq,
    'WW 10-bp periodicity' = ce11_WW_10bp
  ),
  list(
    'Ubiq & Germline promoters' =
      proms[proms$which.tissues %in% c('Ubiq.', 'Germline')],
    'Other promoters' =
      proms[!(proms$which.tissues %in% c('Ubiq.', 'Germline'))]
  ),
  split_by_granges = FALSE,
  split_by_track = TRUE,
  norm = 'zscore'
)
p5

```

plotPeriodicityResults

Plot the output of getPeriodicity()

Description

This function plots some results from the result of `getPeriodicity()`. It plots the raw histogram, the distance-decay normalized histogram and the resulting PSD values. If a shuffled control has been performed by `getPeriodicity()`, it also displays it.

Usage

```
plotPeriodicityResults(
  results,
  periods = c(2, 20),
  filter_periods = TRUE,
  facet_control = TRUE,
  xlim = NULL,
  fdr_threshold = 0.05,
  ...
)
```

Arguments

<code>results</code>	The output of <code>getPeriodicity</code> function.
<code>periods</code>	Vector a numerical vector of length 2, to specify the x-axis limits
<code>filter_periods</code>	Boolean Should the x-axis be constrained to the periods?
<code>facet_control</code>	Boolean should the shuffling plots be faceted?
<code>xlim</code>	Integer x axis upper limit in raw and norm. histograms
<code>fdr_threshold</code>	Float, significance threshold
<code>...</code>	Additional theme arguments passed to <code>theme_ggplot2()</code>

Value

list A list containing four ggplots

Examples

```
data(ce11_TSSs)
periodicity_result <- getPeriodicity(
  ce11_TSSs[['Ubiq.']] [1:100],
  genome = 'BSgenome.Celegans.UCSC.ce11',
  motif = 'TT',
  BPPARAM = setUpBPPARAM(1)
)
head(periodicity_result$PSD)
plotPeriodicityResults(periodicity_result)
plotPeriodicityResults(periodicity_result, xlim = 150)
plotPeriodicityResults(
  periodicity_result, xlim = 150, filter_periods = FALSE
```

```

)
plotPeriodicityResults(
  periodicity_result, xlim = 150, facet_control = FALSE
)

```

setUpBPPARAM

setUpBPPARAM

Description

A function to dynamically select MulticoreParam or SnowParam (if Windows)

Usage

```
setUpBPPARAM(nproc = 1)
```

Arguments

nproc number of processors

Value

A BPPARAM object

Examples

```
BPPARAM <- setUpBPPARAM(1)
```

theme_ggplot2

Personal ggplot2 theming function, adapted from roboto-condensed at <https://github.com/hrbrmstr/hrbrthemes/>

Description

Personal ggplot2 theming function, adapted from roboto-condensed at <https://github.com/hrbrmstr/hrbrthemes/>

Usage

```

theme_ggplot2(
  grid = TRUE,
  border = TRUE,
  base_size = 8,
  plot_title_size = 12,
  plot_title_face = "plain",
  plot_title_margin = 5,
  subtitle_size = 11,
  subtitle_face = "plain",
  subtitle_margin = 5,
  strip_text_size = 10,
  strip_text_face = "bold",

```

```

caption_size = 9,
caption_face = "plain",
caption_margin = 3,
axis_text_size = base_size,
axis_title_size = 9,
axis_title_face = "plain",
axis_title_just = "rt",
panel_spacing = grid::unit(2, "lines"),
grid_col = "#cccccc",
plot_margin = margin(12, 12, 12, 12),
axis_col = "#cccccc",
axis = FALSE,
ticks = FALSE
)

```

Arguments

grid	panel grid ('TRUE', 'FALSE', or a combination of 'X', 'x', 'Y', 'y')
border	border if 'TRUE' add border
base_size	base font size
plot_title_size, plot_title_margin,	plot title size and margin
plot_title_face,	plot title face
subtitle_face, subtitle_size	plot subtitle face and size
subtitle_margin	plot subtitle margin bottom (single numeric value)
strip_text_face, strip_text_size	facet label font face and size
caption_face, caption_size, caption_margin	plot caption face, size and margin
axis_text_size	font size of axis text
axis_title_face, axis_title_size	axis title font face and size
axis_title_just	axis title font justificationk one of '[blmcr]'
panel_spacing	panel spacing (use 'unit()')
grid_col	grid color
plot_margin	plot margin (specify with [ggplot2::margin])
axis_col	axis color
axis	add x or y axes? 'TRUE', 'FALSE', "'xy'"
ticks	ticks if 'TRUE' add ticks

Value

theme A ggplot theme

Examples

```
library(ggplot2)

ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  labs(x="Fuel efficiency (mpg)", y="Weight (tons)",
       title="Seminal ggplot2 scatterplot example") +
  theme_ggplot2()
```

Index

* datasets

- ce11_all_REs, [2](#)
- ce11_ATACseq, [3](#)
- ce11_proms, [3](#)
- ce11_proms_seqs, [4](#)
- ce11_TSSs, [5](#)
- ce11_WW_10bp, [5](#)

- ce11_all_REs, [2](#)
- ce11_ATACseq, [3](#)
- ce11_proms, [3](#)
- ce11_proms_seqs, [4](#)
- ce11_TSSs, [5](#)
- ce11_WW_10bp, [5](#)

- getPeriodicity, [6](#)
- getPeriodicityTrack, [8](#)
- getPeriodicityWithIterations, [9](#)

- plotAggregateCoverage, [11](#)
- plotPeriodicityResults, [14](#)

- setUpBPPARAM, [15](#)

- theme_ggplot2, [15](#)