Package ‘dStruct’

May 3, 2024

Type  Package
Title  Identifying differentially reactive regions from RNA structurome profiling data
Version  1.10.0
Depends  R (>= 4.1)
Description  dStruct identifies differentially reactive regions from RNA structurome profiling data. dStruct is compatible with a broad range of structurome profiling technologies, e.g., SHAPE-MaP, DMS-MaPseq, Structure-Seq, SHAPE-Seq, etc. See Choudhary et al., Genome Biology, 2019 for the underlying method.
Imports  zoo, ggplot2, purrr, reshape2, parallel, IRanges, S4Vectors, rlang, grDevices, stats, utils
License  GPL (>= 2)
biocViews  StatisticalMethod, StructuralPrediction, Sequencing, Software
URL  https://github.com/dataMaster-Kris/dStruct
BugReports  https://github.com/dataMaster-Kris/dStruct/issues
Encoding  UTF-8
LazyData  true
RoxygenNote  7.1.1
Suggests  BiocStyle, knitr, rmarkdown, tidyverse, testthat (>= 3.0.0)
VignetteBuilder  knitr
Config/testthat/edition  3
git_url  https://git.bioconductor.org/packages/dStruct
git_branch  RELEASE_3_19
git_last_commit  85159c4
git_last_commit_date  2024-04-30
Repository  Bioconductor 3.19
Date/Publication  2024-05-03
calcDis

Calculates d score.

Description

d score of a nucleotide is a measure of dissimilarity of its normalized reactivity scores. Consider a transcript and its reactivity profiles from a group of samples. Then, the d score of a nucleotide is \((2/\pi)\) times the arc-tangent of the ratio of the sample standard deviation of its reactivities to their mean.

Usage

calcDis(x)

Arguments

x A numeric vector or matrix.

Value

If input is a numeric vector, a number is returned. For a matrix, a numeric vector is returned.

Author(s)

Krishna Choudhary
References


Examples

```r
# Lower standard deviation of reactivities results in lower d-score.
calcDis(rnorm(10, 1, 0.2))
calcDis(rnorm(10, 1, 0.6))
```

---

**dCombs**

 Assesses within-group or between-group variation.

Description

Given the reactivity profiles for a transcript from multiple samples, and a list of sample identifiers, this function computes the dissimilarity of reactivity scores between the specified samples. These are returned as a sequence of nucleotide-wise $d$ scores.

Usage

```r
dCombs(rdf, combs)
```

Arguments

- `rdf` Data.frame of reactivities for each sample.
- `combs` Data.frame with each column containing groupings of samples.

Value

Nucleotide-wise d scores.

Author(s)

Krishna Choudhary

References

Examples

```r
# Example of a data frame with reactivities.
reacs <- data.frame(matrix(runif(30, 0, 10), 10, 3))

# The columns of data frame with must indicate sample grouping and id.
colnames(reacs) <- c("A1", "A2", "B1")

# Get nucleotide-wise dissimilarity scores for a set of samples.
dCombs(rdf = reacs, combs = data.frame(c("A1", "B1")))
```

---

**dStruct**

*Performs de novo discovery of differentially reactive regions.*

**Description**

This function takes reactivity profiles for samples of two groups as input and identifies differentially reactive regions in three steps (see Choudhary et al., *Genome Biology*, 2019 for details). First, it regroups the samples into homogeneous and heterogeneous sub-groups, which are used to compute the within-group and between-group nucleotide-wise $d$ scores. Second, smoothed between- and within-group $d$ score profiles are compared to construct candidate differential regions. Finally, unsmoothed between- and within-group $d$ scores are compared using the Wilcoxon signed-rank test. The resulting p-values quantify the significance of difference in reactivity patterns between the two input groups.

**Usage**

```r
dStruct(
  rdf,
  reps_A,
  reps_B,
  batches = FALSE,
  min_length = 11,
  check_signal_strength = TRUE,
  check_nucs = TRUE,
  check_quality = TRUE,
  quality = "auto",
  evidence = 0,
  signal_strength = 0.1,
  within_combs = NULL,
  between_combs = NULL,
  ind_regions = TRUE,
  gap = 1,
  get_FDR = TRUE,
  proximity_assisted = FALSE,
  proximity = 10,
  proximity_defined_length = 30
)
```
**Arguments**

- **rdf**
  Dataframe of reactivities for each sample.

- **reps_A**
  Number of replicates of group A.

- **reps_B**
  Number of replicates of group B.

- **batches**
  Logical suggesting if replicates of group A and B were performed in batches and are labelled accordingly. If TRUE, a heterogeneous/homogeneous subset may not have multiple samples from the same batch.

- **min_length**
  Minimum length of constructed regions.

- **check_signal_strength**
  Logical, if TRUE, construction of regions must be based on nucleotides that have a minimum absolute value of reactivity.

- **check_nucs**
  Logical, if TRUE, constructed regions must have a minimum number of nucleotides participating in Wilcoxon signed rank test.

- **check_quality**
  Logical, if TRUE, check constructed regions for quality.

- **quality**
  Worst allowed quality for a region to be tested.

- **evidence**
  Minimum evidence of increase in variation from within-group comparisons to between-group comparisons for a region to be tested.

- **signal_strength**
  Threshold for minimum signal strength.

- **within_combs**
  Dataframe with each column containing groupings of replicates of groups A or B, which will be used to assess within-group variation.

- **between_combs**
  Dataframe with each column containing groupings of replicates of groups A and B, which will be used to assess between-group variation.

- **ind_regions**
  Logical, if TRUE, test each region found in the transcript separately.

- **gap**
  Integer. Join regions if they are separated by these many nucleotides.

- **get_FDR**
  Logical, if FALSE, FDR is not reported.

- **proximity_assisted**
  Logical, if TRUE, proximally located regions are tested together.

- **proximity**
  Maximum distance between constructed regions for them to be considered proximal.

- **proximity_defined_length**
  If performing a "proximity-assisted" test, minimum end-to-end length of a region to be tested.

**Value**

Constructs regions, reports p-value and median difference of between-group and within-group d-scores for each region, and FDR for them.

**Author(s)**

Krishna Choudhary
References

Examples
#Load data from Lai et al., 2019
data(lai2019)

#Run dStruct in de novo discovery mode for a transcript with id YAL042W.
dStruct(rdf = lai2019["YAL042W"], reps_A = 3, reps_B = 2,
       batches = TRUE, min_length = 21,
       between_combs = data.frame(c("A3", "B1", "B2")),
       within_combs = data.frame(c("A1", "A2", "A3")),
       ind_regions = TRUE)

dStructGuided
Performs guided discovery of differentially reactive regions.

Description
This function takes as input reactivity profiles for a transcript region from samples of two groups. First, it regroups the samples into homogeneous and heterogeneous sub-groups, which are used to compute the within-group and between-group nucleotide-wise $d$ scores. If the region meets the quality criteria, the between- and within-group $d$ scores are compared using the Wilcoxon signed-rank test. The resulting p-values quantify the significance of difference in reactivity patterns between the two input groups.

Usage
dStructGuided(
  rdf,
  reps_A,
  reps_B,
  batches = FALSE,
  within_combs = NULL,
  between_combs = NULL,
  check_quality = TRUE,
  quality = "auto",
  evidence = 0
)

Arguments
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rdf</td>
<td>Dataframe of reactivities for each sample. Each column must be labelled as A1, A2, ..., B1, B2, ...</td>
</tr>
<tr>
<td>reps_A</td>
<td>Number of replicates of group A.</td>
</tr>
</tbody>
</table>
**dStructome**

<table>
<thead>
<tr>
<th>Description</th>
<th>Perform de novo or guided discovery of differentially reactive regions for transcriptome-wide data.</th>
</tr>
</thead>
</table>

**Value**

p-value for the tested region (estimated using one-sided Wilcoxon signed rank test) and the median of nucleotide-wise difference of between-group and within-group d-scores.

**Author(s)**

Krishna Choudhary

**References**


**Examples**

```r
# Load Wan et al., 2014 data
data(wan2014)

# Run dStruct in the guided mode on first region in wan2014.
dStructGuided(wan2014[1], reps_A = 2, reps_B = 1)
```

---

<table>
<thead>
<tr>
<th>reps_B</th>
<th>Number of replicates of group B.</th>
</tr>
</thead>
<tbody>
<tr>
<td>batches</td>
<td>Logical suggesting if replicates of group A and B were performed in batches and are labelled accordingly. If TRUE, a heterogeneous/homogeneous subset may not have multiple samples from the same batch.</td>
</tr>
<tr>
<td>within_combs</td>
<td>Data.frame with each column containing groupings of replicates of groups A or B, which will be used to assess within-group variation.</td>
</tr>
<tr>
<td>between_combs</td>
<td>Dataframe with each column containing groupings of replicates of groups A and B, which will be used to assess between-group variation.</td>
</tr>
<tr>
<td>check_quality</td>
<td>Logical, if TRUE, check regions for quality.</td>
</tr>
<tr>
<td>quality</td>
<td>Worst allowed quality for a region to be tested.</td>
</tr>
<tr>
<td>evidence</td>
<td>Minimum evidence of increase in variation from within-group comparisons to between-group comparisons for a region to be tested.</td>
</tr>
</tbody>
</table>
Usage

dStructome(
  rl,
  reps_A,
  reps_B,
  batches = FALSE,
  min_length = 11,
  check_signal_strength = TRUE,
  check_nucs = TRUE,
  check_quality = TRUE,
  quality = "auto",
  evidence = 0,
  signal_strength = 0.1,
  within_combs = NULL,
  between_combs = NULL,
  ind_regions = TRUE,
  gap = 1,
  processes = "auto",
  method = "denovo",
  proximity_assisted = FALSE,
  proximity = 10,
  proximity_defined_length = 30
)

Arguments

rl List of dataframes of reactivities for each sample.
reps_A Number of replicates of group A.
reps_B Number of replicates of group B.
batches Logical suggesting if replicates of group A and B were performed in batches and
are labelled accordingly. If TRUE, a heterogeneous/homogeneous subset may
not have multiple samples from the same batch.
min_length Minimum length of constructed regions.
check_signal_strength Logical, if TRUE, construction of regions must be based on nucleotides that
have a minimum absolute value of reactivity.
check_nucs Logical, if TRUE, constructed regions must have a minimum number of nu-
cleotides participating in Wilcoxon signed rank test.
check_quality Logical, if TRUE, check constructed regions for quality.
quality Worst allowed quality for a region to be tested.
evidence Minimum evidence of increase in variation from within-group comparisons to
between-group comparisons for a region to be tested.
signal_strength Threshold for minimum signal strength.
within_combs Data.frame with each column containing groupings of replicates of groups A or
B, which will be used to assess within-group variation.
### dStructome

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>between_combs</td>
<td>DataFrame with each column containing groupings of replicates of groups A and B, which will be used to assess between-group variation.</td>
</tr>
<tr>
<td>ind_regions</td>
<td>Logical, if TRUE, test each region found in the transcript separately.</td>
</tr>
<tr>
<td>gap</td>
<td>Integer. Join regions if they are separated by these many nucleotides.</td>
</tr>
<tr>
<td>processes</td>
<td>Number of parallel processes to use.</td>
</tr>
<tr>
<td>method</td>
<td>Character specifying either guided or de novo discovery approach.</td>
</tr>
<tr>
<td>proximity_assisted</td>
<td>Logical, if TRUE, proximally located regions are tested together.</td>
</tr>
<tr>
<td>proximity</td>
<td>Maximum distance between constructed regions for them to be considered proximal.</td>
</tr>
<tr>
<td>proximity_defined_length</td>
<td>If performing a &quot;proximity-assisted&quot; test, minimum end-to-end length of a region to be tested.</td>
</tr>
</tbody>
</table>

### Value

Constructs regions, reports p-value and median difference of between-group and within-group d-scores for each region, and FDR for them.

### Author(s)

Krishna Choudhary

### References


### Examples

```r
#Load data from Lai et al., 2019
data(lai2019)

#Run dStruct in de novo discovery mode for all the transcripts in this data in one step.
dStructome(lai2019, 3, 2, batches = TRUE, min_length = 21,
           between_combs = data.frame(c("A3", "B1", "B2")),
           within_combs = data.frame(c("A1", "A2", "A3")),
           ind_regions = TRUE, processes = 1)

#Load data from Wan et al., 2014
data(wan2014)

#Run dStruct in guide discovery mode for all the transcript regions in this data in one step.
dStructome(wan2014, reps_A = 2, reps_B = 1, method = "guided", processes = 1)
```
getCombs

Identifies subgroupings of replicates for assessing within-group and between-group variation.

Description

Regroup all the samples of A and B groups into homogenous and heterogeneous sub-groups. Each homogenous sub-group contains replicates of either group A only or group B only. Each heterogeneous sub-group has a mix of samples from both the groups A and B.

Usage

getCombs(
  reps_A,
  reps_B,
  batches = FALSE,
  between_combs = NULL,
  within_combs = NULL
)

Arguments

reps_A Number of replicates of group A.
reps_B Number of replicates of group B.
batches Logical suggesting if replicates of group A and B were performed in batches and are labelled accordingly. If TRUE, a heterogeneous/homogeneous subset may not have multiple samples from the same batch.
between_combs Dataframe with each column containing groupings of replicates of groups A and B, which will be used to assess between-group variation.
within_combs Dataframe with each column containing groupings of replicates of groups A or B, which will be used to assess within-group variation.

Value

List of two dataframes, containing groupings for within-group and between-group variation.

Author(s)

Krishna Choudhary

References

Examples

# Get heterogeneous and homogeneous set combinations of samples when there are 2 samples of group A and 1 of group B.
getCombs(2, 1)

getContigRegions

Identifies contiguous regions from a list of nucleotide indices.

Description

Given a sequence of nucleotide indices, this function returns integer ranges covered by the indices. There is an option to merge ranges if they are separated by less than a user-specified distance.

Usage

getContigRegions(x, gap = 0)

Arguments

x  A vector of integers.
gap  Include gaps in the ranges if they are shorter than or equal to this length.

Value

IRanges object storing start and end sites of contiguous regions.

Author(s)

Krishna Choudhary

Examples

# Convert an integer vector of nucleotide positions to an IRanges object containing the coordinates of contiguous regions.
nucleotide_positions <- c(1, 3, 2, 8, 4:7, 11:20)
getContigRegions(nucleotide_positions)

# Merge regions if their end points are within 3 nt of each other.
getContigRegions(nucleotide_positions, gap = 3)
getRegions  Constructs potential differentially reactive regions.

Description

This function takes between- and within-group \( d \) scores for a transcript as input and identifies regions where the former is generally larger. Regions that pass minimum quality and minimum signal criteria are returned.

Usage

generateRegions(
  d_within,
  d_spec,
  rdf,
  min_length = 11,
  check_signal_strength = TRUE,
  check_nucs = TRUE,
  check_quality = TRUE,
  quality = 0.5,
  evidence = 0,
  signal_strength = 0.1
)

Arguments

d_within  Nucleotide-wise \( d \) score for within-group variation.
d_spec  Nucleotide-wise \( d \) score for between-group variation.rdf  Dataframe of reactivities for each sample.min_length  Minimum length of constructed regions.
check_signal_strength  Logical, if TRUE, construction of regions must be based on nucleotides that have a minimum absolute value of reactivity.
check_nucs  Logical, if TRUE, constructed regions must have a minimum number of nucleotides participating in Wilcoxon signed rank test.check_quality  Logical, if TRUE, check constructed regions for quality.quality  Worst allowed quality for a region to be tested.evidence  Minimum evidence of increase in variation from within-group comparisons to between-group comparisons for a region to be tested.signal_strength  Threshold for minimum signal strength.

Value

Integer vector of nucleotides that constitute potential differentially reactive regions.
Author(s)
Krishna Choudhary

References

Description
Data from a Structure-seq assay of five samples of *Saccharomyces cerevisiae*, three of which were wild-type samples and two mutant samples. The data was pre-processed to obtain DMS reactivities as described by Lai et al. (2019).

Usage
data("lai2019")

Format
An object of class "list".

Source
Raw data from Lai et al., 2019 in processed form.

References

Examples
data("lai2019")
normalizer

Returns normalizer for reactivity vector.

Description

Assesses normalization factor for raw reactivities using the 2-8 % method. Given a reactivity profile, first, remove 2% of the nucleotides with the highest reactivities. Then, the normalization factor is the mean of reactivities of the 8% of the nucleotides with the next highest reactivities.

Usage

normalizer(raw.estimates)

Arguments

raw.estimates A vector of raw reactivities.

Value

The normalization factor.

Author(s)

Krishna Choudhary

References


Examples

normalizer(c(NA, rnorm(20, 0.5, 0.3), NA, -999))
plotDStructurome

Plots differentially reactive regions.

Description

Given the table of results from dStruct or dStructGuided and the corresponding lists with reactivity scores for all transcripts, this function saves a PDF file with detailed visualizations of reactivities for all differential regions.

Usage

plotDStructurome(
  rl,
  diff_regions,
  outfile,
  fdr = 0.05,
  ylim = c(-0.05, 3),
  del_d_cutoff = 0.01
)

Arguments

rl List of dataframes of reactivities for each sample.
diff_regions Output from dStruct or dStructGuided containing coordinates of regions with significance of differentially reactivity.
outfile The name for pdf file which will be saved.
fdr FDR threshold for plotted regions.
ylim Y-axis limits for plots.
del_d_cutoff Minimum effect size for plotted regions specified in terms of median difference of the between-group and within-group d-scores.

Value

Saves a PDF for all differentially reactive regions. Returns NULL.

Author(s)

Krishna Choudhary

References

Examples

```r
# Load data from Lai et al., 2019
data(lai2019)

# Run dStruct in de novo discovery mode for all the transcripts in this data in one step.
res <- dStructome(lai2019, 3, 2, batches= TRUE, min_length = 21,
between_combs = data.frame(c("A3", "B1", "B2")),
within_combs = data.frame(c("A1", "A2", "A3")),
ind_regions = TRUE, processes = 1)

# Plot the significant results and save to a PDF file.
plotDStructurome(rl = lai2019,
diff_regions = res,
outfile = "significantly_differential_regions",
fdr = 0.05,
ylim = c(-0.05, 3))
```

---

twoEightNormalize Normalizes reactivity vector.

Description

Given a reactivity profile, first, remove 2% of the nucleotides with the highest reactivities. Then, the normalization factor is the mean of reactivities of the 8% of the nucleotides with the next highest re-activities. The raw reactivities are divided by the normalization factor to get normalized reactivities. This is called as 2-8 % normalization and has been a common way to normalize data from RNA structurome profiling technologies such as SHAPE-Seq, Structure-Seq, etc. (see Low and Weeks, 2010, Sloma et al., 2015, and Choudhary et al., 2017).

Usage

twoEightNormalize(raw.estimates)

Arguments

raw.estimates A vector of raw reactivities.

Value

A vector of normalized reactivities.

Author(s)

Krishna Choudhary
References


Examples

twoEightNormalize(c(NA, rnorm(20, 0.5, 0.3), NA, -999))

---

wan2014 Homo sapiens *PARS data*

Description

Data from a PARS assay of a family trio of mother, father, and child. The data was pre-processed to obtain PARS scores as described in Choudhary et al. (2019).

Usage

data(wan2014)

Format

An object of class "list".

Source

Counts data from Wan et al., 2014 in processed form.

References


Examples

data(wan2014)
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