

Package ‘OncoScore’

October 17, 2020

Version 1.16.0

Date 2020-04-13

Title A tool to identify potentially oncogenic genes

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Depends R (>= 4.0.0),

Imports biomaRt, grDevices, graphics, utils, methods,

Suggests BiocGenerics, BiocStyle, knitr, testthat,

Description OncoScore is a tool to measure the association of genes to cancer based on citation frequencies in biomedical literature. The score is evaluated from PubMed literature by dynamically updatable web queries.

Encoding UTF-8

LazyData TRUE

License file LICENSE

URL <https://github.com/danro9685/OncoScore>

BugReports <https://github.com/danro9685/OncoScore>

biocViews BiomedicalInformatics

RoxygenNote 7.1.0

VignetteBuilder knitr

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

git_branch RELEASE_3_11

git_last_commit 40d7b3d

git_last_commit_date 2020-04-27

Date/Publication 2020-10-16

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combine.query.results *combine.query.results*

Description

Merge a set of genes in a unique one in order to account for possible aliases

Usage

```
combine.query.results(query, genes, new.name)
```

Arguments

query	The result of perform.query, perform.query.timeseries or perform.query.from.region
genes	A list of genes to be merged
new.name	A string containing the new name to be used for the new genes

Value

The frequencies of the genes in the cancer related documents and in all the documents retrieved on PubMed

Examples

```
data(query)
combine.query.results(query, c('IDH1', 'IDH2'), 'new_gene')
```

`combine.single.matrix` *combine.single.matrix*

Description

Perform merge procedure on a matrix

Usage

```
combine.single.matrix(query, genes, new.name)
```

Arguments

<code>query</code>	The result of <code>perform.query</code> , <code>perform.query.timeseries</code> or <code>perform.query.from.region</code>
<code>genes</code>	A list of genes to be merged
<code>new.name</code>	A string containing the new name to be used for the new genes

Value

a merged matrix

`compute.frequencies.scores`
compute.frequencies.scores

Description

compute the logarithmic scores based on the frequencies of the genes

Usage

```
compute.frequencies.scores(data, filter.threshold = 1, analysis.mode = "Log2")
```

Arguments

<code>data</code>	input data as result of the function <code>perform.query</code>
<code>filter.threshold</code>	threshold to filter for a minimum number of citations for the genes
<code>analysis.mode</code>	logarithmic scores to be computed, i.e., log10, log2, natural log or log5

Value

the computed scores

`compute.oncoscore` *compute.oncoscore*

Description

compute the OncoScore for a list of genes

Usage

```
compute.oncoscore(
  data,
  filter.threshold = 0,
  analysis.mode = "Log2",
  cutoff.threshold = 21.09,
  file = NULL,
  filter.invalid = TRUE
)
```

Arguments

`data` input data as result of the function `perform.query`

`filter.threshold` threshold to filter for a minimum number of citations for the genes

`analysis.mode` logarithmic scores to be computed, i.e., log10, log2, natural log or log5

`cutoff.threshold` threshold to be used to asses the oncogenes

`file` should I save the results to text files?

`filter.invalid` auto-remove genes with invalid count

Value

the computed OncoScores and the clusters for the genes

Examples

```
data(query)
compute.oncoscore(query)
```

`compute.oncoscore.from.region`
compute.oncoscore.from.region

Description

Perform OncoScore analysis on a given chromosomal region

Usage

```
compute.oncoscore.from.region(  
  chromosome,  
  start = NA,  
  end = NA,  
  gene.num.limit = 100,  
  filter.threshold = NA,  
  analysis.mode = "Log2",  
  cutoff.threshold = 21.09,  
  file = NULL  
)
```

Arguments

chromosome	chromosome to be retrieved
start	initial position to be used
end	final position to be used
gene.num.limit	A limit to the genes to be considered in the analysis; this is done to limit the number of queries to PubMed
filter.threshold	threshold to filter for a minimum number of citations for the genes
analysis.mode	logarithmic scores to be computed, i.e., log10, log2, natural log or log5
cutoff.threshold	threshold to be used to assess the oncogenes
file	should I save the results to text files?

Value

the computed scores

Examples

```
chromosome = 15  
start = 200000  
end = 300000  
compute.oncoscore.from.region(chromosome, start, end)
```

compute.oncoscore.timeseries

compute.oncoscore.timeseries

Description

perform the OncoScore time series analysis for a list of genes and data times

Usage

```
compute.oncoscore.timeseries(
  data,
  filter.threshold = 0,
  analysis.mode = "Log2",
  cutoff.threshold = 21.09,
  file = NULL
)
```

Arguments

`data` input data as result of the function `perform.query.timeseries`

`filter.threshold` threshold to filter for a minimum number of citations for the genes

`analysis.mode` logarithmic scores to be computed, i.e., log10, log2, natural log or log5

`cutoff.threshold` threshold to be used to asses the oncogenes

`file` should I save the results to text files?

Value

the performed OncoScores time series analysis

Examples

```
data(query.timepoints)
compute.oncoscore.timeseries(query.timepoints)
```

estimate.oncogenes	<i>estimate.oncogenes</i>
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Description

estimate the oncoscore for the genes

Usage

```
estimate.oncogenes(data, cutoff.threshold = 21.09)
```

Arguments

`data` input data as result of the function `compute.frequencies.scores`

`cutoff.threshold` threshold to be used to asses the oncogenes

Value

the computed scores and oncogenes

genes	<i>A list of genes</i>
-------	------------------------

Description

This dataset contains a list of genes to be used in the analysis as an example

Usage

genes

Format

txt

Value

list of 5 elements

Source

example data

get.genes.from.biomart	<i>get.genes.from.biomart</i>
------------------------	-------------------------------

Description

Get a gene list from biomart

Usage

```
get.genes.from.biomart(chromosome, start = NA, end = NA)
```

Arguments

chromosome	chromosome to be retrieved
start	initial position to be used
end	final position to be used

Value

A list of genes

Examples

```
chromosome = 15  
start = 200000  
end = 300000  
ch15 = get.genes.from.biomart(chromosome, start, end)
```

`get.list.from.xml` *get.list.from.xml*

Description

process the result of the query

Usage

`get.list.from.xml(webget)`

Arguments

`webget` The result from the query to PubMed

Value

Processed result obtained from the query to PubMed

`get.pubmed.driver.analysis`
get.pubmed.driver.analysis

Description

query PubMed for a list of genes

Usage

`get.pubmed.driver.analysis(keywords, gene)`

Arguments

`keywords` The set of keywords to be used for the query to PubMed

`gene` The name of a gene to be used for the query to PubMed

Value

The frequency for the current gene retrieved with the query on the provided set of keywords

`perform.query` *perform.query*

Description

perform the query to PubMed

Usage

```
perform.query(list.of.genes, gene.num.limit = 100, custom.search = NA)
```

Arguments

- `list.of.genes` The list of genes to be used in the queries to PubMed
- `gene.num.limit` A limit to the genes to be considered in the analysis; this is done to limit the number of queries to PubMed
- `custom.search` A custom set of keywords to be used when querying PubMed

Value

The frequencies of the genes in the cancer related documents and in all the documents retrieved on PubMed

Examples

```
data(genes)
perform.query(genes[1:2])
```

`perform.query.from.region`
perform.query.from.region

Description

Perform the query to PubMed on a given chromosomal region

Usage

```
perform.query.from.region(  
  chromosome,  
  start = NA,  
  end = NA,  
  gene.num.limit = 100  
)
```

Arguments

<code>chromosome</code>	chromosome to be retrieved
<code>start</code>	initial position to be used
<code>end</code>	final position to be used
<code>gene.num.limit</code>	A limit to the genes to be considered in the analysis; this is done to limit the number of queries to PubMed

Value

The frequencies of the genes in the cancer related documents and in all the documents retrieved on PubMed

Examples

```
chromosome = 15
start = 200000
end = 300000
perform.query.from.region(chromosome, start, end)
```

```
perform.query.timeseries
```

```
perform.query.timeseries
```

Description

perform the query to PubMed for the time series analysis

Usage

```
perform.query.timeseries(
  list.of.genes,
  list.of.datatimes,
  gene.num.limit = 100,
  timepoints.limit = 10,
  custom.search = NA
)
```

Arguments

<code>list.of.genes</code>	The list of genes to be used in the queries to PubMed
<code>list.of.datatimes</code>	The list of time points to be used in the queries to PubMed
<code>gene.num.limit</code>	A limit to the genes to be considered in the analysis; this is done to limit the number of queries to PubMed
<code>timepoints.limit</code>	A limit to the time points to be considered in the analysis; this is done to limit the number of queries to PubMed
<code>custom.search</code>	A custom set of keywords to be used when querying PubMed

Value

The frequencies of the genes in the cancer related documents and in all the documents retrieved on PubMed at the specified time points

Examples

```
data(genes)
data(timepoints)
perform.query.timeseries(genes[1:2], timepoints[1:2])
```

<code>plot.oncoscore</code>	<i>plot.oncoscore</i>
-----------------------------	-----------------------

Description

plot the OncoScore for a list of genes

Usage

```
## S3 method for class 'oncoscore'
plot(
  x,
  gene.number = 5,
  main = "OncoScore",
  xlab = "score",
  ylab = "genes",
  file = NA,
  ...
)
```

Arguments

<code>x</code>	input data as result of the function <code>compute.OncoScore</code>
<code>gene.number</code>	number of genes to print
<code>main</code>	the title
<code>xlab</code>	description of x axis (default score)
<code>ylab</code>	description of y axis (default genes)
<code>file</code>	where to save the plot
<code>...</code>	additional parameter to pass to the barplot function

Value

A plot

Examples

```
data(query)
result = compute.oncoscore(query)
plot.oncoscore(result)
```

```
plot.oncoscore.timeseries
      plot.oncoscore.timeseries
```

Description

plot the OncoScore for a list of genes

Usage

```
## S3 method for class 'oncoscore.timeseries'
plot(
  x,
  gene.number = 5,
  incremental = FALSE,
  relative = FALSE,
  main = "OncoScore",
  xlab = "timepoints",
  ylab = "score",
  legend.pos = "top",
  file = NA,
  ...
)
```

Arguments

x	input data as result of the function compute.OncoScore
gene.number	number of genes to print
incremental	display the OncoScore increment
relative	display the incrementa as relative value
main	the title
xlab	description of x asix (default score)
ylab	description of y asix (default genes)
legend.pos	Position of the legend
file	where to save the plot
...	additional parameter to pass to the lines function

Value

A plot

Examples

```
data(query.timepoints)
result = compute.oncoscore.timeseries(query.timepoints)
plot.oncoscore.timeseries(result)
```

query

The result of perform.web.query on genes

Description

This dataset contains the result of perform.web.query on genes

Usage

query

Format

rdata

Value

matrix 5 x 2

Source

example data

query.timepoints

The result of perform.time.series.query on genes and timepoints

Description

This dataset contains the result of perform.time.series.query on genes and timepoints

Usage

query.timepoints

Format

rdata

Value

list of 5 matrix 5 x 2

Source

example data

timepoints	<i>A list of timepoints</i>
------------	-----------------------------

Description

This dataset contains a list of time points to be used in the analysis as an example

Usage

timepoints

Format

txt

Value

list of 5 elements

Source

example data

try.scan	<i>try.scan</i>
----------	-----------------

Description

try to query the given URL

Usage

try.scan(getURL)

Arguments

getURL The given URL

Value

Result obtained from PubMed

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