

# Package ‘OncoScore’

September 19, 2024

**Version** 1.33.0

**Date** 2024-03-21

**Title** A tool to identify potentially oncogenic genes

**Depends** R (>= 4.1.0),

**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

**License** file LICENSE

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

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

**biocViews** BiomedicalInformatics

**RoxygenNote** 7.3.1

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/OncoScore>

**git\_branch** devel

**git\_last\_commit** b7415ab

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-09-18

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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.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)
```

---

<code>estimate.oncogenes</code>	<i>estimate.oncogenes</i>
---------------------------------	---------------------------

---

**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

*A list of genes*

---

**Description**

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

**Usage**

```
data(genes)
```

**Format**

rdata

**Value**

list of 5 elements

**Source**

example data

---

```
get.genes.from.biomart
```

*get.genes.from.biomart*

---

**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
```

---

`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.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**

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

**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.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**

list.of.genes	The list of genes to be used in the queries to PubMed
list.of.datatimes	The list of time points 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
timepoints.limit	A limit to the time points 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 at the specified time points

**Examples**

```
data(genes)
data(timepoints)
```

---

plot.oncoscore	<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**

x	input data as result of the function compute.OncoScore
gene.number	number of genes to print
main	the title
xlab	description of x axis (default score)
ylab	description of y axis (default genes)
file	where to save the plot
...	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**

```
data(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**

```
data(query.timepoints)
```

**Format**

rdata

**Value**

list of 5 matrix 5 x 2

**Source**

example data

timepoints

*A list of timepoints*

---

**Description**

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

**Usage**

```
data(timepoints)
```

**Format**

rdata

**Value**

list of 5 elements

**Source**

example data

---

try.scan

*try.scan*

---

**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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