

# Package ‘recount’

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**Suggests** AnnotationDbi, BiocManager, BiocStyle ( $\geq$  2.5.19), DESeq2, sessioninfo, EnsDb.Hsapiens.v79, GenomicFeatures, knitr ( $\geq$  1.6), org.Hs.eg.db, RefManageR, regionReport ( $\geq$  1.9.4), rmarkdown ( $\geq$  0.9.5), testthat ( $\geq$  2.1.0), covr, pheatmap, DT, edgeR, ggplot2, RColorBrewer

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**Description** Explore and download data from the recount project available at <https://jhubiostatistics.shinyapps.io/recount/>. Using the recount package you can download RangedSummarizedExperiment objects at the gene, exon or exon-exon junctions level, the raw counts, the phenotype metadata used, the urls to the sample coverage bigWig files or the mean coverage bigWig file for a particular study. The RangedSummarizedExperiment objects can be used by different packages for performing differential expression analysis. Using <http://bioconductor.org/packages/derfinder> you can perform annotation-agnostic differential expression analyses with the data from the recount project as described at <http://www.nature.com/nbt/journal/v35/n4/full/nbt.3838.html>.

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**LazyDataCompression** xz

**URL** <https://github.com/leekgroup/recount>

**BugReports** <https://support.bioconductor.org/t/recount/>

**biocViews** Coverage, DifferentialExpression, GeneExpression, RNASeq, Sequencing, Software, DataImport, ImmunoOncology

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<i>recount-package</i>	<i>recount: Explore and download data from the recount project</i>
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## Description

Explore and download data from the recount project available at <https://jhubiostatistics.shinyapps.io/recount/>. Using the *recount* package you can download `RangedSummarizedExperiment` objects at the gene, exon or exon-exon junctions level, the raw counts, the phenotype metadata used, the urls to the sample coverage bigWig files or the mean coverage bigWig file for a particular study. The `RangedSummarizedExperiment` objects can be used by different packages for performing differential expression analysis. Using <http://bioconductor.org/packages/derfinder> you can perform annotation-agnostic differential expression analyses with the data from the recount project as described at <http://www.nature.com/nbt/journal/v35/n4/full/nbt.3838.html>.

## Author(s)

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## See Also

Useful links:

- <https://github.com/leekgroup/recount>
- Report bugs at <https://support.bioconductor.org/t/recount/>

---

abstract_search	<i>Search the abstracts from the SRA studies available via the recount project</i>
-----------------	--

---

### Description

Given a text query, find the SRA project ids (study accession numbers) that contain the text in their abstract as provided by the SRADB Bioconductor package.

### Usage

```
abstract_search(query, id_only = FALSE, ...)
```

### Arguments

query	A character vector with the text to search for via <a href="#">grep</a> in the abstract info available at <a href="#">recount_abstract</a> .
id_only	Whether to only return the project id or to return summary information for the project(s) that match the query.
...	Additional arguments passed to <a href="#">grep</a> .

### Details

Both the query and the abstracts are searched in lower case.

For a more powerful search use the recount project website at <https://jhubiostatistics.shinyapps.io/recount/>.

### Value

If `id_only = TRUE` it returns a character vector with the project SRA ids (accession numbers). If `id_only = FALSE` it returns a subset of [recount\\_abstract](#) for the abstracts that contained the query.

### Author(s)

Leonardo Collado-Torres

### See Also

[browse\\_study](#), [recount\\_abstract](#)

### Examples

```
## Find the Geuvadis consortium project
project_info <- abstract_search("Geuvadis consortium")

## See some summary information for this project
project_info
```

---

add_metadata	<i>Add additional curated metadata to a recount rse object</i>
--------------	--

---

### Description

This function appends sample metadata information to a [RangedSummarizedExperiment-class](#) from the recount2 project. The sample metadata comes from curated efforts independent from the original recount2 project. Currently the only information comes from the recount\_brain project described in more detail at <http://lieberinstitute.github.io/recount-brain/>.

### Usage

```
add_metadata(rse, source = "recount_brain_v2", is_tcga = FALSE, verbose = TRUE)
```

### Arguments

rse	A <a href="#">RangedSummarizedExperiment-class</a> object as downloaded with <a href="#">download_study</a> . If this argument is not specified, the function will return the raw metadata table.
source	A valid source name. The only supported options at this moment are <code>recount_brain_v1</code> and <code>recount_brain_v2</code> .
is_tcga	Set to TRUE only when rse is from TCGA. Otherwise set to FALSE (default).
verbose	If TRUE it will print a message of where the predictions file is being downloaded to.

### Details

For `source = "recount_brain_v1"` and `source = "recount_brain_v2"`, the metadata columns are described at <http://lieberinstitute.github.io/recount-brain/>. Alternatively, you can explore `recount_brain_v2` interactively at <https://jhubiostatistics.shinyapps.io/recount-brain/>.

If you use the `recount_brain` data please cite the Razmara et al. bioRxiv, 2019 <https://www.biorxiv.org/content/10.1101/618025v1>. A bib file is available via `citation('recount')`.

### Value

A [RangedSummarizedExperiment-class](#) object with the sample metadata columns appended to the `colData()` slot.

### Author(s)

Leonardo Collado-Torres

### References

Razmara et al, bioRxiv, 2019. <https://www.biorxiv.org/content/10.1101/618025v1>

**Examples**

```
## Add the sample metadata to an example rse_gene object
rse_gene <- add_metadata(rse_gene_SRP009615, "recount_brain_v2")

## Explore the metadata
colData(rse_gene)

## For a list of studies present in recount_brain check
## http://lieberinstitute.github.io/recount-brain/.
## recount_brain_v2 includes GTEx and TCGA brain samples in addition to the
## recount_brain_v1 data, plus ontology information.

## Obtain all the recount_brain_v2 metadata if you want to
## explore the metadata manually
recount_brain_v2 <- add_metadata(source = "recount_brain_v2")
```

---

add_predictions	<i>Add predicted phenotypes to a recount rse object</i>
-----------------	---

---

**Description**

Shannon Ellis et al (2017) predicted phenotypes based on expression data for the samples in the recount2 project. Using this function you can add the predictions to a [RangedSummarizedExperiment-class](#) object to the colData() slot.

**Usage**

```
add_predictions(rse, is_tcga = FALSE, version = "latest", verbose = TRUE)
```

**Arguments**

rse	A <a href="#">RangedSummarizedExperiment-class</a> object as downloaded with <a href="#">download_study</a> . If this argument is not specified, the function will return the full predictions table.
is_tcga	Set to TRUE only when rse is from TCGA. Otherwise set to FALSE (default).
version	The version number for the predicted phenotypes data. It has to match one of the available numbers at <a href="https://github.com/leekgroup/recount-website/blob/master/predictions/">https://github.com/leekgroup/recount-website/blob/master/predictions/</a> . Feel free to check if there is a newer version than the default. The version used is printed as part of the file name.
verbose	If TRUE it will print a message of where the predictions file is being downloaded to.

**Details**

If you use these predicted phenotypes please cite the Ellis et al bioRxiv pre-print available at <https://www.biorxiv.org/content/early/2017/06/03/145656>. See citation details with citation('recount').

**Value**

A [RangedSummarizedExperiment-class](#) object with the prediction columns appended to the colData() slot. The predicted phenotypes are:

**sex** male or female,

**samplesource** cell\_line or tissue,

**tissue** tissue predicted based off of 30 tissues in GTEx,

**sequencingstrategy** single or paired end sequencing.

For each of the predicted phenotypes there are several columns as described next:

**reported\_phenotype** NA when not available,

**predicted\_phenotype** NA when we did not predict, "Unassigned" when prediction was ambiguous,

**accuracy\_phenotype** accuracy is assigned per dataset based on comparison to samples for which we had reported phenotype information so there are three distinct values per predictor (GTEx, TCGA, SRA) across all studies.

**Author(s)**

Leonardo Collado-Torres

**References**

Ellis et al, bioRxiv, 2017. <https://www.biorxiv.org/content/early/2017/06/03/145656>

**Examples**

```
## Add the predictions to an example rse_gene object
rse_gene <- add_predictions(rse_gene_SRP009615)

## Explore the predictions
colData(rse_gene)

## Download all the latest predictions
PredictedPhenotypes <- add_predictions()
```

---

all\_metadata

*This function downloads the metadata for all projects.*

---

**Description**

Download the metadata from all the projects. This can be useful for finding samples of interests across all projects.

**Usage**

```
all_metadata(subset = "sra", verbose = TRUE)
```

**Arguments**

subset            Either sra, gtex or tcga. Specifies which metadata file to download.  
 verbose          If TRUE it will print a message of where the file is being downloaded to.

**Details**

Note that for subset = 'gtex', there are more variables than the ones we have for 'sra'. This information corresponds to file GTEEx\_Data\_V6\_Annotations\_SampleAttributesDS.txt available at <http://www.gtexportal.org/home/datasets>. There you can find the information describing these variables.

For TCGA we acquired metadata information from 3 different sources:

- GDC: via a json query
- CGC: via json queries and a custom script to merge the tables
- TCGAbiolinks: we used to to parse GDC's XML files For more information, check [https://github.com/leekgroup/recount-website/tree/master/metadata/tcga\\_prep](https://github.com/leekgroup/recount-website/tree/master/metadata/tcga_prep).

**Value**

A `DataFrame-class` object with the phenotype metadata.

**Author(s)**

Leonardo Collado-Torres

**Examples**

```
metadata <- all_metadata()
```

---

browse\_study

*Open a SRA study id in the SRA website*

---

**Description**

Given a SRA study id get the url to browse the study using the SRA website.

**Usage**

```
browse_study(project, browse = interactive())
```

**Arguments**

project          A character vector with at least one SRA study id.  
 browse          Whether to open the resulting URL in the browser.



**Value**

Returns invisibly the URL for exploring the study in the SRA website.

**Author(s)**

Leonardo Collado-Torres

**See Also**

[abstract\\_search](#)

**Examples**

```
## Find the Geuvadis consortium project
id <- abstract_search("Geuvadis consortium", id_only = TRUE)
id

## Explore the Geuvadis consortium project
url <- browse_study(id)

## See the actual URL
url
```

---

coverage_matrix	<i>Given a set of regions for a chromosome, compute the coverage matrix for a given SRA study.</i>
-----------------	--

---

**Description**

Given a set of genomic regions as created by [expressed\\_regions](#), this function computes the coverage matrix for a library size of 40 million 100 bp reads for a given SRA study.

**Usage**

```
coverage_matrix(  
  project,  
  chr,  
  regions,  
  chunksize = 1000,  
  bpparam = NULL,  
  outdir = NULL,  
  chrLen = NULL,  
  verbose = TRUE,  
  verboseLoad = verbose,  
  scale = TRUE,  
  round = FALSE,  
  ...  
)
```

**Arguments**

project	A character vector with one SRA study id.
chr	A character vector with the name of the chromosome.
regions	A <a href="#">GRanges-class</a> object with regions for chr for which to calculate the coverage matrix.
chunksize	A single integer vector defining the chunksize to use for computing the coverage matrix. Regions will be split into different chunks which can be useful when using a parallel instance as defined by <code>bpparam</code> .
bpparam	A <a href="#">BiocParallelParam-class</a> instance which will be used to calculate the coverage matrix in parallel. By default, <a href="#">SerialParam-class</a> will be used.
outdir	The destination directory for the downloaded file(s) that were previously downloaded with <a href="#">download_study</a> . If the files are missing, but <code>outdir</code> is specified, they will get downloaded first. By default <code>outdir</code> is set to <code>NULL</code> which will use the data from the web. We only recommend downloading the full data if you will use it several times.
chrLen	The chromosome length in base pairs. If it's <code>NULL</code> , the chromosome length is extracted from the Rail-RNA runs GitHub repository. Alternatively check the SciServer section on the vignette to see how to access all the recount data via a R Jupyter Notebook.
verbose	If <code>TRUE</code> basic status updates will be printed along the way.
verboseLoad	If <code>TRUE</code> basic status updates for loading the data will be printed.
scale	If <code>TRUE</code> , the coverage counts will be scaled to read counts based on a library size of 40 million reads. Set <code>scale</code> to <code>FALSE</code> if you want the raw coverage counts. The scaling method is by AUC, as in the default option of <a href="#">scale_counts</a> .
round	If <code>TRUE</code> , the counts are rounded to integers. Set to <code>TRUE</code> if you want to match the defaults of <a href="#">scale_counts</a> .
...	Additional arguments passed to <a href="#">download_study</a> when <code>outdir</code> is specified but the required files are missing.

**Details**

When using `outdir = NULL` the information will be accessed from the web on the fly. If you encounter internet access problems, it might be best to first download the BigWig files using [download\\_study](#). This might be the best option if you are accessing all chromosomes for a given project and/or are thinking of using different sets of regions (for example, from different cutoffs applied to [expressed\\_regions](#)). Alternatively check the SciServer section on the vignette to see how to access all the recount data via a R Jupyter Notebook.

If you have `bwtool` installed, you can use <https://github.com/LieberInstitute/recount.bwtool> for faster results. Note that you will need to run [scale\\_counts](#) after running `coverage_matrix_bwtool()`.

**Value**

A [RangedSummarizedExperiment-class](#) object with the counts stored in the assays slot.

**Author(s)**

Leonardo Collado-Torres

**See Also**[download\\_study](#), [findRegions](#), [railMatrix](#)**Examples**

```
if (.Platform$OS.type != "windows") {
  ## Reading BigWig files is not supported by rtracklayer on Windows
  ## Define expressed regions for study DRP002835, chrY
  regions <- expressed_regions("DRP002835", "chrY",
    cutoff = 5L,
    maxClusterGap = 3000L
  )

  ## Now calculate the coverage matrix for this study
  rse <- coverage_matrix("DRP002835", "chrY", regions)

  ## One row per region
  identical(length(regions), nrow(rse))
}
```

---

`download_retry`*Retry multiple times to download a file*

---

**Description**

This function is based on the Bioconductor guidelines for querying data from the web at <http://bioconductor.org/developers/how-to/web-query/>. It will run `download` a set of `N.TRIES` times before giving up. We implemented this function to reduce the number of Bioconductor build errors due to the occasional errors from our data hosting server.

**Usage**

```
download_retry(url, destfile = basename(url), mode = "wb", N.TRIES = 3L, ...)
```

**Arguments**

<code>url</code>	The URL to download. Passed to <a href="#">download</a> .
<code>destfile</code>	The destination file. Defaults to the base name of the URL. Passed to <a href="#">download</a> .
<code>mode</code>	Mode for writing the file. The default <code>wb</code> is used for binary files. This value is passed to <a href="#">download</a> which passes it to <a href="#">download.file</a> .
<code>N.TRIES</code>	The number of download attempts before giving up; default: 3. Should be an integer of length one with a value greater than 0.
<code>...</code>	Additional arguments passed to <a href="#">download</a> .

**Value**

An invisible integer code as specified in [download.file](#).

**Examples**

```
## Download the first files_info.tsv file (version 1)
download_retry(
  recount_url$url[which(recount_url$file_name == "files_info.tsv")[1]]
)
```

---

download\_study

*Download data for a given SRA study id from the recount project*

---

**Description**

Download the gene or exon level [RangedSummarizedExperiment-class](#) objects provided by the recount project. Alternatively download the counts, metadata or file information for a given SRA study id. You can also download the sample bigWig files or the mean coverage bigWig file.

**Usage**

```
download_study(
  project,
  type = "rse-gene",
  outdir = project,
  download = TRUE,
  version = 2,
  ...
)
```

**Arguments**

project	A character vector with one SRA study id.
type	Specifies which files to download. The options are: <ul style="list-style-type: none"> <li><b>rse-gene</b> the gene-level <a href="#">RangedSummarizedExperiment-class</a> object in a file named rse_gene.Rdata.</li> <li><b>rse-exon</b> the exon-level <a href="#">RangedSummarizedExperiment-class</a> object in a file named rse_exon.Rdata.</li> <li><b>rse-jx</b> the exon-exon junction level <a href="#">RangedSummarizedExperiment-class</a> object in a file named rse_jx.Rdata.</li> <li><b>rse-tx</b> the transcript level <a href="#">RangedSummarizedExperiment-class</a> object in a file named rse_tx.RData.</li> <li><b>counts-gene</b> the gene-level counts in a tsv file named counts_gene.tsv.gz.</li> <li><b>counts-exon</b> the exon-level counts in a tsv file named counts_exon.tsv.gz.</li> <li><b>counts-jx</b> the exon-exon junction level counts in a tsv file named counts_jx.tsv.gz.</li> </ul>

	<b>phenotype</b> the phenotype data for the study in a tsv file named project.tsv.
	<b>files-info</b> the files information for the given study (including md5sum hashes) in a tsv file named files_info.tsv.
	<b>samples</b> one bigWig file per sample in the study.
	<b>mean</b> one mean bigWig file for the samples in the study, with each sample normalized to a 40 million 100 bp library using the total coverage sum (area under the coverage curve, AUC) for the given sample.
	<b>all</b> Downloads all the above types. Note that it might take some time if the project has many samples. When using type = 'all' a small delay will be added before each download request to avoid request issues.
	<b>rse-fc</b> Downloads the FANTOM-CAT/recount2 rse file described in Imada, Sanchez, et al., bioRxiv, 2019.
outdir	The destination directory for the downloaded file(s). Alternatively check the SciServer section on the vignette to see how to access all the recount data via a R Jupyter Notebook.
download	Whether to download the files or just get the download urls.
version	A single integer specifying which version of the files to download. Valid options are 1 and 2, as described in <a href="https://jhubiostatistics.shinyapps.io/recount/">https://jhubiostatistics.shinyapps.io/recount/</a> under the documentation tab. Briefly, version 1 are counts based on reduced exons while version 2 are based on disjoint exons. This argument mostly just matters for the exon counts. Defaults to version 2 (disjoint exons). Use version = 1 for backward compatability with exon counts prior to version 1.5.3 of the package.
...	Additional arguments passed to <a href="#">download</a> .

## Details

Check <http://stackoverflow.com/a/34383991> if you need to find the effective URLs. For example, [http://duffel.rail.bio/recount/DRP000366/bw/mean\\_DRP000366.bw](http://duffel.rail.bio/recount/DRP000366/bw/mean_DRP000366.bw) points to a link from SciServer.

Transcript quantifications are described in Fu et al, bioRxiv, 2018. <https://www.biorxiv.org/content/10.1101/247346v2>

FANTOM-CAT/recount2 quantifications are described in Imada, Sanchez, et al., bioRxiv, 2019. <https://www.biorxiv.org/content/10.1101/659490v1>

## Value

Returns invisibly the URL(s) for the files that were downloaded.

## Author(s)

Leonardo Collado-Torres

## Examples

```
## Find the URL to download the RangedSummarizedExperiment for the
## Geuvadis consortium study.
url <- download_study("ERP001942", download = FALSE)

## See the actual URL
url
## Not run:
## Download the example data included in the package for study SRP009615

url2 <- download_study("SRP009615")
url2

## Load the data
load(file.path("SRP009615", "rse_gene.Rdata"))

## Compare the data
library("testthat")
expect_equivalent(rse_gene, rse_gene_SRP009615)

## End(Not run)
```

---

expressed_regions	<i>Identify expressed regions from the mean coverage for a given SRA project</i>
-------------------	--

---

## Description

This function uses the pre-computed mean coverage for a given SRA project to identify the expressed regions (ERs) for a given chromosome. It returns a [GRanges-class](#) object with the expressed regions as defined by [findRegions](#).

## Usage

```
expressed_regions(
  project,
  chr,
  cutoff,
  outdir = NULL,
  maxClusterGap = 300L,
  chrLen = NULL,
  verbose = TRUE,
  ...
)
```

**Arguments**

project	A character vector with one SRA study id.
chr	A character vector with the name of the chromosome.
cutoff	The base-pair level cutoff to use.
outdir	The destination directory for the downloaded file(s) that were previously downloaded with <a href="#">download_study</a> . If the files are missing, but outdir is specified, they will get downloaded first. By default outdir is set to NULL which will use the data from the web. We only recommend downloading the full data if you will use it several times.
maxClusterGap	This determines the maximum gap between candidate ERs.
chrLen	The chromosome length in base pairs. If it's NULL, the chromosome length is extracted from the Rail-RNA runs GitHub repository. Alternatively check the SciServer section on the vignette to see how to access all the recount data via a R Jupyter Notebook.
verbose	If TRUE basic status updates will be printed along the way.
...	Additional arguments passed to <a href="#">download_study</a> when outdir is specified but the required files are missing.

**Value**

A [GRanges-class](#) object as created by [findRegions](#).

**Author(s)**

Leonardo Collado-Torres

**See Also**

[download\\_study](#), [findRegions](#), [railMatrix](#)

**Examples**

```
## Define expressed regions for study SRP009615, chrY
if (.Platform$OS.type != "windows") {
  ## Reading BigWig files is not supported by rtracklayer on Windows
  regions <- expressed_regions("SRP009615", "chrY",
    cutoff = 5L,
    maxClusterGap = 3000L
  )
}
## Not run:
## Define the regions for multiple chrs
regs <- sapply(chrs, expressed_regions, project = "SRP009615", cutoff = 5L)

## You can then combine them into a single GRanges object if you want to
library("GenomicRanges")
single <- unlist(GRangesList(regs))
```

```
## End(Not run)
```

---

find_geo	<i>Find the GEO accession id for a given SRA run</i>
----------	--

---

### Description

Given a SRA run id, this function will retrieve the GEO accession id (starting with GSM) if it's available. Otherwise it will return NA.

### Usage

```
find_geo(run, verbose = FALSE, sleep = 1/2)
```

### Arguments

run	A character vector of length 1 with the SRA run accession id.
verbose	Whether to print a message for the run. Useful when looping over a larger number of SRA run ids.
sleep	The number of seconds (or fraction) to wait before downloading data using <a href="#">get-GEO</a> . This is important if you are looking over <code>geo_info()</code> given the constraints published at <a href="https://www.ncbi.nlm.nih.gov/books/NBK25497/">https://www.ncbi.nlm.nih.gov/books/NBK25497/</a> .

### Details

Although the phenotype information already includes the GEO accession ids, not all projects had GEO entries at the time these tables were created. This function will then be useful to check if there is a GEO accession id for a given sample (run). If there is, you can then retrieve the information using [geo\\_info](#).

### Value

The GEO accession id for the corresponding sample.

### Author(s)

Leonardo Collado-Torres

### Examples

```
## Find the GEO accession id for for SRX110461
find_geo("SRX110461")
```



---

geo\_characteristics    *Build a data.frame from GEO's characteristics for a given sample*

---

### Description

This function builds a data.frame from the GEO characteristics extracted for a given sample. The names of the columns correspond to the field names. For a given SRA project, this information can be combined for all samples as shown in the examples section.

### Usage

```
geo_characteristics(pheno)
```

### Arguments

pheno            A [DataFrame-class](#) as created by [geo\\_info](#).

### Value

A 1 row data.frame with the characteristic fields as column names and the values as the entries on the first row. If the authors of the study used the same names for all samples, you can then combine them using [rbind](#).

### Author(s)

Leonardo Collado-Torres

### Examples

```
## Load required library
library("SummarizedExperiment")

## Get the GEO accession ids
# geoids <- sapply(colData(rse_gene_SRP009615)$run[1:2], find_geo)
## The previous example code works nearly all the time but it
## can occasionally fail depending on how rentrez is doing.
## This code makes sure that the example code runs.
geoids <- tryCatch(
  sapply(colData(rse_gene_SRP009615)$run[1:2], find_geo),
  error = function(e) {
    c(
      "SRR387777" = "GSM836270",
      "SRR387778" = "GSM836271"
    )
  }
)

## Get the data from GEO
geodata <- do.call(rbind, sapply(geoids, geo_info))
```

```
## Add characteristics in a way that we can access easily later on
geodata <- cbind(geodata, geo_characteristics(geodata))

## Explore the original characteristics and the result from
## geo_characteristics()
geodata[, c("characteristics", "cells", "shrna.expression", "treatment")]
```

---

geo\_info

*Extract information from GEO for a given sample*

---

### Description

This function uses GEOquery to extract information for a given sample. The GEO accession ids for the sample can be found in the study phenotype table.

### Usage

```
geo_info(
  geoid,
  verbose = FALSE,
  sleep = 1/2,
  getGPL = FALSE,
  destdir = tempdir(),
  ...
)
```

### Arguments

geoid	A character vector of length 1 with the GEO accession id for a given sample.
verbose	If TRUE the geoid will be shown.
sleep	The number of seconds (or fraction) to wait before downloading data using <a href="#">getGEO</a> . This is important if you are looking over <code>geo_info()</code> given the constraints published at <a href="https://www.ncbi.nlm.nih.gov/books/NBK25497/">https://www.ncbi.nlm.nih.gov/books/NBK25497/</a> .
getGPL	This argument is passed to <a href="#">getGEO</a> and is set to FALSE by default to speed up the process.
destdir	This argument is passed to <a href="#">getGEO</a> .
...	Additional arguments passed to <a href="#">getGEO</a> .

### Value

Returns a [DataFrame-class](#) with the information from GEO available for the given sample.

### Author(s)

Leonardo Collado-Torres, Andrew Jaffe

**Examples**

```
geo_info("GSM836270")
```

---

getRPKM	<i>Compute an RPKM matrix based on a RangedSummarizedExperiment object</i>
---------	--

---

**Description**

For some analyses you might be interested in transforming the counts into RPKMs which you can do with this function.

**Usage**

```
getRPKM(rse, length_var = "bp_length", mapped_var = NULL)
```

**Arguments**

rse	A <a href="#">RangedSummarizedExperiment-class</a> object as downloaded with <a href="#">download_study</a> .
length_var	A length 1 character vector with the column name from <code>rowData(rse)</code> that has the coding length. For gene level objects from recount this is <code>bp_length</code> . If NULL, then it will use <code>width(rowRanges(rse))</code> which should be used for exon RSEs.
mapped_var	A length 1 character vector with the column name from <code>colData(rse)</code> that has the number of reads mapped. For recount RSE object this would be <code>mapped_read_count</code> . If NULL (default) then it will use the column sums of the counts matrix. The results are different because not all mapped reads are mapped to exonic segments of the genome.

**Details**

For gene RSE objects, you will want to specify the `length_var` because otherwise you will be adjusting for the total gene length instead of the total exonic sequence length of the gene.

**Value**

A matrix with the RPKM values.

**Author(s)**

Andrew Jaffe, Leonardo Collado-Torres

**See Also**

[scale\\_counts](#)

**Examples**

```
## get RPKM matrix
rpkm <- getRPKM(rse_gene_SRP009615)

## You can also get an RPKM matrix after running scale_counts()
## with similar RPKM values
rpkm2 <- getRPKM(scale_counts(rse_gene_SRP009615))
rpkm3 <- getRPKM(scale_counts(rse_gene_SRP009615, by = "mapped_reads"))

summary(rpkm - rpkm2)
summary(rpkm - rpkm3)
summary(rpkm2 - rpkm3)
```

---

getTPM	<i>Compute a TPM matrix based on a RangedSummarizedExperiment object</i>
--------	--

---

**Description**

For some analyses you might be interested in transforming the counts into TPMs which you can do with this function. This function uses the gene-level RPKMs to derive TPM values (see Details).

**Usage**

```
getTPM(rse, length_var = "bp_length", mapped_var = NULL)
```

**Arguments**

rse	A <a href="#">RangedSummarizedExperiment-class</a> object as downloaded with <a href="#">download_study</a> .
length_var	A length 1 character vector with the column name from <code>rowData(rse)</code> that has the coding length. For gene level objects from recount this is <code>bp_length</code> . If NULL, then it will use <code>width(rowRanges(rse))</code> which should be used for exon RSEs.
mapped_var	A length 1 character vector with the column name from <code>colData(rse)</code> that has the number of reads mapped. For recount RSE object this would be <code>mapped_read_count</code> . If NULL (default) then it will use the column sums of the counts matrix. The results are different because not all mapped reads are mapped to exonic segments of the genome.

**Details**

For gene RSE objects, you will want to specify the `length_var` because otherwise you will be adjusting for the total gene length instead of the total exonic sequence length of the gene.

As noted in <https://support.bioconductor.org/p/124265/>, Sonali Arora et al computed TPMs in <https://www.biorxiv.org/content> using the formula:  $TPM = FPKM / (\text{sum of FPKM over all genes/transcripts}) * 10^6$

Arora et al mention in their code that the formula comes from <https://doi.org/10.1093/bioinformatics/btp692>; specifically 1.1.1 Comparison to RPKM estimation where they mention an important assumption: Under the assumption of uniformly distributed reads, we note that RPKM measures are estimates of ...

There's also a blog post by Harold Pimentel explaining the relationship between FPKM and TPM: <https://haroldpimentel.wordpress.com/2014/05/08/what-the-fpkm-a-review-rna-seq-expression-units/>.

### Value

A matrix with the TPM values.

### Author(s)

Sonali Arora, Leonardo Collado-Torres

### References

<https://www.biorxiv.org/content/10.1101/445601v2> <https://arxiv.org/abs/1104.3889>

### See Also

[getRPKM](#)

### Examples

```
## Compute the TPM matrix from the raw gene-level base-pair counts.
tpm <- getTPM(rse_gene_SRP009615)
```

---

read_counts	<i>Compute read counts</i>
-------------	----------------------------

---

### Description

As described in the recount workflow, the counts provided by the recount2 project are base-pair counts. You can scale them using [scale\\_counts](#) or compute the read counts using the area under coverage information (AUC). We use the AUC because Rail-RNA soft clips some reads.

### Usage

```
read_counts(rse, use_paired_end = TRUE, round = FALSE)
```

### Arguments

rse	A <a href="#">RangedSummarizedExperiment-class</a> object as downloaded with <a href="#">download_study</a> .
use_paired_end	A logical vector. When TRUE it uses the paired-end flag ( <code>colData(rse)\$paired_end</code> ) to determine whether the sample is paired-end or not. If it's paired-end, then it divides the counts by 2 to return paired-end read counts instead of fragment counts. When FALSE, this information is ignored.
round	Whether to round the counts to integers or not.

**Details**

Check the recount workflow for details about the counts provided by the recount2 project. Note that this function should not be used after [scale\\_counts](#) or it will return non-sensical results.

**Value**

Returns a [RangedSummarizedExperiment-class](#) object with the read counts.

**Author(s)**

Leonardo Collado-Torres

**References**

Collado-Torres L, Nellore A and Jaffe AE. recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor version 1; referees: 1 approved, 2 approved with reservations. F1000Research 2017, 6:1558 doi: 10.12688/f1000research.12223.1.

**See Also**

[scale\\_counts](#)

**Examples**

```
## Difference between read counts and reads downloaded by Rail-RNA
colSums(assays(read_counts(rse_gene_SRP009615))$counts) / 1e6 -
  colData(rse_gene_SRP009615)$reads_downloaded / 1e6

## Paired-end read counts vs fragment counts (single-end counts)
download_study("DRP000499")
load("DRP000499/rse_gene.Rdata")
colSums(assays(read_counts(rse_gene, use_paired_end = FALSE))$counts) /
  colSums(assays(read_counts(rse_gene))$counts)

## Difference between paired-end read counts vs paired-end reads downloaded
colSums(assays(read_counts(rse_gene))$counts) / 1e6 -
  colData(rse_gene)$reads_downloaded / 1e6 / 2
```

---

recount\_abstract

*Summary information at the project level for the recount project*

---

**Description**

A data.frame with summary information at the project level for the studies analyzed in the recount project.

**Format**

A data.frame with 4 columns.

**number\_samples** the number of samples in the study,

**species** the species of the study,

**abstract** the abstract text as provided by the SRAdb Bioconductor package,

**project** the SRA project id.

**References**

<https://jhubiostatistics.shinyapps.io/recount/>

**See Also**

[download\\_study](#)

---

recount\_exons

*Exon annotation used in recount*

---

**Description**

Exon annotation extracted from Gencode v25 (GRCh38.p7) used in recount. Data extracted on October 12th, 2017.

**Format**

A [GRangesList-class](#) with one element per gene. The names match the gene Gencode v25 ids.

**References**

<https://jhubiostatistics.shinyapps.io/recount/>

**See Also**

[reproduce\\_ranges](#), [recount\\_genes](#)

---

recount_genes	<i>Gene annotation used in recount</i>
---------------	--

---

### Description

Gene annotation extracted from Gencode v25 (GRCh38.p7) used in recount. Data extracted on October 12th, 2017. The symbols were updated compared to the version from January 17th, 2017. It includes the sum of the width of the disjoint exons which can be used for normalizing the counts provided in the [RangedSummarizedExperiment-class](#) objects.

### Format

A [GRanges-class](#) with one range per gene. The names match their Gencode v25 ids. The [GRanges-class](#) has three metadata columns.

**gene\_id** the Gencode v25 ids, identical to the names.

**bp\_length** the sum of the width of the disjoint exons for that given gene.

**symbol** a CharacterList with the corresponding gene symbols.

### References

<https://jhubiostatistics.shinyapps.io/recount/>

### See Also

[reproduce\\_ranges](#), [recount\\_exons](#)

---

recount_url	<i>Files and URLs hosted by the recount project</i>
-------------	---

---

### Description

Files and URLs as provided by the recount project. This information is used internally in [download\\_study](#).

### Format

A data.frame with 6 columns.

**path** the original path to the file before being uploaded,

**file\_name** the file name,

**project** the SRA project id,

**version1** A logical vector indicating whether the file was part of version 1 (reduced exons).

**version 2** A logical vector indicating whether the file was updated in version 2 (disjoint exons).

Further details in the recount website documentation tab.

**url** the public URL for the given file.



## References

<https://jhubiostatistics.shinyapps.io/recount/>

## See Also

[download\\_study](#)

---

reproduce_ranges	<i>Reproduce the gene or exons used in the RangedSummarizedExperiment objects</i>
------------------	---

---

## Description

This function reproduces the gene or exon level information used for creating the [RangedSummarizedExperiment-class](#) objects provided by recount. The annotation is based on Gencode v25 with the gene-level information extracted with `genes()` (see [transcripts](#) with default arguments).

## Usage

```
reproduce_ranges(level = "gene", db = "Gencode.v25")
```

## Arguments

level	Either genes or exon. It specifies whether to return Gene or exon level information as a <a href="#">GRanges-class</a> or <a href="#">GRangesList-class</a> object respectively. The gene level information contains the width of the disjoint exons for that given gene which can be used to normalize the counts provided by recount. Can also be both in which case a 2 element list with the exon and the gene output is returned.
db	Either Gencode.v25 (default) or EnsDb.Hsapiens.v79. The default option reproduces the annotation used when creating recount. EnsDb.Hsapiens.v79 can be used for an alternative annotation as showcased in the recount vignette.

## Details

For Gencode.v25, we use the comprehensive gene annotation (regions: CHR) from <https://www.gencodegenes.org/releases/25.html> (GRCh38.p7).

Note that gene symbols have changed over time. This answer in the Bioconductor support forum details how to obtain the latest gene symbol mappings: <https://support.bioconductor.org/p/126148/#126173>.

## Value

Either a [GRanges-class](#) object like `recount_genes` or a [GRangesList-class](#) object like `recount_exons`.

**Author(s)**

Leonardo Collado-Torres

**See Also**

[recount\\_genes](#), [recount\\_exons](#), <https://github.com/nellore>, <https://jhubiostatistics.shinyapps.io/recount/>

**Examples**

```
## Not run:  
## Reproduce gene level information  
genes <- reproduce_ranges()  
  
## Compare against recount_genes  
length(genes)  
length(recount_genes)  
  
## End(Not run)
```

---

rse\_gene\_SRP009615      *RangedSummarizedExperiment at the gene level for study SRP009615*

---

**Description**

[RangedSummarizedExperiment-class](#) at the gene level for study SRP009615. Used as an example in [scale\\_counts](#). Matches the version2 file (details at <https://jhubiostatistics.shinyapps.io/recount/>) under the documentation tab.

**Format**

A [RangedSummarizedExperiment-class](#) as created by the recount project for study with SRA id (accession number) SRP009615.

**References**

<https://jhubiostatistics.shinyapps.io/recount/>

**See Also**

[scale\\_counts](#), [download\\_study](#)

---

`scale_counts`*Scale the raw counts provided by the recount project*

---

## Description

In preparation for a differential expression analysis, you will have to choose how to scale the raw counts provided by the recount project. Note that the raw counts are the sum of the base level coverage so you have to take into account the read length or simply the total coverage for the given sample (default option). You might want to do some further scaling to take into account the gene or exon lengths. If you prefer to calculate read counts without scaling check the function [read\\_counts](#).

## Usage

```
scale_counts(  
  rse,  
  by = "auc",  
  targetSize = 4e+07,  
  L = 100,  
  factor_only = FALSE,  
  round = TRUE  
)
```

## Arguments

<code>rse</code>	A <a href="#">RangedSummarizedExperiment-class</a> object as downloaded with <a href="#">download_study</a> .
<code>by</code>	Either <code>auc</code> or <code>mapped_reads</code> . If set to <code>auc</code> it will scale the counts by the total coverage of the sample. That is, the area under the curve (AUC) of the coverage. If set to <code>mapped_reads</code> it will scale the counts by the number of mapped reads, whether the library was paired-end or not, and the desired read length (L).
<code>targetSize</code>	The target library size in number of single end reads.
<code>L</code>	The target read length. Only used when <code>by = 'mapped_reads'</code> since it cancels out in the calculation when using <code>by = 'auc'</code> .
<code>factor_only</code>	Whether to only return the numeric scaling factor or to return a <a href="#">RangedSummarizedExperiment-class</a> object with the counts scaled. If set to <code>TRUE</code> , you have to multiply the sample counts by this scaling factor.
<code>round</code>	Whether to round the counts to integers or not.

## Details

Rail-RNA <http://rail.bio> uses soft clipping when aligning which is why we recommend using `by = 'auc'`.

If the reads are from a paired-end library, then the `avg_read_length` is the average fragment length. This is taken into account when using `by = 'mapped_reads'`.

**Value**

If `factor_only = TRUE` it returns a numeric vector with the scaling factor for each sample. If `factor_only = FALSE` it returns a [RangedSummarizedExperiment-class](#) object with the counts already scaled.

**Author(s)**

Leonardo Collado-Torres

**See Also**

[download\\_study](#), [read\\_counts](#)

**Examples**

```
## Load an example rse_gene object
rse_gene <- rse_gene_SRP009615

## Scale counts
rse <- scale_counts(rse_gene)

## Find the project used as an example
project_info <- abstract_search("GSE32465")

## See some summary information for this project
project_info

## Use the following code to re-download this file
## Not run:
## Download
download_study(project_info$project)

## Load file
load(file.path(project_info$project, "rse_gene.Rdata"))
identical(rse_gene, rse_gene_SRP009615)

## End(Not run)
```

---

snaptron\_query

*Query Snaptron to get data from exon-exon junctions present in Intropolis*

---

**Description**

This function uses the Snaptron API to query specific exon-exon junctions that are available via Intropolis as described in the vignette.

**Usage**

```
snaptron_query(junctions, version = "srav1", verbose = TRUE, async = TRUE)
```

**Arguments**

junctions	A <a href="#">GRanges-class</a> object with the exon-exon junctions of interest. The chromosome names should be in UCSC format, such as 'chr1'. The strand information is ignored in the query.
version	Either srav1, srav2, gtex or tcga. SRA Version 1 of Intropolis has the exon-exon junctions from about 20 thousand RNA-seq samples in hg19 coordinates. SRA Version 2 has the data from about 50 thousand RNA-seq samples aligned to hg38. GTEx has about 30 million junctions from about 10 thousand samples from the GTEx consortium on hg38 coordinates. Finally, TCGA has about 36 million junctions from about 11 thousand samples from the TCGA consortium on hg38 coordinates.
verbose	If TRUE status updates will be printed.
async	Defaults to TRUE but in some situations it might be preferable to set it to FALSE. This argument gets passed to <a href="#">getURL</a> . Check <a href="https://github.com/ChristopherWilks/snaptron/issues/11">https://github.com/ChristopherWilks/snaptron/issues/11</a> for more details.

**Value**

A [GRanges-class](#) object with the results from the Snaptron query. For information on the different columns please see <http://snaptron.cs.jhu.edu>.

**Author(s)**

Leonardo Collado-Torres

**References**

Please cite <http://snaptron.cs.jhu.edu> if you use this function as Snaptron is a separate project from recount. Thank you!

**Examples**

```
library("GenomicRanges")
## Define some exon-exon junctions (hg19 coordinates)
junctions <- GRanges(seqnames = "chr2", IRanges(
  start = c(28971710:28971712, 29555081:29555083, 29754982:29754984),
  end = c(29462417:29462419, 29923338:29923340, 29917714:29917716)
))

## Check against Snaptron SRA version 1 (hg19 coordinates)
snaptron_query(junctions)
## Not run:
## Check another set of junctions against SRA version 2 (more data, hg38
## coordinates)
junctions_v2 <- GRanges(seqnames = "chr2", IRanges(
```

```
        start = 29532116:29532118, end = 29694848:29694850
    ))
snaptron_query(junctions_v2, version = "srav2")

## Check these junctions in GTEx and TCGA data
snaptron_query(junctions_v2, version = "gtex")
snaptron_query(junctions_v2, version = "tcga")

## End(Not run)
```

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