

# Package ‘cRegulome’

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**Type** Package

**Version** 0.1.1

**Title** Obtain and Visualize Regulome-Gene Expression Correlations in Cancer

**Description** Builds a 'SQLite' database file of pre-calculated transcription factor/microRNA-gene correlations (co-expression) in cancer from the Cistrome Cancer Liu et al. (2011) <doi:10.1186/gb-2011-12-8-r83> and 'miRCancerdb' databases (in press). Provides custom classes and functions to query, tidy and plot the correlation data.

**License** GPL-3

**URL** <https://github.com/MahShaaban/cRegulome>

**BugReports** <https://github.com/MahShaaban/cRegulome/issues>

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**Depends** R(>= 2.10.0)

**Imports** DBI, graphics, httr, RSQLite, UpSetR, VennDiagram, magrittr, dplyr, ggplot2, ggridges, tidyr, reshape2, purrr, grid, R.utils, AnnotationDbi, org.Hs.eg.db, clusterProfiler

**VignetteBuilder** knitr

**Suggests** knitr, rmarkdown, testthat, covr, dbplyr, igraph, readxl

**NeedsCompilation** no

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cmicroRNA	<i>Construct cmicroRNA object</i>
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---

### Description

Constructs an S3 object called cmicroRNA contains data returned by calling [get\\_mir](#). Used to define methods for printing and visualizing microRNA-gene expression correlations.

### Usage

```
cmicroRNA(dat_mir)
```

### Arguments

dat\_mir            A data.frame such as this returned by calling [get\\_mir](#).

### Value

An S3 object of class cmicroRNA

### Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
```

```

dat <- get_mir(conn,
               mir = 'hsa-let-7g',
               study = 'STES',
               min_abs_cor = .3,
               max_num = 5)

# make a cmicroRNA object
cmir <- cmicroRNA(dat)

```

---

cor\_hist

*A histogram of the correlations of microRNA or tf sets*


---

## Description

Plot a [hist](#) of sets of microRNAs or transcription factors-gene correlations in a TCGA study.

## Usage

```
cor_hist(ob, study = NULL, ...)
```

## Arguments

ob	A <a href="#">cmicroRNA</a> or <a href="#">cTF</a> object such as this returned by calling <a href="#">cmicroRNA</a> or <a href="#">cTF</a> .
study	A character vector of The Cancer Genome Atlas (TCGA) study identifiers. To view the available studies in TCGA project, <a href="https://tcga-data.nci.nih.gov/docs/publications/tcga">https://tcga-data.nci.nih.gov/docs/publications/tcga</a> . When left to default NULL all available studies will be included.
...	Other options

## Value

An [hist](#) plot of the correlations values between genes a microRNA or a transcription factor in a TCGA study

## Examples

```

# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
dat <- get_mir(conn,
               mir = c('hsa-let-7g', 'hsa-let-7i'),
               study = 'STES')

```

```
# make a cmicroRNA object
cmir <- cmicroRNA(dat)

# print object
cor_hist(cmir)
```

---

cor\_igraph                      *Make an igraph object*

---

### Description

An igraph object of from [cmicroRNA](#) or [cTF](#) objects.

### Usage

```
cor_igraph(ob)
```

### Arguments

ob                      A [cmicroRNA](#) or [cTF](#) object such as this returned by calling [cmicroRNA](#) or [cTF](#).

### Value

An igraph object

### Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
dat <- get_mir(conn,
               mir = c('hsa-let-7g', 'hsa-let-7i'),
               study = 'STES')

# make a cmicroRNA object
cmir <- cmicroRNA(dat)

# print object
cor_igraph(cmir)
```

---

`cor_joy`*A joy plot of correlation of microRNA or tf sets*

---

## Description

A `ggridges` joy plot of sets of microRNAs or transcription factors-gene correlations in a TCGA study.

## Usage

```
cor_joy(ob, study = NULL, ...)
```

## Arguments

<code>ob</code>	A <code>cmicroRNA</code> or <code>cTF</code> object such as this returned by calling <code>cmicroRNA</code> or <code>cTF</code> .
<code>study</code>	A character vector of The Cancer Genome Atlas (TCGA) study identifiers. To view the available studies in TCGA project, <a href="https://tcga-data.nci.nih.gov/docs/publications/tcga">https://tcga-data.nci.nih.gov/docs/publications/tcga</a> . When left to default NULL all available studies will be included.
<code>...</code>	Other options

## Value

An `ggridges` plot object

## Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
dat <- get_mir(conn,
               mir = c('hsa-let-7g', 'hsa-let-7i'),
               study = 'STES')

# make a cmicroRNA object
cmir <- cmicroRNA(dat)

# print object
cor_joy(cmir)
```

---

`cor_plot`*Plot method for `cmicroRNA` and `cTF` objects*

---

### Description

A dot plot of microRNA/TF correlation in a single study of TCGA. When the object `cmicroRNA/cTF` contains more than one TCGA studies, the argument `study` is a requirement.

### Usage

```
cor_plot(ob, study = NULL, ...)
```

### Arguments

<code>ob</code>	A <code>cmicroRNA</code> or <code>cTF</code> object such as this returned by calling <code>cmicroRNA</code> or <code>cTF</code> .
<code>study</code>	A character vector of The Cancer Genome Atlas (TCGA) study identifiers. To view the available studies in TCGA project, <a href="https://tcga-data.nci.nih.gov/docs/publications/tcga">https://tcga-data.nci.nih.gov/docs/publications/tcga</a> . When left to default NULL all available studies will be included.
<code>...</code>	Other options

### Value

A ggplot object of a dot plot of the correlation values between genes and microRNAs or transcription factors in a TCGA study.

### Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
dat <- get_mir(conn,
               mir = 'hsa-let-7g',
               study = 'STES',
               min_abs_cor = .3,
               max_num = 5)

# make a cmicroRNA object
cmir <- cmicroRNA(dat)

# print object
cor_plot(cmir)
```

---

cor_tidy	<i>Tidy <a href="#">cmicroRNA</a> and <a href="#">cTF</a> objects</i>
----------	---

---

## Description

Tidy [cmicroRNA](#) and [cTF](#) objects

## Usage

```
cor_tidy(ob)
```

## Arguments

ob                    A [cmicroRNA](#) or [cTF](#) object such as this returned by calling [cmicroRNA](#) or [cTF](#).

## Value

A tidy data.frame of four columns. mirna\_base or tfis the microRNA miRBase IDs, feature is the features/genes, cor is the corresponding expression correlations and study is TCGA study ID.

## Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
dat <- get_mir(conn,
  mir = 'hsa-let-7g',
  study = 'STES',
  min_abs_cor = .3,
  max_num = 5)

# make a cmicroRNA object
cmir <- cmicroRNA(dat)

# convert cmicroRNA object to a tidy data.frame
tidy_cmir <- cor_tidy(cmir)
```

---

cor\_upset                    *upset plot of microRNA or tf sets*

---

### Description

`upset` of sets of microRNAs or transcription factors and their correlated features in a TCGA study.

### Usage

```
cor_upset(ob, study = NULL, ...)
```

### Arguments

<code>ob</code>	A <code>cmicroRNA</code> or <code>cTF</code> object such as this returned by calling <code>cmicroRNA</code> or <code>cTF</code> .
<code>study</code>	A character vector of The Cancer Genome Atlas (TCGA) study identifiers. To view the available studies in TCGA project, <a href="https://tcga-data.nci.nih.gov/docs/publications/tcga">https://tcga-data.nci.nih.gov/docs/publications/tcga</a> . When left to default NULL all available studies will be included.
<code>...</code>	Other options

### Value

An `upset` plot

### Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
dat <- get_mir(conn,
               mir = c('hsa-let-7g', 'hsa-let-7i'),
               study = 'STES')

# make a cmicroRNA object
cmir <- cmicroRNA(dat)

# print object
cor_upset(cmir)
```



---

cor_venn_diagram	<i>Venn Diagram of microRNA or transcription factor correlated features</i>
------------------	---

---

## Description

Count and plot the numbers of microRNA correlated features in `cmicroRNA` object.

## Usage

```
cor_venn_diagram(ob, study = NULL, ...)
```

## Arguments

<code>ob</code>	A <code>cmicroRNA</code> or <code>cTF</code> object such as this returned by calling <code>cmicroRNA</code> or <code>cTF</code> .
<code>study</code>	A character vector of The Cancer Genome Atlas (TCGA) study identifiers. To view the available studies in TCGA project, <a href="https://tcga-data.nci.nih.gov/docs/publications/tcga">https://tcga-data.nci.nih.gov/docs/publications/tcga</a> . When left to default NULL all available studies will be included.
<code>...</code>	Other options

## Value

A venn diagram with a circle or an ellipses for each microRNA and the number of correlated features.

## Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# enter a custom query with different arguments
dat <- get_mir(conn,
               mir = c('hsa-let-7g', 'hsa-let-7i'),
               study = 'STES')

# make a cmicroRNA object
cmir <- cmicroRNA(dat)

# print object
cor_venn_diagram(cmir)
```

---

cRegulome

cRegulome *package*

---

### Description

Download, access and visualize Regulome (microRNA and transcription factors) data from miR-Cancer and Cistrome cancer

---

cTF

*Construct cTF object*

---

### Description

Constructs an S3 object called cTF contains data returned by calling [get\\_tf](#). Used to define methods for printing and visualizing transcription factors-gene expression correlations.

### Usage

```
cTF(dat_tf)
```

### Arguments

`dat_tf` A data.frame such as this returned by calling [get\\_tf](#).

### Value

An S3 object of class cTF

### Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
f1 <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), f1)

# enter a custom query with different arguments
dat <- get_tf(conn,
              tf = 'LEF1',
              study = 'STES*',
              min_abs_cor = .3,
              max_num = 5)

# make a cTF object
ctf <- cTF(dat)
```

---

get_db	<i>Get cRegulome.db file</i>
--------	------------------------------

---

### Description

This function calls [download.file](#) to download the pre-build database file of cRegulome. Additionally, the function checks the validity of the pre-defined URL and whether the database file exists in the current working directory to avoid re-downloading it. Typically, users would run this function once at the first time they use the package or to update the database to the latest version.

### Usage

```
get_db(test = FALSE, destfile, ...)
```

### Arguments

test	A logical, default FALSE. When TRUE downloads a database file with the same structure with a subset of the data for speed.
destfile	A character vector for the desired path for the database file. By default, when not specified, is constructed by using <a href="#">tempdir</a> as a directory and the string <code>cRegulome.db.gz</code>
...	Optional arguments passed to <a href="#">download.file</a>

### Value

Downloads a compressed `sqlite` file to the current working directory. The file is named `cRegulome.db.gz` by default and it's not advised to change the name to avoid breaking the other functions that call the database.

### Examples

```
## Not run:
# download a test set of the database
get_db(test = TRUE)

# download the full database file
get_db(test = FALSE)

## End(Not run)

# load the test db file from shipped with the package
db_file <- system.file("extdata", "cRegulome.db", package = "cRegulome")
file.info(db_file)
```

---

get_mir	<i>Get microRNA correlations from cRegulome.db</i>
---------	--

---

### Description

This function access the sqlite database file which is obtained by running [get\\_db](#). Basically, the function provides ways to query the database to the correlation data of the microRNAs of interest. The function returns an error if the database file `cRegulome.db` is not in the working directory.

### Usage

```
get_mir(conn, mir, study = NULL, min_abs_cor = NULL, max_num = NULL,
        targets_only = FALSE)
```

### Arguments

conn	A connection to the database file by <a href="#">dbConnect</a>
mir	A required character vector of the microRNAs of interest. These are the miR-Base ID which are the official identifiers of the widely used miRBase database, <a href="http://www.mirbase.org/">http://www.mirbase.org/</a> .
study	A character vector of The Cancer Genome Atlas (TCGA) study identifiers. To view the available studies in TCGA project, <a href="https://tcga-data.nci.nih.gov/docs/publications/tcga">https://tcga-data.nci.nih.gov/docs/publications/tcga</a> . When left to default NULL all available studies will be included.
min_abs_cor	A numeric, an absolute correlation minimum between 0 and 1 for each mir.
max_num	An integer, maximum number of features to show for each mir in each study.
targets_only	A logical, default FALSE. When TRUE, features will be the microRNA targets as defined in the package <code>targets.Hs.eg.db</code> .

### Value

A tidy data.frame of four columns. `mirna_base` is the microRNA miRBase IDs, `feature` is the features/genes, `cor` is the corresponding expression correlations and `study` is TCGA study ID.

### Examples

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# get microRNA correlations in all studies
get_mir(conn,
```

```

        mir = 'hsa-let-7g')

# get correlations in a particular study
get_mir(conn,
        mir = 'hsa-let-7g',
        study = 'STES')

# enter a custom query with different arguments
get_mir(conn,
        mir = 'hsa-let-7g',
        study = 'STES',
        min_abs_cor = .3,
        max_num = 5)

```

---

get\_tf

*Get transcription factor correlations from cRegulome.db*


---

## Description

This function access the sqlite database file which is obtained by running [get\\_db](#). Basically, the function provides ways to query the database to the correlation data of the transcription factors of interest. The function returns an error if the database file `cRegulome.db` is not in the working directory.

## Usage

```

get_tf(conn, tf, study = NULL, min_abs_cor = NULL, max_num = NULL,
        targets_only = FALSE)

```

## Arguments

conn	A connection to the database file by <a href="#">dbConnect</a>
tf	A required character vector of the transcription factor of interest. These are the HUGO official gene symbols of the genes contains the transcription factor.
study	A character vector of The Cancer Genome Atlas (TCGA) study identifiers. To view the available studies in TCGA project, <a href="https://tcga-data.nci.nih.gov/docs/publications/tcga">https://tcga-data.nci.nih.gov/docs/publications/tcga</a> . When left to default NULL all available studies will be included.
min_abs_cor	A numeric, an absolute correlation minimum between 0 and 1 for each tf.
max_num	An integer, maximum number of features to show for each tf in each study.
targets_only	A logical, default FALSE. When TRUE, features will be the targets of the transcription factors as identified in the Cistrome Cancer, <a href="http://cistrome.org/CistromeCancer/">http://cistrome.org/CistromeCancer/</a>

**Value**

A tidy data.frame of four columns. tf is the official gene symbols of the genes contains the transcription factor, feature is the features/genes, cor is the corresponding expression correlations and study is TCGA study ID.

**Examples**

```
# load required libraries
library(RSQLite)
library(cRegulome)

# locate the testset file and connect
fl <- system.file('extdata', 'cRegulome.db', package = 'cRegulome')
conn <- dbConnect(SQLite(), fl)

# get transcription factors correlations in all studies
get_tf(conn,
        tf = 'LEF1')

# get correlations in a particular study
get_tf(conn,
        tf = 'LEF1',
        study = 'STES*')

# enter a custom query with different arguments
get_tf(conn,
        tf = 'LEF1',
        study = 'STES*',
        min_abs_cor = .3,
        max_num = 5)
```

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