

# **TRGN 527: Applied Data Science and Bioinformatics**

## **UNIT I. Introduction and Basic Data Science**

### **Week 1 – Lecture 5**

**Enrique I. Velazquez Villarreal, M.D., Ph.D., M.P.H., M.S. | Assistant Professor**

Dept. of Translational Genomics

USC | Keck School of Medicine | Norris Comprehensive Cancer Center

Leader of the USC Bioinformatics Core – *USC CaRE2 Health Equity Center*

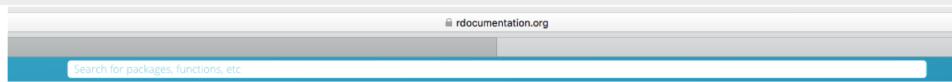
**David W. Craig, Ph.D. | Professor and Vice Chair**

Dept. of Translational Genomics

USC | Keck School of Medicine | Norris Comprehensive Cancer Center

Co-Director, Institute of Translational Genomics

# Installing R packages



The screenshot shows the rdocumentation.org website with the following details:

**biocLite**

From [BioInstaller v1.22.3](#) 99.99th Percentile  
by [Bioconductor Package Maintainer](#)

**Install Or Update Bioconductor And CRAN Packages**

`biocLite` installs or updates Bioconductor and CRAN packages in a Bioconductor release. Upgrading to a new Bioconductor release requires additional steps; see <https://bioconductor.org/install>.

**Keywords** environment

**Usage**

```
biocLite(pkgs=c("Biobase", "IRanges", "AnnotationDbi"), suppressUpdates=FALSE, suppressAutoUpdate=FALSE, siteRepos=character(), ask=TRUE, ...)
```

**Arguments**

**pkgs** character() of package names to install or update. A missing value and suppressUpdates=FALSE updates installed packages, perhaps also installing Biobase, IRanges, and AnnotationDbi if they are not already installed. Package names containing a '/' are treated as github repositories and installed using the `install_github()` function of the `devtools` package.

**suppressUpdates** logical() or character(). When FALSE, `biocLite` asks the user whether old packages should be updated. When TRUE, the user is not prompted to update old packages. When character(), a vector specifying which packages to NOT update.

**suppressAutoUpdate** logical() indicating whether the `BioInstaller` package updates itself.

**siteRepos** character() representing an additional repository in which to look for packages to install. This repository will be prepended to the default repositories (which you can see with `biocinstallRepos`).

**ask** logical() indicating whether to prompt user before installed packages are updated, or the character string 'graphics', which brings up a widget for choosing which packages to update. If TRUE, user can choose whether to update all outdated packages without further prompting, to pick and choose packages to update, or to cancel updating (in a non-interactive session, no packages will be updated). Otherwise, the value is passed to `update.packages`.

**...** Additional arguments.

When installing CRAN or Bioconductor packages, typical arguments include: `lib.loc`, passed to `old.packages` and used to determine the library location of installed packages to be updated; and `lib`, passed to `install.packages` to determine the library location where `pkgs` are to be installed.

When installing github packages, ... is passed to the `devtools` package functions `install_github` and `install`. A typical use is to build vignettes, via `dependencies=TRUE, build_vignettes=TRUE`.

**Details**

Installation of Bioconductor and CRAN packages use R's standard functions for library management -- `install.packages()`, `available.packages()`, `update.packages()`. Installation of github packages uses the `install.github()` function from the `devtools` package. For this reason it usually makes sense, when complicated installation options are needed, to invoke `biocLite()` separately for Bioconductor / CRAN packages and for github packages.

**Value**

`biocLite()` returns the `pkgs` argument, invisibly.

**See Also**

`biocinstallRepos` returns the Bioconductor and CRAN repositories used by `biocLite`.

`install.packages` installs the packages themselves.

`update.packages` updates all installed packages.

`chooseBioCMirror` lets you choose from a list of all public Bioconductor mirror URLs.

`chooseCRANmirror` lets you choose from a list of all public CRAN mirror URLs.

`monograph_group`, `Bioinf_group` and `biocases_group` return package names associated with Bioconductor publications. `all_group` returns the names of all Bioconductor software packages.

# Installing R packages

Using biocLite to install R bioconductor packages:

Example:

- Type the following lines in your R console:

```
➤ source("http://bioconductor.org/biocLite.R")
➤ biocLite("GenomicFeatures")
➤ library(biomaRT)
```

# Installing R packages – First Check your R version

The screenshot shows the RStudio interface with the following details:

- Console Tab:** Displays the R startup message and license information.
- Environment Tab:** Shows the Global Environment pane with the message "Environment is empty".
- File Explorer:** Shows a tree view of the project structure under "Home".

The R startup message includes:

```
R version 3.5.2 (2018-12-20) -- "Eggshell Igloo"
Copyright (C) 2018 The R Foundation for statistical computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

A red circle highlights the first line of the R startup message: "R version 3.5.2 (2018-12-20) -- "Eggshell Igloo"".

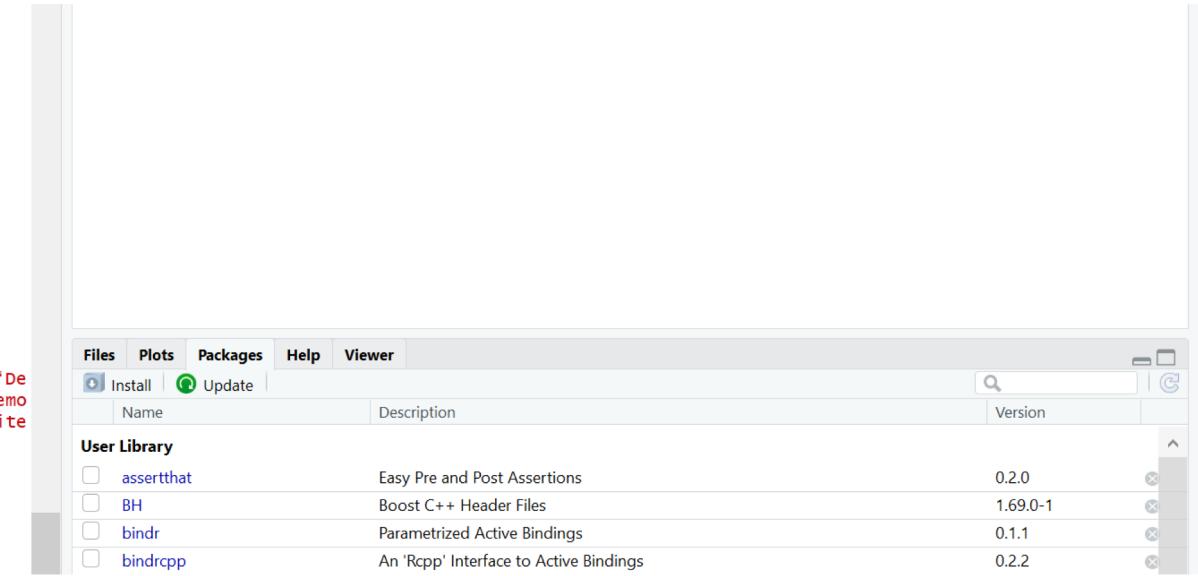
# Installing R packages

```
> source("http://bioconductor.org/biocLite.R")
Installing package into 'C:/Users/davidwcr/Documents/R/win-library/3.5'
(as 'lib' is unspecified)
trying URL 'https://bioconductor.org/packages/3.7/bioc/bin/windows/contrib/3.5/BiocInstaller_1.30.0.zip'
Content type 'application/zip' length 102191 bytes (99 KB)
downloaded 99 KB

package 'BiocInstaller' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
  C:\Users\davidwcr\AppData\Local\Temp\RtmpauYmoT\downloaded_packages
Bioconductor version 3.7 (BiocInstaller 1.30.0), ?biocLite for help
A newer version of Bioconductor is available for this version of R, ?BioconductorUpgrade for help
> biocLite("GenomicFeatures")
Bio mirror: https://bioconductor.org
Using Bioconductor 3.7 (BiocInstaller 1.30.0), R 3.5.2 (2018-12-20).
Installing package(s) 'GenomicFeatures'
also installing the dependencies 'formatR', 'lambda.r', 'futile.options', 'matrixStats', 'futile.logger', 'snow', 'DelayedArray', 'bit', 'prettyunits', 'BiocParallel', 'SummarizedExperiment', 'GenomeInfoDbData', 'bit64', 'blob', 'memoise', 'Rsamtools', 'GenomicAlignments', 'progress', 'GenomeInfoDb', 'GenomicRanges', 'AnnotationDbi', 'DBI', 'RSSQLite', 'rtracklayer', 'biomaRt', 'Biobase'

There is a binary version available but the source version is later:
  binary source needs_compilation
GenomicFeatures 1.32.2 1.32.3          FALSE
```



# Installing R packages

The screenshot shows the RStudio interface during the installation of Bioconductor packages. The top navigation bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, and Help. The main window has tabs for Console and Terminal. The Console tab displays the command-line output of the package installation process.

```
Content type 'application/zip' length 3000735 bytes (2.8 MB)
downloaded 3.7 MB

trying URL 'https://bioconductor.org/packages/3.7/bioc/bin/windows/contrib/3.5/GenomicRanges_1.32.7.zip'
Content type 'application/zip' length 2086262 bytes (2.0 MB)
downloaded 2.0 MB

trying URL 'https://bioconductor.org/packages/3.7/bioc/bin/windows/contrib/3.5/AnnotationDbi_1.42.1.zip'
Content type 'application/zip' length 5255772 bytes (5.0 MB)
downloaded 5.0 MB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.5/DBI_1.0.0.zip'
Content type 'application/zip' length 887758 bytes (866 KB)
downloaded 866 KB

trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.5/RSQLite_2.1.1.zip'
Content type 'application/zip' length 2156505 bytes (2.1 MB)
downloaded 2.1 MB

trying URL 'https://bioconductor.org/packages/3.7/bioc/bin/windows/contrib/3.5/rtracklayer_1.40.6.zip'
Content type 'application/zip' length 3050868 bytes (2.9 MB)
downloaded 2.9 MB

trying URL 'https://bioconductor.org/packages/3.7/bioc/bin/windows/contrib/3.5/biomaRt_2.36.1.zip'
Content type 'application/zip' length 545948 bytes (533 KB)
downloaded 533 KB

trying URL 'https://bioconductor.org/packages/3.7/bioc/bin/windows/contrib/3.5/Biobase_2.40.0.zip'
Content type 'application/zip' length 2413751 bytes (2.3 MB)
downloaded 2.3 MB

package 'formatR' successfully unpacked and MD5 sums checked
package 'lambda.r' successfully unpacked and MD5 sums checked
package 'futile.options' successfully unpacked and MD5 sums checked
package 'matrixStats' successfully unpacked and MD5 sums checked
package 'futile.logger' successfully unpacked and MD5 sums checked
package 'snow' successfully unpacked and MD5 sums checked
package 'DelayedArray' successfully unpacked and MD5 sums checked
package 'bit' successfully unpacked and MD5 sums checked
package 'prettyunits' successfully unpacked and MD5 sums checked
package 'BiocParallel' successfully unpacked and MD5 sums checked
package 'SummarizedExperiment' successfully unpacked and MD5 sums checked
package 'bit64' successfully unpacked and MD5 sums checked
package 'blob' successfully unpacked and MD5 sums checked
package 'memoise' successfully unpacked and MD5 sums checked
package 'Rsamtools' successfully unpacked and MD5 sums checked
package 'GenomicAlignments' successfully unpacked and MD5 sums checked
package 'progress' successfully unpacked and MD5 sums checked
package 'GenomeInfoDb' successfully unpacked and MD5 sums checked
package 'GenomicRanges' successfully unpacked and MD5 sums checked
package 'AnnotationDbi' successfully unpacked and MD5 sums checked
package 'DBI' successfully unpacked and MD5 sums checked
package 'RSQLite' successfully unpacked and MD5 sums checked
package 'rtracklayer' successfully unpacked and MD5 sums checked
package 'biomaRt' successfully unpacked and MD5 sums checked
package 'Biobase' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
C:\Users\davidwcr\AppData\Local\Temp\RtmpauYmoT\downloaded_packages
installing the source packages 'GenomeInfoDbData', 'GenomicFeatures'

trying URL 'https://bioconductor.org/packages/3.7/data/annotation/src/contrib/GenomeInfoDbData_1.1.0.tar.gz'
Content type 'application/x-gzip' length 8204728 bytes (7.8 MB)
downloaded 7.8 MB
```

The right side of the interface shows the Environment pane, which is currently empty. Below it is the Packages pane, which lists the User Library of installed packages. Several packages have been circled in red, including 'rtracklayer', 'biomaRt', and 'Biobase'. The 'BiocInstaller' package is checked.

Name	Description	Version
assertthat	Easy Pre and Post Assertions	0.2.0
BH	Boost C++ Header Files	1.69.0-1
bindr	Parametrized Active Bindings	0.1.1
bindrcpp	An 'Rcpp' Interface to Active Bindings	0.2.2
BiocGenerics	S4 generic functions for Bioconductor	0.28.0
<b>BiocInstaller</b>	Install/Update Bioconductor, CRAN, and github Packages	1.30.0
BiocManager	Access the Bioconductor Project Package Repository	1.30.4
BiocVersion	Set the appropriate version of Bioconductor packages	3.8.0
biomaRt	Genomic Data Retrieval	0.8.0
Biostings	Efficient manipulation of biological strings	2.50.2
bitops	Bitwise Operations	1.0-6
cli	Helpers for Developing Command Line Interfaces	1.0.1
clipr	Read and Write from the System Clipboard	0.4.1
crayon	Colored Terminal Output	1.3.4
curl	A Modern and Flexible Web Client for R	3.2
data.table	Extension of 'data.frame'	1.11.8
digest	Create Compact Hash Digests of R Objects	0.6.18
downloader	Download Files over HTTP and HTTPS	0.4
dplyr	A Grammar of Data Manipulation	0.7.8
fansi	ANSI Control Sequence Aware String Functions	0.4.0
glue	Interpreted String Literals	1.3.0
hms	Pretty Time of Day	0.4.2
httr	Tools for Working with URLs and HTTP	1.4.0
IRanges	Infrastructure for manipulating intervals on sequences	2.16.0
jsonlite	A Robust, High Performance JSON Parser and Generator for R	1.6
magrittr	A Forward-Pipe Operator for R	1.5
mime	Map Filenames to MIME Types	0.6
openssl	Toolkit for Encryption, Signatures and Certificates Based on OpenSSL	1.1
pillar	Coloured Formatting for Columns	1.3.1

# Using “biomaRt” package

The screenshot shows the RStudio interface with the following components:

- Top Bar:** File Edit Code View Plots Session Build Debug Profile Tools Help
- Console Tab:** Shows the command `> library(biomaRt)`. The first two lines are circled in red.
- Environment Tab:** Shows "Environment is empty".
- Packages Tab:** Shows the "User Library" section with a list of packages and their details. The "biomaRt" package is checked.

Name	Description	Version
assertthat	Easy Pre and Post Assertions	0.2.0
BH	Boost C++ Header Files	1.69.0-1
bindr	Parametrized Active Bindings	0.1.1
bindrcpp	An 'Rcpp' Interface to Active Bindings	0.2.2
BiocGenerics	S4 generic functions for Bioconductor	0.28.0
BiocInstaller	Install/Update Bioconductor, CRAN, and github Packages	1.30.0
BiocManager	Access the Bioconductor Project Package Repository	1.30.4
BiocVersion	Set the appropriate version of Bioconductor packages	3.8.0
biomaRt	Genomic Data Retrieval	0.8.0
Biostrings	Efficient manipulation of biological strings	2.50.2
bitops	Bitwise Operations	1.0-6
cli	Helpers for Developing Command Line Interfaces	1.0.1
clipr	Read and Write from the System Clipboard	0.4.1
crayon	Colored Terminal Output	1.3.4
curl	A Modern and Flexible Web Client for R	3.2
data.table	Extension of 'data.frame'	1.11.8
digest	Create Compact Hash Digests of R Objects	0.6.18
downloader	Download Files over HTTP and HTTPS	0.4
dplyr	A Grammar of Data Manipulation	0.7.8
fansi	ANSI Control Sequence Aware String Functions	0.4.0
glue	Interpreted String Literals	1.3.0
hms	Pretty Time of Day	0.4.2
httr	Tools for Working with URLs and HTTP	1.4.0
IRanges	Infrastructure for manipulating intervals on sequences	2.16.0
jsonlite	A Robust, High Performance JSON Parser and Generator for R	1.6
magrittr	A Forward-Pipe Operator for R	1.5
mime	Map Filenames to MIME Types	0.6
openssl	Toolkit for Encryption, Signatures and Certificates Based on OpenSSL	1.1
pillar	Coloured Formatting for Columns	1.3.1

# Using “biomaRt” package

The screenshot shows the RStudio interface with the following details:

- Console Tab:** Displays the R session code and its output. The code includes loading the biomaRt package, setting the working directory, listing available databases, selecting the Ensembl database, and listing datasets.
- Data View:** Shows the "ensembl" dataset as a formal class "Mart". It lists various datasets with their descriptions and versions.
- File View:** Shows the "biomaRt" package listed in the User Library section of the Bioconductor Project Package Repository.

```
> library(biomaRt)
> getwd()
[1] "C:/Users/davidwcr/Documents"
> setwd("C:/Users/davidwcr/Documents/enrique")
> listMarts()
#> biomart      version
#> 1 ENSEMBL_ENSEMBL    Ensembl Genes 95
#> 2 ENSEMBL_MOUSE     Mouse strains 95
#> 3 ENSEMBL_SNPs      Ensembl Variation 95
#> 4 ENSEMBL_FUNCGEN   Ensembl Regulation 95
> ensembl=useMart("ensembl")
> listDatasets(ensembl)

dataset           description
1 acalyptrata_gene_ensembl Eastern happy genes (FastCall1.2)
2 acarolinensis_gene_ensembl Anole lizard genes (AnoCar2.0)
3 acitrinellus_gene_ensembl Midas cichlid genes (Midas_v5)
4 amelanoleuca_gene_ensembl Panda genes (aiIMel1)
5 amexicanus_gene_ensembl Cave fish genes (Astyanax_mexicanus-2.0)
6 anancymaae_gene_ensembl Ma's night monkey genes (Anan_2.0)
7 aocellaris_gene_ensembl Clown anemonefish genes (AmpOce1.0)
8 apercula_gene_ensembl Orange clownfish genes (Nemo_v1)
9 aplatyrhynchos_gene_ensembl Duck genes (BG1_duck_1.0)
10 apolyacanthus_gene_ensembl Spiny chromis genes (ASM210954V1)
11 atestudineus_gene_ensembl Climbing perch genes (fAnaTes1.1)
12 btaurus_gene_ensembl Cow genes (ARS-UCD1.2)
13 caperea_gene_ensembl Brazilian guinea pig genes (CavAp1.0)
14 catys_gene_ensembl Sooty mangabey genes (Caty_1.0)
15 cbelli_gene_ensembl Painted turtle genes (Chrysemys_picta_belli-3.0.3)
16 ccapucinus_gene_ensembl Capuchin genes (Cebus_imitator-1.0)
17 cchokigshd_gene_ensembl Chinese hamster CHOK1GS genes (CHOK1GS_HDV1)
18 ccrigr1_gene_ensembl Chinese hamster CriGr1 genes (CriGr1_1.0)
19 cdingo_gene_ensembl Dingo genes (ASM325472V1)
20 celegans_gene_ensembl Caenorhabditis elegans genes (WCe1235)
21 cfamiliaris_gene_ensembl Dog genes (CanFam3.1)
22 chircus_gene_ensembl Goat genes (ARS1)
23 choffmanni_gene_ensembl Sloth genes (choHof1)
24 cintestinalis_gene_ensembl C.intestinalis genes (KH)
25 cjacchus_gene_ensembl Marmoset genes (ASM275486V1)
26 clanigera_gene_ensembl Long-tailed chinchilla genes (ChiLan1.0)
27 cpalliatius_gene_ensembl Angola colobus genes (Cang.pa_1.0)
28 cporcellus_gene_ensembl Guinea Pig genes (Cavpor3.0)
29 csabaeus_gene_ensembl Vervet-AGM genes (Ch1Sab1.1)
30 csavignyi_gene_ensembl C.savignyi genes (CSAV 2.0)
31 csemilaevis_gene_ensembl Tongue sole genes (Cse.v1.0)
32 csyrichta_gene_ensembl Tarsier genes (Tarsius_syrichta-2.0.1)
33 cvariegatus_gene_ensembl Sheepshead minnow genes (C_variegatus-1.0)
34 dmelanogaster_gene_ensembl Fruitfly genes (BDGP6)
35 dnovenmictus_gene_ensembl Armadillo genes (Dasnov3.0)
36 dordui_gene_ensembl Kangaroo rat genes (Dord_2.0)
37 drerio_gene_ensembl Zebrafish genes (GRCz11)
38 easinus_gene_ensembl Donkey genes (ASM303372V1)
39 eburgeri_gene_ensembl Hagfish genes (Eburgeri_3.2)
40 ecaballus_gene_ensembl Horse genes (EquCab3.0)
41 eeuropaeus_gene_ensembl Hedgehog genes (eriEur1)
42 elucius_gene_ensembl Northern pike genes (Eluc_v3)
43 etelfairi_gene_ensembl Lesser hedgehog tenrec genes (TENREC)
44 falbicoloris_gene_ensembl Flycatcher genes (FicAlb_1.4)
45 fcatus_gene_ensembl Cat genes (Felis_catus_9.0)
46 fdamarensis_gene_ensembl Damara mole rat genes (DMR_v1.0)
47 fhteroclitus_gene_ensembl Mummichog genes (Fundulus_heteroclitus-3.0.2)
48 gaguleatus_gene_ensembl Stickleback genes (BROAD_S1)
49 gaffinis_gene_ensembl Western mosquitofish genes (ASM309773V1)
```

# Using “biomaRt” package

RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Console Terminal ~ /enrique/ R 3.6.2

> listDatasets(ensembl)

dataset	description
1 acalyptrata_gene_ensembl	Eastern happy genes (fAstCall1.2)
2 acarolinensis_gene_ensembl	Anole lizard genes (AnoCar2.0)
3 acitrinellus_gene_ensembl	Midas cichlid genes (Midas_v5)
4 amelanoleuca_gene_ensembl	Panda genes (aiIMe1)
5 amexicanus_gene_ensembl	Cave fish genes (Astyanax_mexicanus-2.0)
6 anancymaae_gene_ensembl	Ma's night monkey genes (Anan_2.0)
7 aocellaris_gene_ensembl	Clown anemonefish genes (Ampocel1.0)
8 apercula_gene_ensembl	Orange clownfish genes (Nemo_v1)
9 aplatyrhynchos_gene_ensembl	Duck genes (BG1_duck_1.0)
10 apolyacanthus_gene_ensembl	Spiny chromis genes (ASM210954v1)
11 atestudineus_gene_ensembl	Climbing perch genes (fAnaTes1.1)
12 btaurus_gene_ensembl	Cow genes (ARS-UCD1.2)
13 caperea_gene_ensembl	Brazilian guinea pig genes (CavAp1.0)
14 catys_gene_ensembl	Sooty mangabey genes (Caty_1.0)
15 cbelli_i_gene_ensembl	Painted turtle genes (Chrysemys_picta_bellii-3.0.3)
16 ccapucinus_gene_ensembl	Capuchin genes (Cebus_imitator-1.0)
17 cchoolgshd_gene_ensembl	Chinese hamster CHOKLGs genes (CHOKLGS_HDV1)
18 ccrigr1_gene_ensembl	Chinese hamster CriGr1 genes (CriGr1_1.0)
19 cdingo_gene_ensembl	Dingo genes (ASM25472v1)
20 celegans_gene_ensembl	Caenorhabditis elegans genes (WBcel235)
21 cfamiliaris_gene_ensembl	Dog genes (CanFam3.1)
22 chircus_gene_ensembl	Goat genes (ARS1)
23 choffmanni_gene_ensembl	Sloth genes (ChoHof1)
24 cintestinalis_gene_ensembl	C.intestinalis genes (KH)
25 cjacchus_gene_ensembl	Marmoset genes (ASM275486v1)
26 clanigera_gene_ensembl	Long-tailed chinchilla genes (Chilan1.0)
27 cpalliatius_gene_ensembl	Angola colobus genes (Cang_pa_1.0)
28 cporcellus_gene_ensembl	Guinea Pig genes (Capvor3.0)
29 csabaeus_gene_ensembl	Vervet-AGM genes (ChlSab1.1)
30 csavignyi_gene_ensembl	C.savignyi genes (CSAV 2.0)
31 csemitaevis_gene_ensembl	Tongue sole genes (Cse_v1.0)
32 csyrichta_gene_ensembl	Tarsier genes (Tarsius_syrichta-2.0.1)
33 cvariegatus_gene_ensembl	Sheepshead minnow genes (C_variegatus-1.0)
34 dmelanogaster_gene_ensembl	Fruitfly genes (BDGP6)
35 dnovemcinctus_gene_ensembl	Armadillo genes (Dasnov3.0)
36 dordoi_gene_ensembl	Kangaroo rat genes (Dord_2.0)
37 drerio_gene_ensembl	Zebrafish genes (GRCz11)
38 easinus_gene_ensembl	Donkey genes (ASM303372v1)
39 eburgeri_gene_ensembl	Hagfish genes (Eburgeri_3.2)
40 ecaballus_gene_ensembl	Horse genes (EquCab3.0)
41 eeuropaeus_gene_ensembl	Hedgehog genes (eriEur1)
42 elucius_gene_ensembl	Northern pike genes (Eluc_v3)
43 etelfairi_gene_ensembl	Lesser hedgehog tenrec genes (TENREC)
44 falbicoloris_gene_ensembl	Flycatcher genes (FicAlb_1.4)
45 fcatus_gene_ensembl	Cat genes (Felis_catus_9.0)
46 fdamarensis_gene_ensembl	Damara mole rat genes (DMR_v1.0)
47 fheteroclitus_gene_ensembl	Mummichog genes (Fundulus_heteroclitus-3.0.2)
48 gaculeatus_gene_ensembl	Stickleback genes (BROAD_S1)
49 gaffinis_gene_ensembl	Western mosquitofish genes (ASM309773v1)
50 gagassizii_gene_ensembl	Agassiz's desert tortoise genes (ASM289641v1)
51 ggallus_gene_ensembl	Chicken genes (GRCg6a)
52 ggorilla_gene_ensembl	Gorilla genes (gorGor4)
53 gmnorhua_gene_ensembl	Cod genes (gadMor1)
54 hburtoni_gene_ensembl	Burton's mouthbrooder genes (AstBur1.0)
55 hcomes_gene_ensembl	Tiger tail seahorse genes (H_comes_QL1_v1)
56 hfemale_gene_ensembl	Naked mole-rat female genes (HetGla_female_1.0)
57 hmale_gene_ensembl	Naked mole-rat male genes (HetGla_1.0)
58 hsapiens_gene_ensembl	Human genes (GRCh38.p12)
59 ipunctatus_gene_ensembl	Channel catfish genes (Ipcoco_1.2)
60 itridcemlineatus_gene_ensembl	Squirrel genes (SpeTri2.0)
61 jjaculus_gene_ensembl	Lesser Egyptian jerboa genes (JacJac1.0)

Environment History Connections

Import Dataset Global Environment List

Files Plots Packages Help Viewer

Install Update Name Description Version

User Library

Name	Description	Version
assertthat	Easy Pre and Post Assertions	0.2.0
BH	Boost C++ Header Files	1.69.0-1
bindr	Parametrized Active Bindings	0.1.1
bindrcpp	An 'Rcpp' Interface to Active Bindings	0.2.2
BiocGenerics	S4 generic functions for Bioconductor	0.28.0
<input checked="" type="checkbox"/> BiocInstaller	Install/Update Bioconductor, CRAN, and github Packages	1.30.0
BiocManager	Access the Bioconductor Project Package Repository	1.30.4
BiocVersion	Set the appropriate version of Bioconductor packages	3.8.0
<input checked="" type="checkbox"/> biomart	Genomic Data Retrieval	0.8.0
Biostings	Efficient manipulation of biological strings	2.50.2
bitops	Bitwise Operations	1.0-6
cli	Helpers for Developing Command Line Interfaces	1.0.1
clipr	Read and Write from the System Clipboard	0.4.1
crayon	Colored Terminal Output	1.3.4
curl	A Modern and Flexible Web Client for R	3.2
data.table	Extension of 'data.frame'	1.11.8
digest	Create Compact Hash Digests of R Objects	0.6.18
downloader	Download Files over HTTP and HTTPS	0.4
dplyr	A Grammar of Data Manipulation	0.7.8
fansi	ANSI Control Sequence Aware String Functions	0.4.0
glue	Interpreted String Literals	1.3.0
hms	Pretty Time of Day	0.4.2
httr	Tools for Working with URLs and HTTP	1.4.0
IRanges	Infrastructure for manipulating intervals on sequences	2.16.0
jsonlite	A Robust, High Performance JSON Parser and Generator for R	1.6
magrittr	A Forward-Pipe Operator for R	1.5
mime	Map Filenames to MIME Types	0.6
openssl	Toolkit for Encryption, Signatures and Certificates Based on OpenSSL	1.1
pillar	Coloured Formatting for Columns	1.3.1