DESeq2 Tool In R

Introduction-
DESeq2 is a comprehensive tool for differential gene expression analysis of RNA-seq data. It provides a suite of functions for data preparation, normalization, differential expression testing, and results visualization.

Need latest version of R and then install R studio which is a IDE which helps to visualize the data successfully.
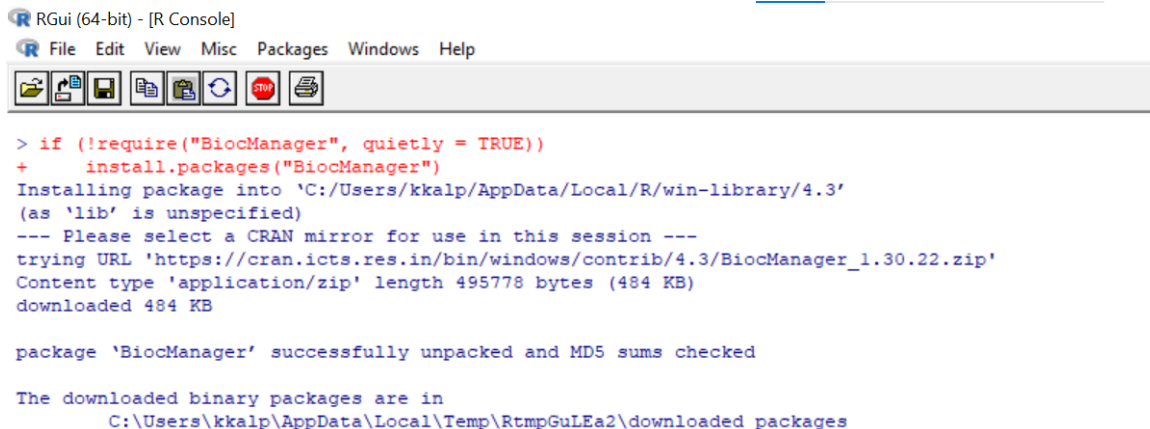
Refer bioconductor site :

Installation

To install this package, start R (version "4.3") and enter:

```
if (!require("BiocManager", quietly = TRUE))
    install.packages("BiocManager")

BiocManager::install("DESeq2")
```

- The provided command is used to install the **BiocManager** package in R, which is a **tool** for managing Bioconductor packages. It checks if the BiocManager package is already installed, and if not, it installs it using the **install.packages()** function.

- if (!require("BiocManager", quietly = TRUE)): This part checks if the **BiocManager** package is already installed using the **require()** function. The quietly = TRUE option suppresses any warning messages that would be generated if the package is not installed.

- **install.packages("BiocManager")**: If the BiocManager package is not installed, this part installs it using the install.packages() function. This function downloads and installs the package from the Comprehensive R Archive Network (CRAN) repository.

Following first command :

```
R RGui (64-bit) - [R Console]
R File  Edit  View  Misc  Packages  Windows  Help

> if (!require("BiocManager", quietly = TRUE))
+     install.packages("BiocManager")
Installing package into 'C:/Users/kkalp/AppData/Local/R/win-library/4.3'
(as 'lib' is unspecified)
--- Please select a CRAN mirror for use in this session ---
trying URL 'https://cran.icts.res.in/bin/windows/contrib/4.3/BiocManager_1.30.22.zip'
Content type 'application/zip' length 495778 bytes (484 KB)
downloaded 484 KB

package 'BiocManager' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
        C:\Users\kkalp\AppData\Local\Temp\RtmpGuLEa2\downloaded_packages
```

Then going for next command:

```
                    C:\Users\kkalp\AppData\Local\Temp\RtmpGuLEa2\downloaded_packages
> BiocManager::install("DESeq2")
'getOption("repos")' replaces Bioconductor standard repositories, see
'help("repositories", package = "BiocManager")' for details.
Replacement repositories:
    CRAN: https://cran.icts.res.in
Bioconductor version 3.18 (BiocManager 1.30.22), R 4.3.2 (2023-10-31 ucrt)
Installing package(s) 'BiocVersion', 'DESeq2'
also installing the dependencies 'bitops', 'formatR', 'colorspace', 'utf8', 'RCurl', 'GenomeInfoDbData', 'zl

trying URL 'https://cran.icts.res.in/bin/windows/contrib/4.3/bitops_1.0-7.zip'
Content type 'application/zip' length 31813 bytes (31 KB)
downloaded 31 KB

trying URL 'https://cran.icts.res.in/bin/windows/contrib/4.3/formatR_1.14.zip'
Content type 'application/zip' length 155284 bytes (151 KB)
downloaded 151 KB

trying URL 'https://cran.icts.res.in/bin/windows/contrib/4.3/colorspace_2.1-0.zip'
Content type 'application/zip' length 2633490 bytes (2.5 MB)
downloaded 2.5 MB

trying URL 'https://cran.icts.res.in/bin/windows/contrib/4.3/utf8_1.2.4.zip'



The downloaded binary packages are in
        C:\Users\kkalp\AppData\Local\Temp\RtmpGuLEa2\downloaded_packages
installing the source package 'GenomeInfoDbData'

trying URL 'https://bioconductor.org/packages/3.18/data/annotation/src/contrib/GenomeInfoDbData_1.2.11.tar.gz'
Content type 'application/x-gzip' length 12284235 bytes (11.7 MB)
downloaded 11.7 MB

* installing *source* package 'GenomeInfoDbData' ...
** using staged installation
** data
** inst
** help
*** installing help indices
** building package indices
** testing if installed package can be loaded from temporary location
** testing if installed package can be loaded from final location
** testing if installed package keeps a record of temporary installation path
* DONE (GenomeInfoDbData)

The downloaded source packages are in
        'C:\Users\kkalp\AppData\Local\Temp\RtmpGuLEa2\downloaded_packages'
Installation paths not writeable, unable to update packages
  path: C:/Program Files/R/R-4.3.2/library
  packages:
    cluster, lattice, Matrix, nlme
```
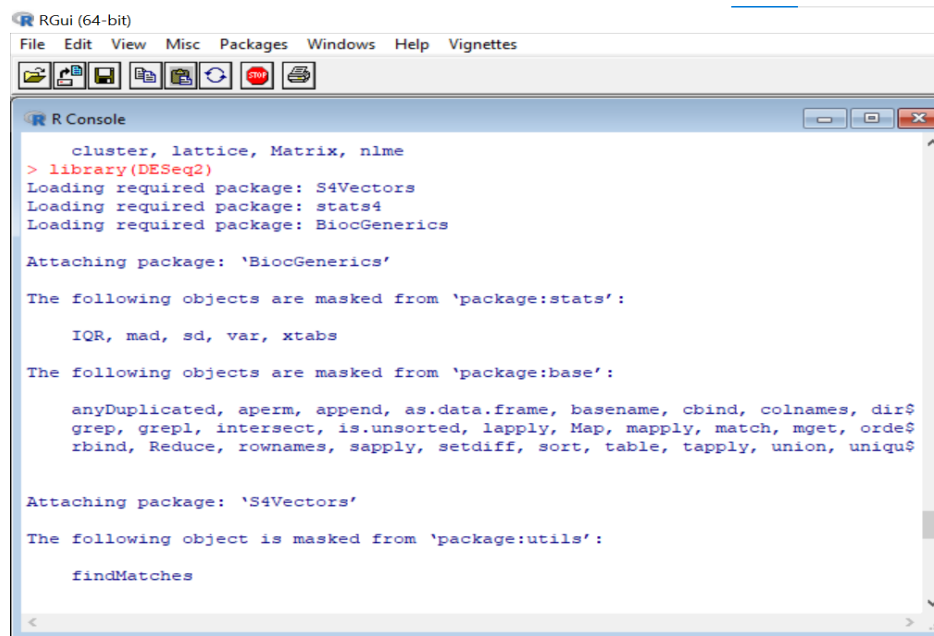
List of packages installed:

```
package 'bitops' successfully unpacked and MD5 sums checked
package 'formatR' successfully unpacked and MD5 sums checked
package 'colorspace' successfully unpacked and MD5 sums checked
package 'utf8' successfully unpacked and MD5 sums checked
package 'RCurl' successfully unpacked and MD5 sums checked
package 'zlibbioc' successfully unpacked and MD5 sums checked
package 'abind' successfully unpacked and MD5 sums checked
package 'crayon' successfully unpacked and MD5 sums checked
package 'SparseArray' 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 'farver' successfully unpacked and MD5 sums checked
package 'labeling' successfully unpacked and MD5 sums checked
package 'munsell' successfully unpacked and MD5 sums checked
package 'R6' successfully unpacked and MD5 sums checked
package 'RColorBrewer' successfully unpacked and MD5 sums checked
package 'viridisLite' successfully unpacked and MD5 sums checked
package 'fansi' successfully unpacked and MD5 sums checked
package 'magrittr' successfully unpacked and MD5 sums checked
package 'pillar' successfully unpacked and MD5 sums checked
package 'pkgconfig' successfully unpacked and MD5 sums checked
package 'GenomeInfoDb' successfully unpacked and MD5 sums checked
package 'XVector' successfully unpacked and MD5 sums checked
package 'S4Arrays' successfully unpacked and MD5 sums checked
package 'DelayedArray' successfully unpacked and MD5 sums checked
package 'futile.logger' successfully unpacked and MD5 sums checked
package 'snow' successfully unpacked and MD5 sums checked
package 'BH' successfully unpacked and MD5 sums checked
package 'cpp11' successfully unpacked and MD5 sums checked
package 'cli' successfully unpacked and MD5 sums checked
package 'glue' successfully unpacked and MD5 sums checked
package 'gtable' successfully unpacked and MD5 sums checked
package 'isoband' successfully unpacked and MD5 sums checked
package 'lifecycle' successfully unpacked and MD5 sums checked
```

```
package 'rlang' successfully unpacked and MD5 sums checked
package 'scales' successfully unpacked and MD5 sums checked
package 'tibble' successfully unpacked and MD5 sums checked
package 'vctrs' successfully unpacked and MD5 sums checked
package 'withr' successfully unpacked and MD5 sums checked
package 'S4Vectors' successfully unpacked and MD5 sums checked
package 'IRanges' successfully unpacked and MD5 sums checked
package 'GenomicRanges' successfully unpacked and MD5 sums checked
package 'SummarizedExperiment' successfully unpacked and MD5 sums checked
package 'BiocGenerics' successfully unpacked and MD5 sums checked
package 'Biobase' successfully unpacked and MD5 sums checked
package 'BiocParallel' successfully unpacked and MD5 sums checked
package 'matrixStats' successfully unpacked and MD5 sums checked
package 'locfit' successfully unpacked and MD5 sums checked
package 'ggplot2' successfully unpacked and MD5 sums checked
package 'Rcpp' successfully unpacked and MD5 sums checked
package 'MatrixGenerics' successfully unpacked and MD5 sums checked
package 'RcppArmadillo' successfully unpacked and MD5 sums checked
package 'BiocVersion' successfully unpacked and MD5 sums checked
package 'DESeq2' successfully unpacked and MD5 sums checked
```

To check if library successfully loaded or not:

For example if we want to install new package then :