

# Installation Guide for the WGCNAapp R Package

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## 1 Install R

If you don't already have it on your computer, download and install the latest version of R for your system (<https://cran.r-project.org>).

You need to install a R version  $\geq 3.2$  to run the application correctly.

## 2 Install dependencies

The WGCNAapp needs other R packages (called dependencies) to be installed in your R environment to function properly.

Open the R software (by default in 'Applications' for Mac and in 'C:\Program Files\R\' with a shortcut on the desktop for Windows). To continue the installation you will have to write the code below in the R software console.

### 2.1 Install Bioconductor dependencies

Install the dependencies packages hosted on Bioconductor by typing/pasting:

```
source("http://bioconductor.org/biocLite.R")
biocLite(c("preprocessCore", "impute", "AnnotationDbi", "GO.db"))
```

Then press the 'Enter'.

You may be asked to update packages.

Update all/some/none? [a/s/n]:

Type *a* to update all and press 'Enter'.

## 2.2 Install CRAN dependencies

Install the dependencies hosted on CRAN by typing/pasting:

```
install.packages(c("shiny", "WGCNA", "stringr", "DT", "networkD3", "gplots",  
                  "plotly", "rmarkdown"))
```

Then press 'Enter'.

If asked to install packages from source:

Do you want to install from sources the packages which needs compilation?  
y/n:

Type *y* to build from source the packages then press 'Enter'.

If you don't have any compiler on your system you should be automatically asked to install one.

When/If asked to choose the CRAN mirror, choose the one that is closest to you (geographically) in the list.

## 2.3 Version

This application was tested with the following version of the dependences:

preprocessCore v1.40.0; impute v1.52.0; AnnotationDbi v1.40.0; GO.db v3.5.0; shiny v1.0.5; WGCNA v1.61;  
stringr v1.2.0; DT v0.4; networkD3 v0.4; gplots v3.0.1; plotly v4.7.1; rmarkdown v1.8

## 3 Install pandoc

For the report feature you will need to have pandoc version  $> 1.12$  installed. You can check if pandoc is already installed by typing/pasting:

```
rmarkdown::pandoc_available()
```

Then press 'Enter'.

If it returns FALSE you don't have pandoc installed, if it returns TRUE you can check which version is installed by typing/pasting:

```
rmarkdown::pandoc_version()
```

If you don't have pandoc or if you have a too old version (*i.e.*  $\leq 1.12$ ) you can install/update it by following this link: <http://pandoc.org/installing.html>.

Then you need to restart R (You don't need to save the session but you can).

## 4 Install WGCNAapp

Download the WGCNAapp R package.

Verify that all dependencies are installed by typing/pasting:

```
list <- c("preprocessCore", "impute", "AnnotationDbi", "GO.db", "shiny", "WGCNA",  
          "stringr", "DT", "networkD3", "gplots", "plotly", "rmarkdown")  
for( i in list){  
  cat( paste0(i, ': ', i %in% installed.packages(), '\n'))  
}
```

Then press ‘Enter’.

If one of the packages shows FALSE, try to install it again.

If all packages show TRUE, you can now install the WGCNAapp package.

If you know in which folder you have downloaded the package into you can type/paste the following (you need to change “path\_where\_you\_downloaded\_the\_package” to correspond to your case):

```
install.packages("path_where_you_downloaded_the_package/WGCNAapp_1.0.tar.gz",  
                 repos=NULL, type="source")
```

Then press ‘Enter’.

Otherwise, you can change the working directory/current folder of R using the menus. Once you are in the right folder, you can type/paste the following:

```
install.packages("WGCNAapp_1.0.tar.gz", repos=NULL, type="source")
```

Then press ‘Enter’.

## 5 Launch the app

Load WGCNAapp by typing/pasting:

```
library(WGCNAapp)
```

Then press ‘Enter’.

Launch the app, by typing/pasting:

```
WGCNAapp()
```

Then press ‘Enter’.

The app will open in your default internet browser.

Any time you wish to open the app after this installation has been completed, simply repeat step 5.

## 6 Formatting your files for upload in the app

Your data has to be formatted in text or csv files (.txt or .csv), with samples as rows and features as columns. The first line of the files must contain the feature names and the first column must contain the sample IDs. The sample IDs from one file must correspond the those in the other file. Clinical trait data will be automatically subsetted and reordered based on sample IDs from the omics data file.

Two files have to be uploaded:

- The first file contains the omics features (continuous data). The data can be submitted as log2 or as normalized log 2 values.
- The second file contains the clinical traits. This data must be in numerical form; qualitative data have to be converted to numerical values (e.g. male=1 and females=2). In the case of binary qualitative data, the user has the option to transform them automatically in the app.