

User Guide

To get started with the offline version of the tool, install R base from the link <https://cran.r-project.org/bin/windows/base/>. Install RStudio compatible to your machine from <https://www.rstudio.com/products/rstudio/download/>. Once you are done, start RStudio and enter the following commands to install the following needed packages.

```
## Not run
## shiny
##Version >=0.14.2
install.packages("shiny")
```

```
## Not run
## markdown
##Version >= 0.7.7
install.packages("markdown")
```

```
## Not run
## plyr
## Version >= 1.8.4
install.packages("plyr")
```

```
## Not run
## data.table
## Version >= 1.10.0
install.packages("data.table")
```

```
## Not run
## dplyr
##Version >= 0.5.0
install.packages("dplyr")
```

```
## Not run
## dtplyr
## Version >= 0.0.2
install.packages("dtplyr")
```

```
## Not run
## tibble
## Version >= 1.3.3
install.packages("tibble")
```

```
## Not run
## shinyjs
##Version >= 0.8
install.packages("shinyjs")
```

```
## Not run
## gtools
## Version >= 3.5.0
install.packages("gtools")
```

```
## Not run
## affyio
##Version >=1.44.0
source("https://bioconductor.org/biocLite.R")
biocLite("affyio")
```

```
## Not run
## affy
## Version >= 1.52.0
source("http://bioconductor.org/biocLite.R")
biocLite("affy")
```

```
## Not run
## oligo
## Version >= 1.40.1
source("https://bioconductor.org/biocLite.R")
biocLite("oligo")
```

```
## Not run
## simpleaffy
##Version >= 2.50.0
source("http://bioconductor.org/biocLite.R")
biocLite("simpleaffy")
```

```
## Not run
## codelink
##Version >= 1.42.0
source("http://bioconductor.org/biocLite.R")
biocLite("codelink")
```

```
## Not run
## lumi
## Version >= 2.26.3
source("http://bioconductor.org/biocLite.R")
biocLite("lumi")
```

```
## Not run
## limma
## Version >= 3.30.6
source("http://bioconductor.org/biocLite.R")
biocLite("limma")
```

```
## Not run
## h10kcod.db
## ~10000 genome package
##Version >= 3.4.0
source("http://bioconductor.org/biocLite.R")
biocLite("h10kcod.db")
```

```
## Not run
## h20kcod.db
## ~20000 genome package
## Version >= 3.4.0
source("http://bioconductor.org/biocLite.R")
biocLite("h20kcod.db")
```

```
## Not run
## hwgcod.db
## Whole human genome package
## version >= 3.4.0
source("http://bioconductor.org/biocLite.R")
biocLite("hwgcod.db")
```

After installing all the packages, shiny package must be loaded before running the MAMGED application. For loading shiny R package, enter **library(shiny)** into the R consol. All other packages can be loaded; however, it is optional here because all the packages are loaded automatically once the application is started. To load all the above installed packages, copy and paste the below commands into the R consol.

```
library(simpleaffy)
library(affy)
library(oligo)
library(shiny)
library(markdown)
library(plyr)
library(data.table)
library(dplyr)
library(dtplyr)
library(tibble)
library(codelink)
```

```
library(lumi)
library(h20kcod.db)
library(h10kcod.db)
library(hwgcod.db)
library(limma)
library(shinyjs)
library(gtools)
library(tools)
library(affyio)
```

Once you are done with all the installation and loading process, put the tool folder in the current working directory. You can also set your working directory at the top of the Rstudio session -> Set Working Directory -> Choose Directory. After setting the path, you can check the current working directory by **getwd()** to make sure that correct working directory is set. To run the program enter **runApp('name of your application')** i.e. the name of tool folder into R, open in browser and work.

Note: If shiny package is not installed and an attempt is made to run the application by `runApp('name of your application')`, R will throw an error **Error: could not find function "runApp"**. To avoid such error, make sure shiny package is loaded before running the application.