

User Guide

To get started with 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 needed packages.

```
install.packages("shiny")
```

```
install.packages("markdown")
```

```
install.packages("plyr")
```

```
install.packages("data.table")
```

```
install.packages("dplyr")
```

```
install.packages("shinyjs")
```

```
## Not run
```

```
## Affy package
```

```
source("http://bioconductor.org/biocLite.R")
```

```
biocLite("affy")
```

```
## Not run
```

```
## simpleaffy package
```

```
source("http://bioconductor.org/biocLite.R")
```

```
biocLite("simpleaffy")
```

```
## Not run
```

```
## codelink package
```

```
source("http://bioconductor.org/biocLite.R")
```

```
biocLite("codelink")
```

```
## Not run
```

```
## lumi package
```

```
source("http://bioconductor.org/biocLite.R")
```

```
biocLite("lumi")
```

```
## Not run
```

```
## limma package
```

```
source("http://bioconductor.org/biocLite.R")
```

```
biocLite("limma")
```

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

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

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

After installing all the packages, all the packages need to be loaded. To load all the above installed packages, copy and paste the below line into the R console.

```
library(affy)
library(shiny)
library(markdown)
library(plyr)
library(data.table)
library(dplyr)
library(codelink)
library(simpleaffy)
library(lumi)
library(h20kcod.db)
library(h10kcod.db)
library(hwgcod.db)
library(limma)
library(shinyjs)
```

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 you can check the current working directory by `getwd()`. 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: To call `runAPP()` function, shiny package should be loaded first by using `library(shiny)`, which otherwise will through an error, **Error: could not find function "runAPP"**.