

First you need to install R

Add R to your repositories by editing the file /etc/apt/sources.list and add the line:

```
deb http://cran.cnr.Berkeley.edu/bin/linux/ubuntu trusty/
```

* Where trusty is the version of ubuntu

Update the repository sources

```
sudo apt-get update
```

Install R

```
sudo apt-get install r-base
```

Install the following packages:

```
sudo apt-get install libxml2 libxml2-dev
```

```
sudo apt-get install libcurl4-openssl-dev
```

```
sudo apt-get install curl
```

Open R and install biocLite

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

```
biocLite()
```

And also other packages which are needed such as:

```
biocLite("GEOquery")
```

Finally install cellmix - http://www.academia.edu/2886152/CellMix_Sample_Analyses

```
# install
```

```
repos <- c("http://web.cbio.uct.ac.za/~renaud/CRAN", getOption("repos"))
```

```
install.packages("CellMix", repos = repos)
```

```
# load
```

```
library(CellMix)
```

* if the installation of cellmix is not successful and it complains about missing packages type

```
biocList("The_Name_Of_The_missing_package")
```

* For running my script I also need R to load mat files so I needed to install:

```
install.packages("R.matlab")
```