

- Install R libraries

<http://cran.r-project.org/bin/windows/base/> (for Windows)

<http://cran.r-project.org/bin/macosx/> (for (Mac) OS X)

- Install Rstudio

[Download the RStudio IDE - RStudio](#)

- # install TDAstats from CRAN by using the command below
`>install.packages("TDAstats")`
- If you want to copy a mat file (let's say dist.mat with 10 columns, and 10 rows) into Rstudio, you can install this package
`> install.packages("R.matlab")`
`>library(R.matlab)`
- Go to the Tools>GlobalChange. Change the working directory to the folder where you've stored your dist.mat file containing the pairwise distances of the genome sequences.
- Use the following commands to copy dist.mat into a matrix variable num in Rstudio
`>dq <-readMat("dist.mat")`
`>num <- matrix(unlist(dq), ncol = 10, nrow =10)`

NOTE: make the necessary changes to the above command^ according to the number of rows and columns you have
- The num variable is now contains the distance matrix in R. To find the homologies, we use the following commands
`>library("TDAstats")`
`>p <- calculate_homology(num, dim =1, threshold = -1, format = "distmat", standardize = FALSE, return_df = FALSE)`
`> plot_barcode(p)`

You will have your barcode.