Install NuclearFRAP (Version 0.0.34)

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January 31, 2014

1 System Requirments

In order to run NuclearFRAP you need to have R (version 3.0.2 or higher) and Matlab installed in your system. Both executables should be in your environmental PATH variable. Typing R or matlab in the console should open the corresponding program. In windows you also require Rtools installed.

NuclearFRAP depends on serveral R packages. To install them from R

- > install.packages(c("Rcell","R.matlab","chron","gridExtra"))
- > source("http://bioconductor.org/biocLite.R")
- > biocLite("EBImage")

NuclearFRAP is not on CRAN, so you have to install it from the local tar.gz. To do so from the command line

R CMD INSTALL NuclearFRAP.tar.gz

Once installed you can load the package

> library(NuclearFRAP)

Note that installing and loading a package are two different things, and you have to load the package using library at the begging of every session, even if you have just installed it.