

```
1 # Bioconductor installs
2 # R. Burke Squires
3 # Source: https://github.com/burkesquires/immunology-
  informatics/tree/master/03_auto_flow_cyto_analysis/
  auto_flow_cyto_analysis
4
5 #####
6 # Normally to install package using R and Bioconductor you
  will type:
7 #####
8
9 # You tell R where to find the source code for the
  Bioconductor packages
10
11 source("https://bioconductor.org/biocLite.R")
12
13 # Now that R now where to find the package information,
14 # you type _biocLite()_ to retrieve teh most recent list of
  packages
15
16 biocLite ()
17
18 # Now that R nows what packages are available, we can install
  a package.
19 # Lets install the _flowCore_ package
20
21 biocLite("flowCore")
22
23 # You only need to install a package once. You can update it
  later on by installing again,
24 # which will install the latest version
25
26 # Before you can actually USE a package you have to load it
  using the library command like this:
27
28 library(flowCore)
29
30 # We can install all of our packages
31
32 biocLite('flowMerge')
33 biocLite("flowQ")
34 biocLite('flowType')
35
36 biocLite('RchyOptimyx')
37
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38 biocLite('rrcov')
39 biocLite('codetools')
40 biocLite('foreach')
41
42
43 install.packages("ROCR")
44 install.packages("sfsmisc")
45 install.packages("GEOmap")
46
47 install.packages("car"); install.packages("RFOC")
48
49
50 library(flowCore)
51 library(flowDensity)
52 library(flowType)
53 library(RchyOptimyx);
54 library(ROCR)
55 library(sfsmisc)
56 library(GEOmap)
57
58 # Before leaving for lunch
59
60 source("http://bioconductor.org/biocLite.R")
61 biocLite('rrcov')
62 biocLite('codetools')
63 biocLite('foreach')
64 biocLite('flowMerge')
65 biocLite('flowType')
66 biocLite('RchyOptimyx')
67 biocLite('Rcpp')
68
69 library(flowType)
70 library(RchyOptimyx)
71
72
73
74 # This is a function that just makes sure you have a package,
or installs it for you without prompting
75 # Gresham Lab Flow Core Guide
76 # https://github.com/GreshamLab/flow
77
78 requireInstall <- function(packageName,isBioconductor=F) {
79   if ( !try(require(packageName,character.only=T)) ) {
80     print(paste0("You don't have ",packageName," accessible, "
81               ,
82               "I'm gonna install it"))
83   }
84   if (isBioconductor) {

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83     source("http://bioconductor.org/biocLite.R")
84     biocLite(packageName)
85   } else {
86     install.packages("packageName", repos = "http://cran.us
      .r-project.org")
87   }
88 }
89 return(1)
90 }
91
92 #Load libraries
93 requireInstall("flowCore", isBioconductor=T)
94
```