

MBatch 01 Installing on Windows  
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## Introduction

These instructions are aimed at people familiar with Windows and R administration, with administrator access to their Windows environment. If using the versions discussed here, it may be possible to install MBatch with minimal administration knowledge.

NOTE: If these instructions are out of date, please see the Linux install instructions for the newest version: [https://github.com/MD-Anderson-Bioinformatics/BatchEffectsPackage/blob/master/docs/MBatch/MBatch\\_01\\_InstallLinux.pdf](https://github.com/MD-Anderson-Bioinformatics/BatchEffectsPackage/blob/master/docs/MBatch/MBatch_01_InstallLinux.pdf)

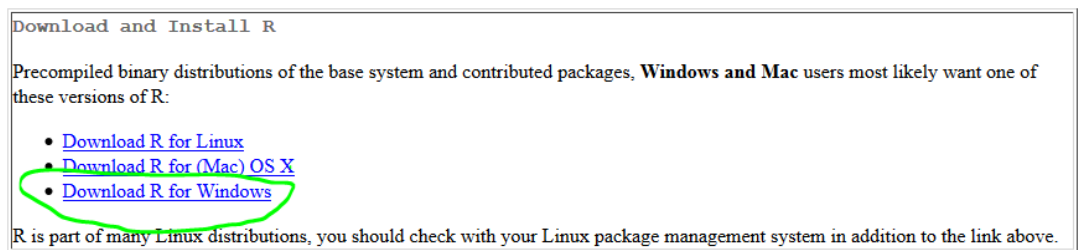
## Target Operating System and Installation

These instructions were tested on Windows 7. These instructions with appropriate modifications should work as a basis for installing MBatch on other systems.

Perform the installs in the order given in this document. Some steps are dependent on previous steps.

## Install R 4.x

MBatch is tested and used with R 4.x on other systems. Use the instructions on a local CRAN mirror (<https://cran.r-project.org/mirrors.html>) under "Download R for Windows" (as shown in the screenshot).



Then follow the "base" link.

## R for Windows

Subdirectories:

[base](#)

Binaries for base distribution. This is what you want to [install R for the first time](#).

[contrib](#)

Binaries of contributed CRAN packages (for R  $\geq$  2.13.x; managed by Uwe Ligges). There is also information on [third party software](#) available for CRAN Windows services and corresponding environment and make variables.

[old contrib](#)

Binaries of contributed CRAN packages for outdated versions of R (for R  $<$  2.13.x; managed by Uwe Ligges).

[Rtools](#)

Tools to build R and R packages. This is what you want to build your own packages on Windows, or to build R itself.

The current version will be a 4.x release (screenshot is from 3.6.x), you can download it from here.

### R-3.6.0 for Windows (32/64 bit)

[Download R 3.6.0 for Windows](#) (80 megabytes, 32/64 bit)

[Installation and other instructions](#)

[New features in this version](#)

If you want to double-check that the package you have downloaded matches the package distributed by CRAN, you can compare the [md5sum](#) of the .exe to the [fingerprint](#) on the master server. You will need a version of md5sum for windows: both [graphical](#) and [command line versions](#) are available.

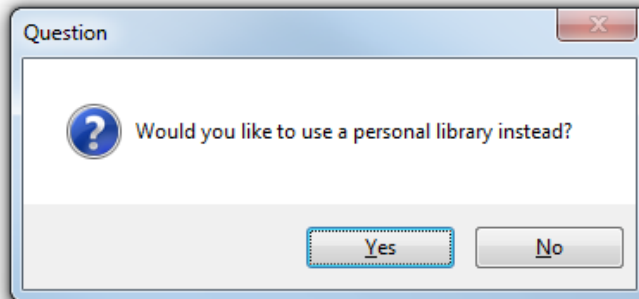
## Setting Up a Personal R Library

If you have not installed any packages in R, you will need to create a personal package for R libraries. Start R by double clicking on the x64 application on your desktop. Note that paths will have changed from 3.4.x to 3.6.x.

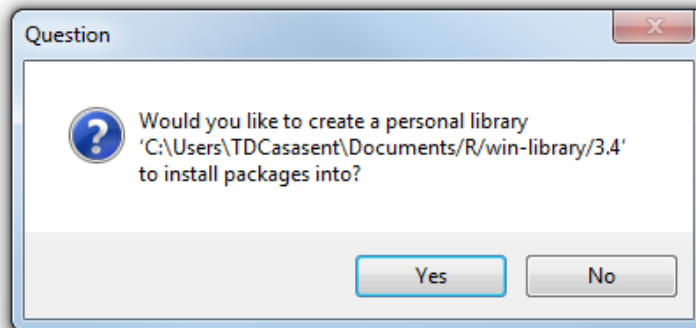
Install a package, as shown below, and create a personal library directory by replying “Yes” to the popups.

```
> install.packages("devtools", repos = "http://cran.revolutionanalytics.com")
```

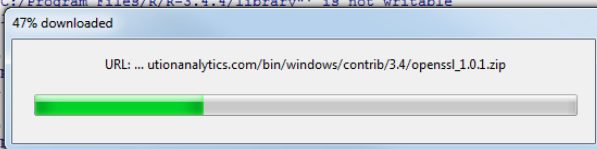
```
> install.packages("devtools", repos = "http://cran.revolutionanalytics.com")
Warning in install.packages("devtools", repos = "http://cran.revolutionanalytics.com") :
  'lib = "C:/Program Files/R/R-3.4.4/library"' is not writable
```



```
> install.packages("devtools", repos = "http://cran.revolutionanalytics.com")
Warning in install.packages("devtools", repos = "http://cran.revolutionanalytics.com") :
  'lib = "C:/Program Files/R/R-3.4.4/library"' is not writable
```



```
> install.packages("devtools", repos = "http://cran.revolutionanalytics.com")
Warning in install.packages("devtools", repos = "http://cran.revolutionanalytics.com") :
  'lib = "C:/Program Files/R/R-3.4.4/library"' is not writable
also installing dependencies: 'openssl', 'whisker', 'digest', 'rstudioapi', 'jsonlite', 'git2r', $
trying URL 'http://cran.revolutionanalytics.com/bin/windows/contrib/3.4/openssl_1.0.1.zip'
Content type 'application/zip' length 3572764 bytes (3.4 MB)
downloaded 47%
trying URL 'http://cran.revolutionanalytics.com/bin/windows/contrib/3.4/openssl_1.0.1.zip'
Content type 'application/zip' length 3572764 bytes (3.4 MB)
downloaded 2.8 MB
```



```
trying URL 'http://cran.revolutionanalytics.com/bin/windows/contrib/3.4/devtools_1.13.5.zip'
Content type 'application/zip' length 443954 bytes (433 KB)
downloaded 433 KB
```

```
package 'mime' successfully unpacked and MD5 sums checked
package 'curl' successfully unpacked and MD5 sums checked
package 'openssl' successfully unpacked and MD5 sums checked
package 'R6' successfully unpacked and MD5 sums checked
package 'httr' successfully unpacked and MD5 sums checked
package 'memoise' successfully unpacked and MD5 sums checked
package 'whisker' successfully unpacked and MD5 sums checked
package 'digest' successfully unpacked and MD5 sums checked
package 'rstudioapi' successfully unpacked and MD5 sums checked
package 'jsonlite' successfully unpacked and MD5 sums checked
package 'git2r' successfully unpacked and MD5 sums checked
package 'withr' successfully unpacked and MD5 sums checked
package 'devtools' successfully unpacked and MD5 sums checked
```

```
The downloaded binary packages are in
  C:\Users\TDCasasent\AppData\Local\Temp\Rtmp8E7Co7\downloaded_packages
> |
```

## Installing Required Packages

MBatch has some required packages.

### Other Required Packages for NGCHM

Within R, run the following installs.

```
# start R (--vanilla says don't load any environments or save any)

R --vanilla

# install packages from CRAN (this installs to site-library so it is available for
all users)

# update to preferred CRAN mirror if desired

# this is at the R command

install.packages("httr", dependencies = TRUE, repos = "http://cran.r-
project.org")

install.packages("magick", dependencies = TRUE, repos = "http://cran.r-
project.org")

install.packages("gert", dependencies = TRUE, repos = "http://cran.r-
project.org")

install.packages("htmlwidgets", dependencies = FALSE, repos = "http://cran.r-
project.org")

install.packages("shiny", dependencies = TRUE, repos = "http://cran.r-
project.org")
```

```

install.packages("usethis", dependencies = TRUE, repos = "http://cran.r-
project.org")

install.packages("covr", dependencies = TRUE, repos = "http://cran.r-
project.org")

install.packages("rversions", dependencies = TRUE, repos = "http://cran.r-
project.org")

install.packages("devtools", dependencies = TRUE, repos = "http://cran.r-
project.org")

library(devtools)

# remotes

devtools::install_github('MD-Anderson-Bioinformatics/tsvio')

devtools::install_github('MD-Anderson-Bioinformatics/NGCHMSupportFiles',
ref='main')

devtools::install_github('MD-Anderson-Bioinformatics/NGCHM-R')

# quit R

# this is at the R command

q()

```

## Other Required Packages

Within R, run the following installs.

```

# start R (--vanilla says don't load any environments or save any)

R --vanilla

message("#*#* reticulate used by MBatch")

install.packages("reticulate", dependencies=TRUE, repos = "http://cran.r-
project.org")

message("#*#* mclust used by oompaBase, ClassDiscovery, and PreProcess (in
install 1)")

install.packages("mclust", dependencies=TRUE, repos = "http://cran.r-
project.org")

message("#*#* Biobase used by oompaBase, ClassDiscovery, and PreProcess
(in install 1)")

install.packages("BiocManager", dependencies=TRUE, repos = "http://cran.r-
project.org")

BiocManager::install(c("Biobase"), update=FALSE)

```

```

message("### oompaBase, ClassDiscovery, and PreProcess")
# used by PCA+ and other clustering algorithms in MBatch
# uses ClassDiscovery functions distanceMatrix and SamplePCA
install.packages(c("oompaBase", "ClassDiscovery", "PreProcess"), dependen-
cies=TRUE, repos=c("http://cran.r-project.org", "http://silicovore.com/OOMPA/"))
message("### Cairo used in MBatch for images")
install.packages("Cairo", dependencies=TRUE, repos = "http://cran.r-
project.org")
message("### BiasedUrn needed for epiR")
install.packages("BiasedUrn", dependencies=TRUE, repos = "http://cran.r-
project.org")
message("### pander needed for epiR")
install.packages("pander", dependencies=TRUE, repos = "http://cran.r-
project.org")
message("### sf needed for epiR")
install.packages("sf", dependencies=TRUE, repos = "http://cran.r-project.org")
message("### lubridate needed for epiR")
install.packages("lubridate", dependencies=TRUE, repos = "http://cran.r-
project.org")
message("### epiR used in correlation density plot")
#install.packages("epiR", dependencies=TRUE, repos = "http://cran.r-
project.org")
#Install version 2.0.40, anything newer fails
install.packages("https://cran.r-project.org/src/contrib/Archive/epiR/epiR_2.0.40.tar.gz")
message("### squash used for dendromat in Supervised Clustering and Hier-
archical Clustering")
install.packages("squash", dependencies=TRUE, repos = "http://cran.r-
project.org")
# used in DAPIR
message("### httr")
install.packages("httr", dependencies=TRUE, repos = "http://cran.r-
project.org")
message("### jsonlite")

```

```

install.packages("jsonlite", dependencies=TRUE, repos = "http://cran.r-
project.org")

# uses dunn.test in MBatchUtils
message("#*#* dunn.test")

install.packages("dunn.test", dependencies=TRUE, repos = "http://cran.r-
project.org")

# used for UMAP
message("#*#* uwot")

install.packages("uwot", dependencies=TRUE, repos = "http://cran.r-
project.org")

message("#*#* devtools")

install.packages("devtools", dependencies=TRUE, repos = "http://cran.r-
project.org")

library(devtools)

message("#*#* jlmelville/vizier")

devtools::install_github("jlmelville/vizier")

# quit R

# this is at the R command

q()

```

## Install MBatch Package

MBatch can be installed from GitHub using the following commands. (The devtools package was installed earlier.)

```

# At Linux command line (this install is for your own user, su to root to install
for everyone)

# start R (--vanilla says don't load any environments or save any)

R --vanilla

# Within R

library(devtools)

devtools::install_github("MD-Anderson-Bioinformatics/BatchEffectsPackage/apps/MBatch")

# quit R

# this is at the R command

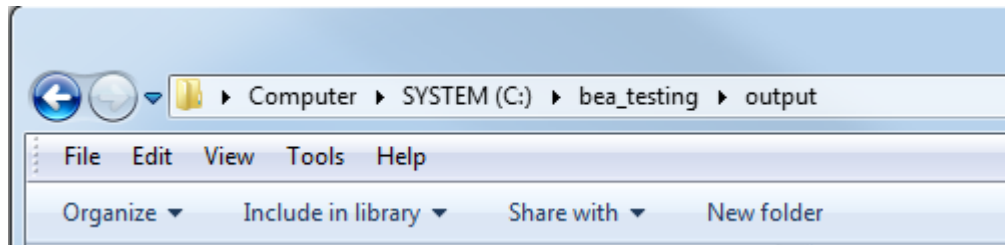
```

q()

Note: As a side note, the "tests" directory installed via devtools is not by default included in install.packages or R CMD INSTALL. If installing MBatch via a different method, to include tests via the command line, use "--install-tests".

## Create base directory for testing

MBatch will use c:\bea\_testing for tests. It also needs a directory named c:\bea\_testing\output. Create both these directories.



## Populating Data for Tests

The files located at [https://github.com/MD-Anderson-Bioinformatics/BatchEffectsPackage/tree/master/data/testing\\_static/MATRIX\\_DATA](https://github.com/MD-Anderson-Bioinformatics/BatchEffectsPackage/tree/master/data/testing_static/MATRIX_DATA) go in the c:\bea\_testing\MATRIX\_DATA folder.

The files located at [https://github.com/MD-Anderson-Bioinformatics/BatchEffectsPackage/tree/master/data/testing\\_static/COMPARE](https://github.com/MD-Anderson-Bioinformatics/BatchEffectsPackage/tree/master/data/testing_static/COMPARE) go in the c:\bea\_testing\COMPARE folder.

## Running the Tests

Finally, run this code to perform the tests. This takes an hour or so to run. Machines with slower processors, slower hard drives, or minimal memory may take longer or be unable to complete the tests.

### # Within R

```
library(MBatch)

# Set these environment variable to override file locations if needed
Sys.setenv(MBATCH_TEST_OUTPUT="c:\\bea_testing\\output")
Sys.setenv(MBATCH_TEST_INPUT="c:\\bea_testing\\MATRIX_DATA")
Sys.setenv(MBATCH_TEST_COMPARE="c:\\bea_testing\\COMPARE")
baseDir <- file.path(system.file(package = "MBatch"), "tests")
message(baseDir)
```



```

testFiles <- list.files(path=baseDir)
print(testFiles)
results <- c()
for(myFile in testFiles)
{
  message("*****")
  message("*****")
  message("**** ", file.path(baseDir, myFile))
  message("*****")
  message("*****")
  test <- source(file.path(baseDir, myFile))
  if (isTRUE(test$value))
  {
    results <- c(results, paste("Test succeeded for ", myFile, sep=""))
  }
  else
  {
    results <- c(results, paste("Test failed for ", myFile, sep=""))
  }
}
print(results)

```

The last part of the output will print whether or not the tests finished properly.

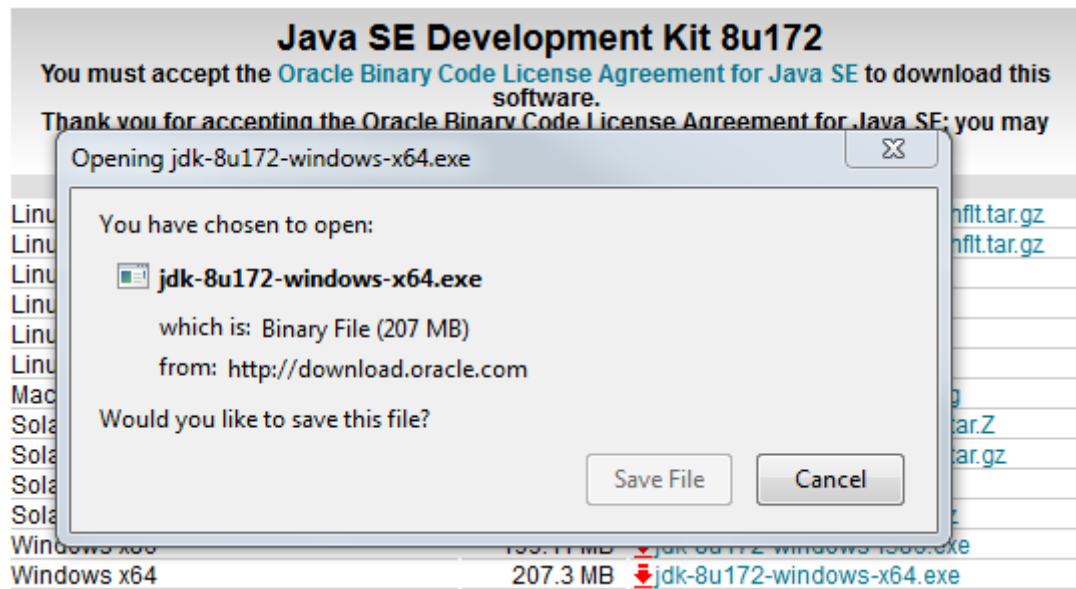
```

2018 05 22 09:59:23.947 DEBUG BSTW5MHDXM2 mbatchStandardLegend before java
2018 05 22 09:59:23.978 DEBUG BSTW5MHDXM2 mbatchStandardLegend after java
No comparable output--no error means 'OK' for now.
> print(results)
[1] "Test succeeded for AN_Adjusted.R"
[2] "Test succeeded for AN_Unadjusted.R"
[3] "Test succeeded for Boxplot_AllSamplesData_Structures.R"
[4] "Test succeeded for Boxplot_AllSamplesRLE_Structures.R"
[5] "Test succeeded for Boxplot_Group_Structures.R"
[6] "Test succeeded for CDP_Files.R"
[7] "Test succeeded for CDP_Plot.R"
[8] "Test succeeded for CDP_Structures.R"
[9] "Test succeeded for EB_withNonParametricPriors.R"
[10] "Test succeeded for EB_withParametricPriors.R"
[11] "Test succeeded for EBNPlus_CombineBatches.R"
[12] "Test succeeded for EBNPlus_Correction_Files.R"
[13] "Test succeeded for EBNPlus_Correction_Structures.R"
[14] "Test succeeded for HierarchicalClustering_Structures.R"
[15] "Test succeeded for MP_ByBatch.R"
[16] "Test succeeded for MP_Overall.R"
[17] "Test succeeded for PCA_DualBatch_Structures.R"
[18] "Test succeeded for PCA_Regular_Structures.R"
[19] "Test succeeded for RBN_Pseudoreplicates.R"
[20] "Test succeeded for RBN_Replicates.R"
[21] "Test succeeded for SupervisedClustering_Batches_Structures.R"
[22] "Test succeeded for SupervisedClustering_Pairs_Structures.R"
> |

```

## Install Open JDK

Many Windows system do not install the JDK needed for compiling Java, and only install a JRE. For Windows, we use the Windows x64 (for 64 bit systems) installation instructions and installer from <http://www.oracle.com/technetwork/java/javase/downloads/jdk8-downloads-2133151.html>. Download and install the JDK8 as per Oracle's instructions.



## rJava Setup for R

For Windows, rJava is installed from the R command line using this R command.  
(Do not use the type="source" option found in the Linux install.)

```
install.packages("rJava", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")
```

The other lines demonstrate a test to make sure the install finished properly.

```
library(rJava)
```

```
.jinit()
```

```
J("java.lang.System")$getProperty("java.version")
```

The output from this will be similar as shown below:

```
> install.packages("rJava", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")
```

Installing package into 'C:/Users/TDCasasent/Documents/R/win-library/3.4'

(as 'lib' is unspecified)

```
trying URL 'http://cran.revolutionanalytics.com/bin/windows/contrib/3.4/rJava_0.9-9.zip'
```

```
Content type 'application/zip' length 720033 bytes (703 KB)
```

```
downloaded 703 KB
```

```
package 'rJava' successfully unpacked and MD5 sums checked
```

The downloaded binary packages are in

```
C:\Users\TDCasasent\AppData\Local\Temp\Rtmp8E7Co7\downloaded_packages
>
>
> library(rJava)
> .jinit()
> J("java.lang.System")$getProperty("java.version")
[1] "1.8.0_172"
```