

1 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.

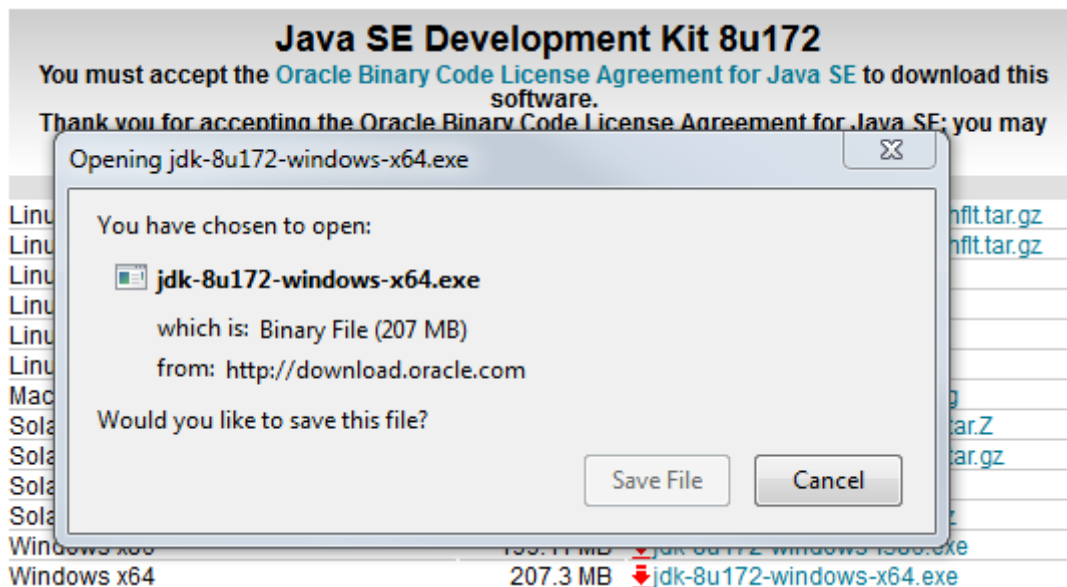
2 Target Operating System and Installation

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.

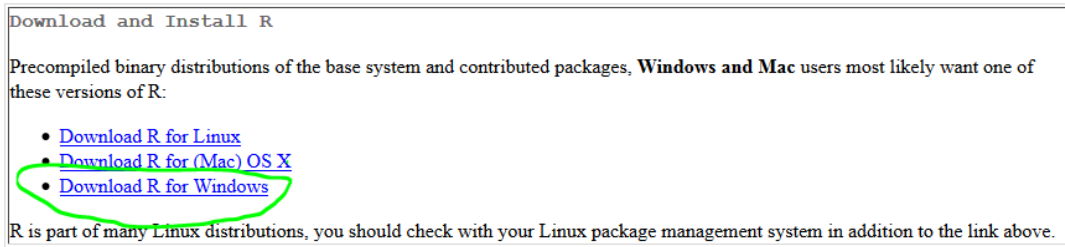
3 Install Open JDK

Many Windows systems 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.



4 Install R 3.4.x

MBatch uses R 3.4.x. It may work with older or newer versions, but packages and R itself tend to change between releases, so it is best to use 3.4.x. 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). Also, see the notes under "Supported branches" for changes to R between 3.3 and 3.4.



Then follow the “base” link.

R for Windows

Subdirectories:

[base](#)

[contrib](#)

[old contrib](#)

[Rtools](#)

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

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.

Binaries of contributed CRAN packages for outdated versions of R (for R $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

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

Then use the “Previous releases” link.

R-3.5.0 for Windows (32/64 bit)

[Download R 3.5.0 for Windows](#) (62 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.

Frequently asked questions

- [Does R run under my version of Windows?](#)
- [How do I update packages in my previous version of R?](#)
- [Should I run 32-bit or 64-bit R?](#)

Please see the [R FAQ](#) for general information about R and the [R Windows FAQ](#) for Windows-specific information.

Other builds

- Patches to this release are incorporated in the [r-patched snapshot build](#).
- A build of the development version (which will eventually become the next major release of R) is available in the [r-devel snapshot build](#).
- [Previous releases](#)

Note to webmasters: A stable link which will redirect to the current Windows binary release is CRAN.MIRROR>/bin/windows/base/release.htm.

Last change: 2018-04-23

Then pick the newest version of 3.4.x.

Previous Releases of R for Windows

This directory contains previous binary releases of R to run on Windows 95, 98, ME, NT4.0, 2000 and XP or later on Intel/clone chips.

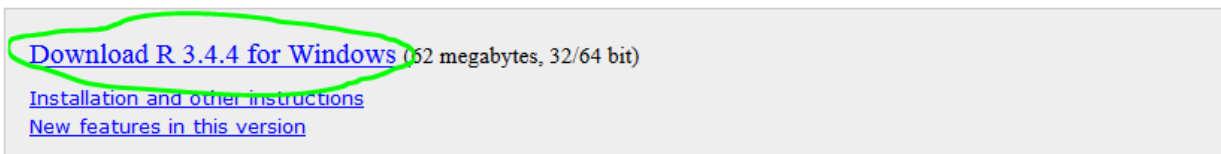
The current release, and links to development snapshots, are available [here](#). Source code for these releases and others is available through [the main CRAN page](#).

In this directory:

[R 3.4.4](#) (March, 2018)
[R 3.4.3](#) (November, 2017)
[R 3.4.2](#) (September, 2017)
[R 3.4.1](#) (June, 2017)
[R 3.4.0](#) (April, 2017)
[R 3.3.3](#) (March, 2017)
[R 3.3.2](#) (October, 2016)
[R 3.3.1](#) (June, 2016)
[R 3.3.0](#) (April, 2016)
[R 3.2.5](#) (April, 2016)
[R 3.2.4](#) (March, 2016)

Then use the “Download R 3.4.X for Windows” link.

R-3.4.4 for Windows (32/64 bit)

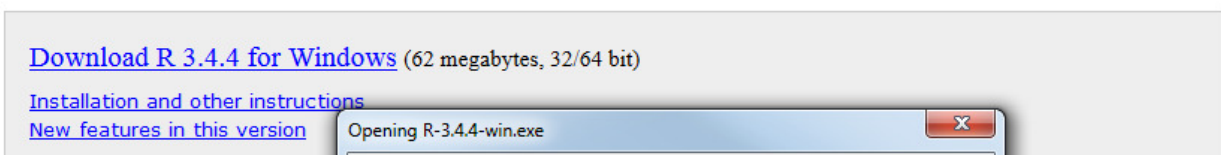


[Download R 3.4.4 for Windows](#) (62 megabytes, 32/64 bit)
[Installation and other instructions](#)
[New features in this version](#)

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.

Download the R install program and follow the instructions provided under “Installation and other instructions”.

R-3.4.4 for Windows (32/64 bit)

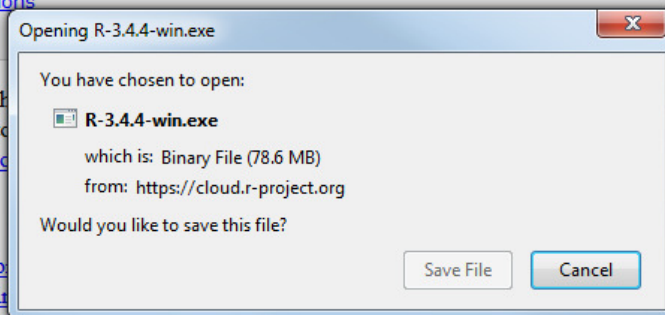


[Download R 3.4.4 for Windows](#) (62 megabytes, 32/64 bit)
[Installation and other instructions](#)
[New features in this version](#)

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.

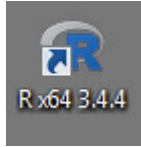
CRAN, you can
um for windows: both

- [Does R run under my version of Windows?](#)
- [How do I update packages in R?](#)
- [Should I run 32-bit or 64-bit R?](#)



5 Setting Up a Personal R Library

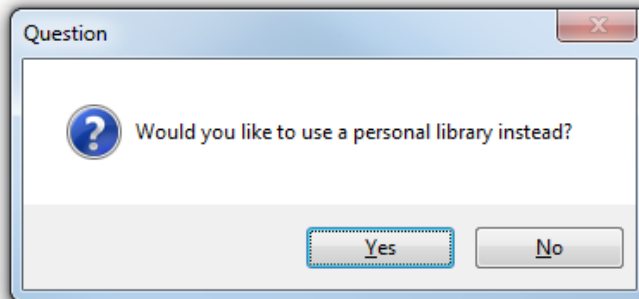
If you have not installed any packages in R, you will need to create a personal package for R libraries. Start R by double clicking on the x64 application on your desktop.



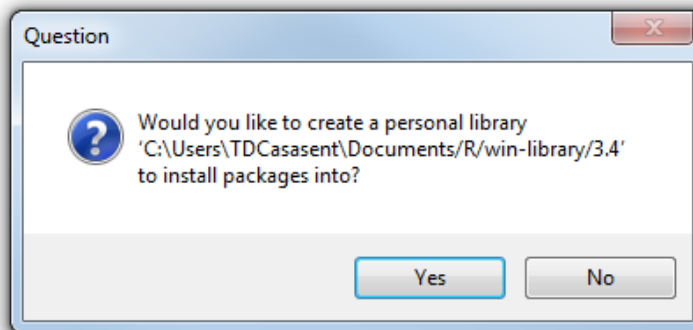
Install a package, as shown below, and create a personal library directory by replying “Yes” to the popups.

```
> 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: 'memoise', '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 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
> |

```

6 Installing Required Packages

MBatch has some required packages.

6.1 rJava Setup for R

For Windows, rJava is installed from the R command line using the command shown below. The other lines demonstrate a test to make sure the install finished properly. (Do not use the `type="source"` option found in the Linux install.)

```
> 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"
```

6.2 Other Required Packages

Within R, run the following installs. (Do not use the type="source" option found in the Linux install.)

```
# 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("Cairo", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")
install.packages("epiR", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")
install.packages("gtools", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")
install.packages("mclust", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")
install.packages("squash", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")
install.packages("httr", dependencies=TRUE, repos = "http://cran.revolutionanalytics.com")

# install packages from Bioconductor (this installs to site-library so it is available for all users)
# if asked about updating a/s/n, choose "a" (all)
# this is at the R command
source("http://bioconductor.org/biocLite.R")
biocLite("limma", ask="a")
biocLite("RBGL", ask="a")
biocLite("graph", ask="a")
biocLite("Biobase", ask="a")
install.packages(c("oompaBase", "ClassDiscovery", "PreProcess"), dependencies=TRUE,
repos=c("http://cran.revolutionanalytics.com", "http://silicovore.com/OOMPA/"))

# install Vennerable from github (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("devtools", repos = "http://cran.revolutionanalytics.com")
library(devtools)
install_github("js229/Vennerable")

#Check that all packages installed properly. Should return [1] TRUE
all(c("Cairo", "epiR", "gtools", "mclust", "squash", "httr", "oompaBase", "ClassDiscovery", "PreProcess", "devtools", "limma", "RBGL", "graph", "Biobase") %in% installed.packages()[,1])
```

```
package 'utf8' successfully unpacked and MD5 sums checked
package 'assertthat' successfully unpacked and MD5 sums checked
package 'pillar' successfully unpacked and MD5 sums checked
package 'pkgconfig' successfully unpacked and MD5 sums checked
package 'lazyeval' successfully unpacked and MD5 sums checked
package 'promises' successfully unpacked and MD5 sums checked
package 'later' successfully unpacked and MD5 sums checked
package 'BH' successfully unpacked and MD5 sums checked
package 'cli' successfully unpacked and MD5 sums checked
package 'crayon' successfully unpacked and MD5 sums checked
package 'praise' successfully unpacked and MD5 sums checked
package 'rlang' successfully unpacked and MD5 sums checked
package 'tibble' successfully unpacked and MD5 sums checked
package 'hms' successfully unpacked and MD5 sums checked
package 'rex' successfully unpacked and MD5 sums checked
package 'httpuv' successfully unpacked and MD5 sums checked
package 'jpeg' successfully unpacked and MD5 sums checked
package 'testthat' successfully unpacked and MD5 sums checked
package 'readr' successfully unpacked and MD5 sums checked
package 'xml2' successfully unpacked and MD5 sums checked
package 'covr' successfully unpacked and MD5 sums checked
package 'httr' successfully unpacked and MD5 sums checked


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


7 Install RStudio

If desired, download and install the Windows RStudio from

(<https://www.rstudio.com/products/rstudio/download/#download>). RStudio is an integrated R environment for developers.

Installers for Supported Platforms

Installers	Size	Date	MD5
RStudio 1.1.453 - Windows Vista/7/8/10	85.8 MB	2018-05-16	bf287e385aef53829204023087e98735
Opening RStudio-1.1.453.exe	74.5 MB	2018-05-16	00a0088424ed06ac434f7a966f602b9c
You have chosen to open:	89.3 MB	2018-05-16	6cfd86770c7b6dbc13e66f4f59c299ce
 RStudio-1.1.453.exe	97.4 MB	2018-05-16	63e36e8138e369d19f9aaf4b0e995bbc
which is: Binary File (85.8 MB)	64.4 MB	2018-05-16	85b3e76c9fad4613bc9cf0de1f34b183
from: https://download1.rstudio.org	88.1 MB	2018-05-16	37cade7e162eab62483e6556e39dedee
Would you like to save this file?	90.6 MB	2018-05-16	44cddd285bc31c41e4eae1d74b8eebb
<input type="button" value="Save File"/> <input type="button" value="Cancel"/>			
Zip/tar archives	Size	Date	MD5
RStudio 1.1.453 - Windows Vista/7/8/10	122.9 MB	2018-05-16	c933e87a1cfla4852e67ebbd867c2bb
RStudio 1.1.453 - Ubuntu 12.04-15.10/Debian 8 (32-bit)	90 MB	2018-05-16	16e3347064194ed2a27f4f40139329e5
RStudio 1.1.453 - Ubuntu 12.04-15.10/Debian 8 (64-bit)	98.3 MB	2018-05-16	db60b00e15d235202466524cd0fbfc25
RStudio 1.1.453 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	88.8 MB	2018-05-16	546642e1fe826f09082fa9fb95e40a81
RStudio 1.1.453 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	91.4 MB	2018-05-16	8df70b969a1786d659826ee3e0da0113

8 Install MBatch Package

MBatch can be installed from GitHub using the following commands. (The devtools package was installed earlier.) Do not use the `install_git` option from the Linux instructions.

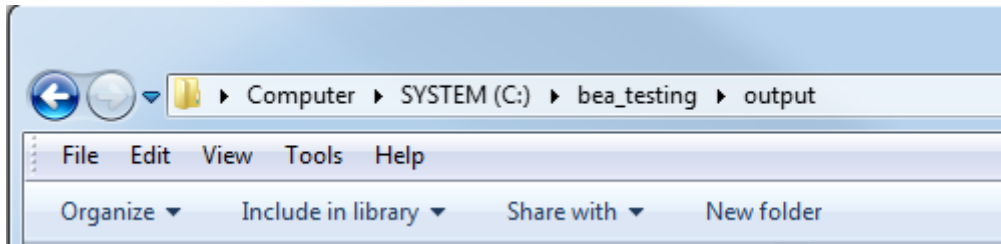
```
# Within R
library(devtools)
devtools::install_github("MD-Anderson-Bioinformatics/MBatch/package")
```

```
readAsGenericMatrix      html
readAsMatrix             html
setLogging               html
writeAsDataframe         html
writeAsMatrix            html
** building package indices
** testing if installed package can be loaded
*** arch - i386
Warning: replacing previous import 'oompaBase::grayscale' by 'squash::grayscale' when loading 'MBatch'
Warning: replacing previous import 'oompaBase::greyscale' by 'squash::greyscale' when loading 'MBatch'
*** arch - x64
Warning: replacing previous import 'oompaBase::grayscale' by 'squash::grayscale' when loading 'MBatch'
Warning: replacing previous import 'oompaBase::greyscale' by 'squash::greyscale' when loading 'MBatch'
* DONE (MBatch)
In R CMD INSTALL
> |
```

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`.

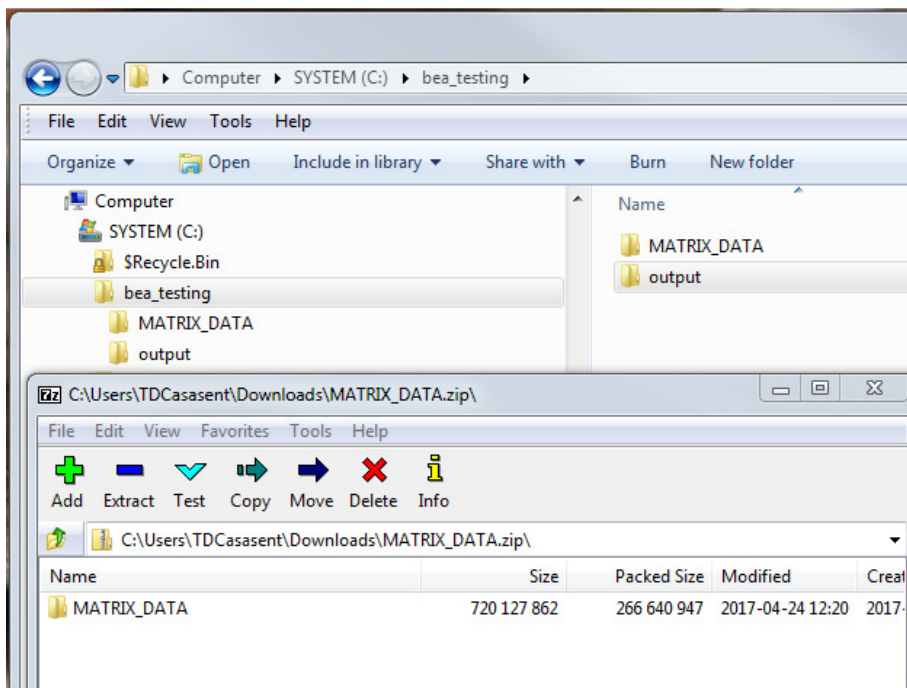
8.1 Create base directory for testing

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

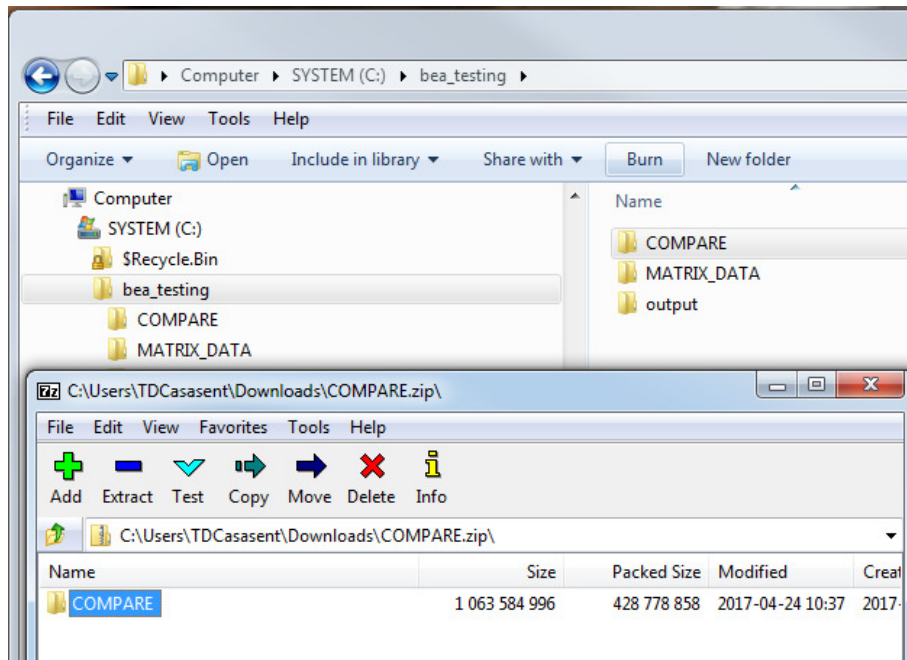


8.2 Populating Data for Tests

The zip file located at http://tcgaddata.mdanderson.org/std_archives/MATRIX_DATA.zip contains the data used by the tests. The folder in the ZIP is copied into c:\bea_testing.



The zip file located at http://tcgadata.mdanderson.org/std_archives/COMPARE.zip contains the data used to confirm the tests. The folder in the ZIP is copied into c:\bea_testing.



8.3 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"
> |
```