

# Installing RnBeads

in 3 easy steps

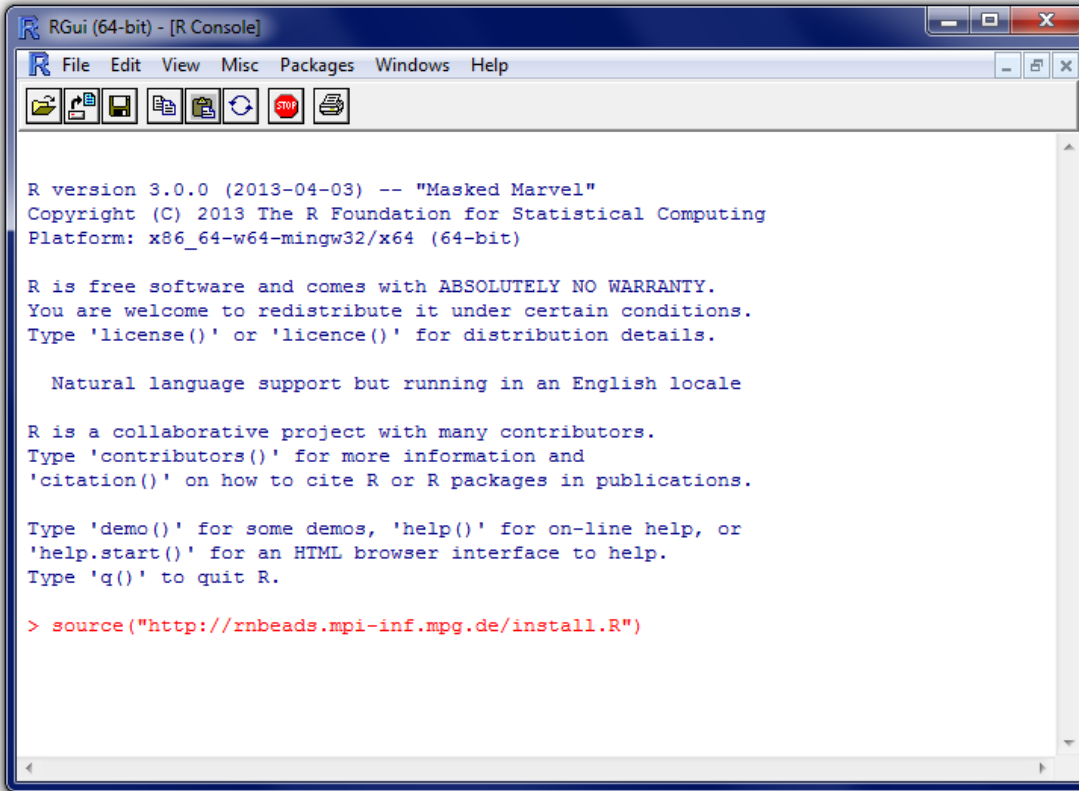


# Notice

The screenshots provided in this tutorial are from installing RnBeads in R 3.0.0 on Windows 7. However, the same steps apply for previous versions of R and other operating systems.



# Step 1 - Download



```
RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help

R version 3.0.0 (2013-04-03) -- "Masked Marvel"
Copyright (C) 2013 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> source("http://rnbeads.mpi-inf.mpg.de/install.R")
```

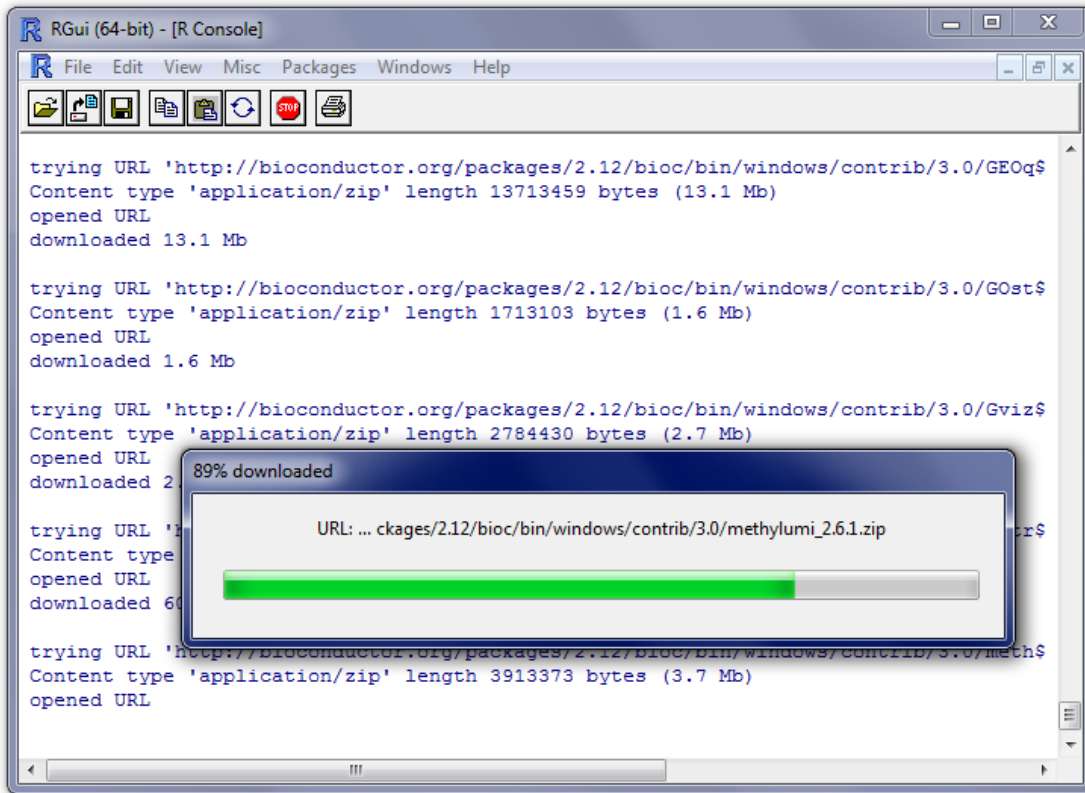
We provide an installation script that takes care of downloading and installing RnBeads.

All you need to do is start an [R](#) session and execute the script using the following command:

```
source("http://rnbeads.mpi-inf.mpg.de/install.R")
```



# Step 1 - Download



```
RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help

trying URL 'http://bioconductor.org/packages/2.12/bioc/bin/windows/contrib/3.0/GEOq$
Content type 'application/zip' length 13713459 bytes (13.1 Mb)
opened URL
downloaded 13.1 Mb

trying URL 'http://bioconductor.org/packages/2.12/bioc/bin/windows/contrib/3.0/GOst$
Content type 'application/zip' length 1713103 bytes (1.6 Mb)
opened URL
downloaded 1.6 Mb

trying URL 'http://bioconductor.org/packages/2.12/bioc/bin/windows/contrib/3.0/Gviz$
Content type 'application/zip' length 2784430 bytes (2.7 Mb)
opened URL
downloaded 2

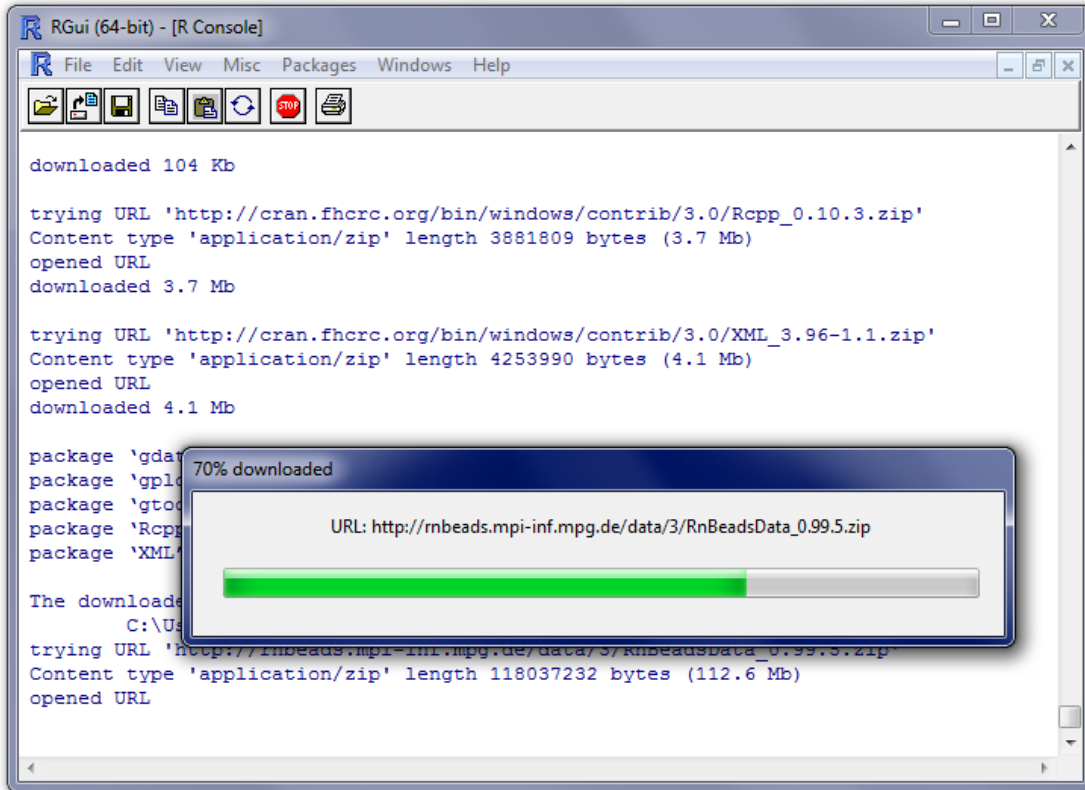
trying URL 'http://bioconductor.org/packages/2.12/bioc/bin/windows/contrib/3.0/methylumi_2.6.1.zip
Content type 'application/zip' length 3913373 bytes (3.7 Mb)
opened URL
```

The script first downloads all external packages used by RnBeads but not present in your current R installation.

These packages are downloaded from the repositories [CRAN](#) and [Bioconductor](#). Depending on the state of your R installation and your Internet connection speed, this may take 15 minutes or more.



# Step 1 - Download



```
downloaded 104 Kb

trying URL 'http://cran.fhcrc.org/bin/windows/contrib/3.0/Rcpp_0.10.3.zip'
Content type 'application/zip' length 3881809 bytes (3.7 Mb)
opened URL
downloaded 3.7 Mb

trying URL 'http://cran.fhcrc.org/bin/windows/contrib/3.0/XML_3.96-1.1.zip'
Content type 'application/zip' length 4253990 bytes (4.1 Mb)
opened URL
downloaded 4.1 Mb

package 'gdata'
package 'ggplot2'
package 'gtsummary'
package 'Rcpp'
package 'XML'

The downloaded source packages are in
  C:\Users\...
trying URL 'http://rnbeads.mpi-inf.mpg.de/data/3/RnBeadsData_0.99.5.zip'
Content type 'application/zip' length 118037232 bytes (112.6 Mb)
opened URL
```

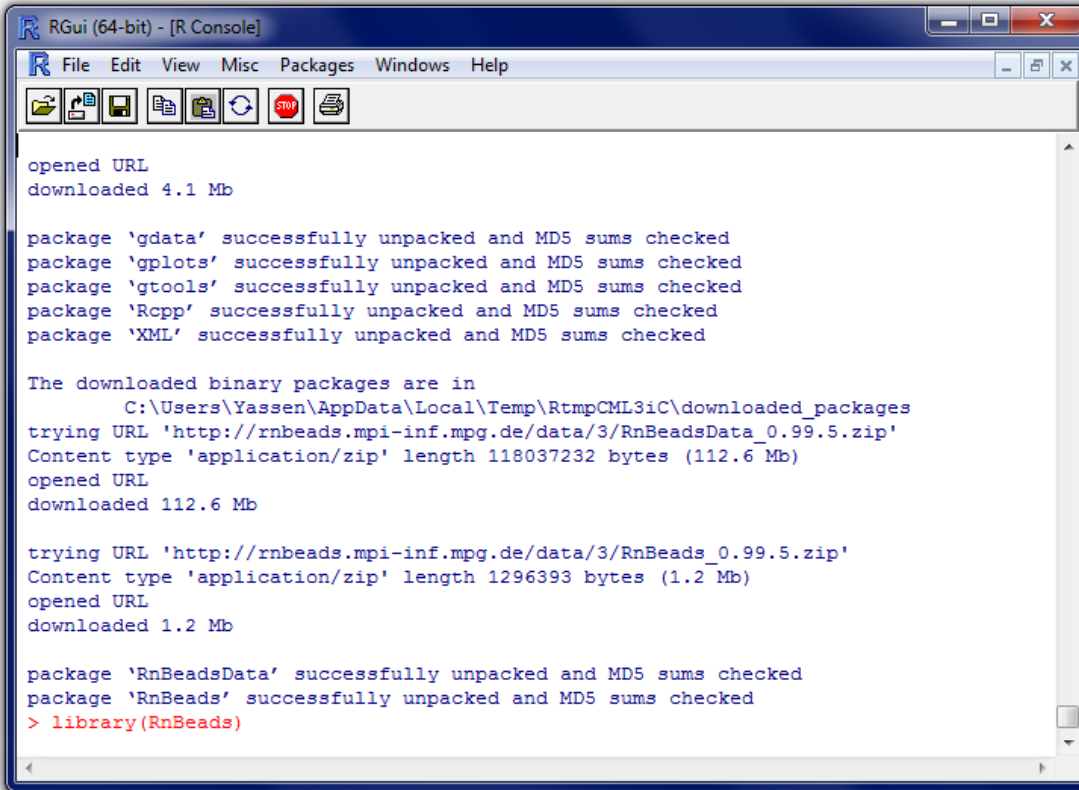
The script first downloads all external packages used by RnBeads but not present in your current R installation.

These packages are downloaded from the repositories [CRAN](#) and [Bioconductor](#). Depending on the state of your R installation and your Internet connection speed, this may take 15 minutes or more.

The last packages to be downloaded and installed are RnBeadsData and RnBeads from our pipeline's official website.



# Step 2 - Start



```
opened URL
downloaded 4.1 Mb

package 'gdata' successfully unpacked and MD5 sums checked
package 'gplots' successfully unpacked and MD5 sums checked
package 'gtools' successfully unpacked and MD5 sums checked
package 'Rcpp' successfully unpacked and MD5 sums checked
package 'XML' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
  C:\Users\Yassen\AppData\Local\Temp\RtmpCML3iC\downloaded_packages
trying URL 'http://rnbeads.mpi-inf.mpg.de/data/3/RnBeadsData_0.99.5.zip'
Content type 'application/zip' length 118037232 bytes (112.6 Mb)
opened URL
downloaded 112.6 Mb

trying URL 'http://rnbeads.mpi-inf.mpg.de/data/3/RnBeads_0.99.5.zip'
Content type 'application/zip' length 1296393 bytes (1.2 Mb)
opened URL
downloaded 1.2 Mb

package 'RnBeadsData' successfully unpacked and MD5 sums checked
package 'RnBeads' successfully unpacked and MD5 sums checked
> library(RnBeads)
```

After downloading and unpacking all files, RnBeads is included as a package in your R installation.

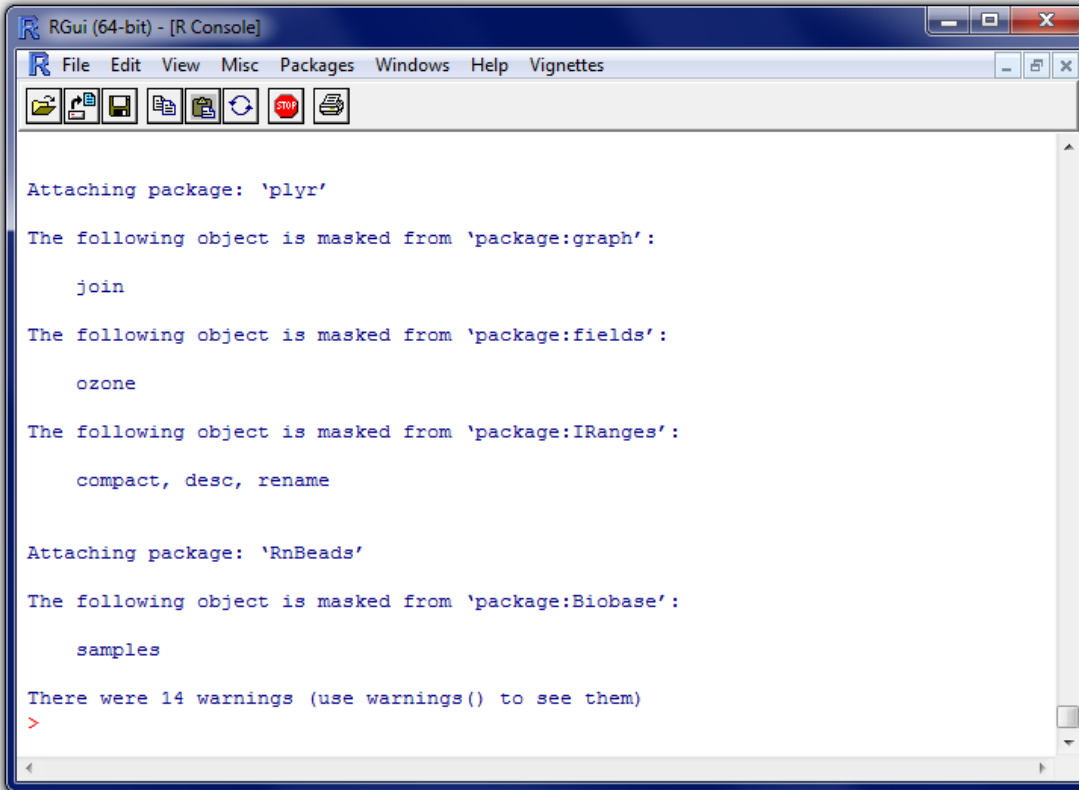
You might see a warning message that RnBeads requires [Ghostscript](#) to be installed and accessible from R. This is what we are going to test now.

We are going to load RnBeads and attempt to create a simple plot. In order to load RnBeads, type the following command in the R session:

```
library(RnBeads)
```



# Step 3 - Validate

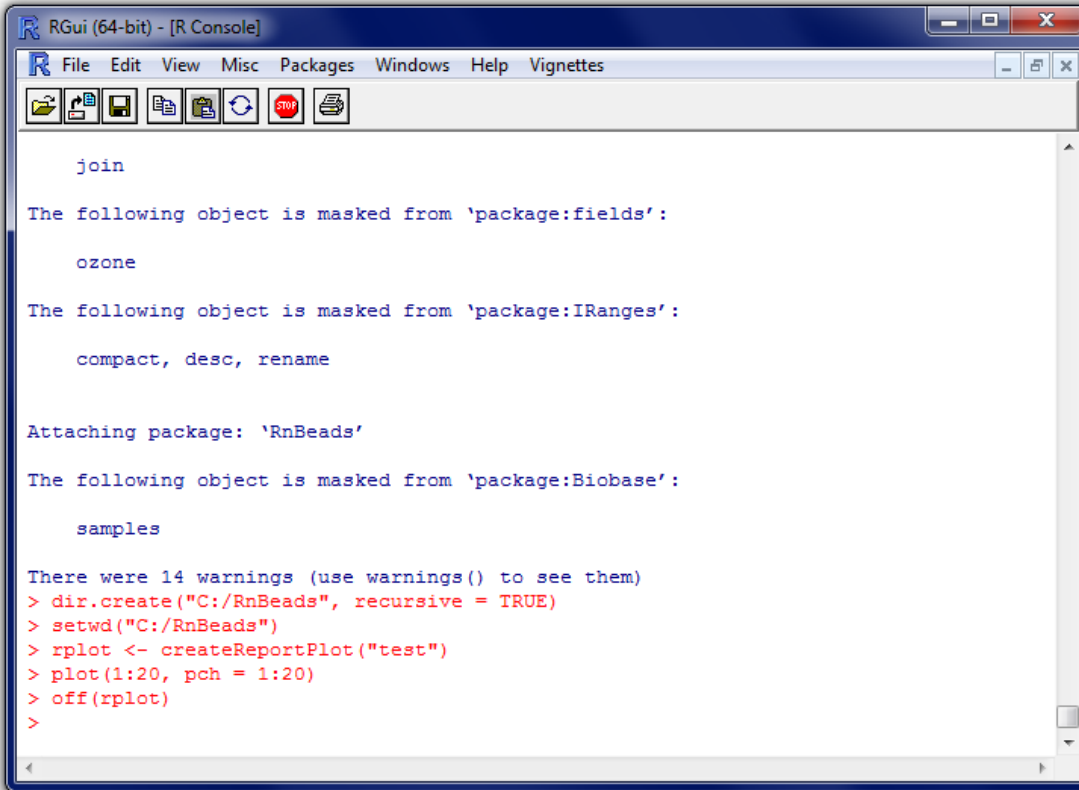


```
RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help Vignettes
Attaching package: 'plyr'
The following object is masked from 'package:graph':
  join
The following object is masked from 'package:fields':
  ozone
The following object is masked from 'package:IRanges':
  compact, desc, rename
Attaching package: 'RnBeads'
The following object is masked from 'package:Biobase':
  samples
There were 14 warnings (use warnings() to see them)
>
```

Upon loading RnBeads, you will probably see several warning messages (related to masked and replaced functions). You can safely ignore them.



# Step 3 - Validate



```
join

The following object is masked from 'package:fields':

  ozone

The following object is masked from 'package:IRanges':

  compact, desc, rename

Attaching package: 'RnBeads'

The following object is masked from 'package:Biobase':

  samples

There were 14 warnings (use warnings() to see them)
> dir.create("C:/RnBeads", recursive = TRUE)
> setwd("C:/RnBeads")
> rplot <- createReportPlot("test")
> plot(1:20, pch = 1:20)
> off(rplot)
>
```

Upon loading RnBeads, you will probably see several warning messages (related to masked and replaced functions). You can safely ignore them.

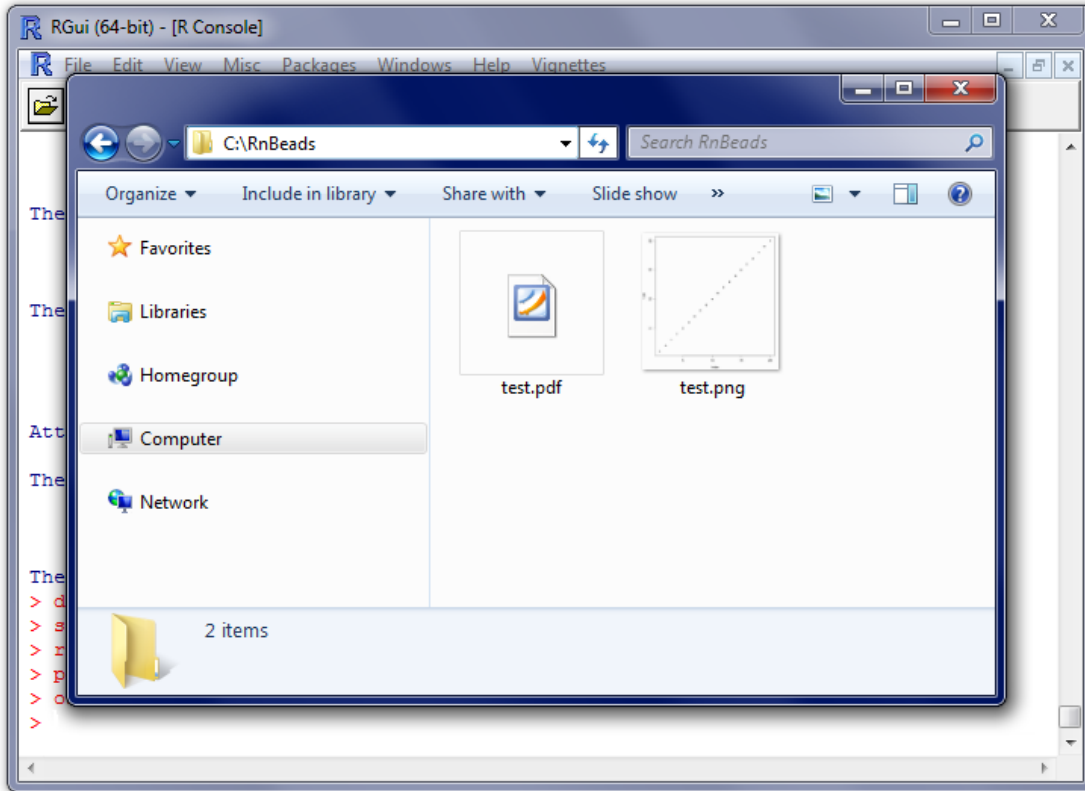
In this last step, you need to create a new temporary directory and save a simple plot in it, in order to make sure that your R installation can access and use Ghostscript. In the code snippet below, the temporary directory is **C:/RnBeads**.

```
dir.create("C:/RnBeads", recursive = TRUE)
setwd("C:/RnBeads")
rplot <- createReportPlot("test")
plot(1:20, pch = 1:20)
off(rplot)
```





# Step 3 - Validate



Now check the contents of the newly created directory, and you will see two files containing our simple plot – a PDF and a PNG file.

If creating the plot resulted in an error in your R session, please check the Ghostscript-related section in the FAQ page on our website:

[rnbeads.mpi-inf.mpg.de/faq.php](http://rnbeads.mpi-inf.mpg.de/faq.php)

