

BioCPR - A tool for correlation plots

BioCPR is an open-source application written in the R programming language. To run BioCPR in a personal system the primary requirement is the latest version of R and R-studio. This supplementary file provides information on how to install R, R-studio and run BioCPR.

Step 1: Installing R

Download and install R by visiting <https://cran.r-project.org/> and select an installer for your operating system.



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[FAQs](#)
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The Comprehensive R Archive Network

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Download R for Linux](#)
- [Download R for \(Mac\) OS X](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2021-05-18, Camp Pontanezen) [R-4.1.0.tar.gz](#), read [what's new](#) in the latest version.
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#)

Questions About R

- If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

What are R and CRAN?

R is 'GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the [R project homepage](#) for further information.

CRAN is a network of ftp and web servers around the world that store identical, up-to-date, versions of code and documentation for R. Please use the CRAN [mirror](#) nearest to you to minimize network load.

Supplementary Figure S1: Screenshot of the download page on the official R website [<https://cran.r-project.org/>].

Step 2: Installing Rstudio

Download RStudio from <https://www.rstudio.com/products/rstudio/download/> for your operating system. RStudio Desktop is sufficient for personal users.

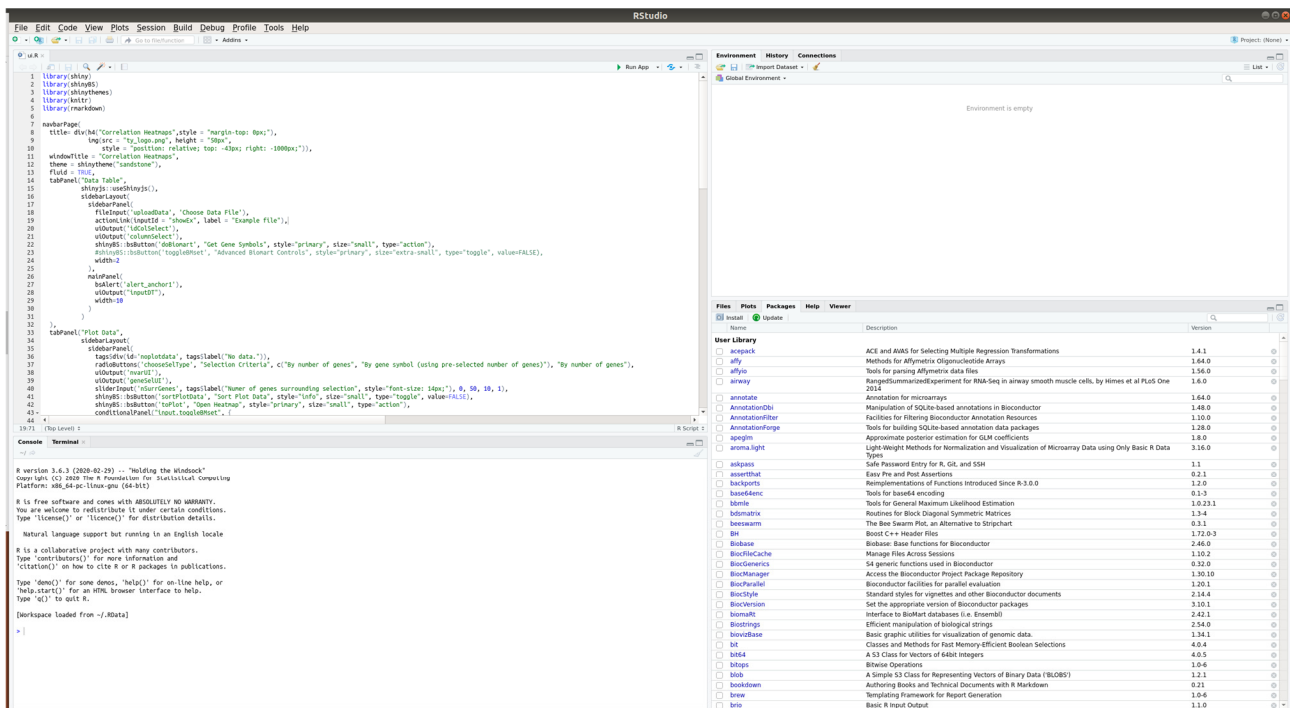
	RStudio Desktop Open Source License	RStudio Desktop Pro Commercial License	RStudio Server Open Source License	RStudio Server Pro Commercial License
	Free	\$995 /year	Free	\$4,975 /year (5 Named Users)
	DOWNLOAD Learn more	BUY Learn more	DOWNLOAD Learn more	BUY Evaluation Learn more
Integrated Tools for R	✓	✓	✓	✓
Priority Support		✓		✓
Access via Web Browser			✓	✓
RStudio Professional Drivers		✓		✓
Connect to RStudio Server Pro remotely		✓		
Enterprise Security				✓
Project Sharing				✓
Manage Multiple R Sessions & Versions				✓
Admin Dashboard				✓
Load Balancing				✓
Auditing and Monitoring				✓
Data Connectivity				✓
Launcher				✓
Tutorial API				✓
License	AGPL	Commercial	AGPL	Commercial

Supplementary Figure S2: Screenshot of the download page on the official RStudio website [<https://rstudio.com/products/rstudio/download/>].

Note: A detailed instruction on installing R and Rstudio on various operating system can be found in the following tutorial; <https://www.datacamp.com/community/tutorials/installing-R-windows-mac-ubuntu>

Step 3: Checking and setting working directory

Check if R and Rstudio are properly working and set the working directory to the folder all the BioCPR files are located (if the git repository is already downloaded).



Supplementary Figure S3: Screenshot of the RStudio startup page.

Step 4: Installing required libraries

Install the required libraries for running BioCPR.

You can install the stable version from CRAN and it will install all the necessary dependencies for running the tool. Please find the commands below;

```
install.packages("heatmapFlex")
install.packages("convertid")
install.packages("readmoRe")
install.packages("coreheat")
```

If you prefer to install the latest development version, there are 4 custom in-built libraries that needs to be installed in addition to libraries from CRAN and BioConductor. Please find the commands below;

```
.libPaths()
libLocation <- .libPaths()[1]

## CRAN packages ##
cranPackages <- c("shinyBS", "shinythemes", "knitr", "rmarkdown", "shinyjs", "plyr", "RColorBrewer",
"R.utils", "gdata", "data.table", "foreach", "ggplot2", "scales", "curl", "openssl", "httr", "Rcurl", "XML",
"WGCNA", "DT", "devtools")
sapply(cranPackages, install.packages, lib = libLocation)

## Bioconductor packages ##

bioConPackages <- c("AnnotationDbi", "biomaRt", "org.Hs.eg.db", "org.Mm.eg.db", "Heatplus", "genefilter",
"impute", "preprocessCore", "GO.db")

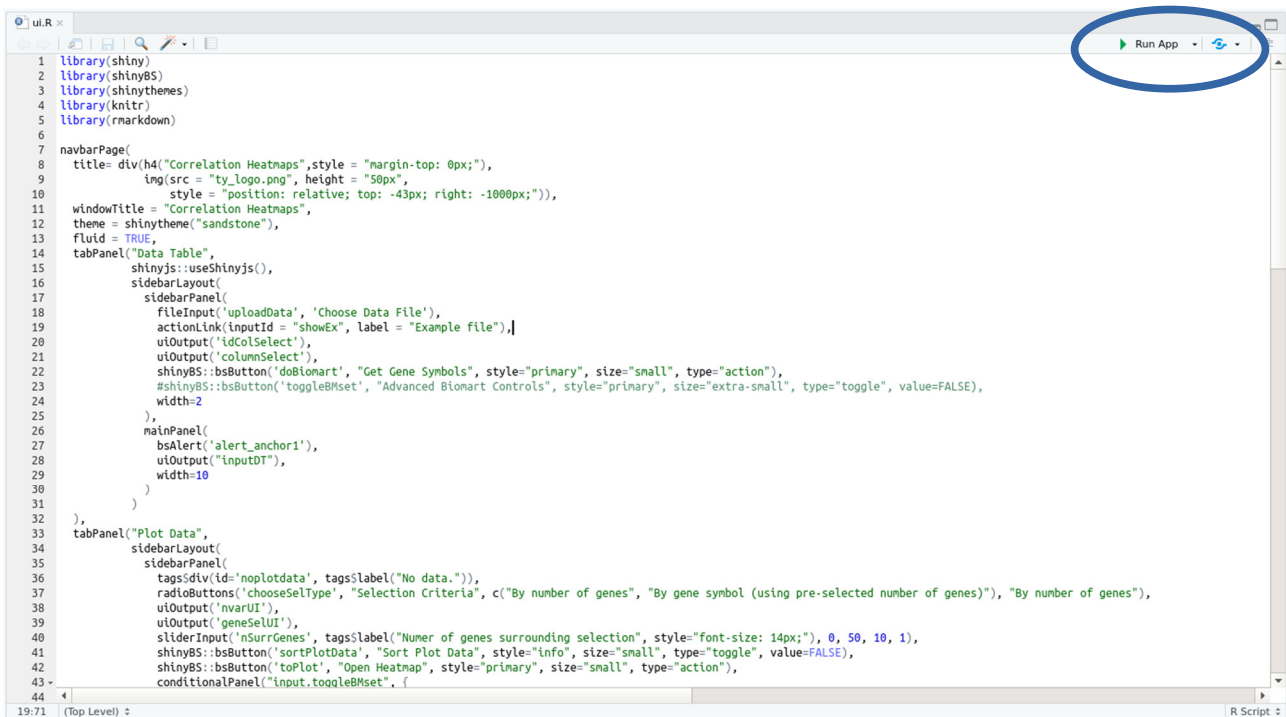
if (!requireNamespace("BiocManager", quietly = TRUE))
install.packages("BiocManager")
BiocManager::install(bioConPackages)
```

```
## In-house packages ##
```

```
install_github("vfey/heatmapFlex")  
install_github("vfey/convertid")  
install_github("vfey/readmoRe")  
install_github("vfey/coreheat")
```

Step 5: Run BioCPR

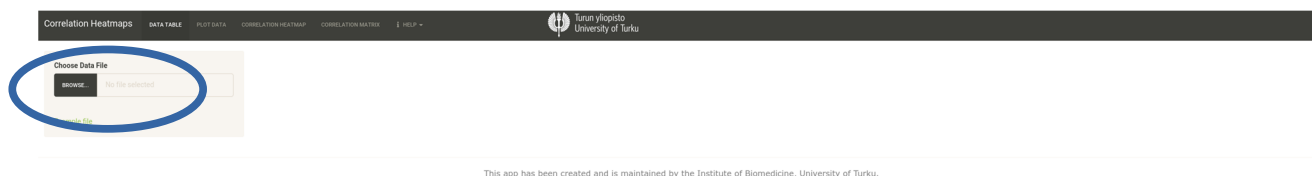
- Download the [git repository](#) and extract the files from the zip file.
- Set the working directory in Rstudio to the BioCPR folder downloaded from github and open the ui.R file in Rstudio.
- After opening the file in Rstudio, A “run App” button should appear and clicking the button will open the BioCPR app in a new screen.



Supplementary Figure S4: Screenshot of the ui.R file in the RStudio interface with the “Run App” button highlighted.

Step 6: Using BioCPR

1. Upon running, the BioCPR interface is initiated. The BioCPR interface is depicted in supplementary Figure S5. You can choose the browse button in the app to upload the sample dataset provided in the git bundle.



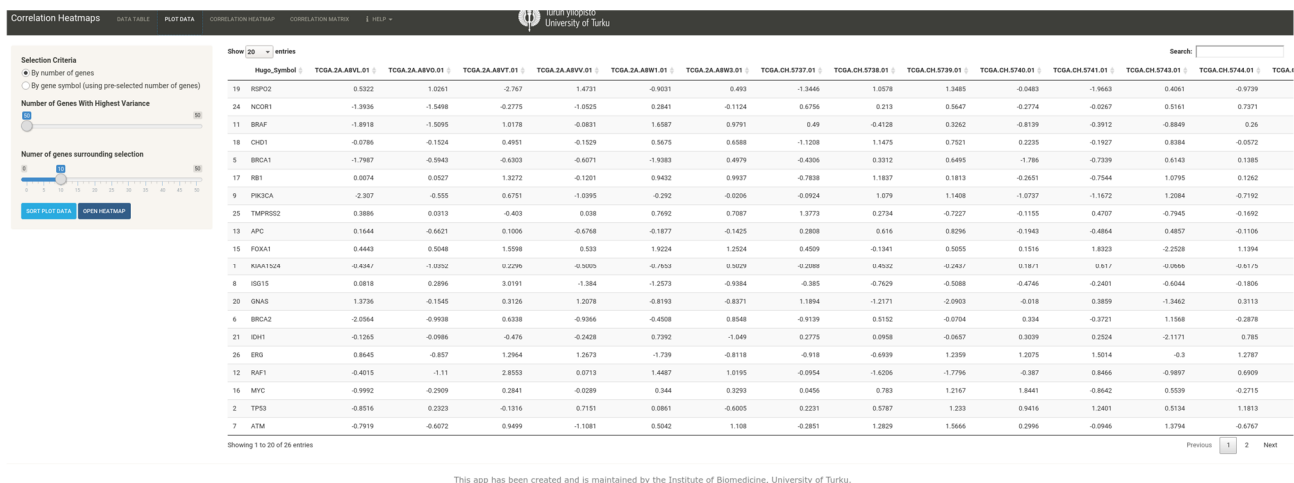
Supplementary Figure S5: Screenshot of the startup page of BioCPR tool.

- Upon uploading the file, the app shows the contents of the file on the right side of the window and the option to select the ID column on the left along with the sample names in the file.

Sample 1	Sample 2	Correlation
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000
TCGA_2A.ARV1.01	TCGA_2A.ARV1.01	1.0000

Supplementary Figure S6: Screenshot of the startup page of BioCPR tool after loading the dataset.

- After reviewing the dataset, we move on to the “PLOT DATA” tab where we select the data to be plotted in the heatmap (Figure S7). We can select either by limiting the number of genes with highest variance between them or by using gene symbol to select required genes while also including genes surrounding them using the “Number of genes surrounding selection” option (Figure S8).



Supplementary Figure S7: Screenshot of the “PLOT DATA” tab where we select the genes for plotting.

Selection Criteria

☐ By number of genes

☒ By gene symbol (using pre-selected number of genes)

Number of Genes With Highest Variance

50

Select gene to display

APC ATM BRCA1

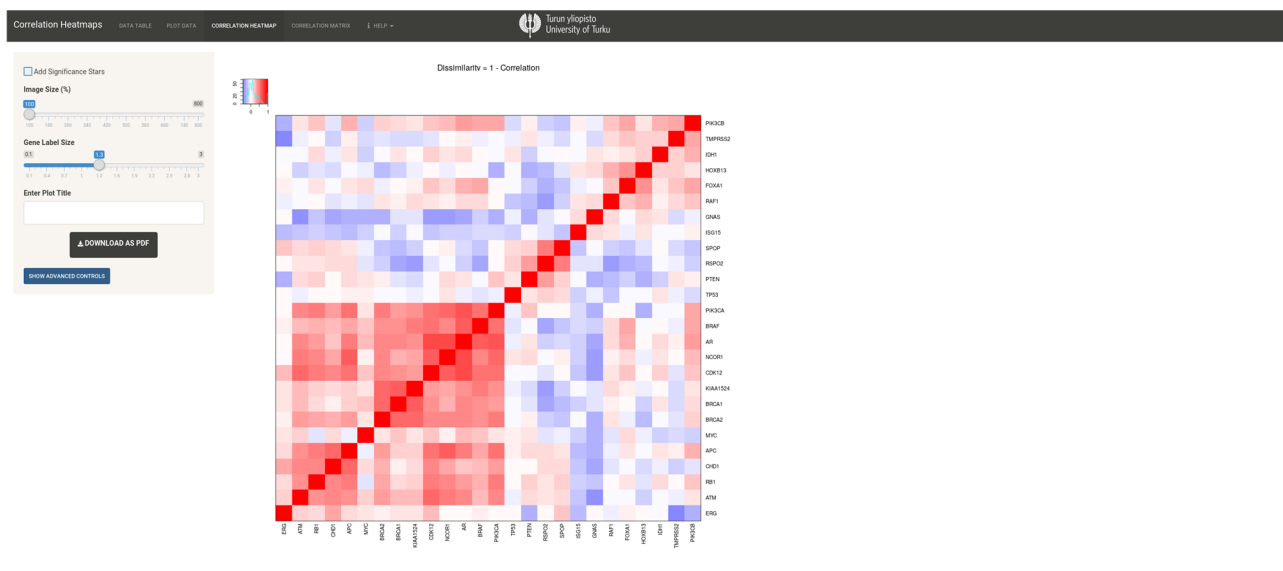
Number of genes surrounding selection

0 50

SORT PLOT DATA OPEN HEATMAP

Supplementary Figure S8: Screenshot of the selection criteria under the plot data tab.

- After selecting the required genes you want to plot, you then move on to the “CORRELATION HEATMAP” tab. Here you can see a visualization of the heatmap of the data selected in the “PLOT DATA” tab (Figure S9). Here you can notice heatmap on the right and the options to edit the heatmap on the left (Figure S10).

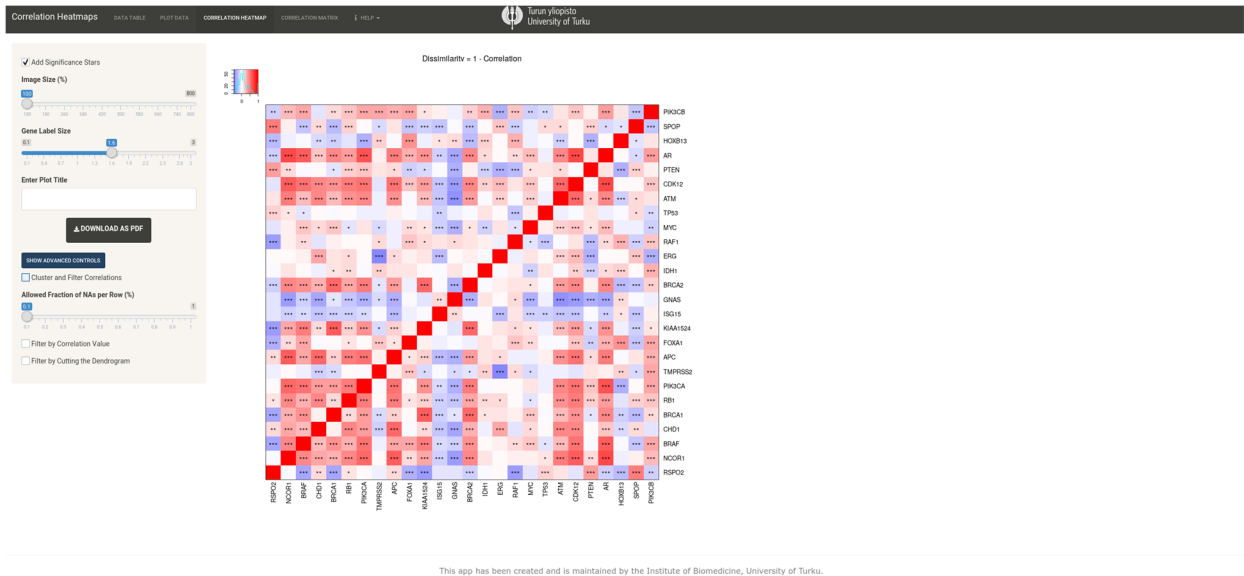


This app has been created and is maintained by the Institute of Biomedicine, University of Turku.

Supplementary Figure S9: Screenshot of the correlation heatmaps generated from data selected in “PLOT DATA” tab.

This screenshot shows the control panel for the 'CORRELATION HEATMAP' tab. It features a checkbox for 'Add Significance Stars'. Below it is a slider for 'Image Size (%)' with a range from 100 to 800 and a current value of 100. Another slider for 'Gene Label Size' has a range from 0.1 to 3 and a current value of 1.3. There is a text input field for 'Enter Plot Title'. At the bottom, there are two buttons: 'DOWNLOAD AS PDF' and 'SHOW ADVANCED CONTROLS'.

Supplementary Figure S10: Screenshot of the options under “CORRELATION HEATMAP” tab.



Supplementary Figure S11: Screenshot of the heatmap with significance stars added.

Using options tab, various parameters of the heatmap can be altered including:

1. Adding significance stars to the heatmap (Figure S11).
2. Adjusting the image size
3. Adjusting the gene label size
4. Advanced options such as removing clustering, filtering by correlation value, cutting the heatmap into dendrogram trees (Figure S12)

☒ Add Significance Stars

Image Size (%)

100 800

100 180 260 340 420 500 580 660 740 800

Gene Label Size

0.1 1.6 3

0.1 0.4 0.7 1 1.3 1.6 1.9 2.2 2.5 2.8 3

Enter Plot Title

[↓ DOWNLOAD AS PDF](#)

[SHOW ADVANCED CONTROLS](#)

☐ Cluster and Filter Correlations

Allowed Fraction of NAs per Row (%)

0.1 1

0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

☒ Filter by Correlation Value

Correlation Filter Threshold

-1 0.5 1

-1 -0.8 -0.6 -0.4 -0.2 0 0.2 0.4 0.6 0.8 1

Correlation Filter Margin per Row (%)

0.05 1

0.001 0.101 0.201 0.301 0.401 0.501 0.601 0.701 0.801 0.901 1

☒ Filter by Cutting the Dendrogram

Threshold for Tree Cutting

0 1 2

0 0.2 0.4 0.6 0.8 1 1.2 1.4 1.6 1.8 2

Number of Genes on a Tree Branch to be Considered a Cluster

1 100

1 11 21 31 41 51 61 71 81 91 100

Supplementary Figure S12: Screenshot of the advanced options for editing heatmap.

5. After editing the heatmap as per our requirements, we can enter a title for our plot and download the edited heatmap using the download button.
6. We can also view the correlation matrix that was used to create the heatmap in the “CORRELATION MATRIX” tab (Figure S13).



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Supplementary Figure S13: Screenshot of the “CORRELATION MATRIX” tab.

7. Finally the help tab, provides a information on frequently asked questions and the format of the data required.

R session information:

— Session info

setting value

version R version 3.5.2 (2018-12-20)

os Ubuntu 18.04.1 LTS

system x86_64, linux-gnu

ui RStudio

language (EN)

collate en_US.UTF-8

ctype en_US.UTF-8

tz Europe/Helsinki

date 2019-01-08

— Packages

package	* version	date	lib source
acepack	1.4.1	2016-10-29 [1]	CRAN (R 3.5.1)
annotate	1.58.0	2018-11-14 [1]	Bioconductor
AnnotationDbi	* 1.42.1	2018-11-14 [1]	Bioconductor
assertthat	0.2.0	2017-04-11 [1]	CRAN (R 3.5.1)
backports	1.1.2	2017-12-13 [1]	CRAN (R 3.5.1)
base64enc	0.1-4	2018-11-14 [1]	local
bindr	0.1.1	2018-03-13 [1]	CRAN (R 3.5.1)
bindrcpp	0.2.2	2018-03-29 [1]	CRAN (R 3.5.1)
Biobase	* 2.40.0	2018-11-14 [1]	Bioconductor
BiocGenerics	* 0.26.0	2018-11-14 [1]	Bioconductor
biomaRt	* 2.36.1	2018-11-14 [1]	Bioconductor
bit	1.1-14	2018-05-29 [1]	CRAN (R 3.5.1)
bit64	0.9-7	2017-05-08 [1]	CRAN (R 3.5.1)
bitops	1.0-6	2013-08-17 [1]	CRAN (R 3.5.1)
blob	1.1.1	2018-03-25 [1]	CRAN (R 3.5.1)
checkmate	1.8.5	2017-10-24 [1]	CRAN (R 3.5.1)
cli	1.0.1	2018-09-25 [1]	CRAN (R 3.5.1)
clipr	* 0.4.1	2018-06-23 [1]	CRAN (R 3.5.2)
cluster	* 2.0.7-1	2018-04-09 [1]	CRAN (R 3.5.1)
codetools	0.2-16	2018-12-24 [4]	CRAN (R 3.5.2)
colorspace	1.4-0	2018-11-05 [1]	R-Forge (R 3.5.1)
coreheat	* 0.1-5	2018-11-14 [2]	local

crayon	1.3.4	2017-09-16 [1]	CRAN (R 3.5.1)
data.table	* 1.11.8	2018-09-30 [1]	CRAN (R 3.5.1)
DBI	1.0.0	2018-05-02 [1]	CRAN (R 3.5.1)
DEoptimR	1.0-8	2016-11-19 [1]	CRAN (R 3.5.1)
digest	* 0.6.18	2018-10-10 [1]	CRAN (R 3.5.1)
doParallel	1.0.14	2018-09-21 [2]	R-Forge (R 3.5.1)
dplyr	0.7.8	2018-11-10 [1]	CRAN (R 3.5.1)
DT	* 0.5	2018-11-05 [2]	CRAN (R 3.5.1)
dynamicTreeCut	1.63-1	2016-03-11 [2]	CRAN (R 3.5.1)
evaluate	0.12	2018-10-09 [1]	CRAN (R 3.5.1)
fastcluster	1.1.25	2018-06-07 [1]	CRAN (R 3.5.1)
fit.models	0.5-14	2017-04-06 [2]	CRAN (R 3.5.1)
foreach	* 1.5.1	2018-08-27 [1]	R-Forge (R 3.5.1)
foreign	0.8-71	2018-07-20 [4]	CRAN (R 3.5.1)
Formula	1.2-3	2018-05-03 [1]	CRAN (R 3.5.1)
gdata	2.18.0	2017-06-06 [1]	CRAN (R 3.5.1)
genefilter	* 1.62.0	2018-11-14 [1]	Bioconductor
ggplot2	* 3.1.0	2018-10-25 [1]	CRAN (R 3.5.1)
glue	1.3.0	2018-07-17 [1]	CRAN (R 3.5.1)
GO.db	3.6.0	2018-11-14 [1]	Bioconductor
gridExtra	2.3	2017-09-09 [1]	CRAN (R 3.5.1)
gtable	0.2.0	2016-02-26 [1]	CRAN (R 3.5.1)
gtools	3.8.1	2018-06-26 [1]	CRAN (R 3.5.1)
heatmapGen	* 0.1-0	2018-11-14 [2]	local
heatmapGen2	* 0.1-3	2018-11-14 [2]	local
Heatplus	* 2.26.0	2018-11-14 [1]	Bioconductor
Hmisc	4.1-1	2018-01-03 [1]	CRAN (R 3.5.1)
hms	0.4.2	2018-03-10 [1]	CRAN (R 3.5.1)
htmlTable	1.12	2018-05-26 [1]	CRAN (R 3.5.1)

htmltools	0.3.6	2017-04-28 [1]	CRAN (R 3.5.1)
htmlwidgets	1.3	2018-09-30 [1]	CRAN (R 3.5.1)
httpuv	1.4.5	2018-07-19 [1]	CRAN (R 3.5.1)
httr	1.3.1	2017-08-20 [1]	CRAN (R 3.5.1)
impute	1.54.0	2018-11-14 [2]	Bioconductor
IRanges	* 2.14.12	2018-09-20 [1]	Bioconductor
iterators	1.0.11	2018-07-05 [1]	R-Forge (R 3.5.1)
jsonlite	1.5	2017-06-01 [1]	CRAN (R 3.5.1)
knitr	* 1.20	2018-02-20 [1]	CRAN (R 3.5.1)
later	0.7.5	2018-09-18 [1]	CRAN (R 3.5.1)
lattice	0.20-38	2018-11-04 [4]	CRAN (R 3.5.1)
latticeExtra	0.6-28	2016-02-09 [1]	CRAN (R 3.5.1)
lazyeval	0.2.1	2017-10-29 [1]	CRAN (R 3.5.1)
magrittr	1.5	2014-11-22 [1]	CRAN (R 3.5.1)
markdown	0.8.1	2018-11-14 [1]	local
MASS	7.3-51.1	2018-11-01 [4]	CRAN (R 3.5.1)
Matrix	1.2-15	2018-11-01 [4]	CRAN (R 3.5.1)
matrixStats	0.54.0	2018-07-23 [1]	CRAN (R 3.5.1)
medseqr	* 0.4-10	2018-11-14 [2]	local
memoise	1.1.0	2017-04-21 [1]	CRAN (R 3.5.1)
mime	0.6.1	2018-11-14 [1]	local
munsell	0.5.0	2018-06-12 [1]	CRAN (R 3.5.1)
mvtnorm	1.0-8	2018-05-31 [1]	CRAN (R 3.5.1)
nnet	7.3-12	2016-02-02 [4]	CRAN (R 3.5.0)
org.Hs.eg.db	* 3.6.0	2018-11-14 [1]	Bioconductor
org.Mm.eg.db	* 3.6.0	2018-11-14 [1]	Bioconductor
PAMhm	* 0.1-1	2018-11-14 [2]	local
pander	* 0.6.3	2018-11-06 [1]	CRAN (R 3.5.2)
pcaPP	1.9-73	2018-01-14 [1]	CRAN (R 3.5.1)

pillar	1.3.0	2018-07-14 [1]	CRAN (R 3.5.1)
pkgconfig	2.0.2	2018-08-16 [1]	CRAN (R 3.5.1)
plyr	* 1.8.4	2016-06-08 [1]	CRAN (R 3.5.1)
preprocessCore	1.42.0	2018-11-14 [1]	Bioconductor
prettyunits	1.0.2	2015-07-13 [1]	CRAN (R 3.5.1)
progress	1.2.0	2018-06-14 [1]	CRAN (R 3.5.1)
promises	1.0.1	2018-04-13 [1]	CRAN (R 3.5.1)
purrr	0.2.5	2018-05-29 [1]	CRAN (R 3.5.1)
R.methodsS3	* 1.7.1	2016-02-16 [1]	CRAN (R 3.5.1)
R.oo	* 1.22.0	2018-04-22 [1]	CRAN (R 3.5.1)
R.utils	* 2.7.0	2018-08-27 [1]	CRAN (R 3.5.1)
R6	2.3.0	2018-10-04 [1]	CRAN (R 3.5.1)
RColorBrewer	* 1.1-2	2014-12-07 [1]	CRAN (R 3.5.1)
Rcpp	1.0.0	2018-11-07 [1]	CRAN (R 3.5.1)
RCurl	1.96-0	2018-11-14 [1]	local
readR	* 0.2-1	2018-11-14 [2]	local
rlang	0.3.0.1	2018-10-25 [1]	CRAN (R 3.5.1)
rmarkdown	* 1.10	2018-06-11 [1]	CRAN (R 3.5.1)
robust	0.4-18	2017-04-27 [2]	R-Forge (R 3.5.1)
robustbase	0.93-3	2018-09-21 [1]	CRAN (R 3.5.1)
rpart	4.1-13	2018-02-23 [4]	CRAN (R 3.5.0)
rprojroot	1.3-2	2018-01-03 [1]	CRAN (R 3.5.1)
rrcov	1.4-7	2018-11-15 [1]	CRAN (R 3.5.1)
RSQLite	2.1.1	2018-05-06 [1]	CRAN (R 3.5.1)
rstudioapi	0.8	2018-10-02 [1]	CRAN (R 3.5.1)
S4Vectors	* 0.18.3	2018-11-14 [1]	Bioconductor
scales	* 1.0.0	2018-08-09 [1]	CRAN (R 3.5.1)
sessioninfo	1.1.1	2018-11-05 [1]	CRAN (R 3.5.1)
shiny	* 1.2.0	2018-11-02 [1]	CRAN (R 3.5.1)

shinyBS	* 0.61	2015-03-31 [1] CRAN (R 3.5.1)
shinyjs	1.0	2018-01-08 [1] CRAN (R 3.5.1)
shinythemes	* 1.1.2	2018-11-06 [1] CRAN (R 3.5.1)
stringi	1.2.4	2018-07-20 [1] CRAN (R 3.5.1)
stringr	1.3.1	2018-05-10 [1] CRAN (R 3.5.1)
survival	2.43-3	2018-11-26 [4] CRAN (R 3.5.1)
tibble	1.4.2	2018-01-22 [1] CRAN (R 3.5.1)
tidyselect	0.2.5	2018-10-11 [1] CRAN (R 3.5.1)
WGCNA	1.66	2018-10-24 [2] CRAN (R 3.5.1)
withr	2.1.2	2018-03-15 [1] CRAN (R 3.5.1)
XML	3.99-0	2018-11-14 [1] local
xtable	1.8-3	2018-08-29 [1] CRAN (R 3.5.1)
yaml	2.2.0	2018-07-25 [1] CRAN (R 3.5.1)