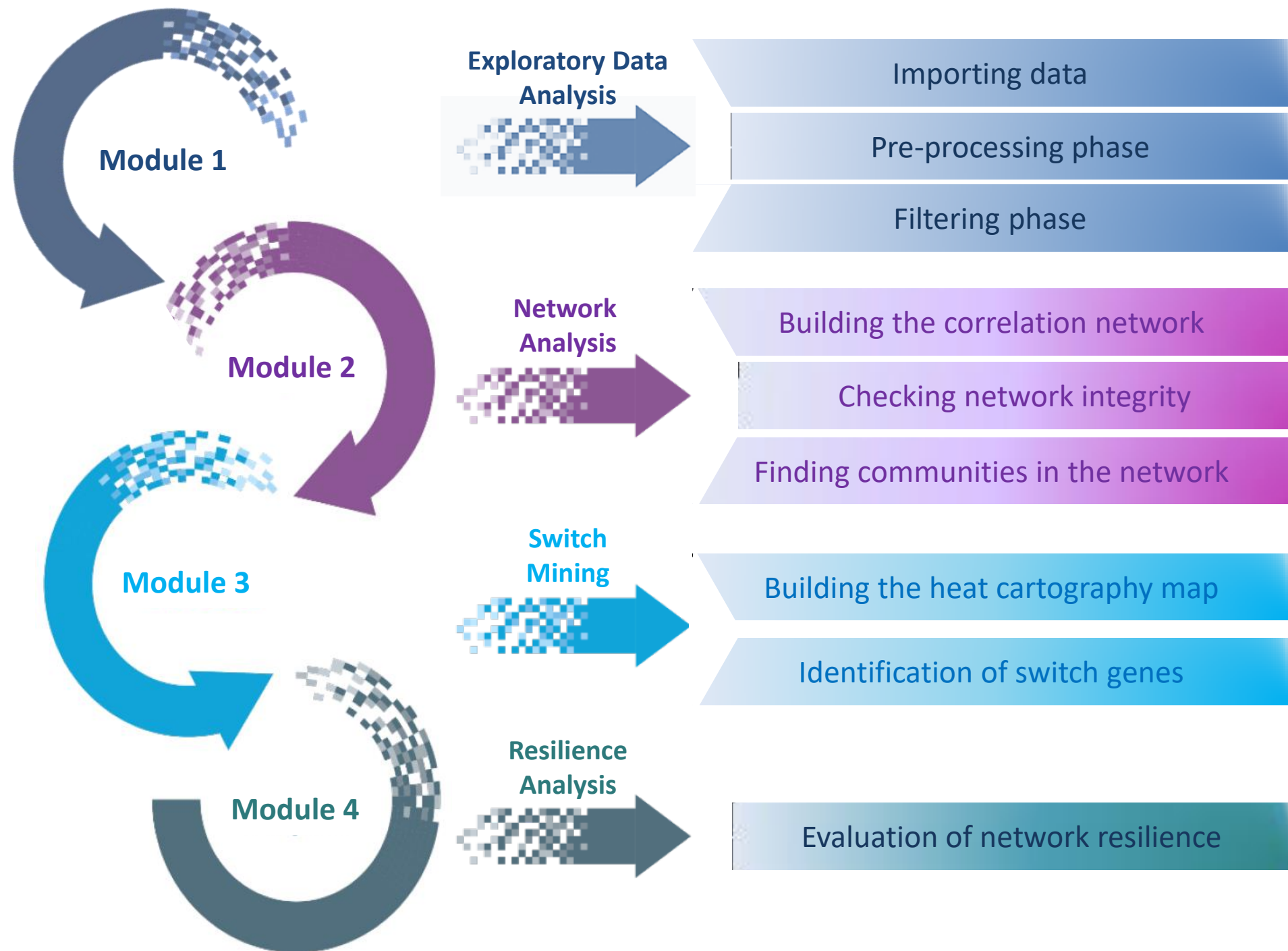




S w I M m e R

SWItchMineR





Module 0: Architecture



SWIMmeR is an open-source R package for the identification of a small pool of genes, called **switch genes**, which are likely to be critically associated with drastic changes in many biological settings.



SWIMmeR is the R implementation of SWIM
(Scientific Reports:7, Article number: 44797 (2017))

GETTING STARTED

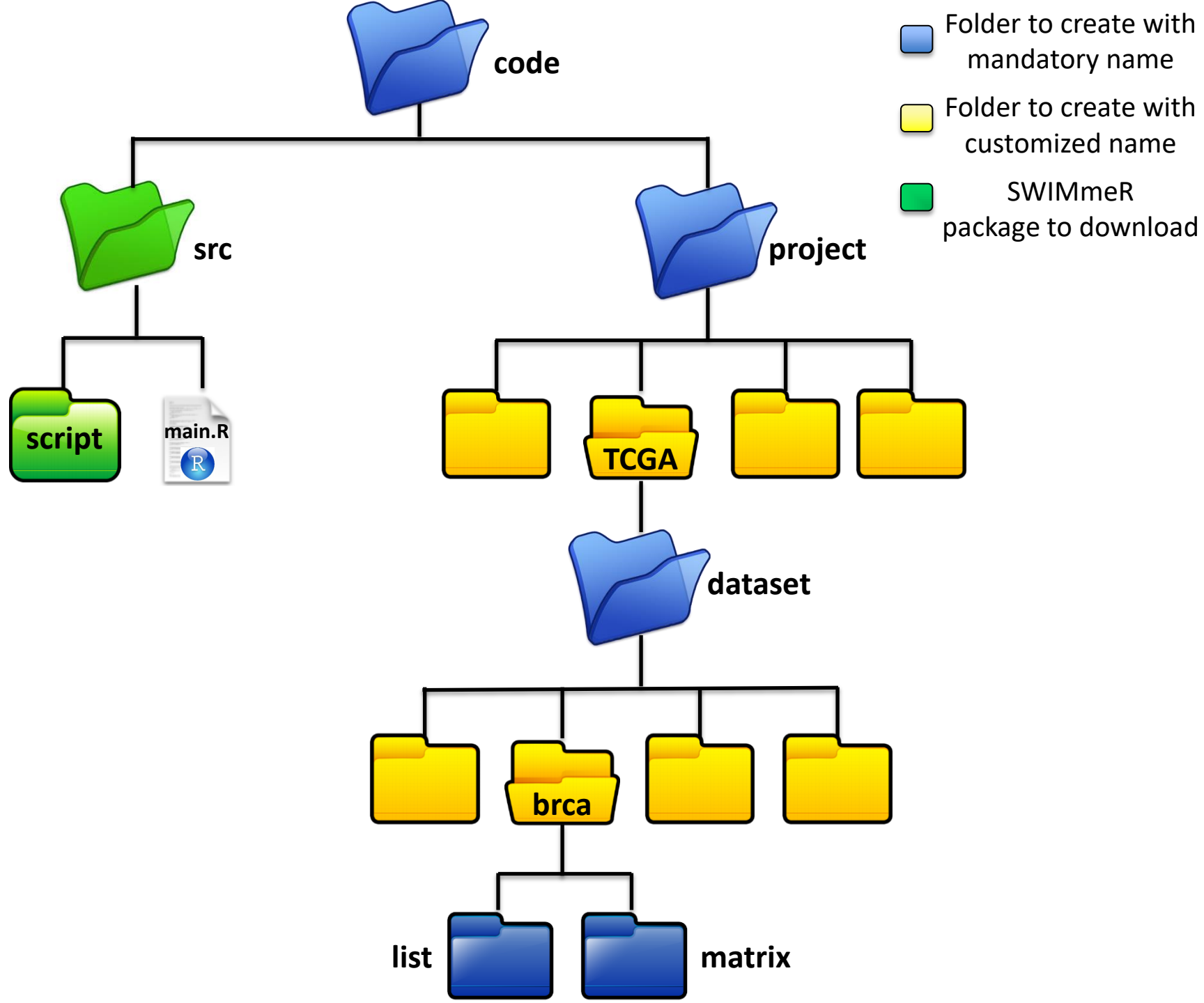


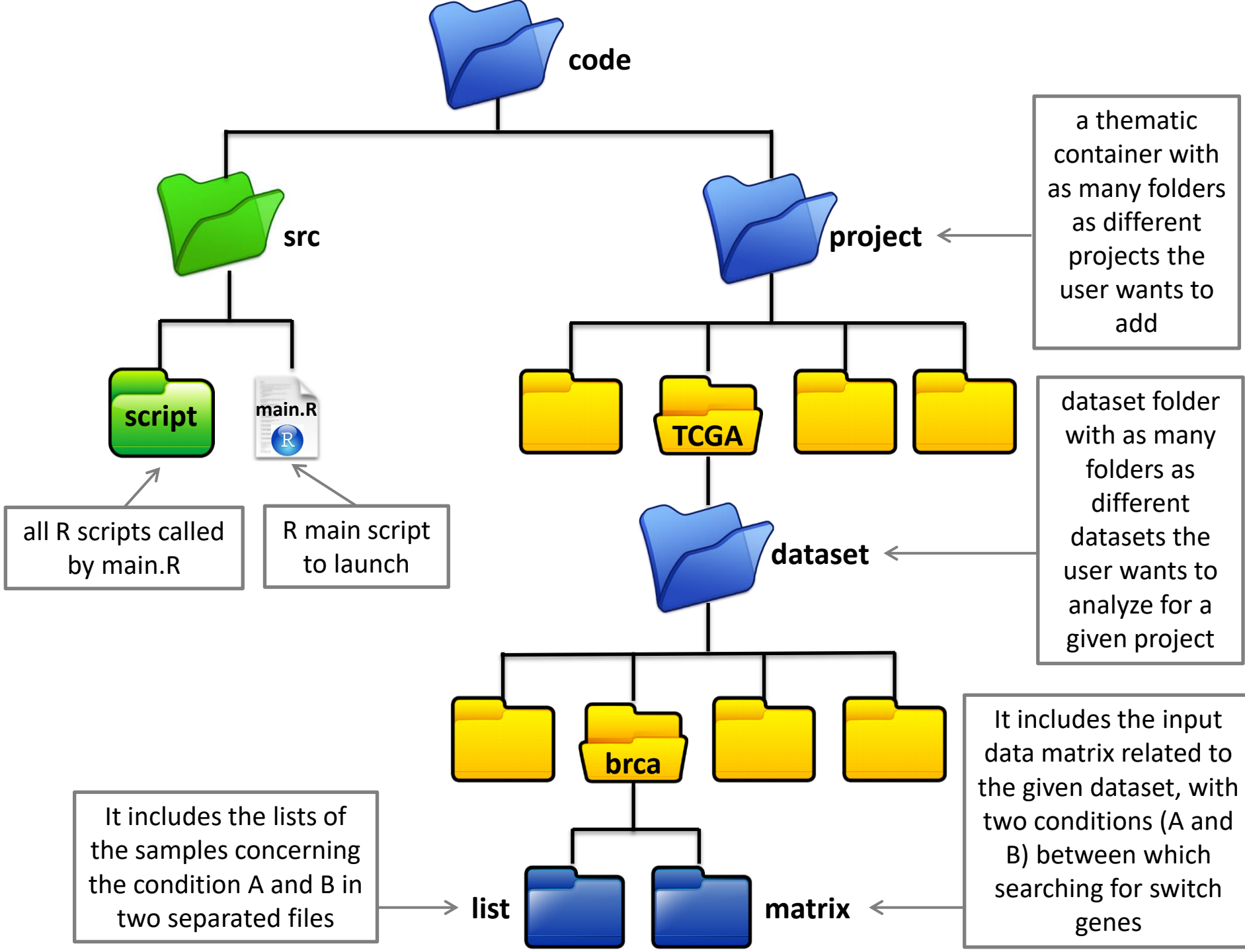
Software requirement

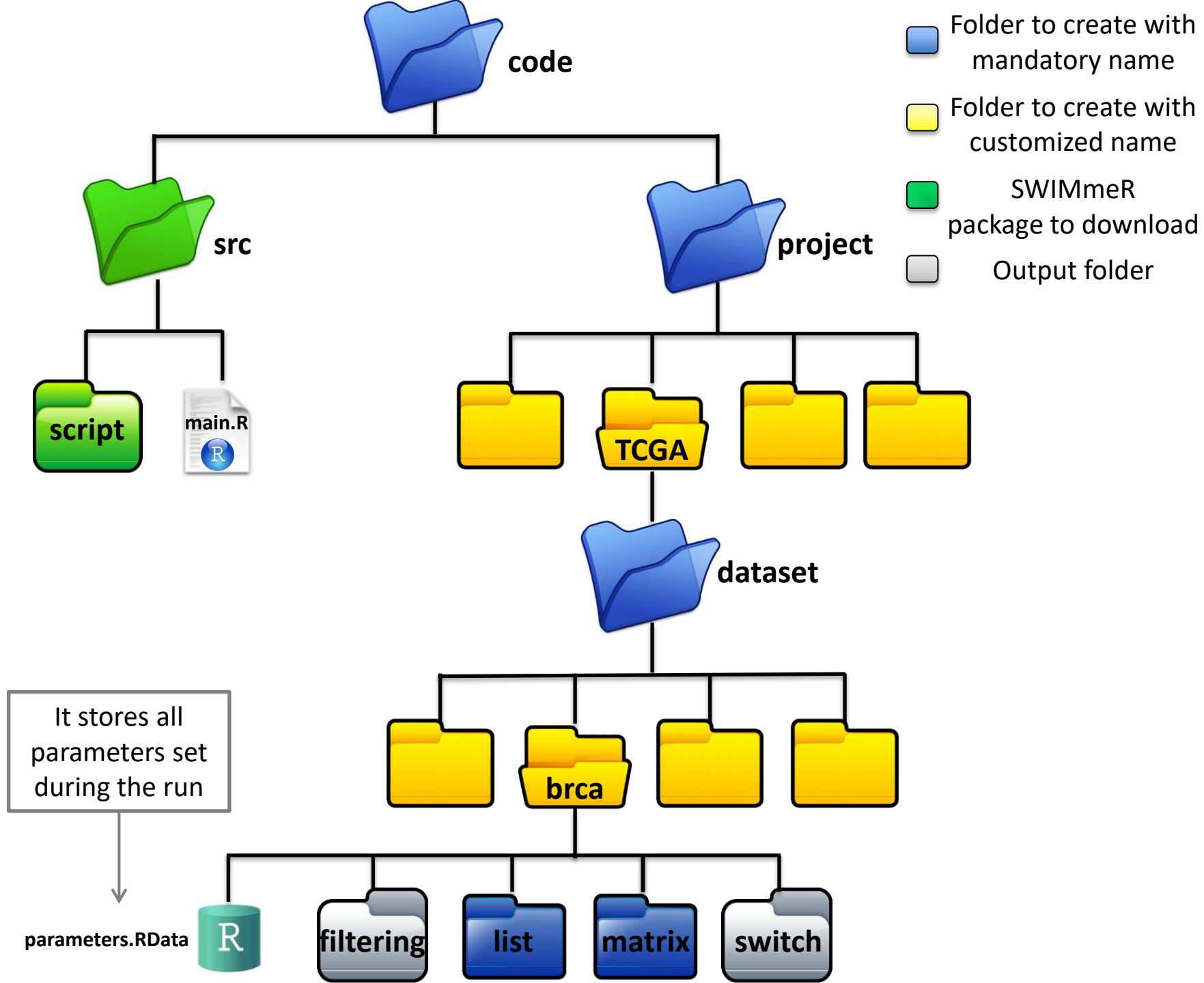
- SWIMmeR has been developed in R (version 3.6.1) and tested on the following operative systems:
 - macOS High Sierra 10.13.6
 - Windows 10 Pro

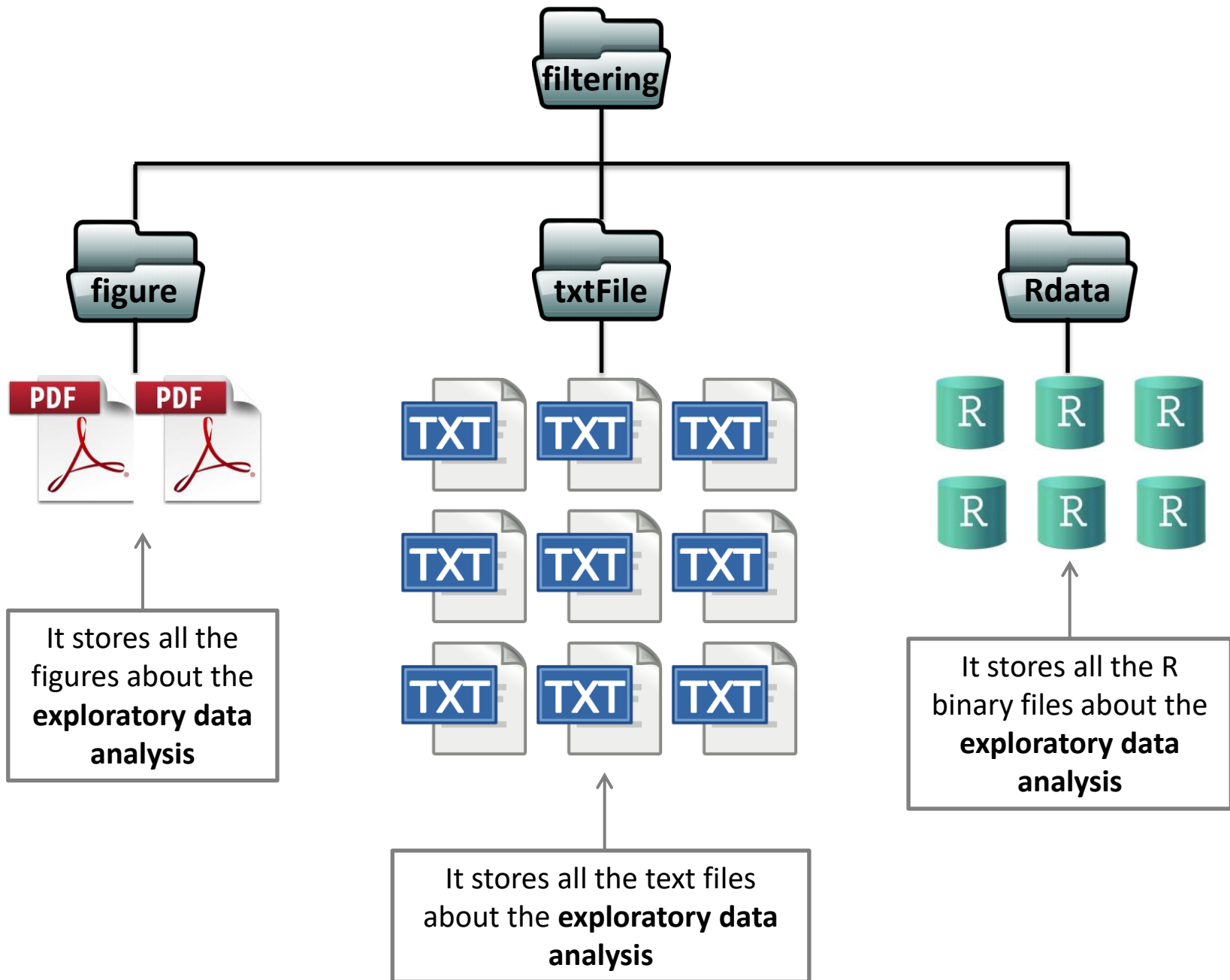
Setting up

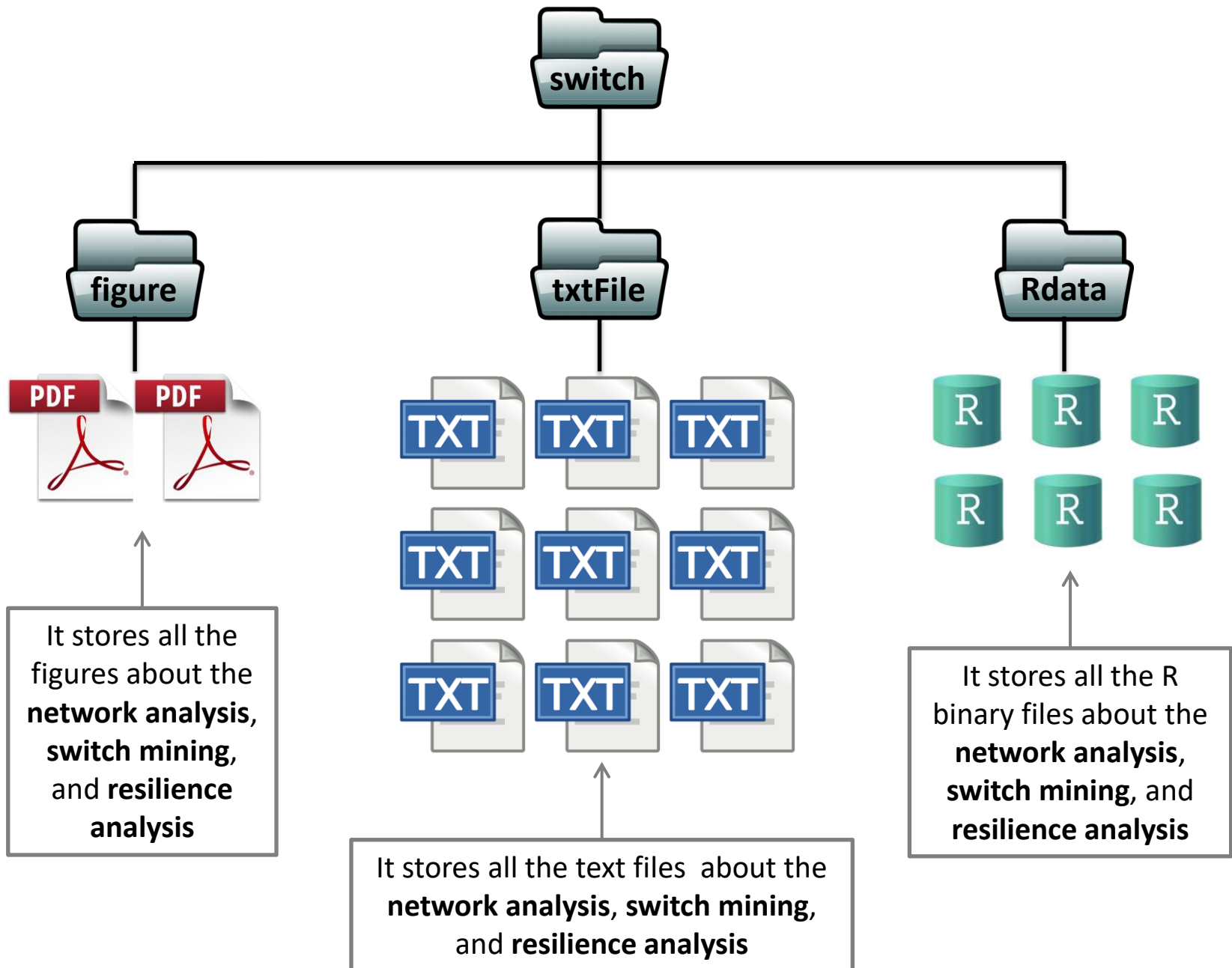
- Install R and R studio
- Download and unzip the SWIMmeR software package (“src” folder)





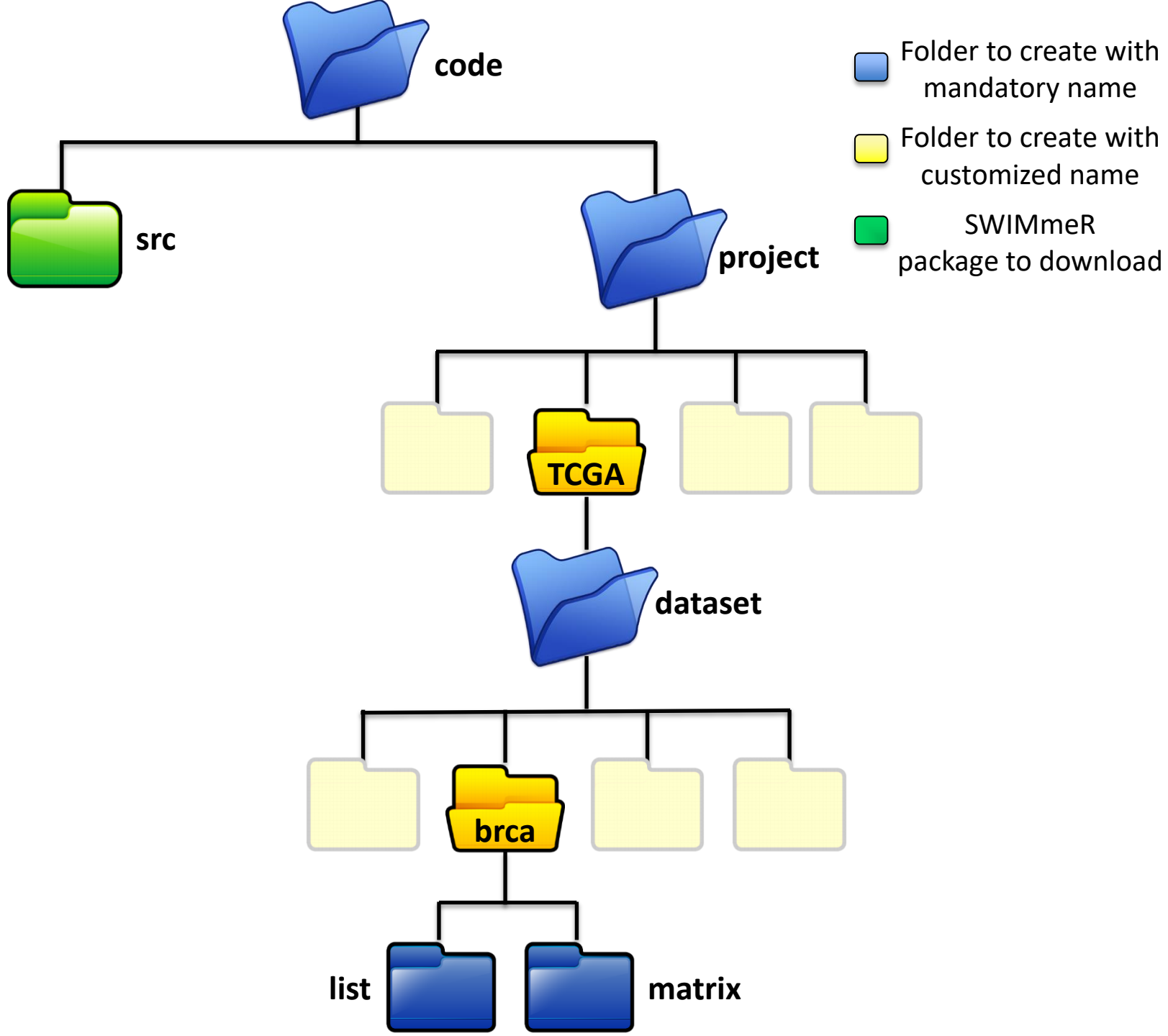


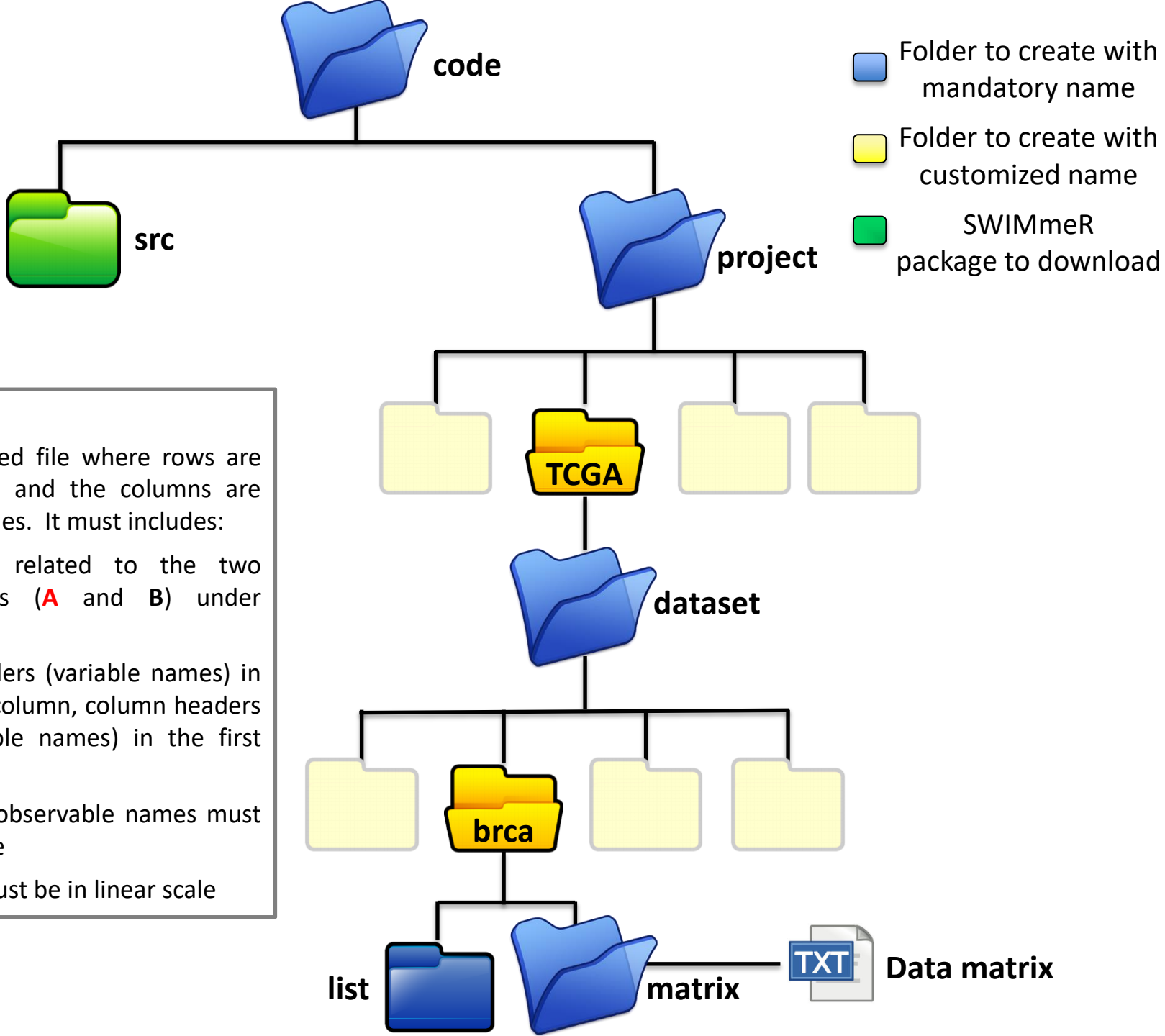




Let's get started







Data matrix:

a tab-delimited file where rows are the variables and the columns are the observables. It must includes:

- all data related to the two conditions (**A** and **B**) under testing
- row headers (variable names) in the first column, column headers (observable names) in the first row
- Variable/observable names must be unique
- Values must be in linear scale

Data matrix - example



Data matrix
N x M

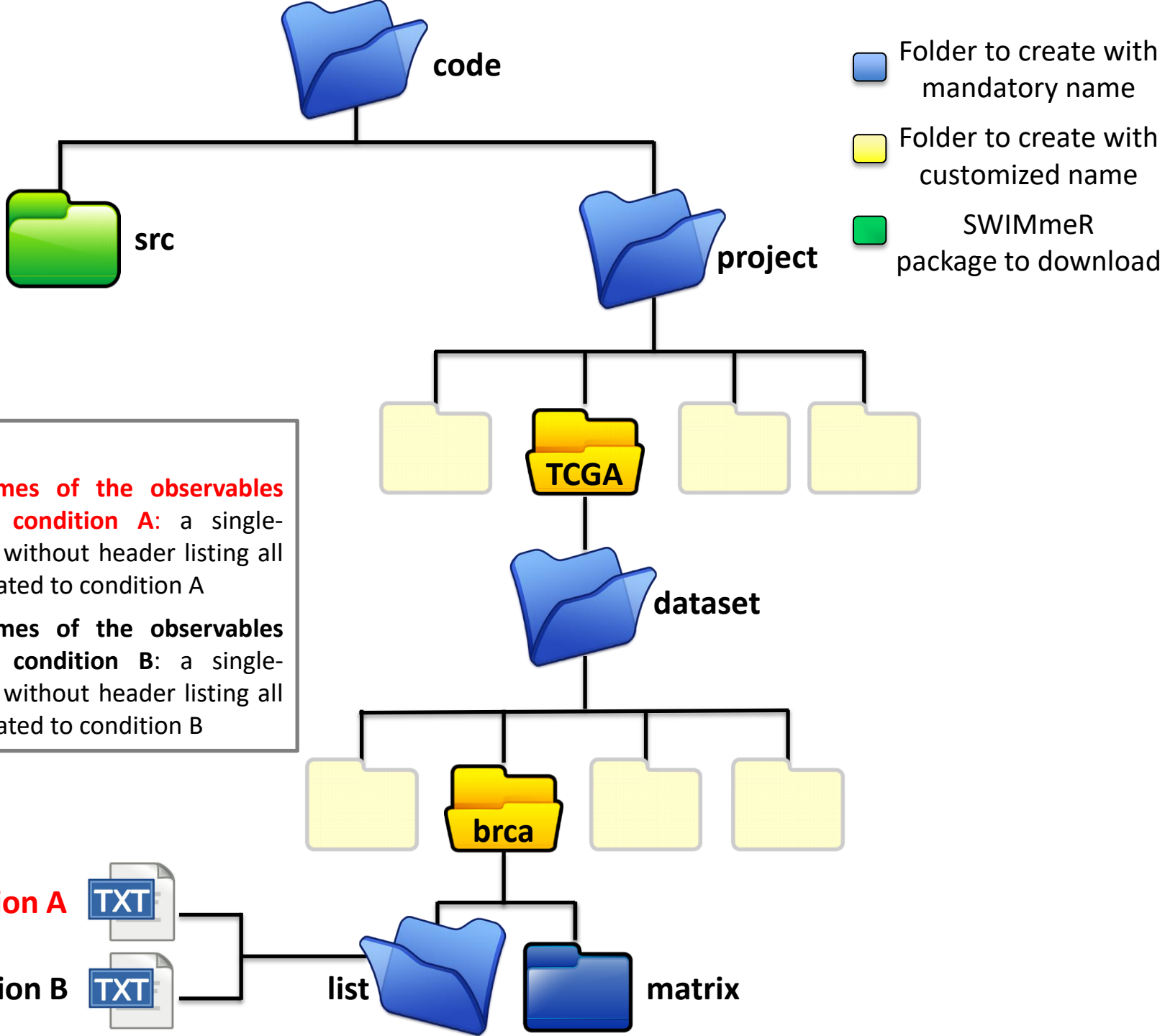
N rows → Transcripts
M columns → Samples

Samples of Condition A – Tumor tissues
Samples of Condition B - Normal tissues

Samples																						
		TCGA-A7-A0CE-11A-21R-A089-07	TCGA-A7-A0D9-11A-53R-A089-07	TCGA-A7-A0D9-01A-31R-A056-07	TCGA-A7-A0DB-01A-11R-A00Z-07	TCGA-A7-A13E-11A-61R-A12P-07	TCGA-A7-A13E-01A-11R-A12P-07	TCGA-A7-A13G-11A-51R-A13Q-07	TCGA-AC-A23H-11A-12R-A157-07	TCGA-AC-A2FB-01A-11R-A17B-07	TCGA-AC-A2FM-11B-32R-A19W-07	...	TCGA-A7-A0CE-01A-11R-A00Z-07	TCGA-A7-A0D9-11A-53R-A089-07	TCGA-A7-A0DB-11A-33R-A089-07	TCGA-A7-A0DC-01A-11R-A00Z-07	TCGA-A7-A13G-11A-51R-A13Q-07	TCGA-A7-A13F-01A-11R-A12P-07	TCGA-A7-A13G-01A-11R-A13Q-07	TCGA-AC-A23H-01A-11R-A157-07	TCGA-AC-A2FB-11A-13R-A17B-07	TCGA-AC-A2FM-01A-11R-A19W-07
Transcripts	AB1G	4.3	3.1	3.3	5.6	2.1	1.6	6.3	5.9	11.2	0.4	...	11.1	26.8	0.9	12.8	4.3	0.0	13.1	5.0	10.3	8.3
	ADAM10	3.9	0.0	0.8	13.5	3.3	4.7	4.7	8.5	3.9	1.2	3.5	13.5	5.2	11.6	4.3	1.2	6.2	4.0	7.5	8.8
										



Caveat: Transcript and samples names must be unique.
Matrix values must be linear. Missing values are treated as 0.



Lists of samples - example

List of samples of condition A - case

TCGA-A7-A0CE-01A-11R-A00Z-07
TCGA-A7-A0D9-01A-31R-A056-07
TCGA-A7-A0DB-01A-11R-A00Z-07
TCGA-A7-A0DC-01A-11R-A00Z-07
TCGA-A7-A13E-01A-11R-A12P-07
TCGA-A7-A13F-01A-11R-A12P-07
TCGA-A7-A13G-01A-11R-A13Q-07
TCGA-AC-A23H-01A-11R-A157-07
.....
TCGA-AC-A2FB-01A-11R-A17B-07
TCGA-AC-A2FM-01A-11R-A19W-07



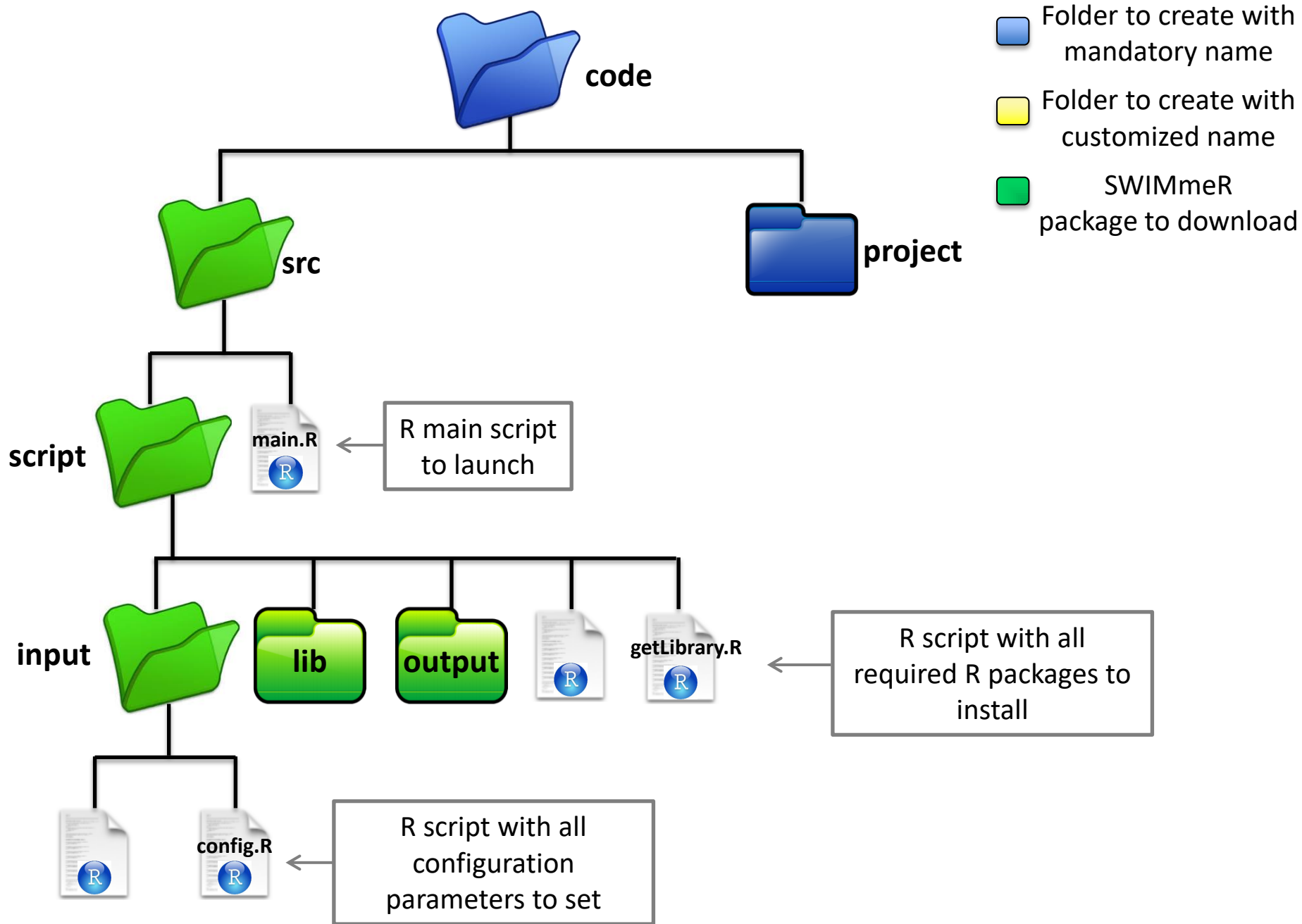
List of samples of condition B - control

TCGA-A7-A0CE-11A-21R-A089-07
TCGA-A7-A0D9-11A-53R-A089-07
TCGA-A7-A0DB-11A-33R-A089-07
TCGA-A7-A0DC-11A-41R-A089-07
TCGA-A7-A13E-11A-61R-A12P-07
TCGA-A7-A13F-11A-42R-A12P-07
TCGA-A7-A13G-11A-51R-A13Q-07
TCGA-AC-A23H-11A-12R-A157-07
.....
TCGA-AC-A2FB-11A-13R-A17B-07
TCGA-AC-A2FM-11B-32R-A19W-07



Ready to launch!





Main file



Initial settings

The screenshot displays the RStudio IDE interface. The main editor window shows the `main.R` script with the following code:

```
1 rm(list=ls())
2
3 options(stringsAsFactors = F)
4
5 setwd("~/SWIMMeR/code")
6 #####
7 source("src/script/getLibrary.R")
8 source("src/script/getSource.R")
9 #####
10 getLibrary()
11 getSource()
12 input_parameter <- config()
13 input_file <- inputFiles()
14 output_file <- outputFiles()
15 #####
16
17 data <- ExploratoryDataAnalysis()
18
19 network <- NetworkAnalysis(data, checkNetIntegrity = T, screePlot = T)
20
21 switch <- SwitchMining()
22
23 saveParameters()
24
25 if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()
26
```

The code is annotated with four modules:

- Module 1** (lines 17-18): `data <- ExploratoryDataAnalysis()`
- Module 2** (lines 19-20): `network <- NetworkAnalysis(data, checkNetIntegrity = T, screePlot = T)`
- Module 3** (lines 21-22): `switch <- SwitchMining()`
- Module 4** (lines 25-26): `if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()`

The console window at the bottom shows the R startup message:

```
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.

> |
```

The file explorer on the right shows the directory structure:

- Home > SWIMMeR > code > src
- Files: `main.R` (616 B, Oct 19, 2020, 5:58 PM) and `script`

A red arrow points to the `main.R` file in the file explorer.

Main file



Initial settings

```
1 rm(list=ls())
2
3 options(stringsAsFactors = F)
4
5 setwd("~/SWIMMeR/code")
6 #####
7 source("src/script/getLibrary.R")
8 source("src/script/getSource.R")
9 #####
10 getLibrary()
11 getSource()
12 input_parameter <- config()
13 input_file <- inputFiles()
14 output_file <- outputFiles()
15 #####
16
17 data <- ExploratoryDataAnalysis()
18
19 network <- NetworkAnalysis(data, checkNetIntegrity = T, screePlot = T)
20
21 switch <- SwitchMining()
22
23 saveParameters()
24
25 if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()
26
```

Module 1

Module 2

Module 3

Module 4

Environment: Global Environment (empty)

Files: Home > SWIMMeR > code > src

Name	Size	Modified
..		
main.R	616 B	Oct 19, 2020, 5:58 PM
script		

Console:

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.

> |

Main file



Initial settings

The screenshot displays the RStudio IDE interface. The main editor window shows the `main.R` script with the following code:

```
1 rm(list=ls())
2
3 options(stringsAsFactors = F)
4
5 setwd("~/SWIMMeR/code")
6 #####
7 source("src/script/getLibrary.R")
8 source("src/script/getSource.R")
9 #####
10 getLibrary()
11 getSource()
12 input_parameter <- config()
13 input_file <- inputFiles()
14 output_file <- outputFiles()
15 #####
16
17 data <- ExploratoryDataAnalysis()
18
19 network <- NetworkAnalysis(data, checkNetIntegrity = T, screePlot = T)
20
21 switch <- SwitchMining()
22
23 saveParameters()
24
25 if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()
26
```

The code is annotated with four modules:

- Module 1** (lines 17-18): `data <- ExploratoryDataAnalysis()`
- Module 2** (lines 19-20): `network <- NetworkAnalysis(data, checkNetIntegrity = T, screePlot = T)`
- Module 3** (lines 21-22): `switch <- SwitchMining()`
- Module 4** (lines 25-26): `if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()`

The console window at the bottom shows the R startup message:

```
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.

>
```

The file explorer on the right shows the directory structure:

- Home > SWIMMeR > code > src
- Files: `main.R` (616 B, Oct 19, 2020, 5:58 PM) and `script` (indicated by a red arrow).

Main file



Initial settings

The screenshot displays the RStudio environment. The main editor window shows the `main.R` script with the following code:

```
1 rm(list=ls())
2
3 options(stringsAsFactors = F)
4
5 setwd("~/SWIMMER/code")
6 #####
7 source("src/script/getLibrary.R")
8 source("src/script/getSource.R")
9 #####
10 getLibrary()
11 getSource()
12 input_parameter <- config()
13 input_file <- inputFiles()
14 output_file <- outputFiles()
15 #####
16
17 data <- ExploratoryDataAnalysis()
18
19 network <- NetworkAnalysis(data, checkNetIntegrity = T, screePlot = T)
20
21 switch <- SwitchMining()
22
23 saveParameters()
24
25 if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()
26
```

The code is annotated with labels on the right side:

- Line 17: **Module 1**
- Line 19: **Module 2**
- Line 21: **Module 3**
- Line 25: **Module 4**

The bottom pane shows the console output:

```
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.

> |
```

The right pane shows the **Files** view of the project directory `Home > SWIMMER > code > src > script`. The file list is as follows:

Name	Size	Modified
..		
getSource.R	3.6 KB	Sep 1, 2020, 8:40 AM
getLibrary.R	369 B	Aug 31, 2020, 3:23 PM
input		
lib		
output		

A red arrow points to the `input` folder.

Main file



Initial settings

main.R

```
1 rm(list=ls())
2
3 options(stringsAsFactors = F)
4
5 setwd("~/SWIMMER/code")
6 #####
7 source("src/script/getLibrary.R")
8 source("src/script/getSource.R")
9 #####
10 getLibrary()
11 getSource()
12 input_parameter <- config()
13 input_file <- inputFiles()
14 output_file <- outputFiles()
15 #####
16
17 data <- ExploratoryDataAnalysis()
18
19 network <- NetworkAnalysis(data,checkNetIntegrity = T, screePlot = T)
20
21 switch <- SwitchMining()
22
23 saveParameters()
24
25 if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()
26
```

Module 1

Module 2

Module 3

Module 4

Console

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.

> |

Environment History Connections

Global Environment

Environment is empty

Files Plots Packages Help Viewer

New Folder Delete Rename More

Home > SWIMMER > code > src > script > input

	Name	Size	Modified
	..		
<input checked="" type="checkbox"/>	config.R	3.7 KB	Sep 29, 2020, 6:51 PM
<input type="checkbox"/>	inputFiles.R	2 KB	Sep 21, 2020, 4:08 PM

Configuration file



Initial settings

The screenshot displays the RStudio interface with the 'config.R' file open in the editor. The file defines a 'config' function that sets up the environment for running SWIMMER. The function includes comments for launching SWIMMER, setting project and dataset names, defining file paths, and specifying input files. It also includes a conditional block for miRNA data and a parameter for paired t-test.

```
1 config <- function(){
2
3   # for executing SWIMMER launch:
4   # source('~/.Documents/SWIMMER/code/src/main.R')
5
6   #####
7   project <- "TCGA"
8   dataset <- "brca"
9   miRNA <- "yes"
10
11   path <- paste0("project/",project,"/dataset/",dataset)
12   #####
13   # input files
14
15   filename_data <- paste0(path,"/matrix/matrice__brca_RNASeq.txt")
16   filename_CTRL <- paste0(path,"/list/Lista__RNASeq_Normal__brca__4wayData.txt")
17   filename_CASE <- paste0(path,"/list/Lista__RNASeq_Tumor__brca__4wayData.txt")
18
19   if(miRNA == "yes"){
20     filename_data_miRNA <- paste0(path,"/matrix/matrice__brca_miRNASeq.txt")
21     filename_CTRL_miRNA <- paste0(path,"/list/Lista__miRNASeq_Normal__brca__4wayData
22     .txt")
23     filename_CASE_miRNA <- paste0(path,"/list/Lista__miRNASeq_Tumor__brca__4wayData.txt"
24   )
25   }
26   #####
27   # input parameters
28
29   paired_ttest <- T           # a logical value indicating whether you want a paired t
30   -test
31 }
```

The console shows the R startup message:

```
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.

> |
```

The Environment pane on the right shows the 'Global Environment' with the message 'Environment is empty'.

The Files pane on the right shows the directory structure: Home > SWIMMER > code > src > script > input. It lists the following files:

Name	Size	Modified
..		
config.R	3.7 KB	Sep 29, 2020, 6:51 PM
inputFiles.R	2 KB	Sep 21, 2020, 4:08 PM

Configuration file



Initial settings

main.R x config.R x

Go to file/function Addins

```
1 config <- function(){
2
3   # for executing SWIMMER launch:
4   # source('~/.Documents/SWIMMER/code/src/main.R')
5
6   #####
7   project <- "TCGA"
8   dataset <- "brca"
9   miRNA <- "yes"
10
11   path <- paste0("project/",project,"/dataset_",dataset,"/")
12   #####
13   # input files
14
15   filename_data <- paste0(path,"/matrix/matrix_",dataset,"_miRNASeq.txt")
16   filename_CTRL <- paste0(path,"/list/Lista_mRNASeq_Normal_",dataset,"_4wayData.txt")
17   filename_CASE <- paste0(path,"/list/Lista_mRNASeq_Tumor_",dataset,"_4wayData.txt")
18
19   if(miRNA == "yes"){
20     filename_data_miRNA <- paste0(path,"/matrix/matrix_",dataset,"_miRNASeq.txt")
21     filename_CTRL_miRNA <- paste0(path,"/list/Lista_mRNASeq_Normal_",dataset,"_4wayData.txt")
22     filename_CASE_miRNA <- paste0(path,"/list/Lista_mRNASeq_Tumor_",dataset,"_4wayData.txt")
23   }
24   #####
25   # input parameters
26
27   paired_ttest <- T # a logical value indicating whether you want a paired t-test
28 }
29
```

Insert *project* name

Insert *dataset* name

Type "yes" if miRNA data are also available, "no" otherwise

Environment History Connections

Import Dataset

Global Environment

Environment is empty

Files Plots Packages Help Viewer

New Folder Delete Rename More

Home > SWIMMER > code > src > script > input

	Name	Size	Modified
<input type="checkbox"/>	..		
<input type="checkbox"/>	config.R	3.7 KB	Sep 29, 2020, 6:51 PM
<input type="checkbox"/>	inputFiles.R	2 KB	Sep 21, 2020, 4:08 PM

Console

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.

> |

Configuration file



Input files

```
1 config <- function(){
2
3   # for executing SWIMMER launch:
4   # source('~/.Documents/SWIMMER/code/src/main.R')
5
6   #####
7   project <- "TCGA"
8   dataset <- "brca"
9   miRNA <- "yes"
10
11   path <- paste0("project/",project,"/dataset/",dataset)
12   #####
13   # input files
14
15   filename_data <- paste0(path,"/matrix/matrice__brca_RNASeq.txt")
16   filename_CTRL <- paste0(path,"/list/Lista__RNASeq_Normal__brca_4wayData.txt")
17   filename_CASE <- paste0(path,"/list/Lista__RNASeq_Tumor__brca_4wayData.txt")
18
19   if(miRNA == "yes"){
20     filename_data_miRNA <- paste0(path,"/matrix/matrice__brca_miRNASeq.txt")
21     filename_CTRL_miRNA <- paste0(path,"/list/Lista__miRNASeq_Normal__brca_4wayData
22     .txt")
23     filename_CASE_miRNA <- paste0(path,"/list/Lista__miRNASeq_Tumor__brca_4wayData.txt"
24   }
25   #####
26   # input parameters
27
28   paired_ttest <- T           # a logical value indicating whether you want a paired t
29   -test
30 }
```

Insert filename for *data matrix*

Insert filename for *list of samples of control condition*

Insert filename for *list of samples of case condition*

Environment is empty

Files	Plots	Packages	Help	Viewer
config.R				
inputFiles.R				

Console

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.

> |

Configuration file



Input files

```
1 config <- function(){
2
3   # for executing SWIMMER launch:
4   # source('~/.Documents/SWIMMER/code/src/main.R')
5
6   #####
7   project <- "TCGA"
8   dataset <- "brca"
9   miRNA <- "yes"
10
11   path <- paste0("project/",project,"/dataset/",dataset)
12   #####
13   # input files
14
15   filename_data <- paste0(path,"/matrix/matrice__brca_RNASeq.txt")
16   filename_CTRL <- paste0(path,"/list/Lista__RNASeq_Normal__brca__4wayData.txt")
17   filename_CASE <- paste0(path,"/list/Lista__RNASeq_Tumor__brca__4wayData.txt")
18
19   if(miRNA == "yes"){
20     filename_data_miRNA <- paste0(path,"/matrix/matrice__brca_miRNASeq.txt")
21     filename_CTRL_miRNA <- paste0(path,"/list/Lista__miRNASeq_Normal__brca__4wayData
22     .txt")
23     filename_CASE_miRNA <- paste0(path,"/list/Lista__miRNASeq_Tumor__brca__4wayData.txt")
24   }
25   #####
26   # input parameters
27   paired_ttest <- T           # a logical value indicating whether you want a paired t
28   -test
29 }
```

Environment is empty

If **miRNA** variable is set to "yes":

- Insert filename for **miRNA** data matrix
- Insert filename for **miRNA** list of samples of **control** condition
- Insert filename for **miRNA** list of samples of **case** condition

Console

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.

> |

Configuration file



**Input parameters:
Module 1**

Type **T** if you want a **paired** t-test, **F** otherwise

Specify the method for **multiple testing correction** (default: "fdr")

Set the threshold for the minimum percentile for the **IQR**

Set the threshold for the maximum **percentage of allowed zeros**

Set the threshold for the **fold-change** (linear scale)

Set the threshold for **adjusted p-value**

```
#####
# input parameters
paired_ttest <- T # a log
correction_method <- "fdr" # method

threshold_prc_iqr <- 0.11
threshold_perc_zeros <- 75
threshold_fc <- 3.4
threshold_pval_adj <- 0.05

if(miRNA == "yes"){
  threshold_prc_iqr_miRNA <- 0.53
  threshold_perc_zeros_miRNA <- 75
  threshold_fc_miRNA <- 3.4
  threshold_pval_adj_miRNA <- 0.05
}

type_correlation <- "pearson"
threshold_prc_corr <- 0.8
threshold_pval_adj_corr <- 0.05
min_rho <- 0.1
max_rho <- 0.9
step_rho <- 0.05

num_clusters <- 3 # set the number of clusters for k-means
iter_max <- 100 # set the maximum number of iterations allowed
num_repeats <- 5 # set the number of times to repeat the clustering (Replicates)

removal_node <- "yes"
#####
```

<input type="checkbox"/> config.R	3.7 KB	Sep 3, 2020, 10:32 AM
<input type="checkbox"/> inputFiles.R	1.9 KB	Sep 2, 2020, 12:45 PM

Configuration file



Input parameters:
Module 1

If **miRNA** variable is set to “yes”: t is empty

Set the threshold for the minimum percentile for the **IQR** for **miRNA**

Set the threshold for the maximum **percentage of allowed zeros** for **miRNAs**

Set the threshold for the **fold-change** (linear scale) for **miRNAs**

Set the threshold for **adjusted p-value** for **miRNAs**

```
#####  
# input parameters  
  
paired_ttest <- T      # a logical value indicating whether y  
correction_method <- "fdr" # method for multiple testing correcti  
  
threshold_prc_iqr <- 0.11  
threshold_perc_zeros <- 75  
threshold_fc <- 3.4  
threshold_pval_adj <- 0.05  
  
if(miRNA == "yes"){  
  threshold_prc_iqr_miRNA <- 0.53  
  threshold_perc_zeros_miRNA <- 75  
  threshold_fc_miRNA <- 3.4  
  threshold_pval_adj_miRNA <- 0.05  
}  
  
type_correlation <- "pearson"  
threshold_prc_corr <- 0.8  
threshold_pval_adj_corr <- 0.05  
min_rho <- 0.1  
max_rho <- 0.9  
step_rho <- 0.05  
  
num_clusters <- 3      # set the number of clusters for k-means  
iter_max <- 100        # set the maximum number of iterations allowed  
num_repeats <- 5       # set the number of times to repeat the clustering (Replicates)  
  
removal_node <- "yes"  
#####
```

Configuration file



**Input parameters:
Module 2**

```
#####  
# input parameters  
  
paired_ttest <- T      # a logical value indicating whether you want a paired t-test  
correction_method <- "fdr" # method for multiple testing correction  
  
threshold_prc_iqr <- 0.11  
threshold_perc_zeros <- 75  
threshold_fc <- 3.4  
threshold_pval_adj <- 0.05  
  
if(miRNA == "yes"){  
  threshold_prc_iqr_miRNA <- 0.53  
  threshold_perc_zeros_miRNA <- 75  
  threshold_fc_miRNA <- 3.4  
  threshold_pval_adj_miRNA <- 0.05  
}  
  
type_correlation <- "pearson"  
threshold_prc_corr <- 0.8  
threshold_pval_adj_corr <- 0.05  
min_rho <- 0.1  
max_rho <- 0.9  
step_rho <- 0.05  
  
num_clusters <- 3      # set the number of clusters  
iter_max <- 100        # set the maximum number of iterations allowed  
num_repeats <- 5      # set the number of repeats  
  
removal_node <- "yes"  
#####
```

Specify the **correlation method** (default: "pearson")

Set the threshold for the **correlation coefficient** (percentile)

Set the threshold for the **correlation adjusted p-value**

Set the **minimum correlation value** to plot network integrity

Set the **maximum correlation value** to plot network integrity

Set the **step** between min_rho and max_rho to plot network integrity

Configuration file



**Input parameters:
Module 2**

```
#####  
# input parameters  
  
paired_ttest <- T      # a logical value indicating whether you want a paired t-test  
correction_method <- "fdr" # method for multiple testing correction  
  
threshold_prc_iqr <- 0.11  
threshold_perc_zeros <- 75  
threshold_fc <- 3.4  
threshold_pval_adj <- 0.05  
  
if(miRNA == "yes"){  
  threshold_prc_iqr_miRNA <- 0.53  
  threshold_perc_zeros_miRNA <- 75  
  threshold_fc_miRNA <- 3.4  
  threshold_pval_adj_miRNA <- 0.05  
}  
  
type_correlation <- "pearson"  
threshold_prc_corr <- 0.8  
threshold_pval_adj_corr <- 0.05  
min_rho <- 0.1  
max_rho <- 0.9  
step_rho <- 0.05  
  
num_clusters <- 3  
iter_max <- 100  
num_repeats <- 5  
  
removal_node <- "yes"  
#####
```

Set the **number of clusters** for k-means

Set the **maximum number of iterations** allowed

Set the number of times to repeat the
clustering (**replicates**)

Environment History Connections

Global Environment

Environment is empty

Files Plots Packages Help Viewer

New Folder Delete Rename More

C: > Users > Giulia > Dropbox > Giulia&Fede > Progetti > SWIMmeR > code > src > script > input

Name	Size	Modified
config.R	3.7 KB	Sep 3, 2020, 10:32 AM
inputFiles.R	1.9 KB	Sep 2, 2020, 12:45 PM

Configuration file



**Input parameters:
Module 4**

The screenshot shows the RStudio interface. The main editor displays the 'config.R' file, which contains input parameters for a Resilience Analysis. A red arrow points to the 'config.R' tab. A blue box highlights the 'Input parameters: Module 4' text. A white box with a black border points to the 'removal_node' parameter, with the text 'Type "yes" if you want to perform the Resilience Analysis (Module 4)'. The file explorer on the right shows the directory structure: C:\Users\Giulia>Dropbox>Giulia&Fede>Progetti>SWIMmeR>code>src>script>input. It lists two files: 'config.R' (3.7 KB, Sep 3, 2020, 10:32 AM) and 'inputFiles.R' (1.9 KB, Sep 2, 2020, 12:45 PM).

```
#####  
# input parameters  
  
paired_ttest <- T      # a logical value indicating whether you want a paired t-test  
correction_method <- "fdr" # method for multiple testing correction  
  
threshold_prc_iqr <- 0.11  
threshold_perc_zeros <- 75  
threshold_fc <- 3.4  
threshold_pval_adj <- 0.05  
  
if(miRNA == "yes"){  
  threshold_prc_iqr_miRNA <- 0.53  
  threshold_perc_zeros_miRNA <- 75  
  threshold_fc_miRNA <- 3.4  
  threshold_pval_adj_miRNA <- 0.05  
}  
  
type_correlation <- "pearson"  
threshold_prc_corr <- 0.8  
threshold_pval_adj_corr <- 0.05  
min_rho <- 0.1  
max_rho <- 0.9  
step_rho <- 0.05  
  
num_clusters <- 3      # set the number of clusters for k-means  
iter_max <- 100        # s  
num_repeats <- 5      # s  
  
removal_node <- "yes"  
#####
```

Type "yes" if you want to perform the Resilience Analysis (Module 4)

Name	Size	Modified
config.R	3.7 KB	Sep 3, 2020, 10:32 AM
inputFiles.R	1.9 KB	Sep 2, 2020, 12:45 PM

SWIMmeR launch!



The screenshot displays the RStudio environment with the following components:

- Source Editor:** Contains the SWIMmeR script with line numbers 6 to 26. The script includes source calls for library and source files, followed by function calls for data exploration, network analysis, and parameter saving.
- Console:** Shows the R startup message and help text. The output includes the R license notice, information about natural language support, and instructions for using help and quitting.
- Environment Panel:** Displays the 'Global Environment' with the message 'Environment is empty'.
- Files Panel:** Shows the file explorer view for the path 'Home > Documents > SWIMmeR > code > src > script'. It lists files and folders: '..', 'getLibrary.R' (369 B, Aug 31, 2020, 3:23 PM), 'getSource.R' (3.6 KB, Sep 1, 2020, 8:40 AM), 'input', 'lib', and 'output'.

```
6 #####
7 source("src/script/getLibrary.R")
8 source("src/script/getSource.R")
9 #####
10 getLibrary()
11 getSource()
12 input_parameter <- config()
13 input_file <- inputFiles()
14 output_file <- outputFiles()
15 #####
16
17 data <- ExploratoryDataAnalysis()
18
19 network <- NetworkAnalysis(data,checkNetIntegrity = F, screePlot = F)
20 |
21 switch <- SwitchMining()
22
23 saveParameters()
24
25 if(input_parameter$removal_node == "yes") resilience <- ResilienceAnalysis()
26
```

Console output:

```
Platform: x86_64-apple-darwin15.6.0 (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.

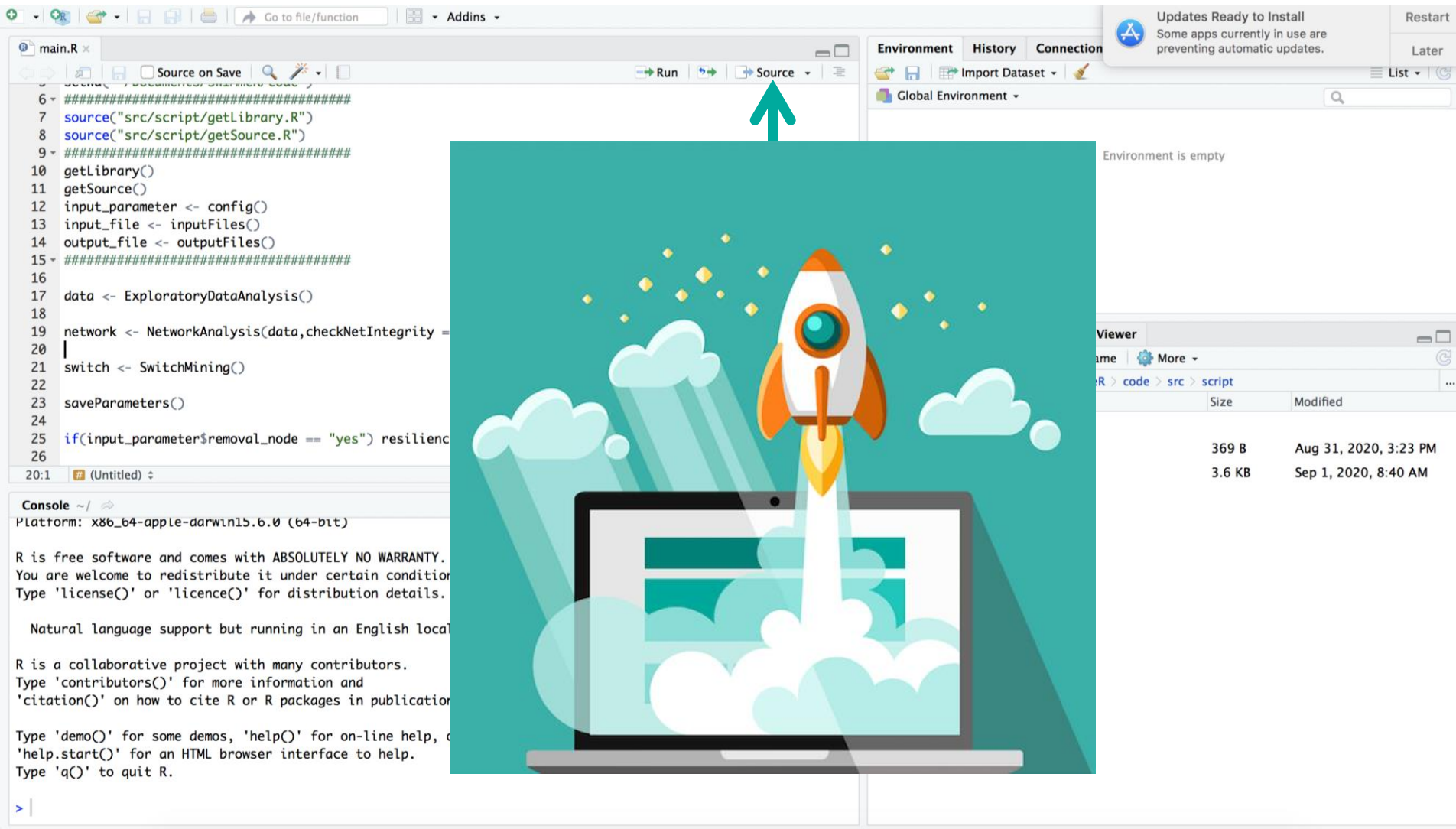
Natural language support but running in an English locale

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.

> |
```

SWIMmeR launch!



The screenshot shows the RStudio IDE interface. The main editor window displays R code for the SWIMmeR package. A green arrow points to the 'Source' button in the top toolbar. A large illustration of a rocket launching from a laptop is overlaid on the center of the screen.

Source Code:

```
#####  
6 source("src/script/getLibrary.R")  
7 source("src/script/getSource.R")  
8 #####  
9 #####  
10 getLibrary()  
11 getSource()  
12 input_parameter <- config()  
13 input_file <- inputFiles()  
14 output_file <- outputFiles()  
15 #####  
16  
17 data <- ExploratoryDataAnalysis()  
18  
19 network <- NetworkAnalysis(data, checkNetIntegrity =  
20 |  
21 switch <- SwitchMining()  
22  
23 saveParameters()  
24  
25 if(input_parameter$removal_node == "yes") resilienc  
26  
20:1 (Untitled) ↵
```

Console:

```
~/  
Platform: x86_64-apple-darwin15.6.0 (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.  
  
> |
```

Environment: Global Environment

Viewer:

File	Size	Modified
R > code > src > script	369 B	Aug 31, 2020, 3:23 PM
	3.6 KB	Sep 1, 2020, 8:40 AM