



Managing
dependencies



Managing and executing
analysis workflow



Versioning and
collaborating on code
(and some other files)



Connecting code
and reporting

and...



Isolating and exporting
environment

Supplementary material

John Doe, Joan Dough, Jan Doh, Dyon Do

18 March, 2018

Read in the data

We have *count data* for three samples:

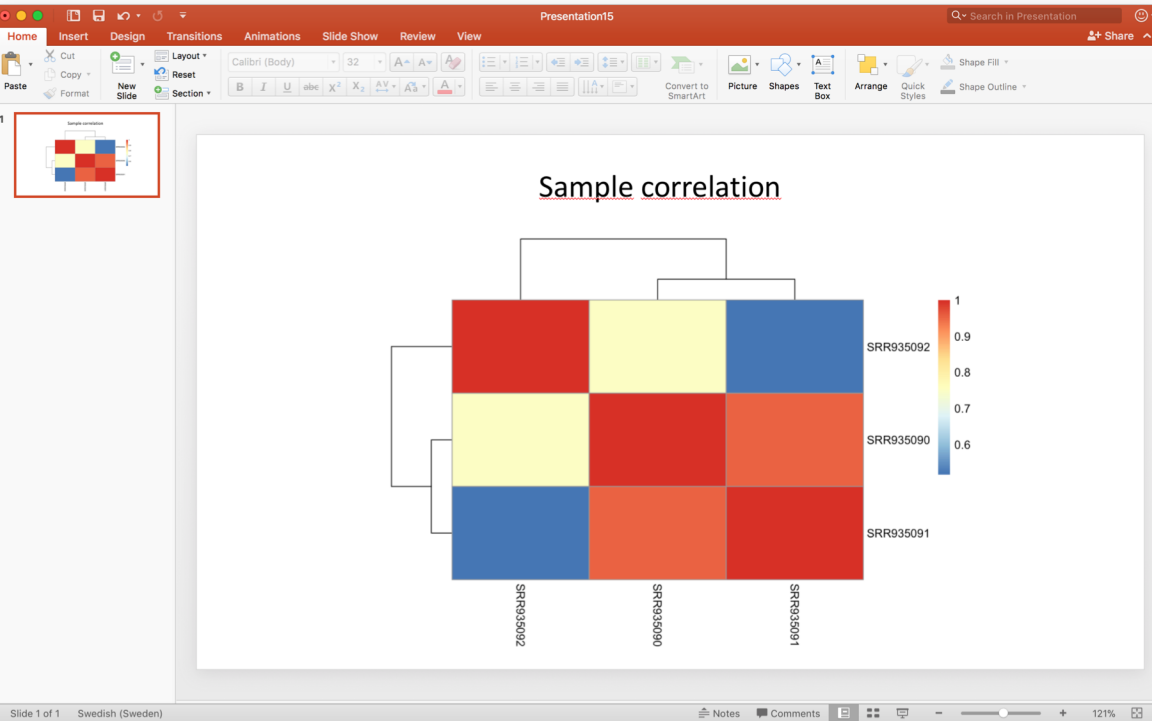
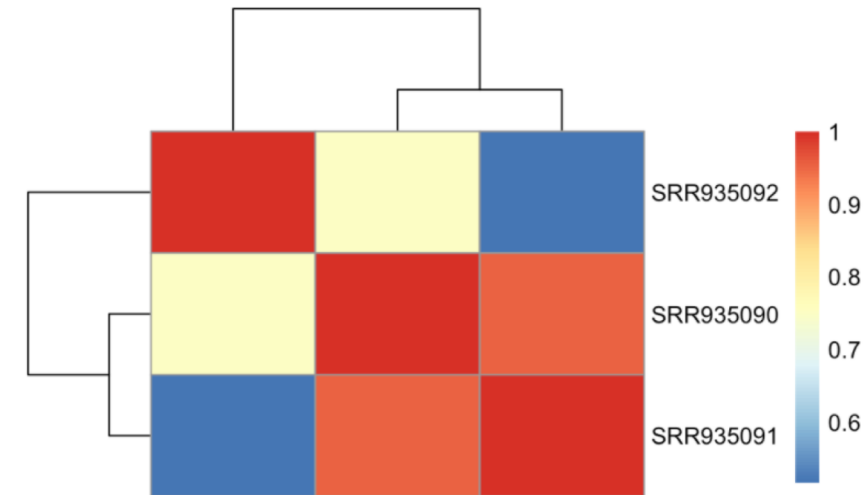
- SRR935090
- SRR935091
- SRR935092

```
# Read counts:
counts_file <- "results/tables/counts.tsv"
counts <- read.delim(counts_file, skip=1, header=F, row.names=1)
sample_names <- t(read.delim(counts_file, nrow=1, header=F))
colnames(counts) <- c("description", gsub(".*(SRR[0-9]*)\\.\\.\\.", "\\1", sample_names))
```

Plot sample correlation

Next, we will plot the sample correlation of the *count data*:

```
heatmap(cor((counts[, -1])), show_colnames=F)
```



- R Markdown makes your analysis more reproducible by connecting your code, figures and descriptive text.
- You can use it to make reproducible reports, rather than e.g. copy-pasting figures into a Word document.
- You can also use it as a notebook, in the same way as lab notebooks are used in a wet lab setting.

```
---  
title: "Supplementary material"  
author: John Doe, Joan Dough, Jan Doh, Dyon Do  
date: "`r format(Sys.time(), '%d %B, %Y')`"  
output: html_document  
---
```

```
```{r, include=FALSE}  
library("pheatmap")
```
```

```
# Read in the data
```

We have *count data* for three samples:

- SRR935090
- SRR935091
- SRR935092

```
```{r}  
Read counts:
counts_file <- "results/tables/counts.tsv"
counts <- read.delim(counts_file, skip=1, header=F, row.names=1)
sample_names <- t(read.delim(counts_file, nrow=1, header=F))
colnames(counts) <- c("description",
 gsub(".*(SRR[0-9]*)\\.\\.\\.","\\1", sample_names))
```
```

```
# Plot sample correlation
```

Next, we will plot the sample correlation of the *count data*:

```
```{r, fig.height=3, fig.width=5}  
pheatmap(cor((counts[, -1])), show_colnames=F)
```
```

Supplementary material

John Doe, Joan Dough, Jan Doh, Dyon Do

18 March, 2018

Read in the data

We have *count data* for three samples:

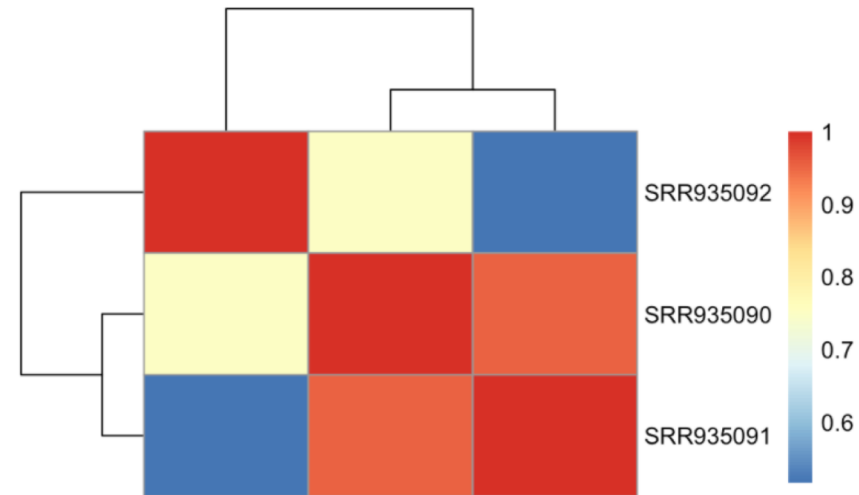
- SRR935090
- SRR935091
- SRR935092

```
# Read counts:  
counts_file <- "results/tables/counts.tsv"  
counts <- read.delim(counts_file, skip=1, header=F, row.names=1)  
sample_names <- t(read.delim(counts_file, nrow=1, header=F))  
colnames(counts) <- c("description", gsub(".*(SRR[0-9]*)\\.\\.\\.","\\1", sample_names))
```

Plot sample correlation

Next, we will plot the sample correlation of the *count data*:

```
pheatmap(cor((counts[, -1])), show_colnames=F)
```



```
```{r, fig.height=3, fig.width=5}
pheatmap(cor((counts[,-1])), show_colnames=F)
```
```

- Document-wide options
- Output format
- Parameters

- Evaluate R code and show output
- Also Bash, Python, Rcpp, SQL, Stan
- Chunk options

```
```{r, fig.height=3, fig.width=5}
pheatmap(cor((counts[,-1])), show_colnames=F)
```
```

- Freely add and format text using markdown

```
---  
title: "Supplementary material"  
author: John Doe, Joan Dough, Jan Doh, Dyon Do  
date: "`r format(Sys.time(), '%d %B, %Y')`"  
output: html_document  
---
```

```
```{r, include=FALSE}  
library("pheatmap")
```
```

```
# Read in the data
```

We have *count data* for three samples:

- SRR935090
- SRR935091
- SRR935092

```
```{r}  
Read counts:
counts_file <- "results/tables/counts.tsv"
counts <- read.delim(counts_file, skip=1, header=F, row.names=1)
sample_names <- t(read.delim(counts_file, nrow=1, header=F))
colnames(counts) <- c("description",
 gsub(".*(SRR[0-9]*)\\.\\.\\.","\\1", sample_names))
```
```

```
# Plot sample correlation
```

Next, we will plot the sample correlation of the *count data*:

```
```{r, fig.height=3, fig.width=5}  
pheatmap(cor((counts[, -1])), show_colnames=F)
```
```

Supplementary material

John Doe, Joan Dough, Jan Doh, Dyon Do

18 March, 2018

Read in the data

We have *count data* for three samples:

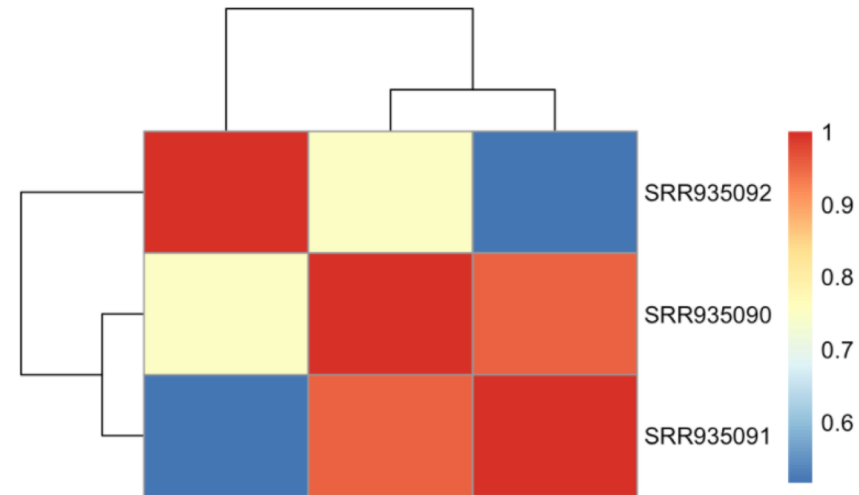
- SRR935090
- SRR935091
- SRR935092

```
# Read counts:  
counts_file <- "results/tables/counts.tsv"  
counts <- read.delim(counts_file, skip=1, header=F, row.names=1)  
sample_names <- t(read.delim(counts_file, nrow=1, header=F))  
colnames(counts) <- c("description", gsub(".*(SRR[0-9]*)\\.\\.\\.","\\1", sample_names))
```

Plot sample correlation

Next, we will plot the sample correlation of the *count data*:

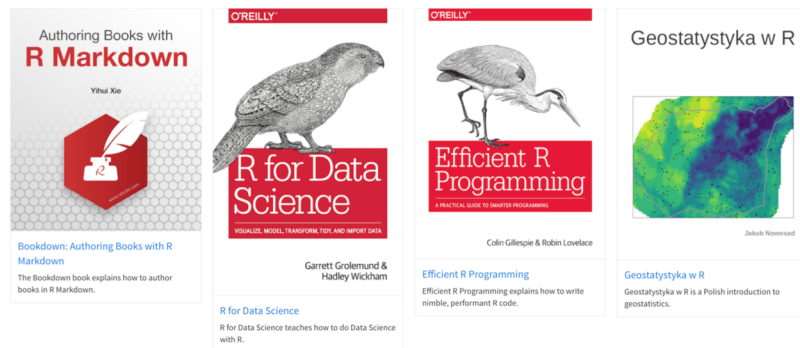
```
pheatmap(cor((counts[, -1])), show_colnames=F)
```



Output formats

- Documents/reports (HTML, PDF, MS Word, Tufte handouts)
- Presentations (Powerpoint, Beamer, Slidy, ioslides, reveal.js)
- Interactive documents and dashboards (HTML widgets, Shiny)
- Books and websites
- Other templates...

Can require different markdown syntax depending on output!



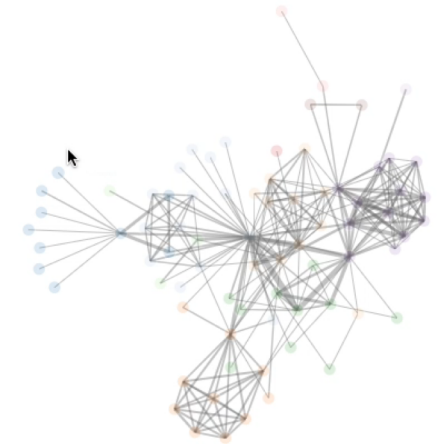
| |
|--------------------------------------|
| Leaflet |
| Geo-spatial mapping |
| dygraphs |
| Time series charting |
| Plotly |
| Interactive graphics with D3 |
| rbokeh |
| R interface to Bokeh |
| Highcharter |
| R interface to Highcharts |
| visNetwork |
| Graph data visualization with vis.js |
| networkD3 |
| Graph data visualization with D3 |
| d3heatmap |
| Interactive heatmaps with D3 |
| DataTables |
| Tabular data display |
| threejs |
| 3D scatterplots and globes |
| rglwidget |
| Render scenes created with rgl |
| DiagrammeR |
| Diagrams and flowcharts |
| MetricsGraphics |
| Scatterplots and line charts with D3 |

networkD3

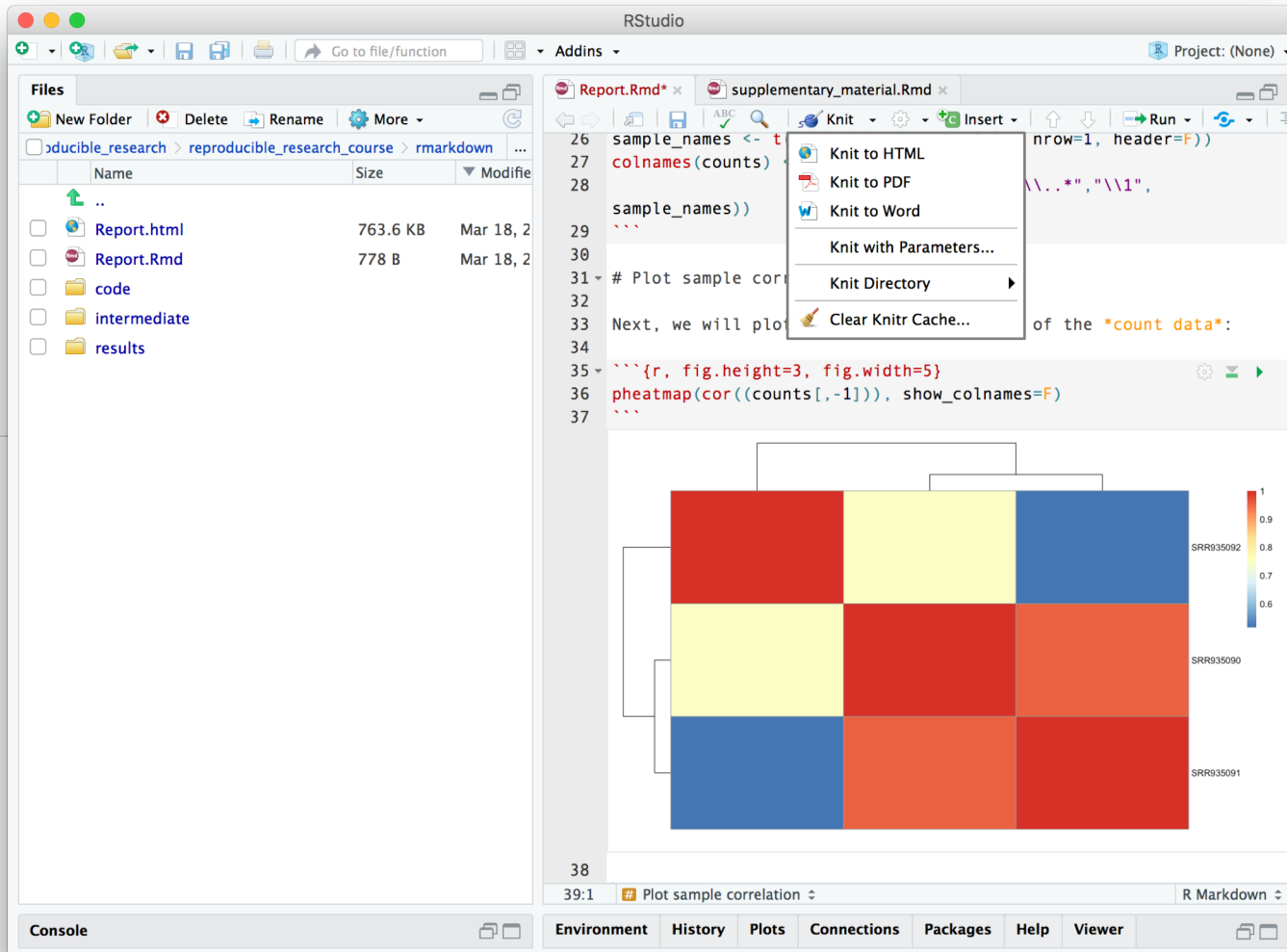
<http://christophergandrud.github.io/networkD3/>

networkD3 provides tools for creating D3 JavaScript network graphs from R.

```
library(networkD3)
data(MisLinks, MisNodes)
forceNetwork(Links = MisLinks, Nodes = MisNodes, Source = "source",
             Target = "target", Value = "value", NodeID = "name",
             Group = "group", opacity = 0.4)
```

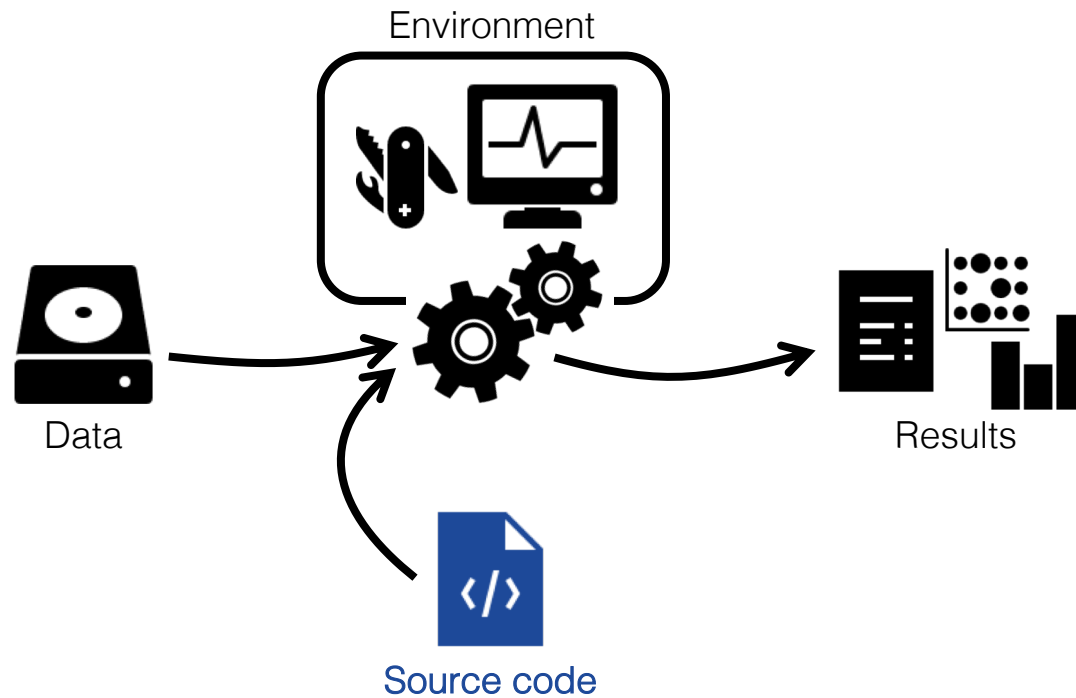


R Markdown in RStudio



- Evaluate inline
- Render from menu
- Render from R console or terminal

```
$ R -e "rmarkdown::render('Report.Rmd')"
```



```
project
|- doc/
|
|- data/
|   |- raw_external/
|   |- raw_internal/
|   |- meta/
|
|- code/
|- notebooks/
|
|- intermediate/
|- scratch/
|- logs/
|
|- results/
|   |- figures/
|   |- tables/
|   |- reports/
|
|- Snakefile
|- config.yml
|- environment.yml
|- Dockerfile
```