

Complements

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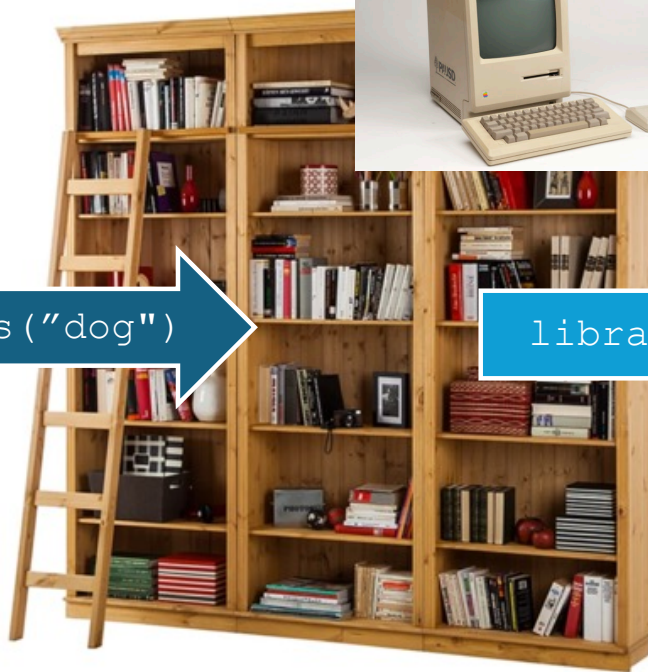
Package installation with **Fripouille**



The Comprehensive R Archive
Network



`install.packages("dog")`



`library(dog)`



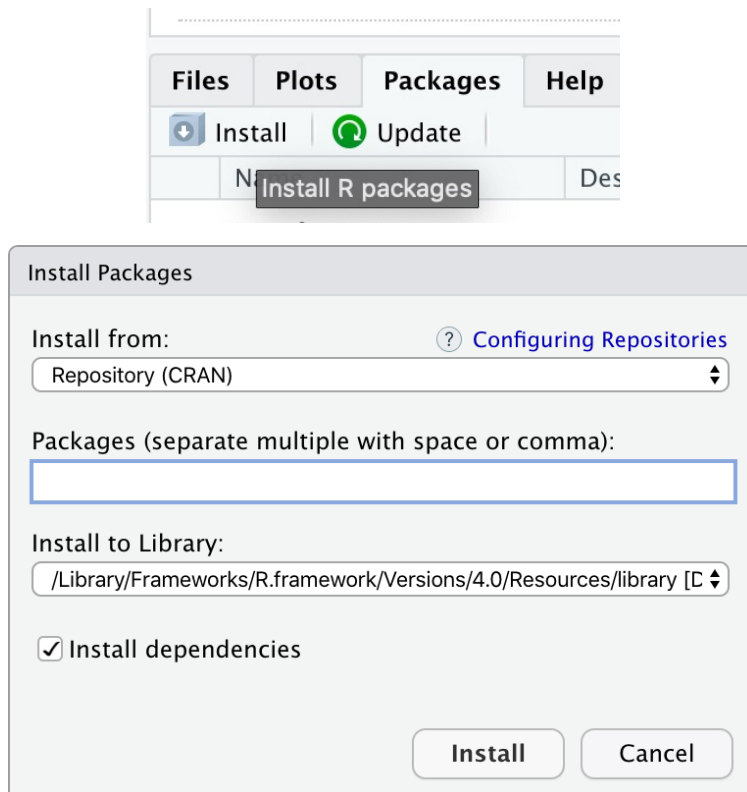
`ouaf()`



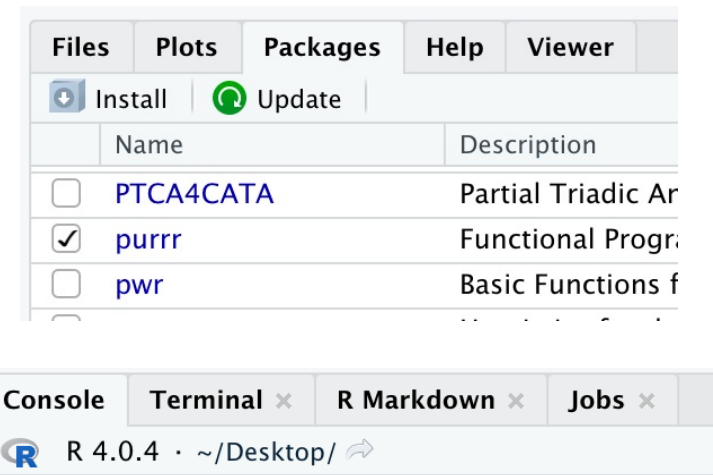
I forgot the names of the commands!



Installation : just once*



Load the library: when needed
(frequently)

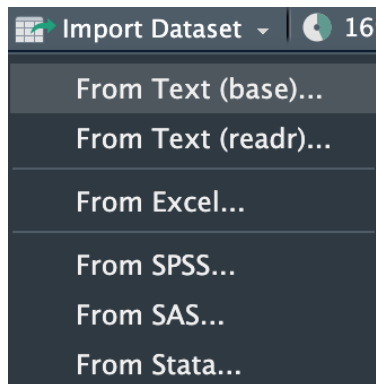


```
> library(purrr)
> aFunctionThatILike(42)
```

*Except to reinstall or update, of course

Import data (with a little help from Rstudio)

- Import Dataset > ...



Import Dataset

Name: covid

Encoding: Automatic

Heading: ☒ Yes ☐ No

Row names: Automatic

Separator: Comma

Decimal: Period

Quote: Double (")

Comment: None

na.strings: NA

☐ Strings as factors

Input File

id,time,status,ABCB1,ABL1,ADA,AHR,AICDA,AIRE,APP,ARG1,ARG2,HC59,0,HC,7.43,6.33,6.87,9.31,3.97,4.23,9.34,6.93,4.87,12.8HC60,0,HC,7.71,6.28,7.34,8.78,4.6,4.44,9.23,6.74,3.74,12.52HC68,0,HC,7.01,6.02,7.09,8.69,3.95,3.81,9.02,5.72,4.66,12.6HC98,0,HC,7.44,6.47,7.31,8.74,3.73,3.73,9.06,6.77,3.83,12.6HC74,0,HC,7.48,6.53,7.14,9.6,3.89,4.33,9.45,6.24,3.99,12.68HC88,0,HC,7.25,6.58,7.13,10.12,3.93,3.88,9.34,7.92,3.88,12.7HC91,0,HC,7.52,6.21,7.06,8.84,4.17,4.17,9.56,7.65,3.66,12.7HC94,0,HC,6.84,6.51,7.59,9.41,3.77,3.95,9.39,6.96,3.95,12.6HC75,0,HC,7.6,6.22,7.07,9.34,3.82,4.71,9.41,6.68,3.82,12.65,5HC76,0,HC,7.27,6.41,6.41,9.4,4.88,3.86,9.08,4.83,3.86,12.84Case1,4,nCOV,7.87,7.13,7.035,9.195,3.125,3.125,9.755,7.72,5Case1,5,nCOV,7.69,7.25,7.26,9.47,3.15,3.15,9.42,7.91,4.32,1Case1,6,nCOV,7.4,6.68,7.07,9.26,2.79,2.79,9.63,8.81,4.71,12Case1,7,nCOV,7.38,6.89,7.05,9.47,3.23,3.23,9.73,7.66,4.82,1Case1.8.nCOV.7.6.57.6.99.9.29.3.09.3.09.9.91.7.69.4.68.12.0

Data Frame

id	time	status	ABCB1	ABL1	ADA	AHR	AICDA
HC59	0	HC	7.43	6.33	6.87	9.31	3.97

Save the commands in your script:

```
covid <- read.csv("covid.csv")
View(covid)
```

Yes, it's useful! (and add comments)

Import Cancel

Extract rows and columns with [,] or \$

- With a dollar sign

```
covid$IFNG
```

- With integers

```
covid[, c(1, 2, 4, 156)]
```

- With booleans

```
covid[covid$status != "HC", ]
```

- With character strings...

```
covid[, c("IFNG")]
```

- Or with combinations of one or several techniques

```
covid$IFNG[covid$status == "HC"]
```

```
covid[covid$status == "nCOV", 1:3]
```

```
covid[
```

```
  covid$status == "nCOV",
```

```
  c("IL1A", "IL1B", "IL1R1")]
```


Colors: the colourpicker Add-in

(super useful)

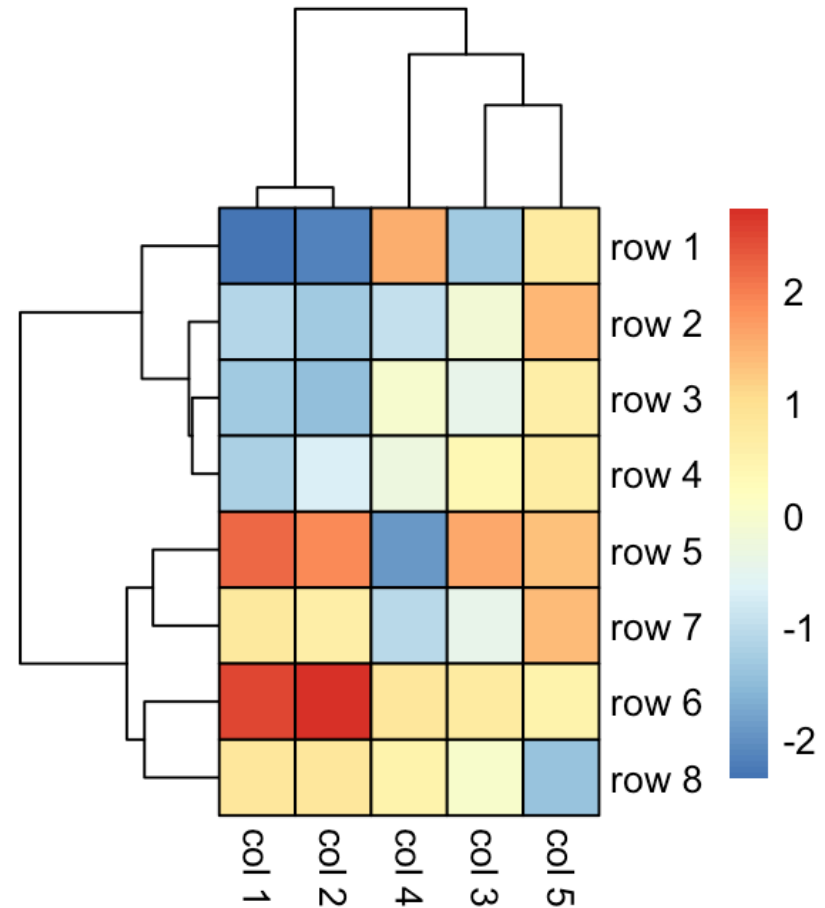


pheatmap: “Pretty” heatmaps

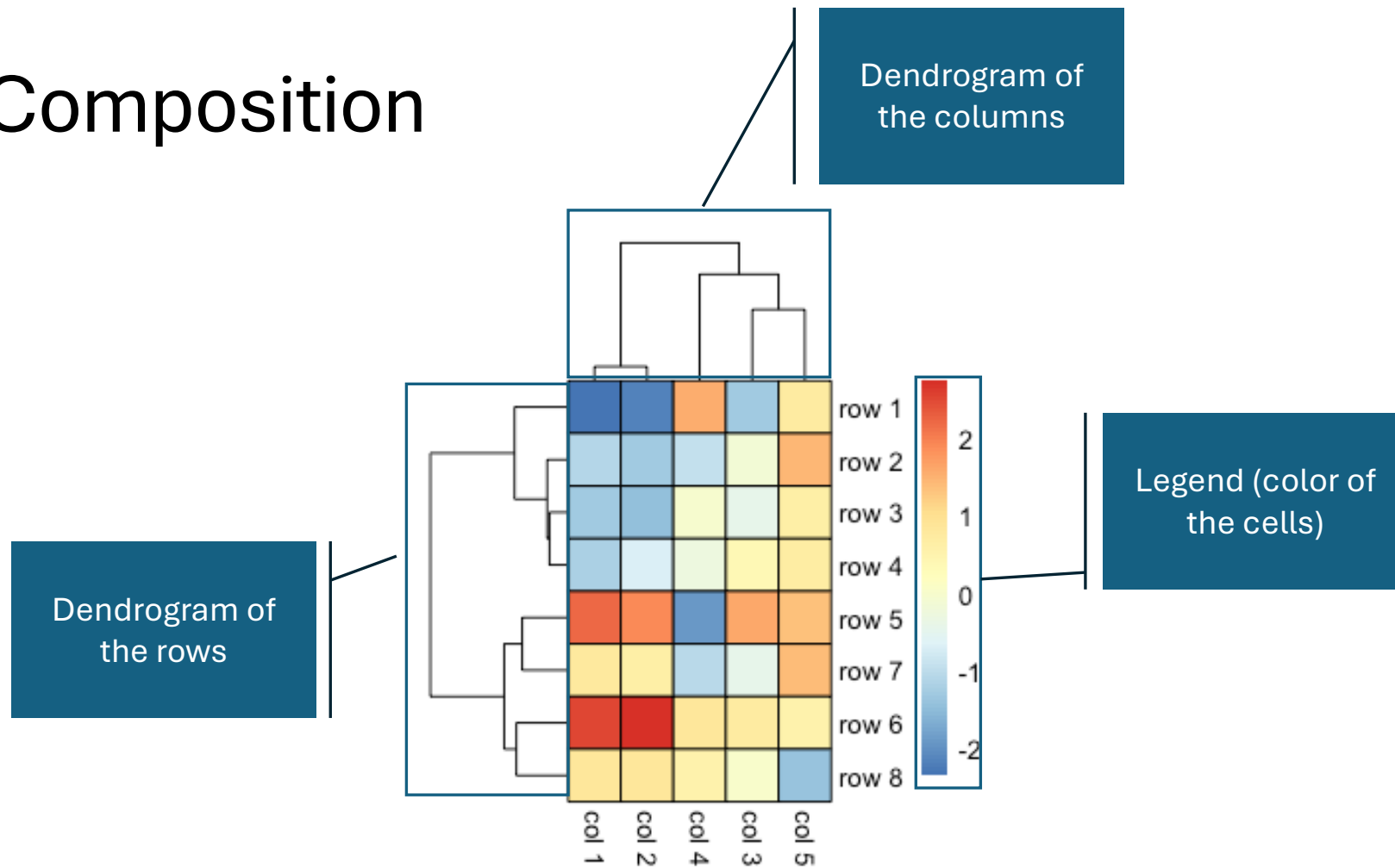


What is it?

	col 1	col 2	col 3	col 4	col 5
row 1	-2.34	-2.16	-1.28	1.54	0.75
row 2	-1.10	-1.30	-0.11	-0.96	1.45
row 3	-1.29	-1.47	-0.44	-0.02	0.65
row 4	-1.18	-0.67	0.39	-0.30	0.70
row 5	2.22	1.92	1.60	-1.90	1.34
row 6	2.53	2.75	0.75	0.86	0.52
row 7	0.78	0.65	-0.41	-1.03	1.38
row 8	0.84	0.83	0.00	0.56	-1.39



Composition



Demo

```
library(pheatmap)
```

```
M <- matrix(rnorm(35), 5, 7)
```

```
dimnames(M) <- list(letters[1:5], LETTERS[1:7])
```

```
pheatmap(mat = M)
```

Exercise

Create a heatmap of the expression of genes IL1A, IL1B, IL1R1, CD4, CD8A, and CD8B.

Bonus constraints:

- show only cases
- use Ward agglomeration method
- use a correlation distance on the columns
- change the colors
-