SciViews : : CHEAT SHEET

SciViews :: R

SciViews::R provides additional functions on top of **tidyverse**. To use it type:

```
SciViews::R

.?topic or about("topic") - get help
```

Read datasets

read() unifies the data importation methods and also loads datasets from R packages.

```
ub <- read(« urchin_bio",
package = "data.io") - Import data from package

ub1 <- read("file.csv") - Import local data

ub1 <- read$csv("file.csv")  or ub1 <-
read("file.csv", type = "csv") - Import local
data
```

write() unifies the data exportation.

```
write(x, files, path)
```

read() and **write()** supports many formats : .txt, .rds, .sas,…

```
Data_types() - Format of data supported
```

Workflow

Function are building blocks. They can be *nested*, *piped* (**%>.%** operator), or used in *successive statements*. A pipeline is usually more readable.

```
ub <- read("urchin_bio", package = "data.io")
```

- Successive statements : select then filter data

```
ub1 <- select(ub, 1:5)
ub2 <- filter(ub1, origin == « Farm")
```

- Nesting function

```
ub2 <- filter(select(ub, 1:5),
   origin == "Farm")
```

- Pipeline with flow

```
ub %>.%
  select(., c(1:5)) %>.%
  filter(., origin == "Farm") -> ub2
```

%>.% is an explicit pipe (dot must be specified). Less ambiguous than tidyverse's pipe %>%.

Data visualisation

chart() uses 4 rules against ggplot()

```
ub <- read("urchin_bio", package = "data.io")
ggplot(data = ub, mapping = aes(x = weight, y = height, colour
= origin) +
   geom_point()
```

1. Replace **ggplot()** by **chart()**

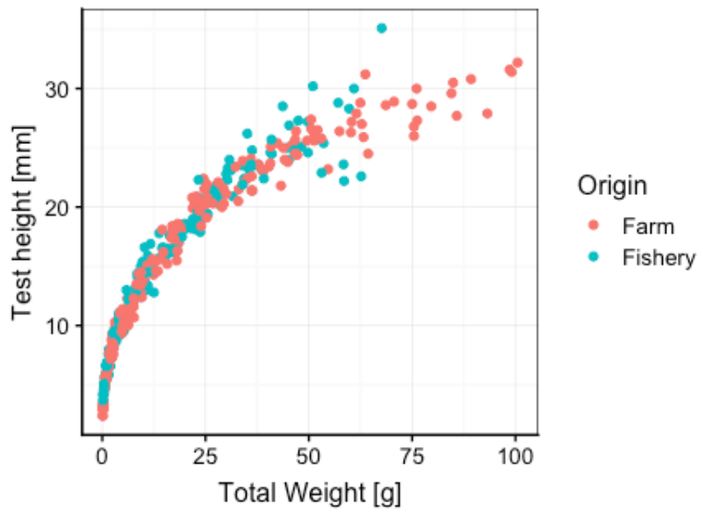
```
chart(data= ub, aes(x = weight, y = height, colour = origin)) +
  geom_point()
```

2. Replace argument **aes()** by **f_aes()** to use formula

```
ggplot(data = ub, f_aes(height ~ weight %col=% origin)) +
  geom_point()
```

3. Use chart with formula syntax

```
chart(ub, formula = height ~ weight %col=% origin) +
  geom_point()
```



In addition **chart()** uses associated metadata (labels and units) to provide a plot close to publication ready.

```
ggplot(data = ub, mapping = aes(x = weight, y = height) +
   geom_point() +
   facet_grid( ~ origin)
```

4. Use facets simply

```
chart(ub, formula = height ~ weight | origin) +
   geom_point()
```

chart() provides a unified interface for base plots, lattice and ggplot2 with argument **type** or with **$**

```
chart(ub, formula = height ~ weight %col=% origin, type =
"geom_point") - type = e.g. "xyplot" or "base"

chart$geom_point(ub, formula = height ~ weight %col=% origin)
```

Reproductible research

Respect the three rules of reproductible research below

1. Organise your analysis in Project with several files

- Data : all datasets
- R : all scripts
- Analysis : all reports, presentations,…

2. Use a portative project

- Use only a relative path

3. Check that all analysis are executables

SciViews snippets

The **SciViews Snippets** in RStudio are organised in a succession of drop-down menu in RStudio.

...	First level	Second level	Description
	..d dataframes	**.dm** managements	Import and write data
		.dr reshape	Rename and arrange columns
		.do observations	Extract rows
		.dv variables	Extract and compute new columns
		.ds summarise	Summarise a datasets
		.dg group data	Group data by factor
		.dc combine	Combine several datasets
	..e exploratory stats	**.es** summary	Summarise datasets
		.ec contingency	Create and visualise a contingency table
	..c charts	**.cu** univariate	plot univariate variable
		.cb bivariate	plot two variables
		.cm multivariate	plot several variables
	..h hypothesis test	**.hc** contingency	Apply a chi2 test
		.hd distribution	Apply a shapiro wilk test
		.hm means	Apply t-test and anova
		.hn nonparametric	Apply WMW and Kruskal-Wallis test
		.hp proportions	Apply a proortion test
		.hv variances	Apply a Bartlett and Levene test
		.hc correlation	Apply a correlation test
	..i (d)istributions	**.iu** uniform	Study a uniform distribution
		.in normal	Study a normal distribution
		.il log-normal	Study a log-normal distribution
		.it t (Student)	Study a Student distribution
		.ib binomial	Study a Binomial distribution
		.ip poissons	Study a Poissons distribution
		.ic chi2	Study a chi2 distribution
		.if F	Study a Fischer distribution
		.ia annotations	Add annotation on the plot of each distribution
	..m models	**.ml** linear	Apply a linear model
		.mt tools	Export linear model in dataframe
	..t tools	**.tm** memory	Quatify de place of an R object

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