



Base R graphics

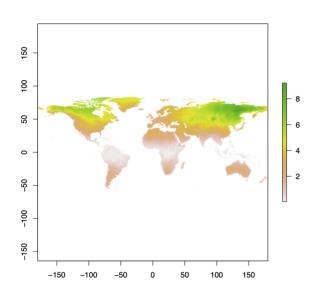
R Foundations for Life Scientists

Marcin Kierczak

Example graphics

Pettersson).





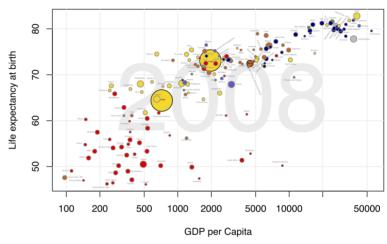
Stability of the climate (courtesy of Dr. Mats



Example graphics







Graphical devices



The concept of a **graphical device** is crucial for understanding R graphics.

A device can be a screen (default) or a file. Some R packages introduce their own devices, e.g. Cairo device. Creating a plot entails:

- opening a graphical device (not necessary for plotting on screen),
- plotting to the graphical device,
- closing the graphical device (very important!)

The most commonly used graphical devices are:

- screen,
- bitmap/raster devices: png(), bmp(), tiff(), jpeg()
- vector devices: svg(), pdf(),
- Cairo versions of the above devices for Windows users they offer higher quality graphics, For more information visit this link.

Working with graphical devices



```
png(filename = 'myplot.png', width = 320, height = 320, antialias = T) plot(x=c(1,2,7), y=c(2,3,5)) dev.off()
```

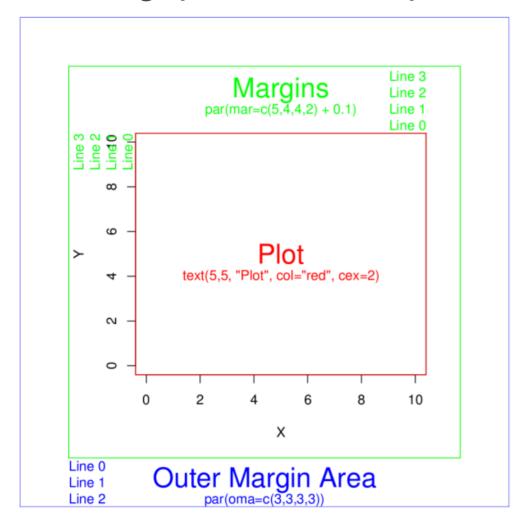
What we did was, in sequence:

- open a graphical device, here png() with some parameters,
- do the actual plotting to the device using plot() and
- close the graphical device using dev.off().

It is of paramount importance to remember to close graphical devices. Otherwise, our plots may end up in some random weird files or on screens.

Standard graphical device viewport





source: rgraphics.limnology.wisc.edu

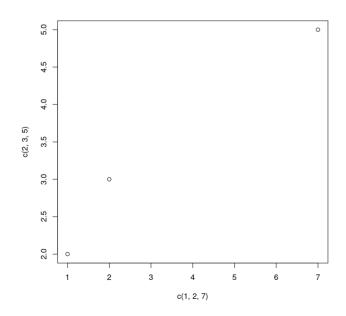
base::plot() basics



base::plot() is a basic command that lets you visualize your data and results. It is very powerful
yet takes some effort to fully master it. Let's begin with plotting three points:

- A(1,2);
- B(2,3);
- C(7,5);

$$plot(x=c(1,2,7), y=c(2,3,5))$$

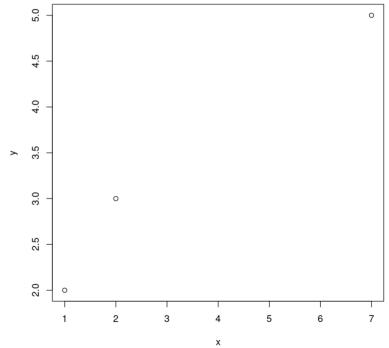


Anatomy of a plot — episode 1



For convenience, we will create a data frame with our points:

```
olot(df)
```



Anatomy of a plot — episode 2



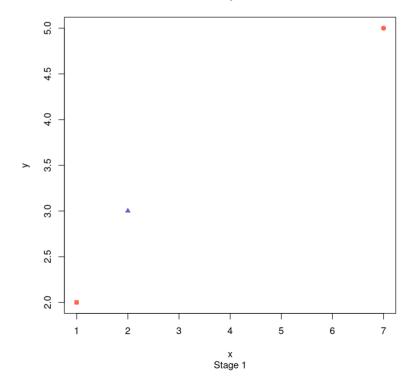
There is many parameters one can set in plot(). Let's have a closer look at some of them:

- pch type of the plotting symbol
- col color of the points
- cex scale for points
- main main title of the plot
- sub subtitle of the plot
- xlab X-axis label
- ylab Y-axis label
- las axis labels orientation
- cex.axis axis lables scale

Let's make our plot a bit fancier...

```
# recycling rule in action!
plot(df, pch = c(15, 17, 19), col = c("tomate
    sub = "Stage 1")
```

Three points



Graphical parameters



Graphical parameters can be set in two different ways:

- as plotting function arguments, e.g. plot(dat, cex = 0.5)
- using par() to set parameters globally

```
# read current graphical parameters
par()
# first, save the current parameters so that you
# can set them back if needed
old_par <- par() # should work in theory, practise varies :-(
# now, modify what you want
par(cex.axis = 0.8, bg='grey')
# do your plotting
plot(.....)
# restore the old parameters if you want
par(old_par)</pre>
```

The pch parameter



A 25	26	*	•	Q	0
•	•	•	•	23	♦
19	20	21	22		24
⊞	SS	M	1 6	•	A
13	14	15		17	18
▽ 7	⊠	*	♦	Ф	XX
	8	9	10	11	12
_ 1	O 2	∆ 3	+ 4	× 5	♦ 6

How to make the pch cheatsheet



```
# create a grid of coordinates
coords <- expand.grid(1:6,1:6)
# make a vector of numerical pch symbols
pch.num <- c(0:25)
# and a vector of character pch symbols
pch.symb <- c('*', '.', 'o', '0', '0', '-', '+', '|', '%', '#')
# plot numerical pch
plot(coords[1:26,1], coords[1:26,2], pch=pch.num,
bty='n', xaxt='n', yaxt='n', bg='red',
xlab='', ylab='')
# and character pch's
points(coords[27:36,1], coords[27:36,2], pch=pch.symb)
# label them
text(coords[,1], coords[,2], c(1:26, pch.symb), pos = 1,
col='slateblue', cex=.8)</pre>
```

Now, make your own cheatsheet for the lty parameter!

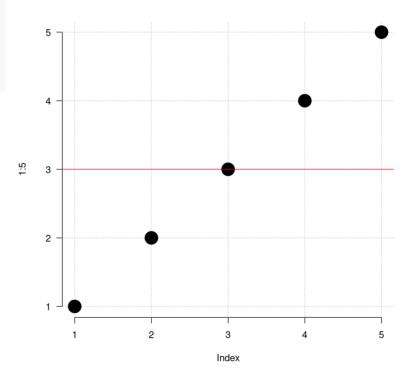
Layers



Elements are added to a plot in the same order you plot them. It is like layers in a graphical program. Think about it! For instance the auxiliary grid lines should be plotted before the actual data points.

```
# make an empty plot
plot(1:5, type = "n", las = 1, bty = "n")
grid(col = "grey", lty = 3)
points(1:5, pch = 19, cex = 3)
abline(h = 3, col = "red")
```

The line overlaps one data point. It is better to plot it before plotting points()



Some thoughts about plotting



There is a few points you should have in mind when working with plots:

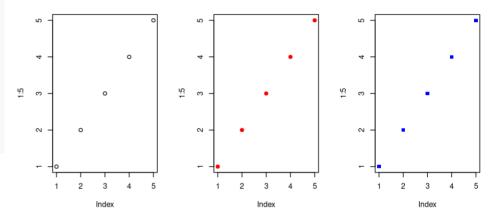
- raster or vector graphics,
- colors, e.g. color-blind people, warm vs. cool colors and optical illusions,
- avoid complications, e.g. 3D plots, pie charts etc.,
- use black and shades of grey for things you do not need to emphasize, i.e. basically everything except your main result,
- avoid 3 axes on one figure.

Many plots on one figure

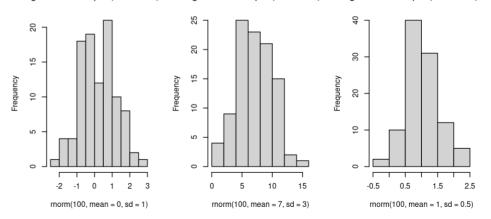


```
par(mfrow=c(2,3))
plot(1:5)
plot(1:5, pch=19, col='red')
plot(1:5, pch=15, col='blue')
hist(rnorm(100, mean = 0, sd=1))
hist(rnorm(100, mean = 7, sd=3))
hist(rnorm(100, mean = 1, sd=0.5))
par(mfrow=c(1,1))
```

Alternative: use par(mfcol=c(3,2)).



Histogram of rnorm(100, mean = 0, sdHistogram of rnorm(100, mean = 7, sdIstogram of rnorm(100, mean = 1, sd



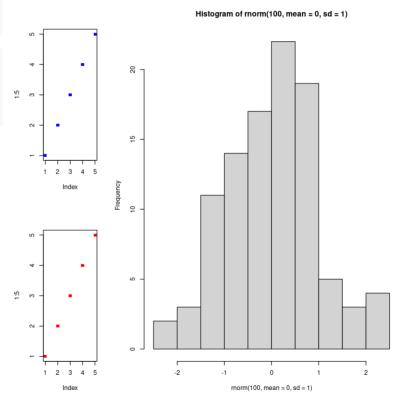
Using graphics::layout()



```
M <- matrix(c(1,2,2,2,3,2,2,2), nrow = 2, nc
layout(mat = M)
plot(1:5, pch=15, col='blue')
hist(rnorm(100, mean = 0, sd=1))
plot(1:5, pch=15, col='red')</pre>
```

```
M <- matrix(c(1,2,2,2,3,2,2), nrow = 2, nc
layout(mat = M)
plot(1:5, pch=15, col='blue')
hist(rnorm(100, mean = 0, sd=1))
plot(1:5, pch=15, col='red')</pre>
```

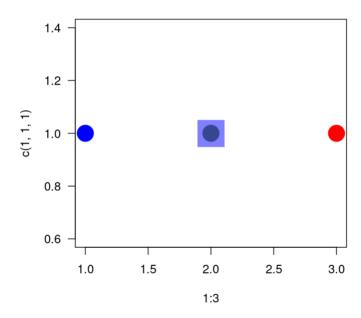
```
M
## [,1] [,2] [,3] [,4]
## [1,] 1 2 2 2
## [2,] 3 2 2 2
```



Defining colors



```
mycol <- c(rgb(0, 0, 1), "olivedrab", "#FF0000")
plot(1:3, c(1, 1, 1), col = mycol, pch = 19, cex = 3)
points(2, 1, col = rgb(0, 0, 1, 0.5), pch = 15, cex = 5)
```



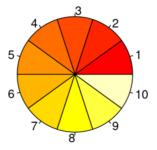
Color palettes



There some built-in palettes: default, hsv, gray, rainbow, terrain.colors, topo.colors, cm.colors, heat.colors

```
mypal <- heat.colors(10)
mypal
pie(x = rep(1, times = 10), col = mypal)

## [1] "#FF0000" "#FF2400" "#FF4900" "#FF6D00" "#FF9200" "#FFB600" "#FFDB00"
## [8] "#FFFF00" "#FFFF40" "#FFFFBF"</pre>
```



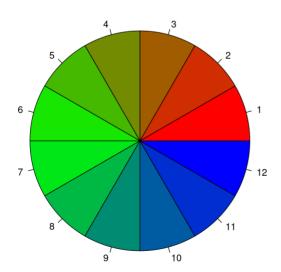
Custom color palettes



You can easily create custom palettes:

```
mypal <- colorRampPalette(c("red", "green",
pie(x = rep(1, times = 12), col = mypal(12))
class(mypal)</pre>
```

```
## [1] "function"
```



Note: grDevices::colorRampPalette() returns a function for generating colors based on the defined custom palette!

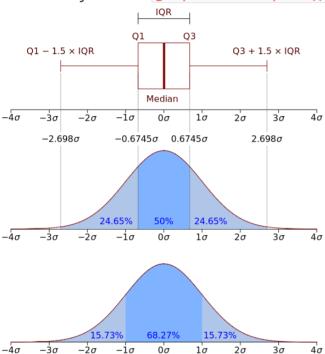
There is an excellent package RColorBrewer that offers a number of pre-made palettes, e.g. color-blind safe palette.

Package wesanderson offers palettes based on Wes Anderson's movies:-)

Box-and-whiskers plot — theory



There are also more specialized R functions used for creating specific types of plots. One commonly used is graphics::boxplot()

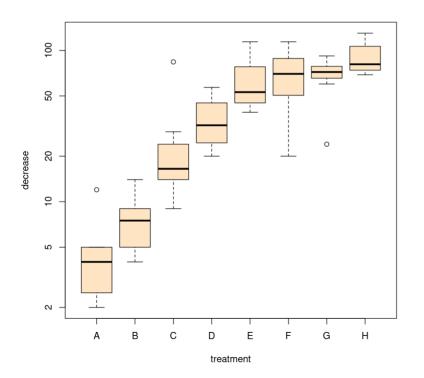


Rule of thumb. If median of one boxplot is outside the box of another, the median difference is likely to be significant $\alpha=5\%$.

Box-and-whiskers plot

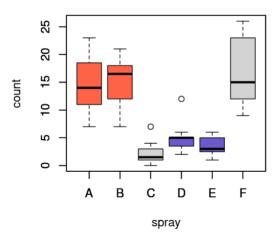


```
boxplot(decrease ~ treatment,
data = OrchardSprays,
log = "y", col = "bisque",
varwidth=TRUE)
```



The add=TRUE parameter in plots allows you to compose plots using previously plotted stuff!

```
attach(InsectSprays)
boxplot(count~spray, data=InsectSprays[spray
boxplot(count~spray, data=InsectSprays[spray
boxplot(count~spray, data=InsectSprays[spray
detach(InsectSprays)
```

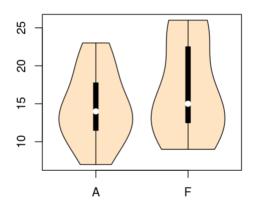


Violin plots



Package vioplot empowers your graphics repertoire with a variation of box-and-whiskers plot called *violin plot*.

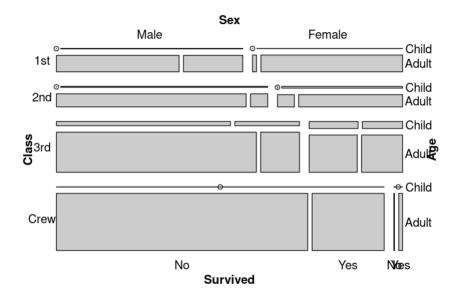
```
attach(InsectSprays)
vioplot::vioplot(count[spray=="A"],
count[spray=="F"],
col="bisque",
names=c("A","F"))
detach(InsectSprays)
```



A violin plot is very similar to a boxplot, but it also visualizes distribution of your datapoints.

Plotting categorical data



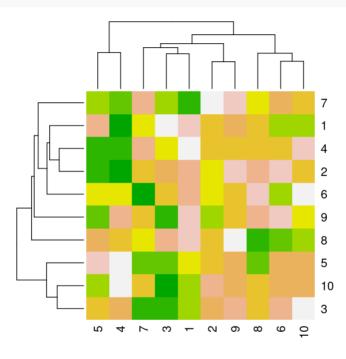


Package vcd provides a lot of ways of visualizing categorical data.

Plotting simple heatmaps



```
heatmap(matrix(rnorm(100, mean = 0, sd = 1), nrow = 10),
col=terrain.colors(10))
```



Thank you! Questions?



