

# R programming in Life Sciences

## Introduction to R graphics.

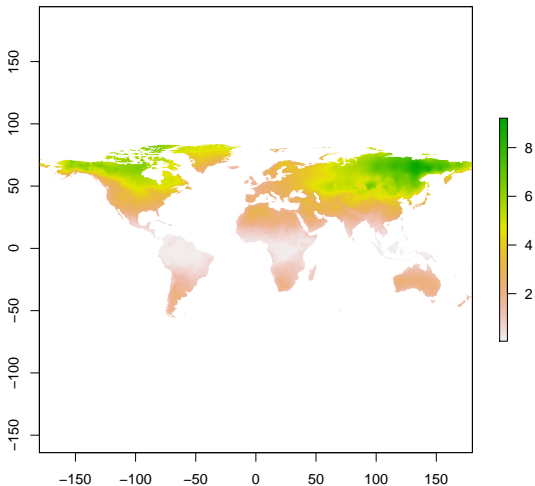
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Uppsala, SWEDEN

04 Nov 2016, Uppsala

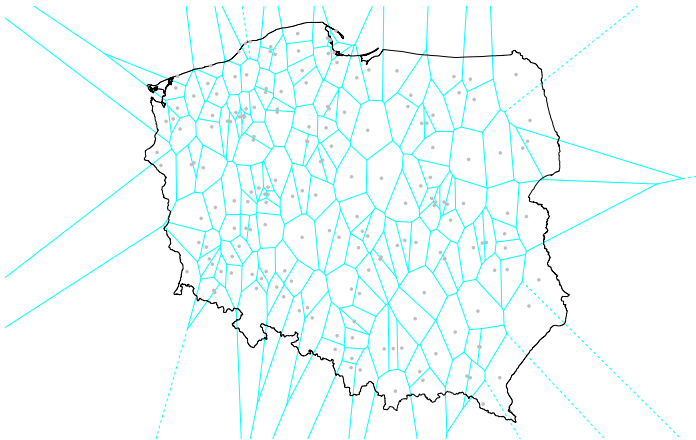
# Graphics

Example – stability of the climate, courtesy of dr. Mats Pettersson



# Graphics

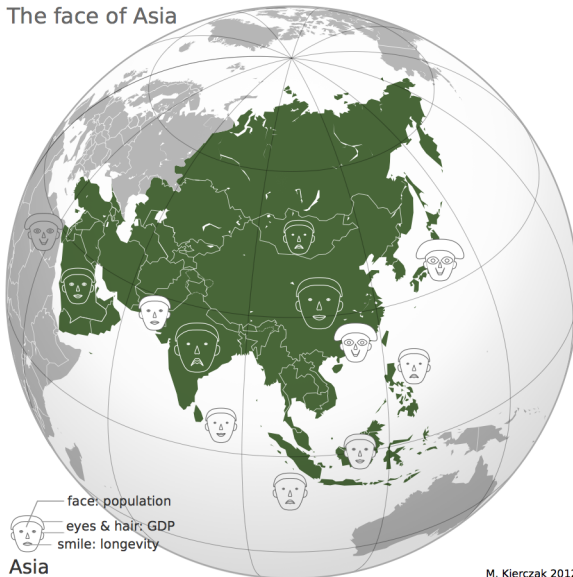
## Example – airport-based Voronoi tessellation of Poland



# Graphics

## Example – The face of Asia

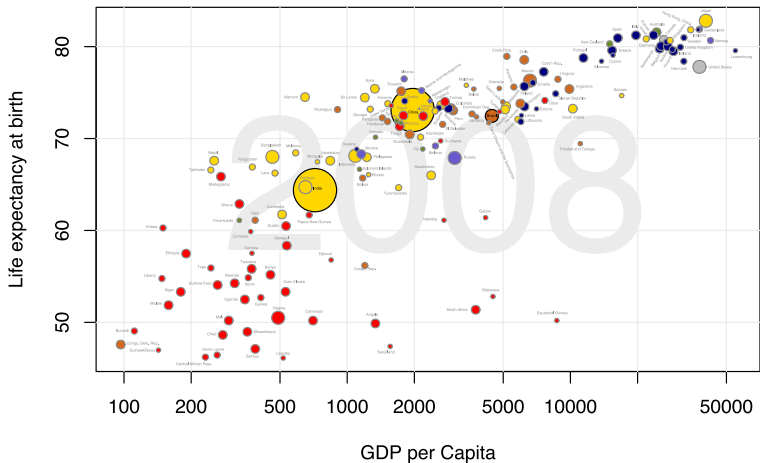
### The face of Asia



M. Kierczak 2012

# Graphics

## Example – Gapminder-type plot



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 <http://stat.ethz.ch/R-manual/R-devel/library/grDevices/html/Devices.html>

# Graphics

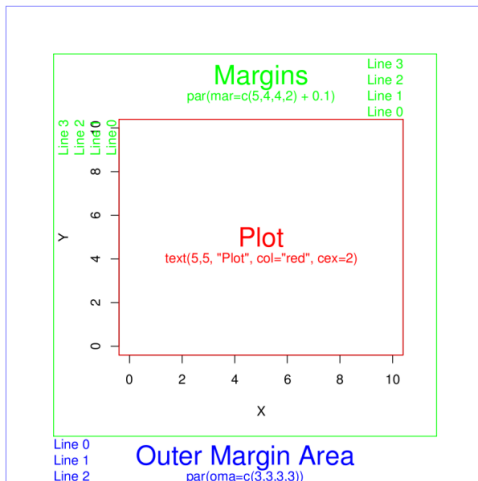
## Working with graphical devices

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



# Graphics

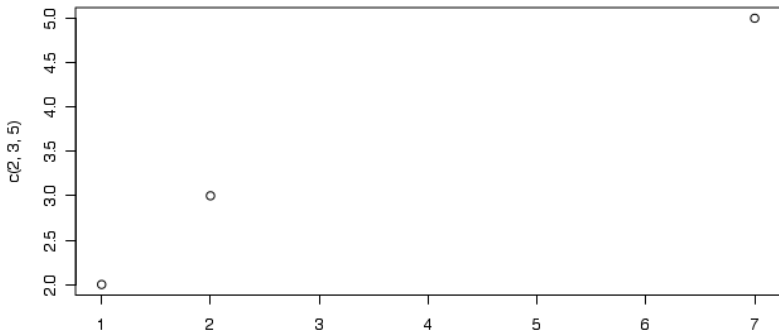
## Standard graphical device viewport



source: [rgraphics.limnology.wisc.edu](http://rgraphics.limnology.wisc.edu)

`plot()` is the 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))
```



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

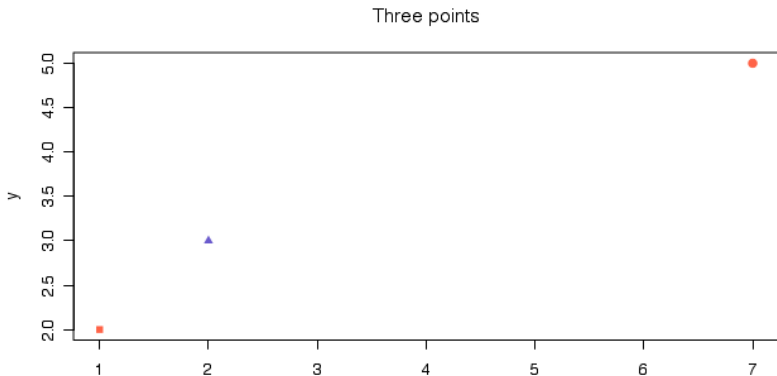
```
df <- data.frame(x=c(1,2,7), y=c(2,3,5),  
                 row.names=c("A", "B", "C"))
```

```
df
```

```
##   x y  
## A 1 2  
## B 2 3  
## C 7 5
```

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

```
plot(df, pch=c(15,17,19),  
      col=c("tomato", "slateblue"), # recycling rule in action!  
      main="Three points", sub="Stage 1")
```



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 labels scale

Graphical parameters can be set in two different ways:

- as plotting function arguments, e.g. `plot(dat, cex=0.5)`
- using `par()`

```
# read current graphical parameters
par()
# first, save the current parameters so that you
# can set them back if needed
opar <- 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(opar)
```

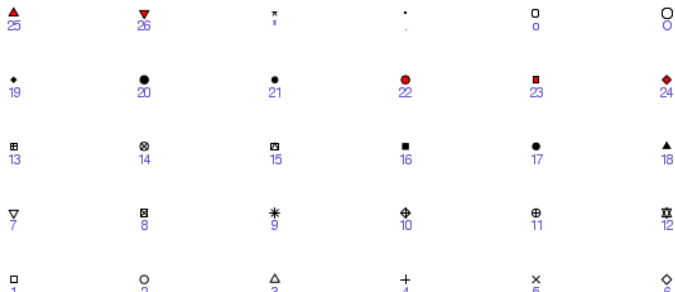
# Graphics

## Graphical parameters – pch

```
# 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)
```

# Graphics

## Graphical parameters – pch result

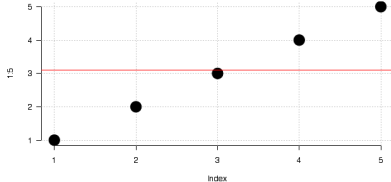


Now, make your only cheatsheet for the **lty** parameter!



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')  
# plot grid  
grid(col='grey', lty=3)  
# plot the actual data  
points(1:5, pch=19, cex=3)  
# plot a line  
abline(h = 3.1, col='red')  
# you see, it overlaps the  
# data point. It is better  
# to plot it before points()
```



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 greys for things you do not need to emphasize, i.e. basically everything except your main result,
- avoid 3 axis.

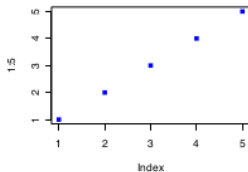
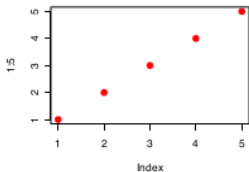
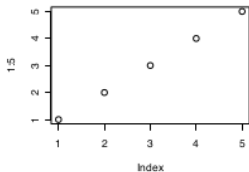
# Graphics

## Many plots on one figure

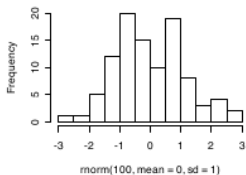
```
par(mfrow=c(2,3))
plot(1:5)
plot(1:5, pch=19, col='red')
plot(1:5, pch=15, col='blue')
hist(rnorm(100, mean = 0, sd=1))
hist(rnorm(100, mean = 7, sd=3))
hist(rnorm(100, mean = 1, sd=0.5))
par(mfrow=c(1,1))
```

# Graphics

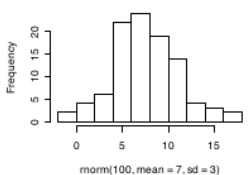
Many plots on one figure – result



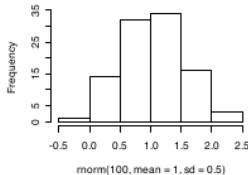
Histogram of `morm(100, mean = 0, sd = 1)`



Histogram of `morm(100, mean = 7, sd = 3)`



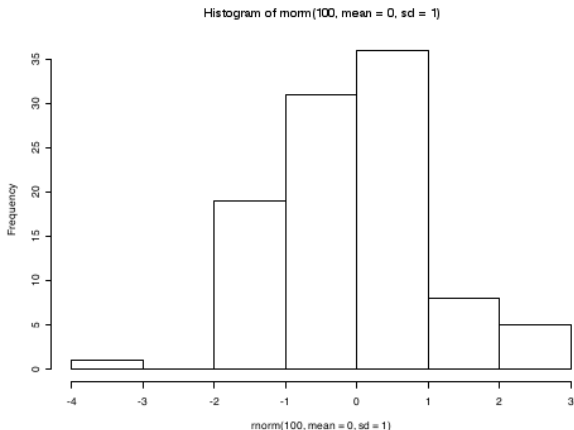
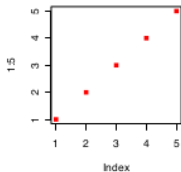
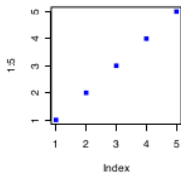
Histogram of `morm(100, mean = 1, sd = 0.5)`



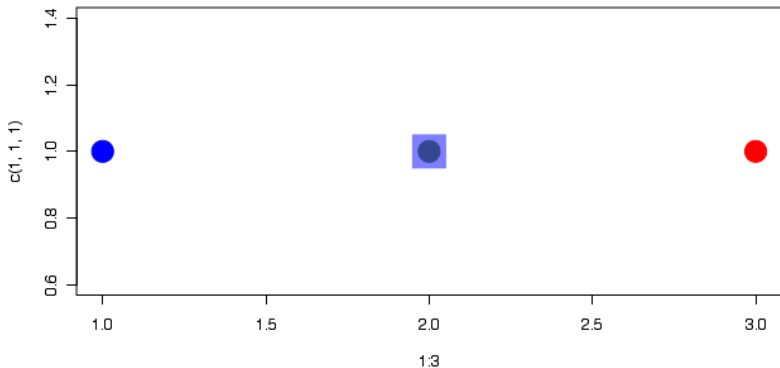
# Graphics

## Many plots on one figure – layout

```
layout(matrix(c(1, 2, 2, 2, 3, 2, 2, 2), nrow = 2, ncol = 4, byrow = T),  
plot(1:5, pch = 15, col = "blue"),  
hist(rnorm(100, mean = 0, sd = 1)),  
plot(1:5, pch = 15, col = "red"))
```



```
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)
```

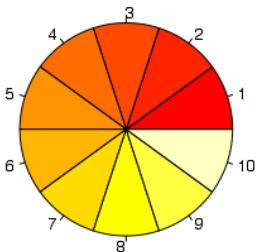


There some built-in palettes: default, hsv, gray, rainbow, terrain.colors, topo.colors, cm.colors, heat.colors

```
mypal <- heat.colors(10)
mypal

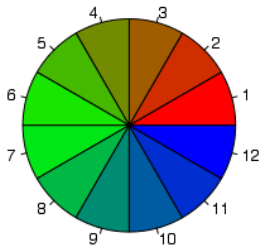
## [1] "#FF0000FF" "#FF2400FF" "#FF4900FF" "#FF6D00FF" "#FF9200FF"
## [6] "#FFB600FF" "#FFDB00FF" "#FFFF00FF" "#FFFF40FF" "#FFFFBFFF"

pie(x = rep(1, times = 10), col = mypal)
```



You can easily create custom palettes:

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



Note that `colorRampPalette` returns a function!



- 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 movies:-)

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

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

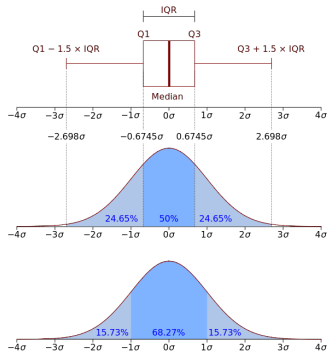
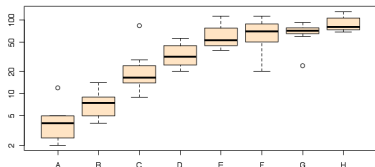


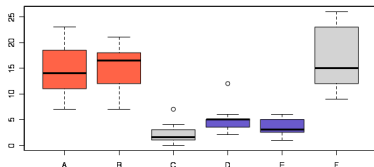
Figure: source:  
[commons.wikimedia.org](https://commons.wikimedia.org)

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



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

```
attach(InsectSprays)
boxplot(count~spray,
        data=InsectSprays[spray %in% c("C","F"),],
        col="lightgray")
boxplot(count~spray,
        data=InsectSprays[spray %in% c("A","B"),],
        col="tomato", add=T)
boxplot(count~spray,
        data=InsectSprays[spray %in% c("D","E"),],
        col="slateblue", add=T)
detach(InsectSprays)
```

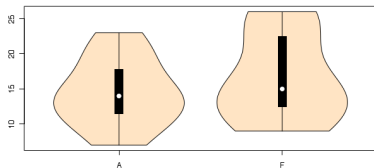


Package `vioplot` lets you plot *violin plots*. A violin plot is very similar to a boxplot, but it also visualizes distribution of your datapoints.

```
library(vioplot)
```

```
## Loading required package: sm  
## Package 'sm', version  
2.2-5.4: type help(sm) for  
summary information
```

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



# Graph gallery

## Categorical data with vcd

```
library(vcd) # load the vcd package

## Loading required package: grid

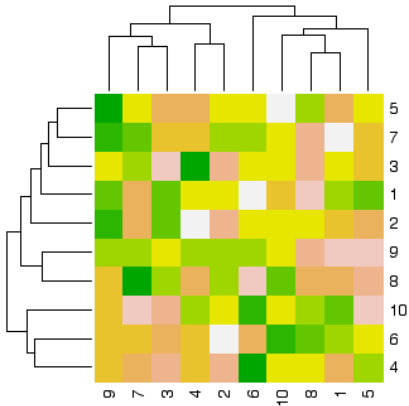
data(Titanic) # Load the data
mosaic(Titanic, labeling=labeling_border(rot_labels = c(0,0,0,0))) # Plot the data
```



# Graph gallery

## Heatmaps

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



For more awesome examples visit: <http://www.r-graph-gallery.com>