探索式資料分析
統計圖表

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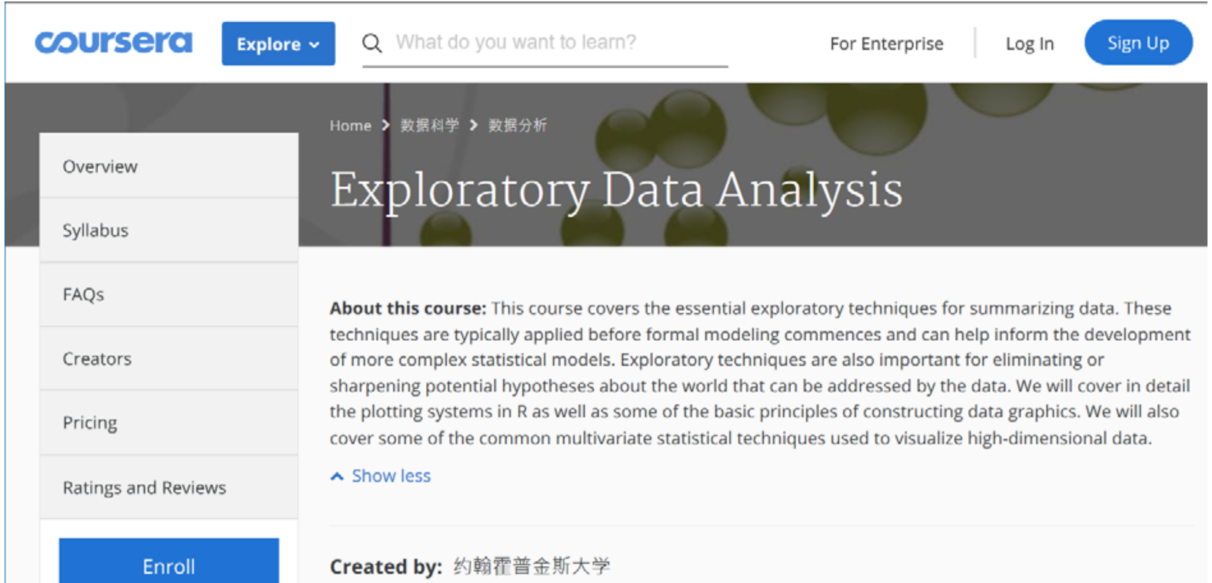
http://www.hmwu.idv.tw

主要參考書目

https://www.coursera.org/learn/exploratory-data-analysis



Exploratory Data Analysis

About this course: This course covers the essential exploratory techniques for summarizing data. These techniques are typically applied before formal modeling commences and can help inform the development of more complex statistical models. Exploratory techniques are also important for eliminating or sharpening potential hypotheses about the world that can be addressed by the data. We will cover in detail the plotting systems in R as well as some of the basic principles of constructing data graphics. We will also cover some of the common multivariate statistical techniques used to visualize high-dimensional data.

Created by: 约翰霍普金斯大学

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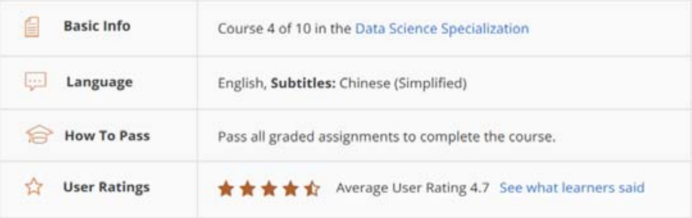
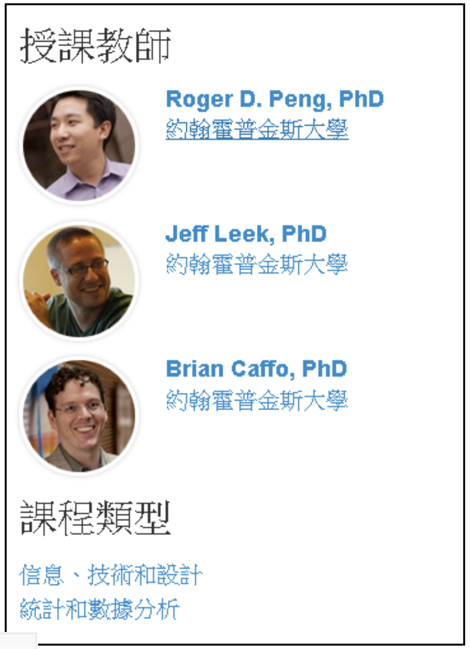


Basic Info	Course 4 of 10 in the Data Science Specialization
Language	English, **Subtitles:** Chinese (Simplified)
How To Pass	Pass all graded assignments to complete the course.
User Ratings	★★★★☆ Average User Rating 4.7 See what learners said



授課教師

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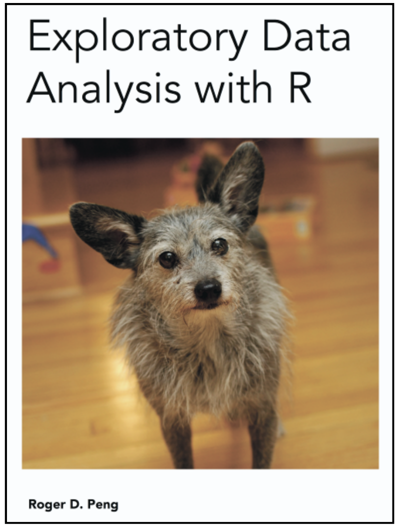
課程類型

信息、技術和設計
統計和數據分析

EDA with R: Course Content

- Making exploratory graphs
- Principles of analytic graphics
- Plotting systems and graphics devices in R
- The base, lattice, and ggplot2 plotting systems in R
- Clustering methods (群集分析)
- Dimension reduction techniques (維度縮減)



Exploratory Data Analysis with R

Roger D. Peng

John Tukey (1915~2000): 統計學界的畢卡索

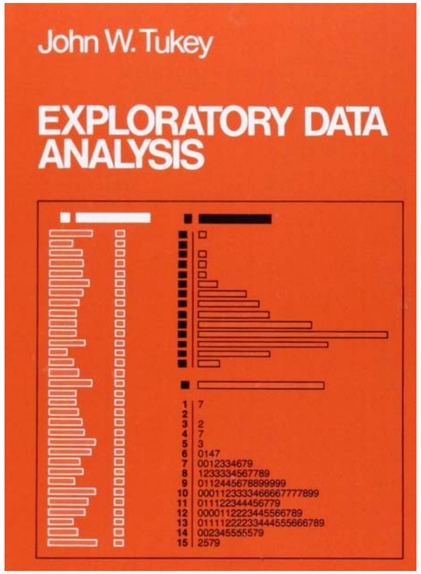
生平

- 布朗大學**化學**學士及碩士。
- 1939年: 普林斯頓大學**數學**博士。(數理統計)
- 二次大戰加入火砲控制研究室，以及後來加入**AT&T**貝爾實驗室(**創立統計組**)，接觸統計上的實際問題。

「對正確的問題有個近似的答案，

勝過對錯的問題有精確的答案。」

"An approximate answer to the right question is worth a great deal more than a precise answer to the wrong question."



John W. Tukey

EXPLORATORY DATA ANALYSIS

對後世的貢獻

- 發明快速傅立葉轉換(FFT)。
- 創造bit (位元)及 software(軟體) 。
- 探索性的資料分析 (Exploratory Data Analysis, EDA, 1977)

Source: http://www.unige.ch/ses/sococ/cl/bib/eda/tukey.html

「統計應該是科學，而非數學！」

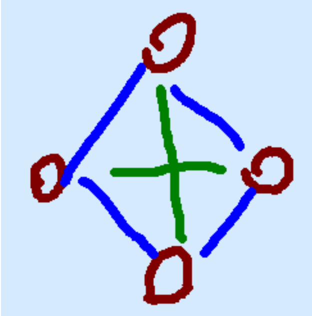
Stanford Linear Accelerator (1973)

他曾挑戰當時主流的數理統計學家，堅持 data analysis 是統計分析中不可忽視的步驟，數學的假設需要 data 加以驗證才可行。 Tukey 說過統計應該是科學，而非數學！

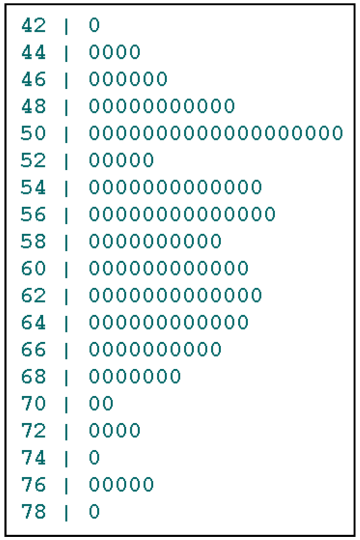
數學思維 vs 統計思維

証明在哪裏? vs 數據在哪裏?

"Let the data speak for themselves"

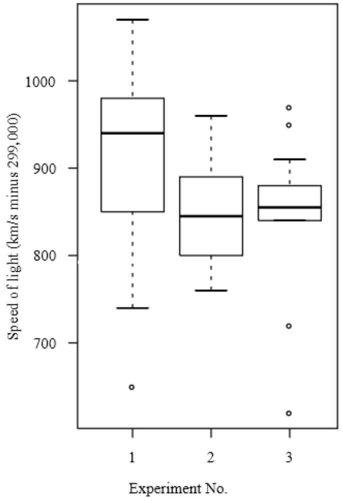


Stem and Leaf Plot



```
42 | 0
44 | 0000
46 | 000000
48 | 00000000000
50 | 0000000000000000000
52 | 00000
54 | 0000000000000
56 | 00000000000000
58 | 0000000000
60 | 000000000000
62 | 0000000000000
64 | 000000000000
66 | 0000000000
68 | 0000000
70 | 00
72 | 0000
74 | 0
76 | 00000
78 | 0
```

Box-and-whisker plot



What is EDA?

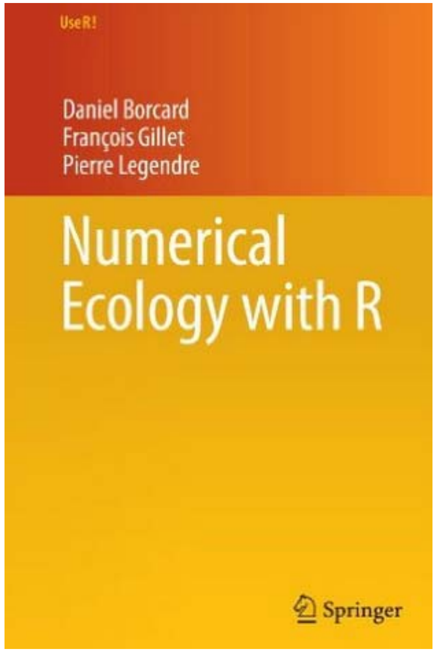
- Exploratory Data Analysis (EDA) is an **approach/philosophy** for data analysis that employs a variety of techniques (mostly **graphical**) to
  - maximize **insight** into a data set;
  - uncover underlying **structure**;
  - extract important variables;
  - detect **outliers** and anomalies (detection of mistakes);
  - test underlying **assumptions**;
  - develop parsimonious **models** (preliminary selection of appropriate models);
  - determine **optimal** factor settings;
  - determine **relationships** among the explanatory variables; and
  - assess the direction and rough size of relationships between explanatory and **outcome variables**.

- You should always look at every variable - you will learn something!

Source: http://www.itl.nist.gov/div898/handbook/eda/section1/eda11.htm

What Do They Say About EDA?

- **Daniel Borcard, Francois Gillet, Pierre Legendre (2011):**
  - A first exploratory look at the data can tell much about them.
  - Information about simple parameters and distributions of variables is important to consider in order to choose more advanced analyses correctly.
  - EDA is often neglected by people who are eager to jump to more sophisticated analyses. It should have an important place.



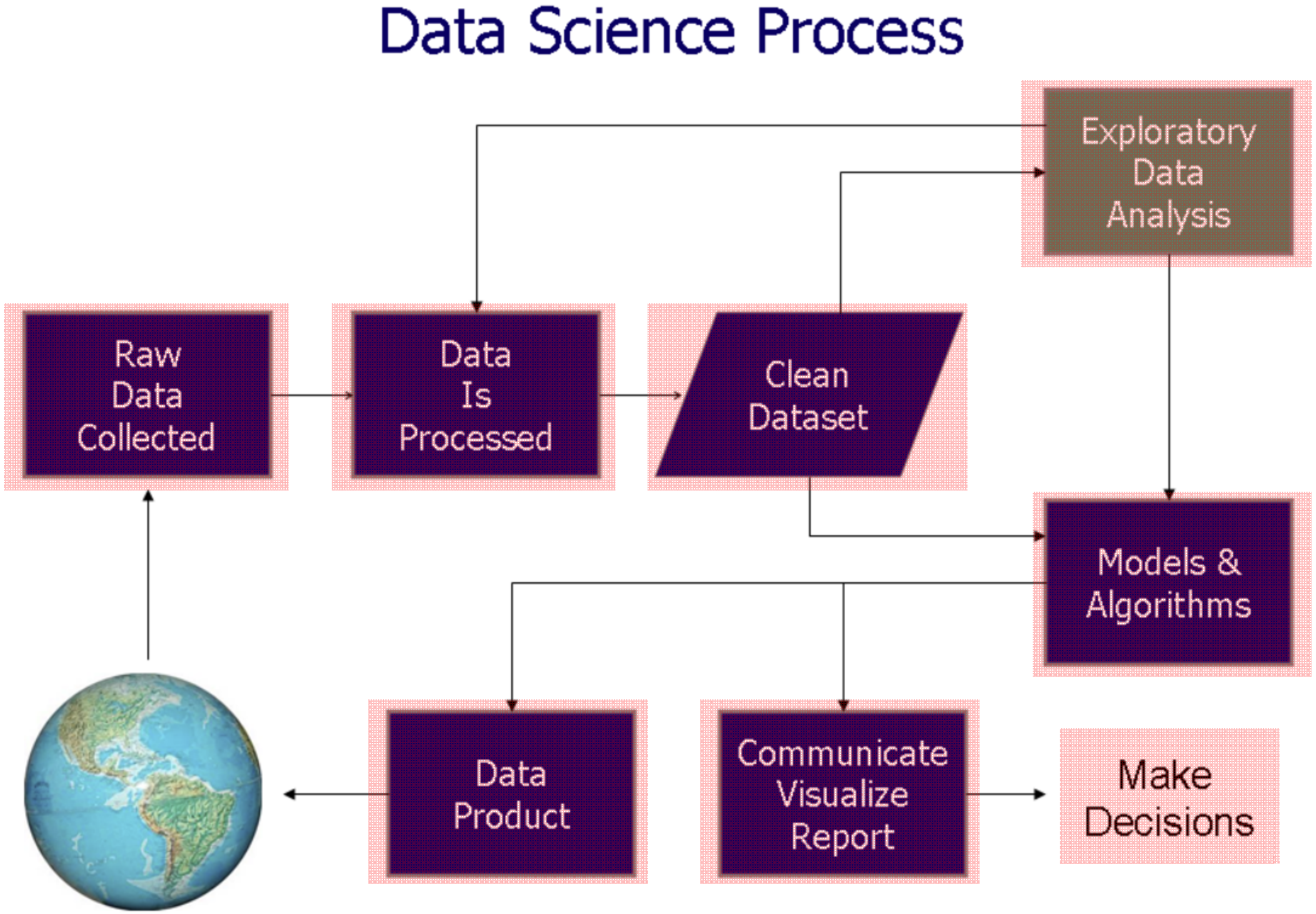
What Do They Say About EDA?

- **Howard J. Seltman (2015)**, Experimental Design and Analysis.
  - EDA need not be restricted to techniques you have seen before; sometimes you need to invent a new way of looking at your data.
  - Perform whatever steps are necessary to become more familiar with your data, check for obvious mistakes, learn about variable distributions, and learn about relationships between variables.
  - EDA is not an exact science, it is a very important art!

Source: google images

Data Analysis Procedures

- Statistics and data analysis procedures can broadly be split into two parts: (1) **Graphical techniques.** (2) **Quantitative techniques.**



Data Science Process

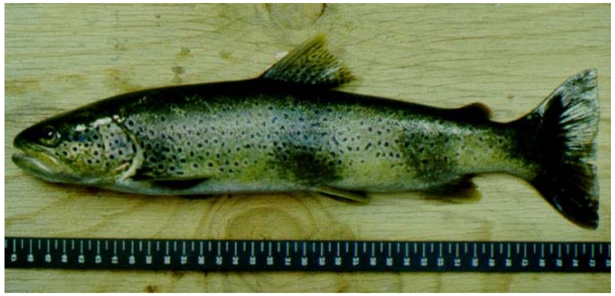
Source: https://en.wikipedia.org/wiki/Exploratory_data_analysis

例子1: The Doubs Fish Data

- **Fish communities** were good biological indicators of these water bodies: Verneaux (1973) (Verneaux et al. 2003) proposed to use **fish species** to characterize ecological zones along European rivers and streams. (River Doubs, 杜河)

- Verneaux proposed a **typology** in four zones, and he named each one after a characteristic species:
  - the **trout (鱒魚，鮭鱒魚) zone** (from the brown trout Salmo trutta fario),
  - the **grayling (鱒魚) zone** (from Thymallus),
  - the **barbell (鲃, 有觸鬚的魚) zone** (from Barbus) and
  - the **bream (歐鯿, 鯉科淡水魚) zone** (from the common bream Abramis brama).

- The two upper zones are considered as the “**Salmonid (鮭魚) region**" and the two lowermost ones constitute the “**Cyprinid (鯉科之魚) region**” .

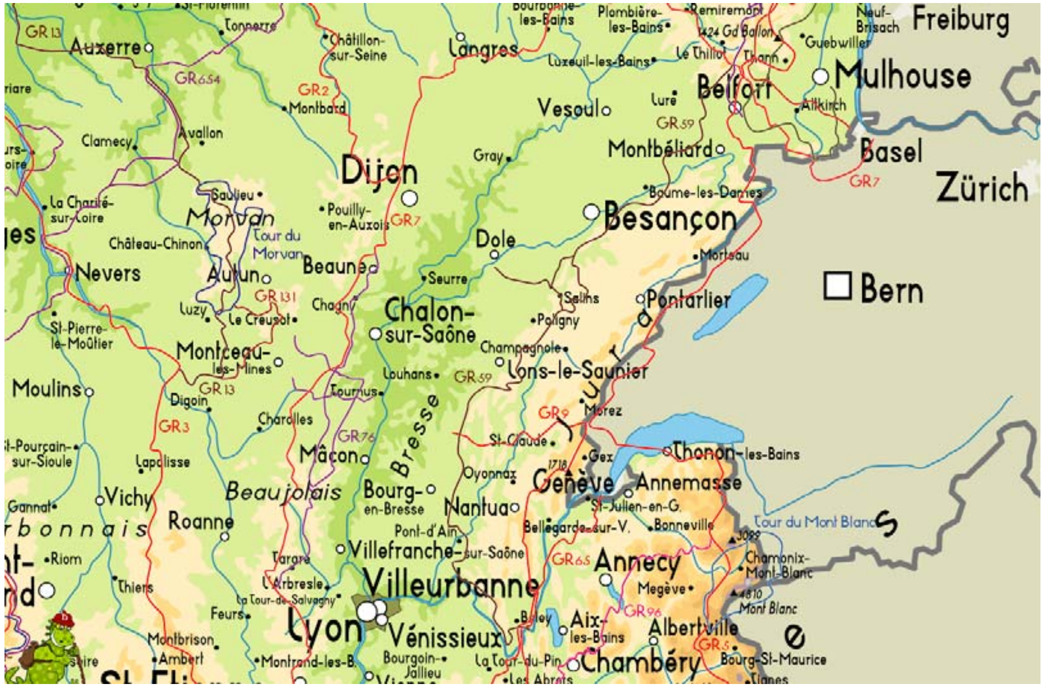


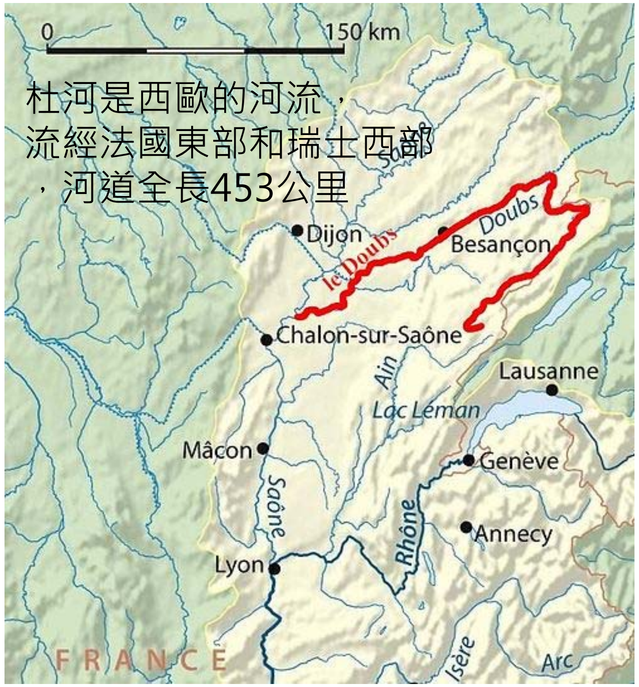
D. Borcard et al., Numerical Ecology with R, Use R, DOI 10.1007/978-1-4419-7976-6_2, © Springer Science+Business Media, LLC 2011

Image Source:

http://www.qub.ac.uk/bb-old/prodohl/TroutConcert/images/gallery/c_lagiader-me07-18-trout.jpg
http://www.bamboorods.ch/guiding/bilder/grayling2.jpg
https://en.wikipedia.org/wiki/Barbus_barbus#/media/File:Barbel.jpg
http://www.ultimateangling.co.za/index.php?topic=15775.0

River Doubs Map




杜河是西歐的河流，流經法國東部和瑞士西部，河道全長453公里

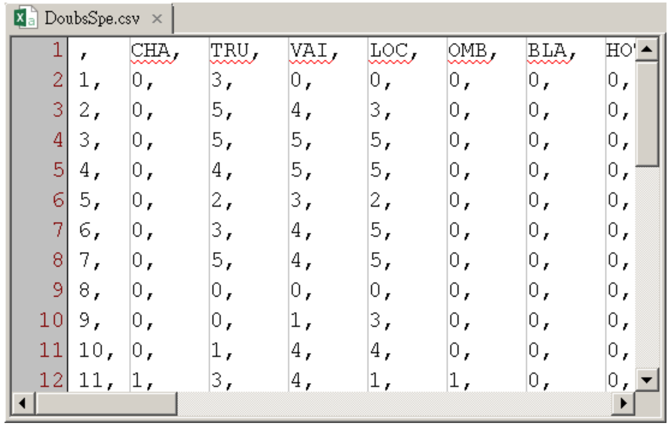
Source: https://en.wikipedia.org/wiki/Doubs_%28river%29

- 背景知識、問題
- 資料收集方式、變數資訊
- 參與人角色 (分析者、廠商、顧主、客戶、居民、...)
- 資料處理、探索(分析)方法
- 呈現: 資料/過程/結果。

The Doubs Fish Data: 檔案

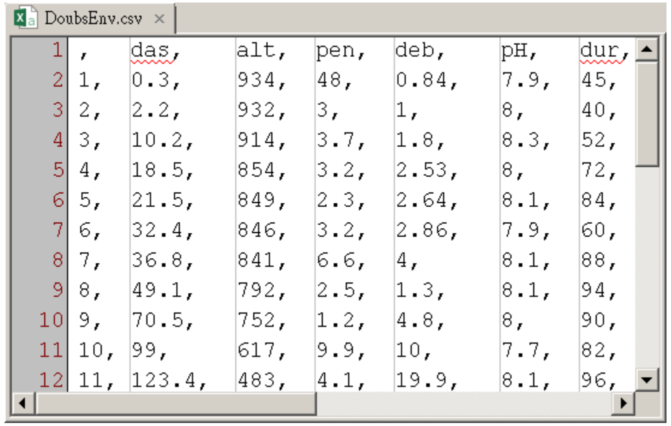
- The Doubs data set have been collected at 30 sites along the Doubs River (near the France–Switzerland border in the Jura Mountains.)

- **DoubsSpe**: contains coded abundances (豐富充足) of 27 fish species.
- **DoubsEnv**: contains 11 environmental variables related to the hydrology, geomorphology and chemistry of the river.
- **DoubsSpa**: contains the geographical coordinates (Cartesian, X and Y) of the sites.



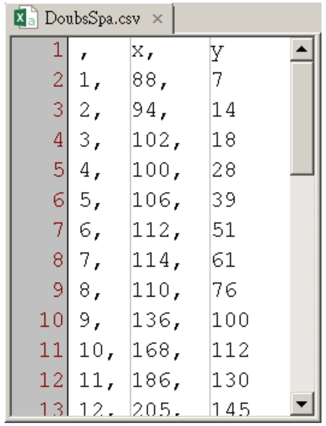
DoubsSpe.csv

```
,    CHA, TRU, VAI, LOC, OMB, BLA, HO'
1,   0,   3,   0,   0,   0,   0,   0,
2,   0,   5,   4,   3,   0,   0,   0,
3,   0,   5,   5,   5,   0,   0,   0,
4,   0,   4,   5,   5,   0,   0,   0,
5,   0,   2,   3,   2,   0,   0,   0,
6,   0,   3,   4,   5,   0,   0,   0,
7,   0,   5,   4,   5,   0,   0,   0,
8,   0,   0,   0,   0,   0,   0,   0,
9,   0,   0,   1,   3,   0,   0,   0,
10,  0,   1,   4,   4,   0,   0,   0,
11,  1,   3,   4,   1,   1,   0,   0,
```



DoubsEnv.csv

```
,   das,   alt, pen, deb,   pH,  dur,
1,  0.3,   934, 48,  0.84,  7.9, 45,
2,  2.2,   932, 3,   1,     8,   40,
3,  10.2,  914, 3.7, 1.8,   8.3, 52,
4,  18.5,  854, 3.2, 2.53,  8,   72,
5,  21.5,  849, 2.3, 2.64,  8.1, 84,
6,  32.4,  846, 3.2, 2.86,  7.9, 60,
7,  36.8,  841, 6.6, 4,     8.1, 88,
8,  49.1,  792, 2.5, 1.3,   8.1, 94,
9,  70.5,  752, 1.2, 4.8,   8,   90,
10, 99,    617, 9.9, 10,    7.7, 82,
11, 123.4, 483, 4.1, 19.9,  8.1, 96,
```



DoubsSpa.csv

```
,   x,   y
1,  88,  7
2,  94,  14
3,  102, 18
4,  100, 28
5,  106, 39
6,  112, 51
7,  114, 61
8,  110, 76
9,  136, 100
10, 168, 112
11, 186, 130
12, 205, 145
```

The Doubs Fish Data: 前置處理

- Verneaux used a semi-quantitative, species-specific, abundance scale (0–5) so that comparisons between species abundances make sense. (However, species-specific codes cannot be understood as unbiased estimates of the true abundances (number or density of individuals) or biomasses at the sites.) [你需要一位data domain專家]

- Working with the environmental data available in the R package **ade4** (version 1.4-14), we corrected a mistake in the das variable and restored the variables to their original units (Table 1.1.)

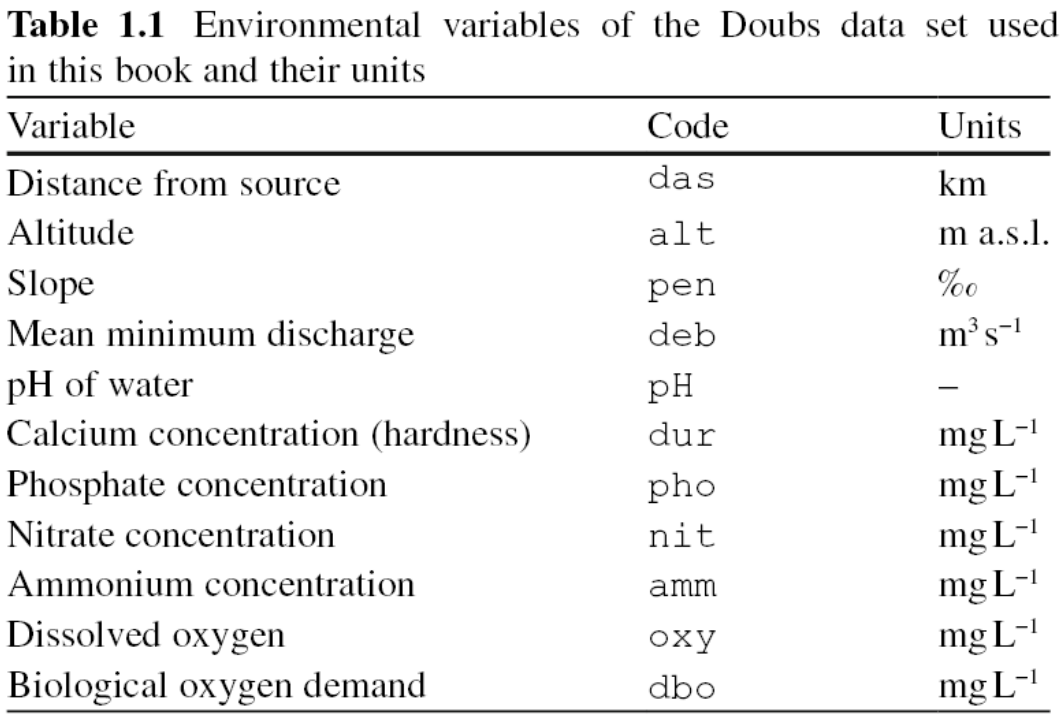


Table 1.1 Environmental variables of the Doubs data set used in this book and their units

Variable	Code	Units
Distance from source	das	km
Altitude	alt	m a.s.l.
Slope	pen	‰
Mean minimum discharge	deb	$m^3 s^{-1}$
pH of water	pH	–
Calcium concentration (hardness)	dur	$mg L^{-1}$
Phosphate concentration	pho	$mg L^{-1}$
Nitrate concentration	nit	$mg L^{-1}$
Ammonium concentration	amm	$mg L^{-1}$
Dissolved oxygen	oxy	$mg L^{-1}$
Biological oxygen demand	dbo	$mg L^{-1}$

Data Extraction: Read Data

- 每一檔案之大小、資料維度、關聯。
- (報告中)列出每一變數之
  - 名稱、所代表意義。
  - 型態(連續、類別、順序、時間等等)、單位
  - 編碼、範圍(五數摘要)、遺失值比例(分佈)。
- 若是類別變數，則列出每一類別之次數分佈、交叉次數表。

```
> # Load the required package, vegan: Community Ecology Package
> library(vegan)

> # Load additionnal functions
> # (files must be in the working directory)
> source("panelutils.R")

> # Import the data from CSV files
> # Species (community) data frame (fish abundances)
> spe <- read.csv("DoubsSpe.csv", row.names=1)
> # Environmental data frame
> env <- read.csv("DoubsEnv.csv", row.names=1)
> # Spatial data frame
> spa <- read.csv("DoubsSpa.csv", row.names=1)
```

```
> library(ade4)
> data(doubs)
> ?doubs
```

Source: Borcard D., Gillet F. & Legendre P. Numerical Ecology with R, Springer, 2011

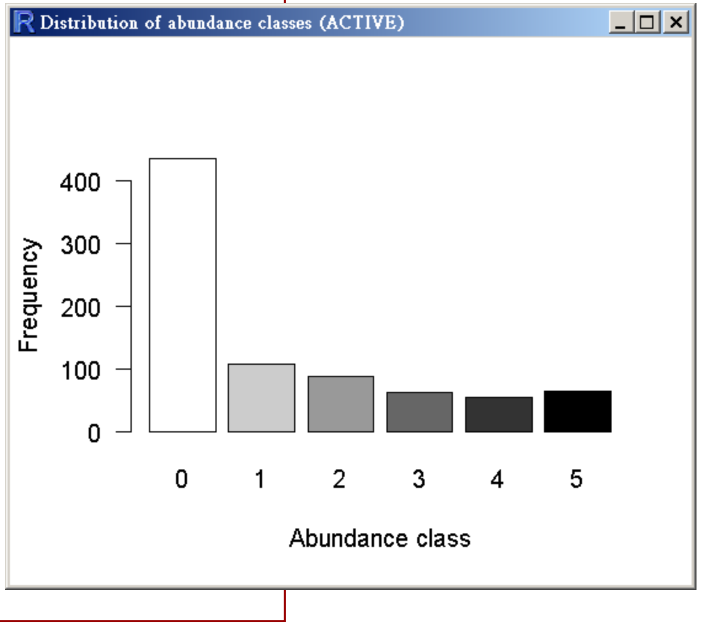
Species Data: First Contact
Basic functions

```
> spe   # Display the whole data frame in the console
   CHA TRU VAI LOC OMB BLA HOT TOX VAN CHE BAR SPI GOU BRO PER BOU PSO ROT
1    0   3   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
...
> spe[1:5,1:10]    # Display only 5 lines and 10 columns
  CHA TRU VAI LOC OMB BLA HOT TOX VAN CHE
1   0   3   0   0   0   0   0   0   0   0
...
> head(spe)    # Display only the first few lines
  CHA TRU VAI LOC OMB BLA HOT TOX VAN CHE BAR SPI GOU BRO PER BOU PSO ROT CAR
1   0   3   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
...
> nrow(spe)    # Number of rows (sites)
[1] 30
> ncol(spe)    # Number of columns (species)
[1] 27
> dim(spe)    # Dimensions of the data frame (rows, columns)
[1] 30 27
> colnames(spe)    # Column labels (descriptors = species)
 [1] "CHA" "TRU" "VAI" "LOC" "OMB" "BLA" "HOT" "TOX" "VAN" "CHE" "BAR" "SPI"
...
> rownames(spe)    # Row labels (objects = sites)
 [1] "1"  "2"  "3"  "4"  "5"  "6"  "7"  "8"  "9"  "10" "11" "12" "13" "14"
...
> summary(spe)    # Descriptive statistics for columns
      CHA            TRU            VAI             LOC             OMB
 Min.   :0.00   Min.   :0.00   Min.   :0.000   Min.   :0.000   Min.   :0.00
 1st Qu.:0.00   1st Qu.:0.00   1st Qu.:0.000   1st Qu.:1.000   1st Qu.:0.00
 Median :0.00   Median :1.00   Median :3.000   Median :2.000   Median :0.00
 Mean   :0.50   Mean   :1.90   Mean   :2.267   Mean   :2.433   Mean   :0.50
 3rd Qu.:0.75   3rd Qu.:3.75   3rd Qu.:4.000   3rd Qu.:4.000   3rd Qu.:0.75
 Max.   :3.00   Max.   :5.00   Max.   :5.000   Max.   :5.000   Max.   :4.00
  ...
```

Overall Distribution of Abundances (Dominance Codes)

Compare median and mean abundances. Are most distributions symmetrical?

```
> # Minimum and maximum of abundance values in the whole data set
> range(spe)
[1] 0 5
> # Count cases for each abundance class
> (ab <- table(unlist(spe)))
  0   1   2   3   4   5
435 108  87  62  54  64
> # Create a graphic window with title
> windows(title="Distribution of abundance classes")
>
> # Barplot of the distribution, all species confounded
> barplot(ab, las=1, xlab="Abundance class",
+  ylab="Frequency", col=gray(5:0/5))
> # Number of absences
> sum(spe==0)
[1] 435
> # Proportion of zeros in the community data set
> sum(spe==0)/(nrow(spe)*ncol(spe))
[1] 0.537037
```



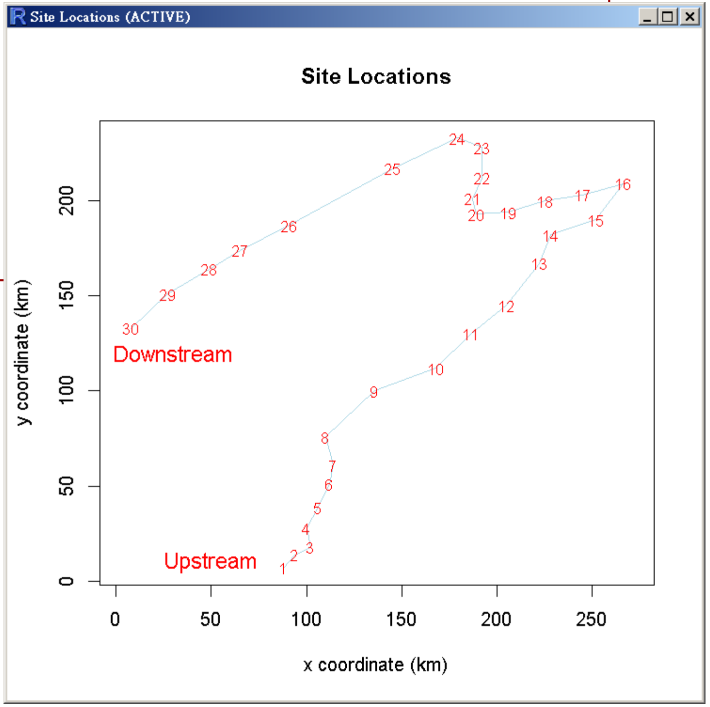
How do you interpret the high frequency of zeros (absences) in the data frame?

google "sparse data"

Species Data: A Closer Look
Map of the Locations of the Sites

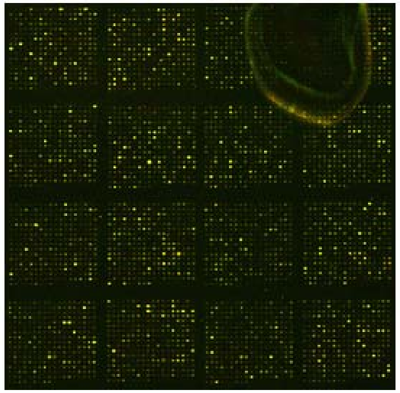
```
> windows(title="Site Locations")
> # Create an empty frame (proportional axes 1:1, with titles)
> # Geographic coordinates x and y from the spa data frame
> plot(spa, asp=1, type="n", main="Site Locations",
+ xlab="x coordinate (km)", ylab="y coordinate (km)")
> # Add a blue line connecting the sites (Doubs river)
> lines(spa, col="light blue")
> # Add site labels
> text(spa, row.names(spa), cex=0.8, col="red")
> # Add text blocks
> text(50, 10, "Upstream", cex=1.2, col="red")
> text(30, 120, "Downstream", cex=1.2, col="red")
```

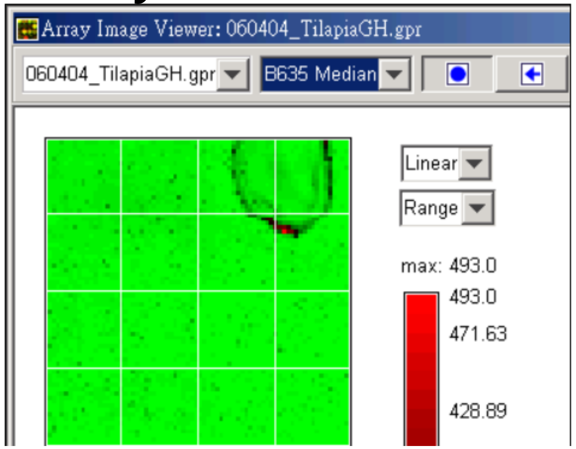
The river looks more real, but where are the fish?



註: 重建 Reconstruction

生物晶片 (Microarray)





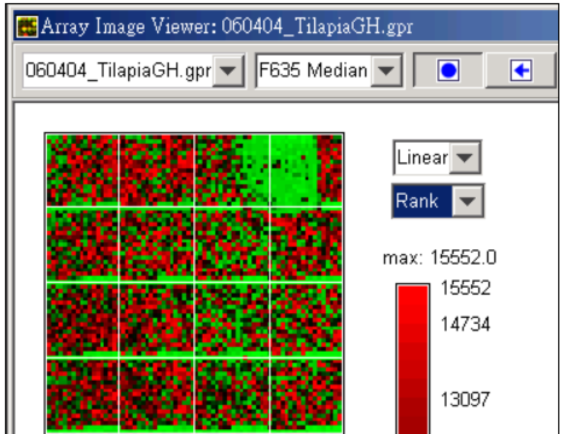
Array Image Viewer: 060404_TilapiaGH.gpr

060404_TilapiaGH.gpr ▼ B635 Median ▼

Linear ▼

Range ▼

max: 493.0



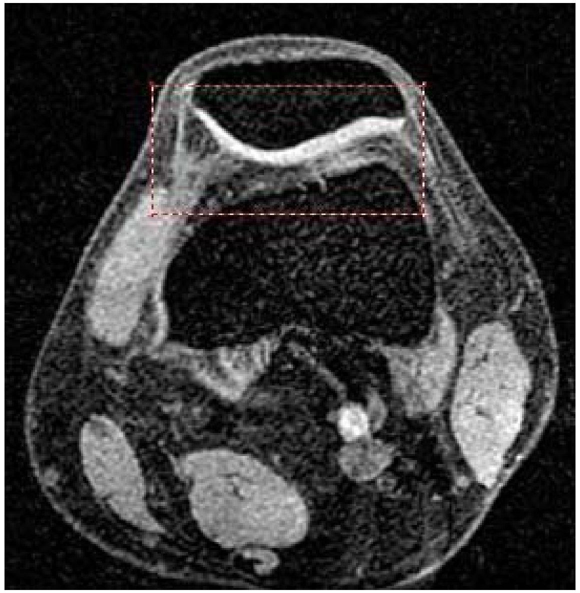
Array Image Viewer: 060404_TilapiaGH.gpr

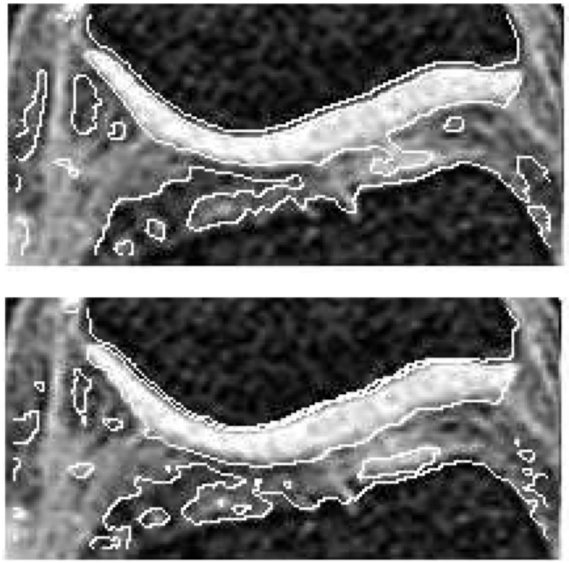
060404_TilapiaGH.gpr ▼ F635 Median ▼

Linear ▼

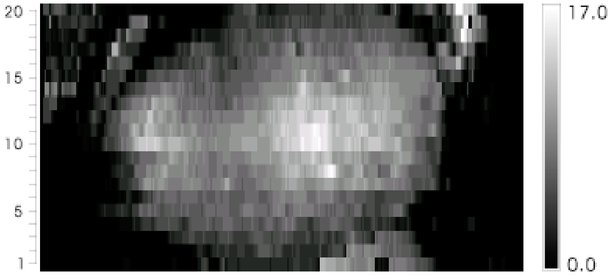
Rank ▼

max: 15552.0



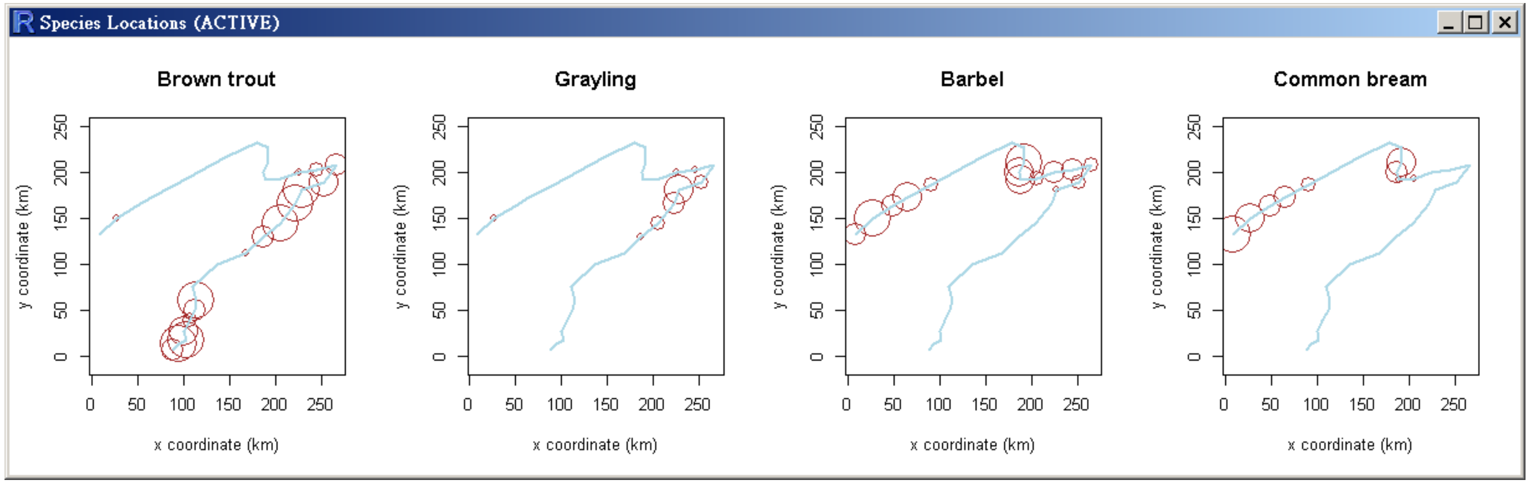


醫學影像 (fMRI)



Maps of Some Fish Species

```
> # New graphic window (size 9x9 inches)
> windows(title="Species Locations", 9, 9)
> par(mfrow=c(1,4))
> # Plot four species
> xl <- "x coordinate (km)",
> yl <- "y coordinate (km)"
> plot(spa, asp=1, col="brown", cex=spe$TRU, main="Brown trout", xlab=xl, ylab=yl)
> lines(spa, col="light blue", lwd=2)
> plot(spa, asp=1, col="brown", cex=spe$OMB, main="Grayling", xlab=xl, ylab=yl)
> lines(spa, col="light blue", lwd=2)
> plot(spa, asp=1, col="brown", cex=spe$BAR, main="Barbel", xlab=xl, ylab=yl)
> lines(spa, col="light blue", lwd=2)
> plot(spa, asp=1, col="brown", cex=spe$BCO, main="Common bream", xlab=xl, ylab=yl)
> lines(spa, col="light blue", lwd=2)
```



Bubble maps of the abundance of four fish species

From these graphs you should understand why these four species were chose as ecological indicators.

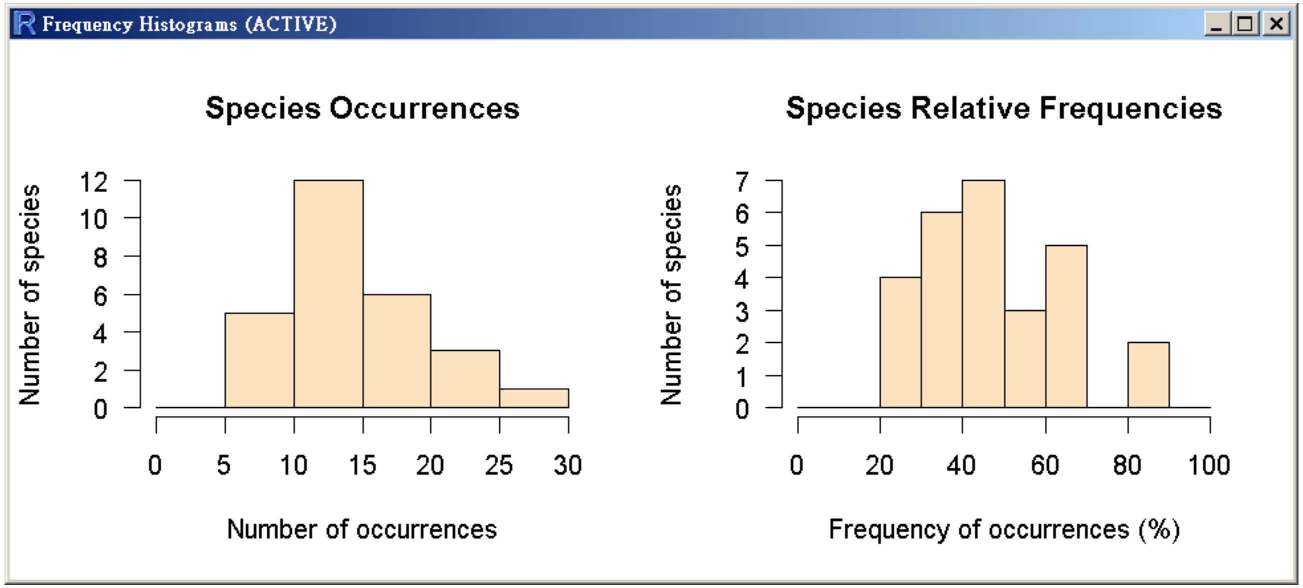
Compare Species: Number of Occurrences

At how many sites does each species occur? Calculate the relative frequencies of species (proportion of the number of sites) and plot histograms.

```
> # Compute the number of sites where each species is present
> # To sum by columns, the second argument of apply(), MARGIN, is set to 2
> spe.pres <- apply(spe > 0, 2, sum)
> # Sort the results in increasing order
> sort(spe.pres)
PCH CHA OMB BLA BCO BBO TOX BOU ROT ANG HOT SPI CAR GRE PSO BAR ABL PER TRU TAN
  7   8   8   8   9  10  11  11  11  11  12  12  12  12  13  14  14  15  17  17
VAN BRO GAR VAI GOU LOC CHE
 18  18  18  20  20  24  25
> # Compute percentage frequencies
> spe.relf <- 100*spe.pres/nrow(spe)
> # Round the sorted output to 1 digit
> round(sort(spe.relf), 1)
 PCH  CHA  OMB  BLA  BCO  BBO  TOX  BOU  ROT  ANG  HOT  SPI  CAR  GRE  PSO  BAR
23.3 26.7 26.7 26.7 30.0 33.3 36.7 36.7 36.7 36.7 40.0 40.0 40.0 40.0 43.3 46.7
 ABL  PER  TRU  TAN  VAN  BRO  GAR  VAI  GOU  LOC  CHE
46.7 50.0 56.7 56.7 60.0 60.0 60.0 66.7 66.7 80.0 83.3
```

Compare Species: Number of Occurrences

```
> # Plot the histograms
> windows(title="Frequency Histograms",8,5)
> # Divide the window horizontally
> par(mfrow=c(1,2))
> hist(spe.pres, main="Species Occurrences", right=FALSE, las=1,
+ xlab="Number of occurrences", ylab="Number of species",
+ breaks=seq(0,30,by=5), col="bisque")
> hist(spe.relf, main="Species Relative Frequencies", right=FALSE,
+ las=1, xlab="Frequency of occurrences (%)", ylab="Number of species",
+ breaks=seq(0, 100, by=10), col="bisque")
```



Compare Sites: Species Richness

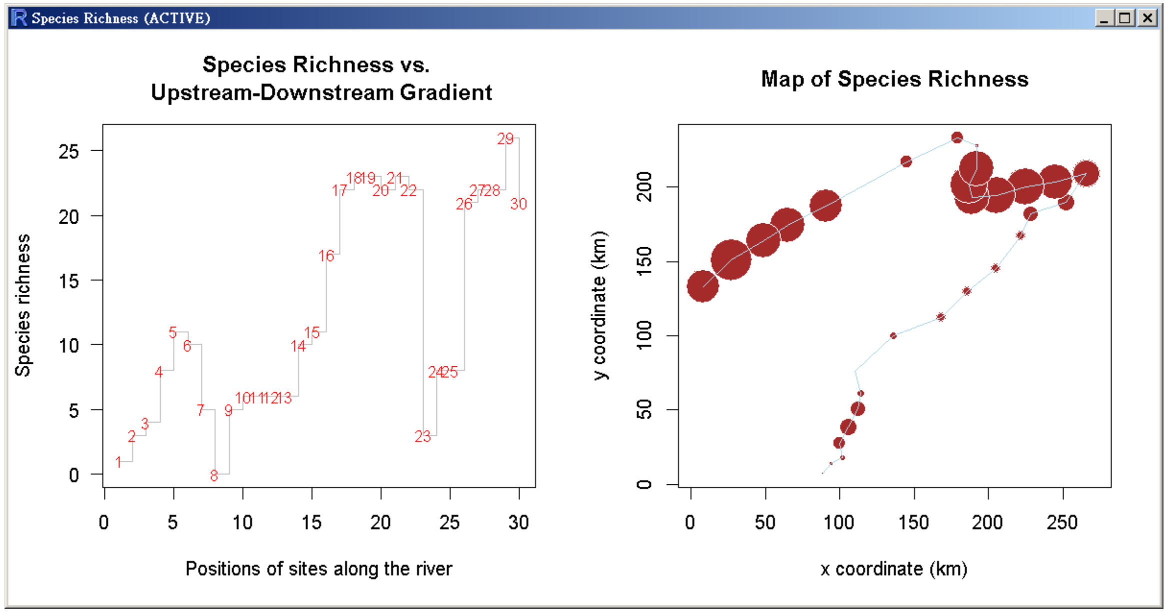
Now that we have seen at how many sites each species is present, we may want to know how many species are present at each site (species richness).

```
> # Compute the number of species at each site
> # To sum by rows, the second argument of apply(), MARGIN, is set to 1
> sit.pres <- apply(spe > 0, 1, sum)
> # Sort the results in increasing order
> sort(sit.pres)
 8  1  2 23  3  7  9 10 11 12 13  4 24 25  6 14  5 15 16 26 30 17 20 22 27 28 18 19
 0  1  3  3  4  5  5  6  6  6  6  8  8  8 10 10 11 11 17 21 21 22 22 22 22 22 23 23
21 29
23 26
```

Compare Sites: Species Richness

```
> windows(title="Species Richness", 10, 5)
> par(mfrow=c(1,2))
> # Plot species richness vs. position of the sites along the river
> plot(sit.pres,type="s", las=1, col="gray",
+ main="Species Richness vs. \n Upstream-Downstream Gradient",
+ xlab="Positions of sites along the river", ylab="Species richness")
> text(sit.pres, row.names(spe), cex=.8, col="red")
> # Use geographic coordinates to plot a bubble map
> plot(spa, asp=1, main="Map of Species Richness", pch=21, col="white",
+ bg="brown", cex=5*sit.pres/max(sit.pres), xlab="x coordinate (km)",
+ ylab="y coordinate (km)")
> lines(spa, col="light blue")
```

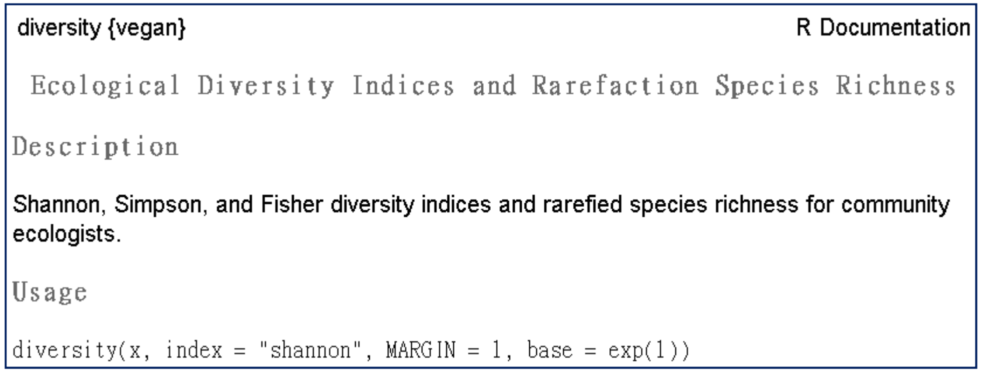
Can you identify richness hot spots along the river?



Compute Alpha Diversity Indices of the Fish Communities

Finally, one can easily compute classical diversity indices from the data. Let us do it with the function **diversity()** of the **vegan** package.

生態多樣性指標



diversity {vegan}　　R Documentation

Ecological Diversity Indices and Rarefaction Species Richness

Description

Shannon, Simpson, and Fisher diversity indices and rarefied species richness for community ecologists.

Usage

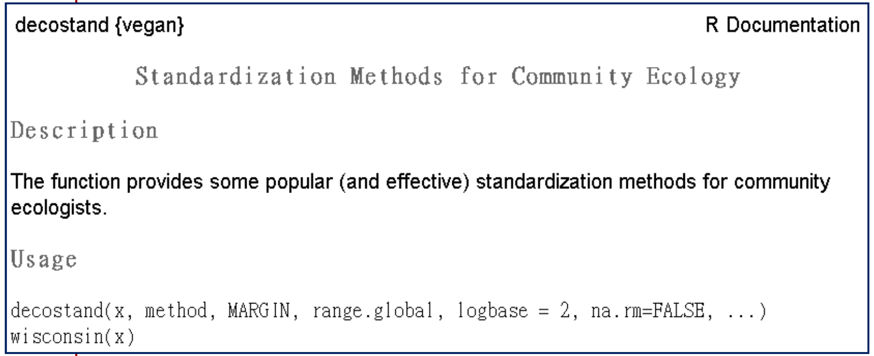
```
diversity(x, index = "shannon", MARGIN = 1, base = exp(1))
```

```
> # Get help on the diversity() function
> ?diversity
>
> N0 <- rowSums(spe > 0)         # Species richness
> H <- diversity(spe)            # Shannon entropy
> N1 <- exp(H)                   # Shannon diversity (number of abundant species)
> N2 <- diversity(spe, "inv")    # Simpson diversity (number of dominant species)
> J <- H/log(N0)                 # Pielou evenness
> E10 <- N1/N0                   # Shannon evenness (Hill's ratio)
> E20 <- N2/N0                   # Simpson evenness (Hill's ratio)
> (div <- data.frame(N0, H, N1, N2, E10, E20, J))
  N0        H        N1        N2       E10       E20         J
1  1 0.000000  1.000000  1.000000 1.0000000 1.0000000       NaN
2  3 1.077556  2.937493  2.880000 0.9791642 0.9600000 0.9808340
3  4 1.263741  3.538634  3.368421 0.8846584 0.8421053 0.9115962
4  8 1.882039  6.566883  5.727273 0.8208604 0.7159091 0.9050696
5 11 2.329070 10.268387  9.633333 0.9334897 0.8757576 0.9712976
6 10 2.108294  8.234184  7.000000 0.8234184 0.7000000 0.9156205
...
```

Transformation and Standardization of the Species Data

- The **decostand()** function of the **vegan** package provides many options for common standardization of ecological data.
- In this function, standardization, as contrasted with simple transformation (such as square root, log or presence–absence), means that the values are not transformed individually but relative to other values in the data table.
- Standardization can be done relative to sites (site profiles), species (species profiles), or both (double profiles), depending on the focus of the analysis.

```
> # Get help on the decostand() function
> ?decostand
> ## Simple transformations
> # Partial view of the raw data (abundance codes)
> spe[1:5, 2:4]
  TRU VAI LOC
1   3   0   0
...
> # Transform abundances to presence-absence (1-0)
> spe.pa <- decostand(spe, method="pa")
> spe.pa[1:5, 2:4]
  TRU VAI LOC
1   1   0   0
...
```



decostand {vegan} R Documentation

Standardization Methods for Community Ecology

Description

The function provides some popular (and effective) standardization methods for community ecologists.

Usage

```
decostand(x, method, MARGIN, range.global, logbase = 2, na.rm=FALSE, ...)
wisconsin(x)
```

Transformation and Standardization of the Species Data

```
> Species profiles: 2 methods: presence-absence or abundance data
> ## Species profiles: standardization by column
> # Scale abundances by dividing them by the maximum value for each species
> # Note: MARGIN=2 (column, default value) for this method
> spe.scal <- decostand(spe, "max")
> spe.scal[1:5,2:4]
  TRU VAI LOC
1 0.6 0.0 0.0
...
> # Display the maximum by column
> apply(spe.scal, 2, max)
CHA TRU VAI LOC OMB BLA HOT TOX VAN CHE BAR SPI GOU BRO PER BOU PSO ROT CAR TAN
  1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1
BCO PCH GRE GAR BBO ABL ANG
  1   1   1   1   1   1   1
> # Scale abundances by dividing them by the species totals
> # (relative abundance by species)
> # Note: MARGIN=2 for this method
> spe.relsp <- decostand(spe, "total", MARGIN=2)
> spe.relsp[1:5,2:4]
         TRU        VAI        LOC
1 0.05263158 0.00000000 0.00000000
...
> # Display the sum by column
> apply(spe.relsp, 2, sum)
CHA TRU VAI LOC OMB BLA HOT TOX VAN CHE BAR SPI GOU BRO PER BOU PSO ROT CAR TAN BCO
  1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1
PCH GRE GAR BBO ABL ANG
  1   1   1   1   1   1
```

Did the scaling work properly? Keep an eye on the results by a plot or by the use of summary statistics

Scale Abundances by Dividing Them by the Site Totals

```
> ## Site profiles: 3 methods; presence-absence or abundance data
> ## standardization by row
> # Scale abundances by dividing them by the site totals
> # (relative abundance, or relative frequencies, per site)
> # (relative abundance by site)
> # Note: MARGIN=1 (default value) for this method
> spe.rel <- decostand(spe, "total")
> spe.rel[1:5,2:4]
         TRU        VAI        LOC
1 1.00000000 0.00000000 0.00000000
...
> # Display the sum of row vectors to determine if the scaling worked properly
> apply(spe.rel, 1, sum)
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
 1  1  1  1  1  1  1  0  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
29 30
 1  1
> # Give a length of 1 to each row vector (Euclidean norm)
> spe.norm <- decostand(spe, "normalize")
> spe.norm[1:5,2:4]
        TRU       VAI       LOC
1 1.0000000 0.0000000 0.0000000
...
> # Verify the norm of row vectors
> norm <- function(x) sqrt(x%*%x)
> apply(spe.norm, 1, norm)
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
 1  1  1  1  1  1  1  0  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
29 30
 1  1
```

The chord transformation: the Euclidean distance function applied to chord-transformed data produces a chord distance matrix. Useful before PCA and K-means.

Compute Relative Frequencies by Rows (Site Profiles)

- The Hellinger transformation can be also be obtained by applying the chord transformation to square-root-transformed species data.

```
> # Compute relative frequencies by rows (site profiles), then square root
> # Compute square root of relative abundances by site
> spe.hel <- decostand(spe, "hellinger")
> spe.hel[1:5,2:4]
        TRU       VAI       LOC
1 1.0000000 0.0000000 0.0000000
2 0.6454972 0.5773503 0.5000000
3 0.5590170 0.5590170 0.5590170
4 0.4364358 0.4879500 0.4879500
5 0.2425356 0.2970443 0.2425356
> # Check the norm of row vectors
> apply(spe.hel, 1, norm)
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 
 1  1  1  1  1  1  1  0  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1 
29 30 
 1  1 
```

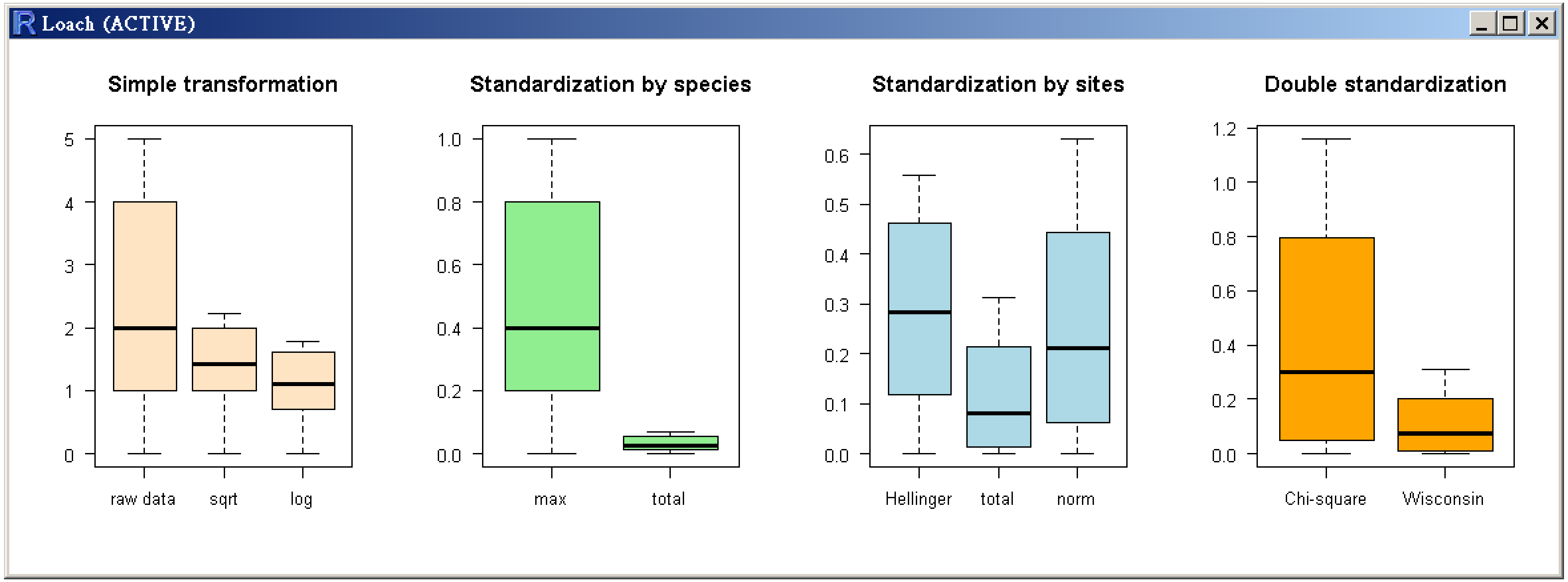
http://artax.karlin.mff.cuni.cz/r-help/library/analogue/html/tran.html

Standardization by Both Columns and Rows

```
> # Chi-square transformation
> spe.chi <- decostand(spe, "chi.square")
> spe.chi[1:5,2:4]
        TRU       VAI       LOC
1 4.1969078 0.0000000 0.0000000
2 1.7487116 1.2808290 0.9271402
3 1.3115337 1.2007772 1.1589253
4 0.7994110 0.9148778 0.8829907
5 0.2468769 0.3390430 0.2181506
> # Check what happened to site 8 where no species was found
> spe.chi[7:9,]
  CHA      TRU       VAI       LOC OMB BLA HOT TOX      VAN       CHE BAR SPI GOU BRO
7   0 1.311534 0.9606217 1.1589253   0   0   0   0 0.302004 0.2646384   0   0   0   0
8   0 0.000000 0.0000000 0.0000000   0   0   0   0 0.000000 0.0000000   0   0   0   0
9   0 0.000000 0.2744634 0.7946916   0   0   0   0 0.000000 1.5122194   0   0   0   0
  PER BOU PSO ROT CAR       TAN BCO PCH GRE      GAR BBO ABL ANG
7   0   0   0   0   0 0.0000000   0   0   0 0.000000   0   0   0
8   0   0   0   0   0 0.0000000   0   0   0 0.000000   0   0   0
9   0   0   0   0   0 0.3373903   0   0   0 1.140587   0   0   0
> # Wisconsin standardization
> # Abundances are first ranged by species maxima and then by site totals
> spe.wis <- wisconsin(spe)
> spe.wis[1:5,2:4]
         TRU        VAI        LOC
1 1.00000000 0.00000000 0.00000000
2 0.41666667 0.33333333 0.25000000
3 0.31250000 0.31250000 0.31250000
4 0.19047619 0.23809524 0.23809524
5 0.05882353 0.08823529 0.05882353
```

Boxplots of Transformed Abundances of a Common Species (Stone Loach)

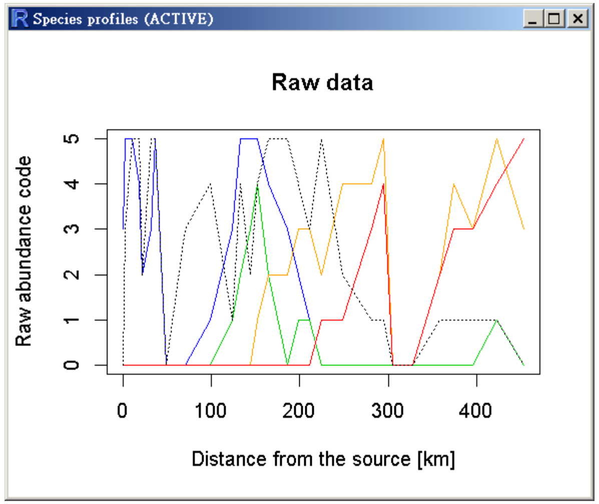
```
> windows(title="Loach") # 泥鰍
> par(mfrow=c(1,4))
> boxplot(spe$LOC, sqrt(spe$LOC), log1p(spe$LOC), las=1, main="Simple transformation",
+ names=c("raw data", "sqrt", "log"), col="bisque")
> boxplot(spe.scal$LOC, spe.relsp$LOC, las=1, main="Standardization by species",
+ names=c("max", "total"), col="lightgreen")
> boxplot(spe.hel$LOC, spe.rel$LOC, spe.norm$LOC, las=1, main="Standardization by sites",
+ names=c("Hellinger", "total", "norm"), col="lightblue")
> boxplot(spe.chi$LOC, spe.wis$LOC, las=1, main="Double standardization",
+ names=c("Chi-square", "Wisconsin"), col="orange")
```

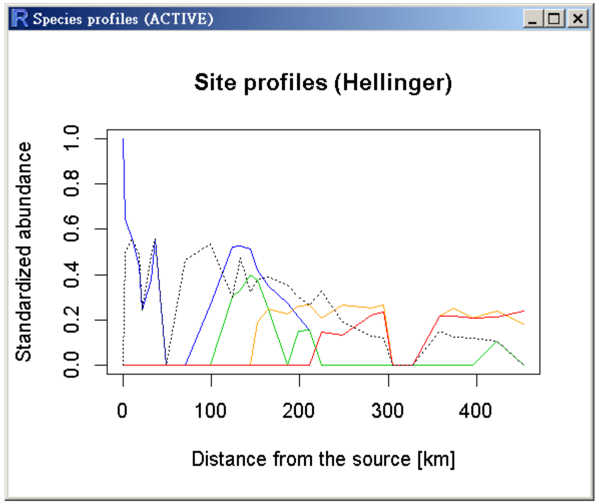


Boxplots of transformed abundances of a common species, Nemacheilus barbatulus (**stone loach**)

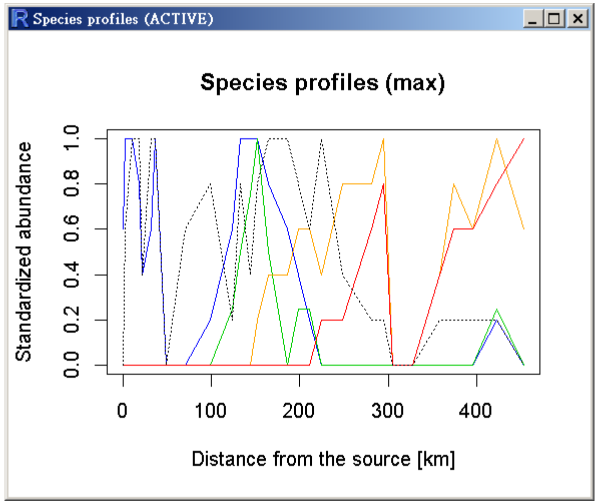
Plot Profiles Along the Upstream-Downstream Gradient

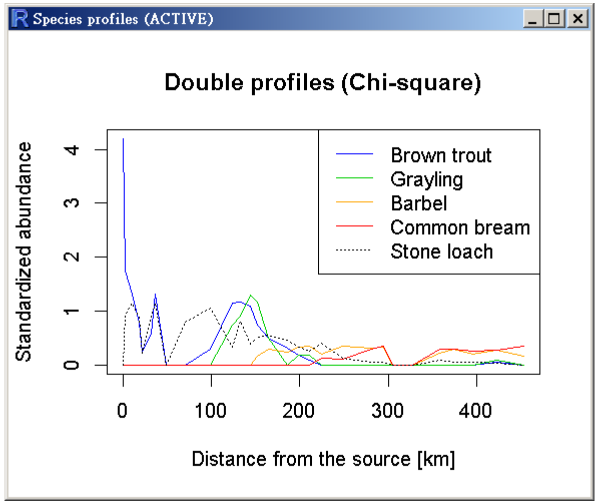
Another way to compare the effects of transformations on species profiles is to plot them along the river course.





Compare the profiles and explain the differences.





Plot Profiles Along the Upstream-Downstream Gradient

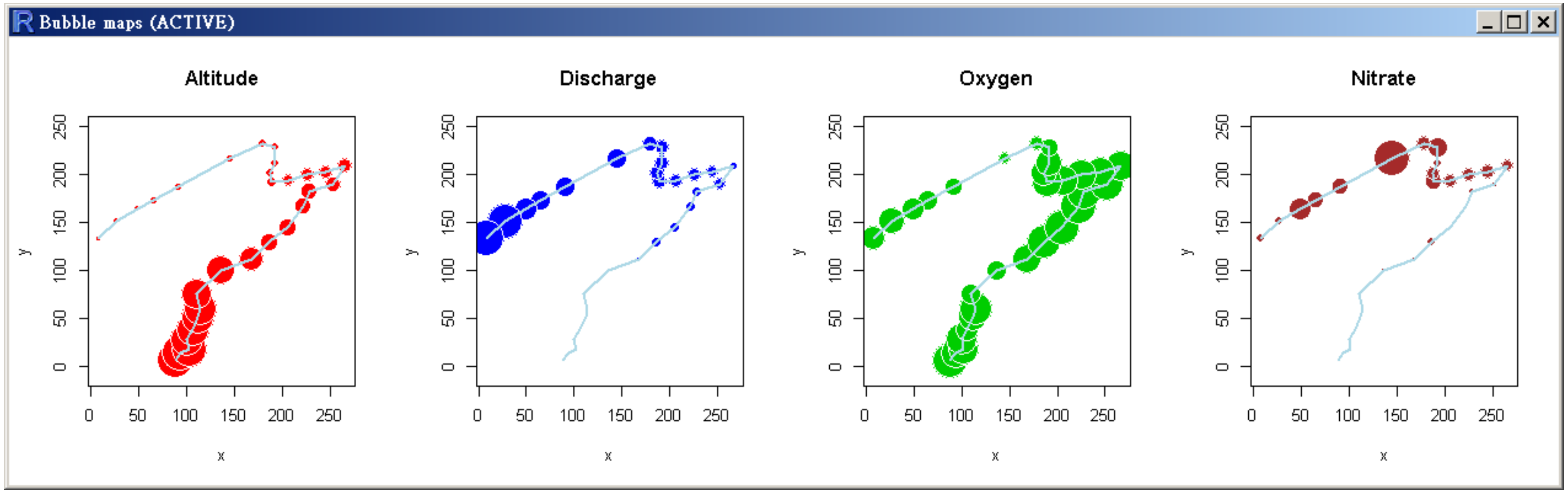
```
> windows(title="Species profiles", 9, 9)
> plot(env$das, spe$TRU, type="l", col=4, main="Raw data",
+ xlab="Distance from the source [km]", ylab="Raw abundance code")
> lines(env$das, spe$OMB, col=3); lines(env$das, spe$BAR, col="orange")
> lines(env$das, spe$BCO, col=2); lines(env$das, spe$LOC, col=1, lty="dotted")
>
> plot(env$das, spe.scal$TRU, type="l", col=4, main="Species profiles (max)",
+ xlab="Distance from the source [km]", ylab="Standardized abundance")
> lines(env$das, spe.scal$OMB, col=3); lines(env$das, spe.scal$BAR, col="orange")
> lines(env$das, spe.scal$BCO, col=2); lines(env$das, spe.scal$LOC, col=1, lty="dotted")

> plot(env$das, spe.hel$TRU, type="l", col=4, main="Site profiles (Hellinger)",
+ xlab="Distance from the source [km]", ylab="Standardized abundance")
> lines(env$das, spe.hel$OMB, col=3); lines(env$das, spe.hel$BAR, col="orange")
> lines(env$das, spe.hel$BCO, col=2); lines(env$das, spe.hel$LOC, col=1, lty="dotted")
>
> plot(env$das, spe.chi$TRU, type="l", col=4, main="Double profiles (Chi-square)",
+ xlab="Distance from the source [km]", ylab="Standardized abundance")
> lines(env$das, spe.chi$OMB, col=3); lines(env$das, spe.chi$BAR, col="orange")
> lines(env$das, spe.chi$BCO, col=2); lines(env$das, spe.chi$LOC, col=1, lty="dotted")
> legend("topright", c("Brown trout", "Grayling", "Barbel", "Common bream", "Stone loach"),
+ col=c(4,3,"orange",2,1), lty=c(rep(1,4),3))
```

Bubble Maps of Some Environmental Variables

```
> windows(title="Bubble maps", 9, 9)
> par(mfrow=c(1,4))
> plot(spa, asp=1, main="Altitude", pch=21, col="white",
+ bg="red", cex=5*env$alt/max(env$alt), xlab="x", ylab="y")
> lines(spa, col="light blue", lwd=2)
> plot(spa, asp=1, main="Discharge", pch=21, col="white",
+ bg="blue", cex=5*env$deb/max(env$deb), xlab="x", ylab="y")
> lines(spa, col="light blue", lwd=2)
> plot(spa, asp=1, main="Oxygen", pch=21, col="white",
+ bg="green3", cex=5*env$oxy/max(env$oxy), xlab="x", ylab="y")
> lines(spa, col="light blue", lwd=2)
> plot(spa, asp=1, main="Nitrate", pch=21, col="white",
+ bg="brown", cex=5*env$nit/max(env$nit), xlab="x", ylab="y")
> lines(spa, col="light blue", lwd=2)
```

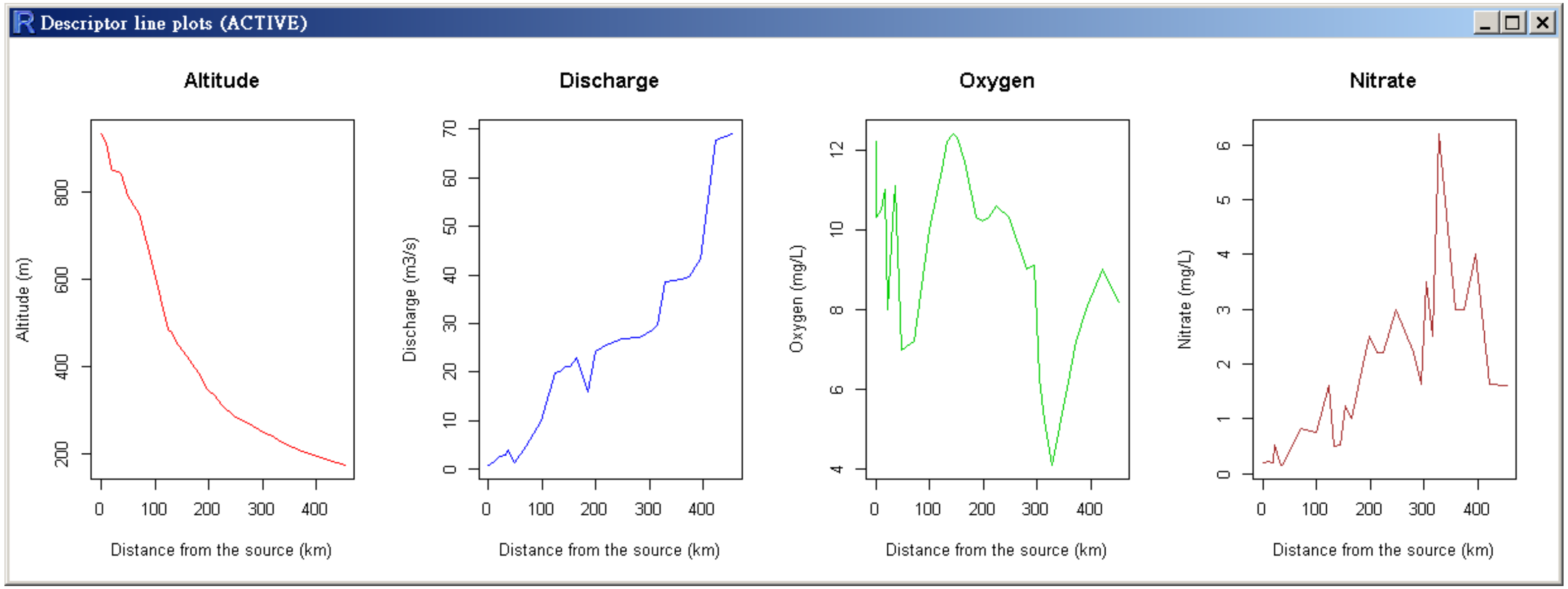
Apply the basic functions to **env**. While examining the **summary()**, note how the variables differ from the species data in values and spatial distributions. Draw maps of some of the environmental variables.



Which ones of these maps display an upstream-downstream gradient? How could you explain the spatial patterns of the other variables?

Examine the Variation of Some Descriptors Along the Stream: Line Plots

```
> windows(title="Descriptor line plots")
> par(mfrow=c(1,4))
> plot(env$das, env$alt, type="l", xlab="Distance from the source (km)",
+ ylab="Altitude (m)", col="red", main="Altitude")
> plot(env$das, env$deb, type="l", xlab="Distance from the source (km)",
+ ylab="Discharge (m3/s)", col="blue", main="Discharge")
> plot(env$das, env$oxy, type="l", xlab="Distance from the source (km)",
+ ylab="Oxygen (mg/L)", col="green3", main="Oxygen")
> plot(env$das, env$nit, type="l", xlab="Distance from the source (km)",
+ ylab="Nitrate (mg/L)", col="brown", main="Nitrate")
```



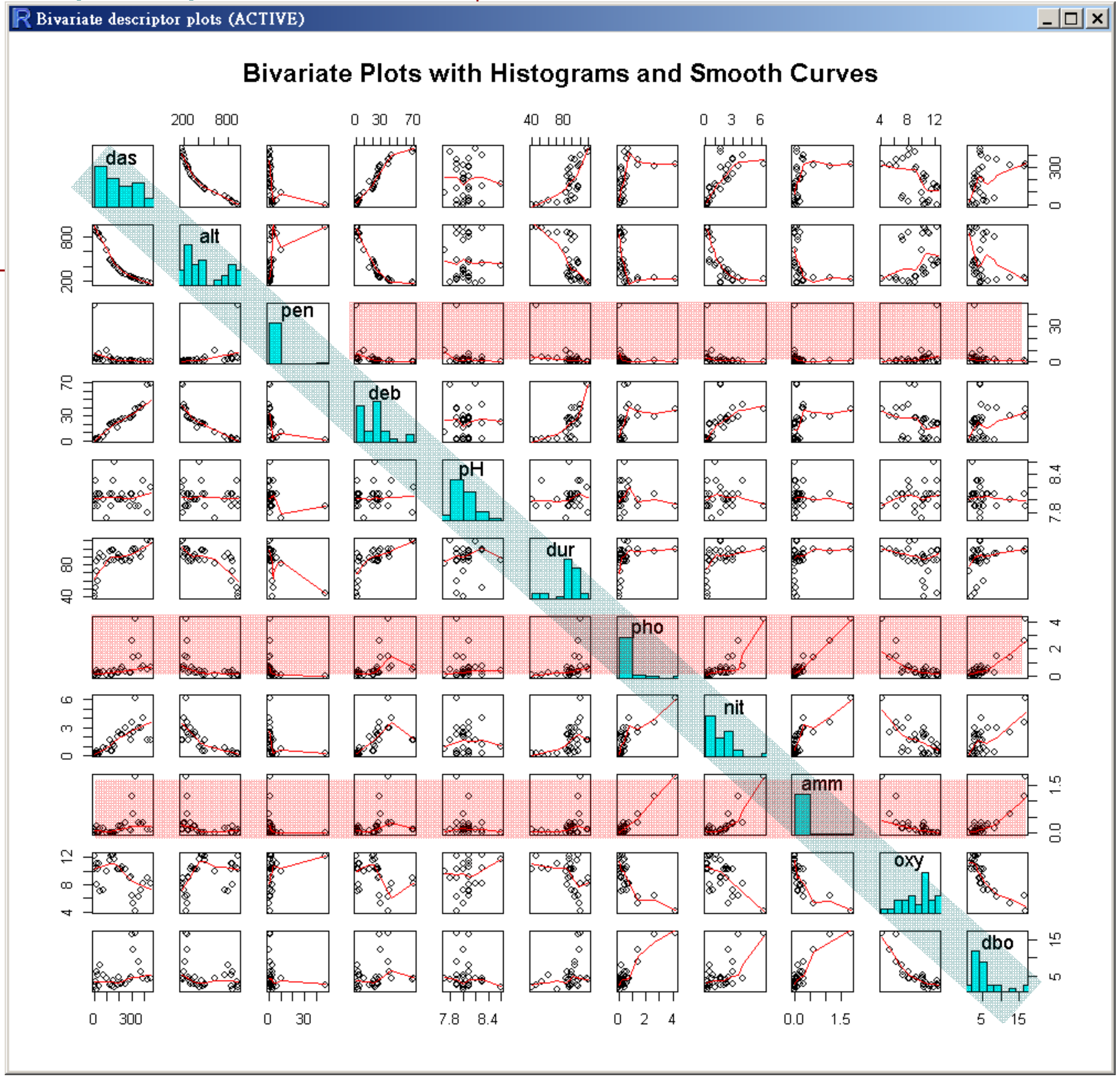
Note the scalings.

Scatter Plots for All Pairs of Environmental Variables

```
> windows(title="Bivariate descriptor plots")
> source("panelutils.R")
> op <- par(mfrow=c(1,1), pty="s")
> pairs(env, panel=panel.smooth,
diag.panel=panel.hist,
main="Bivariate Plots with
Histograms and Smooth Curves")
> par(op)
```

- Do many variables seem normally distributed?

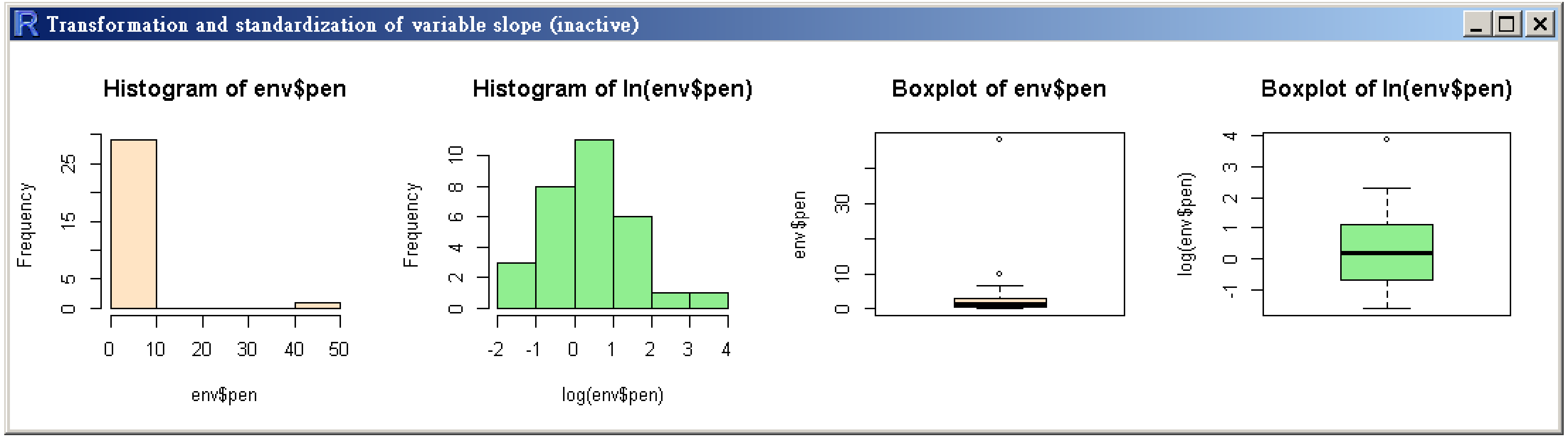
- Do many scatter plots show linear or at least monotonic relationships?



Simple Transformation of An Environmental Variable

- Simple transformations, such as the log transformation, can be used to improve the distributions of some variables (make it closer to the normal distribution).
- Because environmental variables are dimensionally heterogeneous (expressed in different units and scales), many statistical analyses require their standardization to zero mean and unit variance. These centred and scaled variables are called z-scores.

```
> range(env$pen)   #河道坡度
[1]  0.2 48.0
> # Log-transformation of the slope variable (y = ln(x))
> # Compare histograms and boxplots of raw and transformed values
> windows(title="Transformation and standardization of variable slope")
> par(mfrow=c(1,4))
> hist(env$pen, col="bisque", right=FALSE)
> hist(log(env$pen), col="light green", right=F, main="Histogram of ln(env$pen)")
> boxplot(env$pen, col="bisque", main="Boxplot of env$pen", ylab="env$pen")
> boxplot(log(env$pen), col="light green", main="Boxplot of ln(env$pen)",
+ ylab="log(env$pen)")
```



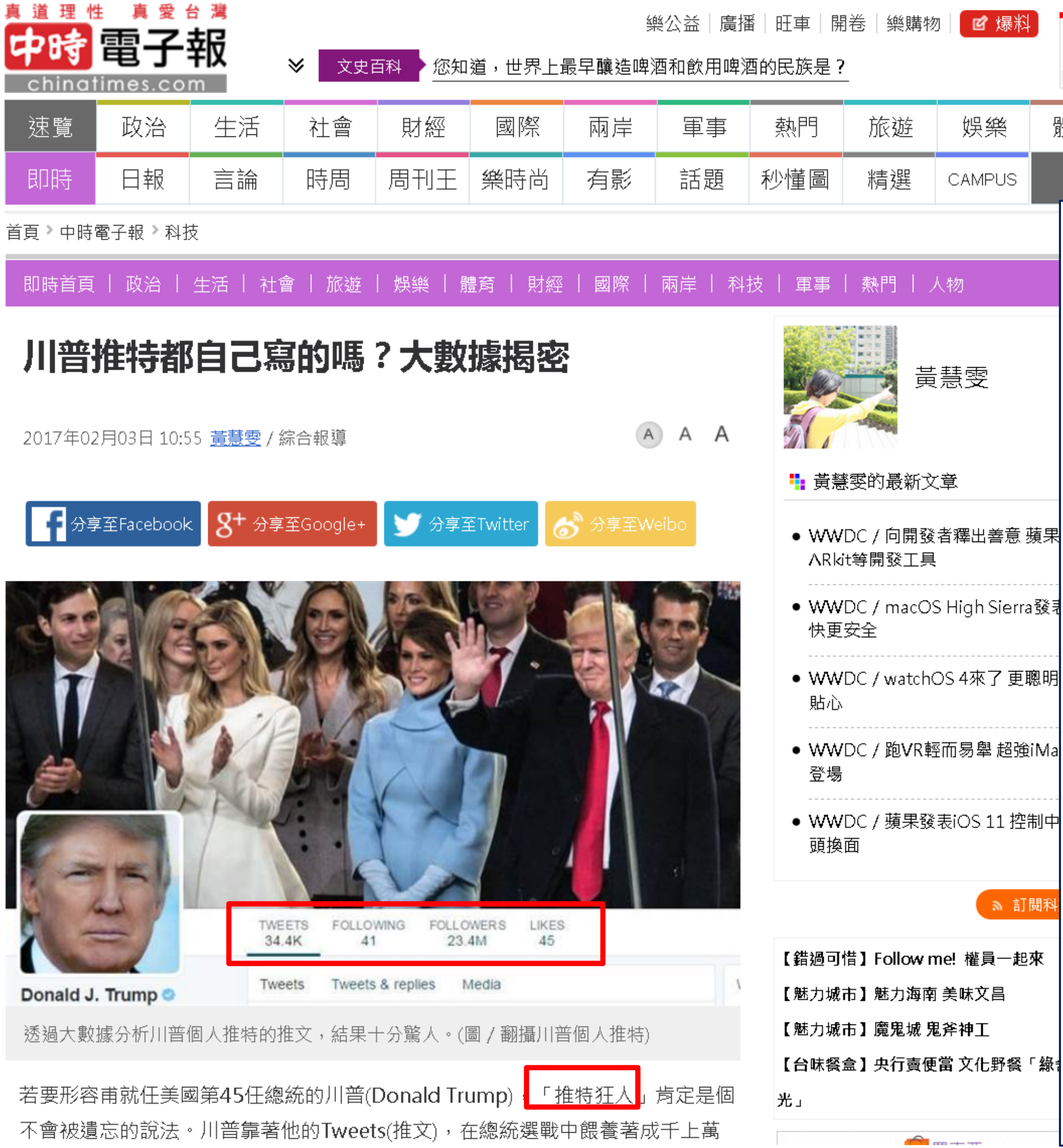
Standardization of All Environmental Variables

```
> # Center and scale = standardize variables (z-scores)
> env.z <- decostand(env, "standardize")
> apply(env.z, 2, mean)   # means = 0
          das           alt           pen           deb            pH           dur
 1.000429e-16  1.814232e-18 -1.659010e-17  1.233099e-17 -4.096709e-15  3.348595e-16
          pho           nit           amm           oxy           dbo
 1.327063e-17 -8.925898e-17 -4.289646e-17 -2.886092e-16  7.656545e-17
> apply(env.z, 2, sd)   # standard deviations = 1
das alt pen deb  pH dur pho nit amm oxy dbo
  1   1   1   1   1   1   1   1   1   1   1
>
> # Same standardization using the scale() function (which returns a matrix)
> env.z <- as.data.frame(scale(env))
> env.z
           das          alt         pen         deb         pH          dur
1  -1.34949526  1.667360909  5.14106053 -1.18004457 -0.8635475 -2.436958124
2  -1.33585215  1.659991358 -0.05737533 -1.17120570 -0.2878492 -2.733425049
...
```

小結 & 想想看

- The EDA tools allow researchers to obtain a general impression of their data.
- Information about simple parameters and distributions of variables is important to consider in order to choose more advanced analyses correctly.
- Graphical representations may help generate hypotheses about the processes acting behind the scene. (try heatmap!)
- **想想看: Doubs Fish Data經過這一連串的資料探索，還有哪一些有趣的問題可以提出? (季節? 人口、工廠分佈? 這些資料可以得到嗎?)**

例子2: 川普推特誰寫的?



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中時電子報 chinatimes.com

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文史百科 您知道，世界上最早釀造啤酒和飲用啤酒的民族是？

六月 6

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即時 | 日報 | 言論 | 時周 | 周刊王 | 樂時尚 | 有影 | 話題 | 秒懂圖 | 精選 | CAMPUS

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川普推特都自己寫的嗎？大數據揭密

2017年02月03日 10:55 黃慧雯 / 綜合報導　A A A

分享至Facebook　分享至Google+　分享至Twitter　分享至Weibo

透過大數據分析川普個人推特的推文，結果十分驚人。(圖 / 翻攝川普個人推特)

若要形容甫就任美國第45任總統的川普(Donald Trump)，「推特狂人」肯定是個不會被遺忘的說法。川普靠著他的Tweets(推文)，在總統選戰中餵養著成千上萬

黃慧雯

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ARkit等開發工具
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貼心
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訂閱科

【錯過可惜】Follow me! 權員一起來

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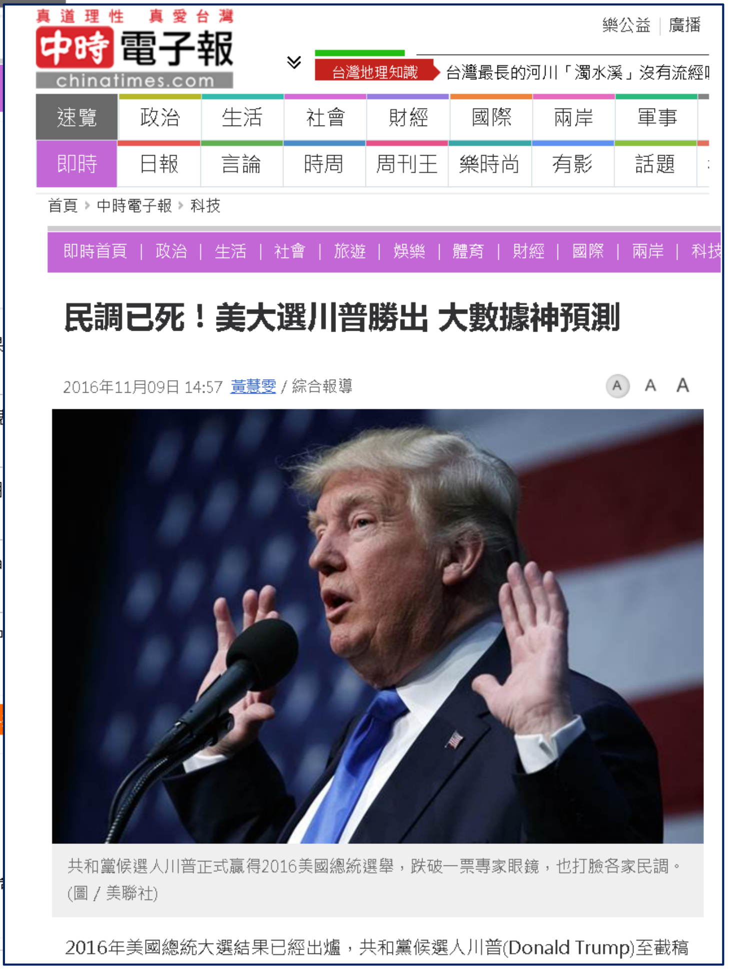
【魅力城市】魔鬼城 鬼斧神工

【台味餐盒】央行賣便當 文化野餐「綠

光」



真 道 理 性　真 愛 台 灣

中時電子報 chinatimes.com

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台灣地理知識 台灣最長的河川「濁水溪」沒有流經

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民調已死！美大選川普勝出 大數據神預測

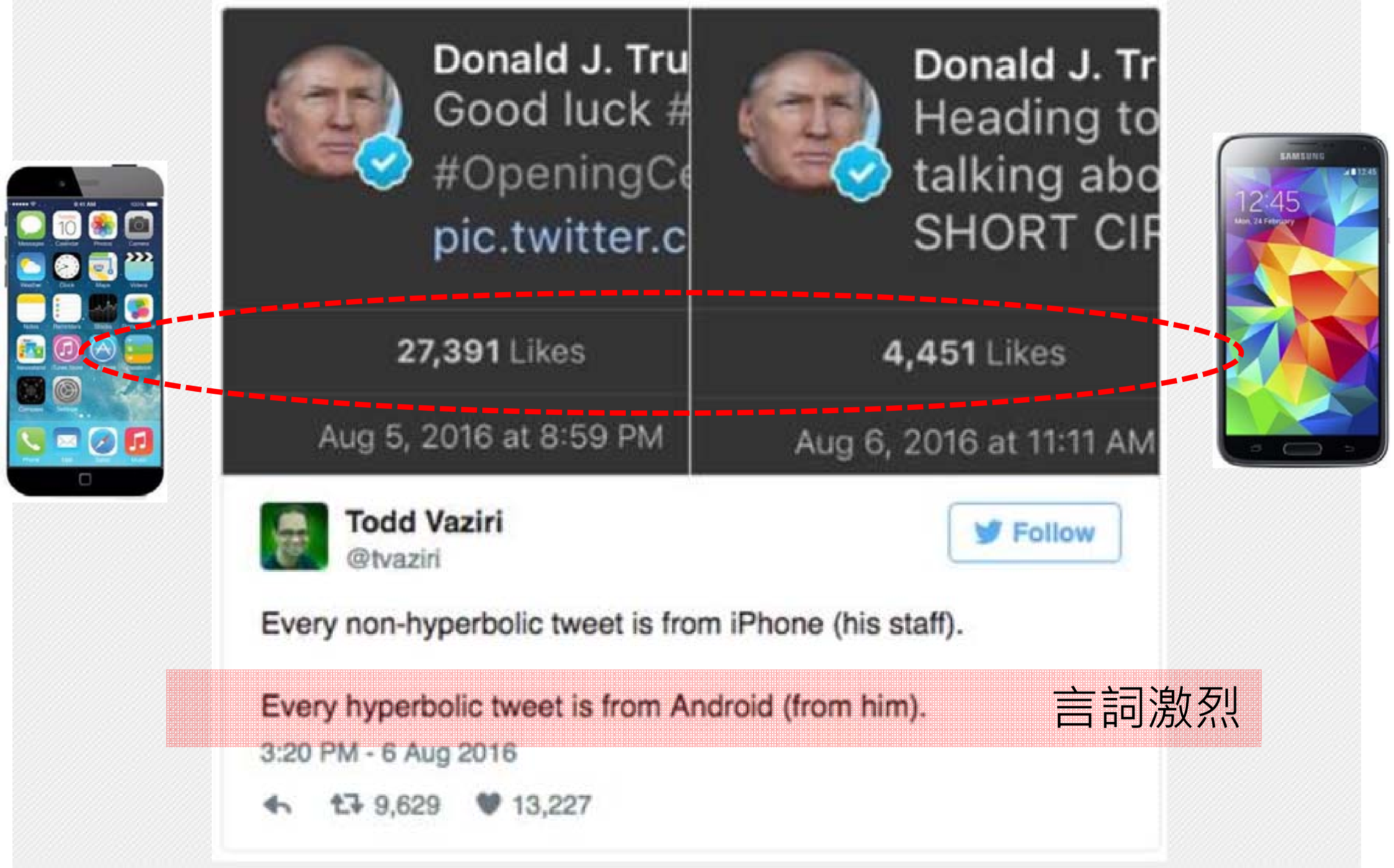
2016年11月09日 14:57 黃慧雯 / 綜合報導　A A A

共和黨候選人川普正式贏得2016美國總統選舉，跌破一票專家眼鏡，也打臉各家民調。(圖 / 美聯社)

2016年美國總統大選結果已經出爐，共和黨候選人川普(Donald Trump)至截稿

有疑問?

數據分析師David Robinson發現，川普發表祝賀內容時，是透過iPhone；而用來抨擊選戰對手時，則是透過Android手機。到底川普個人推特推文的差異，從何而來？這些推文是不是由他一個人包辦，



Donald J. Tru
Good luck #
#OpeningC
pic.twitter.c

27,391 Likes

Aug 5, 2016 at 8:59 PM

Donald J. Tr
Heading to
talking abo
SHORT CIR

4,451 Likes

Aug 6, 2016 at 11:11 AM

Todd Vaziri
@tvaziri
Follow

Every non-hyperbolic tweet is from iPhone (his staff).

Every hyperbolic tweet is from Android (from him). 言詞激烈

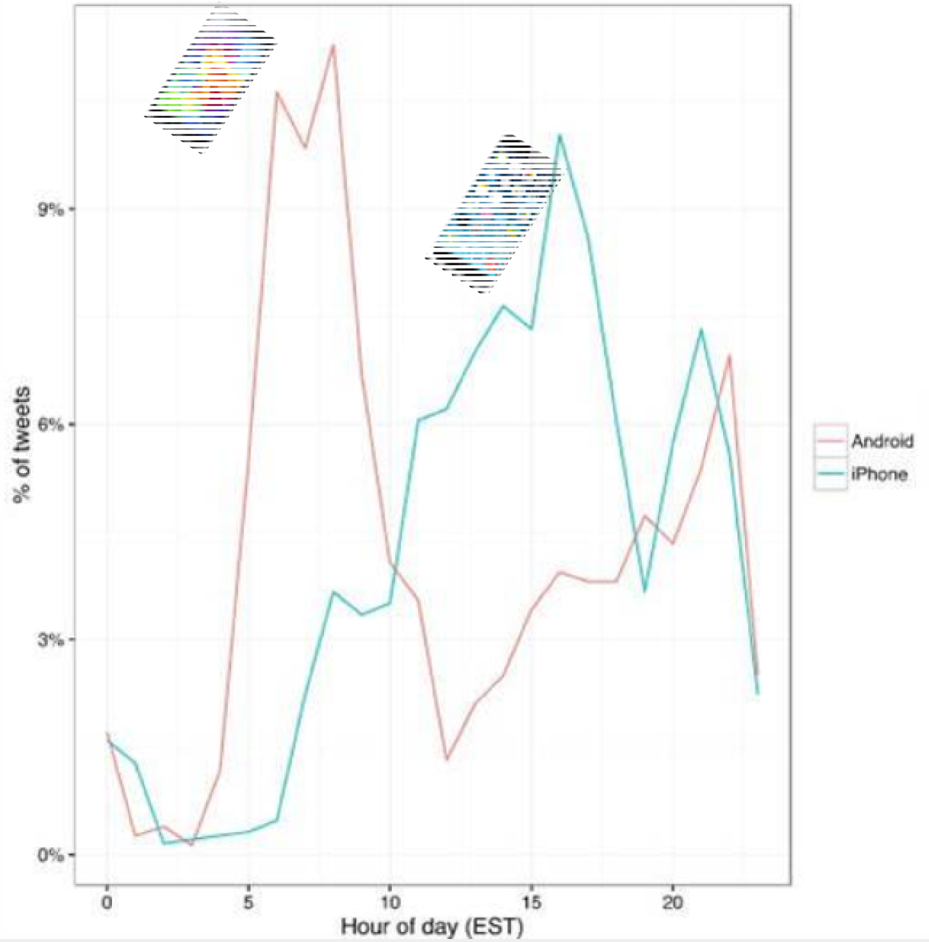
3:20 PM - 6 Aug 2016

9,629 13,227

Twitter網友發現川普推文分別來自iPhone與Android手機端，且發文內容風格迥異。(圖 / 翻攝DZone)

發文時間對比

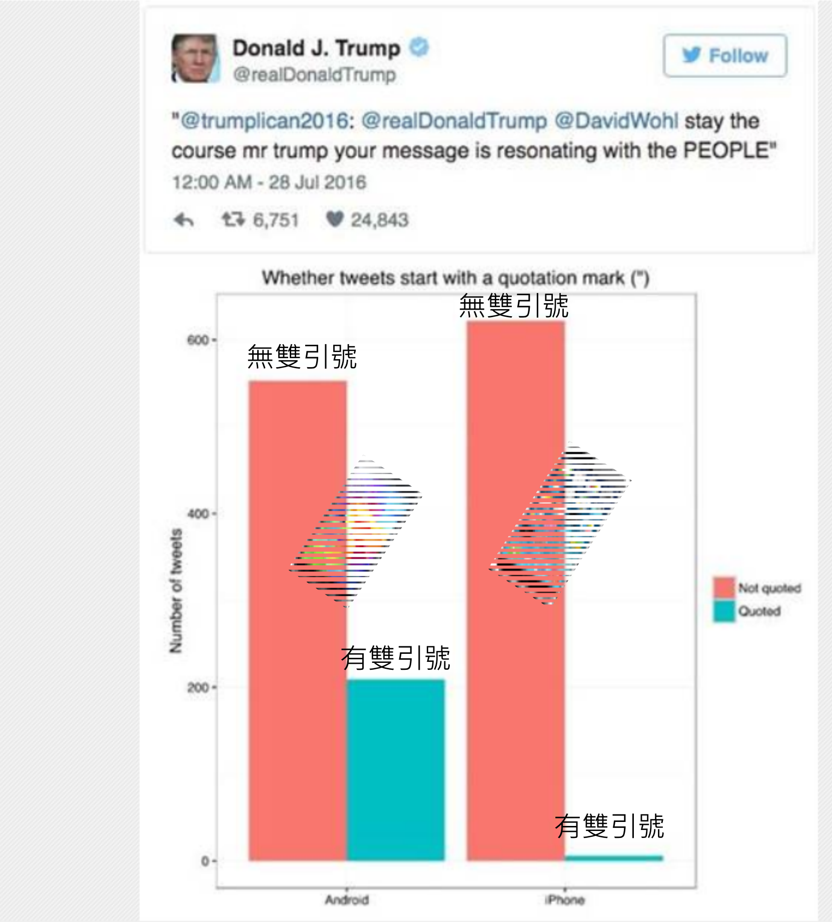
→川普習慣在早上發推文；而他的助理或團隊習慣在下午或晚上發推文



就推文時間分析來看，可看出來自Android手機的推文時間大多落在早上，與來自iPhone端的推文時間區間不同。(圖 / 翻攝DZone)

發文習慣對比

→川普轉推慣用雙引號，他的團隊則沒有這個習慣



Donald J. Trump
@realDonaldTrump

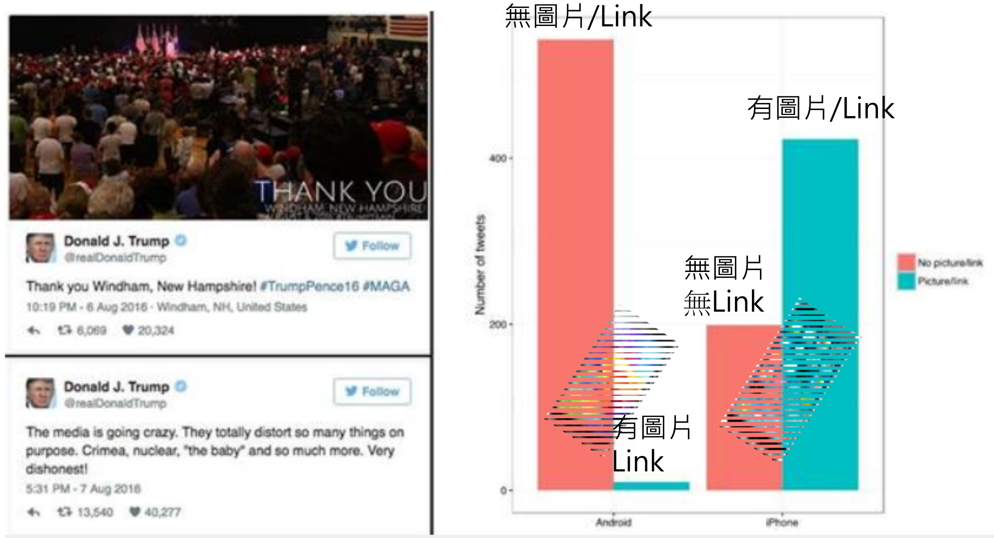
"@trumplican2016: @realDonaldTrump @DavidWohl stay the course mr trump your message is resonating with the PEOPLE"

12:00 AM - 28 Jul 2016

6,751 24,843

川普轉推推文多愛用雙引號。(圖 / 翻攝DZone)

→川普的推文都以文字為主，少附link以及圖片



Donald J. Trump
@realDonaldTrump

Thank you Windham, New Hampshire! #TrumpPence16 #MAGA

10:19 PM - 6 Aug 2016 - Windham, NH, United States

6,069 20,324

Donald J. Trump
@realDonaldTrump

The media is going crazy. They totally distort so many things on purpose. Crimea, nuclear, "the baby" and so much more. Very dishonest!

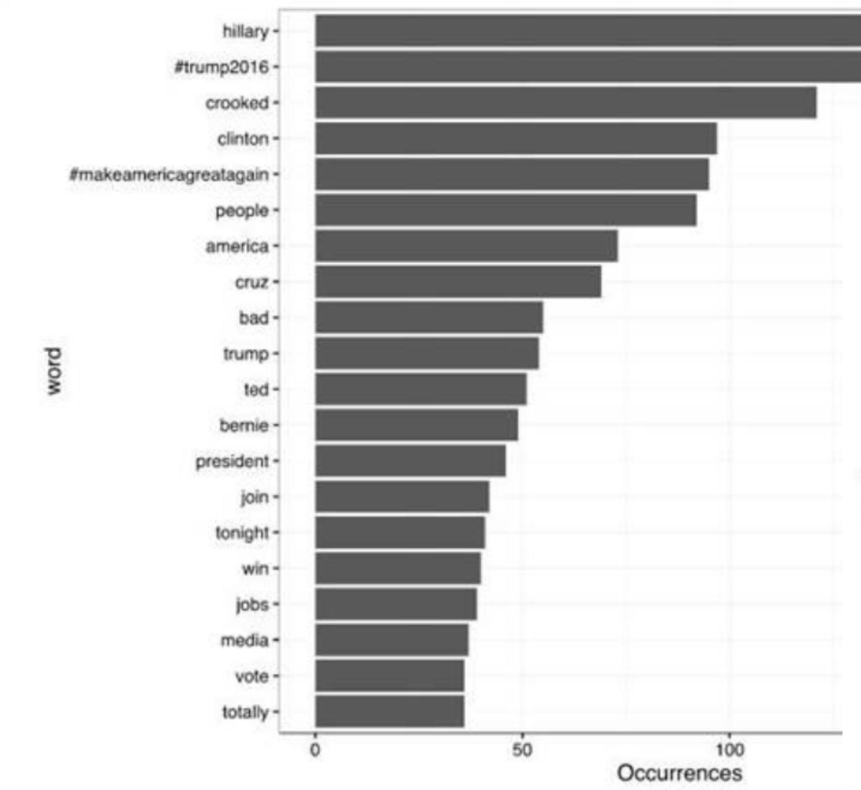
5:31 PM - 7 Aug 2016

13,540 40,277

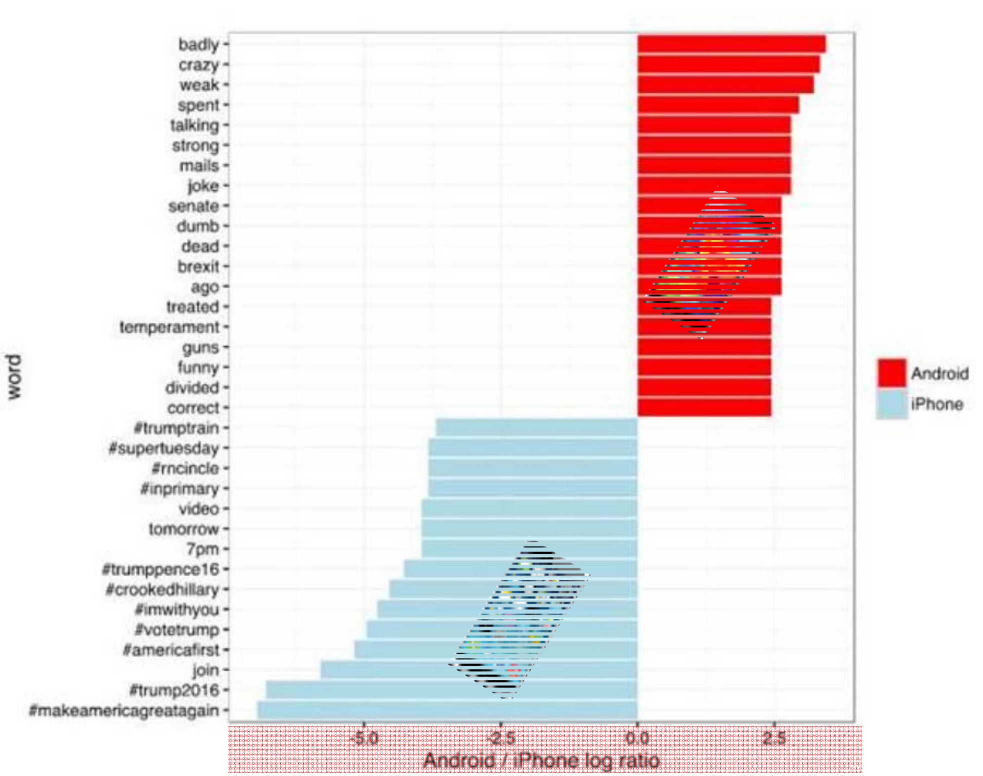
川普的推文很少用link以及圖片(如左下)，來自iPhone的推文習慣不同，常附圖片。(圖 / 翻攝DZone)

發推文文字對比

就發推文時使用的文字來看，以下是來自Android手機的推文常見字



川普推文常用字。(圖 / 翻攝DZone)



Android帳號推文與iPhone推文常用字的對比。(圖 / 翻攝DZone)

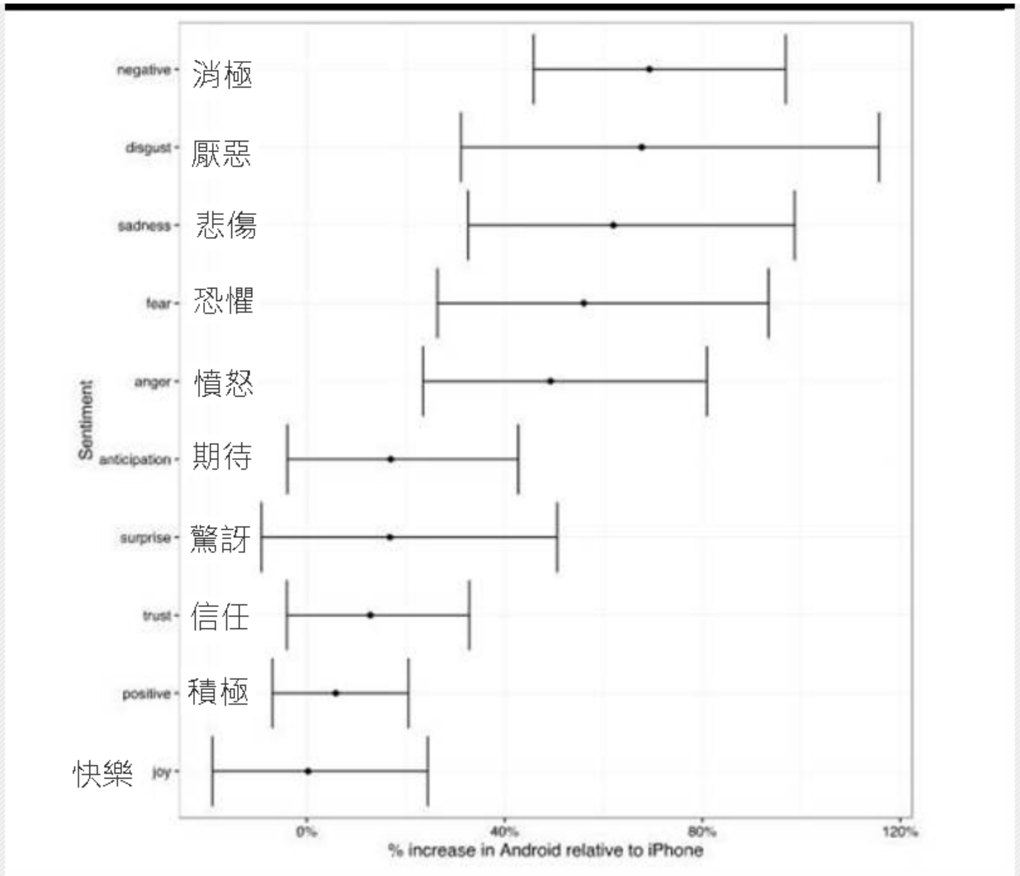
情感分析

- 用 tidytext 當中的NRC Word-Emotion Association辭典，數據分析師將推文的用詞跟「積極、消極、憤怒、期待、厭惡、恐懼、快樂、悲傷、驚訝、信任」這十種情緒進行了**關聯分析**，結果發現：

- Android手機的推文中(共4901個字)，總共有321個字與「**憤怒**」的情感有關、有207個字與「**厭惡**」的情緒有關。

- 而透過**Poisson test** 分析後，更可明顯發現Android手機的推文更喜歡使用強烈情緒性的字眼，若透過**95%信賴區間**來看，就能看出Android手機推文與iPhone推文的不同。

→從結果來看，Android手機端的推文，使用「厭惡、悲傷、恐懼、憤怒」等消極情緒字眼的比例比iPhone的推文高出40%~80%。

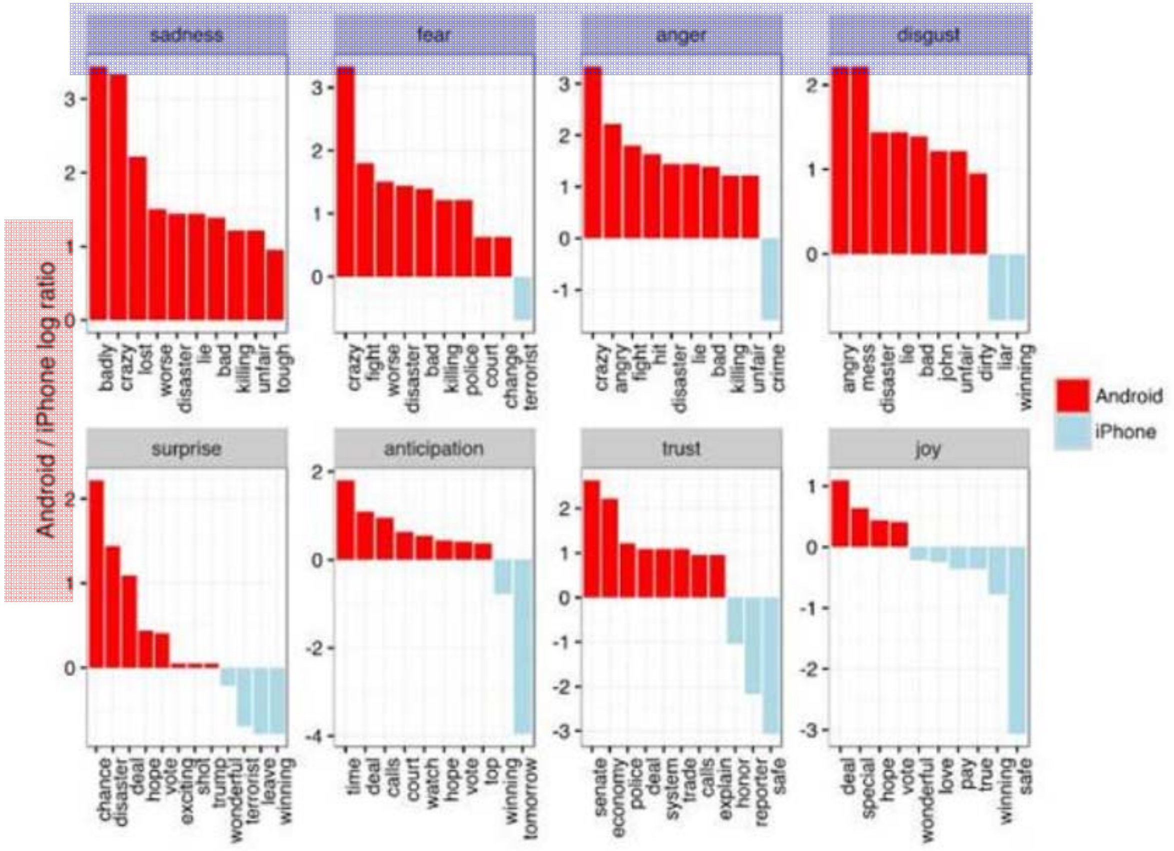


以95%信賴區間來看來看Android手機推文與情緒的關聯性。(圖 / 翻攝DZone)

總結: 川普推特誰寫的?

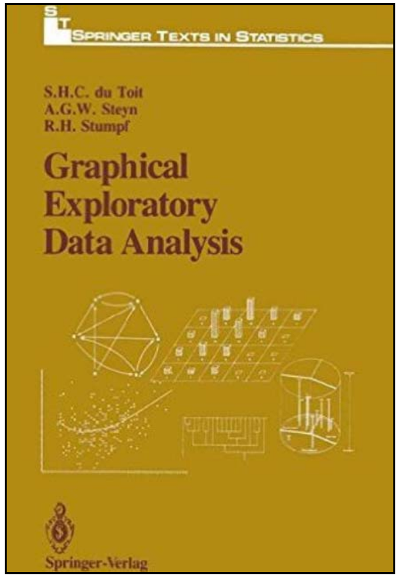
- 從川普個人推特帳號的**單則推文**中，可能看不出個所以然。然而在**大數據的分析下**，卻能很清楚看出脈絡。

- 川普個人推特的推文，來自Android手機的發文與來自iPhone的發文，明顯是由不同人所寫，因為發推時間、推文內容、標籤使用率、轉發方式都截然不同。且**來自Android手機的推文也顯得更為激烈與消極**。
- 川普個人用來發推的行動裝置，就是三星的Galaxy系列手機。基於上述分析，幾乎可以確定來自Android手機的推文是由川普本人所發；而來自iPhone的推文，則應該是出於他助理團隊之手。



Android手機推文愛用情緒性字詞的比例比iPhone推文高出很多。(圖 / 翻攝DZone)

推薦書目


Springer Texts in Statistics

S.H.C. du Toit
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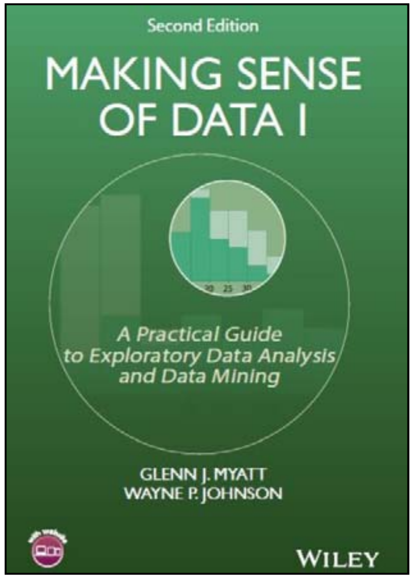
Graphical Exploratory Data Analysis

Springer-Verlag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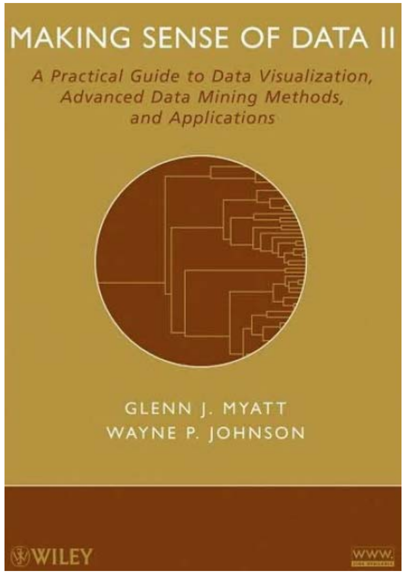
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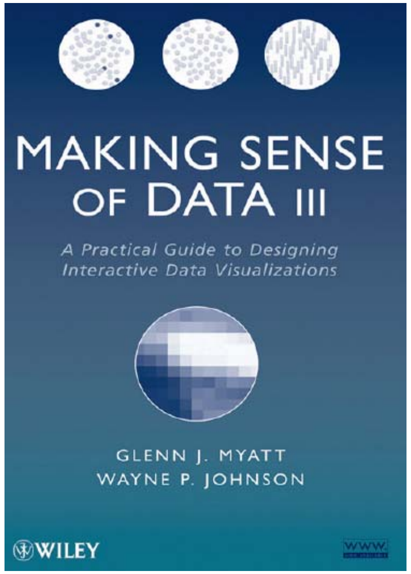
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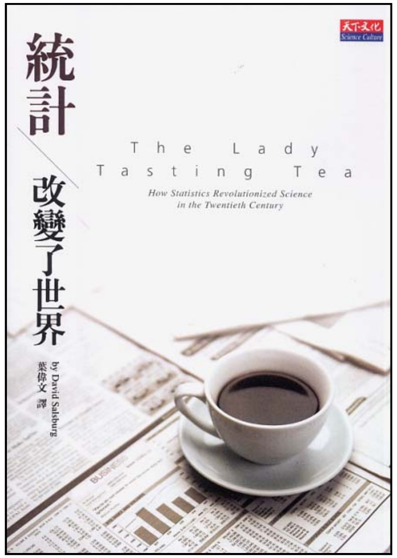
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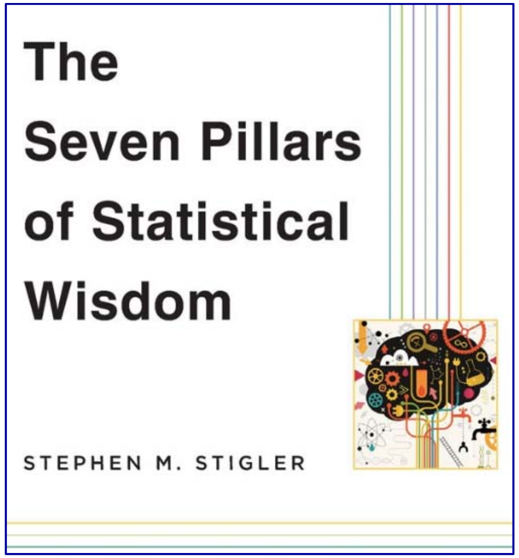
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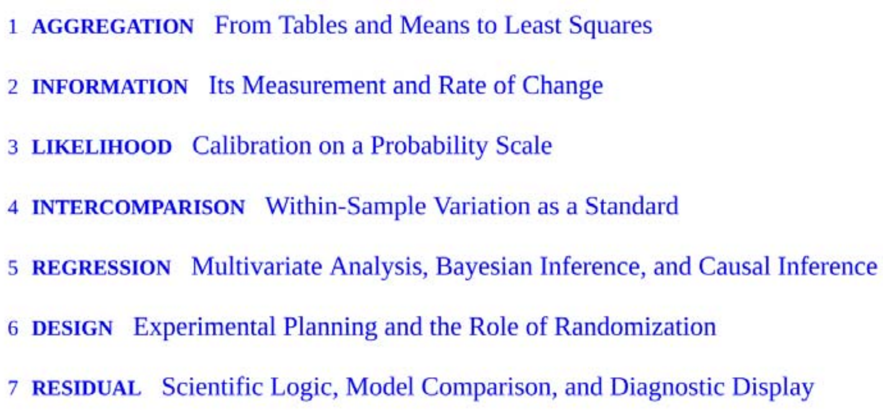
STEPHEN M. STIGLER



1 AGGREGATION From Tables and Means to Least Squares

2 INFORMATION Its Measurement and Rate of Change

3 LIKELIHOOD Calibration on a Probability Scale

4 INTERCOMPARISON Within-Sample Variation as a Standard

5 REGRESSION Multivariate Analysis, Bayesian Inference, and Causal Inference

6 DESIGN Experimental Planning and the Role of Randomization

7 RESIDUAL Scientific Logic, Model Comparison, and Diagnostic Display

Infovis and Statistical Graphics: Different Goals, Different Looks

Journal of Computational and Graphical Statistics, Volume 22, 2013 - Issue 1

- **Infovis and Statistical Graphics: Different Goals, Different Looks**
  Andrew Gelman & Antony Unwin, Pages: 2-28
- **InfoVis Is So Much More**: A Comment on Gelman and Unwin and an Invitation to Consider the Opportunities, Robert Kosara, Pages: 29-32
- **InfoVis and Statistical Graphics: Comment**
  Paul Murrell, Pages: 33-37
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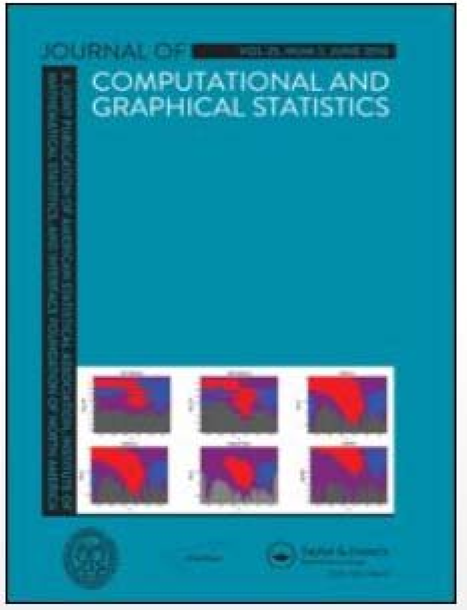
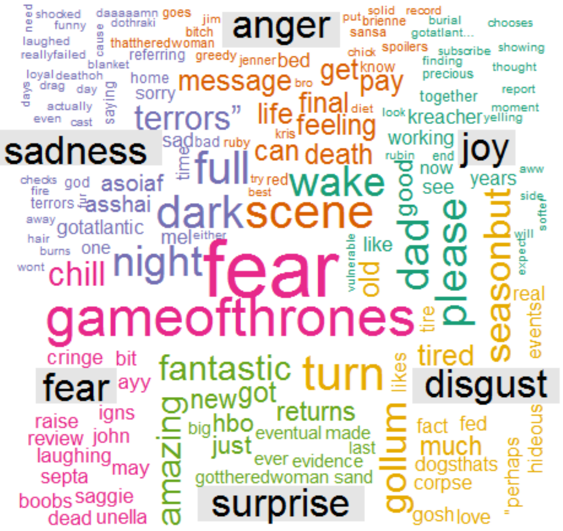
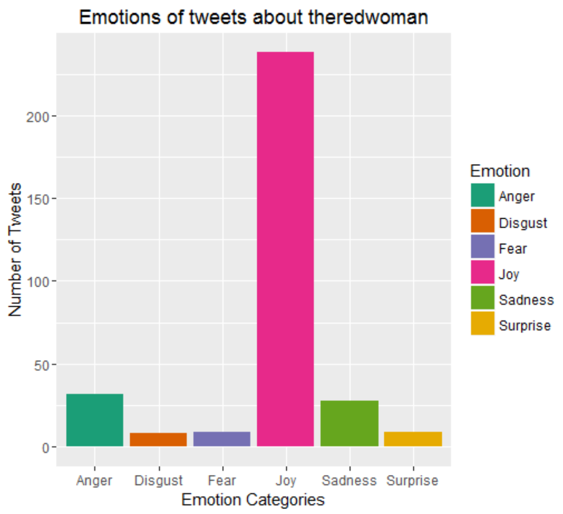


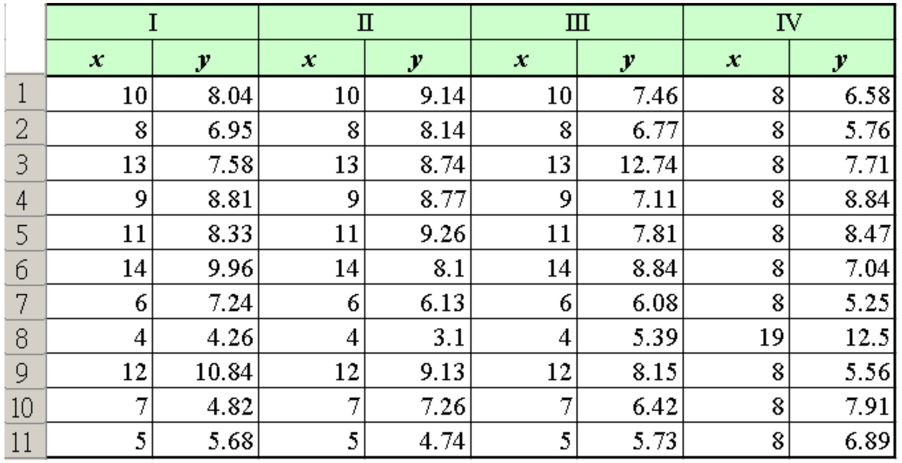




http://emarketingwall.com/how-twitter-responded-to-the-latest-episode-of-game-of-thrones

Why Data Visualization?

- It is not about "infographics", the beautiful, heavily customized products of expert graphic designers.
- Data visualization can provide clear understanding of patterns in data, detect hidden structures in data, condense information.
- **Anscombe's quartet** comprises four datasets. They were constructed in 1973 by the statistician Francis Anscombe to demonstrate both the importance of graphing data before analyzing it and the effect of outliers on statistical properties.
- Four datasets have nearly identical simple statistical properties, yet appear very different when graphed.



	I		II		III		IV	
	x	*y*	*x*	*y*	*x*	*y*	*x*	*y*
1	10	8.04	10	9.14	10	7.46	8	6.58
2	8	6.95	8	8.14	8	6.77	8	5.76
3	13	7.58	13	8.74	13	12.74	8	7.71
4	9	8.81	9	8.77	9	7.11	8	8.84
5	11	8.33	11	9.26	11	7.81	8	8.47
6	14	9.96	14	8.1	14	8.84	8	7.04
7	6	7.24	6	6.13	6	6.08	8	5.25
8	4	4.26	4	3.1	4	5.39	19	12.5
9	12	10.84	12	9.13	12	8.15	8	5.56
10	7	4.82	7	7.26	7	6.42	8	7.91
11	5	5.68	5	4.74	5	5.73	8	6.89

Mean of x in each case: 9 (exact)

Sample variance of x in each case: 11 (exact)

Mean of y in each case: 7.50 (to 2 decimal places)

Sample variance of y in each case: 4.122 or 4.127 (to 3 decimal places)

Correlation between x and y in each case: 0.816 (to 3 decimal places)

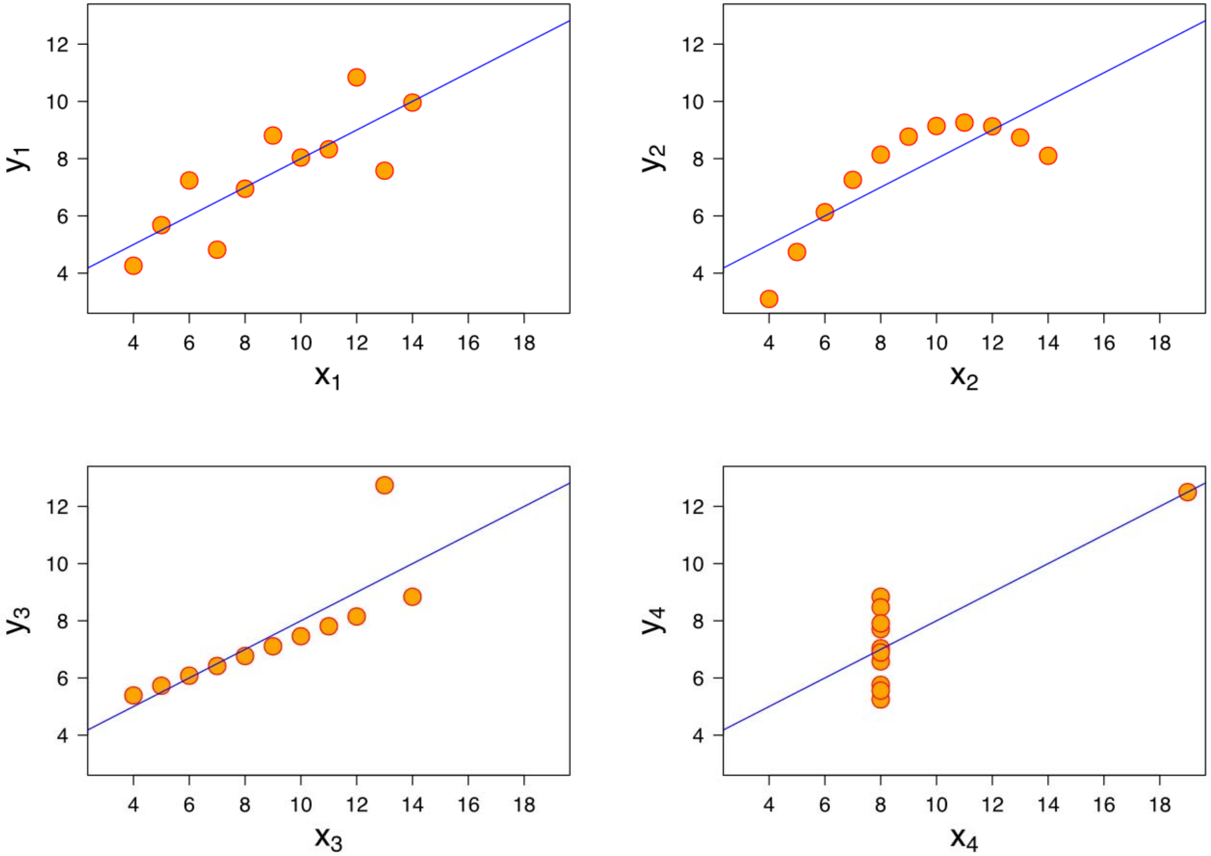
Linear regression line in each case: $y = 3.00 + 0.500x$ (to 2 and 3 decimal places, respectively)

https://en.wikipedia.org/wiki/Anscombe's_quartet

http://ryanwomack.com/IASSIST/DataViz/

Anscombe's Quartet

- Mean of x in each case: 9 (exact)
- Sample variance of x in each case: 11 (exact)
- Mean of y in each case: 7.50 (to 2 decimal places)
- Sample variance of y in each case: 4.122 or 4.127 (to 3 decimal places)
- Correlation between x and y in each case: 0.816 (to 3 decimal places)
- Linear regression line in each case: $y = 3.00 + 0.500x$ (to 2 and 3 decimal places, respectively)



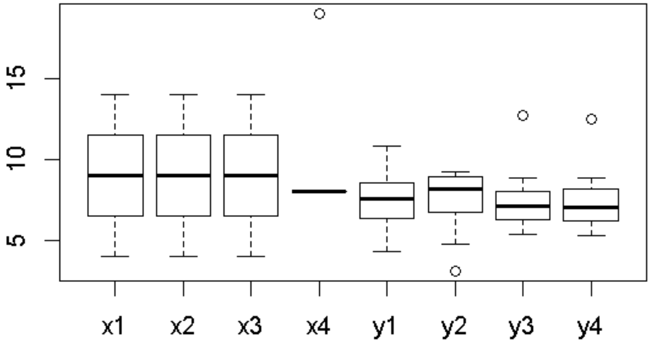
anscombe {datasets}

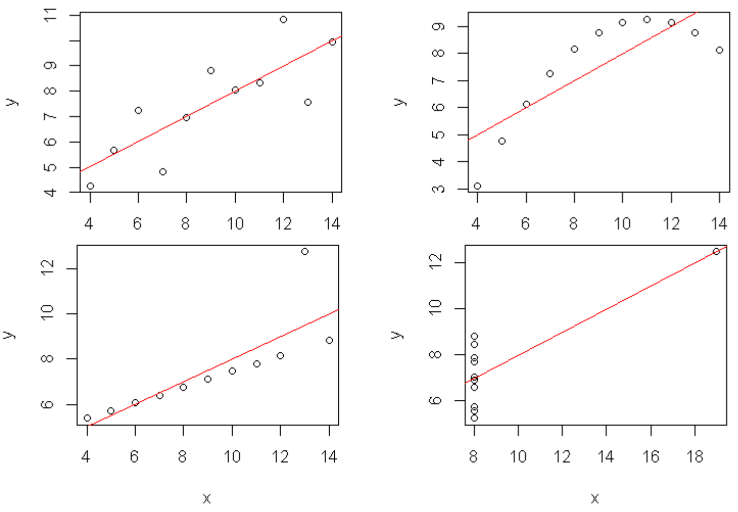
Anscombe's Quartet of ‘Identical’ Simple Linear Regressions

```
> head(anscombe, 3)
  x1 x2 x3 x4   y1   y2    y3   y4
1 10 10 10  8 8.04 9.14  7.46 6.58
2  8  8  8  8 6.95 8.14  6.77 5.76
3 13 13 13  8 7.58 8.74 12.74 7.71
> apply(anscombe, 2, mean)
      x1       x2       x3       x4       y1       y2       y3       y4 
9.000000 9.000000 9.000000 9.000000 7.500909 7.500909 7.500000 7.500909 
> apply(anscombe, 2, sd)
      x1       x2       x3       x4       y1       y2       y3       y4 
3.316625 3.316625 3.316625 3.316625 2.031568 2.031657 2.030424 2.030579 
> mapply(cor, anscombe[,1:4], anscombe[,5:8])
       x1        x2        x3        x4 
0.8164205 0.8162365 0.8162867 0.8165214 
> mapply(function(x, y) lm(y~x)$coefficients, anscombe[, 1:4], anscombe[, 5:8])
                   x1       x2        x3        x4
(Intercept) 3.0000909 3.000909 3.0024545 3.0017273
x           0.5000909 0.500000 0.4997273 0.4999091
```

```
par(mfrow=c(2, 2))
regplot <- function(x, y){
  plot(y~x)
  abline(lm(y~x), col="red")
}
mapply(regplot, anscombe[, 1:4], anscombe[, 5:8])
```

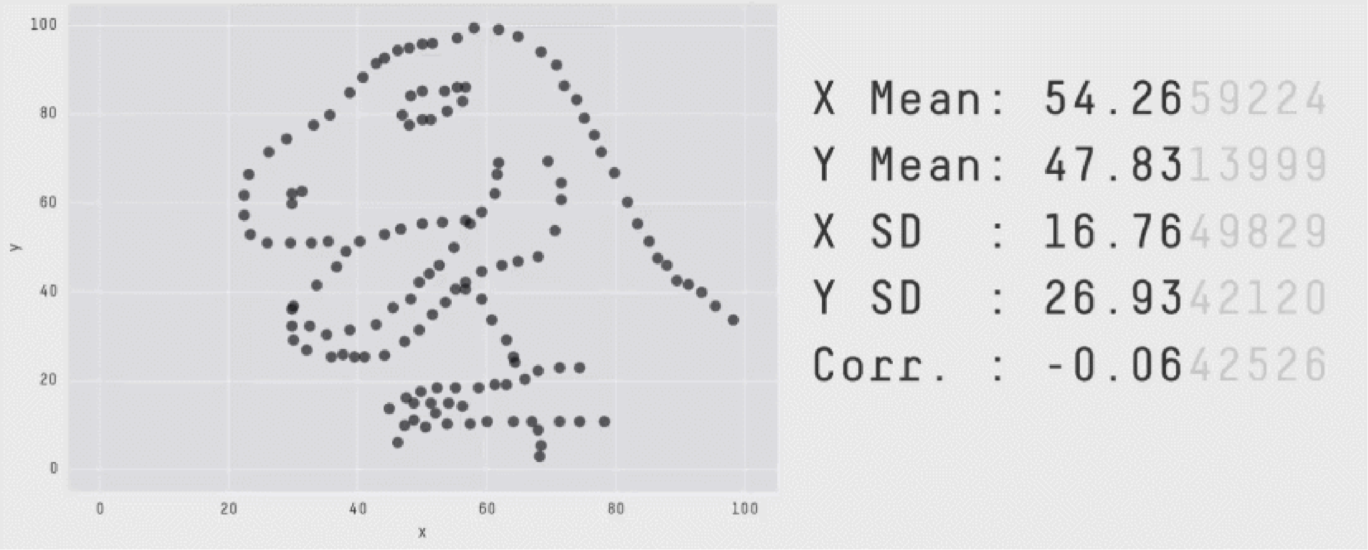
boxplot(anscombe)



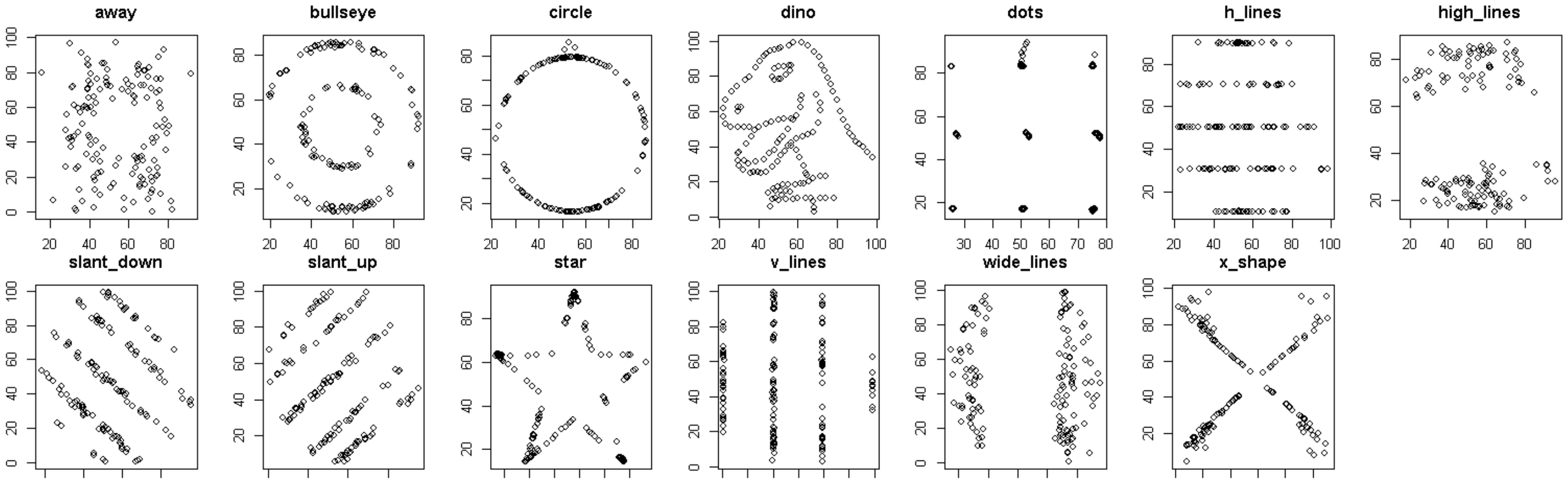


The Datasaurus Dozen

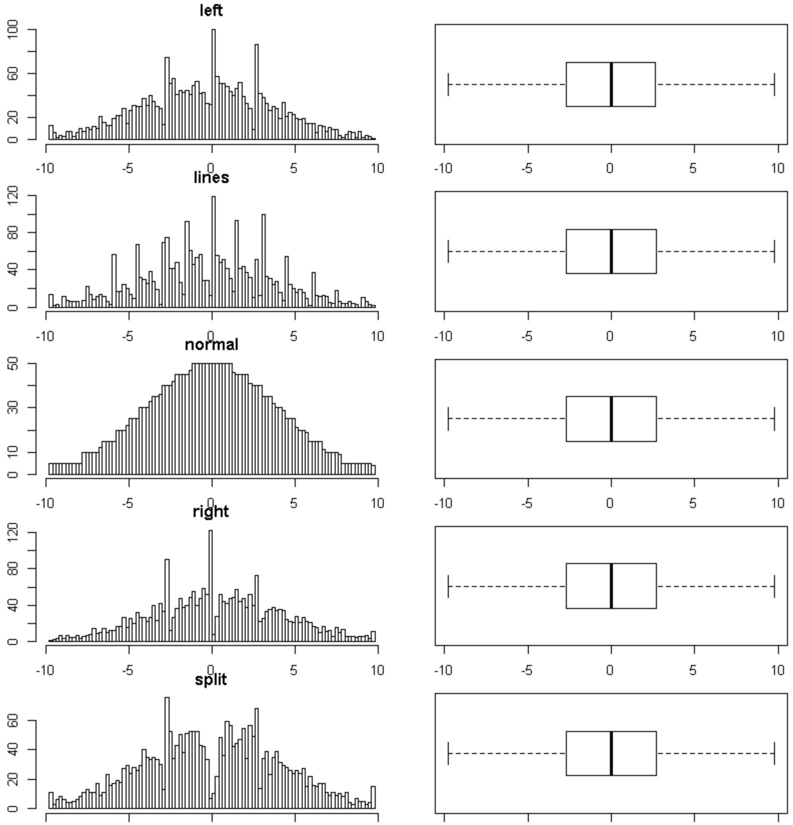
```
install.packages("datasauRus")
```

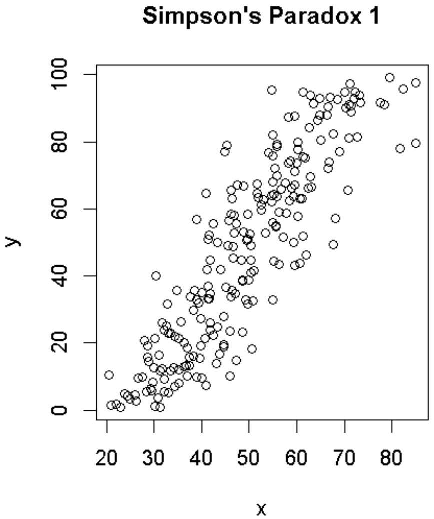


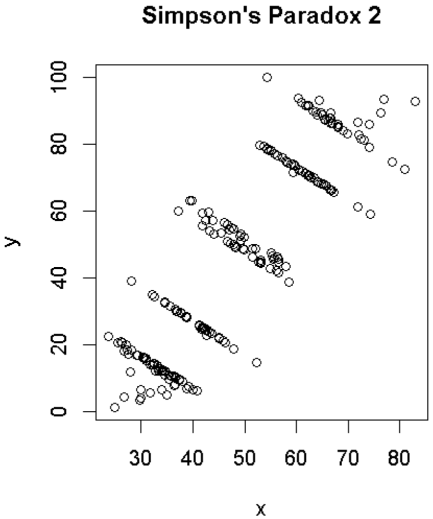
Justin Matejka and George Fitzmaurice, Same Stats, Different Graphs: Generating Datasets with Varied Appearance and Identical Statistics through Simulated Annealing. https://www.autodeskresearch.com/publications/samestats



The Datasaurus Dozen
More examples



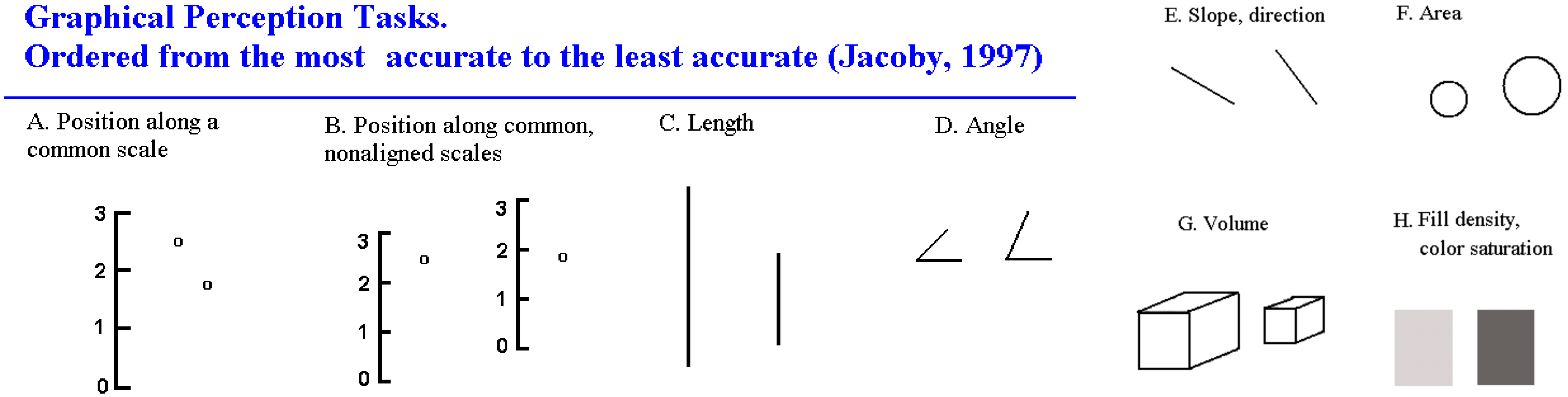




Graphical Perception

Human reception and comprehension of graphical information involves three fundamental perceptual task:

- **Detection**: the visual recognition of a geometric aspect that encodes a physical value. The basic information from the data must be discernible in the graph.
- **Assembly**: the process of discerning patterned regularities among the discrete elements of a graphical display.
- **Estimation**: the visual assessment of the relative magnitudes of two or more quantitative physical values.

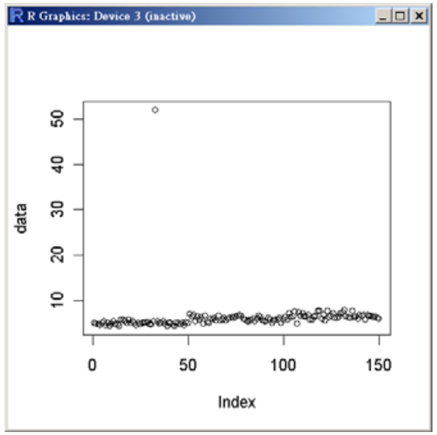


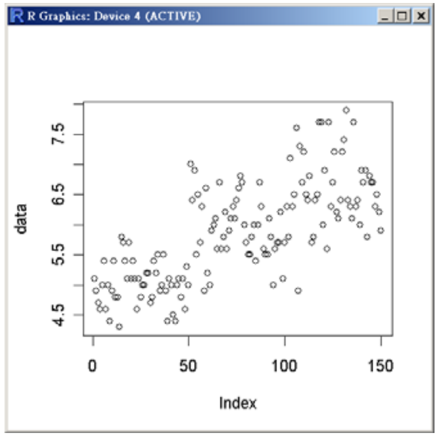
Graphical Perception Tasks.
Ordered from the most accurate to the least accurate (Jacoby, 1997)

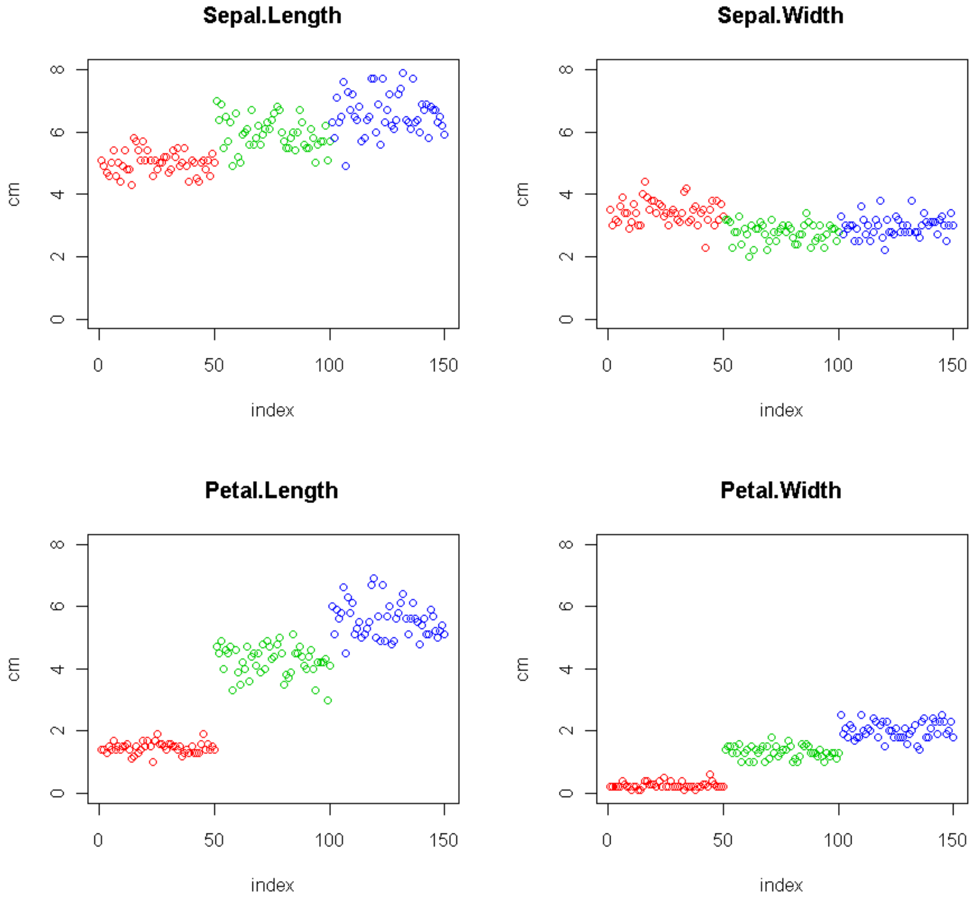
A. Position along a common scale
3
2
1
0
B. Position along common, nonaligned scales
3
2
1
0
3
2
1
0
C. Length
D. Angle
E. Slope, direction
F. Area
G. Volume
H. Fill density, color saturation

Index Plot

- Index plot takes a single argument which is a continuous variable and plots the values on the y axis, with the x coordinate determined by the position of the number in the vector.
- Useful for error checking.



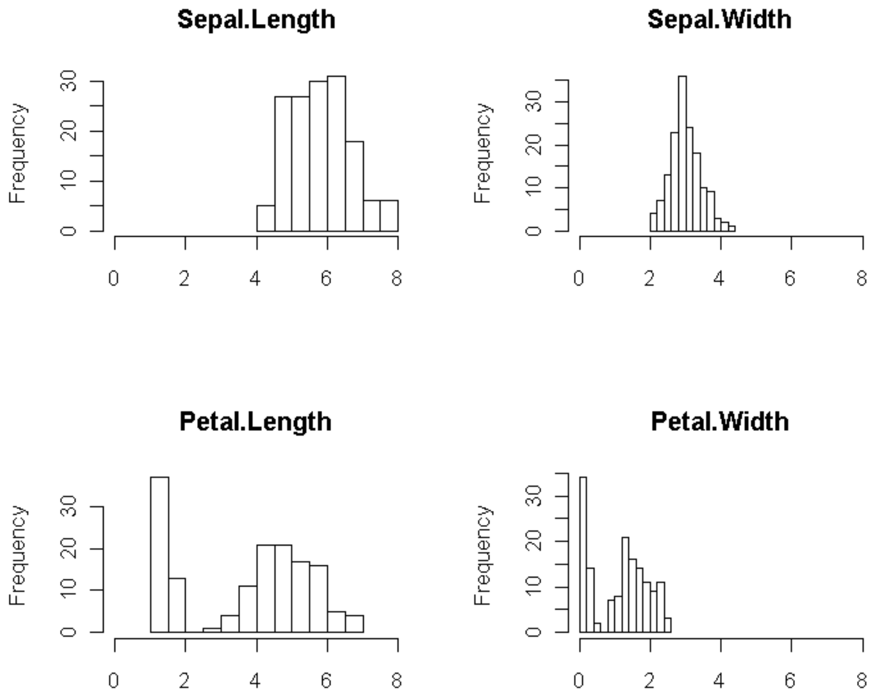




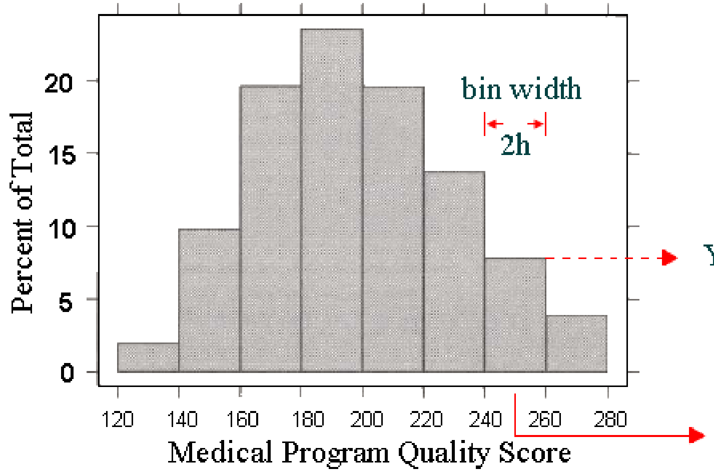
直方圖 (Histogram) (1/3)

The histogram shows:

1. center of the data (location)
2. spread of the data (scale)
3. skewness of the data
4. presence of outliers
5. presence of multiple modes in the data.



O. Bin origin at 120, bin widths of 20.



bin_7

$$Y_7 = \frac{\#\text{ observations within bin}_7}{(2h)\, n}$$

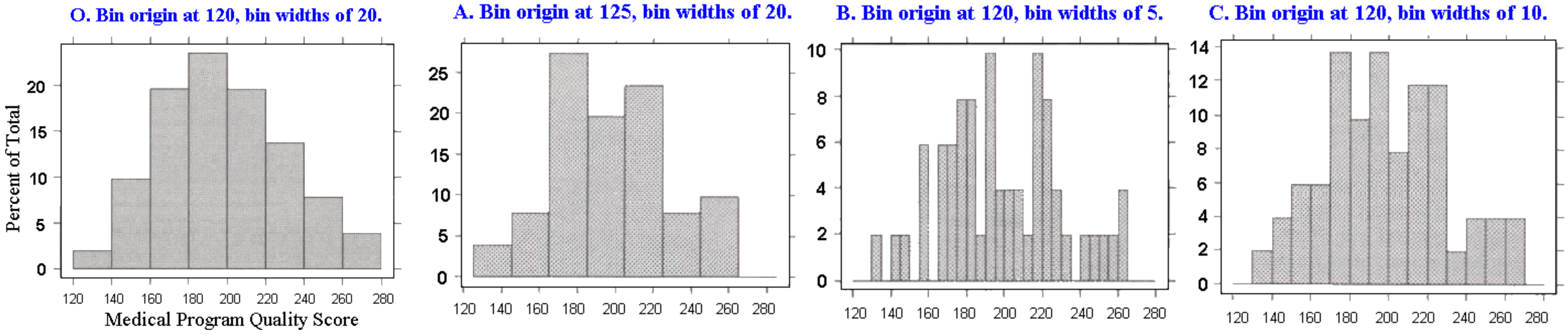
Changes in bin origin and bin widths affect the shape of the histogram

直方圖 (Histogram) (2/3)

- 1/2h adjusts the height of each bar so that the total area enclosed by the entire histogram is 1.
- The area covered by each bar can be interpreted as the probability of an observation falling within that bar.

Disadvantage for displaying a variable's distribution:

- selection of origin of the bins.
- selection of bin widths.
- the very use of the bins is a distortion of information because any data variability within the bins cannot be displayed in the histogram.



O. Bin origin at 120, bin widths of 20.

A. Bin origin at 125, bin widths of 20.

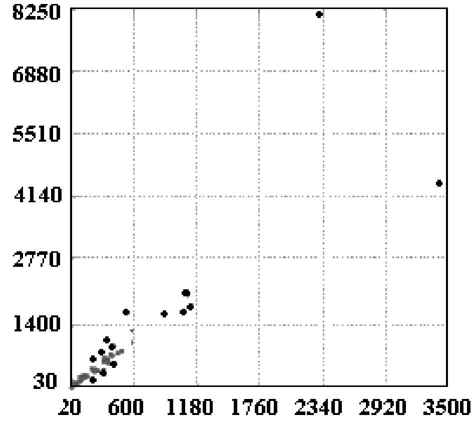
B. Bin origin at 120, bin widths of 5.

C. Bin origin at 120, bin widths of 10.

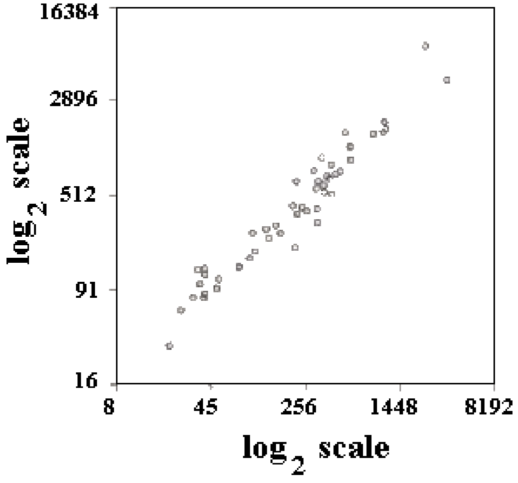
Figure Sources: Jacoby (1997).

Extensions of Scatterplots

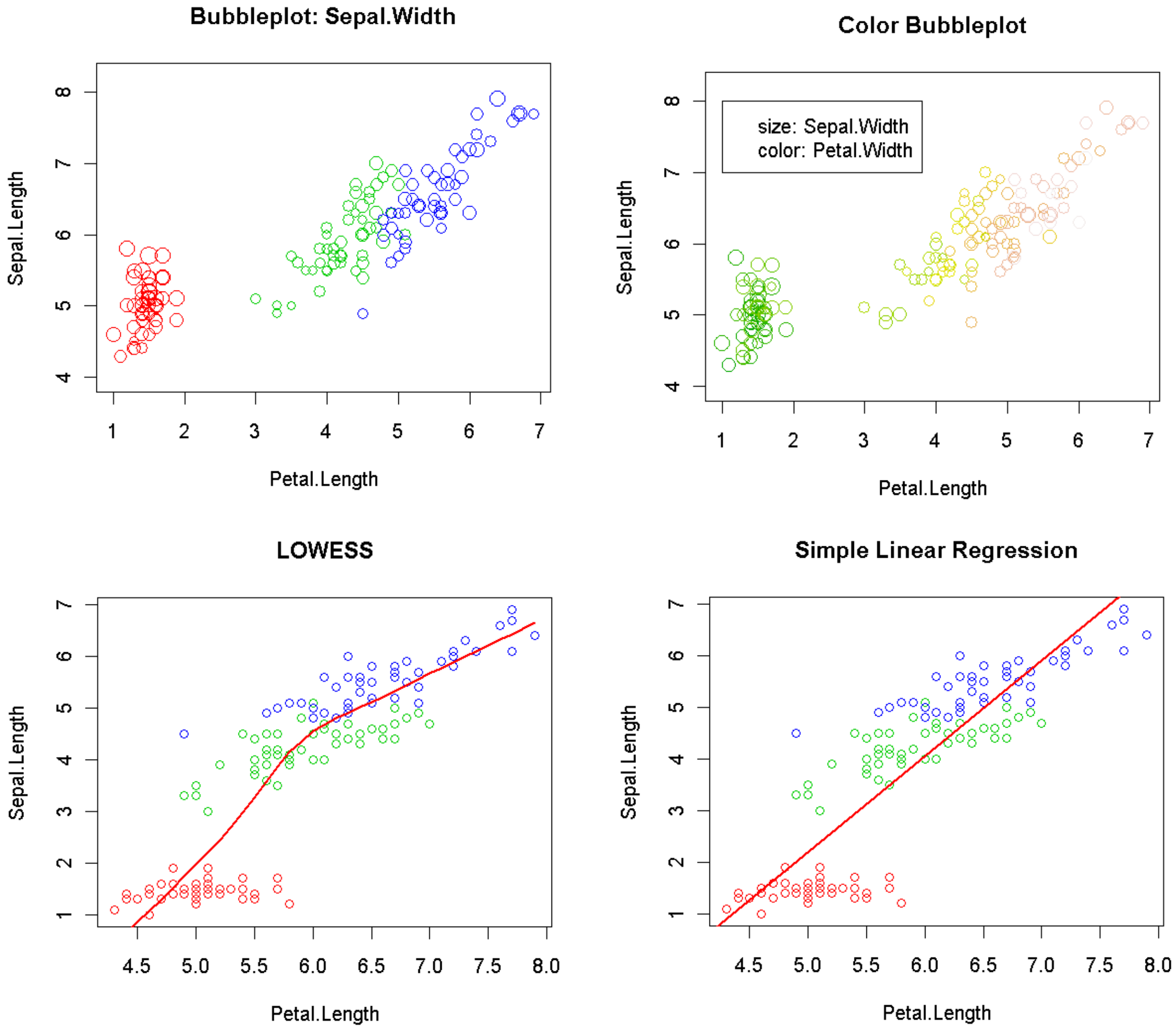
Poorly-Constructed



Better



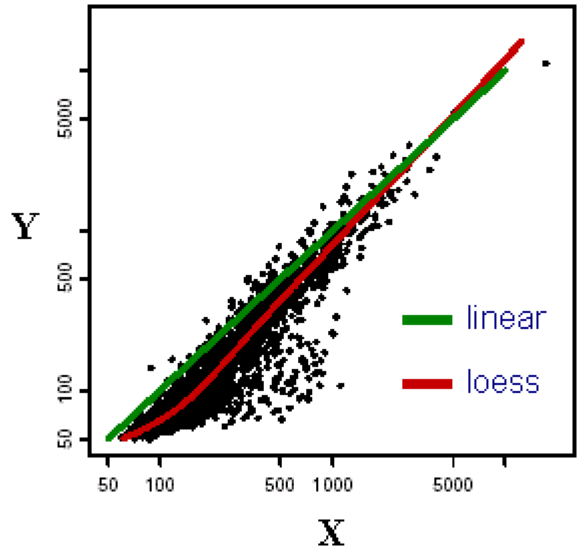
With a smoothing curve



MA plot
Scatterplot for Gene Expression Data

- **MA plots** can show the intensity-dependent ratio of raw microarray data.

Original basis



Oligo	cDNA

$X = PM_1$,
$Y = PM_2$
	X= Cy3
	Y= Cy5

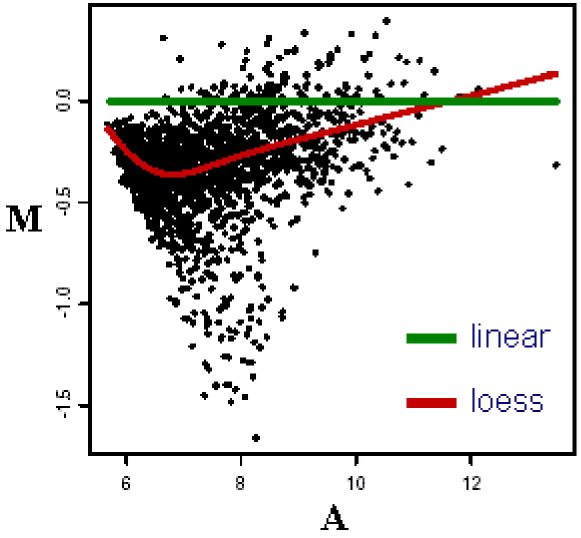
$X = PM_1 - MM_1$, $Y = PM_2 - MM_2$	

→

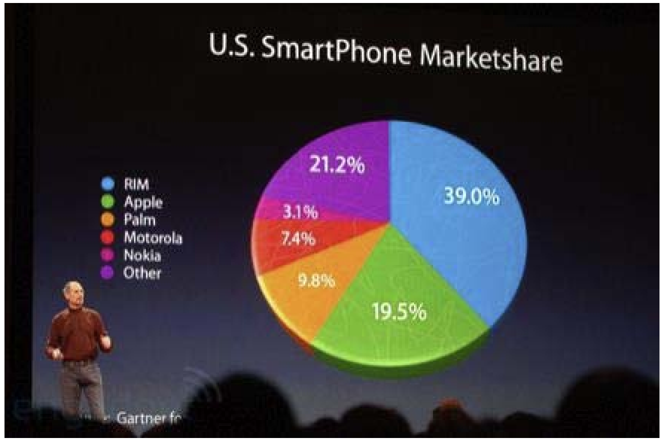
$$M = \log_2\left(\frac{Y}{X}\right)$$

$$A = \frac{1}{2}\log_2(X\,Y)$$

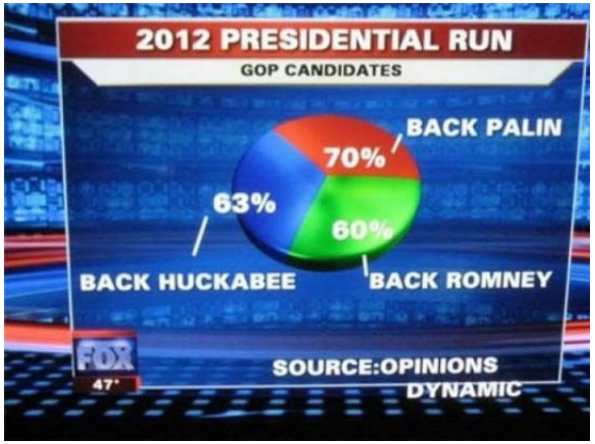
Basis of *M*

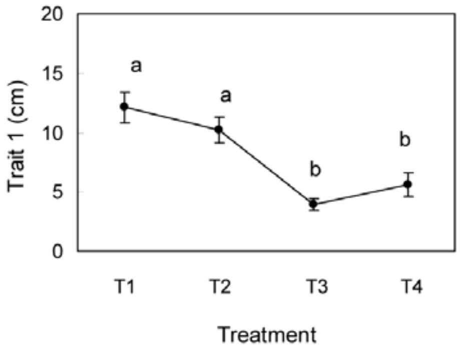


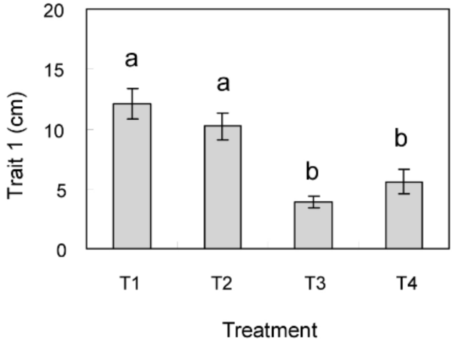
圖表的誤用



Source: https://www.managertoday.com.tw/articles/view/51480

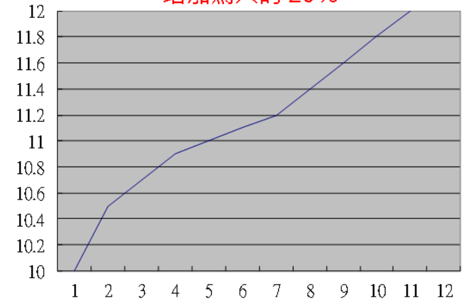






Source: http://ir.tari.gov.tw:8080/bitstream/345210000/3094/1/journal_arc_60-1-6.pdf

增加驚人的 20%



Misleading Graphs: Real Life Examples
http://www.statisticshowto.com/misleading-graphs/

The top ten worst graphs
https://www.biostat.wisc.edu/~kbroman/topten_worstgraphs/

Bad Infographics: 11 Mistakes You Never Want to Make
http://blog.visme.co/bad-infographics/

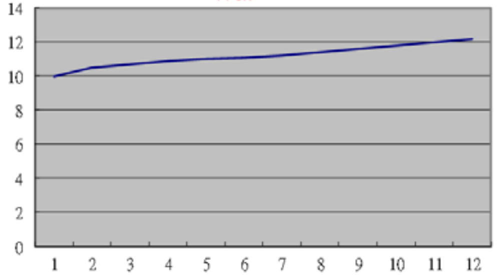
13 Graphs That Are Clearly Lying
https://www.buzzfeed.com/katienotopoulos/graphs-that-lied-to-us?utm_term=.qsnBZa6Qa#.xePkLjDaj

11 Most Useless And Misleading Infographics On The Internet
https://io9.gizmodo.com/11-most-useless-and-misleading-infographics-on-the-inte-1688239674

The most misleading charts of 2015, fixed
https://qz.com/580859/the-most-misleading-charts-of-2015-fixed/

Misleading graph
https://en.wikipedia.org/wiki/Misleading_graph

增加 20%



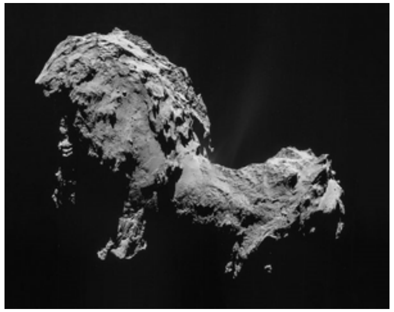
範例: rgl, explore a comet

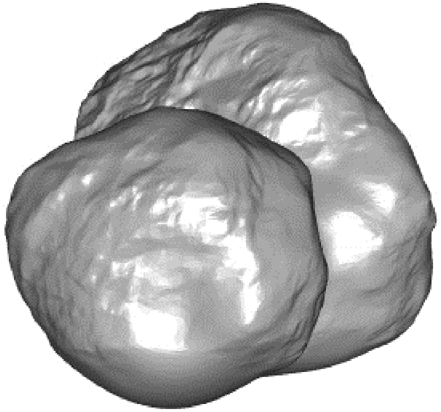
Explore a comet with R's "rgl" package

December 24, 2014

http://blog.revolutionanalytics.com/2014/12/explore-a-comet-with-rs-rgl-package.html

"Last month, the Philae lander touched down on comet Churyumov–Gerasimenko. In the process, the lander and the orbiting Rosetta probe captured detailed data on the geometry of the comet, which the ESA published as a shape file. ..."





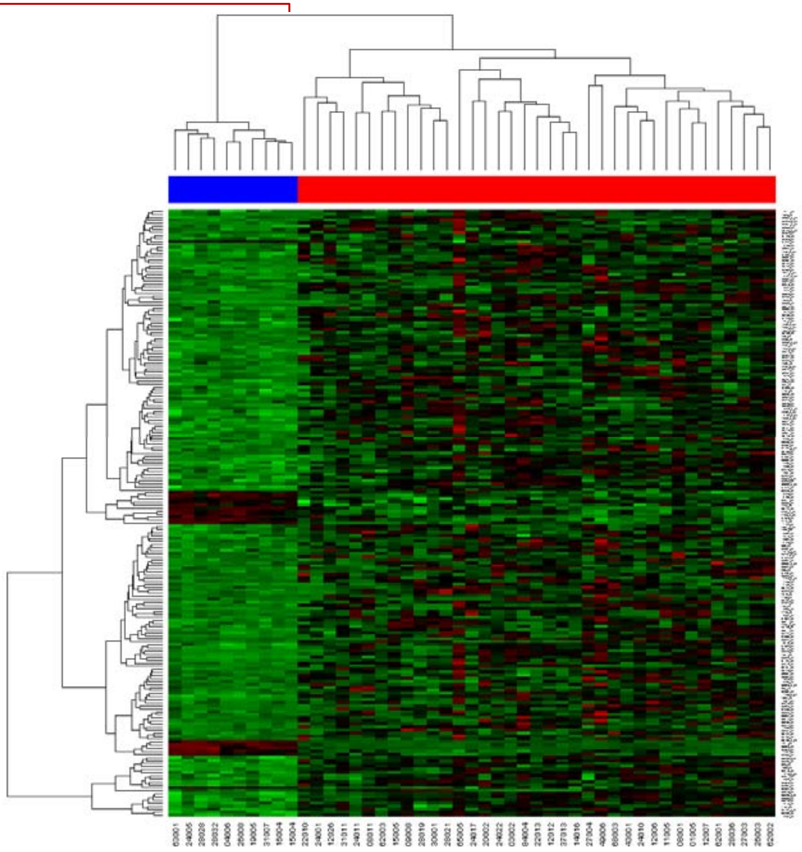
https://en.wikipedia.org/wiki/67P/Churyumov%E2%80%93Gerasimenko

```
> open3d()
> # comet <- readOBJ(url("http://sci.esa.int/science-e/www/object/doc.cfm?fobjectid=54726"))
> comet <- readOBJ("ESA_Rosetta_OSIRIS_67P_SHAP2P.obj")
> class(comet)
[1] "mesh3d"  "shape3d"
> str(comet)
List of 6
 $ vb           : num [1:4, 1:31456] -0.394 0.402 0.443 1 -0.163 ...
 $ it           : num [1:3, 1:62908] 14327 6959 18747 8258 15598 ...
 $ primitivetype: chr "triangle"
 $ material     : NULL
 $ normals      : NULL
 $ texcoords    : NULL
 - attr(*, "class")= chr [1:2] "mesh3d" "shape3d"
> shade3d(comet, col="gray")
```

```
# it: indices for triangular faces
# ib: indices for quad faces
# vb: matrix of vertices: 4xn matrix (rows
x, y, z, h) or equivalent vector, where h
indicates scaling of each plotted quad
```

heatmap {stats}

```
> source("https://bioconductor.org/biocLite.R")
> biocLite("ALL")
> library(ALL)
> data(ALL)
> ALL
> str(ALL)
> dim(exprs(ALL))
[1] 12625   128
> exprs(ALL)[1:3, 1:5]
             01005    01010    03002    04006    04007
1000_at   7.597323 7.479445 7.567593 7.384684 7.905312
1001_at   5.046194 4.932537 4.799294 4.922627 4.844565
1002_f_at 3.900466 4.208155 3.886169 4.206798 3.416923
> table(ALL$mol.biol)

ALL1/AF4  BCR/ABL E2A/PBX1      NEG   NUP-98  p15/p16
      10       37        5       74        1        1
> eset <- ALL[, ALL$mol.biol %in%
                c("BCR/ABL", "ALL1/AF4")]
> dim(exprs(eset))
[1] 12625    47
> f <- factor(as.character(eset$mol.biol))
> eset.p <- apply(exprs(eset), 1, function(x) t.test(x ~ f)$p.value)
> selected.eset <- eset[eset.p < 0.00001, ]
> dim(selected.eset)
Features  Samples
     200       47
> ma.col <- colorRampPalette(c("green", "black", "red"))(200)
> var.col <- ifelse(f=="ALL1/AF4", "blue", "red")
> heatmap(exprs(selected.eset), col=ma.col, ColSideColors=var.col,
          scale="row")
```

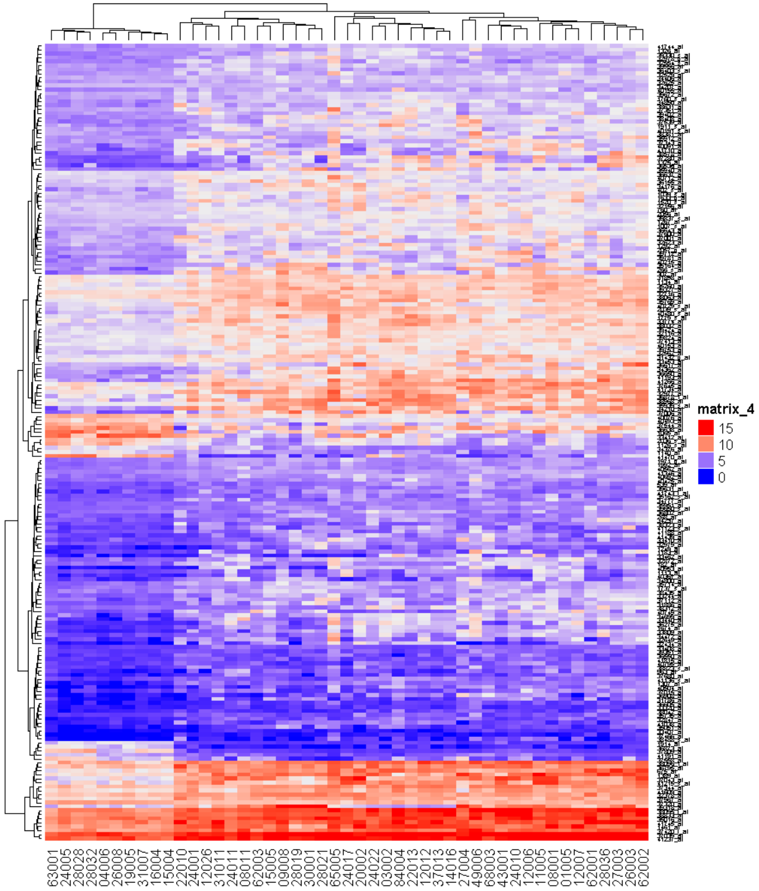


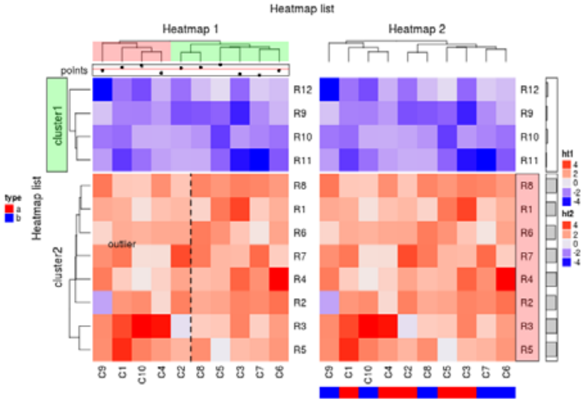
Complex Heatmap

http://www.bioconductor.org/packages/devel/bioc/html/ComplexHeatmap.html

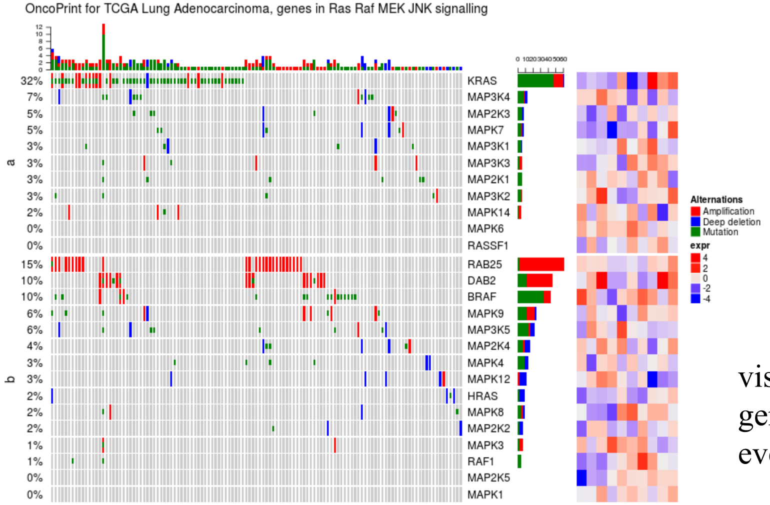
```
> source("https://bioconductor.org/biocLite.R")
> biocLite("ComplexHeatmap")
> library(ComplexHeatmap)
> Heatmap(exprs(selected.eset))
```

Zuguang Gu, Roland Eils, Matthias Schlesner, Complex heatmaps reveal patterns and correlations in multidimensional genomic data, Bioinformatics, Volume 32, Issue 18, 15 September 2016, Pages 2847–2849.





One famous GO game
Player
player1
player2

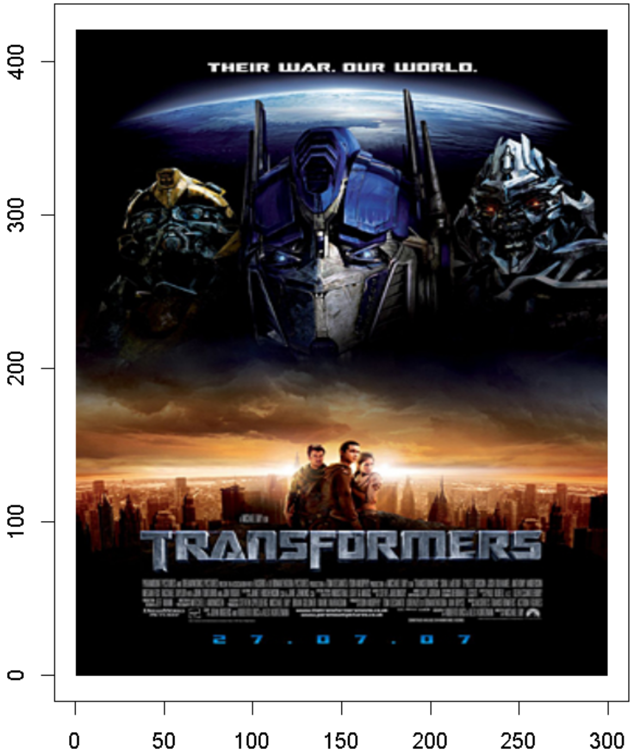


visualize multiple genomic alteration events by heatmap

讀取外部影像檔案

```
> install.packages(c("tiff", "jpeg", "png", "fftwtools"),
repos="http://cran.csie.ntu.edu.tw")
> library(EBImage) # (Repositories: BioC Software)
> Transformers <- readImage("Transformers07.jpg")
> (dims <- dim(Transformers))
[1] 300 421   3
> Transformers
Image
  colorMode    : Color
  storage.mode : double
  dim          : 300 421 3
  frames.total : 3
  frames.render: 1

imageData(object)[1:5,1:6,1]
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    0    0    0    0    0    0
[2,]    0    0    0    0    0    0
[3,]    0    0    0    0    0    0
[4,]    0    0    0    0    0    0
[5,]    0    0    0    0    0    0
> plot(c(0, dims[1]), c(0, dims[2]), type='n',
+ xlab="", ylab="")
> rasterImage(Transformers, 0, 0, dims[1], dims[2])
```

```
> source("https://bioconductor.org/biocLite.R")
> biocLite("EBImage")
```

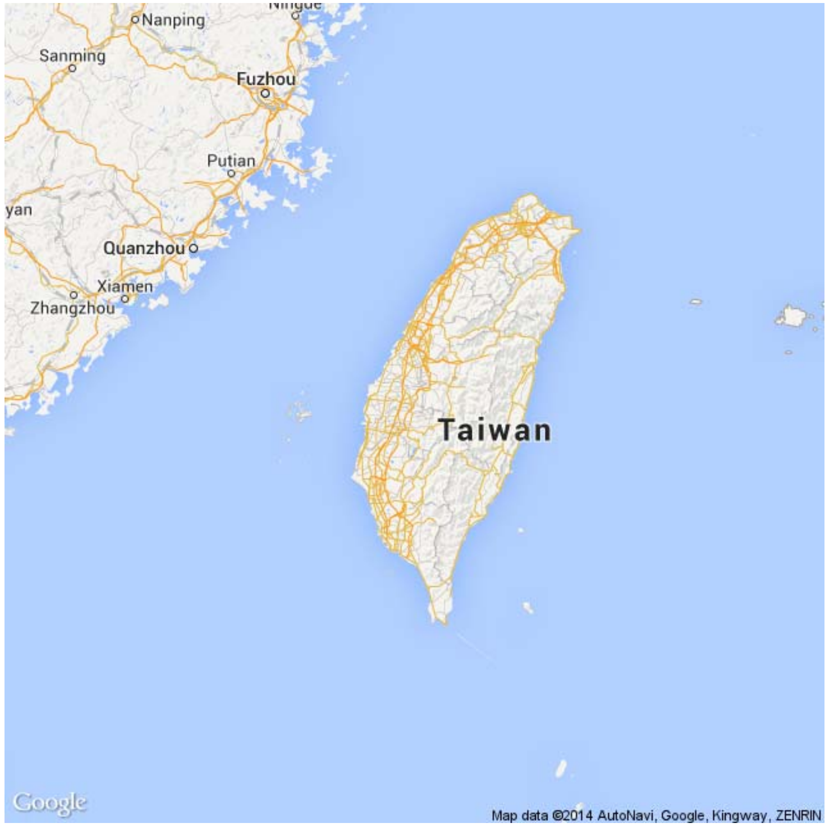


https://en.wikipedia.org/wiki/Transformers_(film)

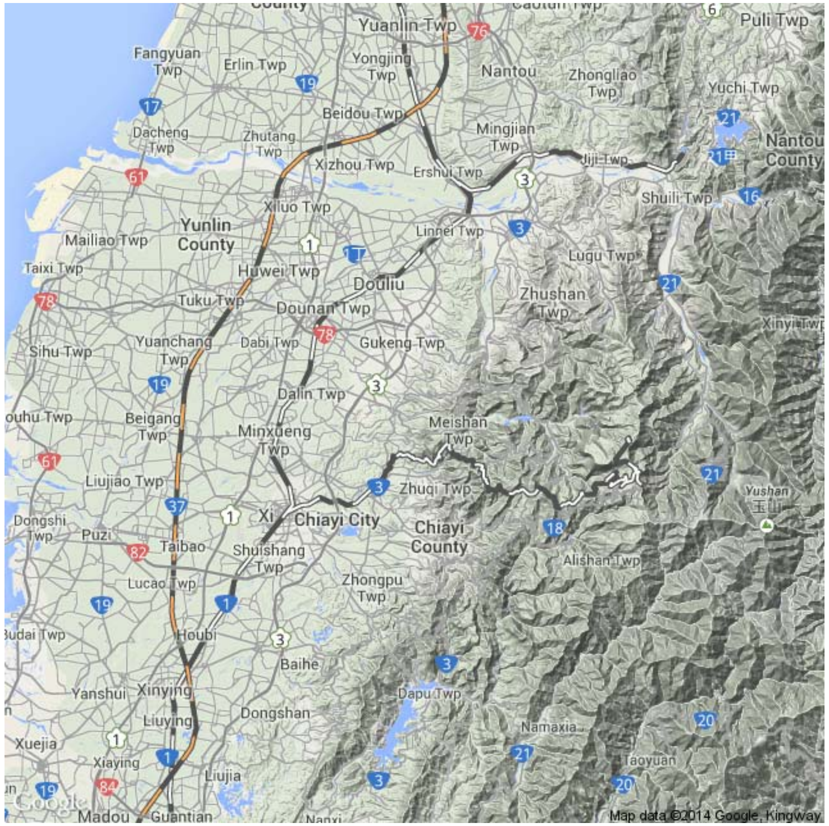
```
> #install.packages("jpeg")
> library(jpeg)
> Transformers <- readJPEG("Transformers07.jpg")
```

台灣地圖

```
TaiwanMap <- GetMap(center=c(lat = 23.58, lon =120.58), zoom =7, destfile =
"Taiwan1.png")
TaiwanMap <- GetMap(center=c(lat = 23.58, lon =120.58), zoom = 10, destfile =
"Taiwan2.png", maptype = "terrain")
```



Map data ©2014 AutoNavi, Google, Kingway, ZENRIN



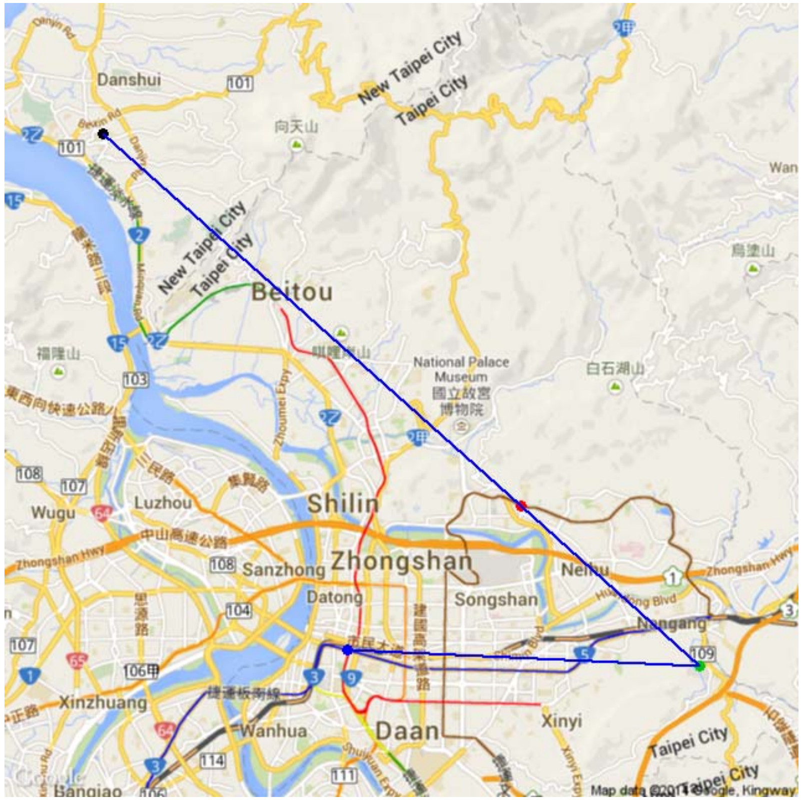
Map data ©2014 Google, Kingway

於地圖上標記

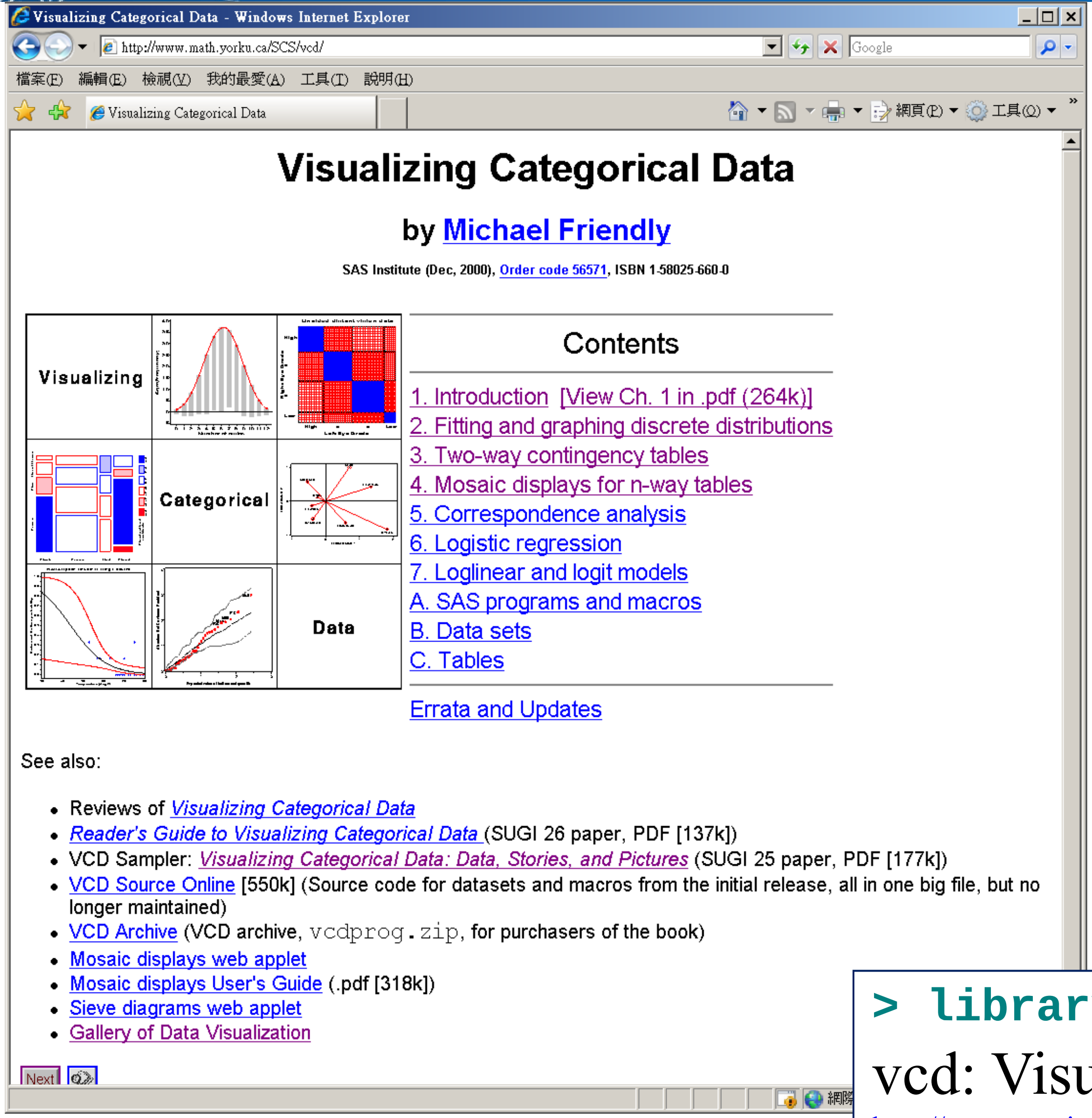
```
my.lat <- c(25.175339, 25.082288, 25.042185, 25.046254)
my.lon <- c(121.450003, 121.565481, 121.614548, 121.517532)
bb = qbbox(my.lat, my.lon)
print(bb)
MyMap <- GetMap.bbox(bb$lonR, bb$latR, destfile = "my.png", maptype = "roadmap")

My.markers <- cbind.data.frame(lat = my.lat, lon = my.lon)
tmp <-  PlotOnStaticMap(MyMap, lat = My.markers[,"lat"], lon = My.markers[,"lon"], destfile =
"my.png", cex=2.5, pch=20, col=1:4, add=F)
```

查詢經緯度
http://card.url.com.tw/realads/map_latlng.php

- 淡江大學 25.175339, 121.450003
- 台北市的地理中心位置: 內湖區環山路和內湖路一段跟基湖路口: 25.082288, 121.565481
- 中研院 25.042185, 121.614548
- 捷運台北站: 25.046254,121.517532



類別資料的視覺化: vcd
Visualizing Categorical Data


Visualizing Categorical Data - Windows Internet Explorer
http://www.math.yorku.ca/SCS/vcd/
Google
檔案(F) 編輯(E) 檢視(V) 我的最愛(A) 工具(T) 說明(H)
Visualizing Categorical Data
網頁(P) 工具(O)
Visualizing
Categorical
Data
Next

Visualizing Categorical Data

by Michael Friendly

SAS Institute (Dec, 2000), Order code 56571, ISBN 1-58025-660-0

Contents

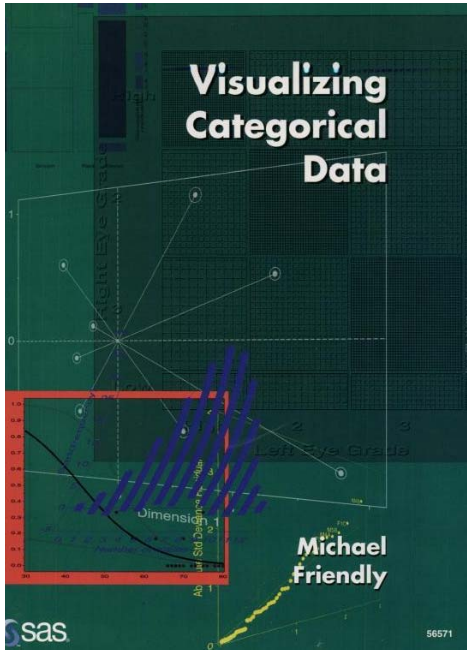
1. Introduction [View Ch. 1 in .pdf (264k)]
2. Fitting and graphing discrete distributions
3. Two-way contingency tables
4. Mosaic displays for n-way tables
5. Correspondence analysis
6. Logistic regression
7. Loglinear and logit models
A. SAS programs and macros
B. Data sets
C. Tables

Errata and Updates

See also:

- Reviews of *Visualizing Categorical Data*
- *Reader's Guide to Visualizing Categorical Data* (SUGI 26 paper, PDF [137k])
- VCD Sampler: *Visualizing Categorical Data: Data, Stories, and Pictures* (SUGI 25 paper, PDF [177k])
- VCD Source Online [550k] (Source code for datasets and macros from the initial release, all in one big file, but no longer maintained)
- VCD Archive (VCD archive, `vcdprog.zip`, for purchasers of the book)
- Mosaic displays web applet
- Mosaic displays User's Guide (.pdf [318k])
- Sieve diagrams web applet
- Gallery of Data Visualization

- Fourfold Display for 2x2 Tables
- Association Plots
- Mosaic Display

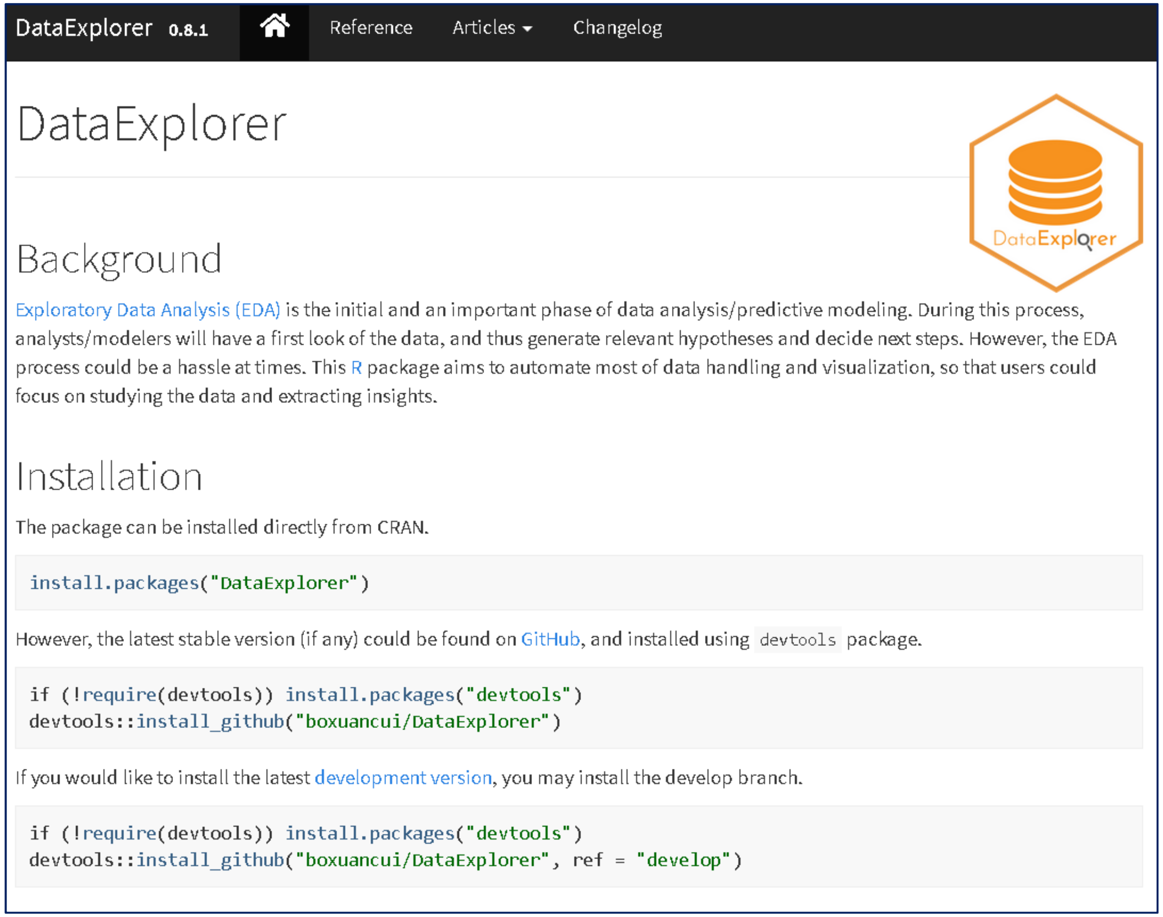


```
> library(vcd)
```

vcd: Visualizing Categorical Data
http://cran.r-project.org/web/packages/vcd/index.html

DataExplorer: Automate Data Exploration and Treatment

http://boxuancui.github.io/DataExplorer/



DataExplorer

Background

Exploratory Data Analysis (EDA) is the initial and an important phase of data analysis/predictive modeling. During this process, analysts/modelers will have a first look of the data, and thus generate relevant hypotheses and decide next steps. However, the EDA process could be a hassle at times. This R package aims to automate most of data handling and visualization, so that users could focus on studying the data and extracting insights.

Installation

The package can be installed directly from CRAN.

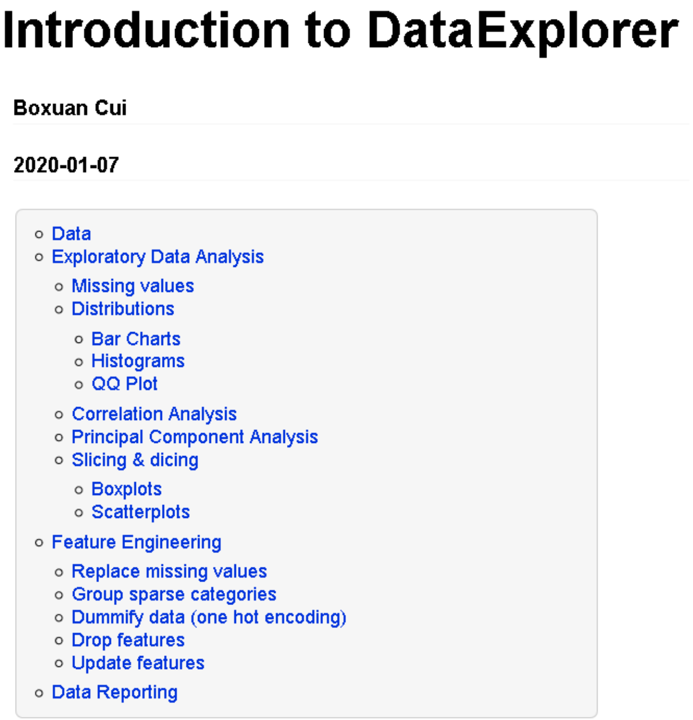
```
install.packages("DataExplorer")
```

However, the latest stable version (if any) could be found on GitHub, and installed using `devtools` package.

```
if (!require(devtools)) install.packages("devtools")
devtools::install_github("boxuancui/DataExplorer")
```

If you would like to install the latest development version, you may install the develop branch.

```
if (!require(devtools)) install.packages("devtools")
devtools::install_github("boxuancui/DataExplorer", ref = "develop")
```



Introduction to DataExplorer

Boxuan Cui

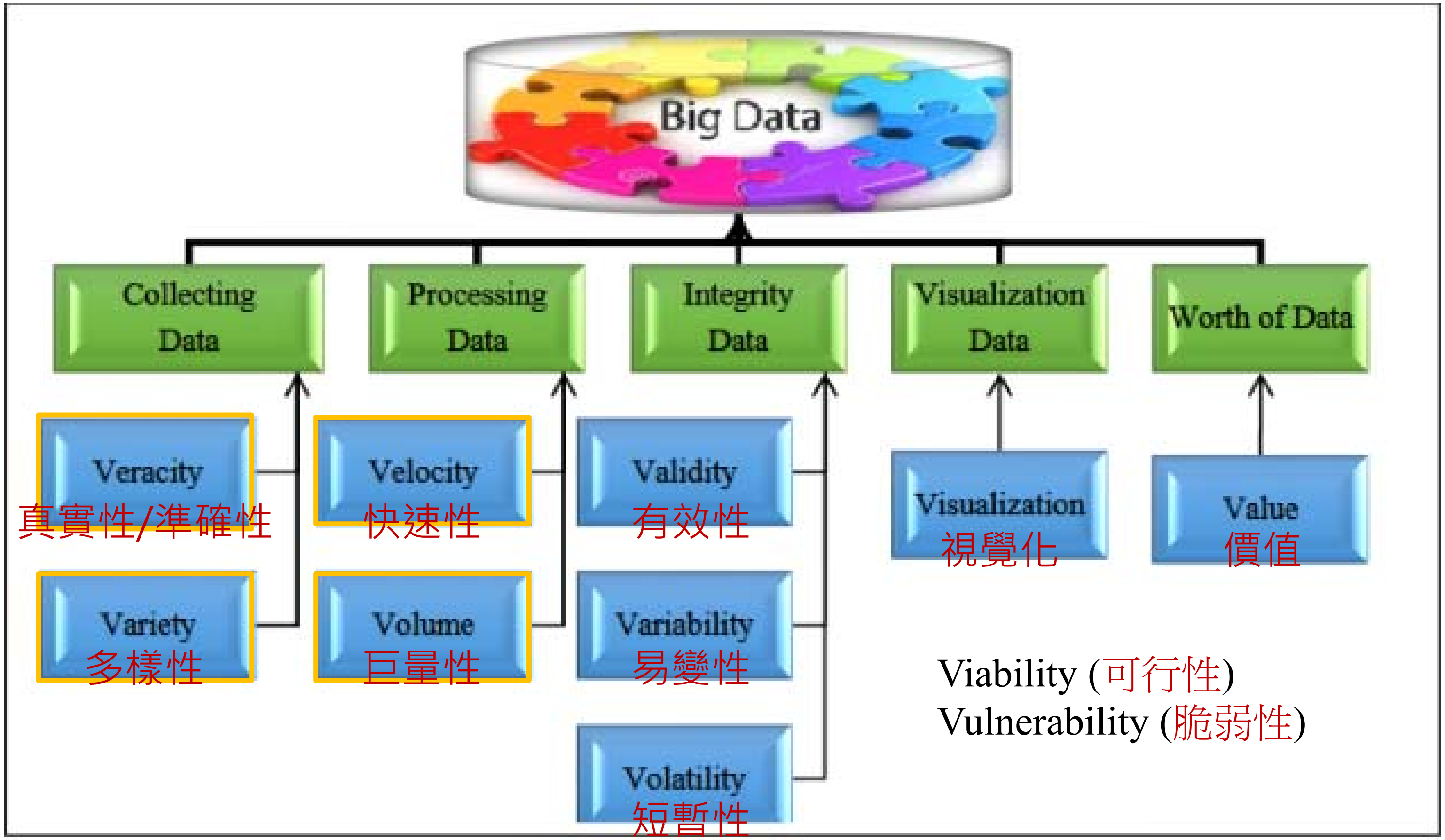
2020-01-07

- Data
- Exploratory Data Analysis
  - Missing values
  - Distributions
    - Bar Charts
    - Histograms
    - QQ Plot
  - Correlation Analysis
  - Principal Component Analysis
  - Slicing & dicing
    - Boxplots
    - Scatterplots
- Feature Engineering
  - Replace missing values
  - Group sparse categories
  - Dummify data (one hot encoding)
  - Drop features
  - Update features
- Data Reporting

https://cran.r-project.org/web/packages/DataExplorer/vignettes/dataexplorer-intro.html

Big Data: The Era of 9 Vs

- Visualization:
  - Visualization will be key to making big data an integral part of decision making.
  - Visualization will be the only way to make big data accessible to a large audience.
  - Visualization will be essential to the analysis of big data so it can be of highest value.



Categorization of Big Data V's

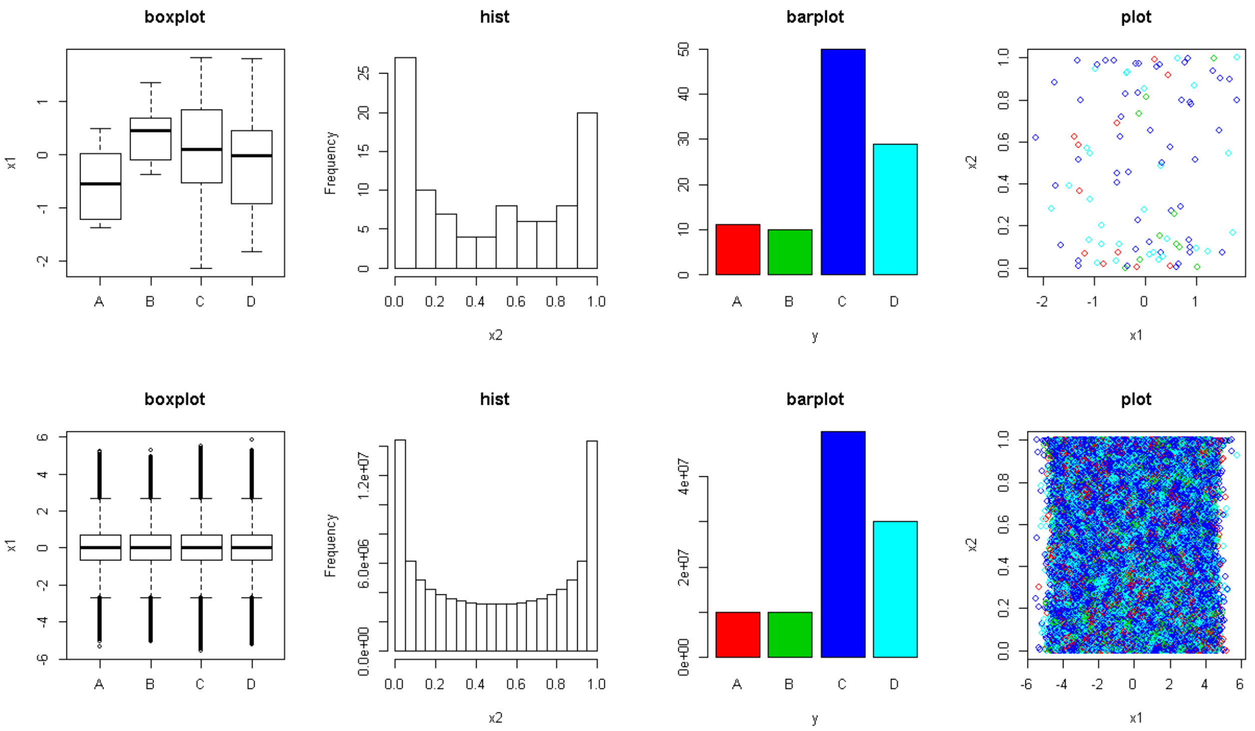
http://blogs.systweak.com/2017/03/big-data-vs-represents-characteristics-or-challenges-of-big-data/

The Challenge of Visualizing Big Data

```
> n <- 1e+02
```

a large p?

```
> n <- 1e+08
```

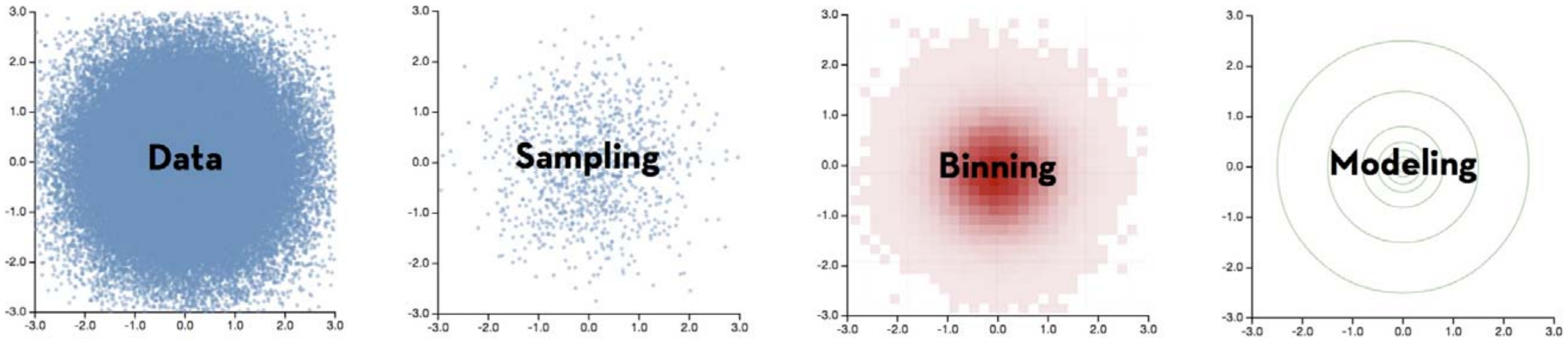


```
> n <- 1e+02
> y <- as.factor(sample(LETTERS[1:4], n, replace=T, prob=c(0.1, 0.1, 0.5, 0.3)))
> x1  <- rnorm(n)
> x2  <- rbeta(n, 0.5, 0.5)
> xydata <- data.frame(y, x1, x2)
> par(mfrow=c(1,4))
> boxplot(x1~y, data=xydata, ylab="x1", main="boxplot")
> hist(x2, xlab="x2", main="hist")
> barplot(table(y), xlab="y", col = 2:5, main="barplot")
> plot(x1, x2, main="plot", col=as.integer(y)+1)
```

Two principles:
Look at Less Data;
or Look at Data Faster

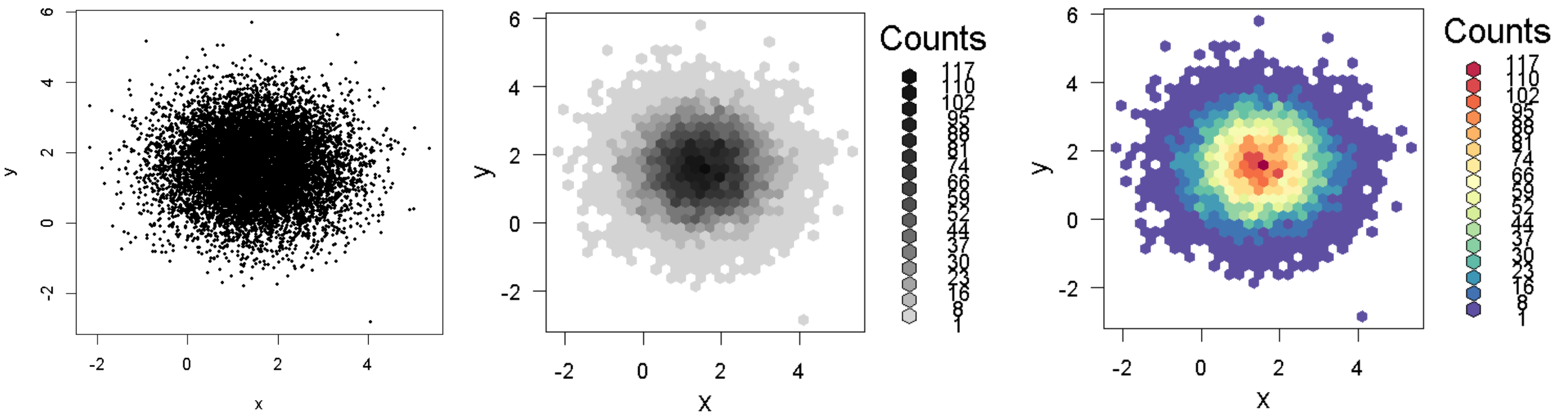
How Can We Visualize and Interact with Billion+ Record Databases in Real-time?

- Two central challenges:
  - need to keep visualizations perceptually effective regardless of the number of input data points.
  - need to support real-time interaction to enable rapid and iterative exploratory analysis.
- Perceptual and interactive scalability should be limited by the chosen resolution of the visualized data, not the number of records.



http://skandel.github.io/slides/strata2013/part1

hexbin Package: Hexagonal Binning Routines



```
> x <- rnorm(mean=1.5, 10000)
> y <- rnorm(mean=1.6, 10000)
> my.data <- data.frame(x, y)
>
> pk <- c("RColorBrewer", "hexbin", "gplots")
> install.packages(pk, repos="http://cran.csie.ntu.edu.tw")
> library(RColorBrewer)
> # create rainbow color
> col_rb <- colorRampPalette(rev(brewer.pal(11, 'Spectral')))
> # scatterplot
> plot(my.data, pch=16, col='black', cex=0.5)
> library(hexbin)
> h <- hexbin(my.data) # create a hexbin object
> h
'hexbin' object from call: hexbin(x = my.data)
n = 10000  points in    nc = 598  hexagon cells in grid dimensions  36 by 31
> plot(h) # in grey level
> plot(h, colramp=col_rb) # rainbow color
```

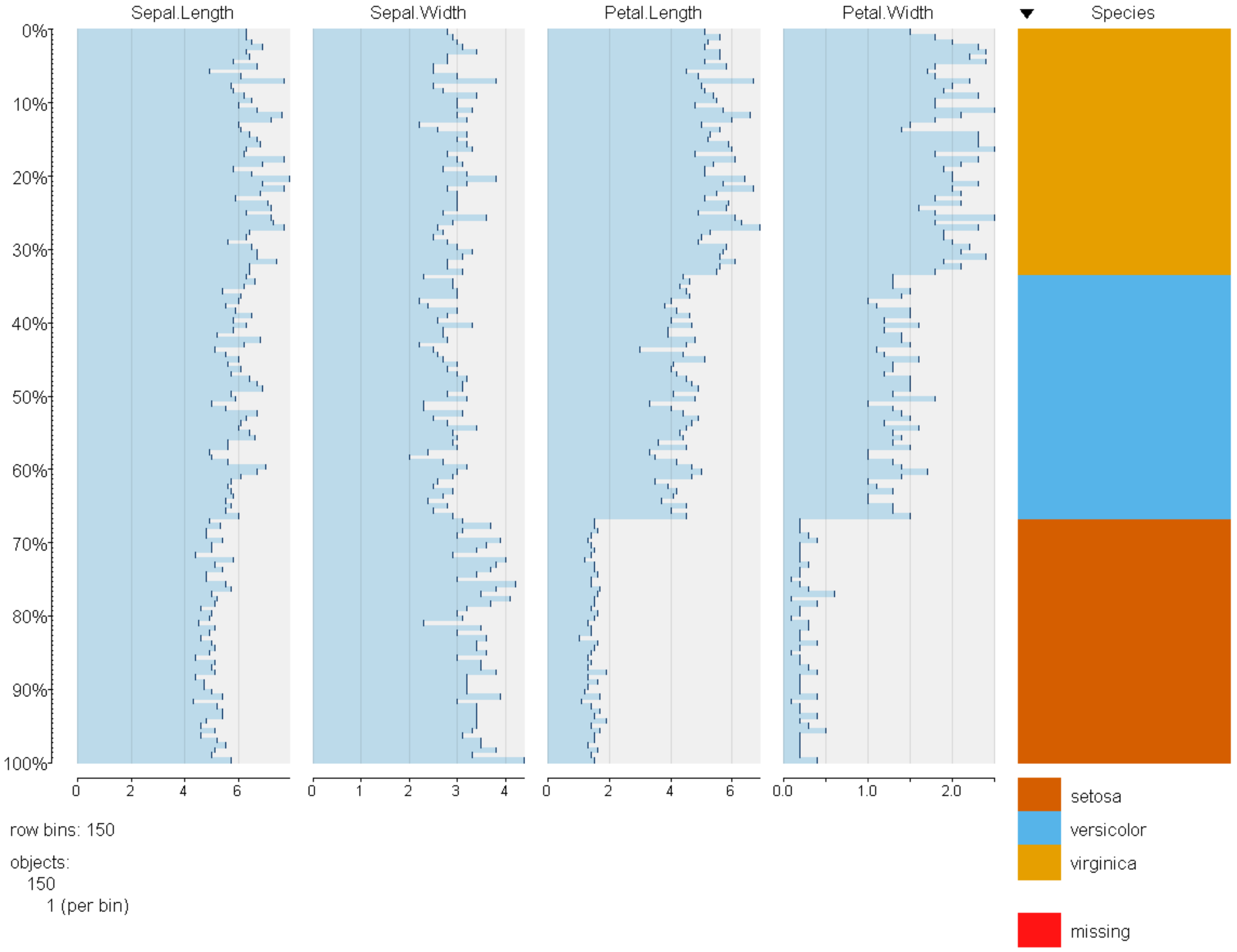
tabplot: Tableplot, a Visualization of Large Datasets

- A tableplot is a visualisation of a (large) dataset with a dozen of variables, both numeric and categorical.
  - Each column represents a variable and each row bin is an aggregate of a certain number of records.
  - Numeric variables are visualized as bar charts, and
  - categorical variables as stacked bar charts. Missing values are taken into account.
  - Also supports large '**ffdf**' datasets from the '**ff**' package.
  - https://github.com/mtennekes/tabplot
  - https://cran.r-project.org/web/packages/tabplot/vignettes/tabplot-vignette.html
- Tennekes, M., Jonge, E. de, Daas, P.J.H. (2013) Visualizing and Inspecting Large Datasets with Tableplots, Journal of Data Science 11 (1), 43-58.

```
tableplot(dat, select, subset = NULL, sortCol = 1, decreasing = TRUE,
  nBins = 100, from = 0, to = 100, nCols = ncol(dat), sample = FALSE,
  sampleBinSize = 1000, scales = "auto", numMode = "mb-sdb-ml",
  max_levels = 50, pals = list("Set1", "Set2", "Set3", "Set4"),
  change_palette_type_at = 20, rev_legend = FALSE, colorNA = "#FF1414",
  colorNA_num = "gray75", numPals = "OrBu", limitsX = NULL,
  bias_brokenX = 0.8, IQR_bias = 5, select_string = NULL,
  subset_string = NULL, colNames = NULL, filter = NULL, plot = TRUE,
  ...)
```

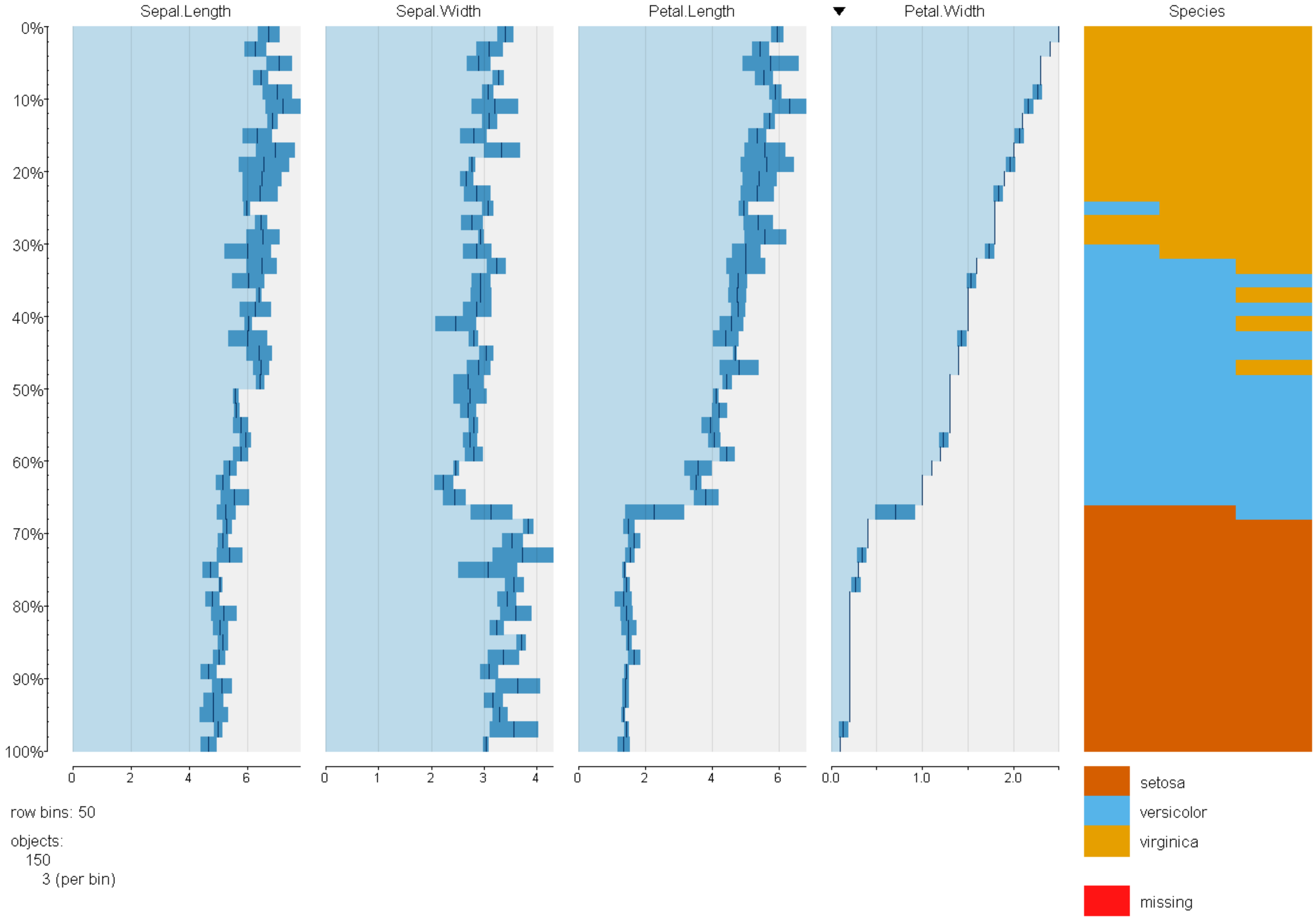
tableplot(iris, nBins=150, sortCol=5)

```
> install.packages("tabplot")
> library(tabplot)
> tableplot(iris, nBins=150, sortCol=5)
```



tableplot(iris, nBins=50, sortCol=4)

```
> tableplot(iris, nBins=50, sortCol=4)
```

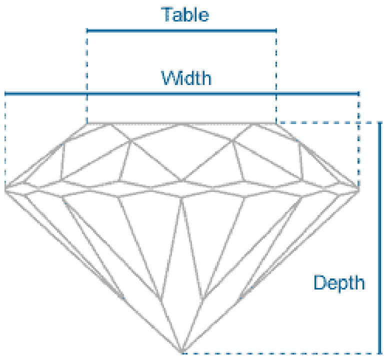


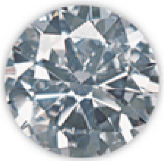
tableplot(diamonds)

```
> require(ggplot2)
> data(diamonds)
> dim(diamonds)
[1] 53940    10
> head(diamonds)
# A tibble: 6 x 10
  carat       cut color clarity depth table price     x     y     z
  <dbl>     <ord> <ord>   <ord> <dbl> <dbl> <int> <dbl> <dbl> <dbl>
1  0.23     Ideal     E     SI2  61.5    55   326  3.95  3.98  2.43
2  0.21   Premium     E     SI1  59.8    61   326  3.89  3.84  2.31
3  0.23      Good     E     VS1  56.9    65   327  4.05  4.07  2.31
4  0.29   Premium     I     VS2  62.4    58   334  4.20  4.23  2.63
5  0.31      Good     J     SI2  63.3    58   335  4.34  4.35  2.75
6  0.24 Very Good     J    VVS2  62.8    57   336  3.94  3.96  2.48
> tableplot(diamonds)
```

Details

- price. price in US dollars (\$326--\$18,823)
- carat. weight of the diamond (0.2--5.01)
- cut. quality of the cut (Fair, Good, Very Good, Premium, Ideal)
- colour. diamond colour, from J (worst) to D (best)
- clarity. a measurement of how clear the diamond is (I1 (worst), SI1, SI2, VS1, VS2, VVS1, VVS2, IF (best))
- x. length in mm (0--10.74)
- y. width in mm (0--58.9)
- z. depth in mm (0--31.8)
- depth. total depth percentage = z / mean(x, y) = 2 * z / (x + y) (43--79)
- table. width of top of diamond relative to widest point (43--95)



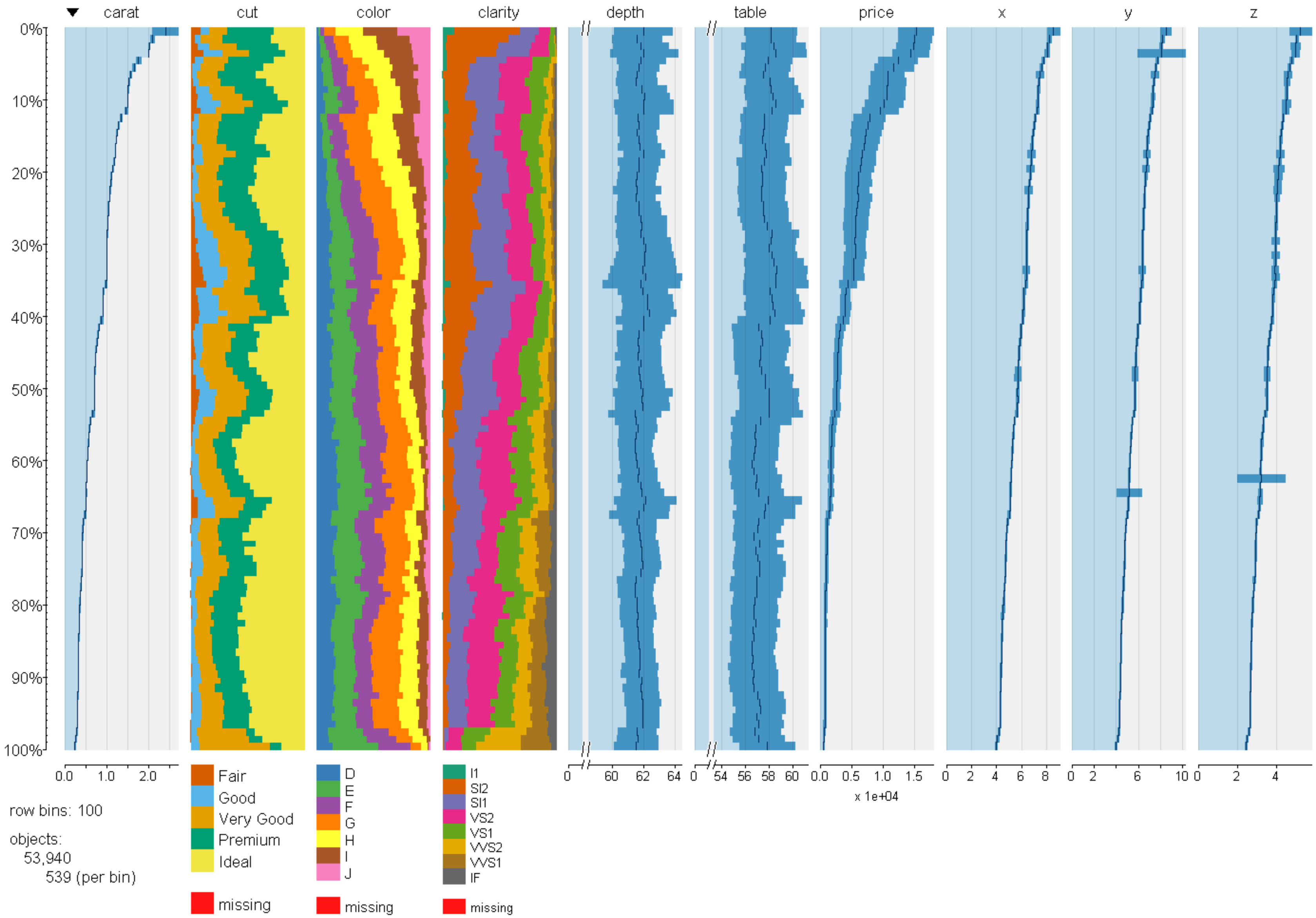
Excellent Ideal	
Very Good	
Good	
Fair	
Poor	

http://www.lumeradiamonds.com/diamond-education/diamond-cut

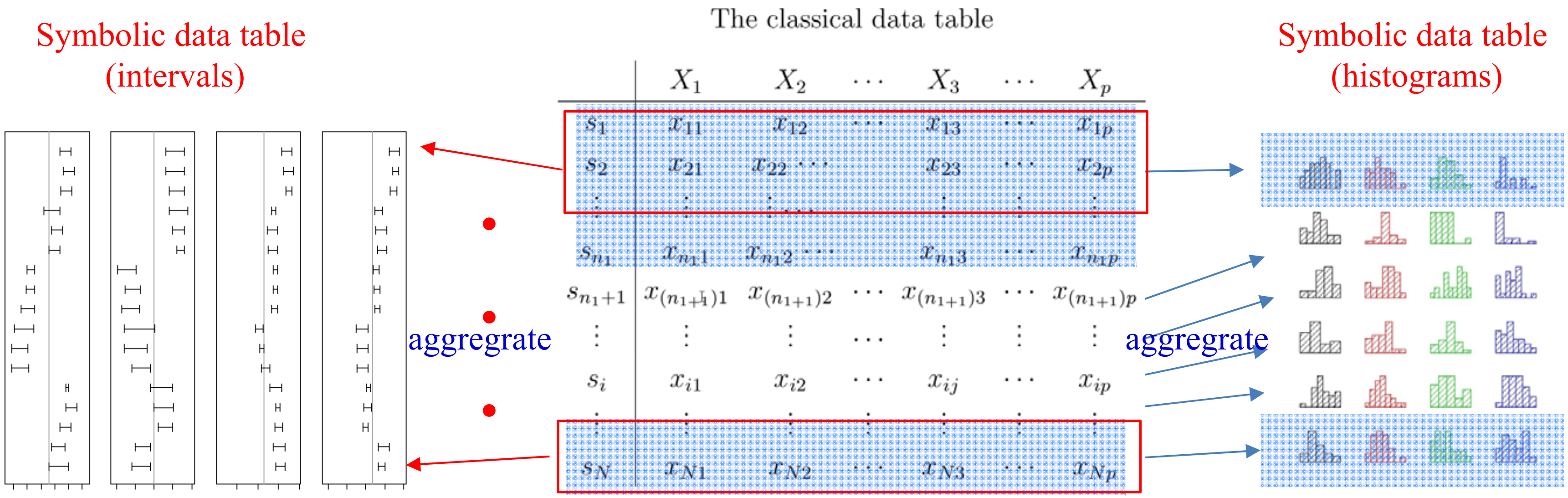
http://docs.ggplot2.org/0.9.3.1/diamonds.html

http://yourdiamondteacher.com/diamond-4cs/cut/

tableplot(diamonds)



Symbolic Data Analysis (Billard and Diday, JASA 2003)



Symbolic data table (intervals)

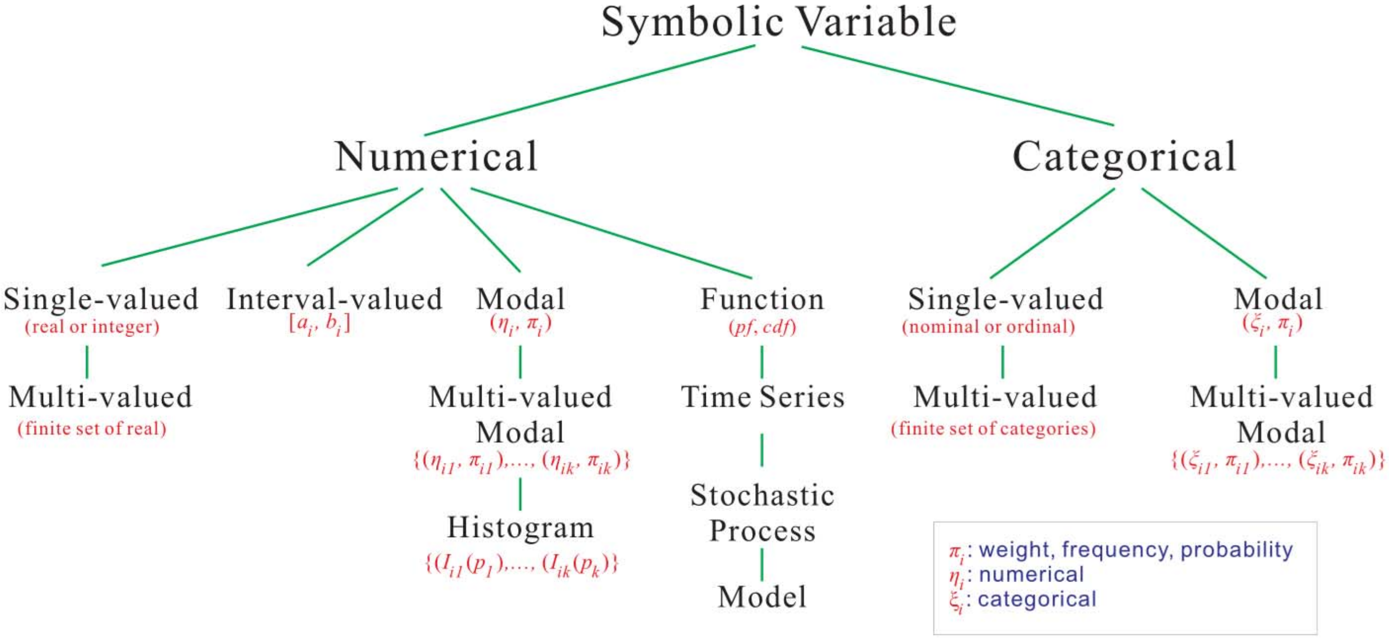
aggregate

The classical data table

	X_1	X_2	$\cdots$	X_3	$\cdots$	X_p
s_1	x_{11}	x_{12}	$\cdots$	x_{13}	$\cdots$	x_{1p}
s_2	x_{21}	$x_{22}\cdots$		x_{23}	$\cdots$	x_{2p}
$\vdots$	$\vdots$	$\vdots\ \cdots$		$\vdots$	$\vdots$	$\vdots$
s_{n_1}	x_{n_11}	$x_{n_12}\cdots$		x_{n_13}	$\cdots$	x_{n_1p}
s_{n_1+1}	$x_{(n_1+1)1}$	$x_{(n_1+1)2}$	$\cdots$	$x_{(n_1+1)3}$	$\cdots$	$x_{(n_1+1)p}$
$\vdots$	$\vdots$	$\vdots$	$\cdots$	$\vdots$	$\vdots$	$\vdots$
s_i	x_{i1}	x_{i2}	$\cdots$	x_{ij}	$\cdots$	x_{ip}
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
s_N	x_{N1}	x_{N2}	$\cdots$	x_{N3}	$\cdots$	x_{Np}

aggregate

Symbolic data table (histograms)



Symbolic Variable

- Numerical
  - Single-valued (real or integer)
    - Multi-valued (finite set of real)
  - Interval-valued $[a_i, b_i]$
  - Modal (η_i, π_i)
    - Multi-valued Modal $\{(\eta_{i1}, \pi_{i1}), \ldots, (\eta_{ik}, \pi_{ik})\}$
      - Histogram $\{(I_{i1}(p_1), \ldots, (I_{ik}(p_k)\}$
  - Function (*pf, cdf*)
    - Time Series
      - Stochastic Process
        - Model
- Categorical
  - Single-valued (nominal or ordinal)
    - Multi-valued (finite set of categories)
  - Modal (ξ_i, π_i)
    - Multi-valued Modal $\{(\xi_{i1}, \pi_{i1}), \ldots, (\xi_{ik}, \pi_{ik})\}$

π_i: weight, frequency, probability
η_i: numerical
ξ_i: categorical

資料無邊界!

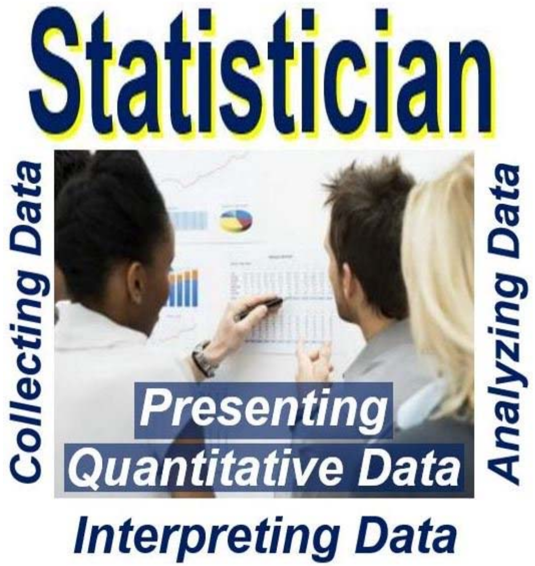
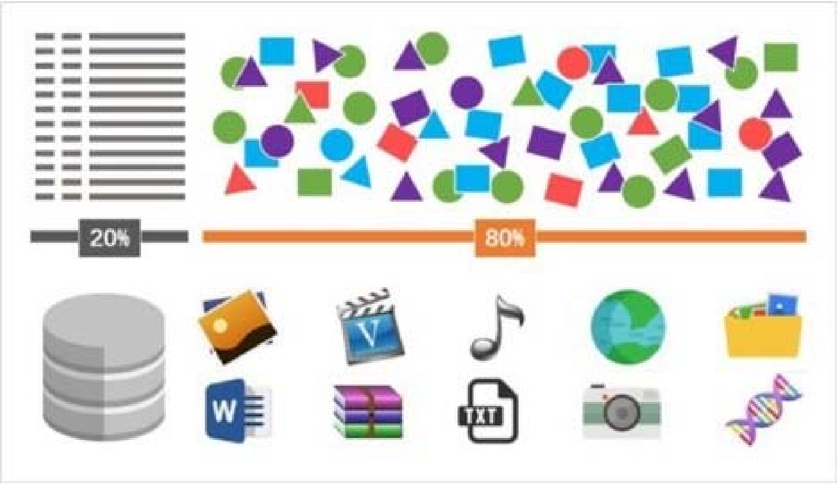
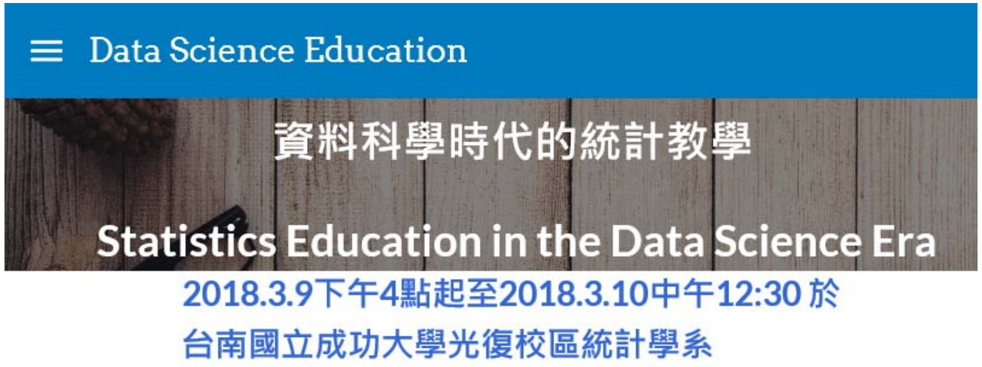


Image source: http://marketbusinessnews.com/financial-glossary/what-is-a-statistician

- 統計教學裡的範例幾乎都是結構性的數據。
- 大數據時代，80%的資料是非結構性的，統計課程如何面對?





≡ Data Science Education

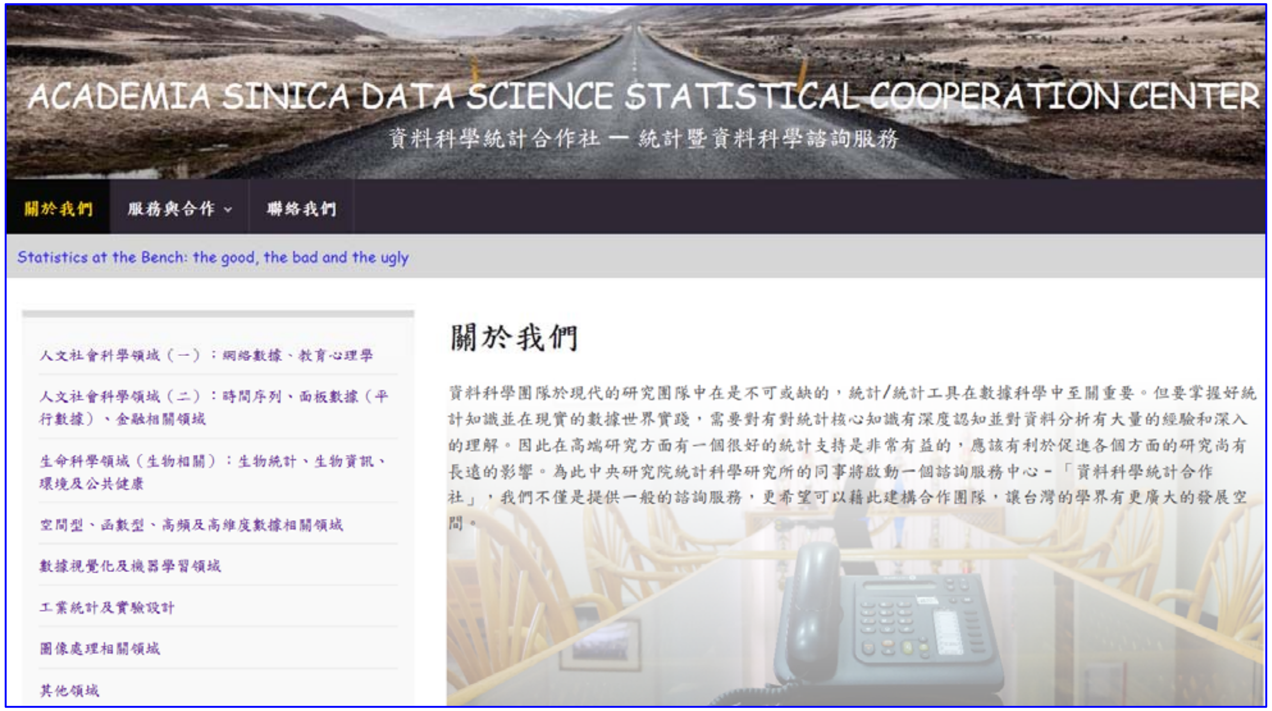
資料科學時代的統計教學

Statistics Education in the Data Science Era

2018.3.9下午4點起至2018.3.10中午12:30 於
台南國立成功大學光復校區統計學系

2018統計教學工作坊 18~19 May, 2018
Lounge (2F),
Institute of Statistical Science, AS

未來方向?



ACADEMIA SINICA DATA SCIENCE STATISTICAL COOPERATION CENTER

資料科學統計合作社 — 統計暨資料科學諮詢服務

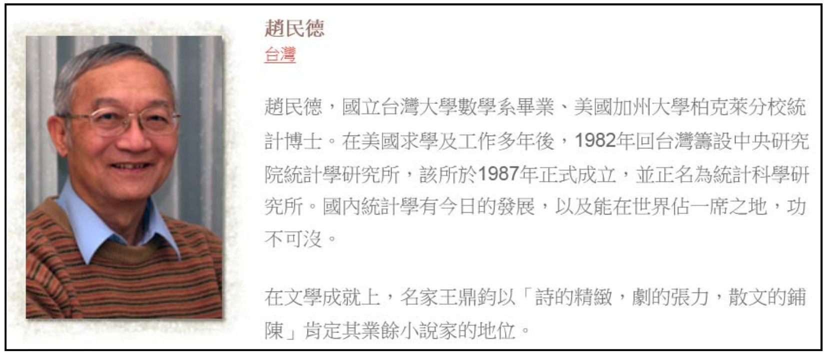
Statistics at the Bench: the good, the bad and the ugly

- 人文社會科學領域（一）：網絡數據、教育心理學
- 人文社會科學領域（二）：時間序列、面板數據（平行數據）、金融相關領域
- 生命科學領域（生物相關）：生物統計、生物資訊、環境及公共健康
- 空間型、函數型、高頻及高維度數據相關領域
- 數據視覺化及機器學習領域
- 工業統計及實驗設計
- 圖像處理相關領域
- 其他領域

關於我們

資料科學團隊於現代的研究團隊中在是不可或缺的，統計/統計工具在數據科學中至關重要。但要掌握好統計知識並在現實的數據世界實踐，需要對有對統計核心知識有深度認知並對資料分析有大量的經驗和深入的理解。因此在高端研究方面有一個很好的統計支持是非常有益的，應該有利於促進各個方面的研究尚有長遠的影響。為此中央研究院統計科學研究所的同事將啟動一個諮詢服務中心 – 「資料科學統計合作社」，我們不僅是提供一般的諮詢服務，更希望可以藉此建構合作團隊，讓台灣的學界有更廣大的發展空間。

趙民德，1999，「統計已死，統計萬歲！」第八屆南區統計研討會演說稿



趙民德

台灣

趙民德，國立台灣大學數學系畢業、美國加州大學柏克萊分校統計博士。在美國求學及工作多年後，1982年回台灣籌設中央研究院統計學研究所，該所於1987年正式成立，並正名為統計科學研究所。國內統計學有今日的發展，以及能在世界佔一席之地，功不可沒。

在文學成就上，名家王鼎鈞以「詩的精緻，劇的張力，散文的鋪陳」肯定其業餘小說家的地位。

“統計有沒有死？會不會萬歲？

只要有米倉，就會有老鼠；只要有數據，就會發展處理數據的方法。但是不是叫做統計學、或者叫做computer science 的data mining，就要看這一代的統計人如何因應變局。”