

# R 語言設計概念與農業應用

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# 安裝 R 與 Rstudio

- R 下載:
  - Windows: <https://cran.r-project.org/bin/windows/base/>
  - Mac: <https://cran.r-project.org/bin/macosx/>
  - 下載後雙擊滑鼠左鍵下載檔案進入安裝畫面
- Rstudio 下載: <https://posit.co/download/rstudio-desktop/>

OS	Download	Size	SHA-256
Windows 10/11	<a href="#">RSTUDIO-2023.03.0-386.EXE</a> ↓	208.08 MB	<a href="#">885432DB</a>
macOS 11+	<a href="#">RSTUDIO-2023.03.0-386.DMG</a> ↓	374.55 MB	<a href="#">ED87B818</a>

# What is R?

- R 並非專用統計軟體, 而是可用來執行分析的環境:
  - 匯入適當的 package (套件)
  - 應用套件內提供之 function (函式)
- Packages 由許多熱心人士編寫並免費提供學術使用。



# 方便使用的 R 介面

The screenshot displays the RStudio interface with several components:

- Editor:** The main workspace contains R Markdown code for a Shiny application. It includes a title, runtime settings, and a histogram plot of `faithful$eruptions` with interactive sliders for `n_breaks` and `bw_adjust`. An orange box labeled "Editor" is overlaid on the code.
- Environment:** The top right pane shows the current environment with a function `ff` defined as `function (x)`.
- R Console:** The bottom left pane shows the R terminal output, including the R version (3.1.1), copyright information, and the execution of the following commands:

```
> plot(rnorm(100))
> hist(rnorm(100))
> hist(rnorm(100),col="lightblue")
>
```

An orange box labeled "R Console" is overlaid on the terminal output.
- Plots:** The bottom right pane displays a histogram titled "Histogram of rnorm(100)". The x-axis is labeled "rnorm(100)" and the y-axis is labeled "Frequency". The histogram bars are light blue. A context menu is open over the plot, showing options: "Save Plot as Image...", "Save Plot as PDF...", and "Copy Plot".

# R的優缺點

- 優點:
  - 免費軟體
  - 完善的說明文件與討論區
  - 漂亮的圖型介面
  - 程式容易根據使用者需求做修改
- 缺點:
  - 並無 **user friendly** 之使用者介面
  - 需詳知函式名稱與程式編寫邏輯
  - 說明文件與討論區使用英文

<http://cran.csie.ntu.edu.tw/>  
or <https://cran.r-project.org>



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[Contributed](#)

## The Comprehensive R Archive Network

### Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Download R for Linux](#) ([Debian](#), [Fedora/Redhat](#), [Ubuntu](#))
- [Download R for macOS](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

### Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2023-04-21, Already Tomorrow) [R-4.3.0.tar.gz](#), read [what's new](#) in the latest version.
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#)

### Questions About R

- If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

<https://agstats.io/post/keeping-up-with-r/>

# R packages for Agricultural Research

Finding the R packages that support your research

Julia Piaskowski

Last updated on Oct 14, 2022 · 17 min read · R, CRAN, agriculture









<http://www.hmwu.idv.tw/index.php/r-software>



**R統計軟體教學/R語言程式設計/學習講義 (R Software Learning Materials)**

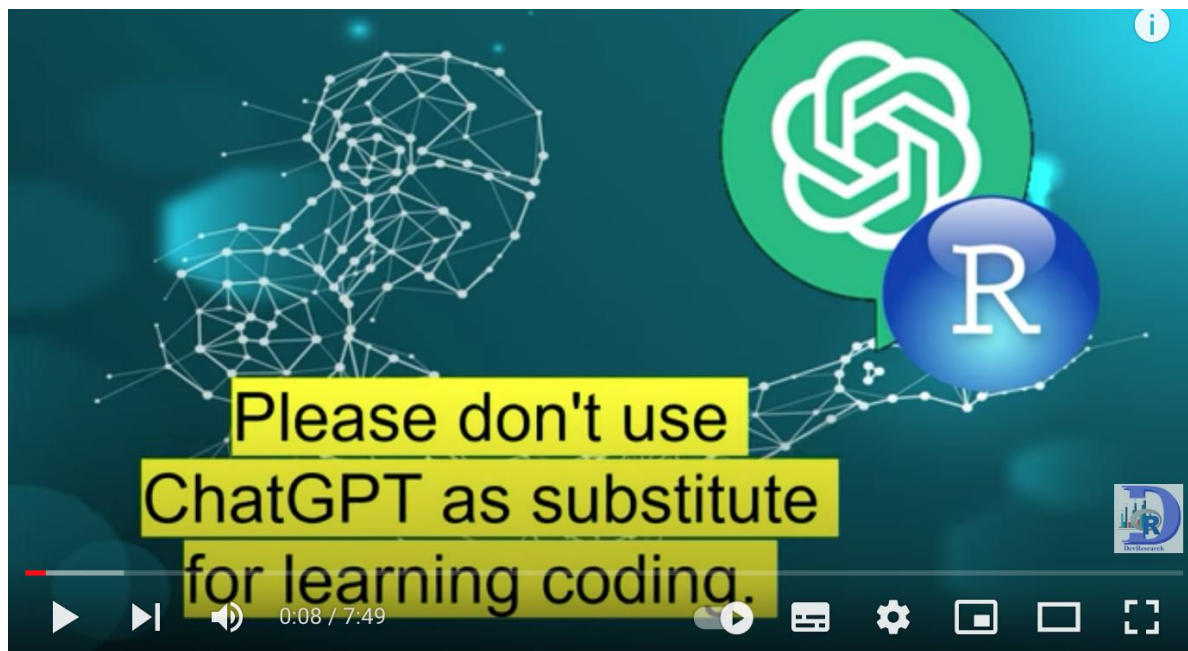
[https://youtube.com/playlist?list=PL3tdy4h3sD63W3T3JGhBusRcT-uxTM\\_2P](https://youtube.com/playlist?list=PL3tdy4h3sD63W3T3JGhBusRcT-uxTM_2P)



- 1  統計學實習第01堂：R語言環境與基本變數運算  
陳昱權 · 觀看次數：719次 · 2年前 · 45:05
- 2  統計學實習第02堂：R語言資料框架與資料輸入  
Roland Huang · 觀看次數：273次 · 2年前 · 38:24
- 3  統計學實習第3堂：敘述統計與R語言繪圖  
Roland Huang · 觀看次數：249次 · 2年前 · 45:14
- 4  統計學實習第4堂：sampling與機率  
Roland Huang · 觀看次數：124次 · 2年前 · 39:24
- 5  統計學實習第05堂：離散隨機變數  
Roland Huang · 觀看次數：125次 · 2年前 · 39:38
- 6  統計學實習第06堂：連續隨機變數與曲線

# ChatGPT for coding: “程式語言翻譯機”

<https://www.youtube.com/watch?v=9FQuy2Q5-1M>



<https://www.youtube.com/watch?v=Y3H1yTUPV0Y>







王宏恩 · 追蹤

1小時 · 地球



本日新發現：原來可以叫ChatGPT直接把R跑回歸模型出來的純文字統計結果完整的解釋出來...而且還超詳細的...

Just realize that ChatGPT can even explain every detail in the plain-text output of regression model in Rstudio. It is very interesting that AI can interpret such a format.

The screenshot shows the RStudio console output on the left and a ChatGPT explanation on the right. The RStudio output includes the following text:

```
can you explain the result generated by R below?  
  
Call:  
lm(formula = Fauci ~ covid * Trump, data = ANES2020)  
  
Residuals:  
  Min   1Q Median   3Q   Max  
-86.003 -13.037  4.028 13.997 61.092  
  
Coefficients:  
              Estimate Std. Error t value Pr(>|t|)  
(Intercept) 86.003362   0.392262 219.250 < 2e-16 ***  
covid      -10.932146   2.010123  -5.439 5.55e-08 ***  
Trump       -0.470953   0.007103 -66.304 < 2e-16 ***  
covid:Trump  0.135179   0.035404  3.818 0.000136 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 23.74 on 7226 degrees of freedom  
(因為不存在，1050 個觀測量被刪除了)  
Multiple R-squared:  0.3845, Adjusted R-squared:  0.384  
F-statistic: 1505 on 3 and 7226 DF, p-value: < 2.2e-16
```

The ChatGPT explanation on the right provides a detailed interpretation of the R output, including the response variable 'Fauci', explanatory variables 'covid' and 'Trump', and the interaction term 'covid:Trump'. It lists key interpretations of the output:

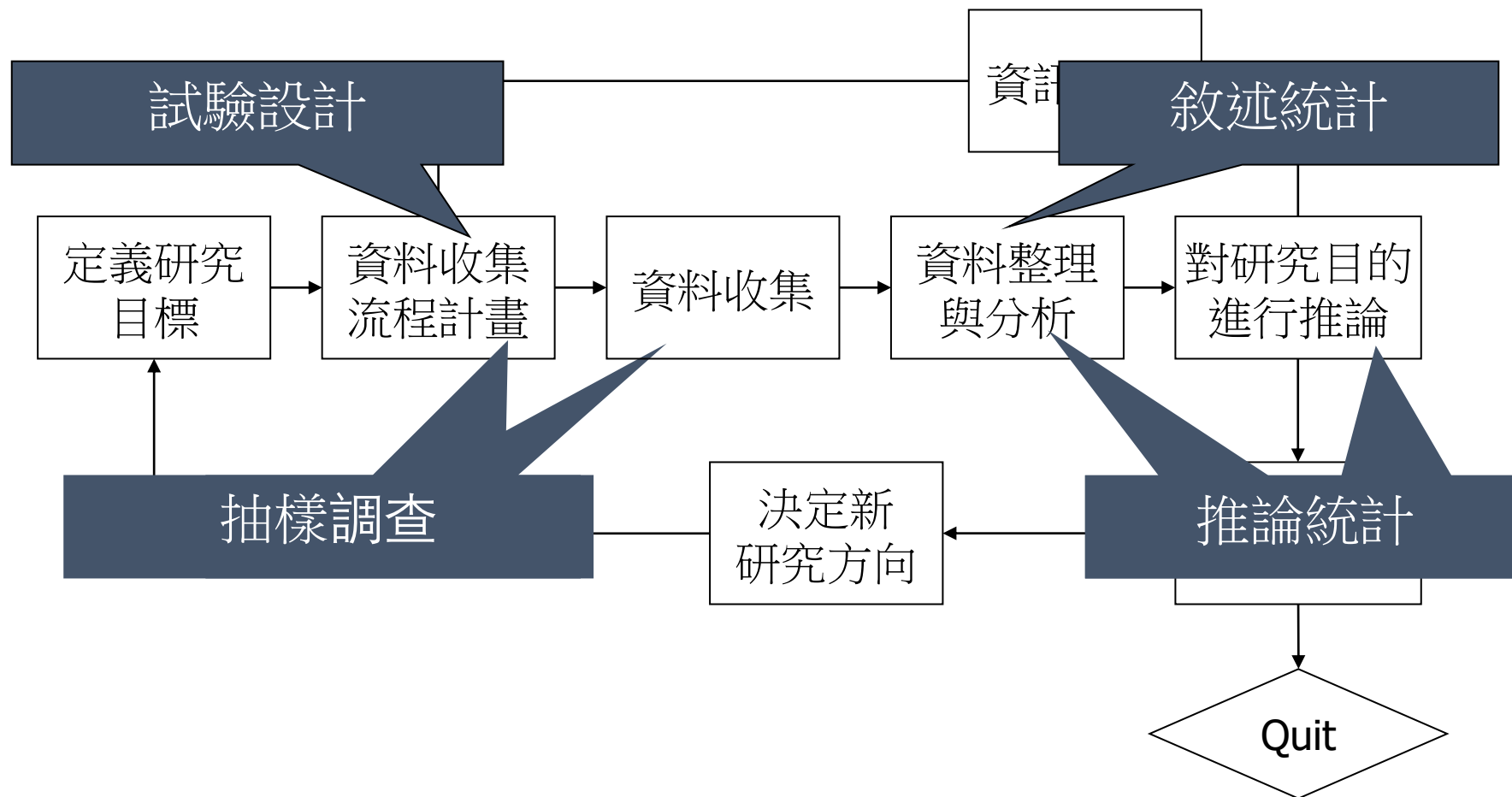
- The intercept coefficient estimates the average value of 'Fauci' when 'covid' and 'Trump' are both equal to zero. It is highly significant ( $p < 2e-16$ ) and equals 86.003.
- The 'covid' coefficient estimates the change in 'Fauci' associated with a one-unit increase in 'covid' when 'Trump' is held constant. It is significantly negative ( $p = 5.55e-08$ ) and equals -10.932.
- The 'Trump' coefficient estimates the change in 'Fauci' associated with a one-unit increase in 'Trump' when 'covid' is held constant. It is highly significant ( $p < 2e-16$ ) and equals -0.471.
- The 'covid:Trump' coefficient estimates the change in the slope of the relationship between 'Fauci' and 'covid' when 'Trump' increases by one unit. It is significant ( $p = 0.000136$ ) and equals 0.135, which suggests that the effect of 'covid' on 'Fauci' depends on the value of 'Trump'.
- The residual standard error measures the variability of the response variable around the fitted values of the model. It is estimated to be 23.74, which is relatively large.
- The multiple R-squared value (0.3845) measures the proportion of the total variation in 'Fauci' that is explained by the model. It suggests that the model explains a moderate amount of the variation in 'Fauci'.
- The adjusted R-squared value (0.3843) is similar to the multiple R-squared but takes into account the number of predictors in the model.
- The F-statistic tests the overall significance of the model, and its associated p-value ( $< 2.2e-16$ ) indicates that the model as a whole is highly significant.



# R 語言應用

- 資料收集 - 開放資料、試驗設計
- 了解資料 - 圖表與摘要統計值
- 建立模型 - 傳統統計方法、機器學習的分類與預測
- 進階應用 - 影像辨識、生物資訊

# 研究進行流程



# Agricolae for Experimental Design

## Completely randomized design (CRD)

```
> trt <- c("A", "B", "C")
> repeticion <- c(4, 3, 4)
> outdesign <- design.crd(trt,r=repeticion,seed=777,serie=0)
> book1 <- outdesign$book
> head(book1)
```

```
plots r trt
1     1 1  C
2     2 1  A
3     3 1  B
4     4 2  A
5     5 3  A
6     6 2  C
```

```
Excel:write.csv(book1,"book1.csv",row.names=FALSE)
```

## Randomized complete block design (RCBD)

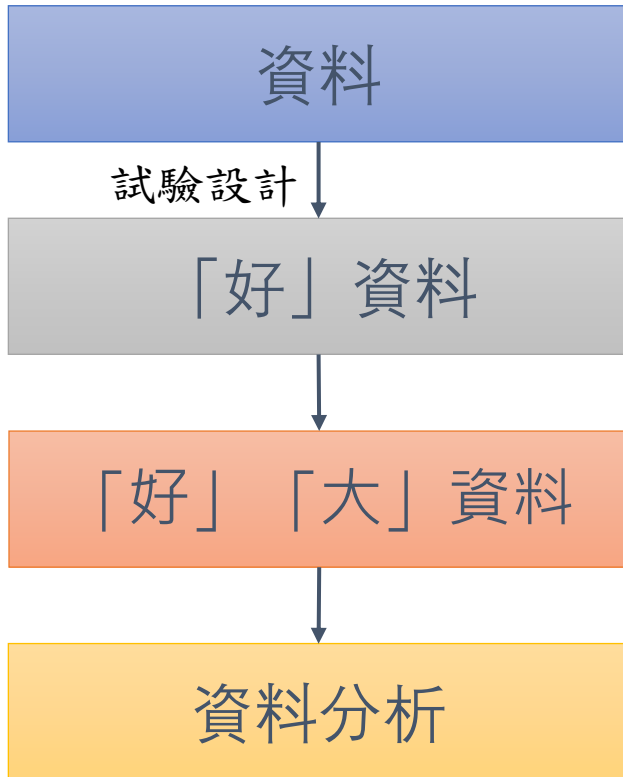
```
> trt <- c("A", "B", "C","D","E")
> repeticion <- 4
> outdesign <- design.rcbd(trt,r=repeticion, seed=-513, serie=2)
> # book2 <- outdesign$book
> book2<- zigzag(outdesign) # zigzag numeration
> print(outdesign$sketch)
```

```
      [,1] [,2] [,3] [,4] [,5]
[1,] "E"  "B"  "D"  "A"  "C"
[2,] "B"  "A"  "D"  "C"  "E"
[3,] "C"  "E"  "A"  "B"  "D"
[4,] "D"  "C"  "E"  "B"  "A"
```

```
> print(matrix(book2[,1],byrow = TRUE, ncol = 5))
```

```
      [,1] [,2] [,3] [,4] [,5]
[1,] 101  102  103  104  105
[2,] 205  204  203  202  201
[3,] 301  302  303  304  305
[4,] 405  404  403  402  401
```

# 從資料收集出發



氮肥用量與產量：

氮肥 (Kg) (X)	0	0.5	1.0	1.5	2.0	2.5
產量 (Kg) (Y)	10	18	32	48	55	62



氮肥用量 (X)	低	中	高
產量 (Kg) (Y)	10	18	32



Y (response)	X (predictor)	
	類別變數	連續變數
類別變數	列聯表 / 比率資料分析	廣義線性模式 (logistic regression, etc.)
連續變數	平均數檢定	迴歸與相關

列聯表 / 比率資料分析  
平均數檢定

Categorical Y

比例  
 $H_0: \pi = \pi_0$  or  $H_0: \pi_i = \pi_j$

單一樣本 兩獨立樣本 成對樣本 >2 獨立樣本

可用常態分布近似 Otherwise

1 2 3 4

- 1: z test or chi-squared test  $\sum \frac{(O-E)^2}{E}$
- 2: Binomial test
- 3: Fisher's exact test
- 4: McNemar test

Numerical Y

平均值  
 $H_0: \mu = \mu_0$  or  $H_0: \mu_i = \mu_j$

單一樣本 兩獨立樣本 成對樣本 >2 獨立樣本

Normal Normal 成對值相減為 Normal Normal 且變方同質 Otherwise

σ已知 σ未知 σ<sub>i</sub>已知 σ<sub>i</sub>未知且σ<sub>1</sub>=σ<sub>2</sub> σ<sub>i</sub>未知且σ<sub>1</sub>≠σ<sub>2</sub> 5 6 7 8 9 10 11

- 5: one-sample z test
- 6: one-sample t test
- 7: two-sample z test
- 8: two-sample t-test
- 9: Welch two-sample t-test
- 10: 變方分析 (ANOVA)
- 11: 變數轉換或無母數法

變方  
 $H_0: \sigma = \sigma_0$  or  $H_0: \sigma_i = \sigma_j$

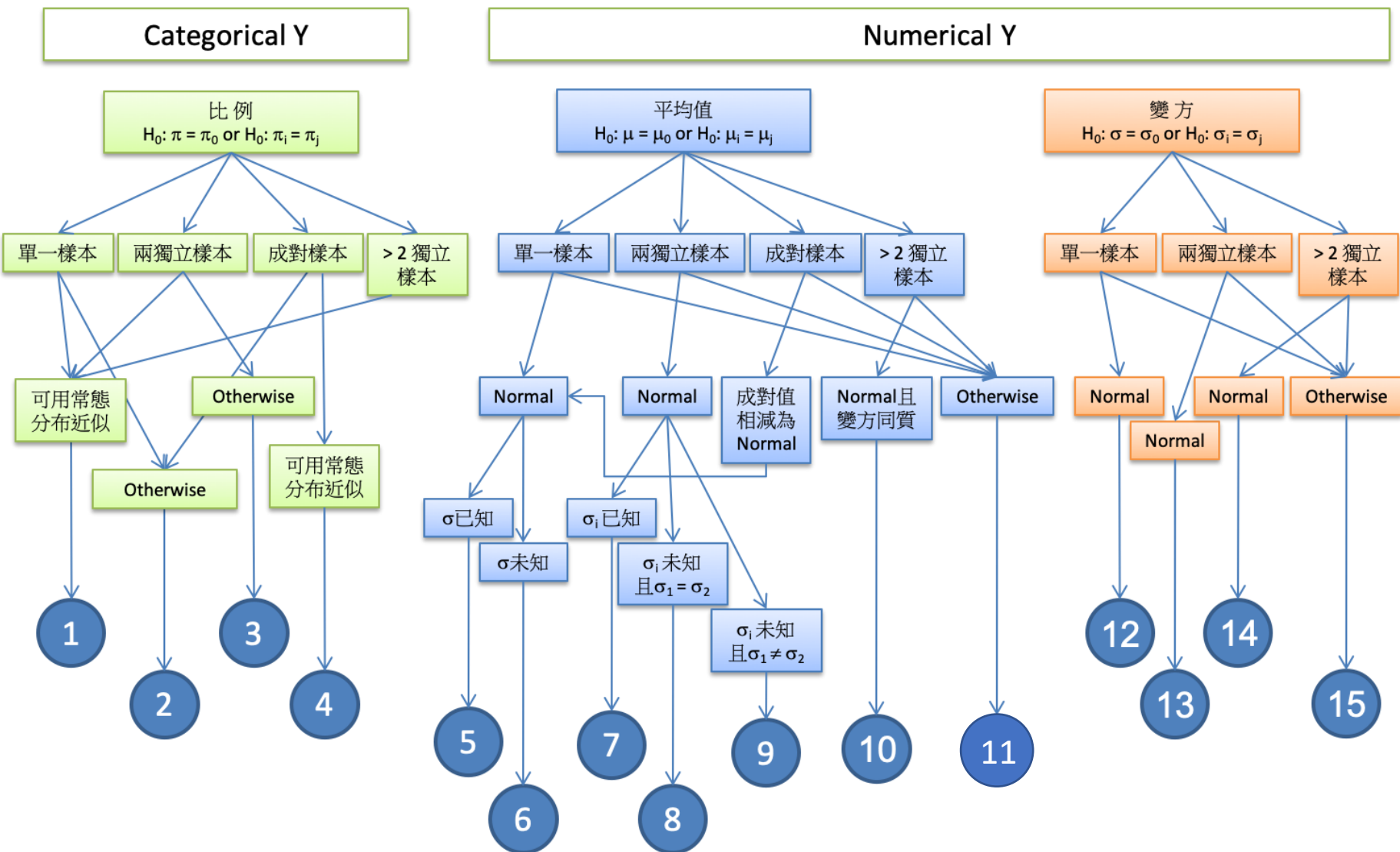
單一樣本 兩獨立樣本 >2 獨立樣本

Normal Normal Otherwise

12 13 14 15

- 12: chi-squared test  $\frac{(n-1)S^2}{\sigma^2}$
- 13: F-test
- 14: Bartlett's test
- 15: Levene's test

列聯表 / 比率資料分析  
平均數檢定



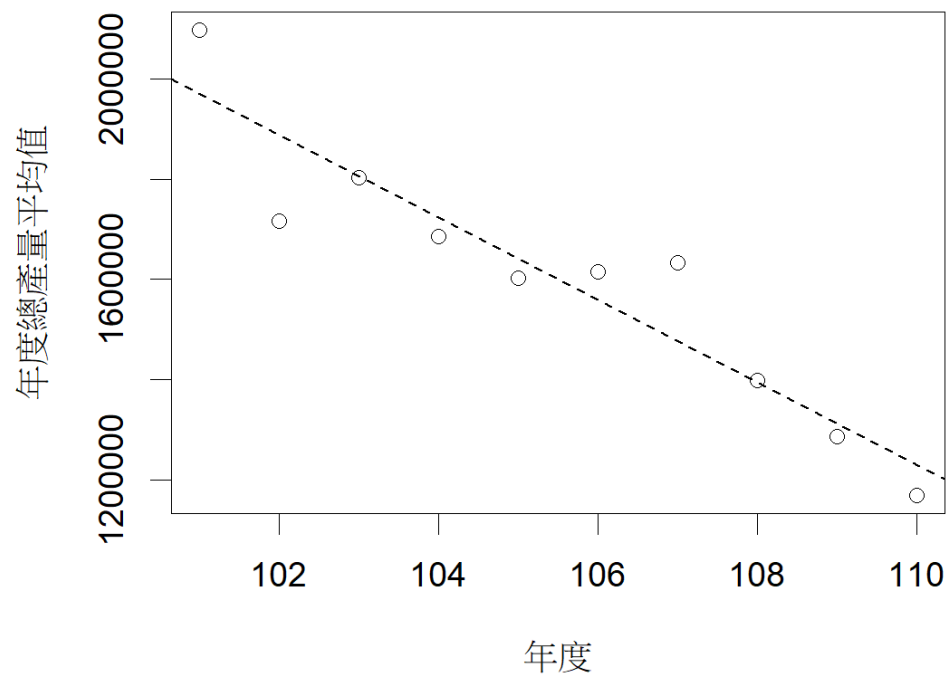
1: prop.test or chisq.test  
2: binom.test  
3: fisher.test  
4: mcnemar.test

5: N/A [qnorm; pnorm]  
6: t.test  
7: t.test  
8: t.test  
9: t.test

10: aov or lm  
11: boxcox (MASS); kruskal.test

12: N/A [qchisq]  
13: var.test  
14: bartlett.test  
15: leveneTest (car)

## 迴歸與相關



圖、西瓜總收量年度平均值散佈圖。虛線為最小平方最佳配適直線：年度平均總收量估計值 =  $10246280 - 82011 \times \text{年度}$ ，相關係數  $r = -0.94$ 。

```
cor(mean.yield.by.year, c(101:110))
Out = lm(mean.yield.by.year ~ c(101:110))
summary(Out)
plot(101:110,mean.yield.by.year,
      xlab="年度",ylab="年度單位面積產量平均值")
abline(lm(mean.yield.by.year~c(101:110)),lty=2,lwd=1.5)
```

```
Call:
lm(formula = mean.prod.by.year ~ c(101:110))

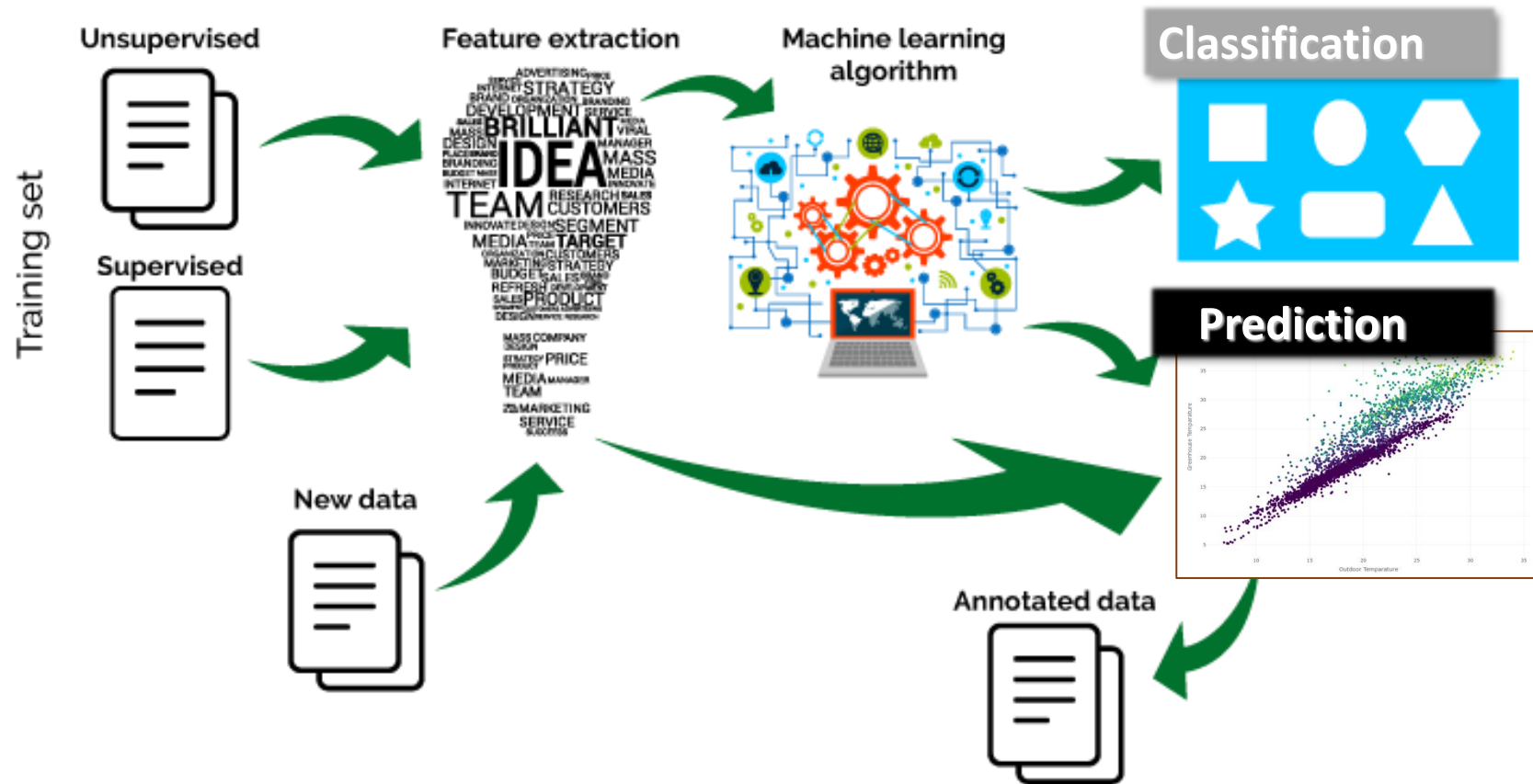
Residuals:
    Min       1Q   Median       3Q      Max
-169035  -39416  -14930   41955  154057

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) 10141151    1153149   8.794 2.20e-05 ***
c(101:110)   -81104      10926  -7.423 7.45e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 99240 on 8 degrees of freedom
Multiple R-squared:  0.8732,    Adjusted R-squared:  0.8574
F-statistic: 55.1 on 1 and 8 DF,  p-value: 7.455e-05
```



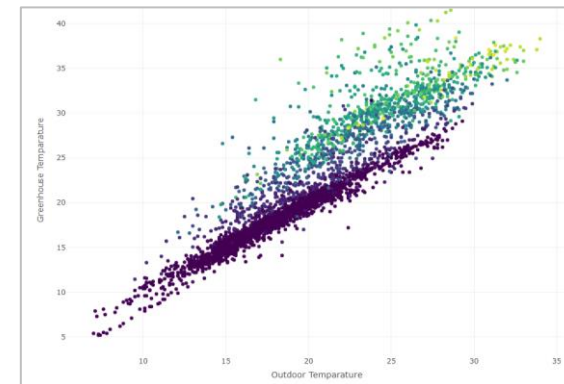
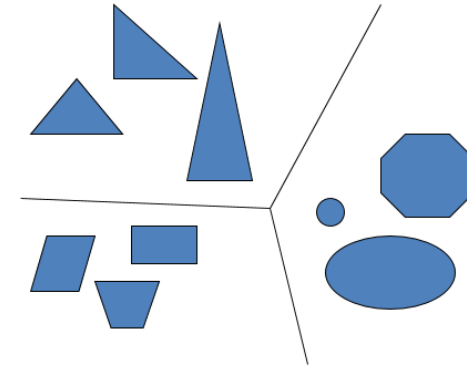
# Machine Learning



<https://www.pantechsolutions.net/blog/machine-learning-projects-and-ideas/>

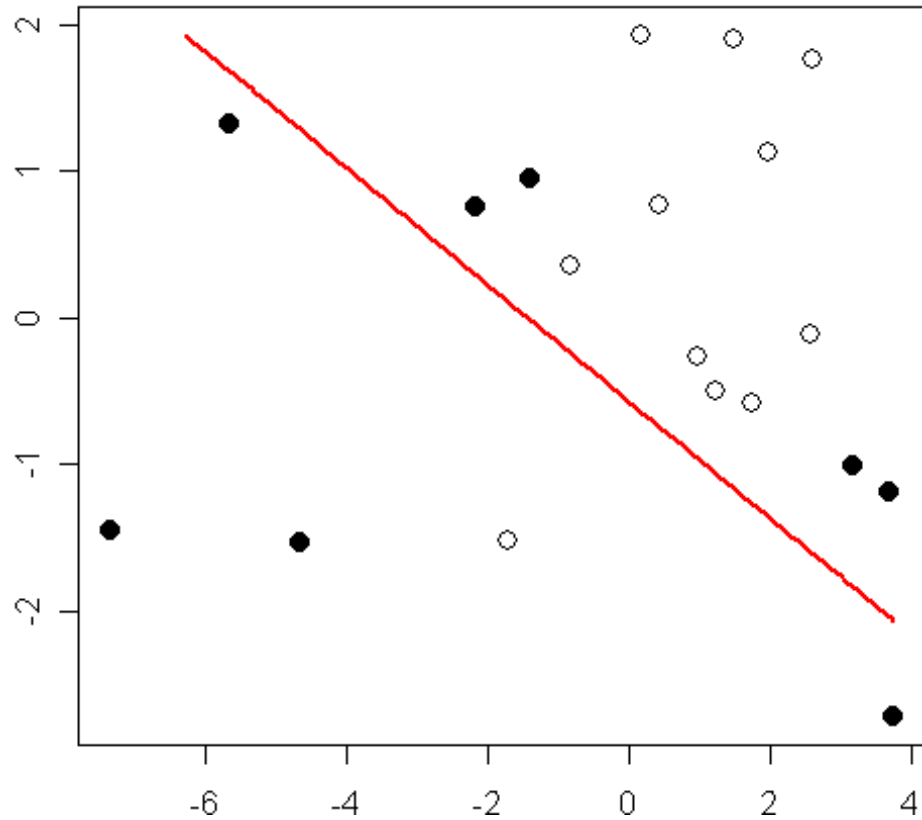
# Objectives of Machine Learning

- **Classification:**
  - Discover **clusters of samples** having similar patterns in features
- **Prediction:**
  - Build up a **predictive model** to represent a continuous response of the target variable.

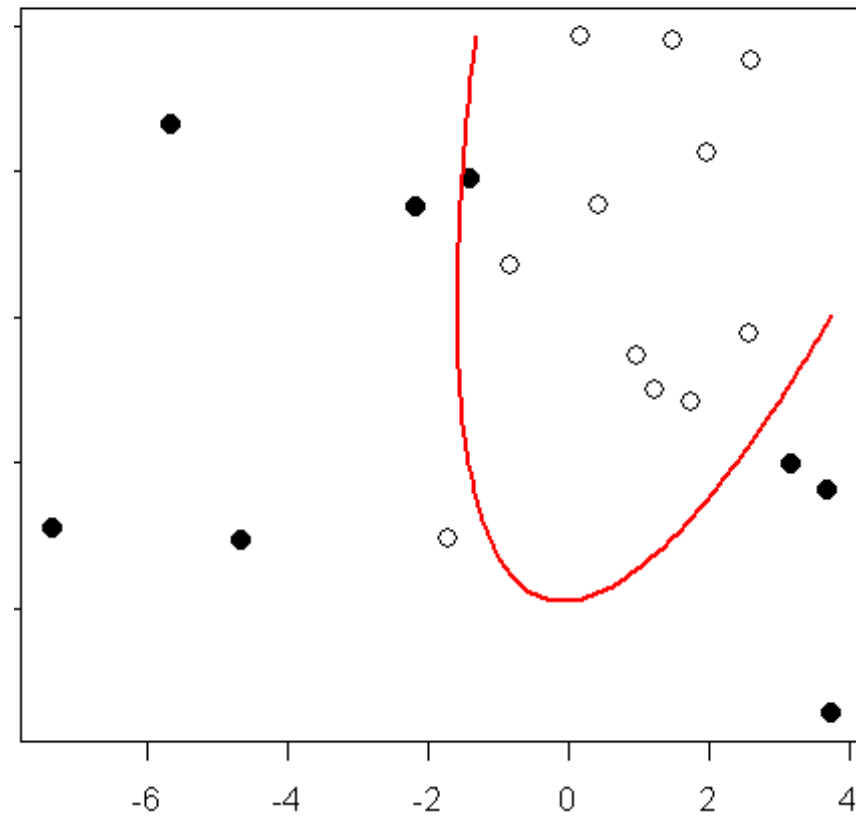


# Linear vs Quadratic Discriminant Analysis for Classification

**LDA** `MASS::lda`



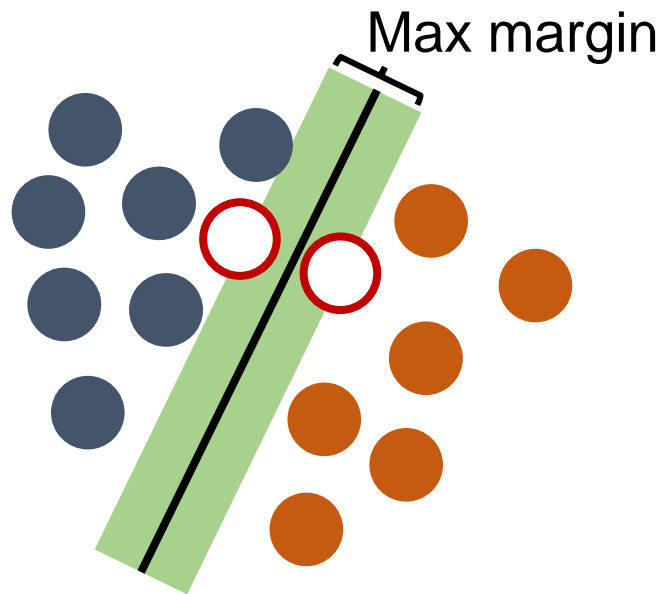
**QDA** `MASS::qda`



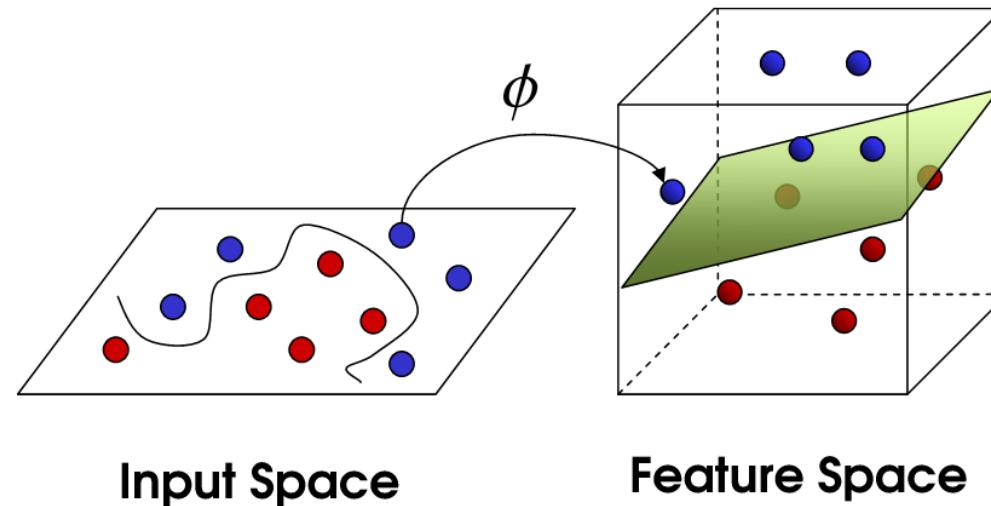
# Support Vector Machine (SVM)

e1071::svm

Linear classification:



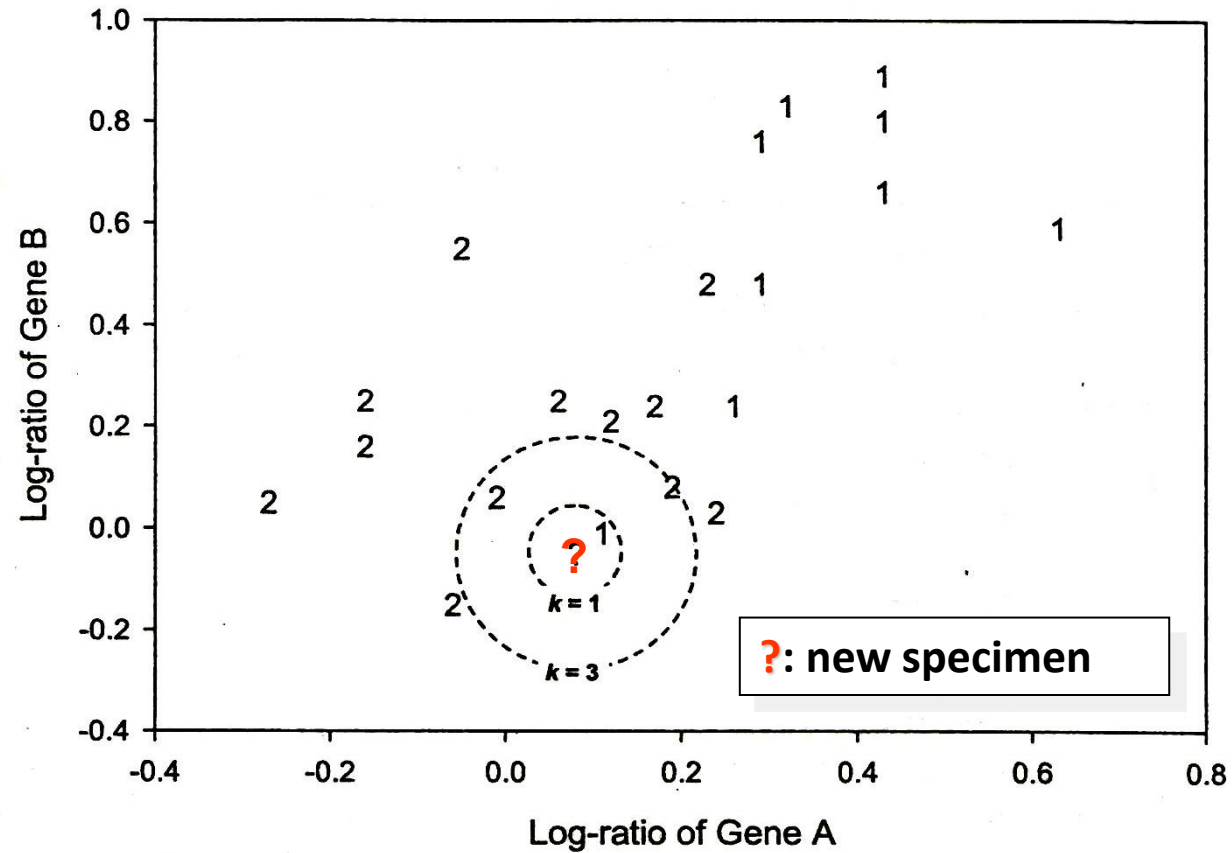
Non-linear classification:



Multiple Kernel learning [Alpaydin, Chapter 13.8]

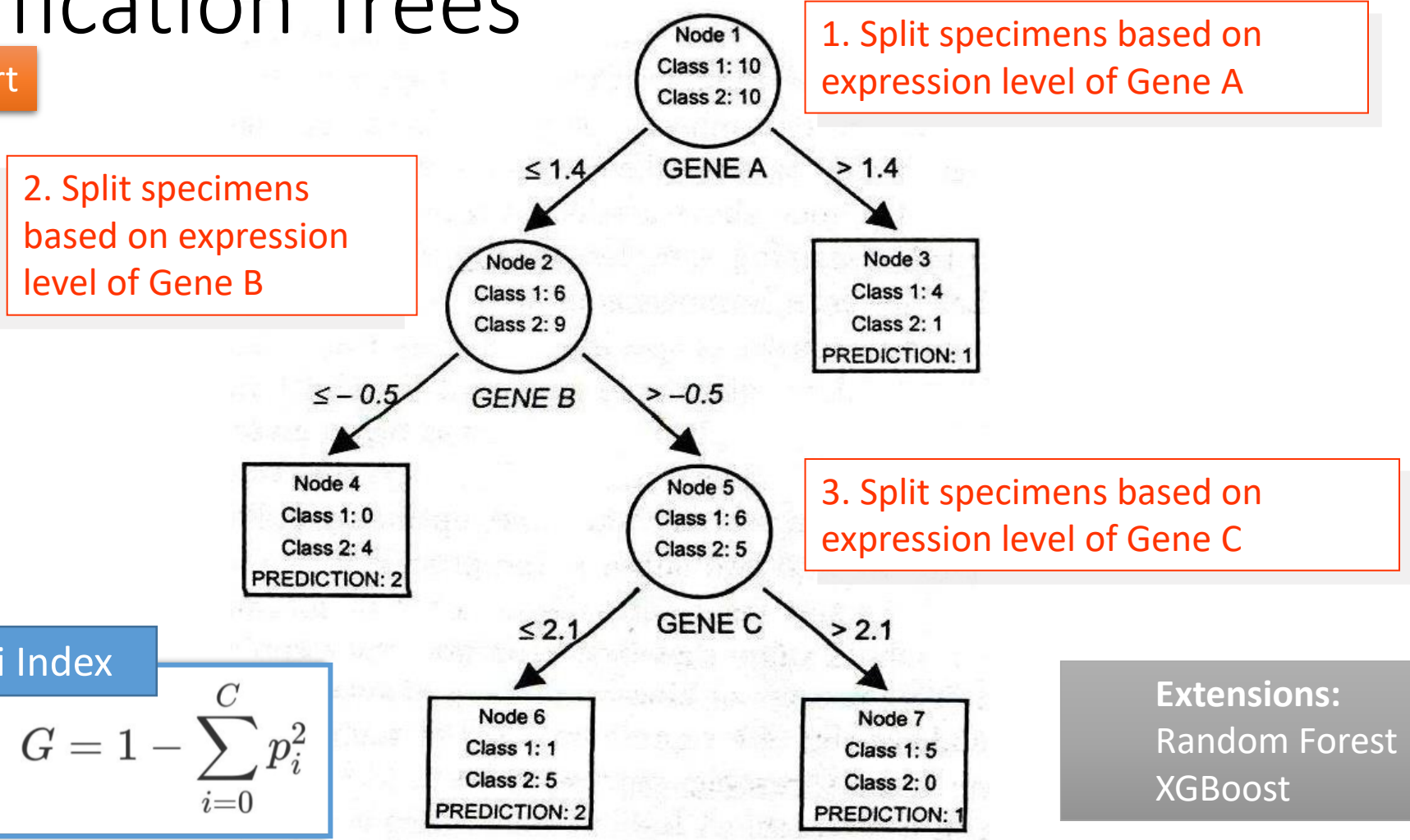
# Nearest neighbor classification (kNN)

class::knn



# Classification Trees

rpart::rpart

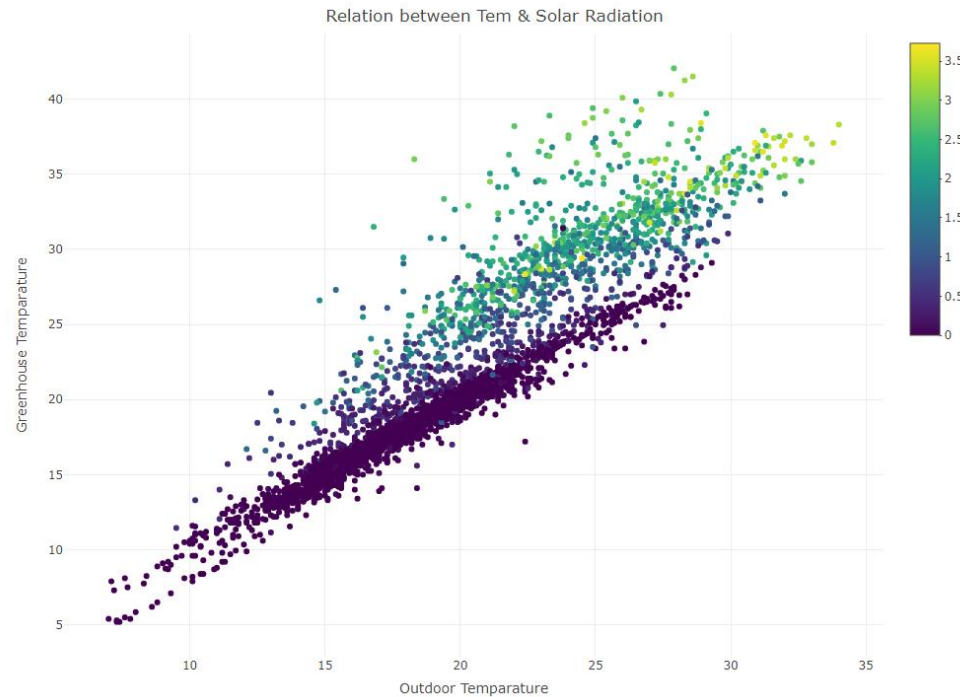


Gini Index

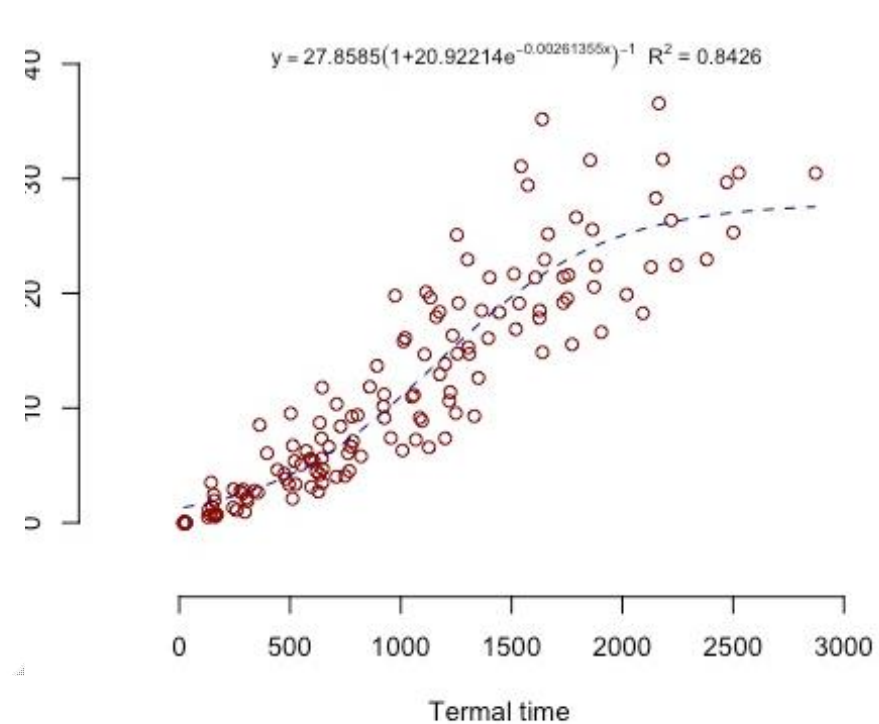
$$G = 1 - \sum_{i=0}^C p_i^2$$

# Regression Model (Prediction)

stats::lm



Linear Multiple Regression Model

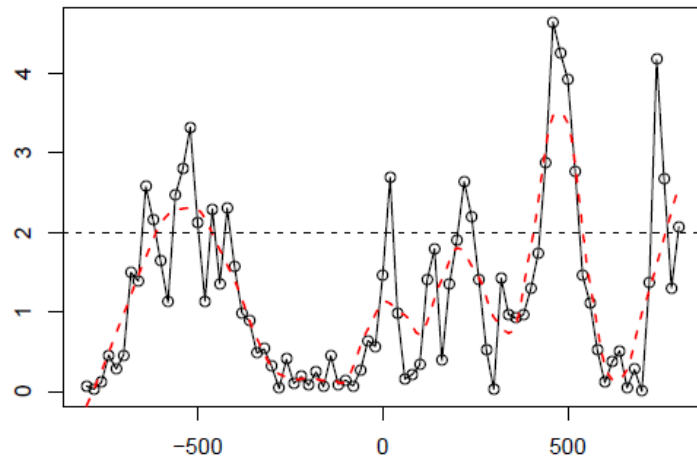


Nonlinear Gompertz Model

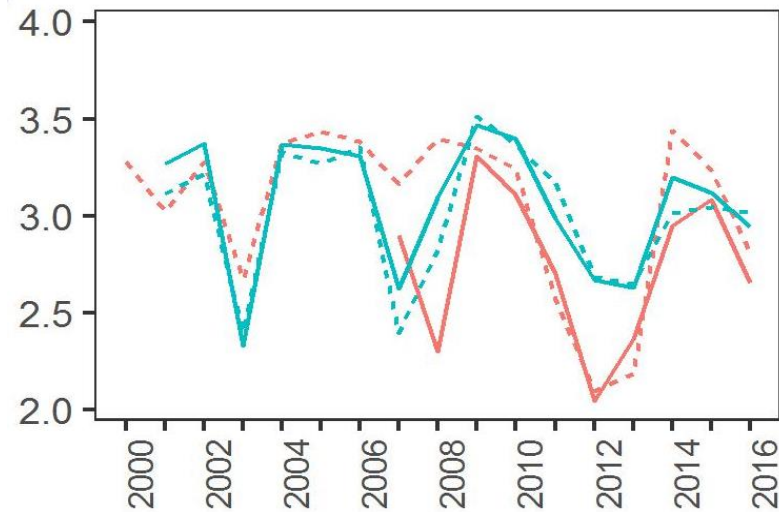
# Other Models for Prediction

```
stats::loess
```

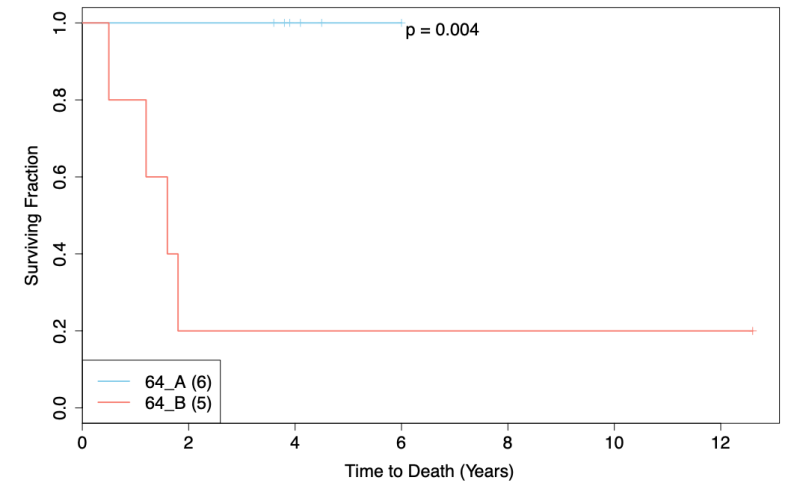
## LOESS



## Time-series



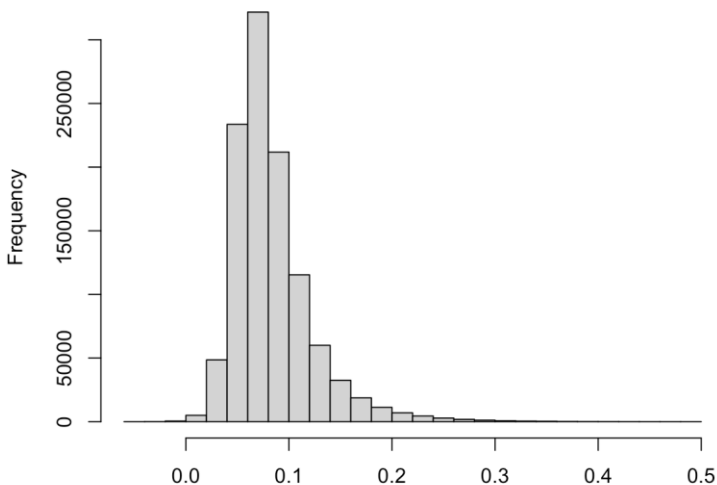
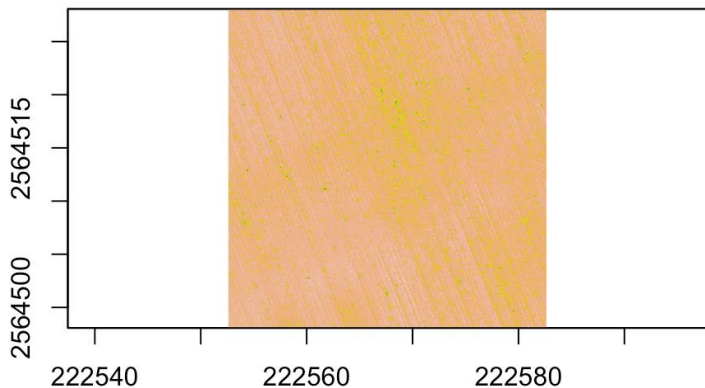
## Survival





	ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
SUPERVISED LEARNING	<b>NBC</b> Naïve Bayes classifier	A classification technique based on Bayes' Theorem with an assumption of independence among predictors. In simple terms, a Naive Bayes classifier assumes that the presence of a particular feature in a class is unrelated to the presence of any other feature	e1071::naiveBayes	naiveBayes(class ~ ., data = x)
	<b>KNN</b> k-Nearest Neighbours	A non-parametric method used for classification and regression. In both cases, the input consists of the k closest training examples in the feature space. The output depends on whether k-NN is used for classification or regression	class::knn	knn(train, test, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
	<b>REG</b> Linear Regression	Model the linear relationship between a scalar dependant variable Y and one or more explanatory variables (or independent variables) denoted X	stats::lm	lm(dist ~ speed, data=cars)
	<b>LREG</b> Logistic Regression	Used to predict a binary outcome (1 / 0, Yes / No, True / False) given a set of independent variables.	stats::glm	glm(Y ~ ., family = binomial (link = 'logit'), data = X)
	<b>TM</b> Tree-Based Models	The idea is to consecutively divide (branch) the training dataset based on the input features until an assignment criterion with respect to the target variable into a "data bucket" (leaf) is reached	rpart::rpart	rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
	<b>ANN</b> Artificial Neural Network	Neural networks are built from units called perceptrons. Perceptrons have one or more inputs, an activation function and an output. An ANN model is built up by combining perceptrons in structured layers.	neuralnet::neuralnet	neuralnet(f,data=train_,hidden=c(5,3),linear.output=T)
	<b>SVM</b> Support Vector Machine	A data classification method that separates data using hyperplanes	e1071::svm	svm(formula, data = NULL, ..., subset, na.action = na.omit, scale = TRUE)
UNSUPERVISED LEARNING	<b>PCA</b> Principal Component Analysis	A procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.	stats::prcomp stats::princomp FactoMineR::PCA ade4::dudi.pca amap::acp	<b>stats</b> : prcomp(formula, data = NULL, subset, na.action, ...) <b>stats</b> : princomp(formula, data = NULL, subset, na.action, ...) <b>FactoMineR</b> : PCA(decathlon, quanti.sup = 11:12, quali.sup=13) <b>ade4</b> : dudi.pca(deug\$stab, center = deug\$cent, scale = FALSE, scan = FALSE) <b>amap</b> : acp(lubisch)
	<b>KMC</b> k-Mean Clustering	Aims at partitioning n observations into k clusters in which each observation belongs to the cluster with the nearest mean	stats::kmeans	kmeans(x, centers, iter.max = 10, nstart = 1, algorithm = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"), trace=FALSE)
	<b>HCL</b> Hierarchical Clustering	An approach which builds a hierarchy from the bottom-up, and doesn't require the number of clusters to be specified beforehand.	stats::hclust	hclust(d, method = "complete", members = NULL)

# 影像辨識



```
rm(list=ls())
library(raster)
library(rgdal) # support file reading in "raster"

setwd("~/Dropbox/00_course/NTU-ImageAnalysis/ppt/")
ff = c("small_red.tif", "small_green.tif", "small_blue.tif", "small_nir.tif")

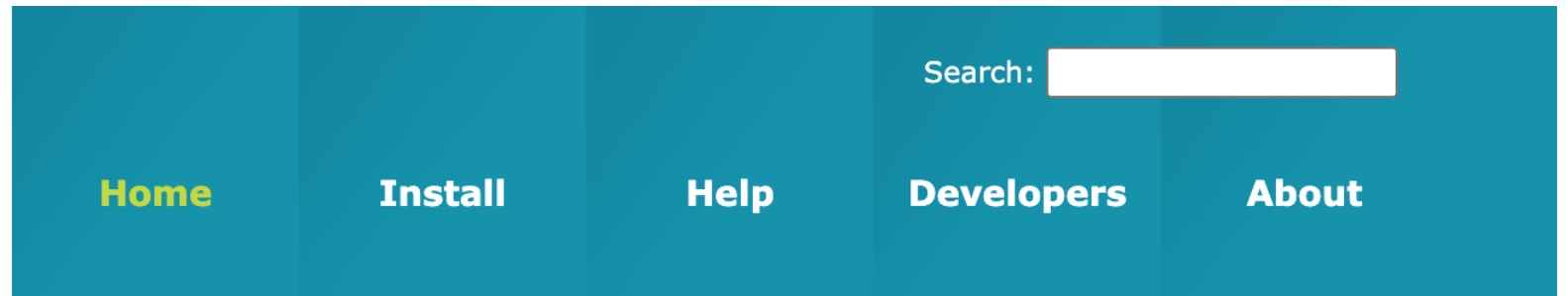
# data import
img = stack(ff)
# convert data into rasterbrick for faster processing
img_br = brick(img)
minValue(img_br)
maxValue(img_br)
plot(img_br)

### Faster Raster Calculations of NDVI with the Overlay Function
### https://www.earthdatascience.org/courses/earth-analytics/multi
ndvi.fun = function(r,n){
  (n-r)/(n+r)
}
ndvi = overlay(img_br[[1]],img_br[[4]],fun=ndvi.fun)

plot(ndvi)
hist(ndvi)
```

# BioConductor

- BioConductor is the R software project for the analysis of biomedical and genomic data
  - Microarrays
  - Genome sequence data
  - Pathway graphs



<https://www.bioconductor.org/>

# BioConductor

## 1.2 於 R console 中安裝 Bioconductor

**Windows** 使用者 R 桌面圖示上按右鍵以「系統管理員身份執行」最新版本 R, **MacOS** 使用者依正常方式開啟 R 後, 於 > 符號後執行以下程式安裝 bioconductor

```
install.packages("BiocManager")
BiocManager::install() #安裝基本 Bioconductor 套件
#若過程中出現 Update all/some/none? [a/s/n]: 輸入a

#安裝課堂中會用到的其他套件
BiocManager::install("affyilmGUI")
BiocManager::install("DESeq2")
BiocManager::install("WGCNA")
```

# Common Workflows in BioC

[https://www.bioconductor.org/packages/release/BiocViews.html#\\_\\_\\_Workflow](https://www.bioconductor.org/packages/release/BiocViews.html#___Workflow)



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## Bioconductor Workflows

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## RNA-seq workflow: gene-level exploratory analysis and differential expression

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16 October, 2019

### Abstract

Here we walk through an end-to-end gene-level RNA-seq differential expression workflow using Bioconductor packages. We will start from the FASTQ files, show how these were quantified to the reference transcripts, and prepare gene-level count datasets for downstream analysis. We will perform exploratory data analysis (EDA) for quality assessment and to explore the relationship between samples, perform differential gene expression analysis, and visually explore the results.

### Contents

# Summary

- R 語言是具有彈性的工具，現在開始學習、永遠不嫌晚
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- 善用網路與AI工具，建立自我學習的能力
- 透過社群共學也是一個好途徑~