AI、大數據與品質研討會

中華民國品質學會

主題：品質控制在生物資訊的應用

主講人：李明昌 博士

2021年4月26日

大綱

- R語言與RStudio軟體簡介
- Bioconductor實務應用
- 品質控制技術
- 結論與未來展望

個人簡介

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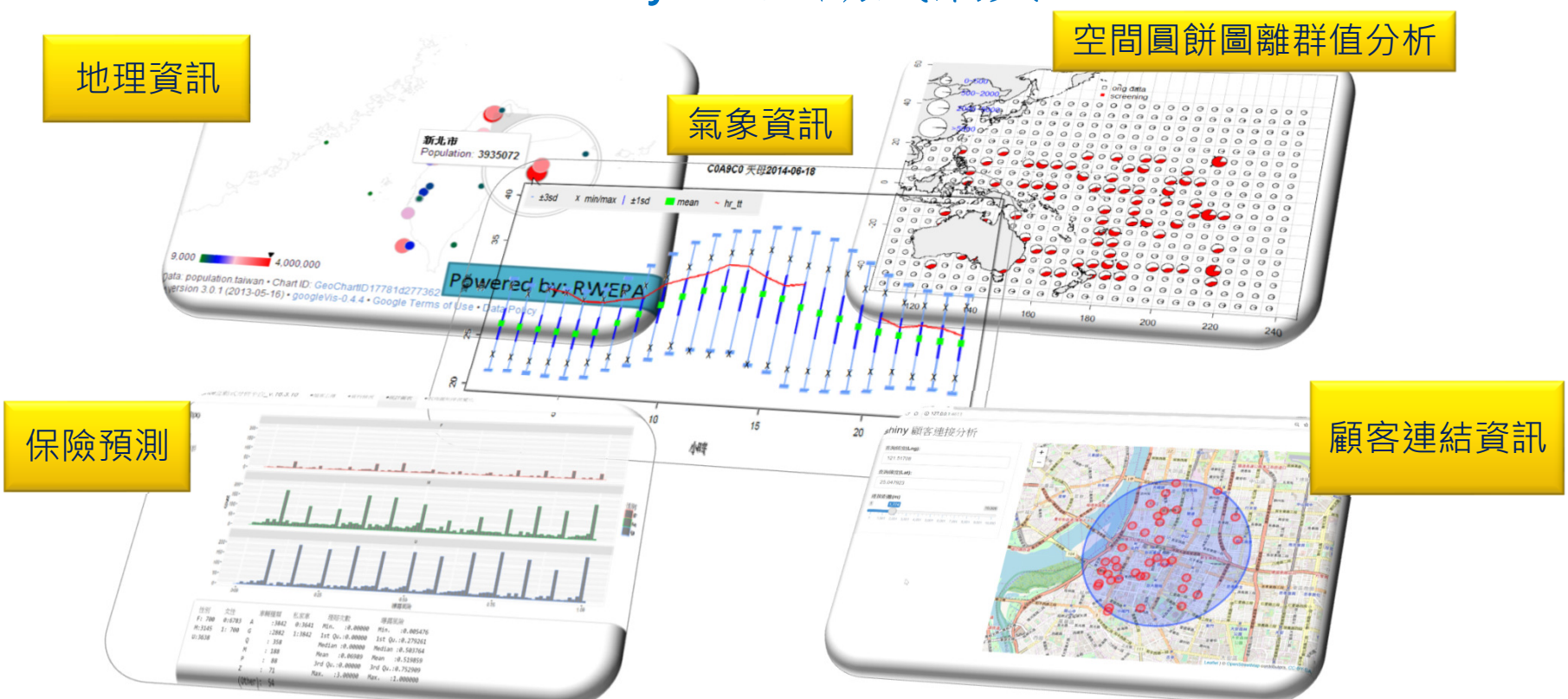
  臺灣資料科學與商業應用協會 常務理事
- 學歷：中原大學 工業與系統工程所 博士
- 經歷：
  - 育達科技大學 資訊管理系(所) 專任助理教授
  - 佛光大學 兼任教師
  - 國立台北商業大學 兼任教師
  - 東吳大學 兼任教師
  - 崇友實業 行銷企劃專員
  - 國航船務代理股份有限公司 海運市場運籌管理員
- 國內外各大專院校、資策會、工業技術研究院、國家發展委員會、中央氣象局、公平交易委員會、各縣市政府與日本名古屋產業大學等公民營單位演講達280多場，2460小時以上。
- 連絡資訊：
  - RWEPA網站：http://rwepa.blogspot.com/
  - E-MAIL: *alan9956@gmail.com*

資料分析/視覺化成果?

R + shiny → 互動式網頁



網頁呈現

中央氣象局 1,600萬筆資料

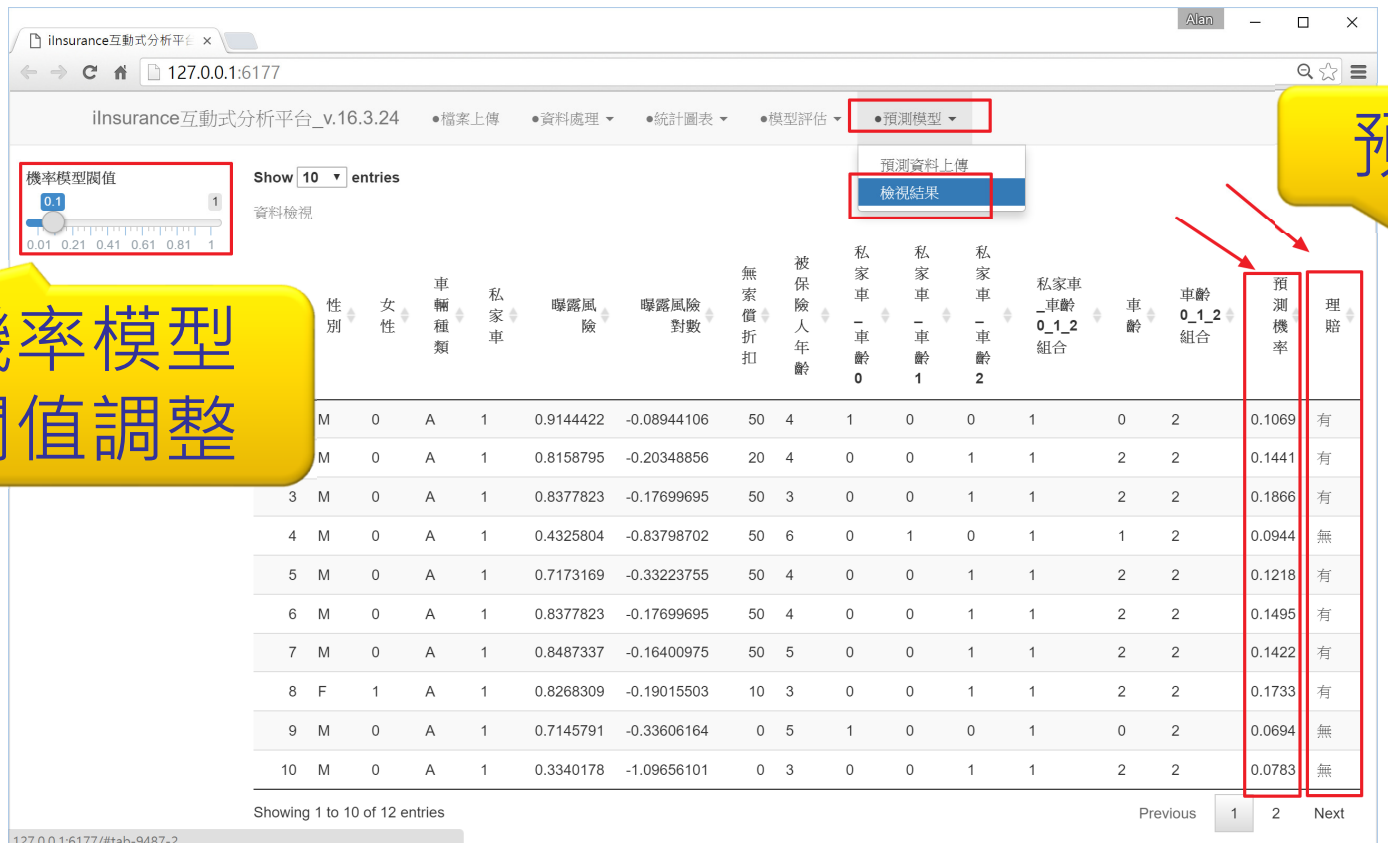
異常偵測

動態繪圖

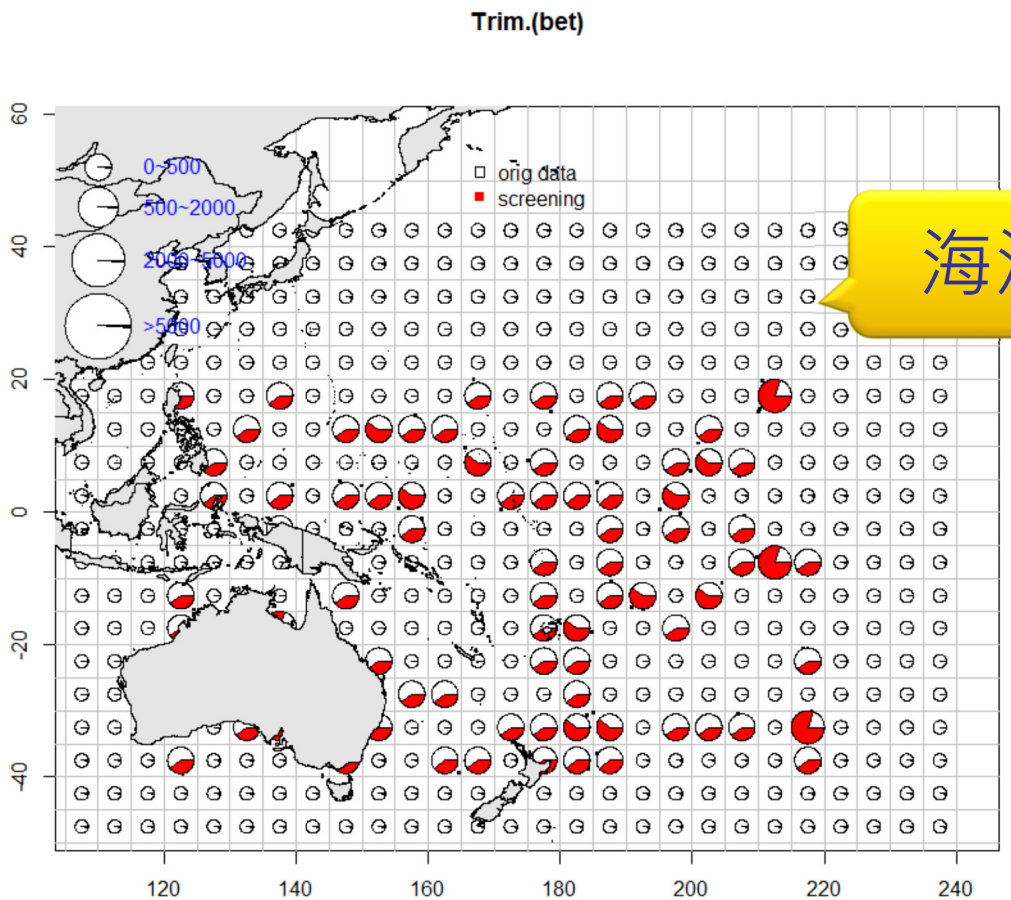
客製化選單

R統計運算

保險預測模型

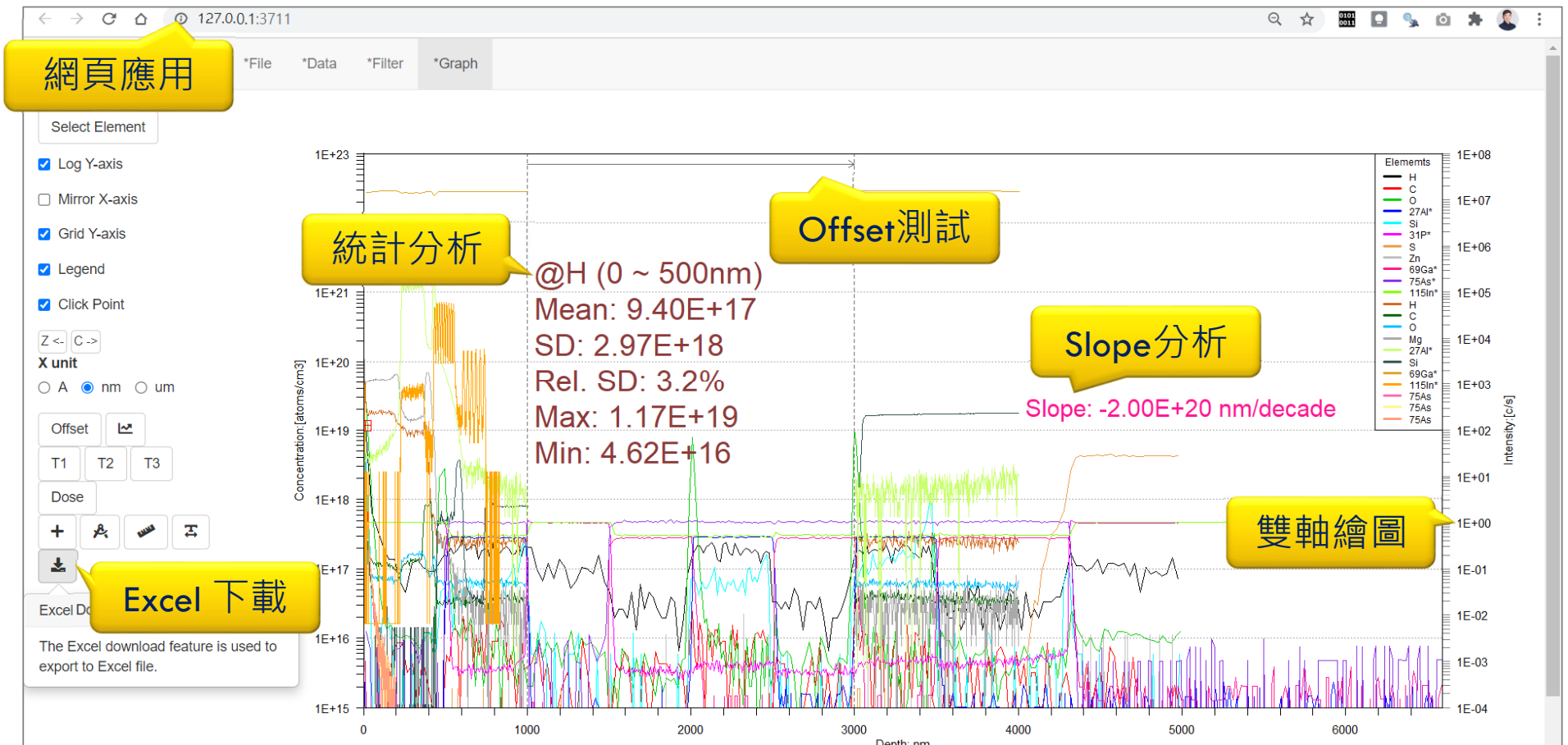

Alan
iInsurance互動式分析平台
127.0.0.1:6177
iInsurance互動式分析平台_v.16.3.24
●檔案上傳
●資料處理
●統計圖表
●模型評估
●預測模型
預測資料上傳
檢視結果
機率模型閥值
0.1
1
0.01 0.21 0.41 0.61 0.81 1
Show 10 entries
資料檢視
性別 女性 車輛種類 私家車 曝露風險 曝露風險對數 無索償折扣 被保險人年齡 私家車_車齡0 私家車_車齡1 私家車_車齡2 私家車_車齡0_1_2組合 車齡 車齡0_1_2組合 預測機率 理賠
1 M 0 A 1 0.9144422 -0.08944106 50 4 1 0 0 1 0 2 0.1069 有
2 M 0 A 1 0.8158795 -0.20348856 20 4 0 0 1 1 2 2 0.1441 有
3 M 0 A 1 0.8377823 -0.17699695 50 3 0 0 1 1 2 2 0.1866 有
4 M 0 A 1 0.4325804 -0.83798702 50 6 0 1 0 1 1 2 0.0944 無
5 M 0 A 1 0.7173169 -0.33223755 50 4 0 0 1 1 2 2 0.1218 有
6 M 0 A 1 0.8377823 -0.17699695 50 4 0 0 1 1 2 2 0.1495 有
7 M 0 A 1 0.8487337 -0.16400975 50 5 0 0 1 1 2 2 0.1422 有
8 F 1 A 1 0.8268309 -0.19015503 10 3 0 0 1 1 2 2 0.1733 有
9 M 0 A 1 0.7145791 -0.33606164 0 5 1 0 0 1 0 2 0.0694 無
10 M 0 A 1 0.3340178 -1.09656101 0 3 0 0 1 1 2 2 0.0783 無
Showing 1 to 10 of 12 entries
Previous 1 2 Next
127.0.0.1:6177/#tab-9487-2
預測結果
機率模型
閥值調整

空間圓餅圖離群值分析

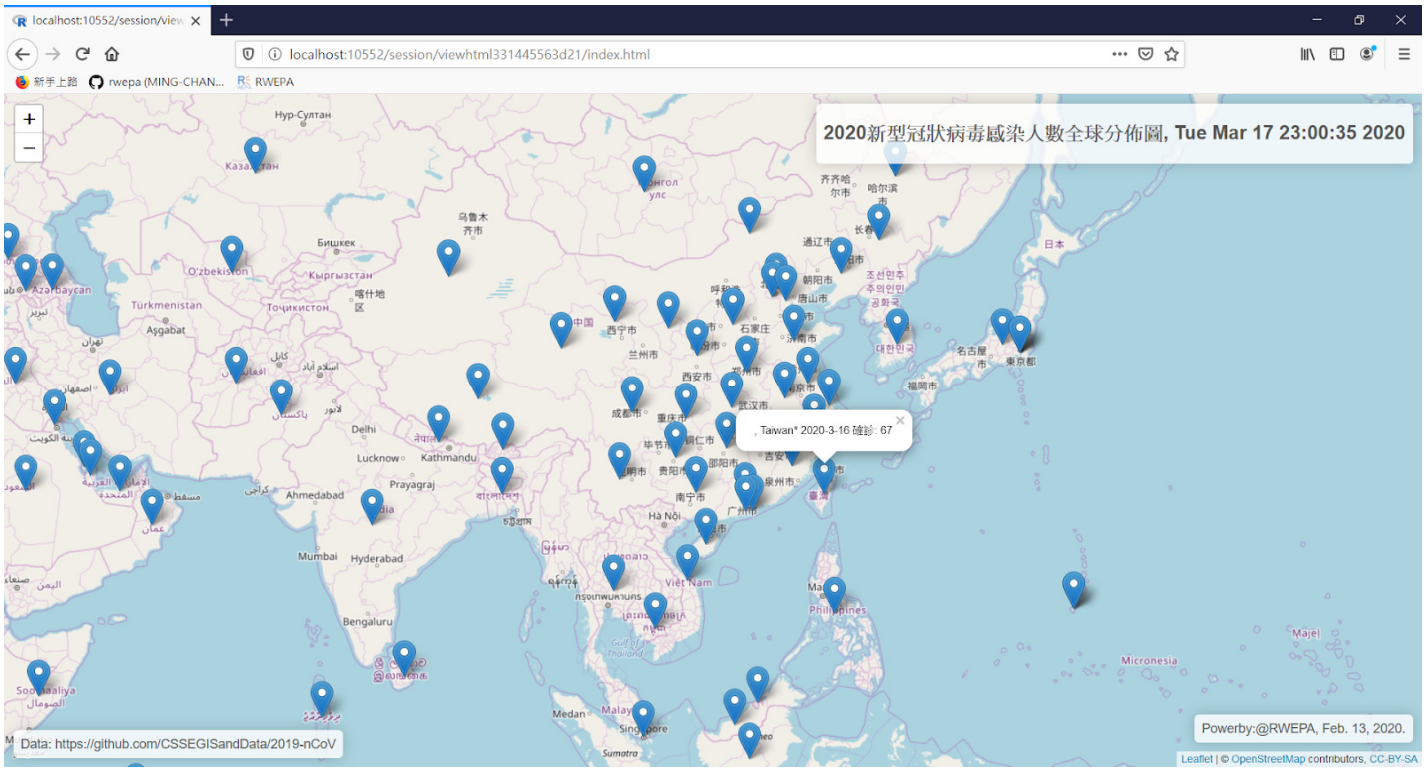


海洋生態視覺化

離子資料分析與視覺化應用



2020新型冠狀病毒視覺化



http://rwepa.blogspot.com/2020/02/2019nCoV.html

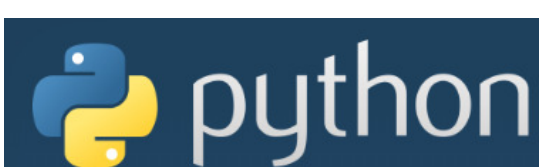
大數據分析工具

- Microsoft Excel 2019: 104萬餘筆資料限制

	A	B	C	D	E	F	G
1	WEEK_END_DATE	STORE_NUM	UPC	UNITS	VISITS	HHS	SPEND
1048572	14-Jan-09	367	1111009477	13	13	13	18.07
1048573	14-Jan-09	367	1111009497	20	18	18	27.8
1048574	14-Jan-09	367	1111009507	14	14	14	19.32
1048575	14-Jan-09	367	1111035398	4	3	3	14
1048576	14-Jan-09	367	1111038078	3	3	3	7.5

1,048,576筆資料限制

- 免費: 核心程式 + 套件(模組) + IDE



大數據分析免費工具

軟體	Python	R	Julia
Released	1991	2000	2012
用途	程式語言 系統結合	統計,繪圖,視覺化 程式語言	科學計算 程式語言
版本	自由軟體 物件導向	自由軟體 物件導向	自由軟體 物件導向
附加功能	免費模組	免費套件	免費模組
使用者	工科+ 商管	商管+ 工科	商管+ 工科

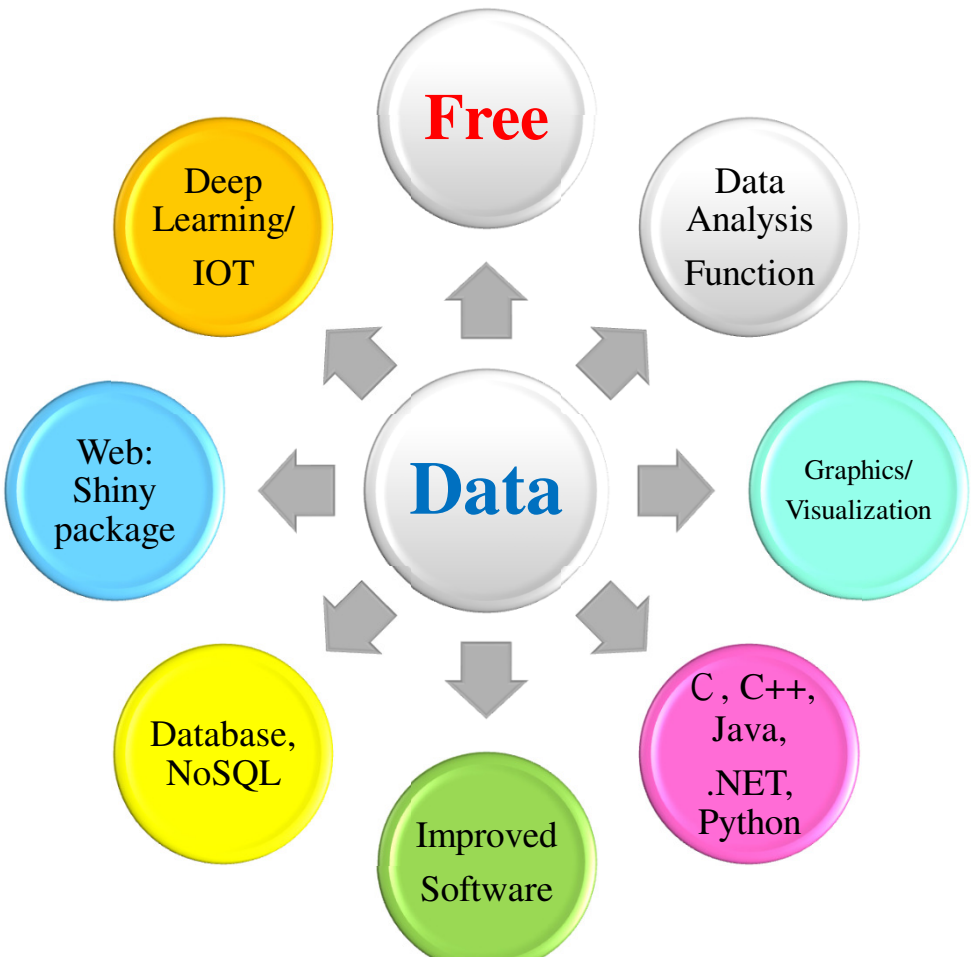
1.R語言與RStudio軟體簡介

R 安裝與簡介

認識R

- 1976 - 貝爾實驗室 John Chambers, Rick Becker, and Allan Wilks研發S 語言。
- 1993 - Ross Ihaka and Robert Gentlemen, University of Auckland, New Zealand 研發R 語言。
  - **R** 是一種基於 **S** 語言所發展出具備統計分析、繪圖與資料視覺化的程式語言。
- 1997年－R的核心開發團隊 (R development core team) 成立，專責R原始碼的修改與編寫。
  - 2000年2月 － R 1.0.0
  - 2013年3月 － R 2.15.3
  - 2021年3月 － R 4.0.5

R-八大功能

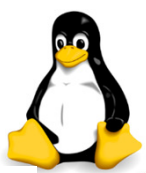

Free
Data Analysis Function
Graphics/ Visualization
C , C++, Java, .NET, Python
Improved Software
Database, NoSQL
Web: Shiny package
Deep Learning/ IOT
Data

R-下載

- 官網: http://www.r-project.org/
- 選取左側 Download \ CRAN
- 選取Taiwan CRAN

Taiwan
https://cran.csie.ntu.edu.tw/

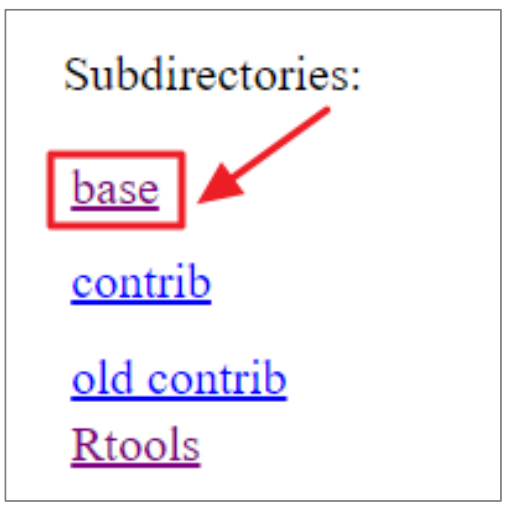
- 選取 Download R for Windows



- Download R for Linux
- Download R for (Mac) OS X
- Download R for Windows

R-下載 (續)

- 選取 base → 下載 [R-4.0.5-win.exe]

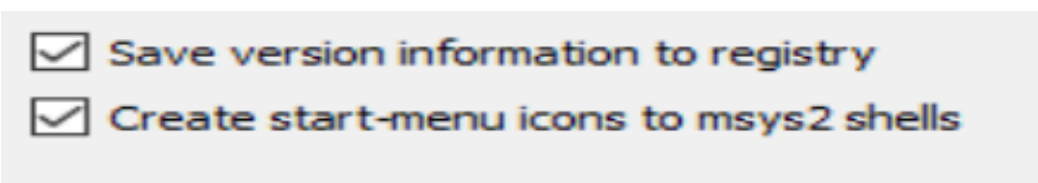


- R安裝路徑: 保留原路徑,不要修改
- https://github.com/rwepa/DataDemo/blob/master/windows_intall_R.pdf

下載並安裝 Rtools

- Rtools for Windows: 一定要保留原路徑 C:\rtools40

On Windows 64-bit: rtools40-x86_64.exe (recommended: includes both i386 and x64 compilers)



R官方網頁

[Home]

Download

CRAN

下載

繪圖

ject

R

Logo

Contributors

What's New?

Reporting

The R Project for Statistical Computing

Getting Started

統計計算

R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To **download R**, please choose your preferred CRAN mirror.

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.

R Manuals

The R Manuals

edited by the R Development Core Team.

The following manuals for R were created on Debian Linux and may differ from the manuals for Mac or Windows on platform-specific pages, but most parts version of the manuals for each platform are part of the respective R installations. The manuals change with R, hence we provide versions for the most recent version for the patched release version (R-patched) and finally a version for the forthcoming R version that is still in development (R-devel).

Here they can be downloaded as PDF files, EPUB files, or directly browsed as HTML:

Manual	R-release	R-patched
An Introduction to R is based on the former "Notes on R", gives an introduction to the language and how to use R for doing statistical analysis and graphics.	HTML | PDF | EPUB	HTML | PDF | EPUB
R Data Import/Export describes the import and export facilities available either in R itself or via packages which are available from CRAN.	HTML | PDF | EPUB	HTML | PDF | EPUB
R Installation and Administration	HTML | PDF | EPUB	HTML | PDF | EPUB
Writing R Extensions covers how to create your own packages, write R help files, and the foreign language (C, C++, Fortran, ...) interfaces.	HTML | PDF | EPUB	HTML | PDF | EPUB
A draft of **The R language definition** documents the language *per se*. That is, the objects that it works on, and the details of the expression evaluati process, which are useful to know when programming R functions.		
R Internals: a guide to the internal structures of R and coding standar the core team working on R itself.		
The R Reference Index: contains all help files of the R standard and recommended packages in printable form. (9MB, approx. 3500 pages)		

contributed documentation
(貢獻文件, 免費啦)

Translations of manuals into other languages than English are available from the contributed documentation section (only a few translations are available).

R Manuals (續)

Contributed Documentation

English --- Other Languages

Manuals, tutorials, etc. provided by users of R. The R core team does not take any responsibility for contents, but we appreciate the effort very much and encourage everybody to contribute to this list! To submit, follow the submission instructions on the CRAN main page. All material below is available directly from CRAN, you may also want to look at the list of other R documentation available on the Internet.

Note: Please use the directory listing to sort by name, size or date (e.g., to see which documents have been updated latetly).

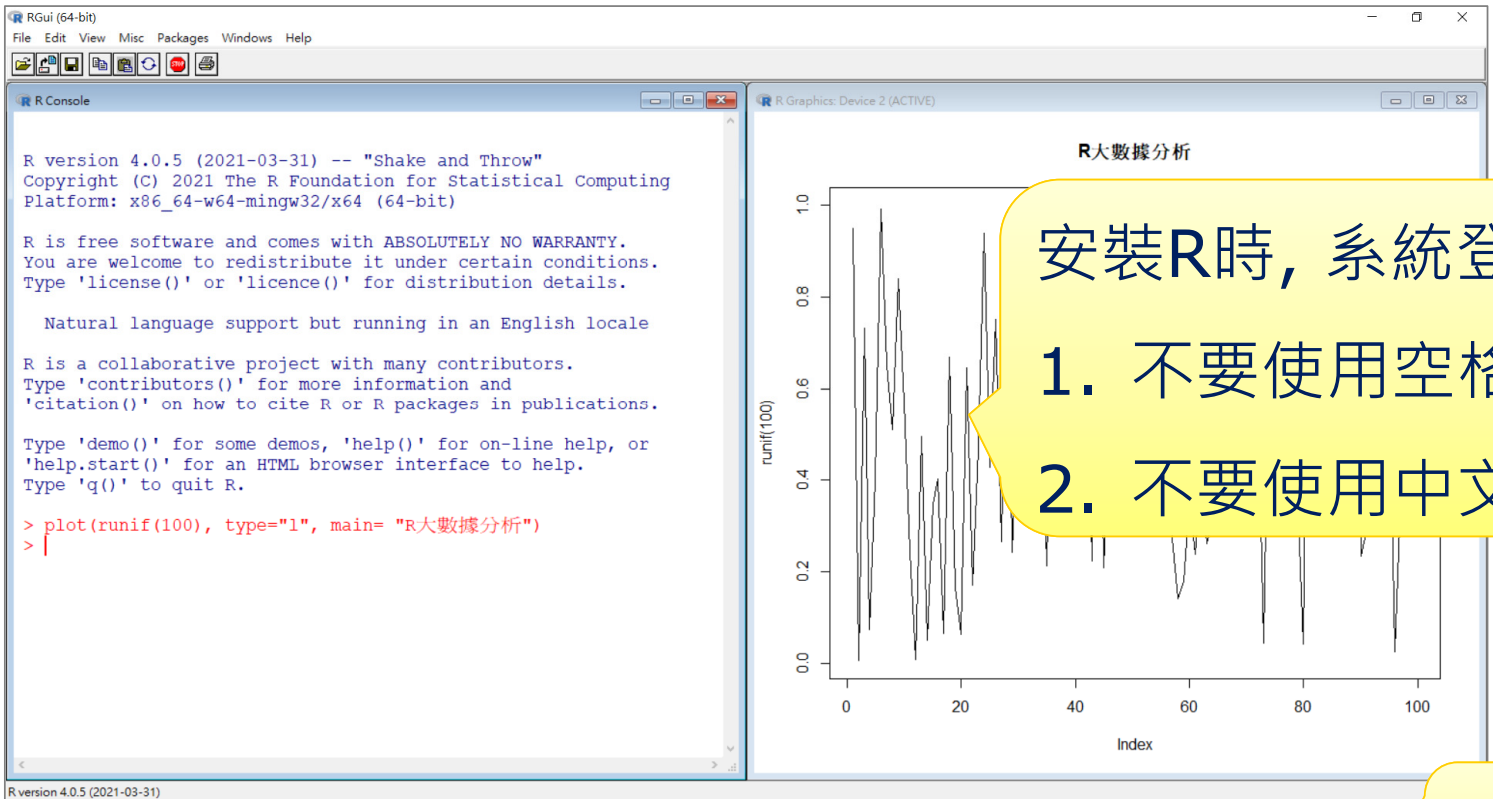
English Documents

Documents with more than 100 pages:

好書!

- **"Visual Statistics. Use R!"** by Alexey Shipunov (PDF, 2016-06-06, 301 page
  are accessible from Alexey Shipunov's English R page .
- **"Using R for Data Analysis and Graphics - Introduction, Examples and Commentary"** by John Maindonald (PDF, data sets and scripts are available at JM's homepage).
- **"Practical Regression and Anova using R"** by Julian Faraway (PDF, data sets and scripts are available at the book homepage).

R 執行畫面 - Windows



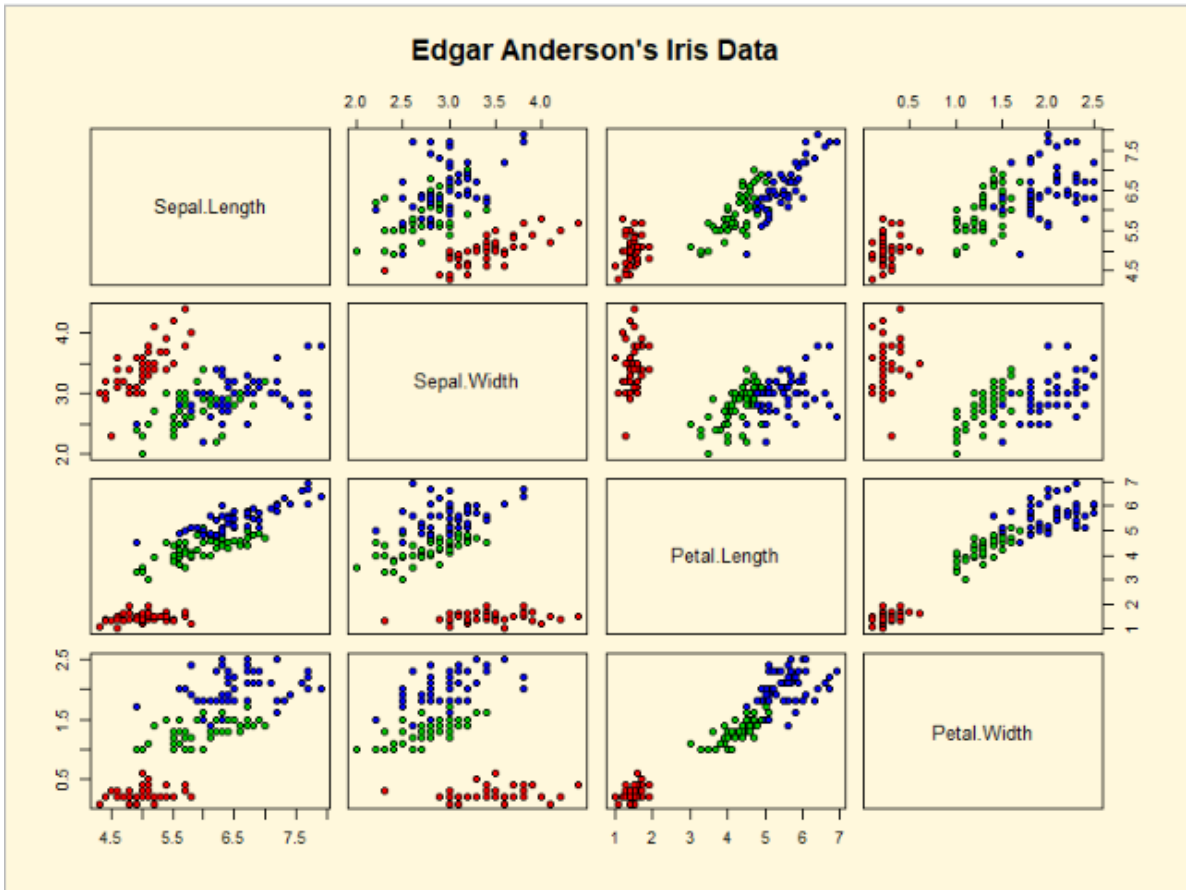
安裝R時，系統登入名稱：

1. 不要使用空格
2. 不要使用中文字

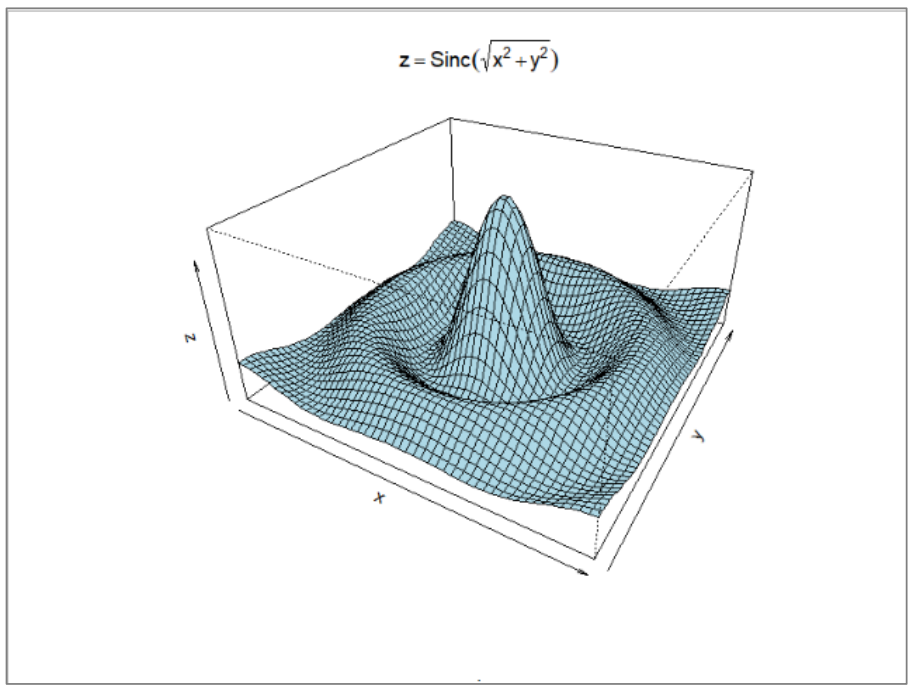
plot(runif(100), type="*l*", main= "R大數據分析")

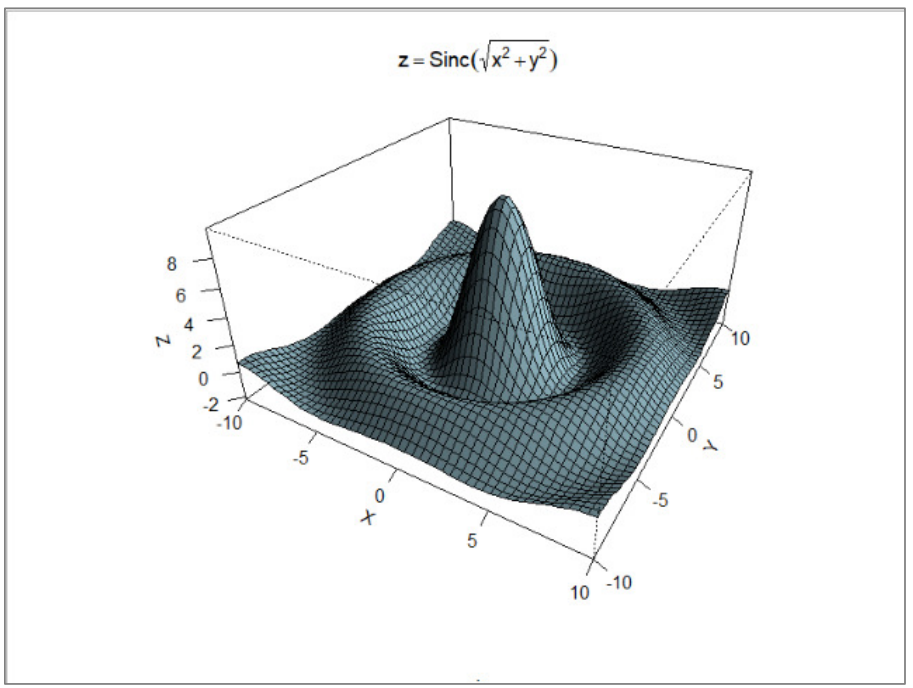
大小寫須一致

demo(graphics)



demo(persp)



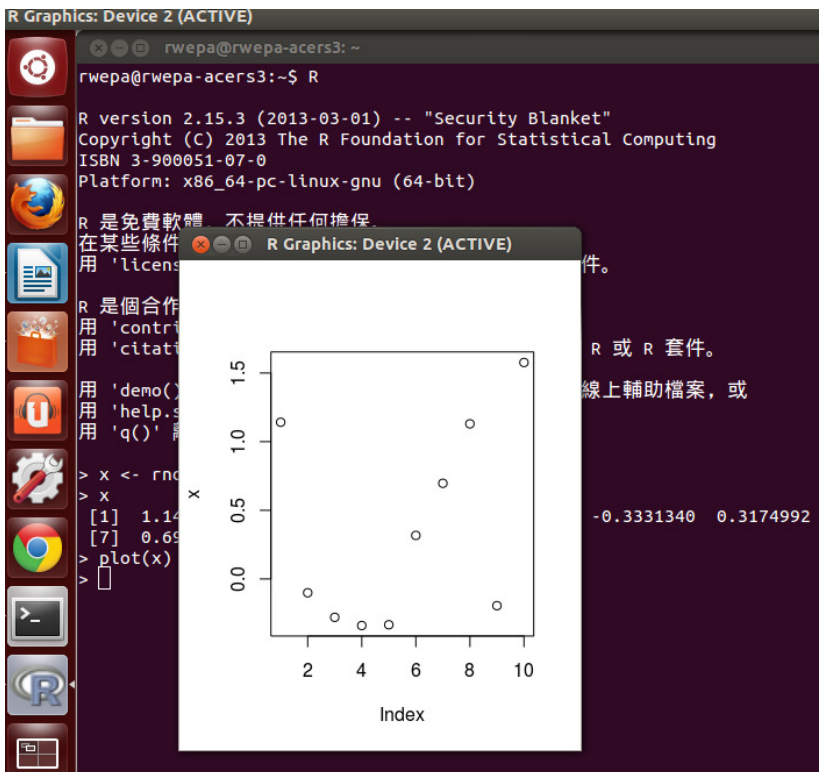


R for Mac

- https://youtu.be/72MYRBNo5Bk

R for Ubuntu

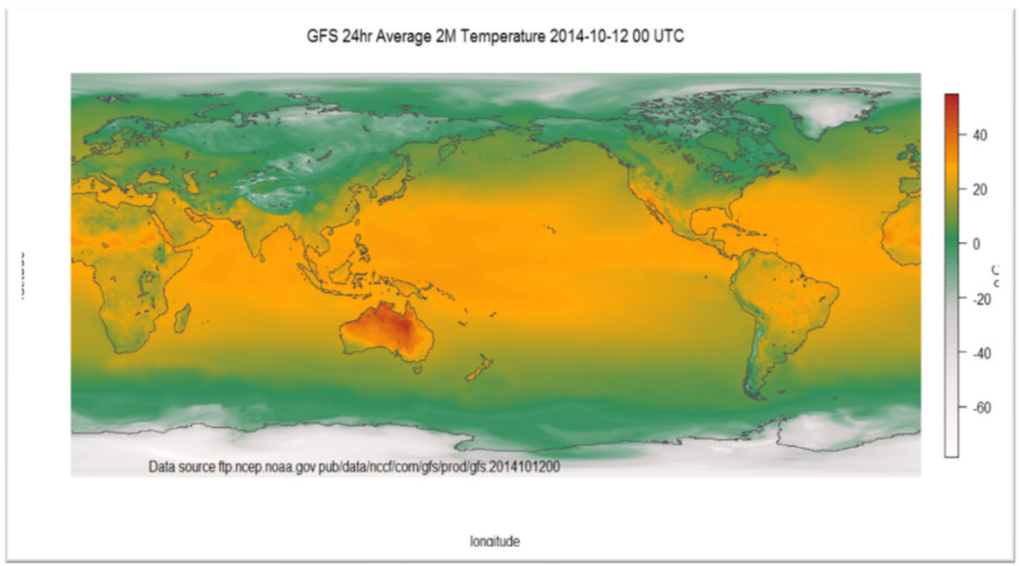
- http://rwepa.blogspot.com/2013/05/ubuntu-r.html



RStudio 安裝與簡介

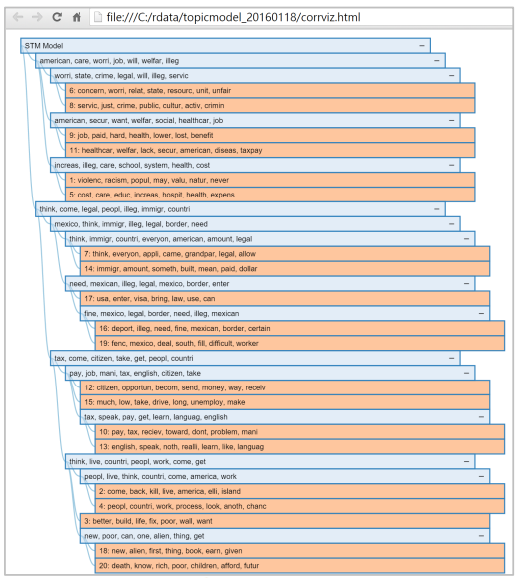
整合式開發環境 - RStudio

- http://www.rstudio.com/



視覺化應用

(全球2M氣溫圖)



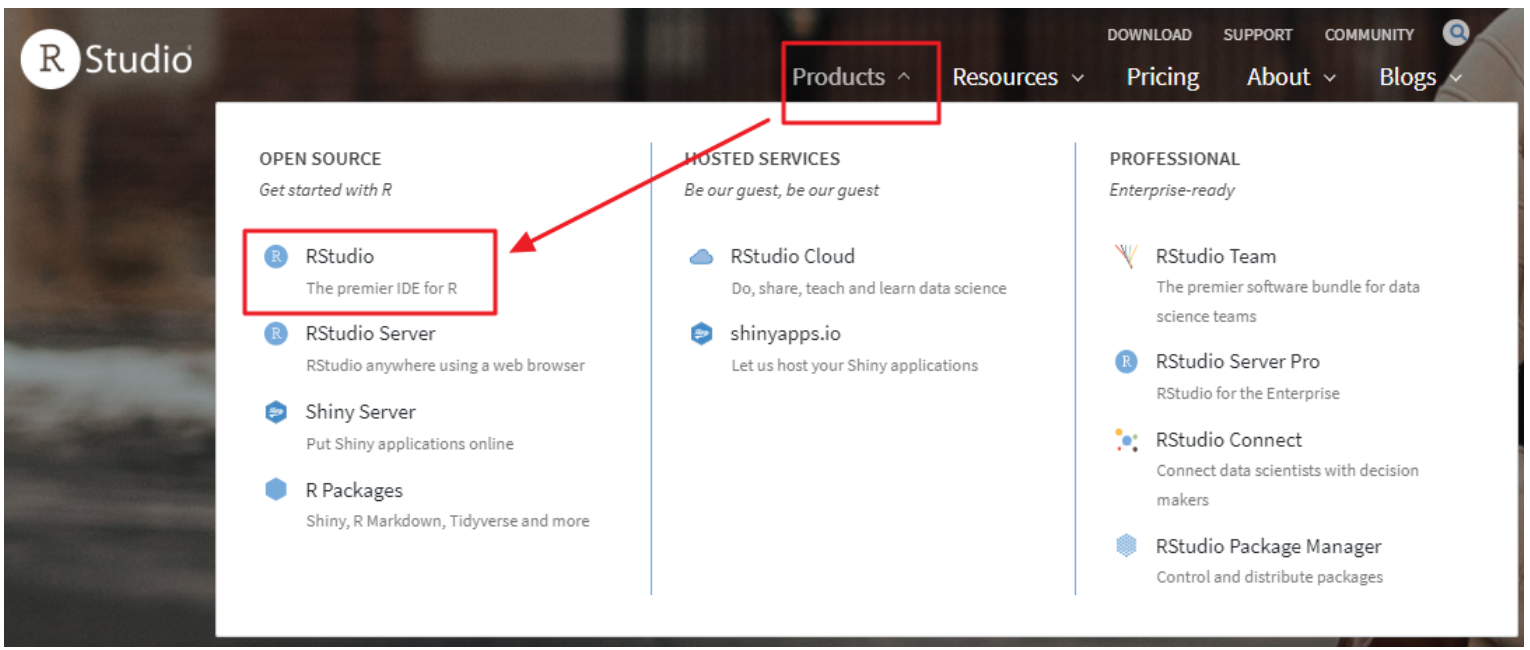
主題模型

RStudio - 特性

- 支援智慧輸入 (按Tab)
- 高亮度顯示程式碼
- 整合R程式, 控制台, 變數清單, 繪圖視窗
- 整合資料庫匯入 SQL, Spark
- 整合R套件: shiny, rmarkdown
- 安裝注意:
  - 先安裝R, 再安裝 RStudio
  - 安裝 RStudio時, 請先關閉R

RStudio 下載

- http://www.rstudio.com/



RStudio 下載 (續)

	RStudio Desktop	RStudio Desktop	RStudio Server	RStudio Server Pro
	Open Source License	Commercial License	Open Source License	Commercial License
	Free	$995	Free	$4,975
	單機版	ear	伺服器版本	/year (Named Users)
	DOWNLOAD	BUY	DOWNLOAD	BUY
	Learn more	Learn more	Learn more	Evaluation | Learn more
Integrated Tools for R	✓	✓	✓	✓
Priority Support		✓		✓
Access via Web Browser			✓	✓
Enterprise Security				✓
Project Sharing				

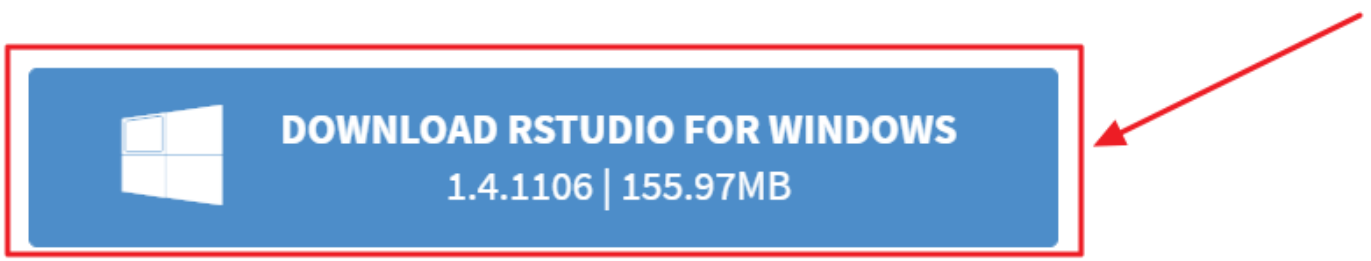
免費版

RStudio 下載 (續)

RStudio Desktop 1.4.1106 - Release Notes

1. Install R. RStudio requires R 3.0.1+.

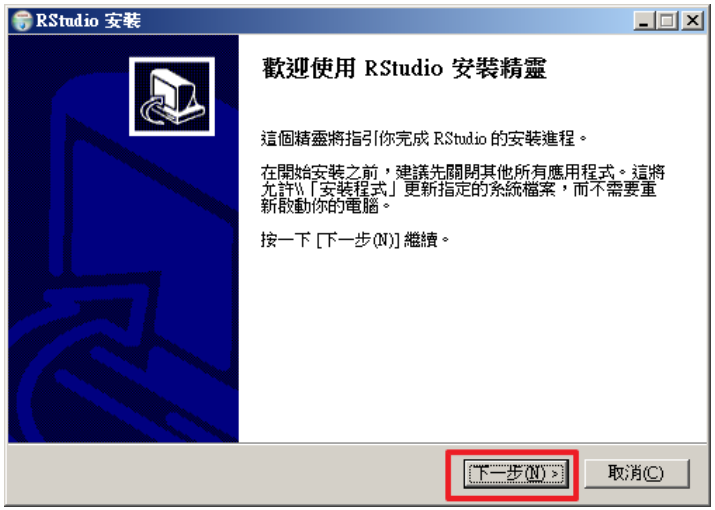
2. Download RStudio Desktop. Recommended for your system:



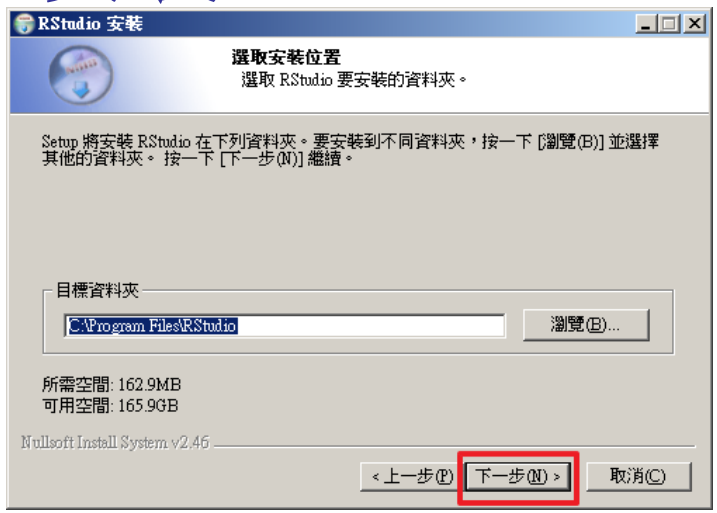
Requires Windows 10/8 (64-bit)

RStudio 安裝

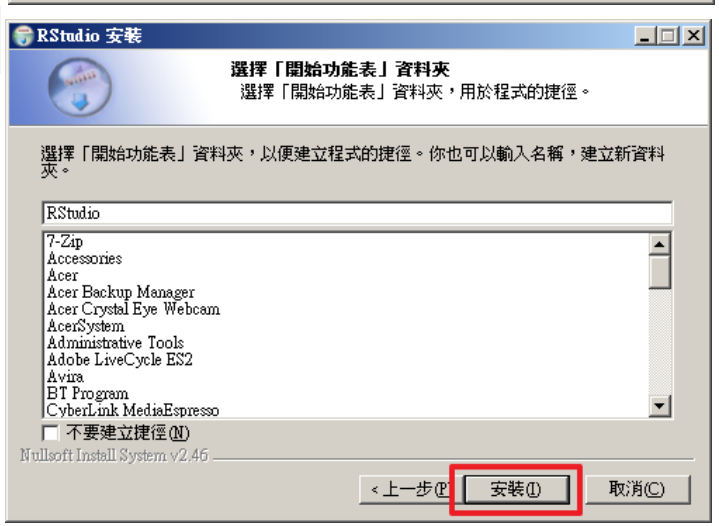
1



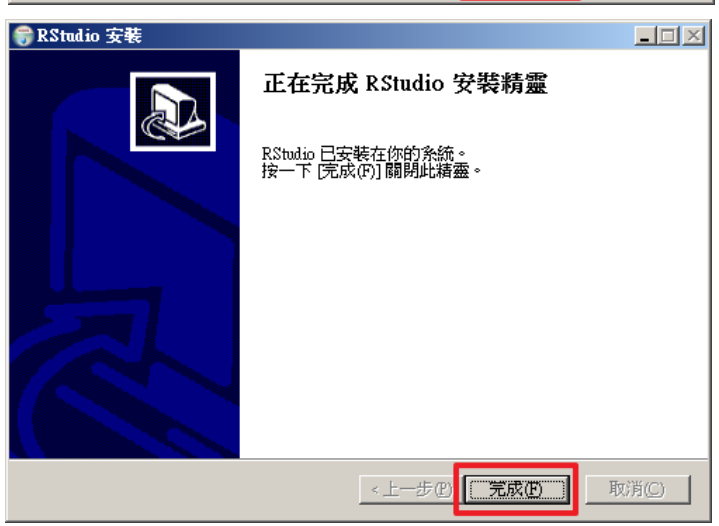
2



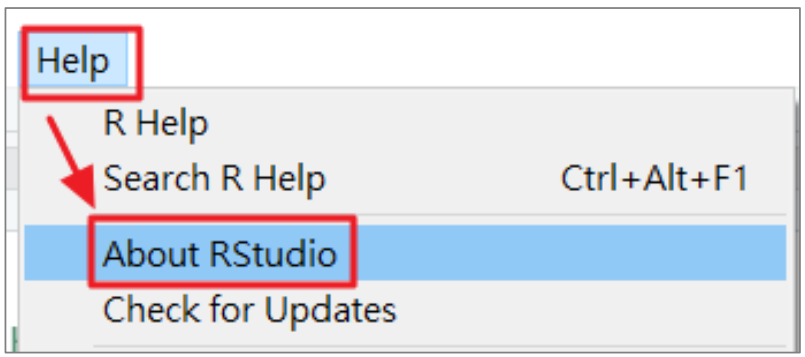
3



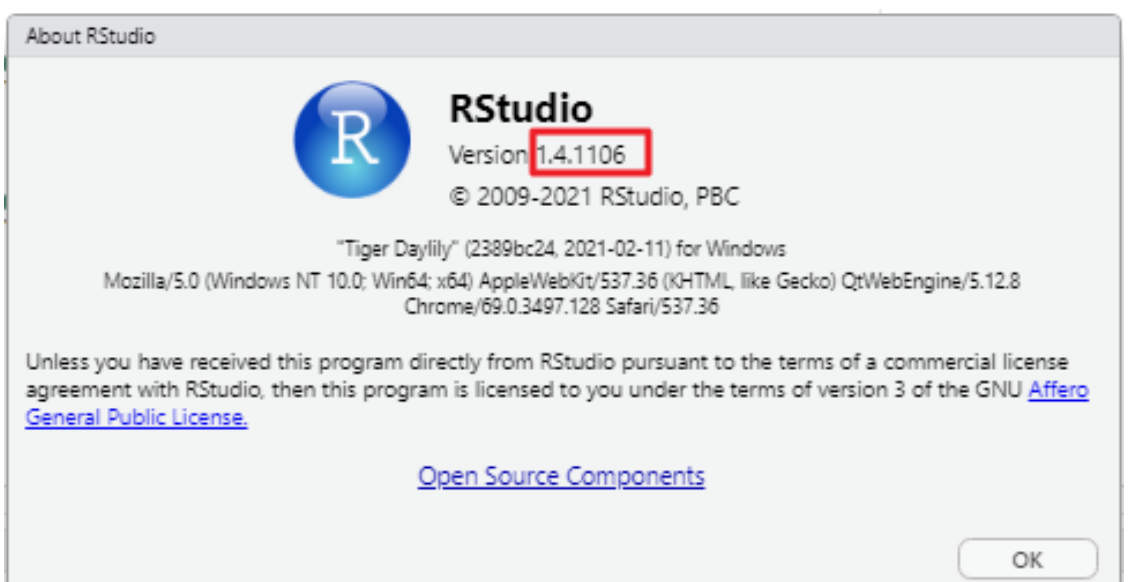
4



RStudio 版本訊息

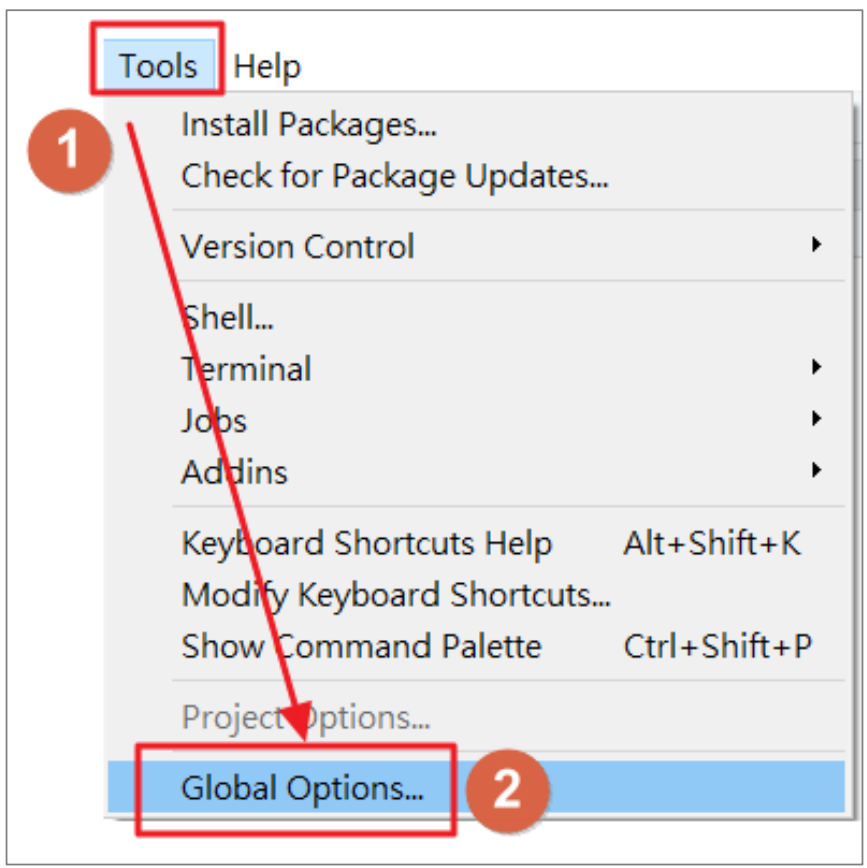


Help \
About RStudio

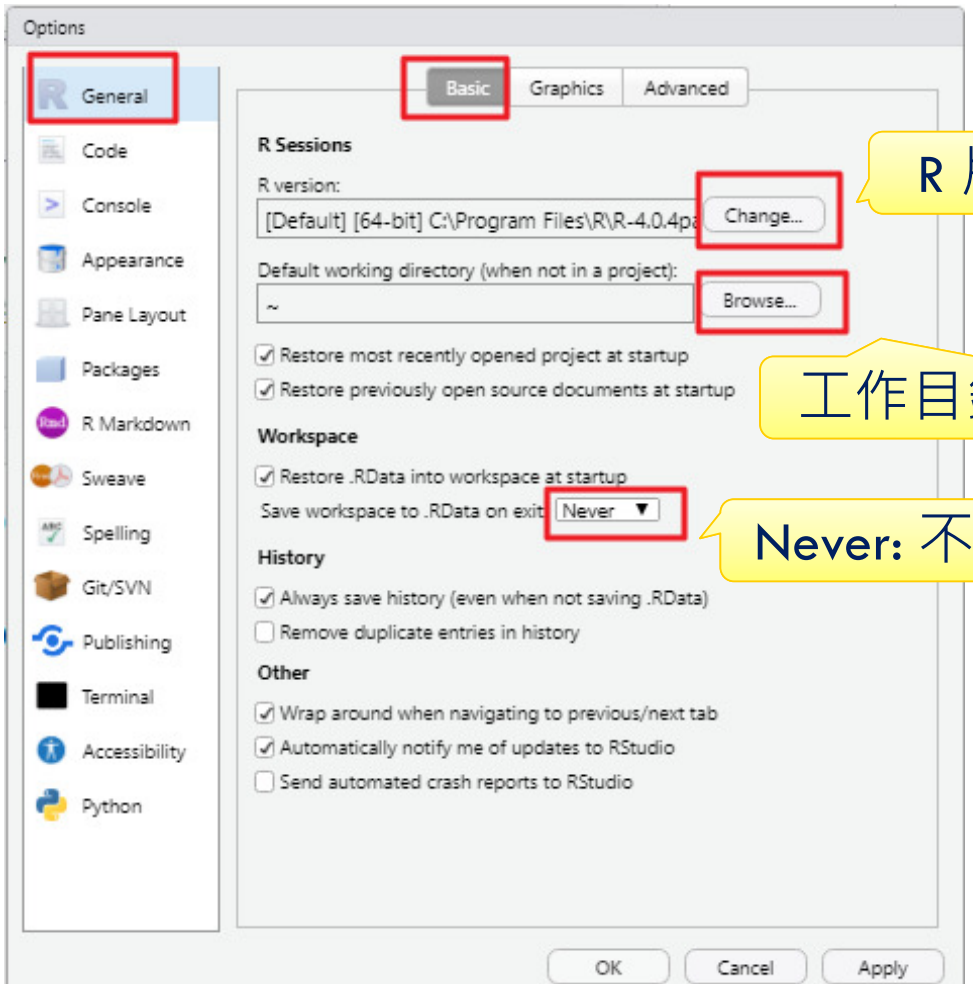


RStudio - 選項設定

- Tools \ Global Options



General \ Basic

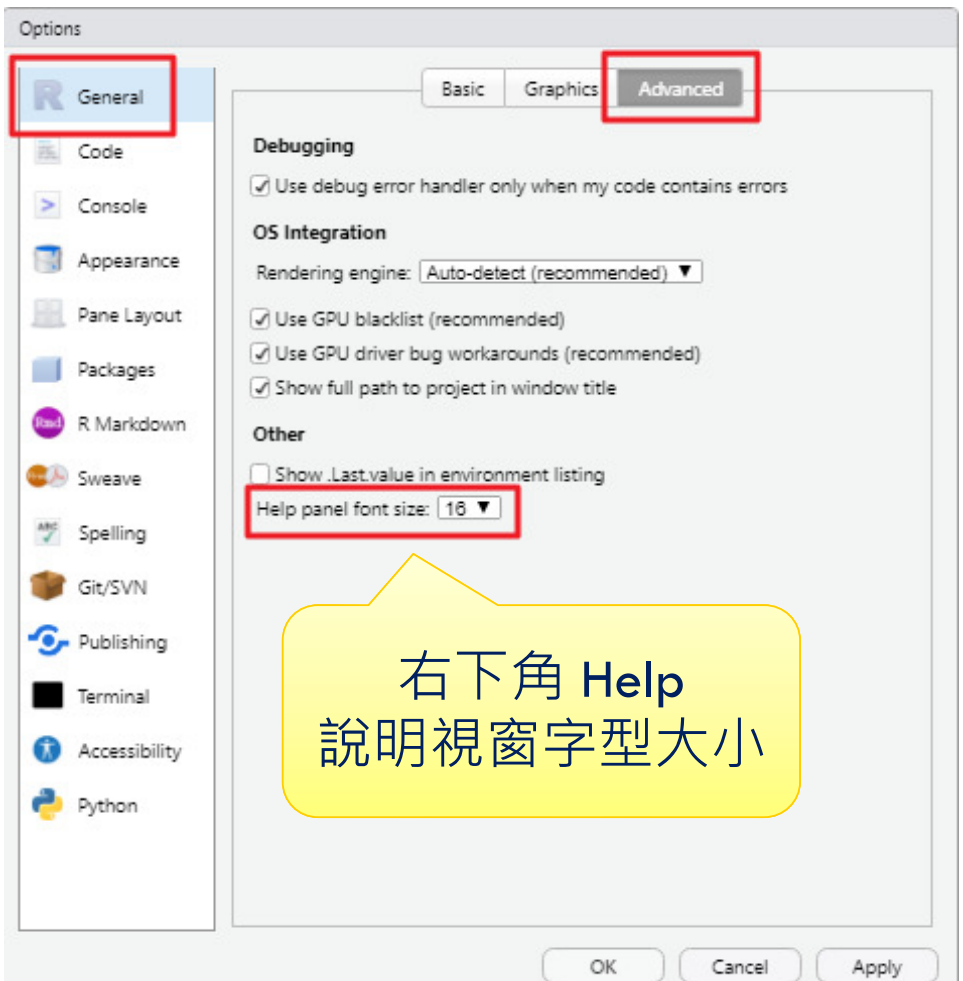


R 版本

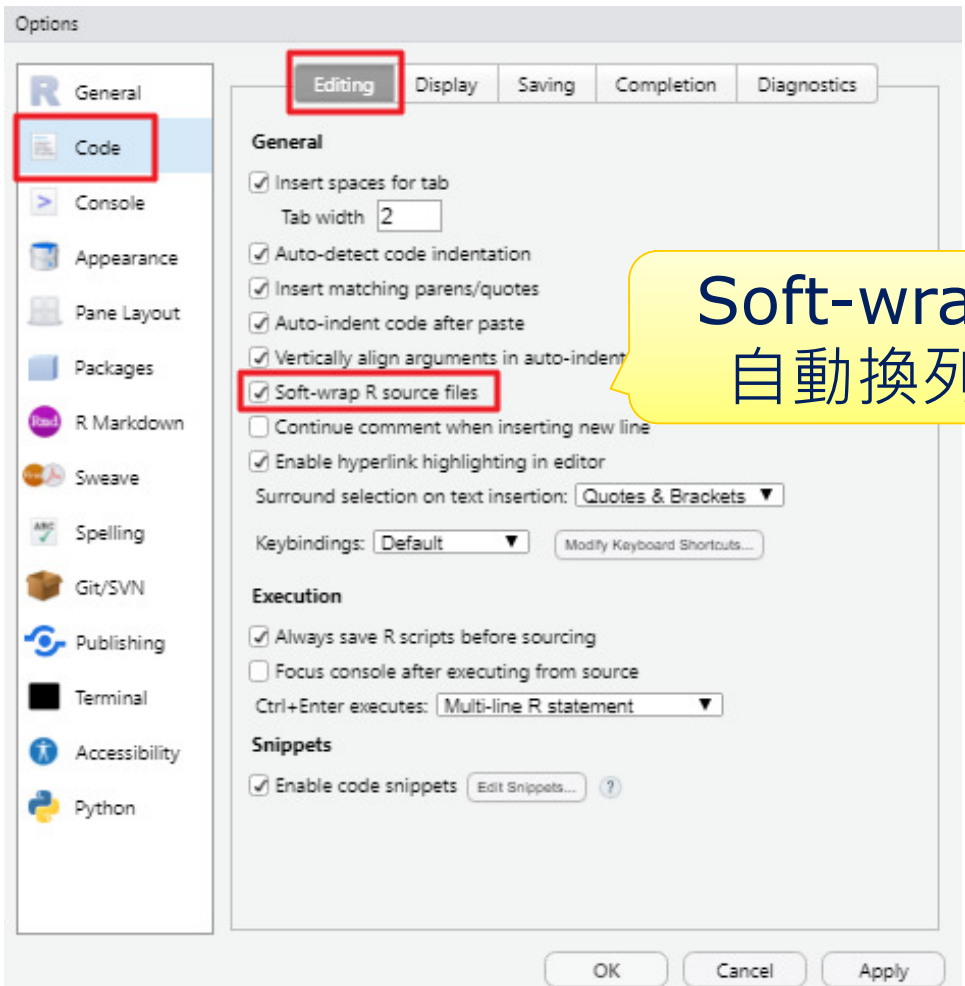
工作目錄 C:/rdata

Never: 不用儲存RData

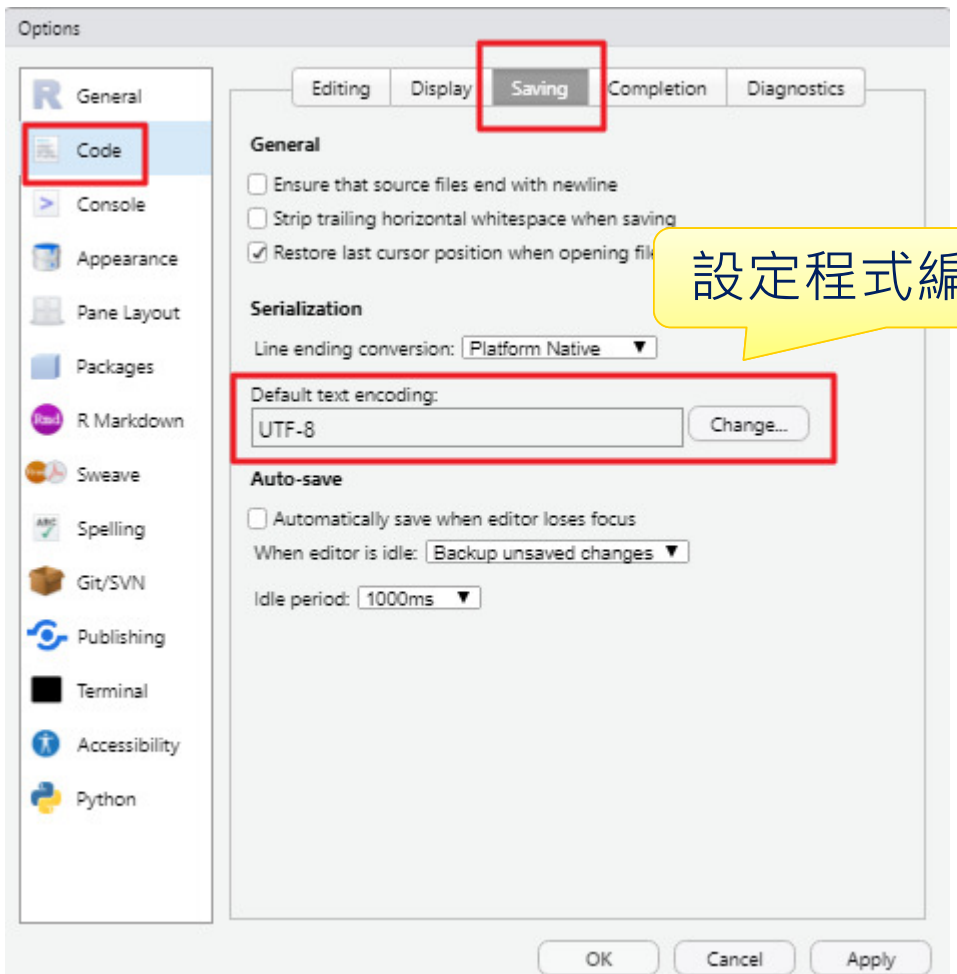
General \ Advanced



Code \ Editing



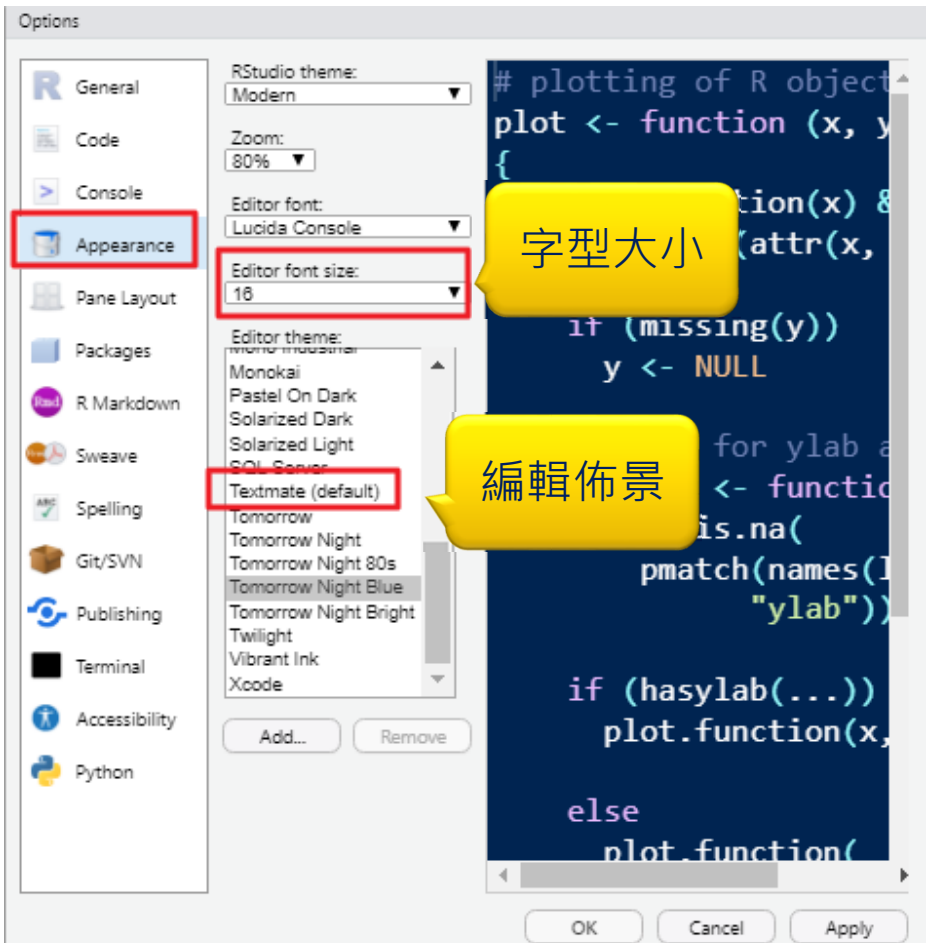
Code \ Saving


Options
General
Code
Console
Appearance
Pane Layout
Packages
R Markdown
Sweave
Spelling
Git/SVN
Publishing
Terminal
Accessibility
Python
Editing
Display
Saving
Completion
Diagnostics
General
Ensure that source files end with newline
Strip trailing horizontal whitespace when saving
Restore last cursor position when opening fil
Serialization
Line ending conversion: Platform Native
Default text encoding:
UTF-8
Change...
Auto-save
Automatically save when editor loses focus
When editor is idle: Backup unsaved changes
Idle period: 1000ms
OK
Cancel
Apply
設定程式編碼 UTF-8

RStudio-選項設定(續)

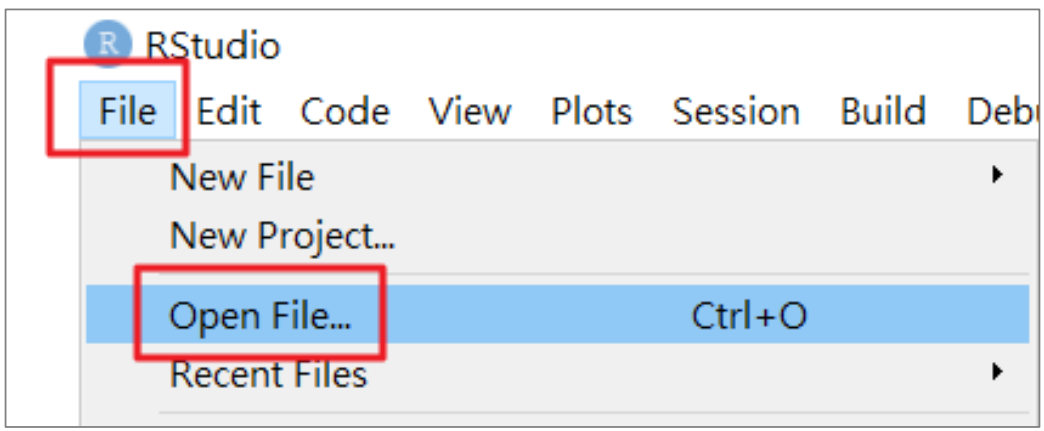
- Appearance \ Editor theme
- 預設值: TextMate

設定完成,須重新啟動RStudio



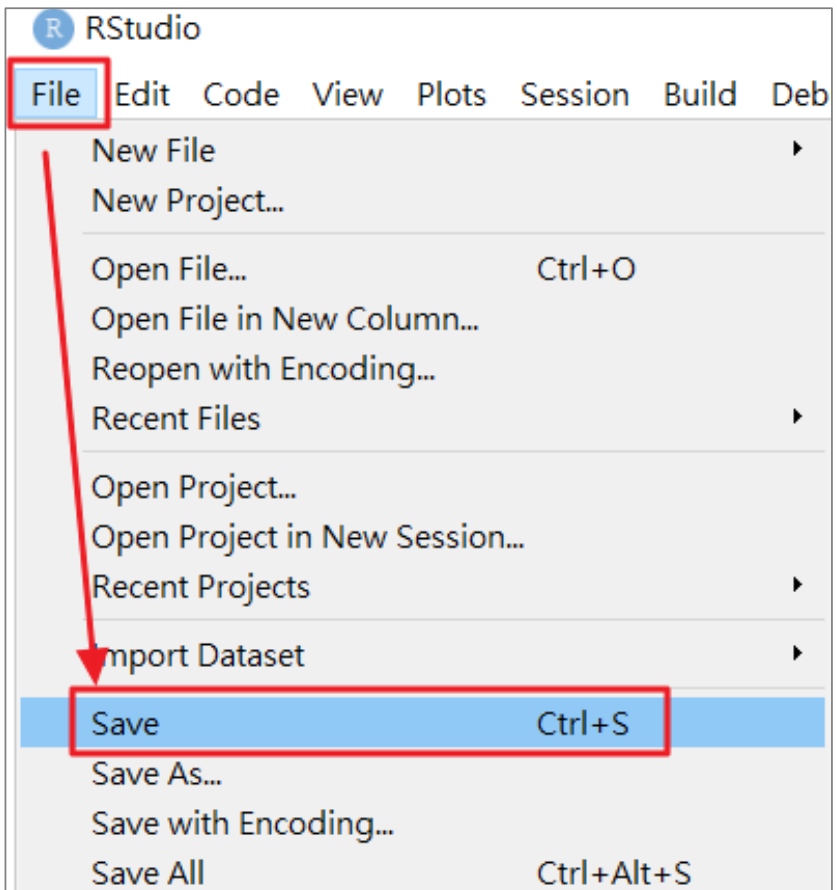
開啟檔案

- File \ Open File

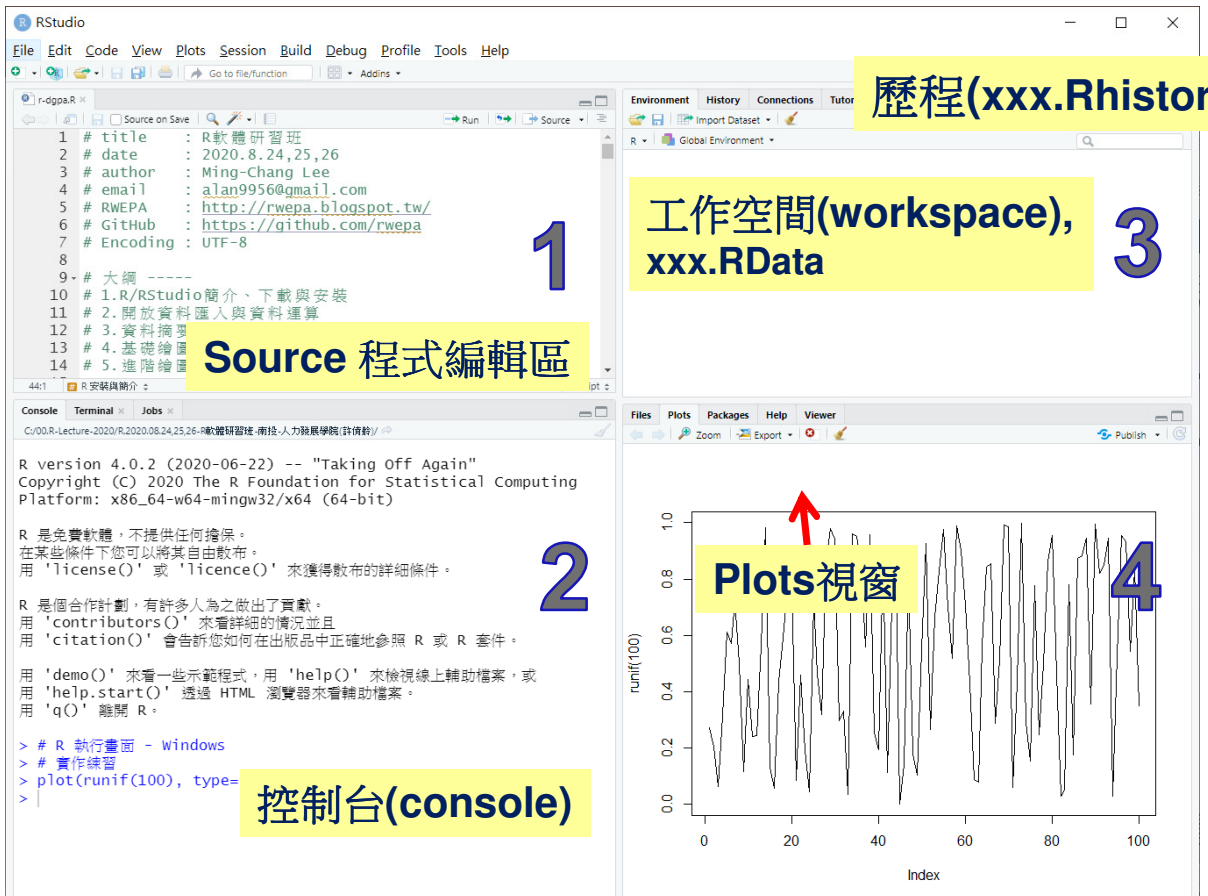


儲存檔案

- File \ Save (CTRL + S)
- 檔名: xxx.R



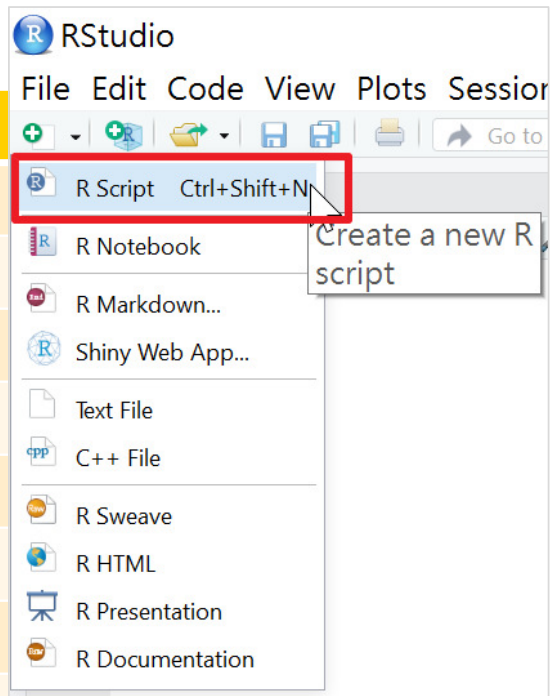
R/RStudio環境的基礎觀念



CTRL + SHIFT + F10: 重新啟動R

RStudio 快速鍵

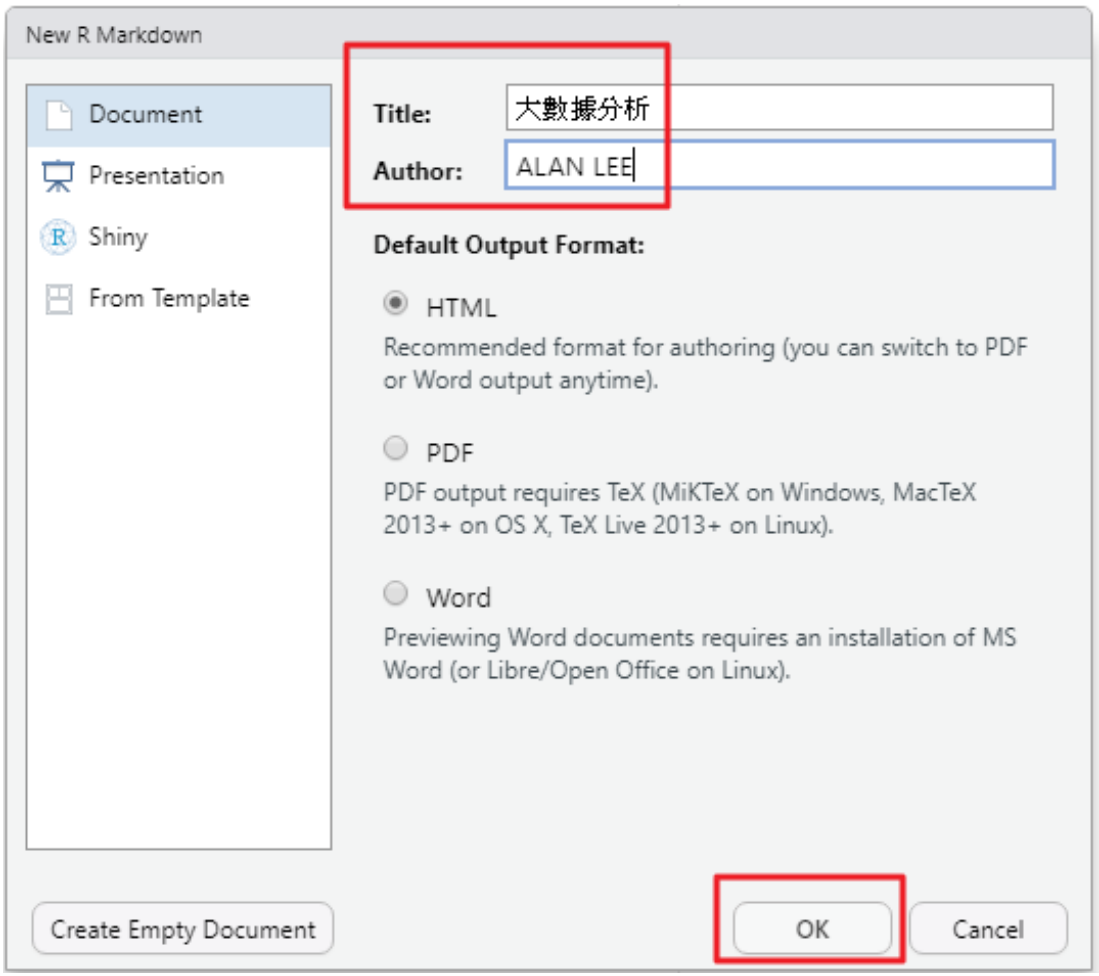
快速鍵功能	功能
Ctrl + Shift + N	建立新的R程式
Ctrl + S	儲存檔案
Ctrl + Shift + R	建立章節 (-----)
Alt + -	指派符號
Ctrl + Shift + C	註解
Ctrl + Enter	執行程式
Ctrl + Shift + F10	重新啟動R
Alt + Shift + K	快速鍵總表 (Esc 退出)



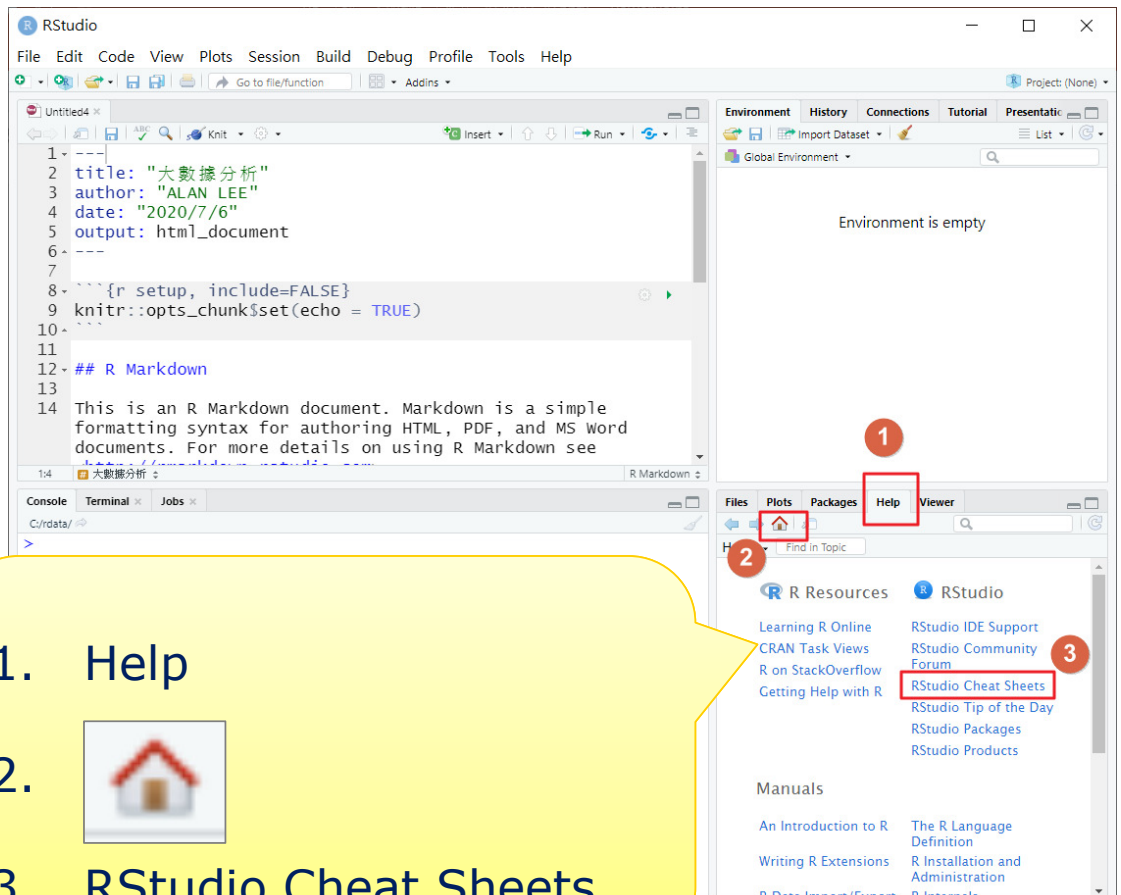
R Markdown

R標記語言

RStudio - Markdown



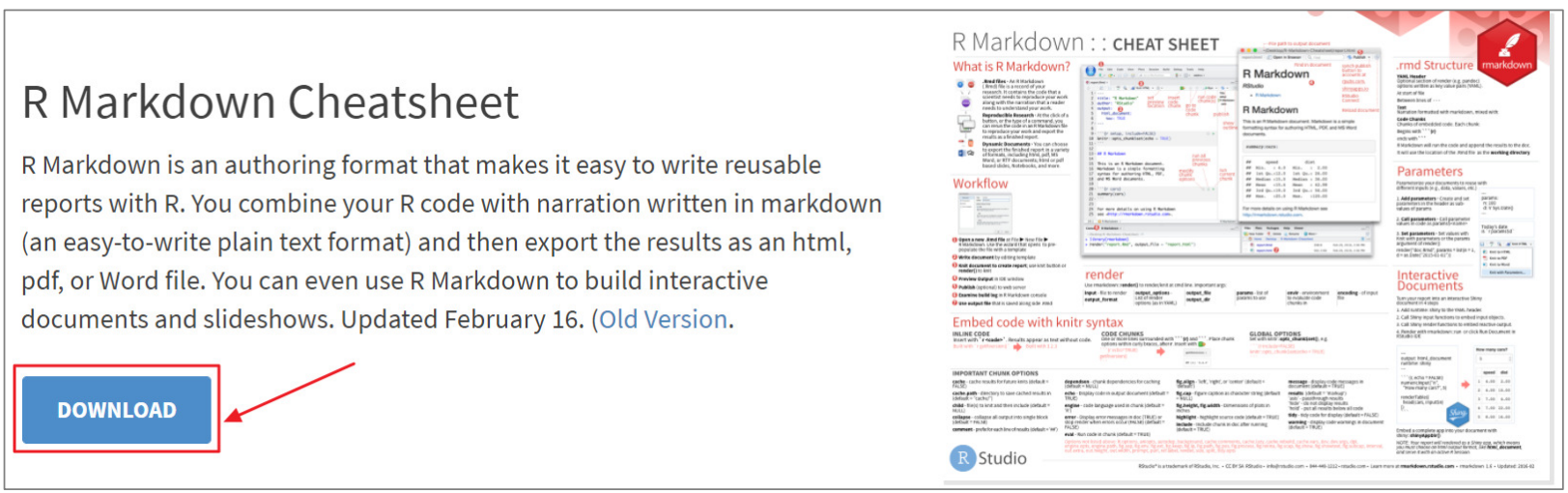
RStudio - Markdown (續)



1. Help
2.
3. RStudio Cheat Sheets

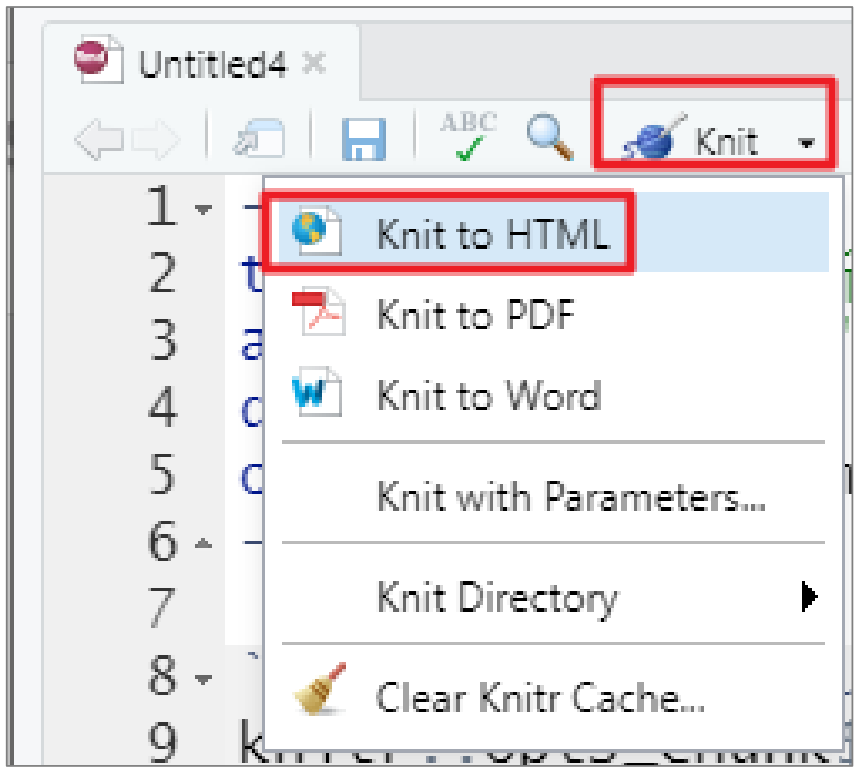
R Markdown Cheatsheet 線上說明

- https://www.rstudio.com/resources/cheatsheets/

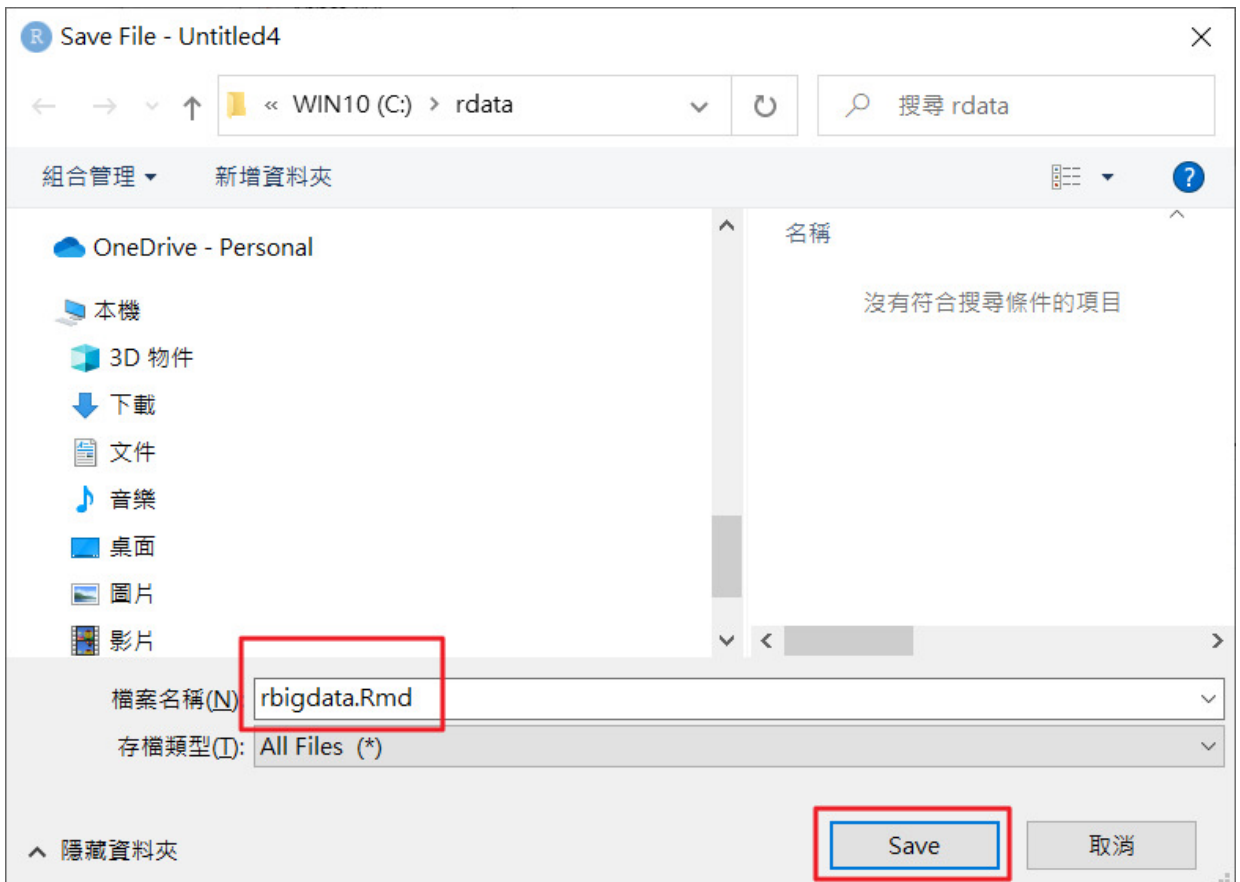


RStudio - Markdown (續)

- Knit HTML
- Knit PDF
- Knit Word



RStudio - Markdown (續)

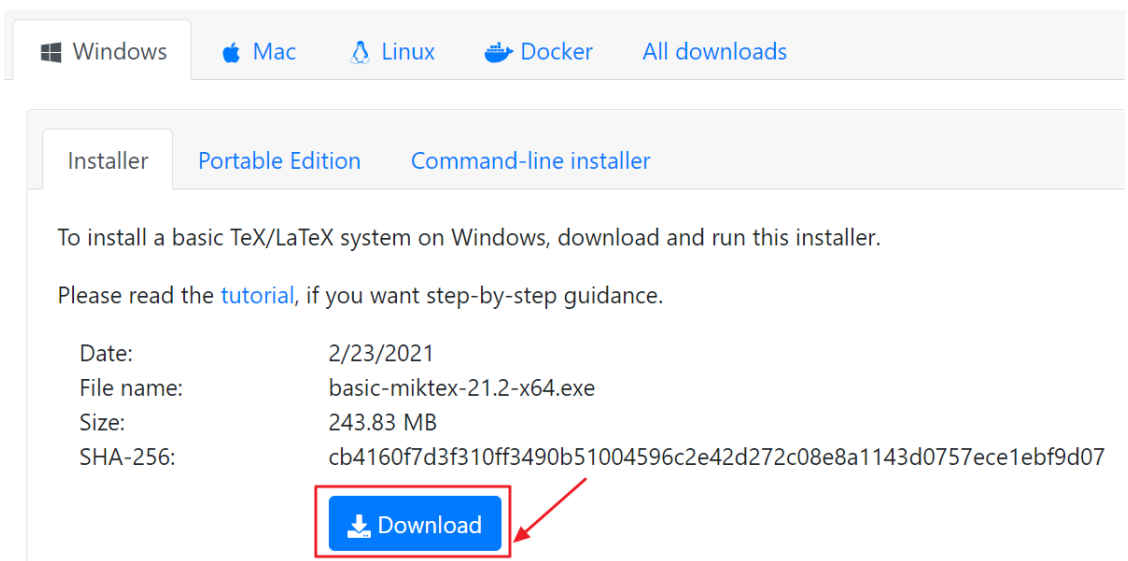


Knit to HTML

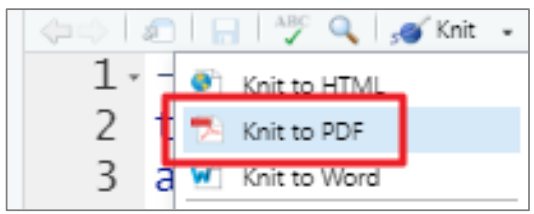

大數據分析
檔案 | C:/rdata/rbigdata.html
輸出HTML
大數據分析
ALAN LEE
2020/7/6
R Markdown
R程式碼
summary(cars)
報表
Including Plots
You can also embed plots, for example:
圖形
pressure

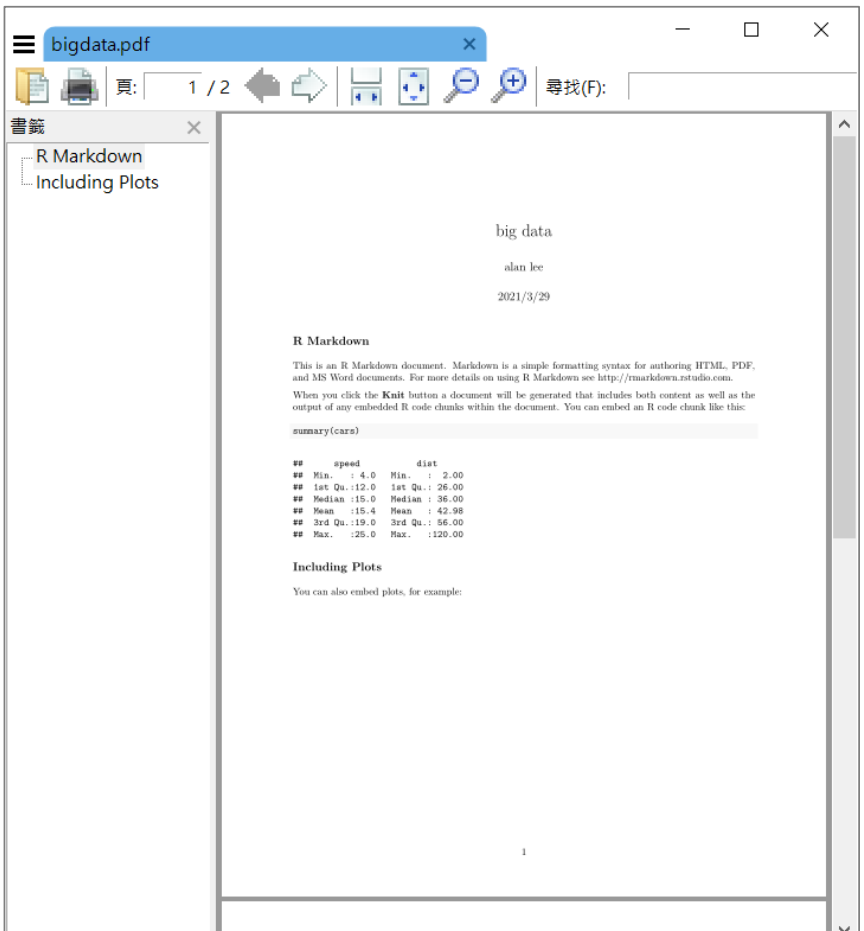
RStudio - Markdown : PDF

- 下載 Miktex: https://miktex.org/download
- basic-miktex-21.2-x64.exe (243.83MB)

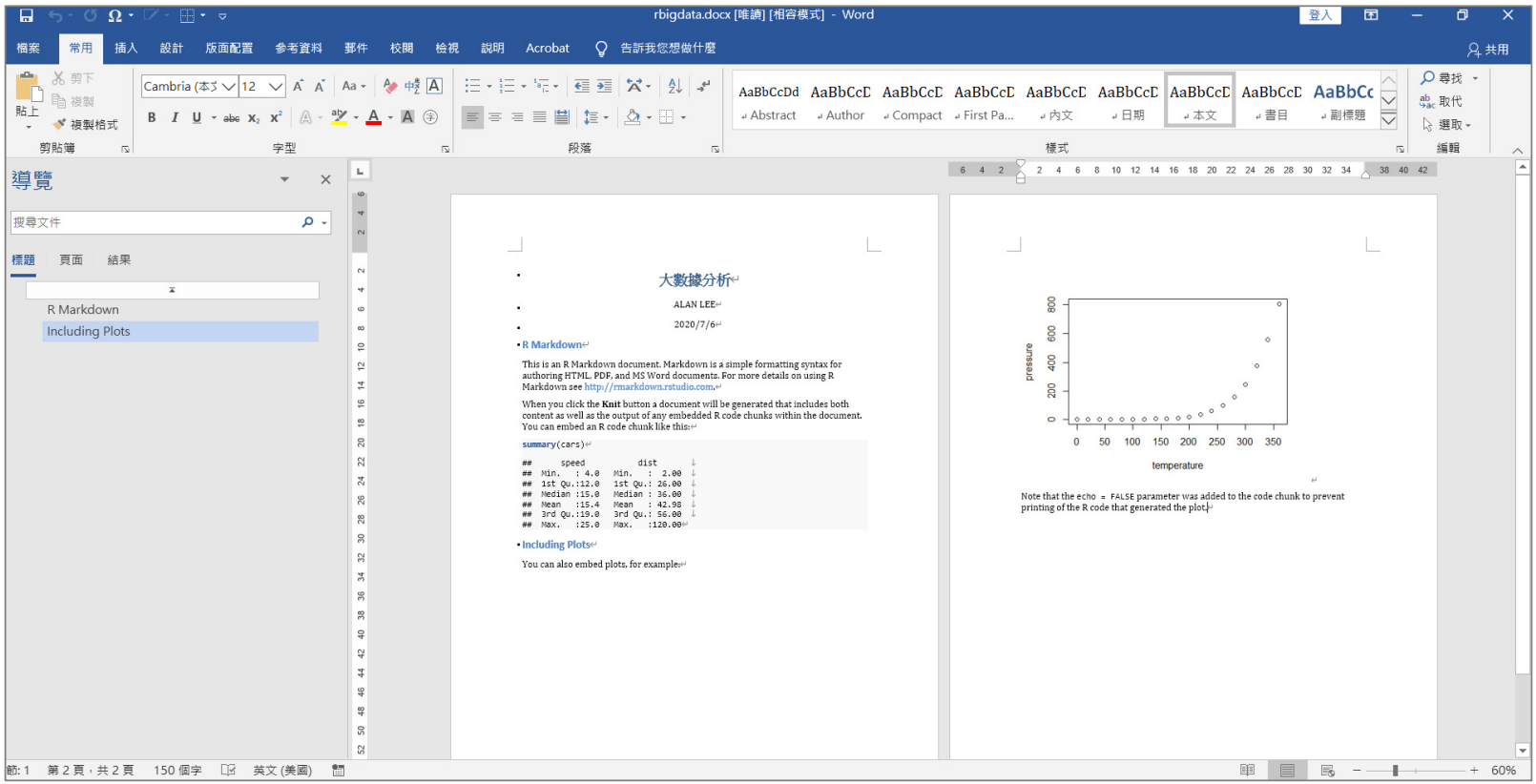


Knit to PDF


Knit
Knit to HTML
Knit to PDF
Knit to Word


bigdata.pdf
頁: 1 / 2
尋找(F):
書籤
R Markdown
Including Plots
big data
alan lee
2021/3/29
R Markdown
This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.
When you click the Knit button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:
summary(cars)
speed dist
Min. : 4.0 Min. : 2.00
1st Qu.:12.0 1st Qu.: 26.00
Median :15.0 Median : 36.00
Mean :15.4 Mean : 42.98
3rd Qu.:19.0 3rd Qu.: 56.00
Max. :25.0 Max. :120.00
Including Plots
You can also embed plots, for example:
1

RStudio - Markdown : Word



R學習

- http://rwepa.blogspot.com/

工作目錄

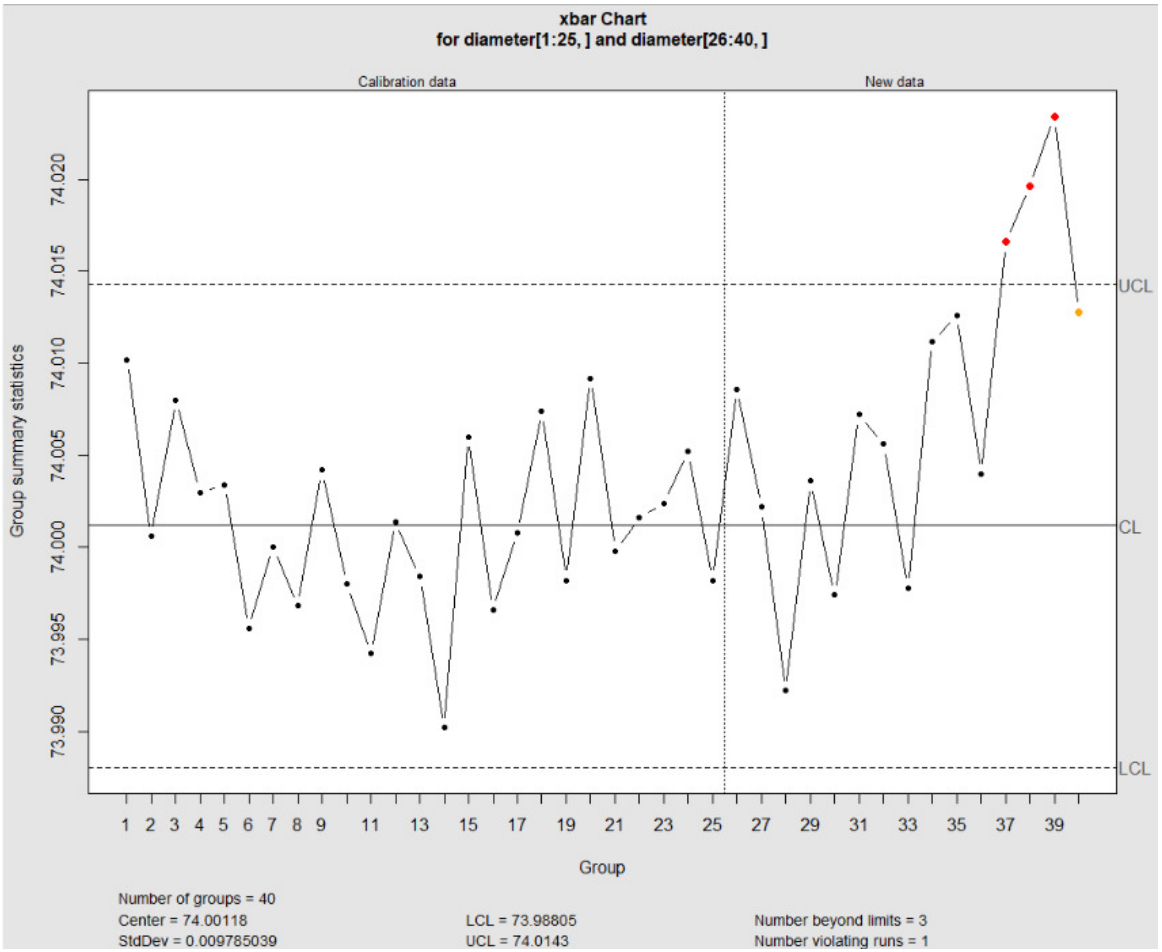
```
> # 取得工作目錄
> getwd()
[1] "C:/Users/88697/Documents"
>
> # 設定工作目錄
> # 先建立 C:/rdata 資料夾
> setwd("C:/rdata")
>
> getwd()
[1] "C:/rdata"
>
```

qcc: Quality Control Charts

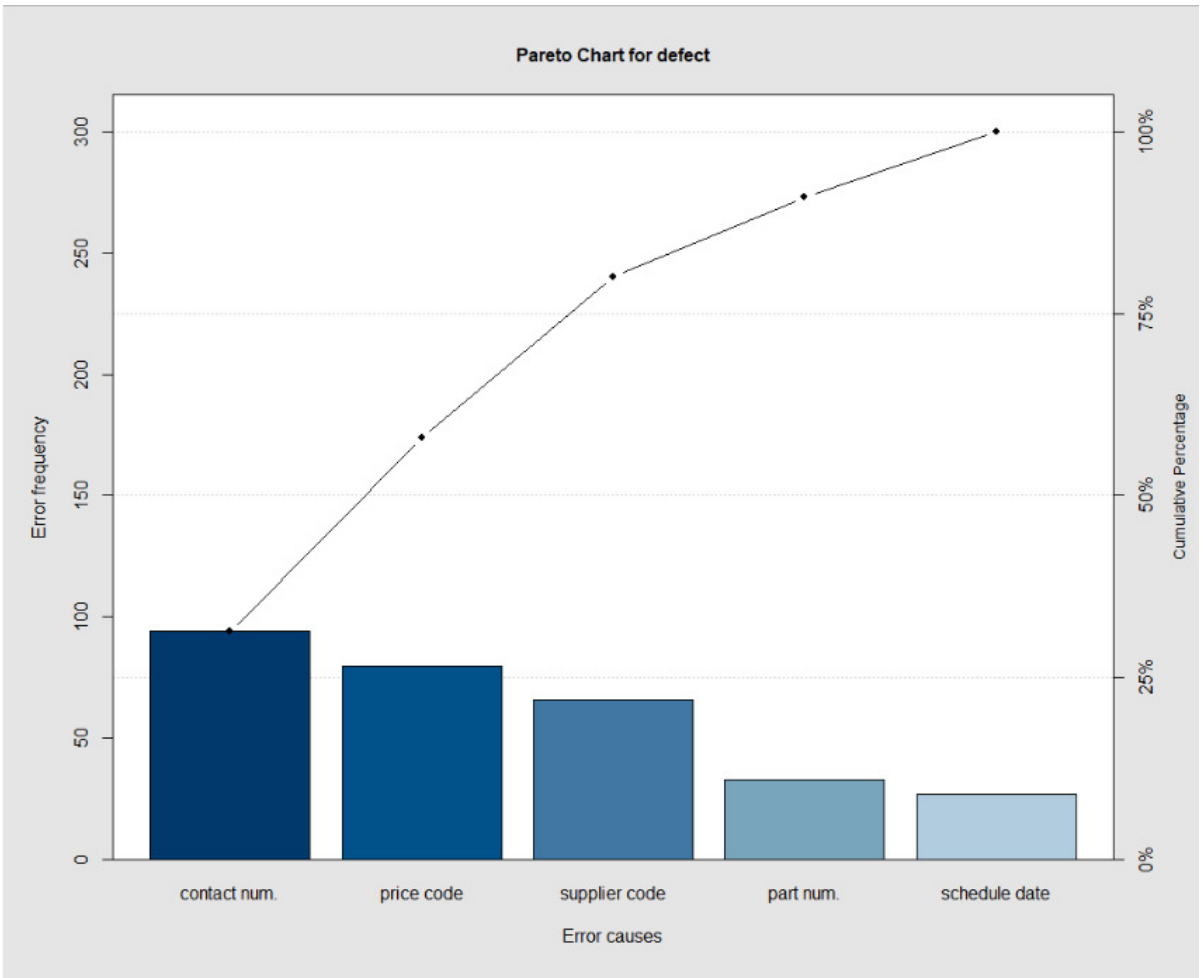
- https://cran.r-project.org/web/packages/qcc/index.html

```
> # qcc package
> # https://cran.r-project.org/web/packages/qcc/index.html
>
> library(qcc)
  __ _  ___ ___
 / _  |/ __/ __|  Quality Control Charts and
| (_| | (_| (__   Statistical Process Control
 \__  |\___\___|
    |_|           version 2.7
Type 'citation("qcc")' for citing this R package in publications.
>
> # x-bar chart
> data(pistonrings)
> diameter = with(pistonrings, qcc.groups(diameter, sample))
> head(diameter)
    [,1]   [,2]   [,3]   [,4]   [,5]
1 74.030 74.002 74.019 73.992 74.008
2 73.995 73.992 74.001 74.011 74.004
3 73.988 74.024 74.021 74.005 74.002
4 74.002 73.996 73.993 74.015 74.009
5 73.992 74.007 74.015 73.989 74.014
6 74.009 73.994 73.997 73.985 73.993
> qcc(diameter[1:25,], type="xbar", newdata=diameter[26:40,])
List of 15
 $ call        : language qcc(data = diameter[1:25, ], type = "xbar", newdata = diameter[26:40, ])
 $ type        : chr "xbar"
 $ data.name   : chr "diameter[1:25, ]"
 $ data        : num [1:25, 1:5] 74 74 74 74 74 ...
  ..- attr(*, "dimnames")=List of 2
 $ statistics  : Named num [1:25] 74 74 74 74 74 ...
  ..- attr(*, "names")= chr [1:25] "1" "2" "3" "4" ...
```

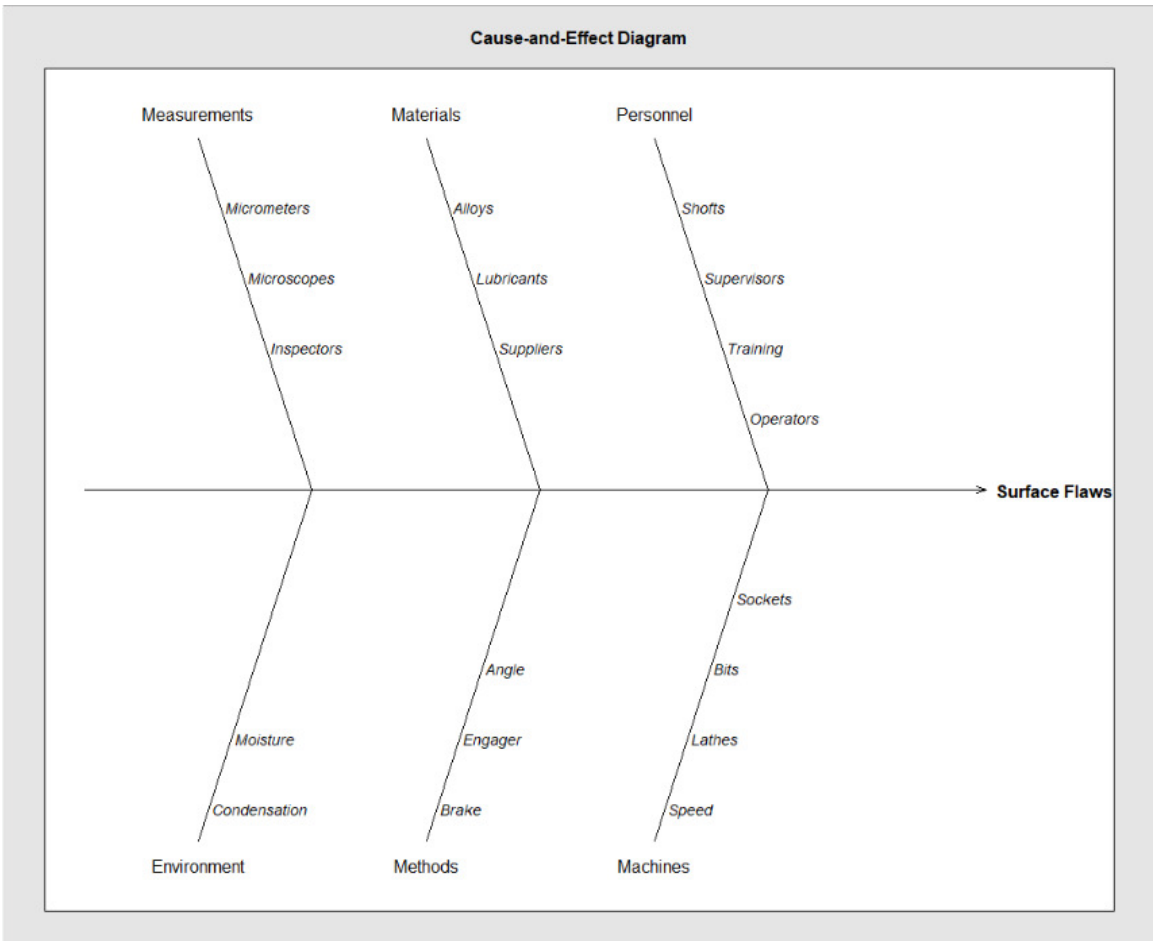
$\bar{x}$ chart (平均值管製圖)



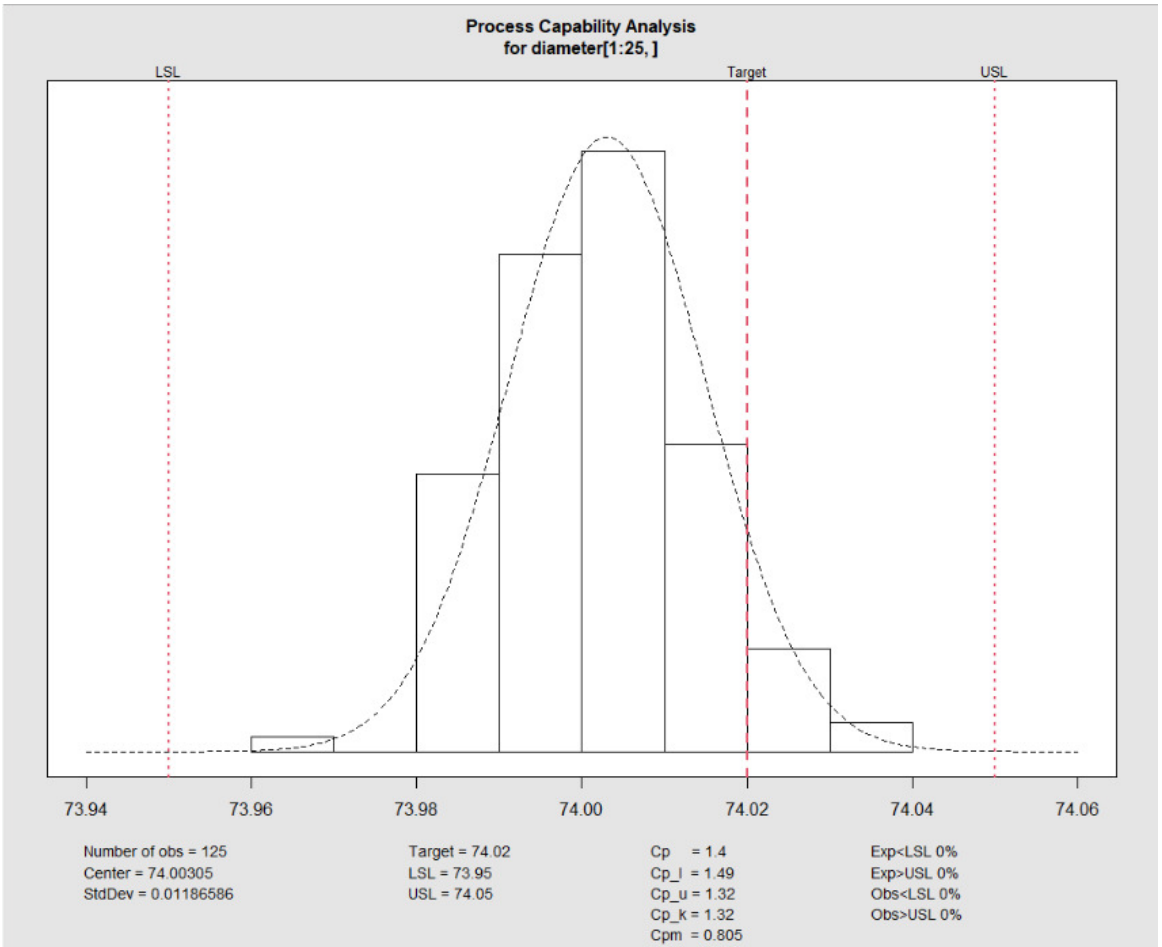
Pareto chart (柏拉圖)



Cause and effect diagram (要因分析圖)
魚骨圖(Fishbone Diagram), 石川圖(Iskiawa Diagram)

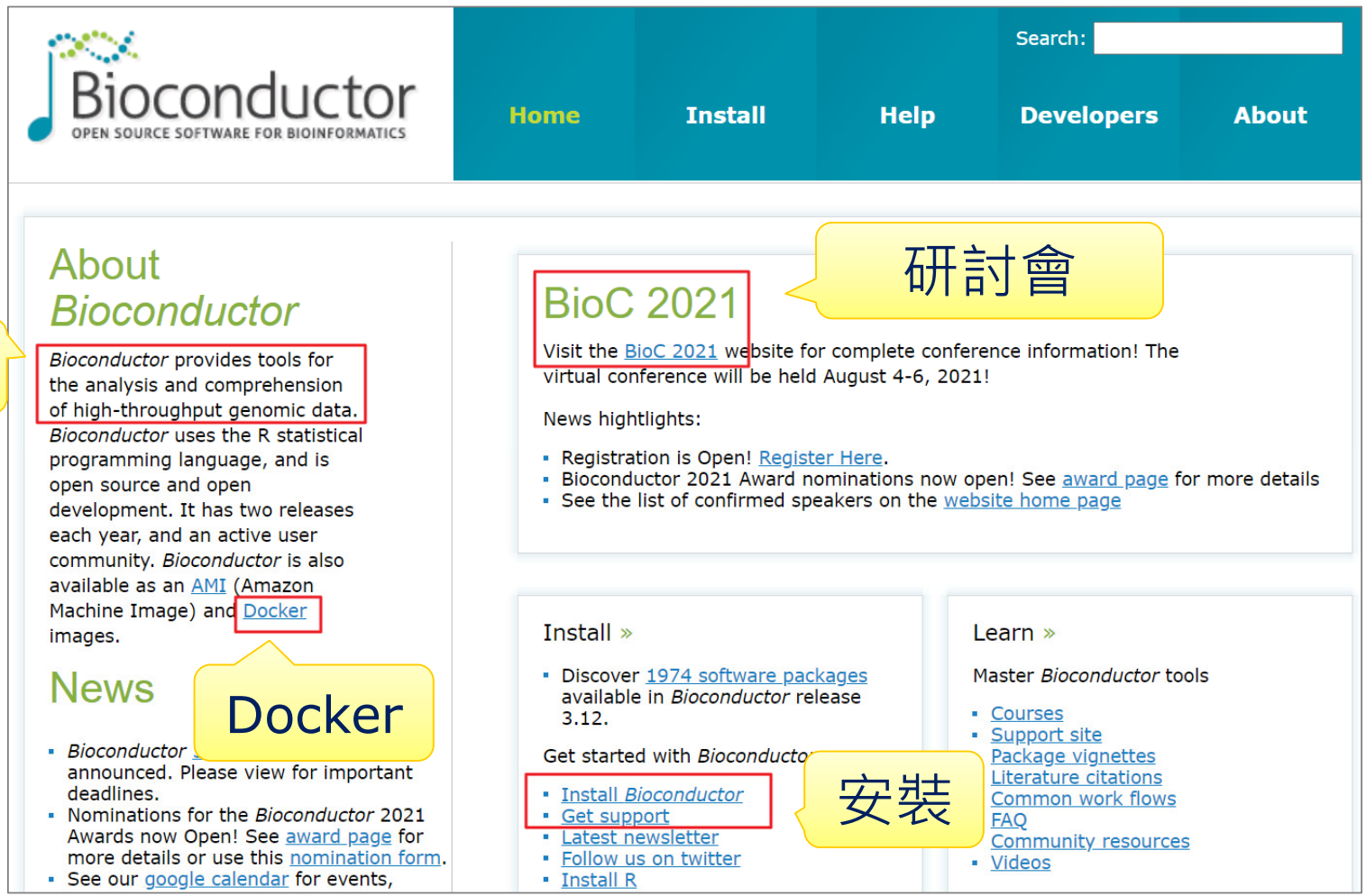


process capability index (製程能力 Cp)



2.Bioconductor實務應用

https://www.bioconductor.org/



安裝 Bioconductor 基礎套件

```
# 安裝 Bioconductor 基礎套件
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")

BiocManager::install(version = "3.12")
```

Common work flows

Bioconductor version 3.12 (Release)

Autocomplete biocViews search:

- Software (1975)
- AnnotationData (971)
- ExperimentData (398)
- Workflow (28)
  - AnnotationWorkflow (3)
  - BasicWorkflow (5)
  - EpigeneticsWorkflow (4)
  - GeneExpressionWorkflow (11)
  - GenomicVariantsWorkflow (2)
  - ImmunoOncologyWorkflow (14)
  - ProteomicsWorkflow (2)
  - ResourceQueryingWorkflow (2)
  - SingleCellWorkflow (2)

Packages found under Workflow:

Rank based on number of downloads: lower numbers are more frequently downloaded.

Show All entries Search table:

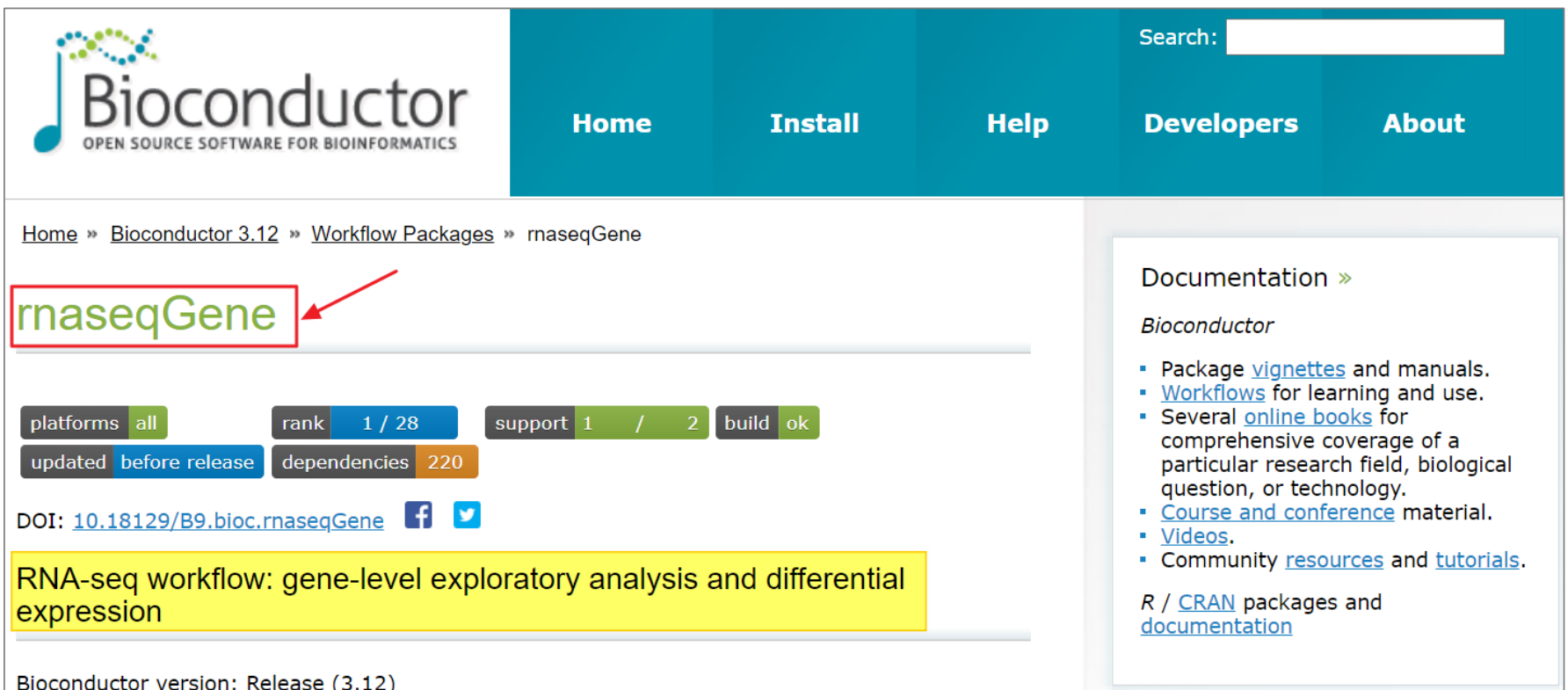
Package	Maintainer	Title	Rank
rnaseqGene	Michael Love	RNA-seq workflow: gene-level exploratory analysis and differential expression	1
liftOver	Bioconductor Package Maintainer	Changing genomic coordinate systems with rtracklayer::liftOver	2
RNAseq123	Matthew Ritchie	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR	3
TCGAWorkflow	go edraoui Silva	TCGA Workflow Analyze cancer genomics and epigenomics data using Bioconductor packages	4
methylationArrayAnalysis	Jovana Maksimovic	A cross-package Bioconductor workflow for analysing methylation array data	5

第1名

含中文說明

rnaseqGene 套件

- https://bioconductor.org/packages/release/workflows/html/rnaseqGene.html



rnaseqGene 套件 - 功能

- 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 aligned to the reference genome, and prepare a count matrix which tallies the number of RNA-seq reads/fragments within each gene for each sample.
- 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.

FASTA 檔案

NC_001477.fasta

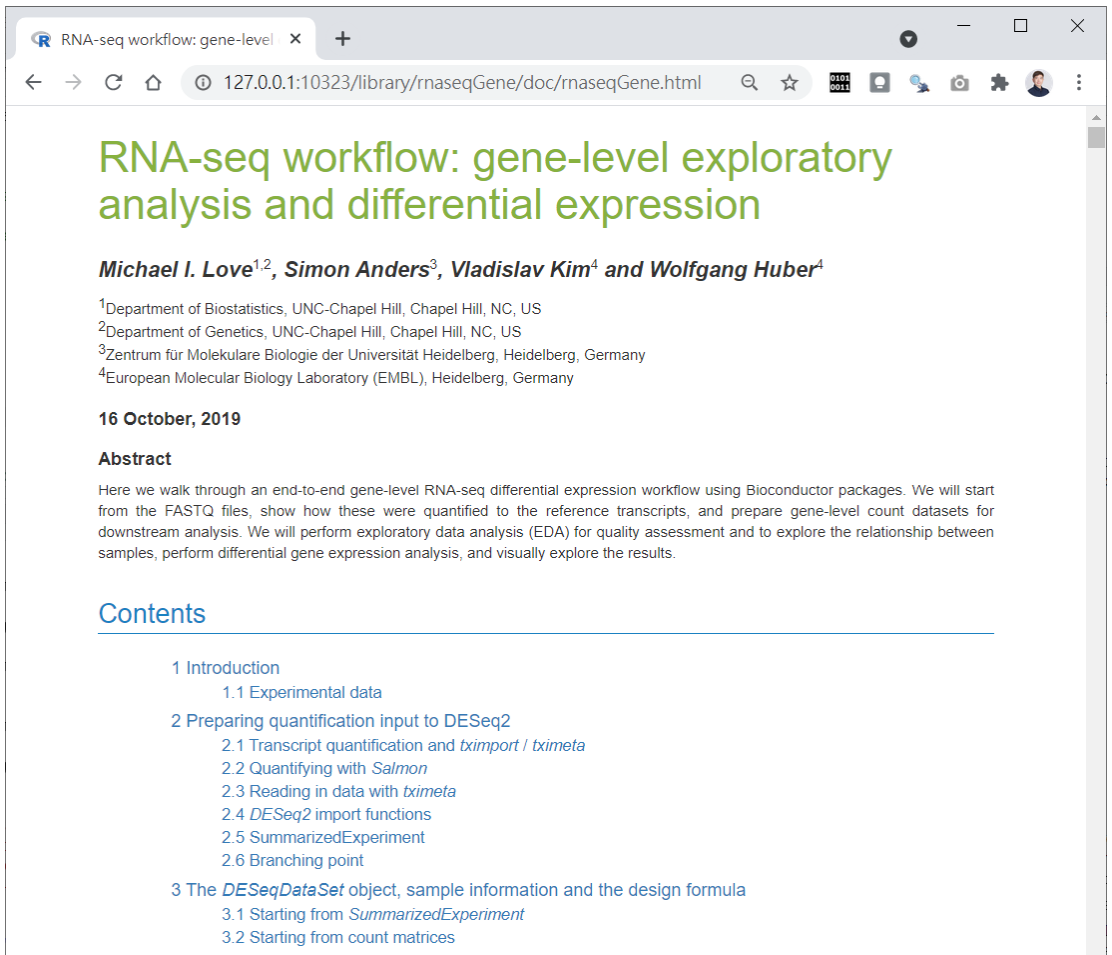
```
>NC_001477.1 Dengue virus 1, complete genome
AGTTGTTAGTCTACGTGGACCGACAAGAACAGTTTCGAATCGGAAGCTTGCTTAACGTAGTTCTAACAGT
TTTTTATTAGAGAGCAGATCTCTGATGAACAACCAACGGAAAAAGACGGGTCGACCGTCTTTCAATATGC
TGAAACGCGCGAGAAACCGCGTGTCAACTGTTTCACAGTTGGCGAAGAGATTCTCAAAAGGATTGCTTTC
AGGCCAAGGACCCATGAAATTGGTGATGGCTTTTATAGCATTCCTAAGATTTCTAGCCATACCTCCAACA
GCAGGAATTTTGGCTAGATGGGGCTCATTCAAGAAGAATGGAGCGATCAAAGTGTTACGGGGTTTCAAGA
AAGAAATCTCAAACATGTTGAACATAATGAACAGGAGGAAAAGATCTGTGACCATGCTCCTCATGCTGCT
```

安裝 rnaseqGene 套件

```
> BiocManager::install("rnaseqGene")
'getOption("repos")' replaces Bioconductor standard repositories, see '?repositories' for details

replacement repositories:
    CRAN: https://cran.rstudio.com/

Bioconductor version 3.12 (BiocManager 1.30.12), R 4.0.5 (2021-03-31)
Installing package(s) 'rnaseqGene'
also installing the dependencies ‘fs’, ‘sass’, ‘jquerylib’, ‘backports’, ‘httpuv’, ‘sourcetools’, ‘later’, ‘p
ap’, ‘commonmark’, ‘bslib’, ‘htmlwidgets’, ‘crosstalk’, ‘formatR’, ‘checkmate’, ‘rstudioapi’, ‘cpp11’, ‘sys’
ime’, ‘stringi’, ‘lazyeval’, ‘assertthat’, ‘shiny’, ‘DT’, ‘cli’, ‘utf8’, ‘lambda.r’, ‘futile.options’, ‘numD
x’, ‘mvtnorm’, ‘colorspace’, ‘bit’, ‘cachem’, ‘Formula’, ‘data.table’, ‘htmlTable’, ‘viridis’, ‘forcats’, ‘r
 ‘hms’, ‘prettyunits’, ‘askpass’, ‘htmltools’, ‘xfun’, ‘tinytex’, ‘evaluate’, ‘highr’, ‘markdown’, ‘stringr’
```

rnaseqGene 套件 - 線上說明

```
# 線上說明
browseVignettes("rnaseqGene")
```



3.品質控制技術

品質控制

- 在實驗或陣列中獲得的資料的質量對於資料分析和正確解釋微陣列資料是重要環結之一。
- 單個或幾個異常資料都可能破壞大型數據集的分析結果。在首先確保數據質量可以接受之前，不應進行分析。
- 如果樣品在收集後未立即正確處理，則RNA易於快速降解（degradation）而影響分析結果。
- 若樣品的品質不合格最直接影響的就是產出的資料量不足或是導致資料豐富度不夠而無法呈現最真實的分析結果。

qcmetrics 套件

- https://www.bioconductor.org/packages/release/bioc/html/qcmetrics.html

qcmetrics 套件 demo

```
> # qcmetrics套件
> # https://www.bioconductor.org/packages/release/bioc/html/qcmetrics.html
>
> # BiocManager::install("qcmetrics")
> library("qcmetrics")
>
> # 建立 QcMetric 物件
> qc <- QcMetric(name = "A test metric")
> class(qc)
[1] "QcMetric"
attr(,"package")
[1] "qcmetrics"
> qc
Object of class "QcMetric"
 Name: A test metric
 Status: NA
 Data: empty
>
> # qcdata: 實際儲存資料
> qcdata(qc, "x") <- rnorm(100)
> qcdata(qc) ## all available qcdata
[1] "x"
```

函數 show

```
> qc
Object of class "QcMetric"
 Name: A test metric
 Status: NA
 Data: x
> show(qc)
Object of class "QcMetric"
 Name: A test metric
 Status: NA
 Data: x
> summary(qcdata(qc, "x"))
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-3.13692 -0.65860 -0.04072  0.01924  0.68710  2.44919
> # status: 狀態屬性 {TRUE, FALSE}
> status(qc) <- TRUE
> qc
Object of class "QcMetric"
 Name: A test metric
 Status: TRUE
 Data: x
>
```

函數 boxplot

```
> # 預設繪圖有錯誤
> plot(qc)
Warning message:
In x@plot(x, ...) : No specific plot function defined
> # 新增繪圖方法
> plot(qc) <- function(object, ... ) boxplot(qcdata(object, "x"), ...)
>
> # 繪製盒鬚圖
> plot(qc, main = "qcmetrics繪圖")
```

1 2

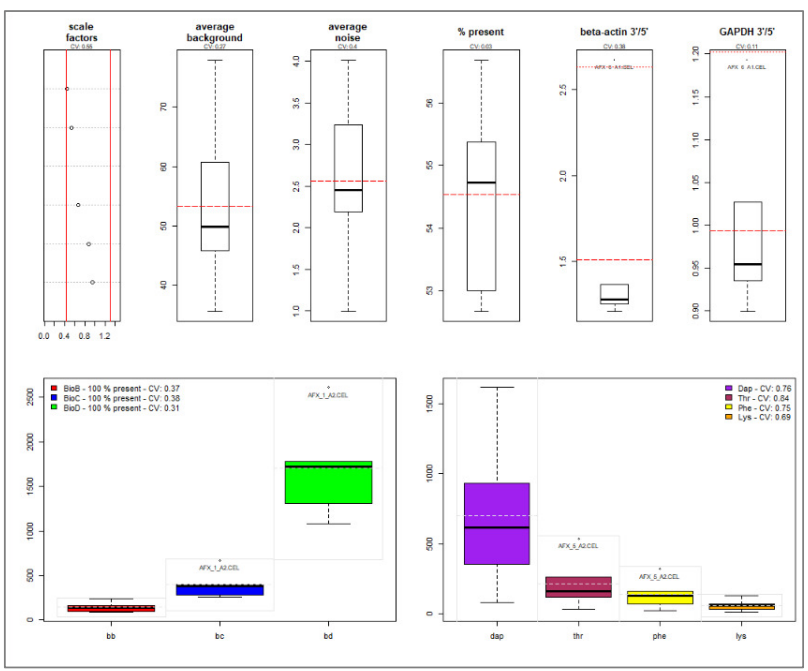
Metadata 元資料

```
> # 建立元資料 metadata
> metadata(qcm) <- list(author = "李明昌(ALAN LEE)",
+                       lab = "Big array lab")
> qcm
Object of class "QcMetrics"
 containing 1 QC metrics.
 and 2 metadata variables.
> mdata(qcm)
$author
[1] "李明昌(ALAN LEE)"

$lab
[1] "Big array lab"

> # 更新元資料
> metadata(qcm) <- list(author = "李明昌(ALAN LEE)",
+                       lab = "Big array lab",
+                       organization = "中華民國品質學會")
> mdata(qcm)
$author
[1] "李明昌(ALAN LEE)"

$lab
[1] "Big array lab"

$organization
[1] "中華民國品質學會"
```

函數 yaqc – 計算 YAQC統計

```
# MAQCsubsetAFX套件內建資料集 refA
# BiocManager::install("MAQCsubsetAFX")

library("MAQCsubsetAFX")
data(refA)
refA

library("affy")

# 計算 RNA degradation
deg <- AffyRNAdeg(refA)
deg

# BiocManager::install("yaqcaffy")
library("yaqcaffy")

# 計算 YAQCStats
yqc <- yaqc(refA)
show(yqc)

plot(yqc)
```

```
> refA
AffyBatch object
size of arrays=1164x1164 features (19 kb)
cdf=HG-U133_Plus_2 (54675 affyids)
number of samples=6
number of genes=54675
annotation=hgu133plus2
notes=
>
```



函數 qcReport – 建立報表

```
> # qcReport 建立報表
> qcReport(maqcm,
+          reportname = "RNA-deg",
+          type = "html",
+          author = "Ming-Chang Lee")
Report written to RNA-deg.html
>
```

file:///C:/rdata/RNA-deg.html

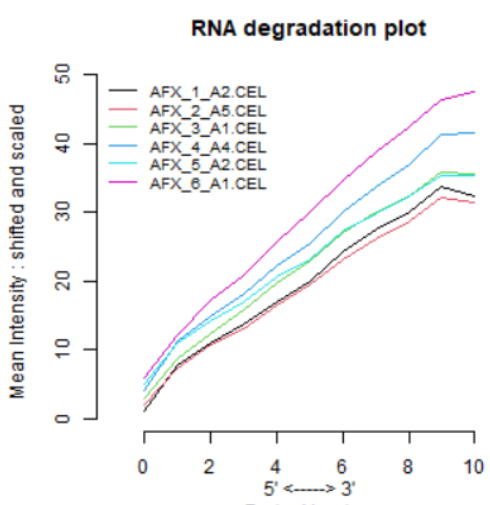
Quality control report generated with `qcmetrics`

Author: Ming-Chang Lee

Date: Thu Apr 22 21:42:36 2021

Affy RNA degradation slopes

```
## Object of class "QcMetric"
##  Name: Affy RNA degradation slopes
##  Status: TRUE
##  Data: deg
```



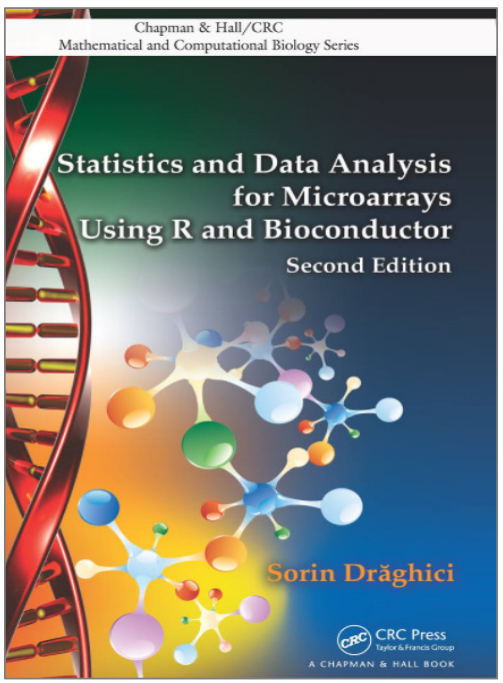
4.結論與未來展望

Recap

- R, RStudio 簡介 - qcc 套件
- Bioconductor 實務應用 - rnaseqGene 套件
- 品質控制技術 - qcmetrics 套件
- 生物資訊研究方向
  - Tallulah S. Andrews, Vladimir Yu Kiselev, Davis McCarthy & Martin Hemberg , Tutorial: guidelines for the computational analysis of *single-cell RNA sequencing data*, Nature Protocols volume 16, pages 1–9 (2021)
  - https://www.nature.com/articles/s41596-020-00409-w

參考資料

- Sorin Drăghici (2012), Statistics and Data Analysis for Microarrays: Using R and Bioconductor, Second Edition, CRC Press, 2012.
- Gatto L (2020), qcmetrics: A Framework for Quality Control. R package version 1.28.0, https://github.com/lgatto/qcmetrics.
- R教學-基礎篇(免費)
  - http://rwepa.blogspot.tw/2013/01/r-201174.html
- R入門資料分析與視覺化應用教學(付費)
  - https://courses.mastertalks.tw/courses/R-teacher
- R商業預測與應用(付費)
  - https://courses.mastertalks.tw/courses/R-2-teacher



謝謝您的聆聽

Q & A

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http://rwepa.blogspot.tw/