

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

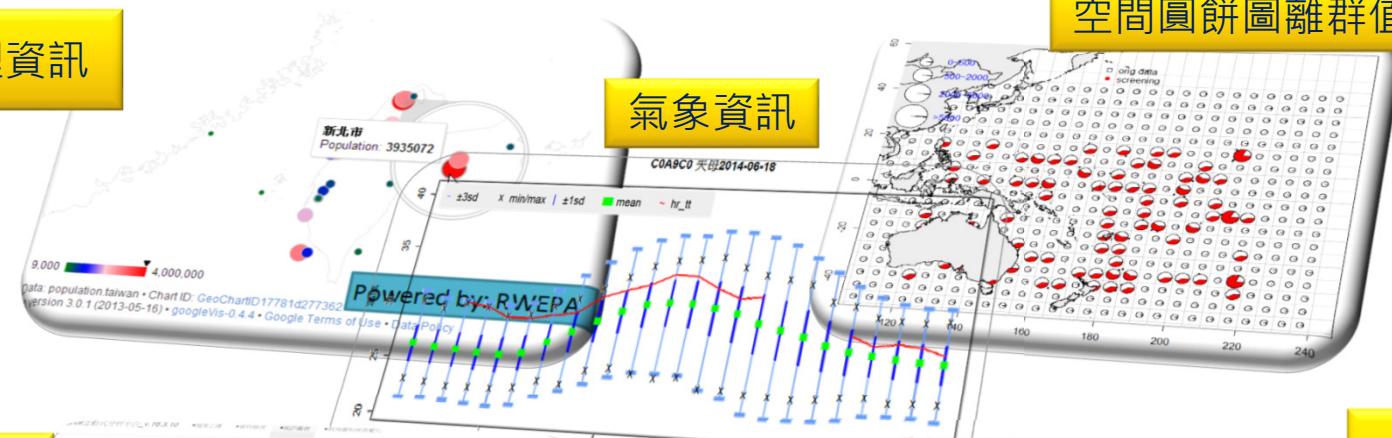
- 姓名：李明昌 (ALAN LEE)
- 現職：中華R軟體學會 常務理事
臺灣資料科學與商業應用協會 常務理事
- 學歷：中原大學 工業與系統工程所 博士
- 經歷：
 - 育達科技大學 資訊管理系(所) 專任助理教授
 - 佛光大學 兼任教師
 - 國立台北商業大學 兼任教師
 - 東吳大學 兼任教師
 - 崇友實業 行銷企劃專員
 - 國航船務代理股份有限公司 海運市場運籌管理員
- 連絡資訊：
 - RWEPA網站：<http://rwepa.blogspot.com/>
 - E-MAIL: ***alan9956@gmail.com***
 - GitHub: <https://github.com/rwepa>
 - FB: <https://www.facebook.com/rbigdata>



資料分析/視覺化成果?

R + shiny → 互動式網頁

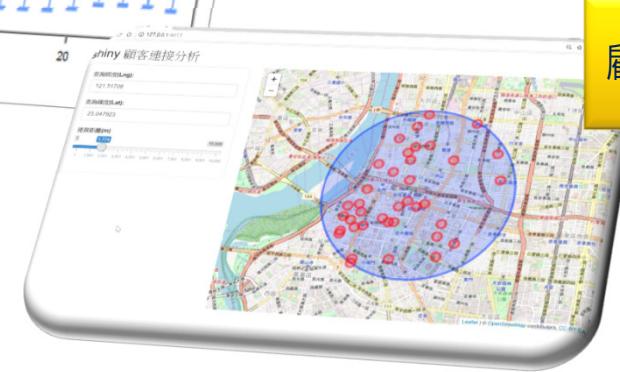
地理資訊



保險預測



顧客連結資訊



網頁呈現

中央氣象局 1,600萬筆資料



保險預測模型

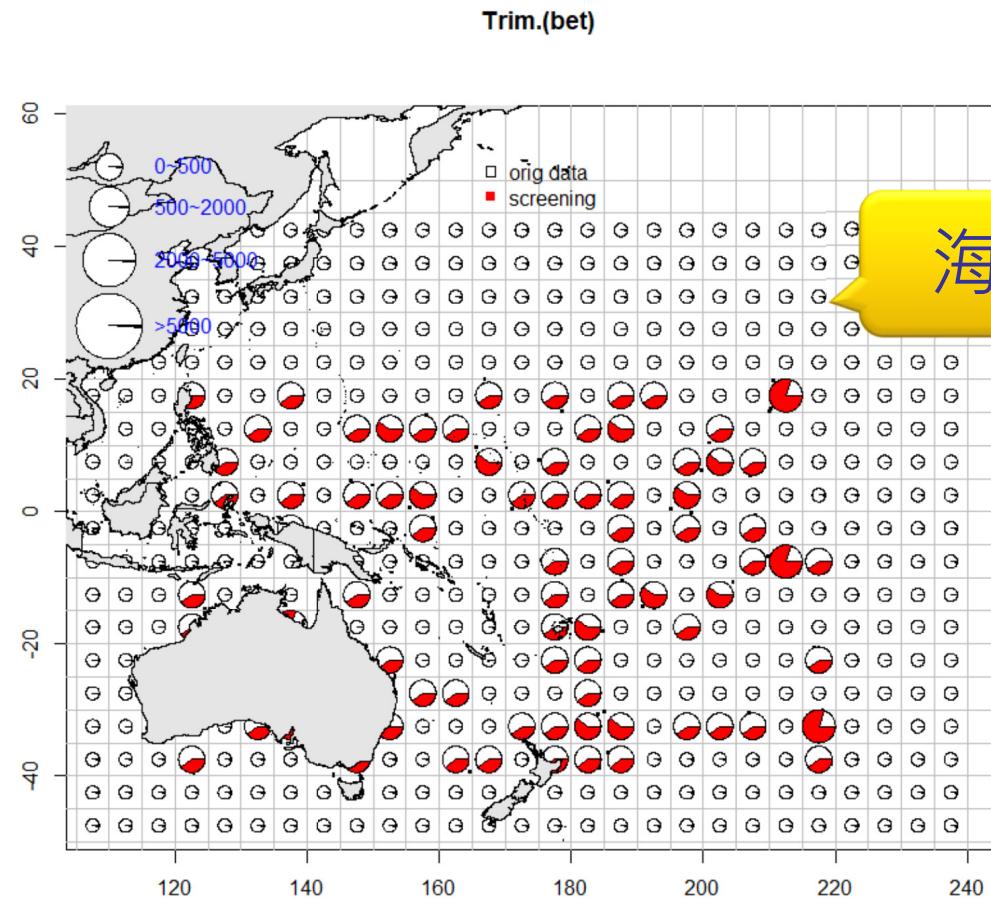
機率模型閥值調整

預測結果

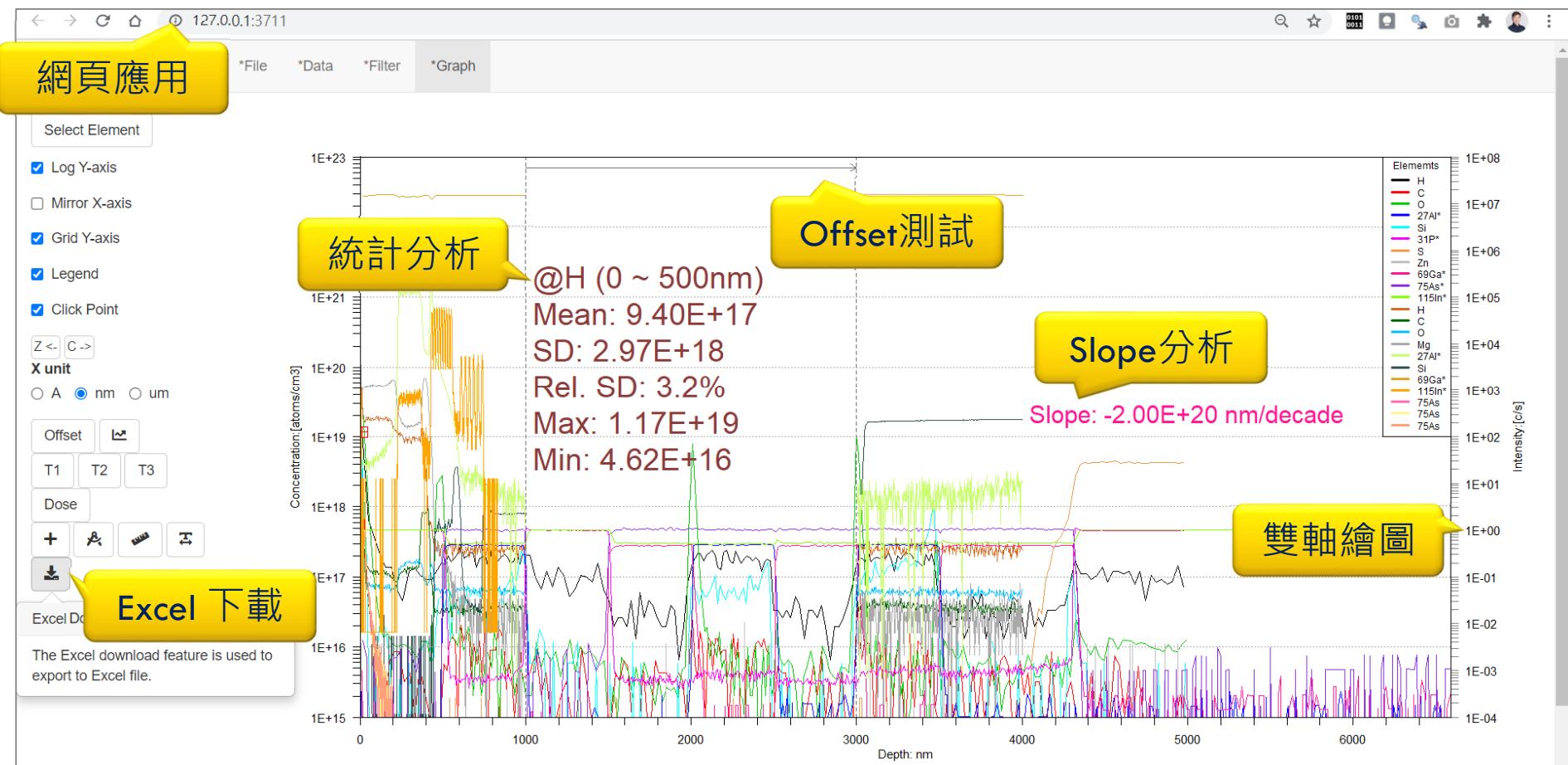
The screenshot shows the iInsurance interactive analysis platform version v.16.3.24. The top navigation bar includes links for file upload, data processing, statistical charts, model evaluation, and prediction models. A red box highlights the 'Prediction Model' dropdown. Below it, a yellow box highlights the 'Probability Model Threshold' section, which contains a slider set to 0.1 and a numerical scale from 0.01 to 1. Another red box highlights the 'View Results' button in the 'Prediction Results' panel. A large yellow callout points to the 'Prediction Results' table, which displays 10 entries of predicted probability and claim status. The table includes columns for gender, vehicle type, exposure risk, exposure risk count, discount factor, insured person age, private car age 0, private car age 1, private car age 2, private car age 0-1-2 combination, car age 0-1-2 combination, predicted probability, and claim status.

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 0_1_2 組合	預測機率	理賠		
M	0	A	1	0.9144422	-0.08944106	50	4	1	0	0	1	0	2	0.1069	有	
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

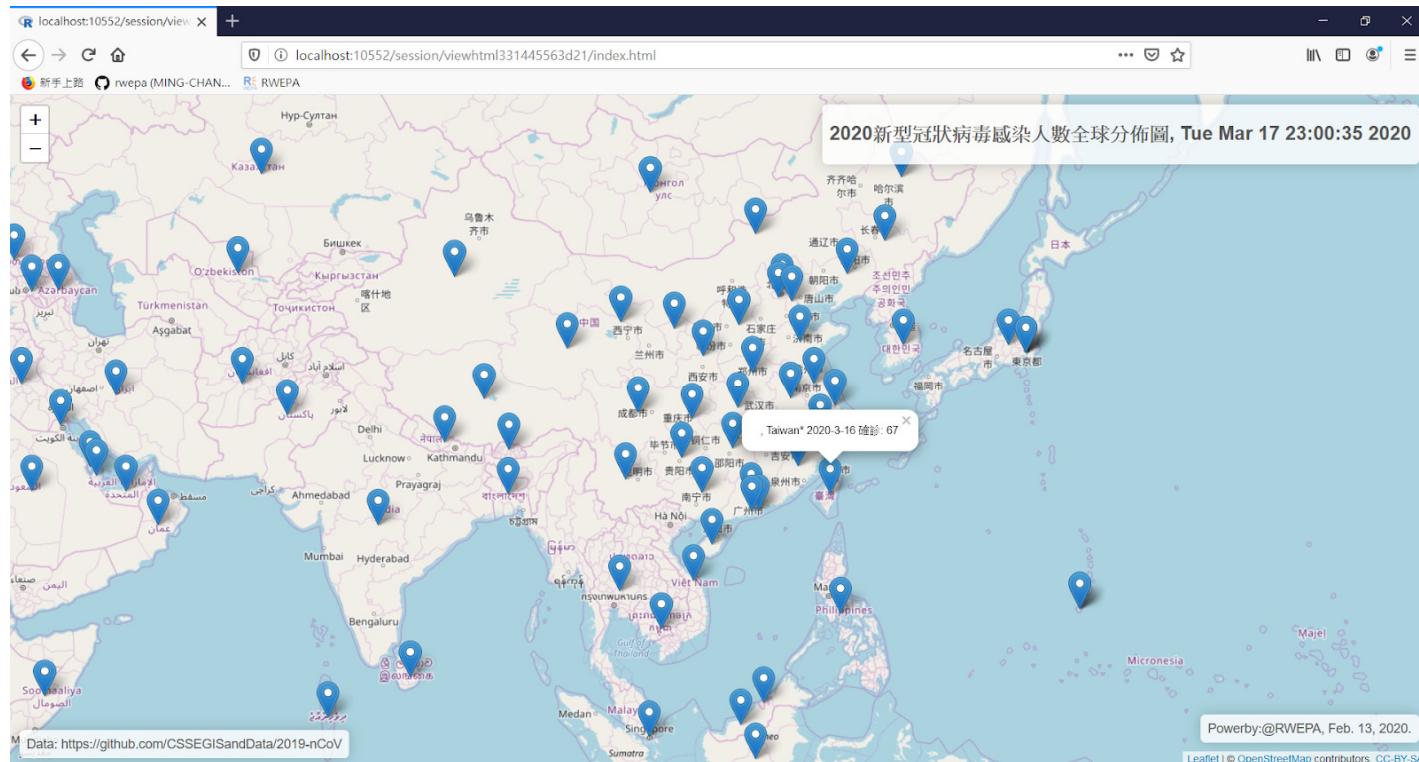
空間圓餅圖離群值分析



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 Gentleman, 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



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]



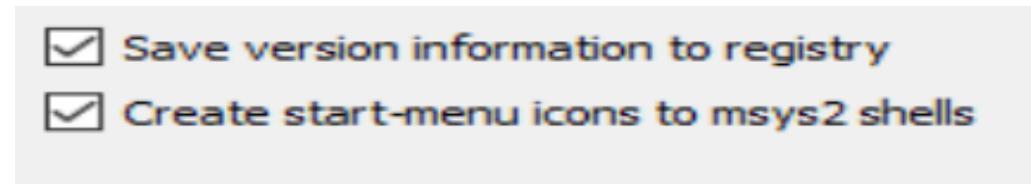
- R安裝路徑: 保留原路徑,不要修改
- https://github.com/rwepa/DataDemo/blob/master/windows_intall_R.pdf

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](#)[Project](#)[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 <i>per se</i> . That is, the objects that it works on, and the details of the expression evaluation process, which are useful to know when programming R functions.		
R Internals : a guide to the internal structures of R and coding standards 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 lately).

English Documents

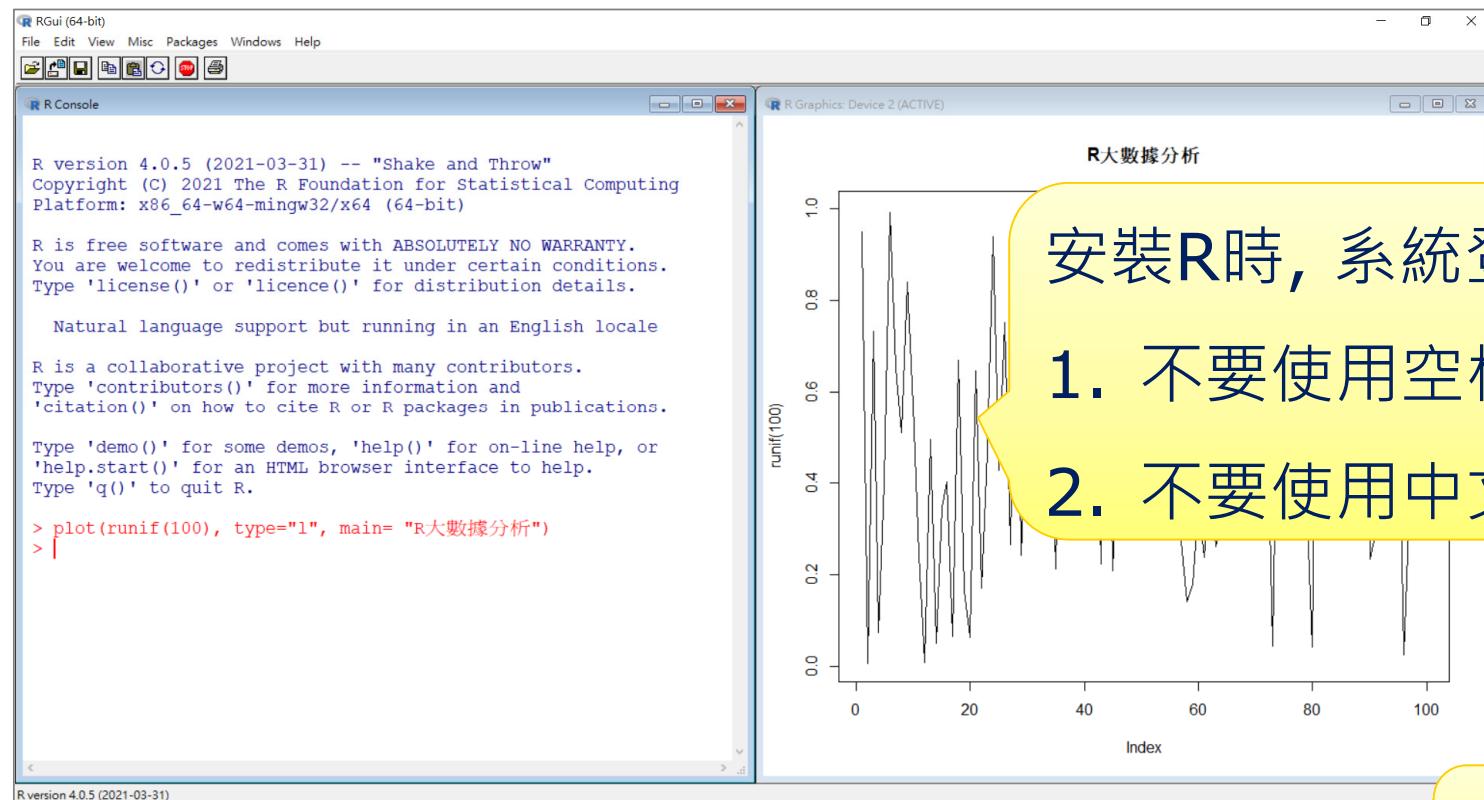
Documents with more than 100 pages:

- “**Visual Statistics. Use R!**” by Alexey Shipunov ([PDF](#), 2016-06-06, 301 pages) 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](#)).



好書!

R 執行畫面 - Windows



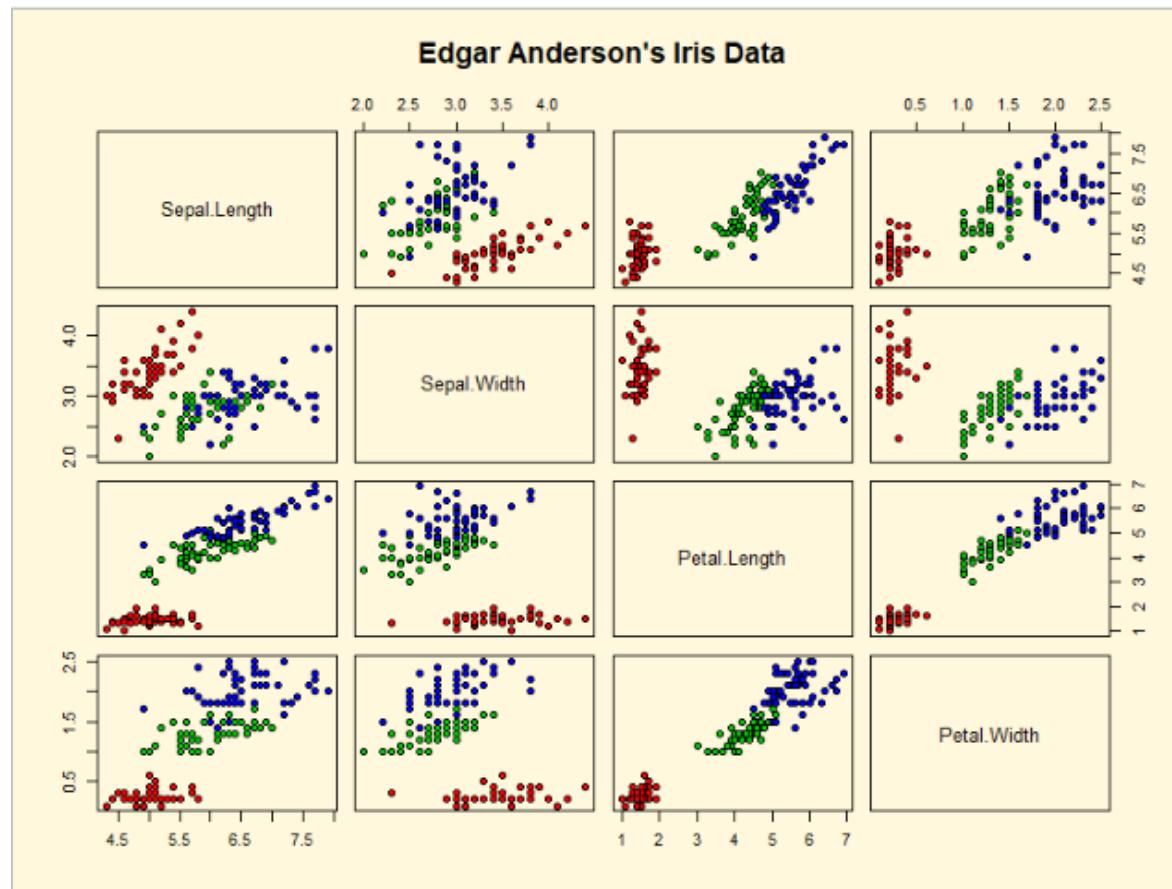
安裝R時，系統登入名稱：

1. 不要使用空格
2. 不要使用中文字

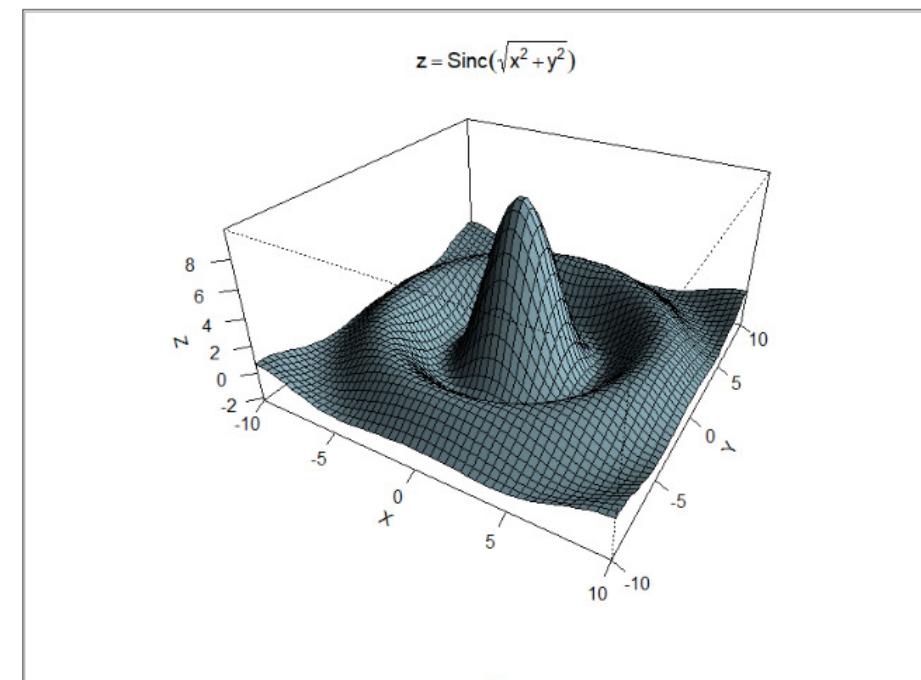
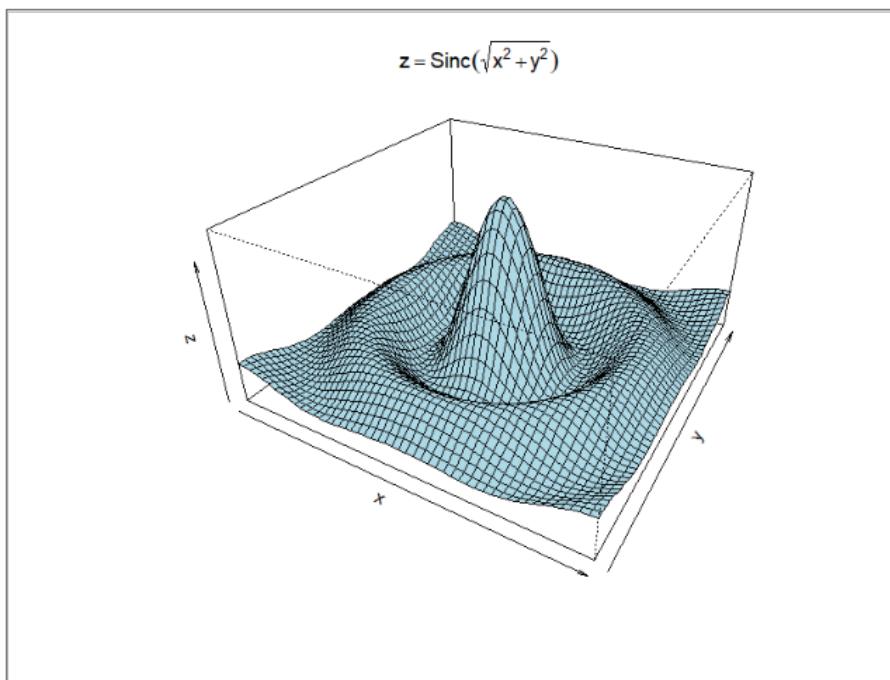
```
plot(runif(100), type="l", main= "R大數據分析")
```

大小寫
須一致

demo(graphics)



demo(persp)



R for Mac

- <https://youtu.be/72MYRBNo5Bk>



Mac OS X 安裝 R 軟體

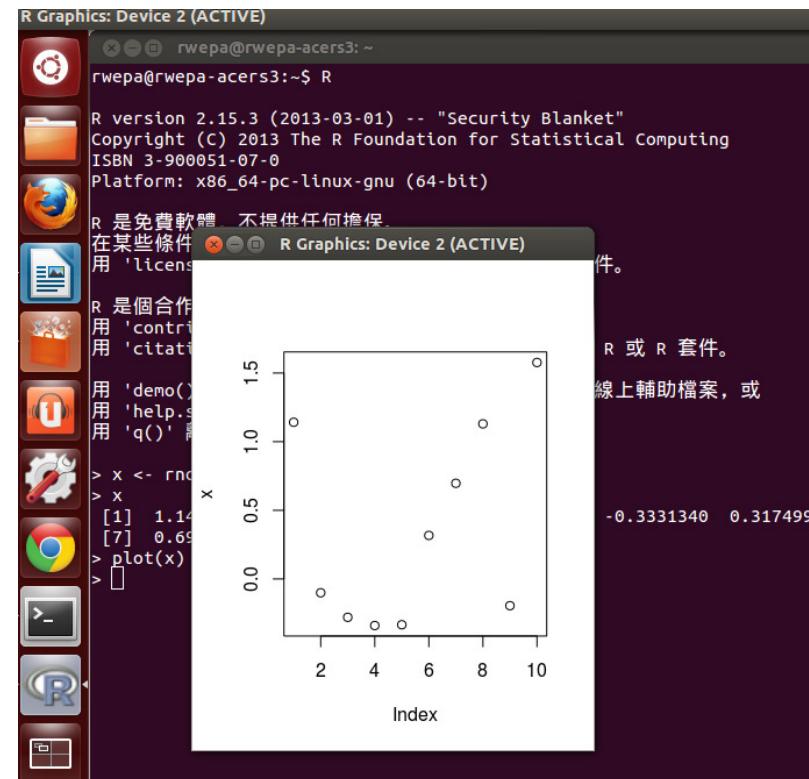
育達科技大學
資訊管理系
李明昌
alan9956@gmail.com

R
WEPa
Since 2013

更多訊息 <http://rwepa.blogspot.tw/>

R for Ubuntu

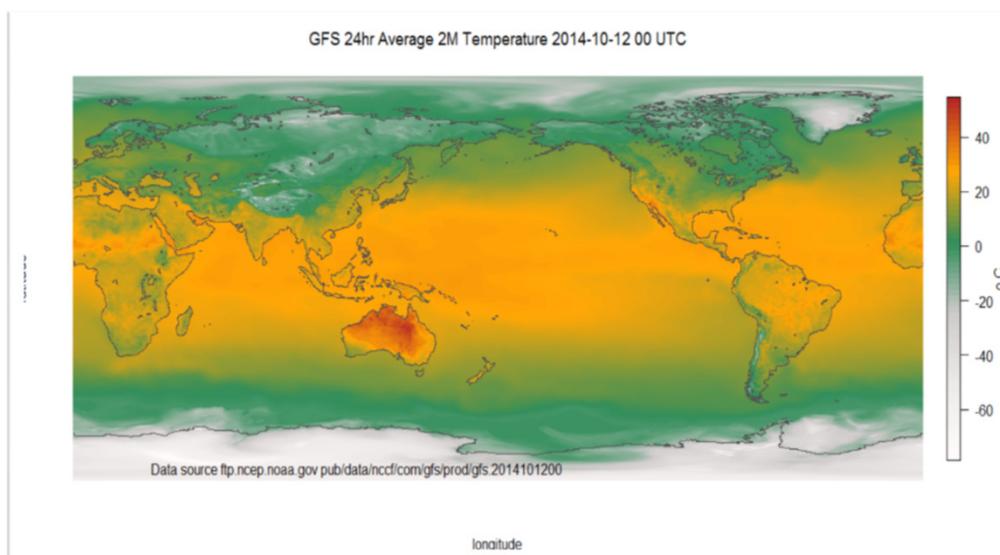
- <http://rwepa.blogspot.com/2013/05/ubuntu-r.html>



RStudio 安裝與簡介

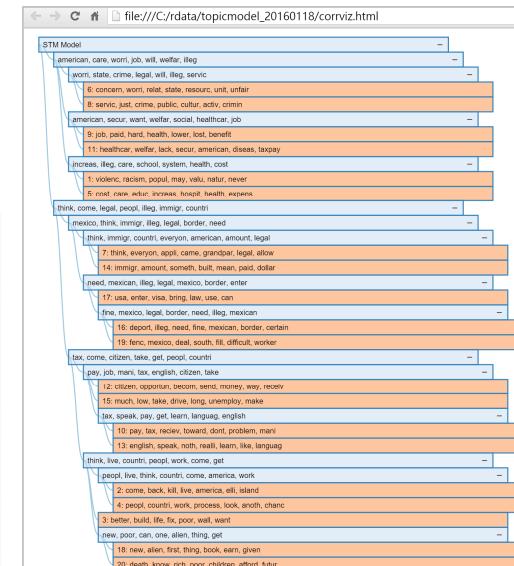
整合式開發環境 - RStudio

- <http://www.rstudio.com/>



視覺化應用

(全球2M氣溫圖)



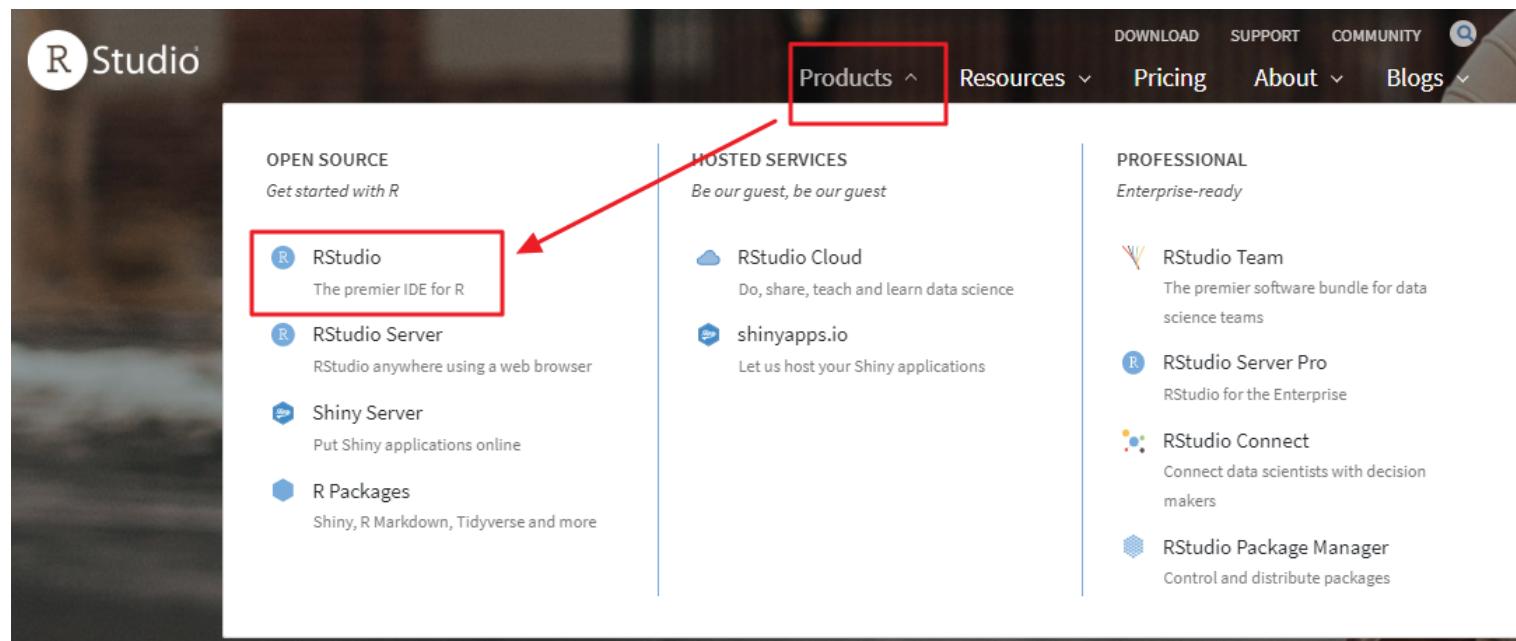
主題模型

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

Open Source License

Free

RStudio Desktop

Commercial License

\$995

RStudio Server

Open Source License

Free

RStudio Server Pro

Commercial License

\$4,975**單機版****DOWNLOAD****BUY****DOWNLOAD****BUY****伺服器版本**/year
(Named Users)

Integrated Tools for R

Priority Support

Access via Web Browser

Enterprise Security

Project Sharing

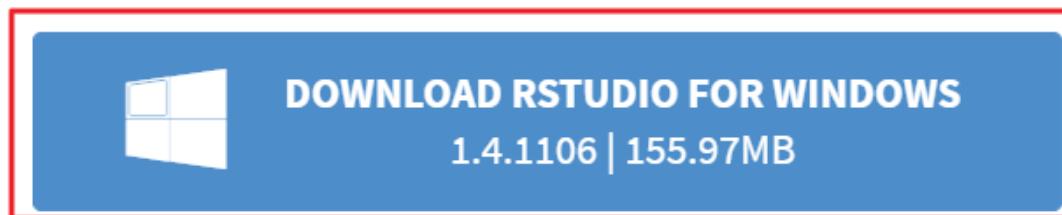
免費版[Learn more](#)[Learn more](#)[Learn more](#)[Evaluation | Learn more](#)

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:

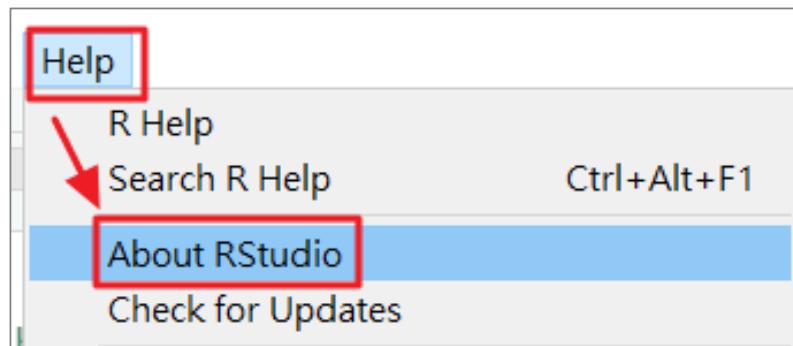


Requires Windows 10/8 (64-bit)

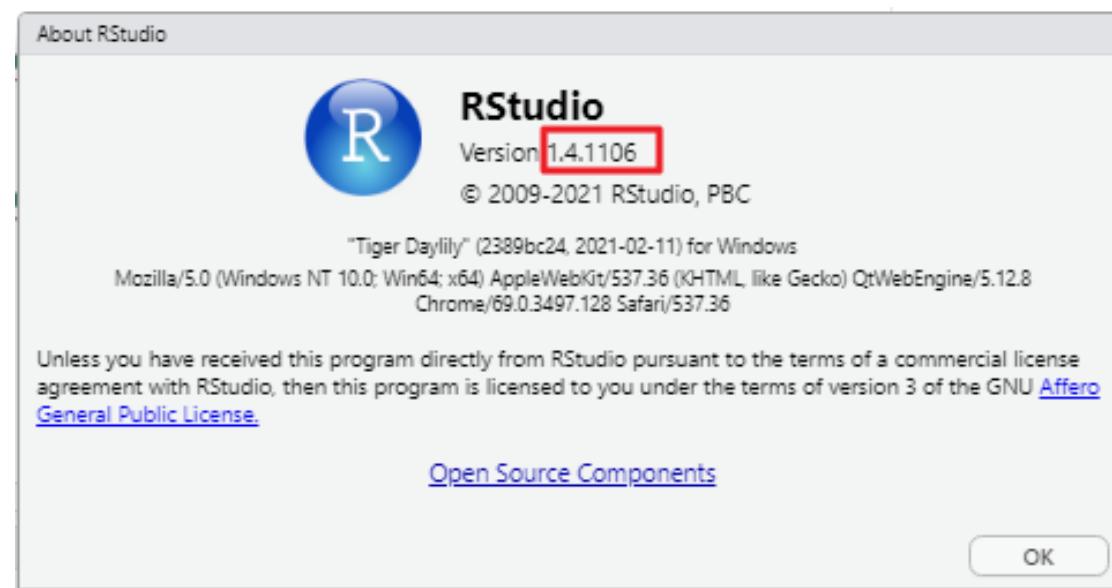
RStudio 安裝



RStudio 版本訊息

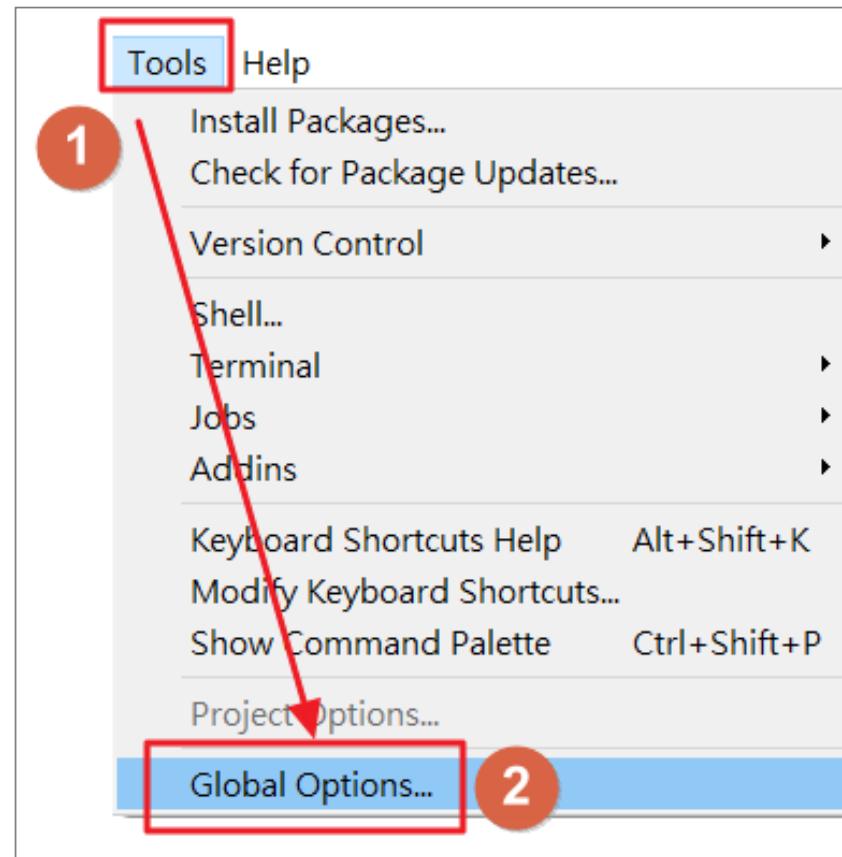


Help \
About RStudio

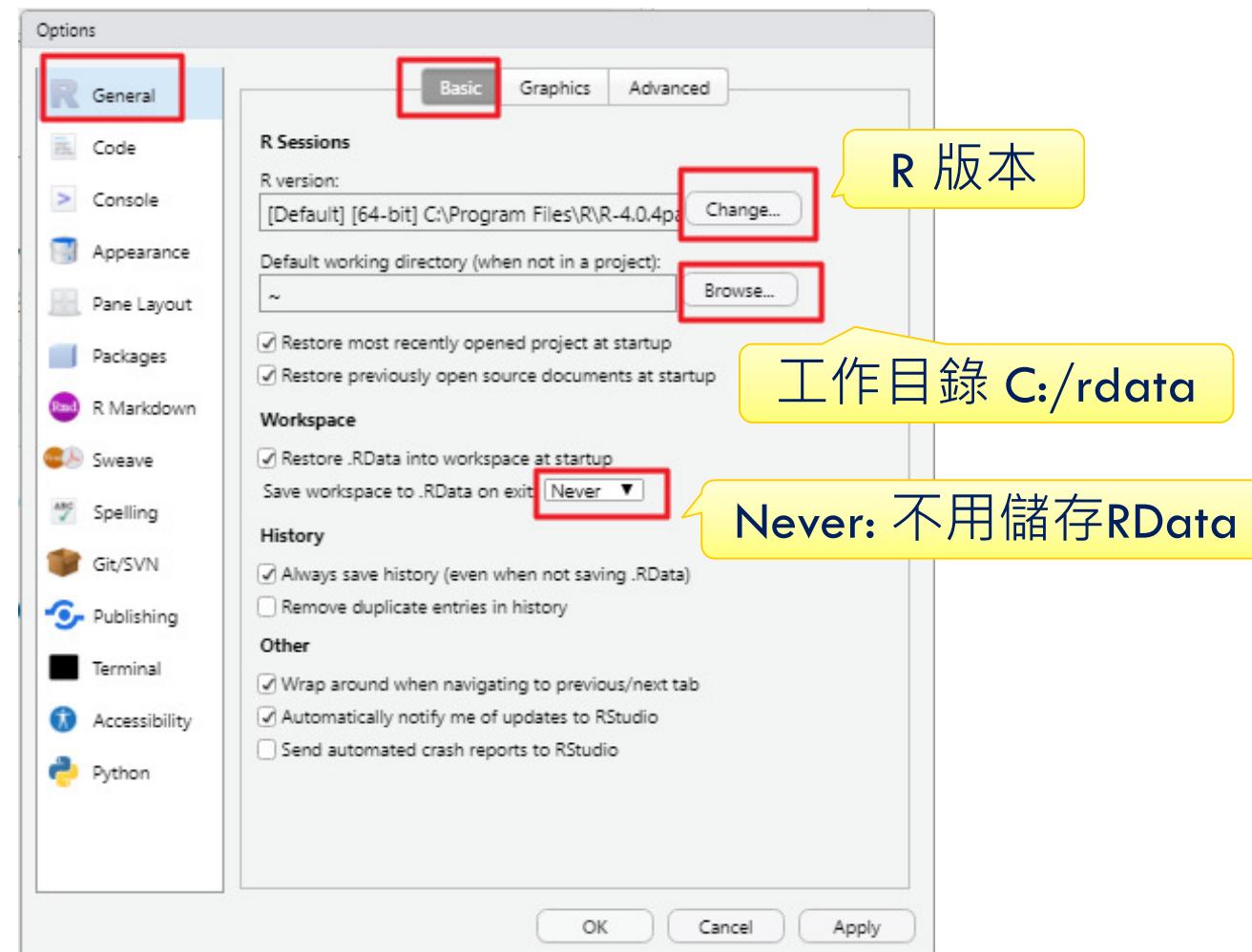


RStudio - 選項設定

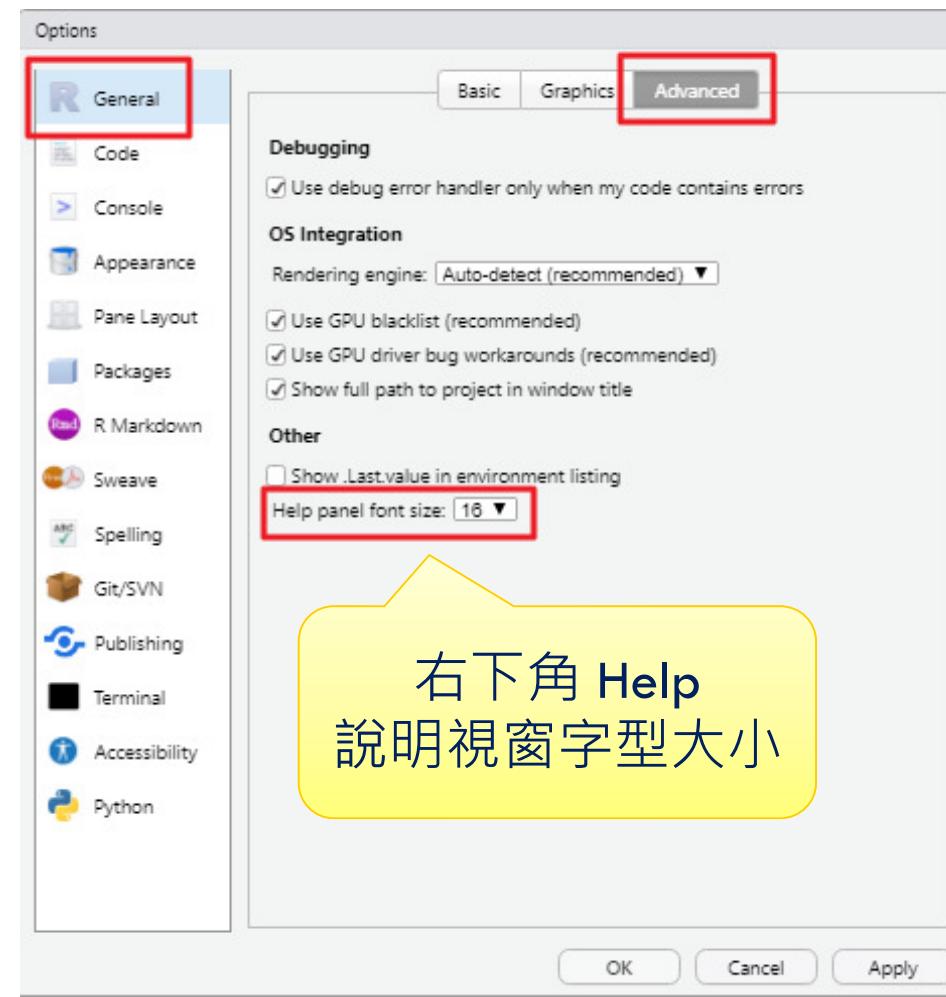
■ Tools \ Global Options



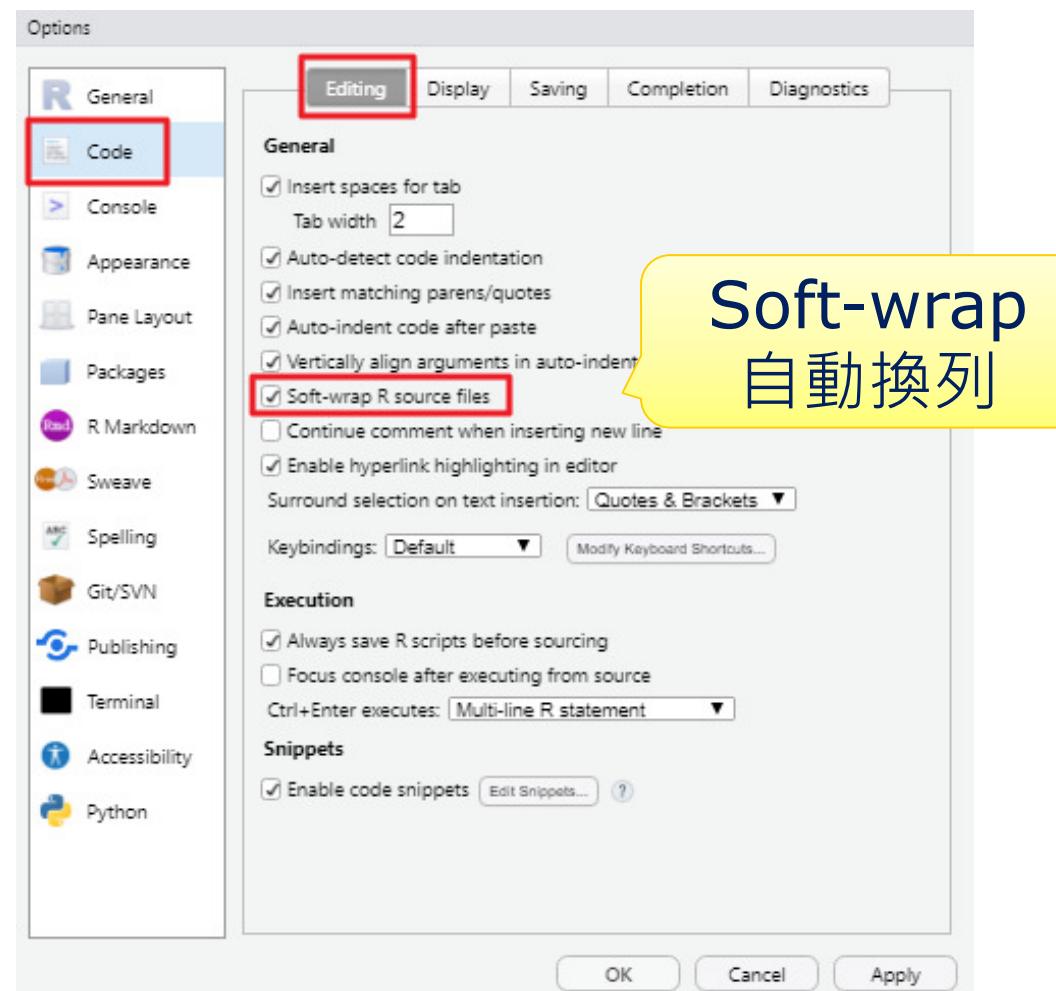
General \ Basic



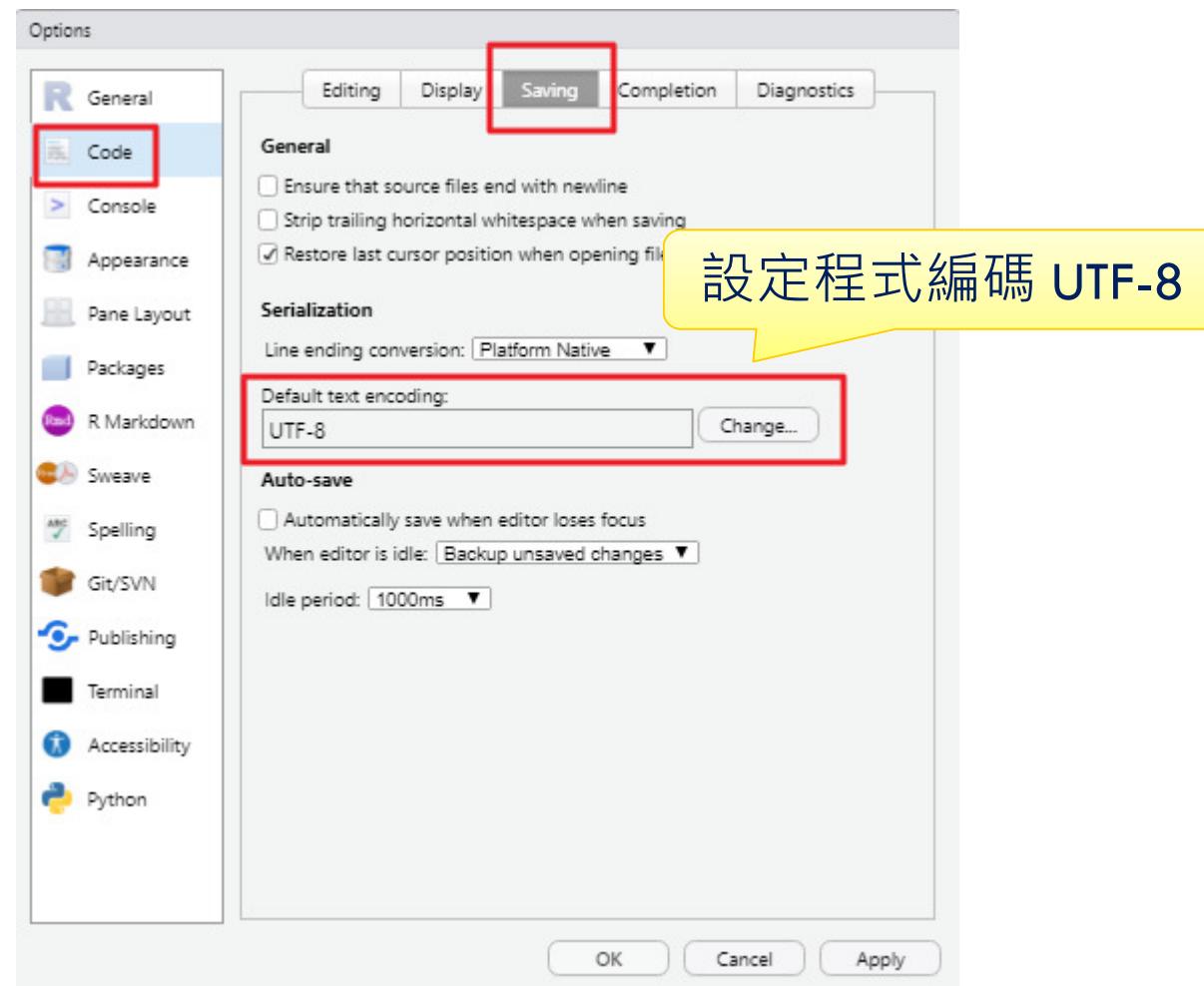
General \ Advanced



Code \ Editing



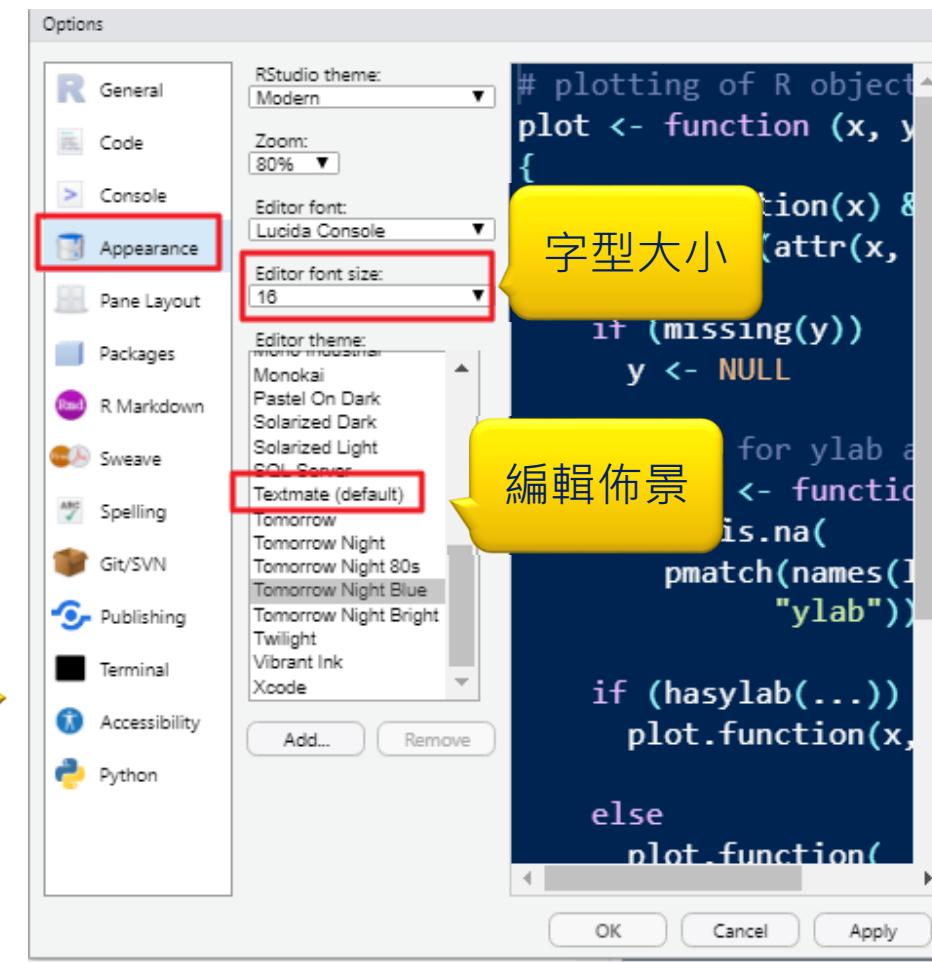
Code \ Saving



RStudio-選項設定(續)

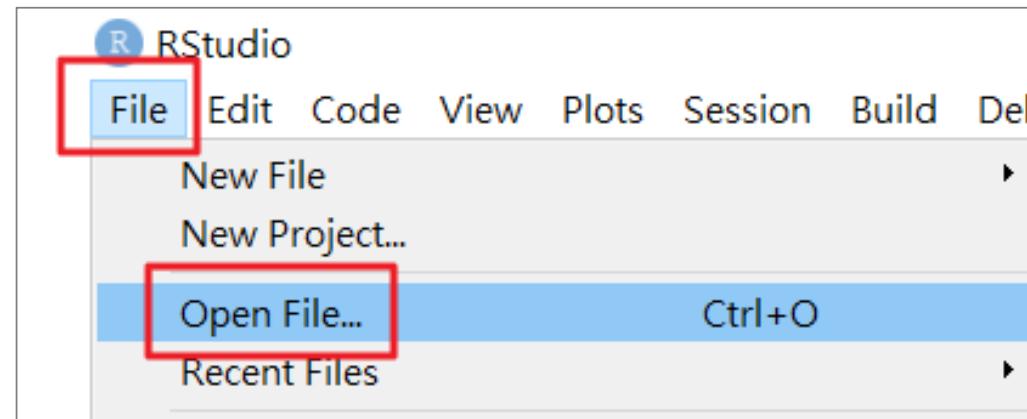
- Appearance \ Editor theme
- 預設值:
TextMate

設定完成,須重
新啟動RStudio



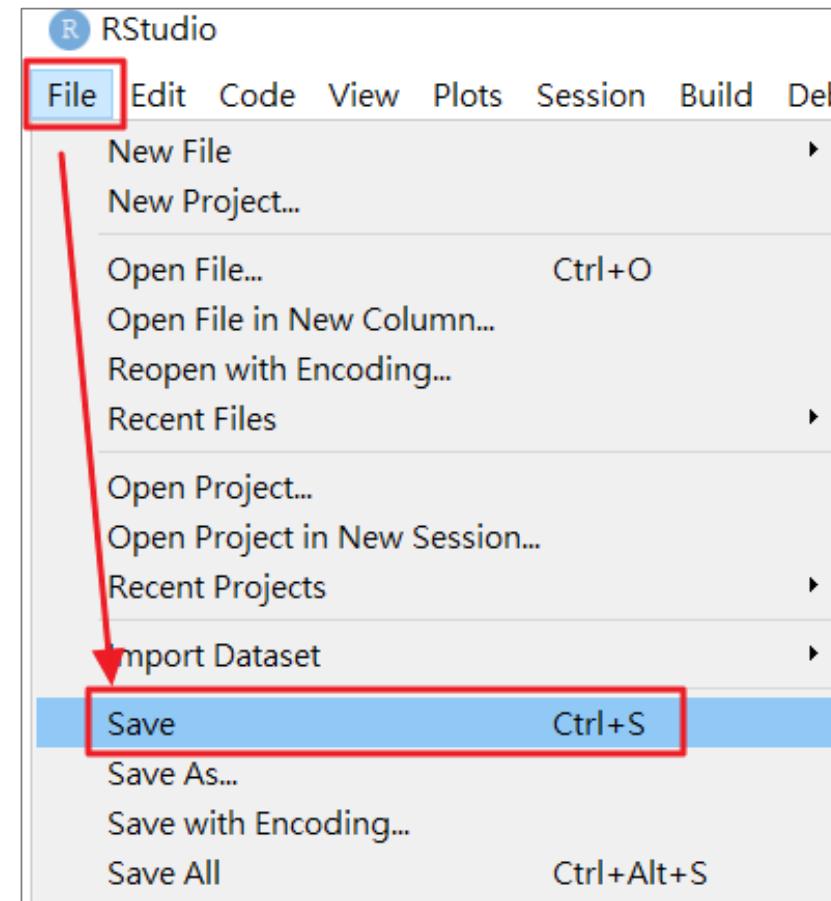
開啟檔案

- File \ Open File

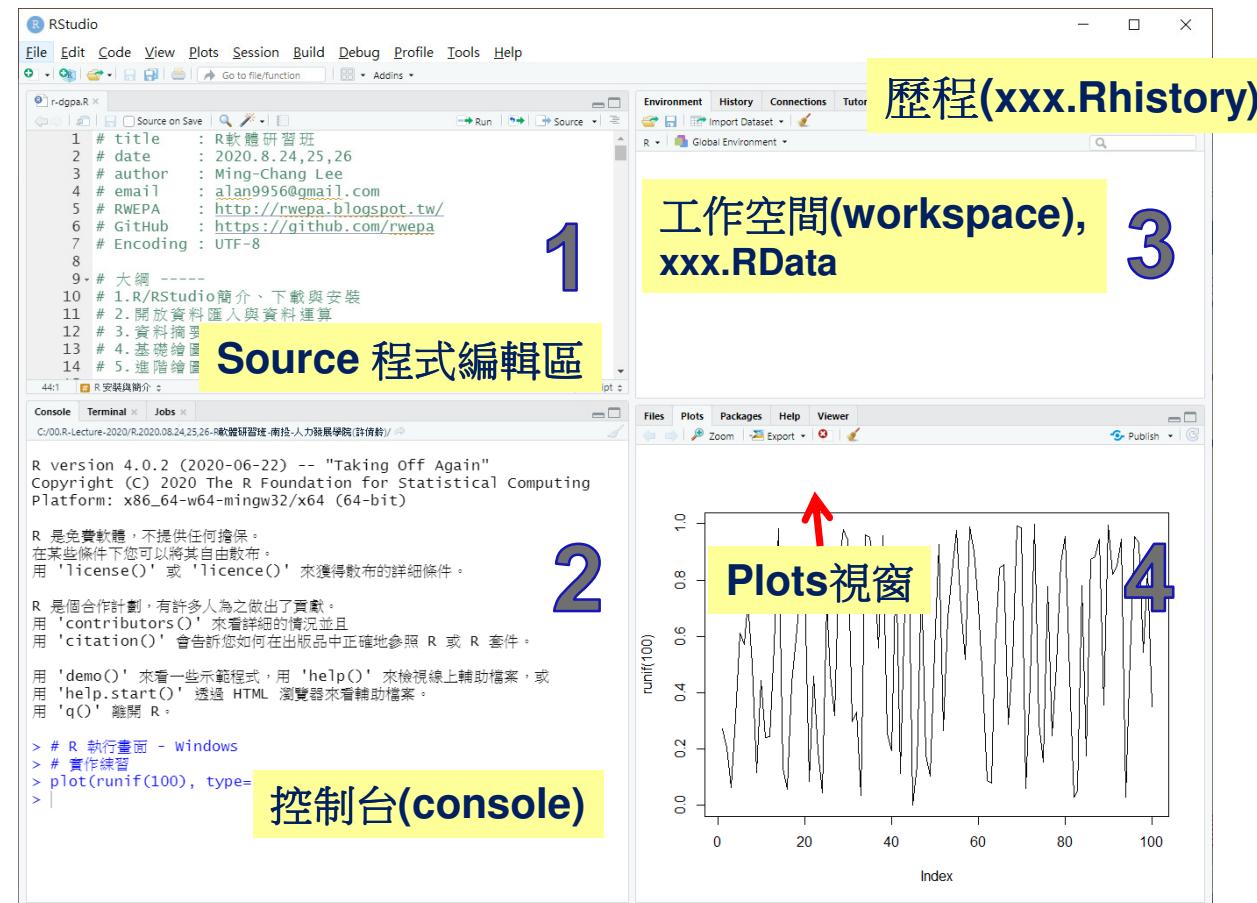


儲存檔案

- File \ Save
(CTRL + S)
- 檔名: xxx.R



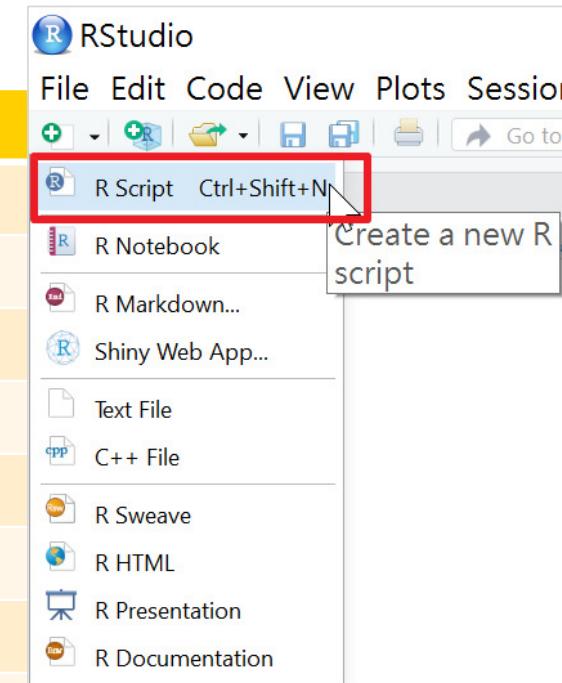
R/RStudio環境的基礎觀念



CTRL + SHIFT + F10: 重新啟動R

RStudio 快速鍵

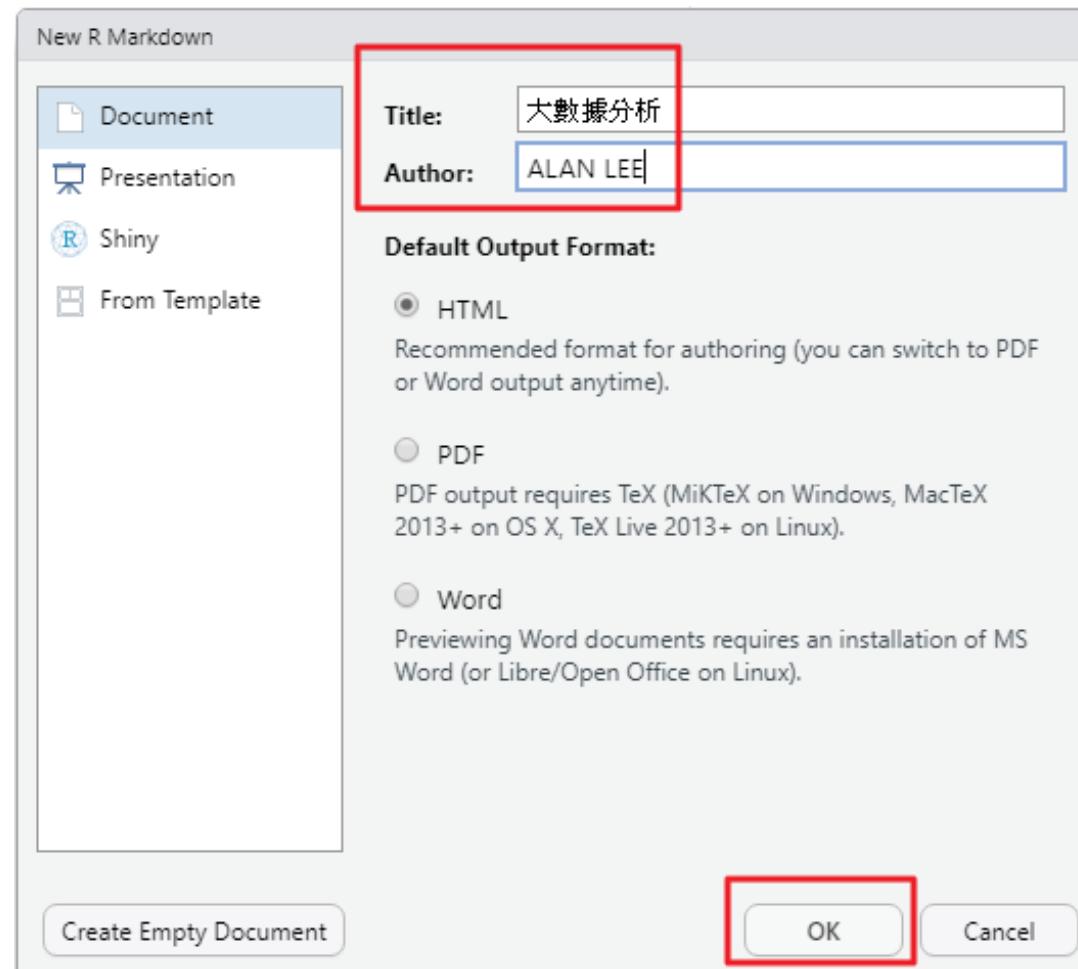
快速鍵功能	功能
Ctrl + Shift + N	建立新的R程式
Ctrl + S	儲存檔案
Ctrl + Shift + R	建立章節 (-----)
Alt + -	指派符號
Ctrl + Shift + C	註解
Ctrl + Enter	執行程式
Ctrl + Shift + F10	重新啟動R
Alt + Shift + K	快速鍵總表 (Esc 退出)



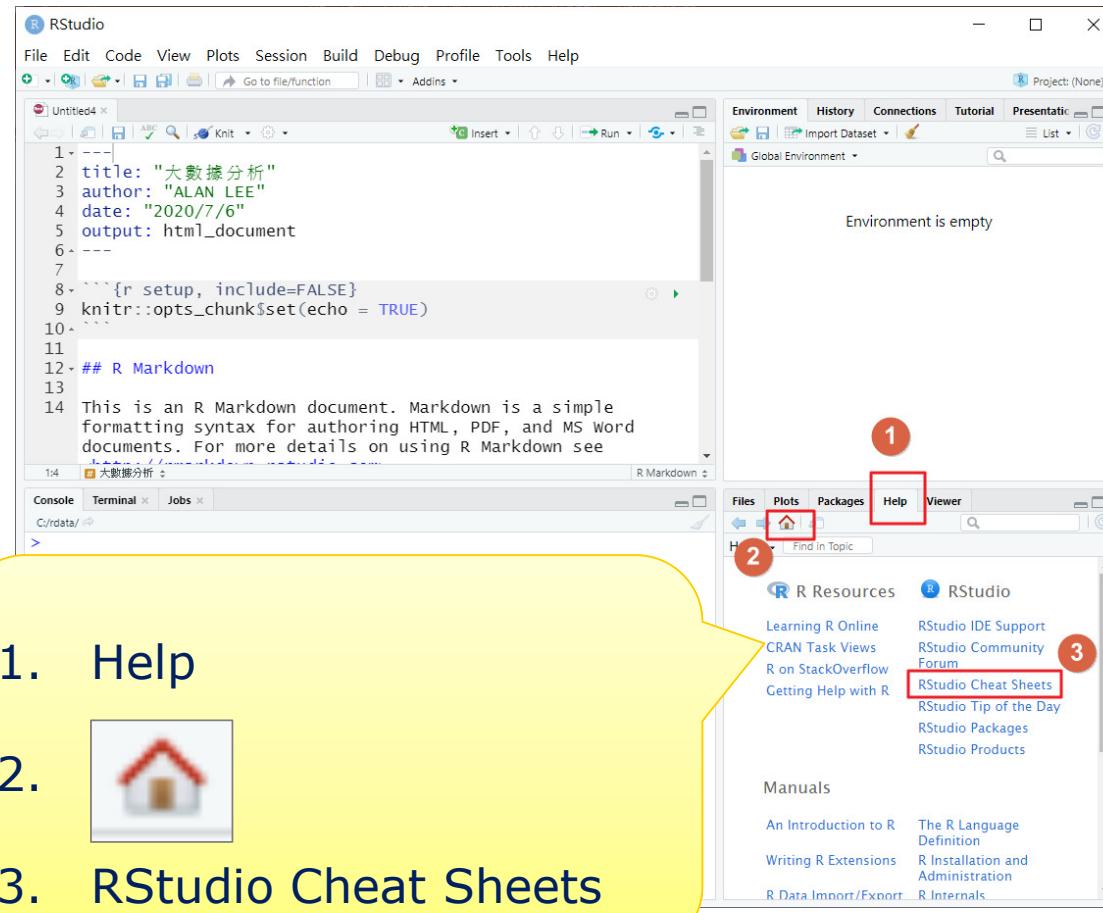
R Markdown

R標記語言

RStudio - Markdown



RStudio - Markdown (續)



The screenshot shows the RStudio interface. On the left, a code editor window displays an R Markdown document with the following content:

```
1 ---  
2 title: "大數據分析"  
3 author: "ALAN LEE"  
4 date: "2020/7/6"  
5 output: html_document  
6 ---  
7  
8 ``{r setup, include=FALSE}  
9 knitr::opts_chunk$set(echo = TRUE)  
10 ``  
11  
12 ## R Markdown  
13  
14 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  
15 http://rstudio.com/r-markdown
```

The RStudio menu bar is visible at the top, and the global environment pane on the right shows "Environment is empty". A yellow callout box on the left side of the image highlights the following three resources:

1. Help
2. Home icon
3. RStudio Cheat Sheets

The "Help" menu is open, showing various links. The "RStudio Cheat Sheets" link is highlighted with a red box and a circled number 3. Other visible links include "R Resources", "Learning R Online", "CRAN Task Views", "R on StackOverflow", "Getting Help with R", "RStudio IDE Support", "RStudio Community Forum", "RStudio Tip of the Day", "RStudio Packages", and "RStudio Products".

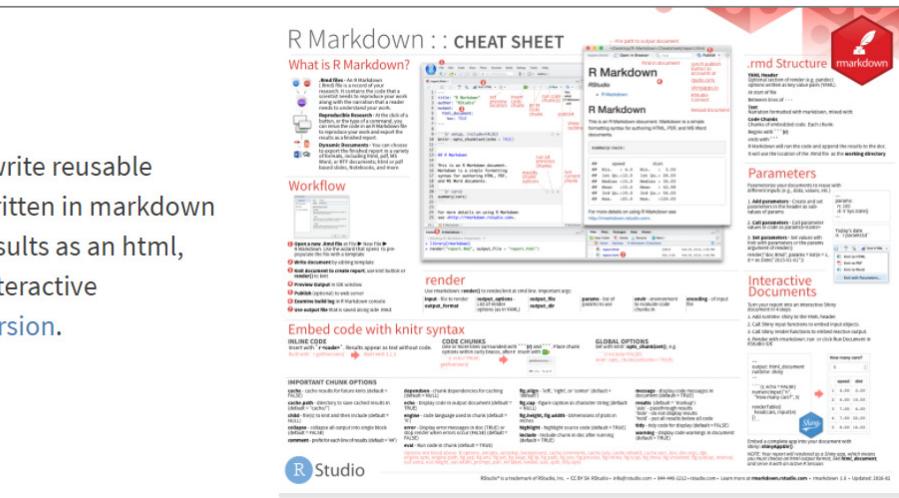
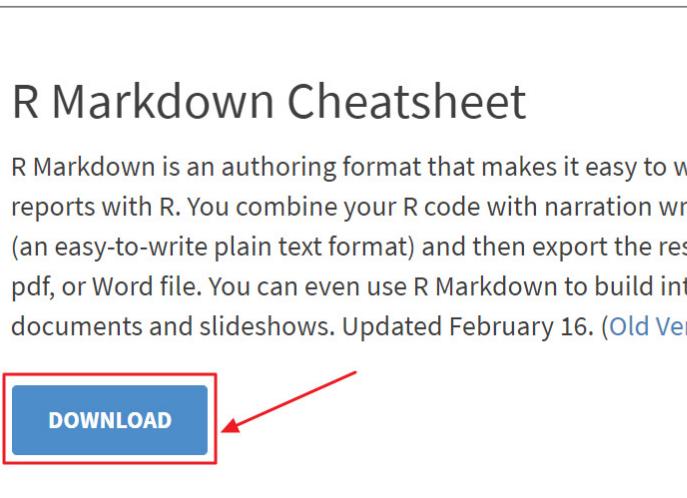
R Markdown Cheatsheet 線上說明

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

R Markdown Cheatsheet

R Markdown is an authoring format that makes it easy to write reusable reports with R. You combine your R code with narration written in markdown (an easy-to-write plain text format) and then export the results as an html, pdf, or Word file. You can even use R Markdown to build interactive documents and slideshows. Updated February 16. ([Old Version](#)).

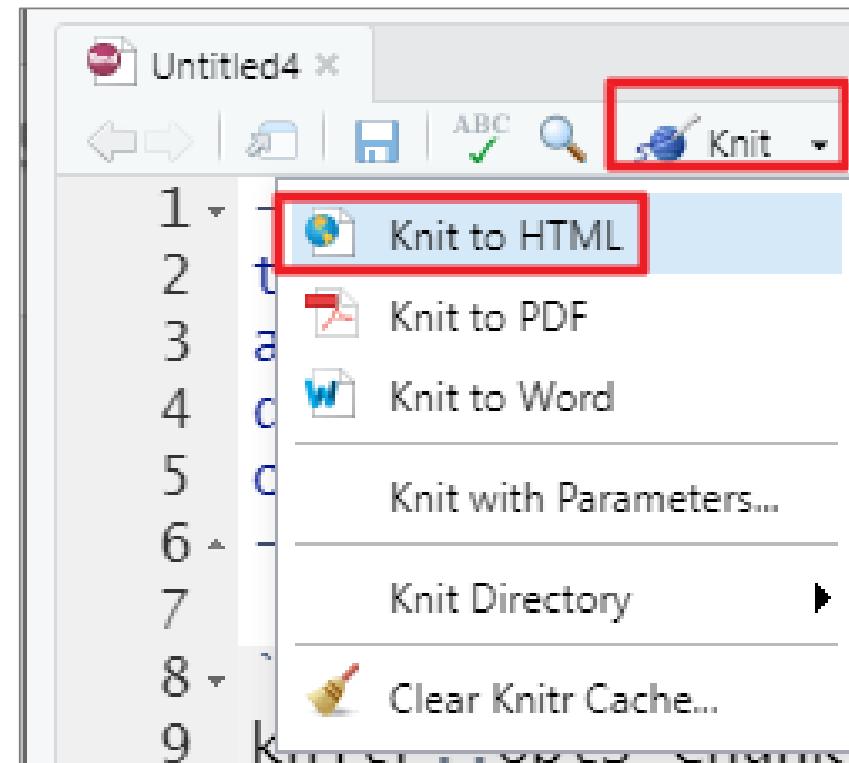
[DOWNLOAD](#)



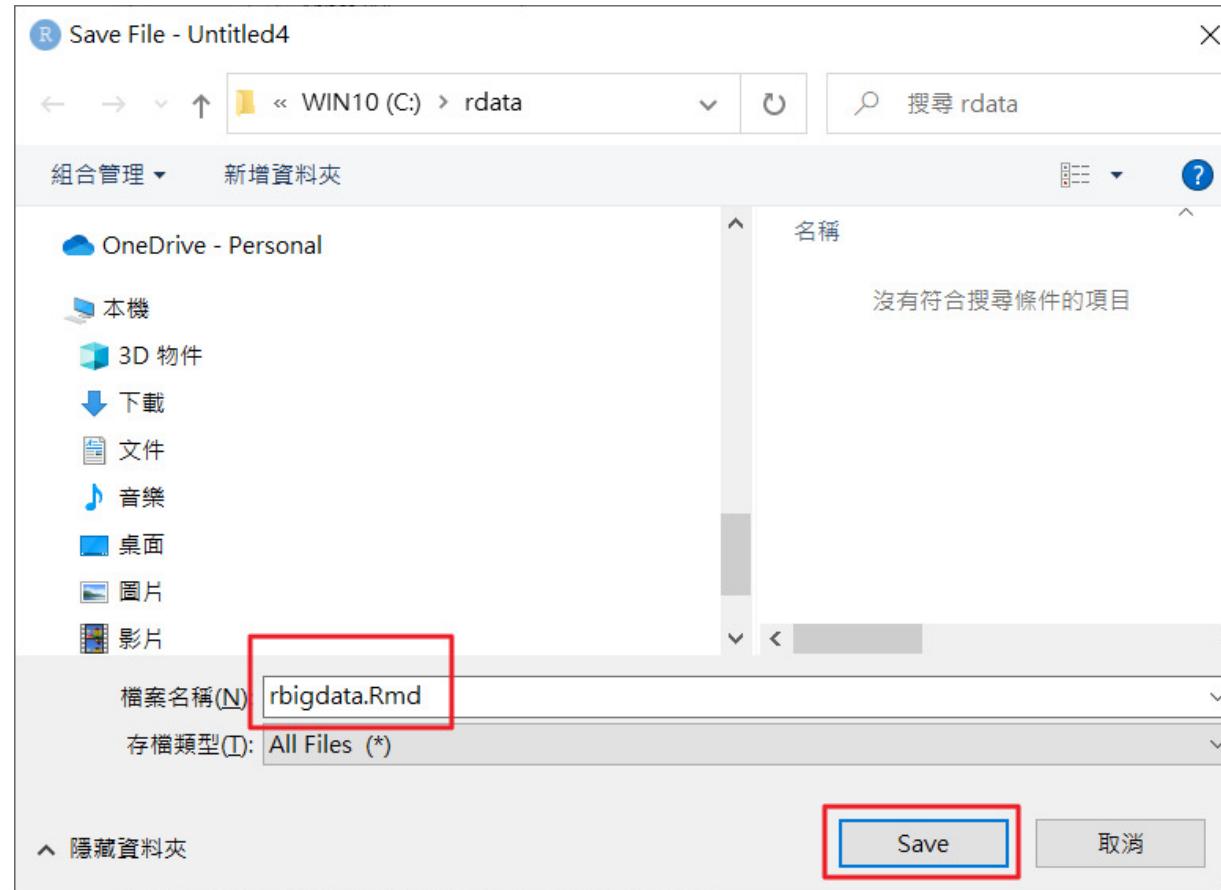
The screenshot shows the R Markdown Cheatsheet page. It includes a 'What is R Markdown?' section with a brief description and a 'Workflow' diagram. Below these are sections for 'R Markdown', 'Parameters', 'Interactive Documents', and 'How many?'. A red arrow points from the 'DOWNLOAD' button to the 'Workflow' diagram.

RStudio - Markdown (續)

- Knit HTML
- Knit PDF
- Knit Word



RStudio - Markdown (續)



Knit to HTML



大數據分析
ALAN LEE
2020/7/6

R Markdown

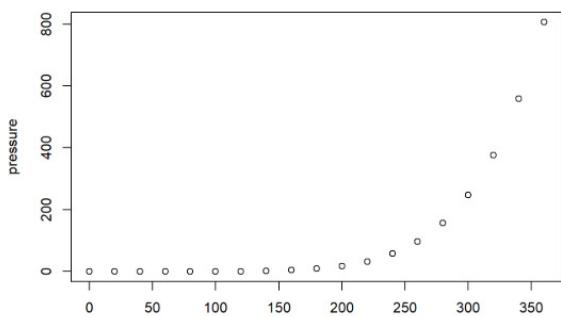
This is an R Markdown document. When you click the Knit button, it will be processed by R Markdown and stored in the current working directory. You can also embed plots, for example:

```
summary(cars)
```

```
##      speed         dist
## Min.   :4.00   Min.   : 2.00
## 1st Qu.:12.00  1st Qu.:26.00
## Median :15.00  Median :36.00
## Mean   :15.40  Mean   :42.98
## 3rd Qu.:19.00  3rd Qu.:56.00
## Max.   :25.00  Max.   :120.00
```

Including Plots

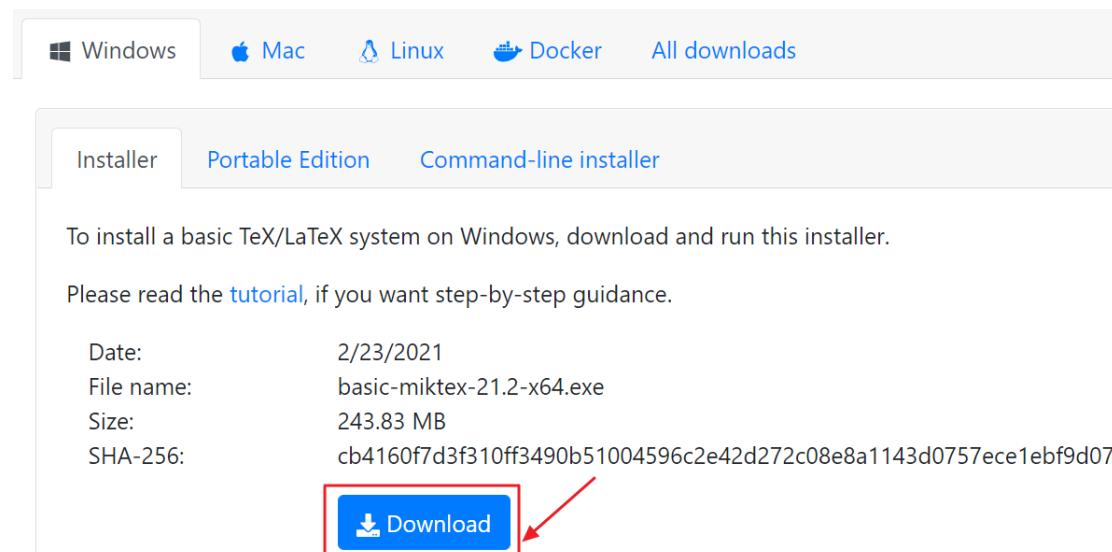
You can also embed plots, for example:



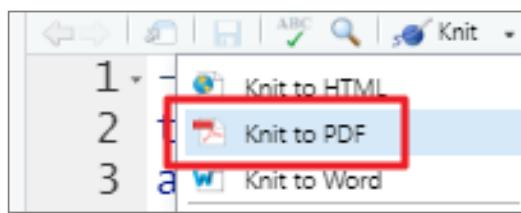
A scatter plot showing the relationship between 'speed' (X-axis, ranging from 0 to 350) and 'pressure' (Y-axis, ranging from 0 to 800). The data points show a positive correlation, with most points clustered below 200 speed and below 400 pressure, and a few outliers at higher speeds and pressures.

RStudio - Markdown : PDF

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



Knit to PDF



A screenshot of a PDF viewer displaying a document titled 'bigdata.pdf'. The document contains the following text:

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:

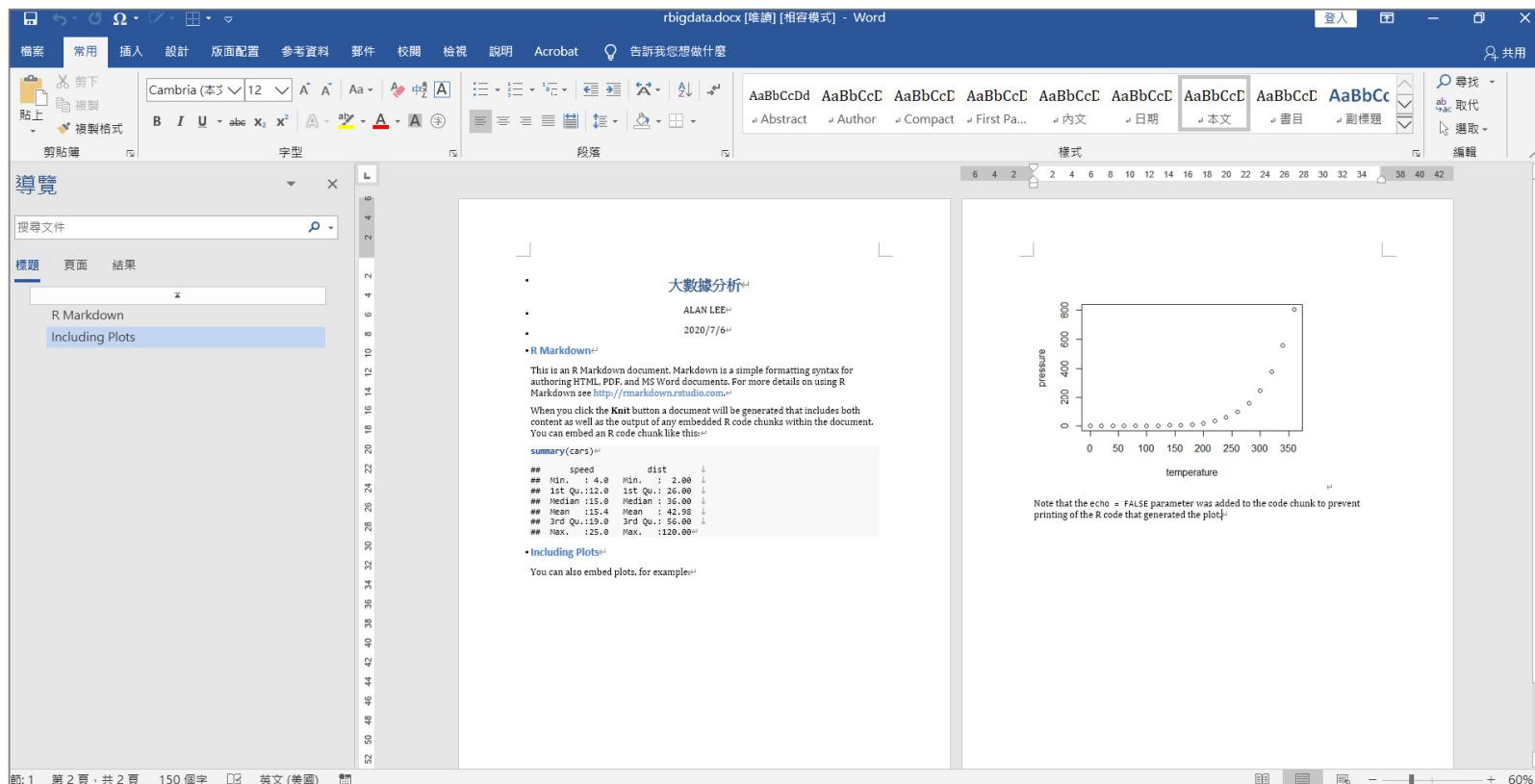
```
summary(cars)
```

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:

RStudio - Markdown : Word



R學習

- <http://rwepa.blogspot.com/>

The screenshot shows the homepage of the RWEPA blog. At the top left is the RWEPA logo with 'Since 2013'. To its right is a block of R code demonstrating shinyUI and ggmap. Below this is a welcome message in Chinese and English. A central section displays several R plots and maps. On the right side, there's a search bar and a sidebar with a list of links. A red speech bubble on the right points to the sidebar with the text '免費教學' (Free Teaching). A yellow speech bubble at the bottom right points to the sidebar with the text '下載 R,RStudio' (Download R, RStudio).

歡迎光臨 RWEPA 部落格
Welcome to RWEPA blog

歡迎來到 RWEPA blog, 成立宗旨為提供免費R軟體的相關資訊。R包括大量套件可應用於不同領域, 例如: 2D/3D互動式繪圖, 資料視覺化, 資料探勘, 線性與非線性最佳化問題, 時間序列, 空間資料, 財務分析, 多變量分析, 問卷調查, 實驗設計, 統計製程管制, 存活分析, 臨床實驗分析, 社會網絡分析, 生物資訊, 醫學統計等。

2021年4月12日 星期一

2021-R軟體與Shiny Web應用程式設計

免費教學

搜尋此網誌 (例: task)

GitHub DataDemo

iPAS-R-tutorial

iPAS-Python-tutorial

★★★R入門資料分析與視覺化(付費,中文字幕)

★★★R商業預測與應用(付費,中文字幕)

★★★R語言-直播課程(付費)

R教學-基礎篇/程式碼(免費)

Python程式設計PDF(免費)

★R 4.0.5-Wndows下載

★RStudio-1.4.1106下載

★RStudio Daily

R-bloggers

下載 R,RStudio

工作目錄

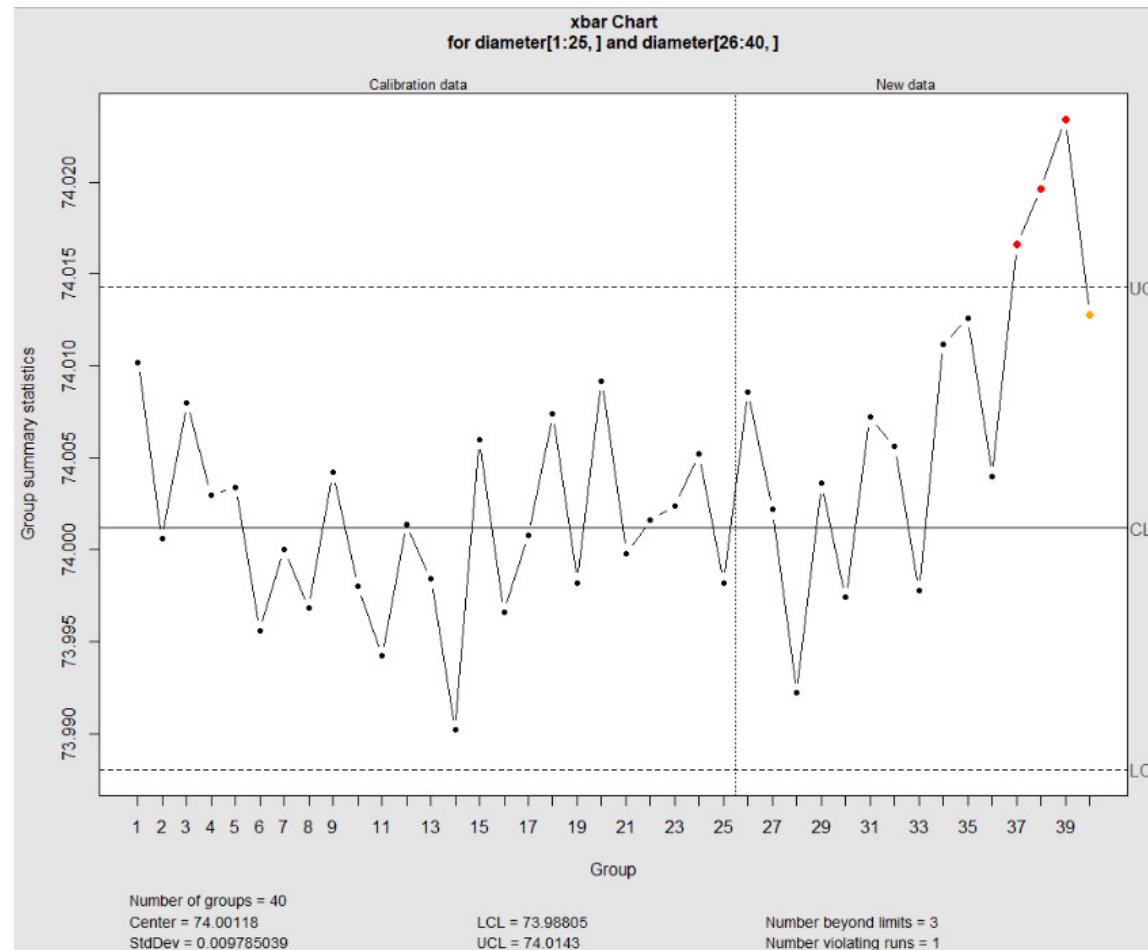
```
> # 取得工作目錄  
> getwd()  
[1] "C:/Users/88697/Documents"  
>  
> # 設定工作目錄  
> # 先建立 C:/rdata 資料夾  
> setwd("C:/rdata")  
>  
> getwd()  
[1] "C:/rdata"  
>
```

qcc: Quality Control Charts

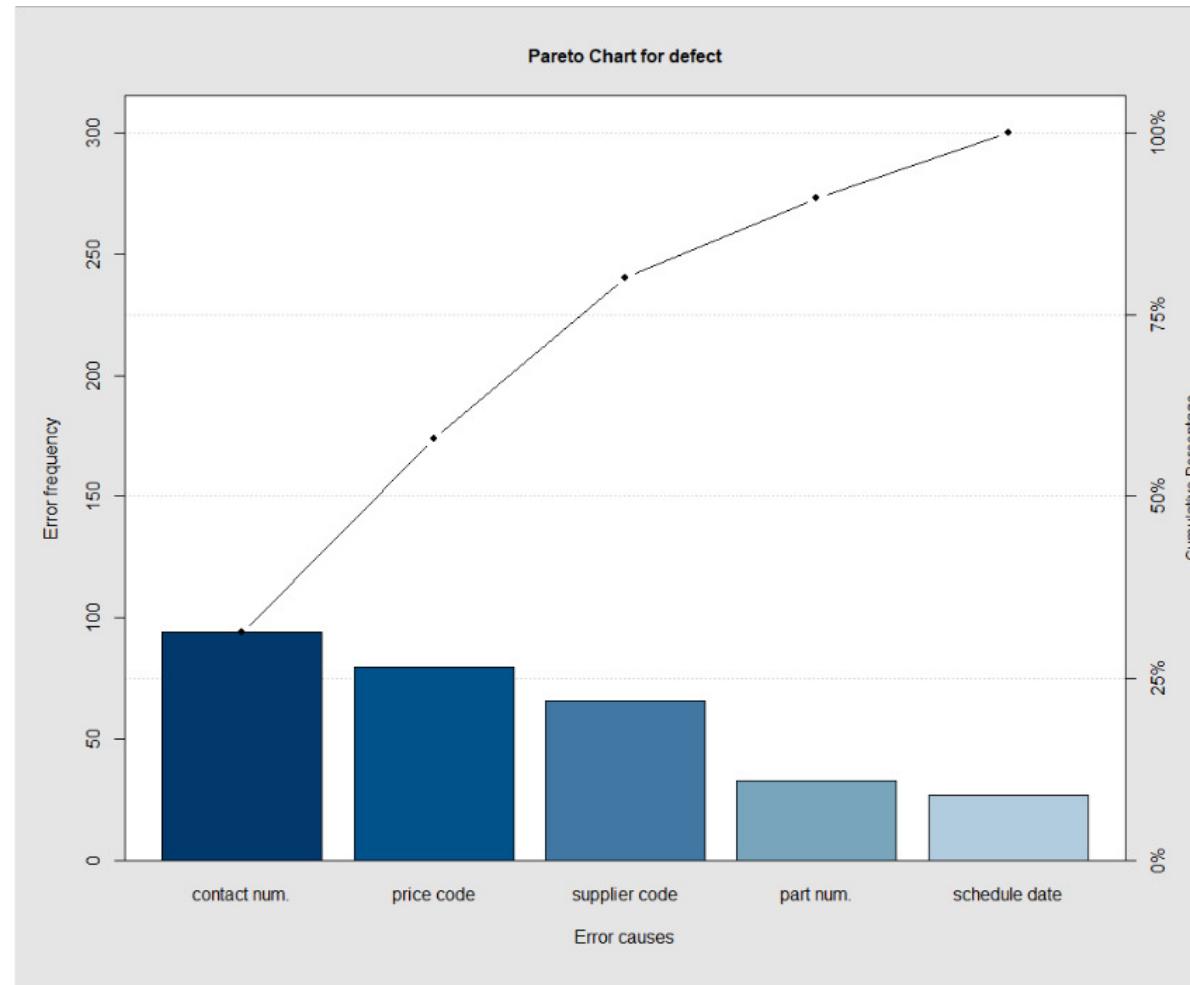
- <https://cran.r-project.org/web/packages/qcc/index.html>

```
> # qcc package
> # https://cran.r-project.org/web/packages/qcc/index.html
>
> library(qcc)
[1] "Quality Control Charts and"
[2] "Statistical Process Control"
[3] "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)

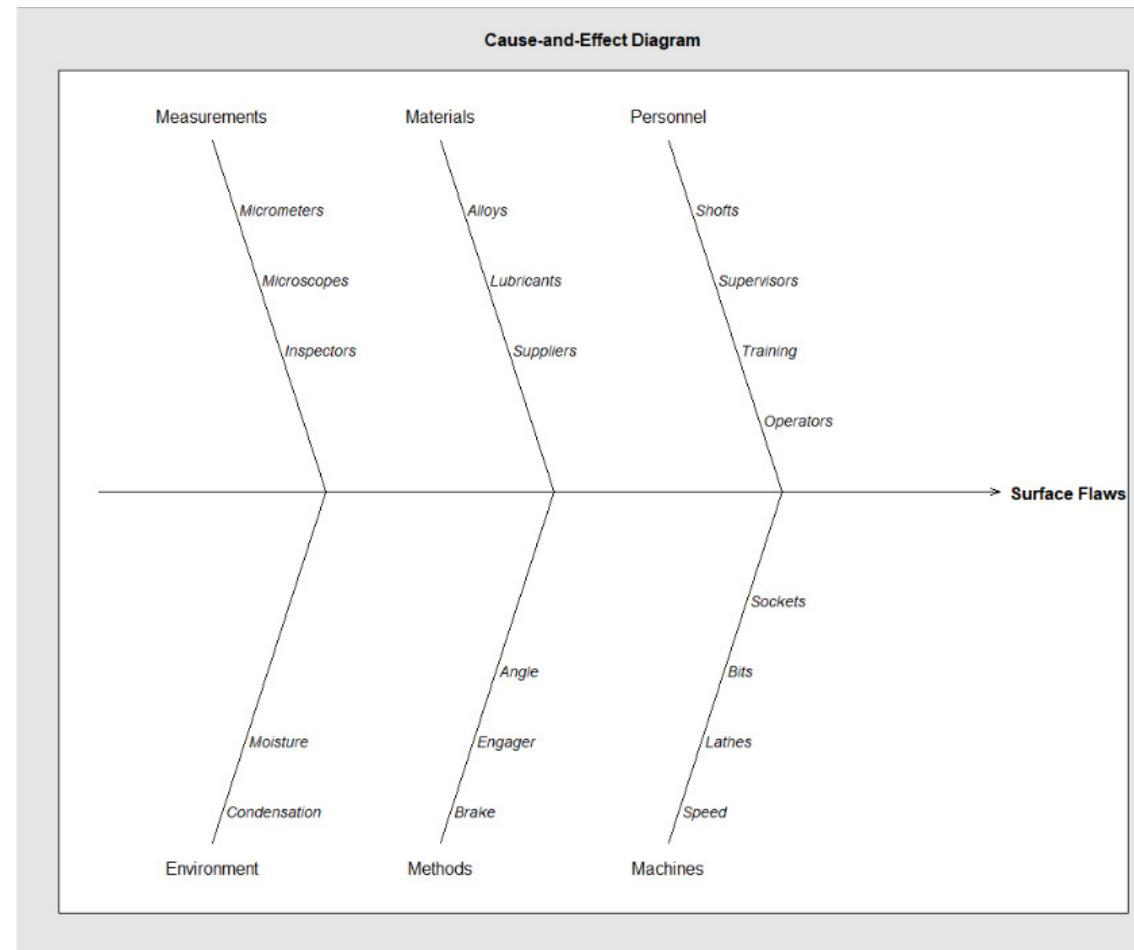


Pareto chart (柏拉圖)

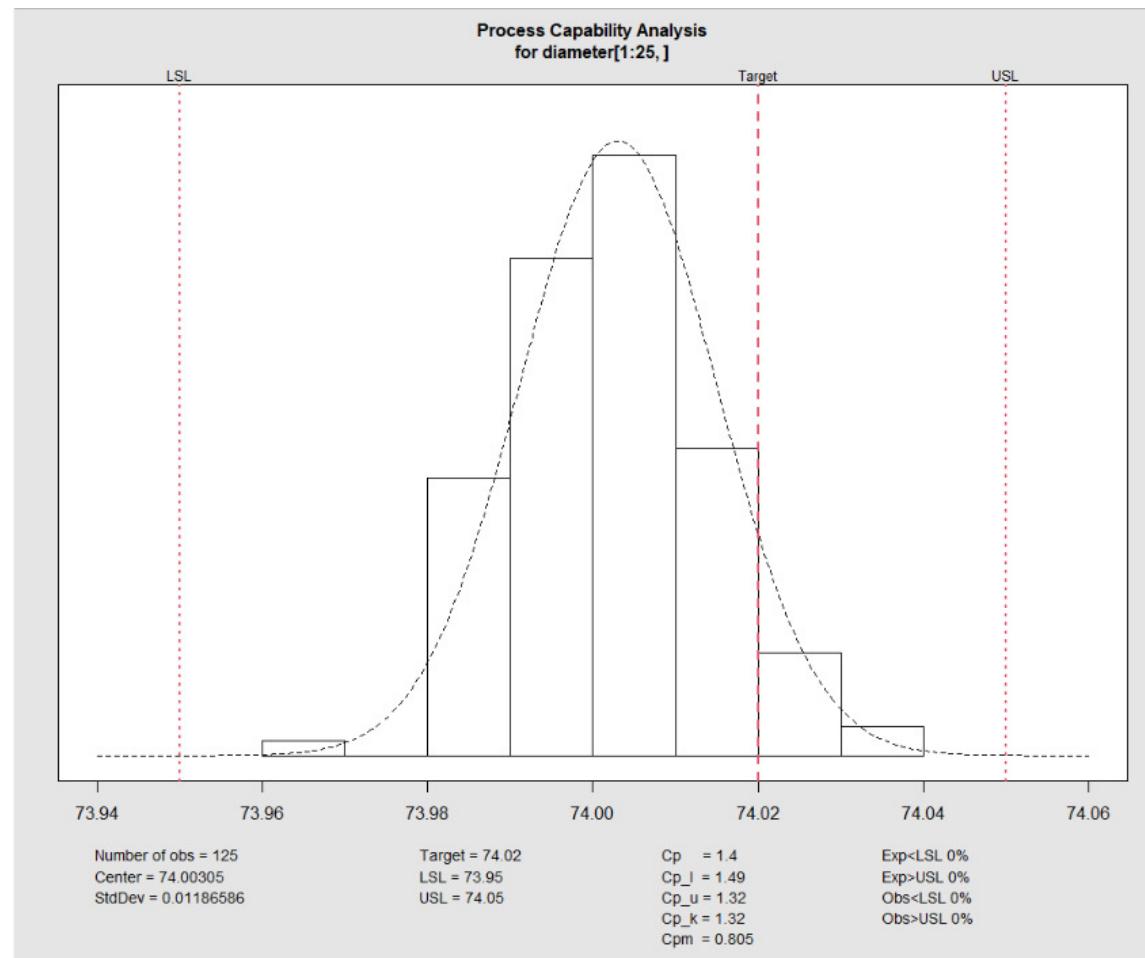


Cause and effect diagram (要因分析圖)

魚骨圖(Fishbone Diagram), 石川圖(Ischiawa Diagram)

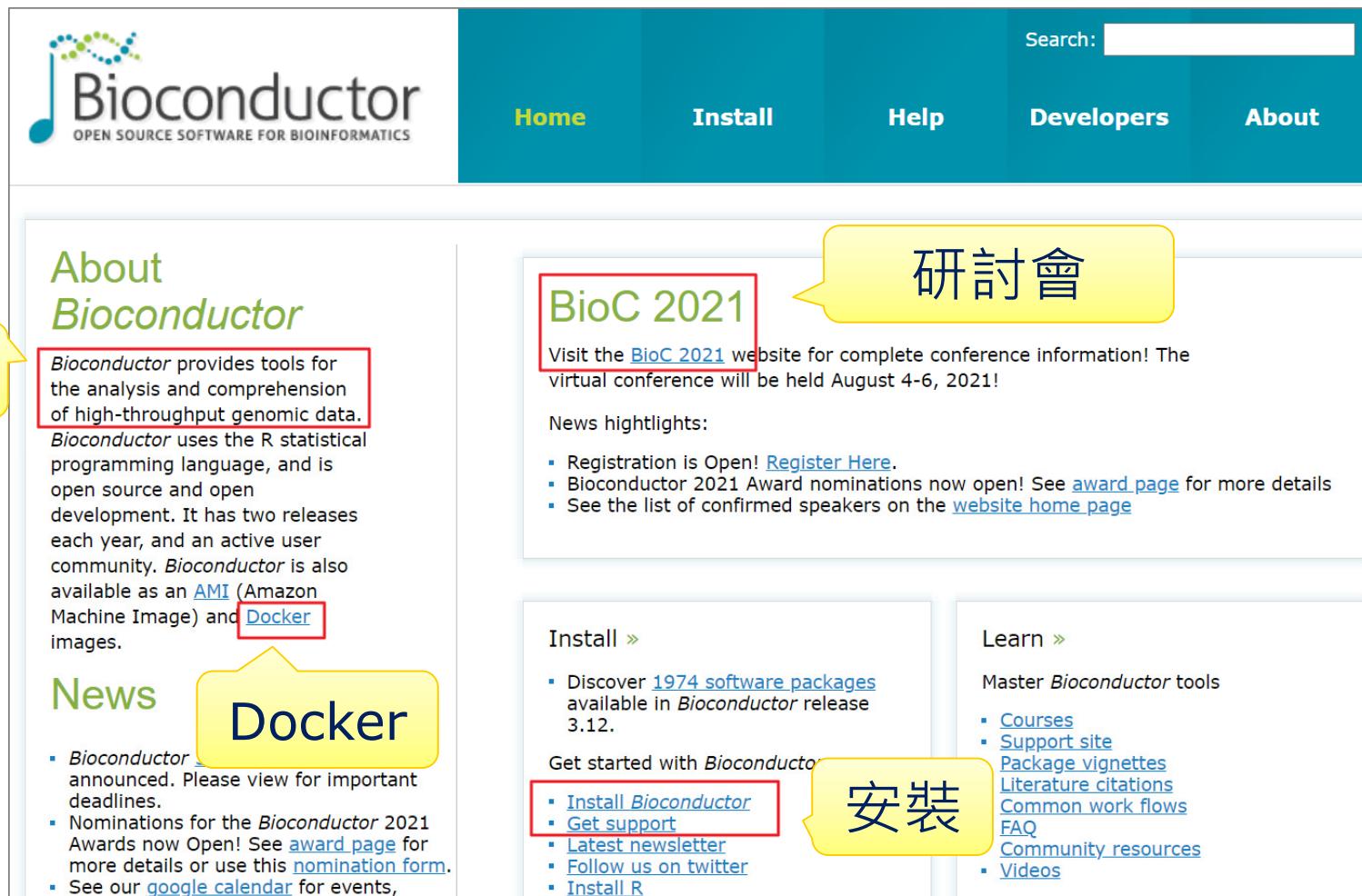


process capability index (製程能力 Cp)



2.Bioconductor實務應用

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



功能

About Bioconductor

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data.

Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community. Bioconductor is also available as an [AMI](#) (Amazon Machine Image) and [Docker](#) images.

News

Docker

- Bioconductor announced. Please view for important deadlines.*
- Nominations for the Bioconductor 2021 Awards now Open! See [award page](#) for more details or use this [nomination form](#).*
- See our [google calendar](#) for events,*

Search:

Home **Install** **Help** **Developers** **About**

BioC 2021

Visit the [BioC 2021](#) website for complete conference information! The virtual conference will be held August 4-6, 2021!

News highlights:

- Registration is Open! [Register Here](#).
- Bioconductor 2021 Award nominations now open! See [award page](#) for more details
- See the list of confirmed speakers on the [website home page](#)

Install »

- Discover [1974 software packages](#) available in Bioconductor release 3.12.

Get started with Bioconductor

- [Install Bioconductor](#)
- [Get support](#)
- [Latest newsletter](#)
- [Follow us on twitter](#)
- [Install R](#)

Learn »

Master Bioconductor tools

- [Courses](#)
- [Support site](#)
- [Package vignettes](#)
- [Literature citations](#)
- [Common work flows](#)
- [FAQ](#)
- [Community resources](#)
- [Videos](#)

安裝

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.

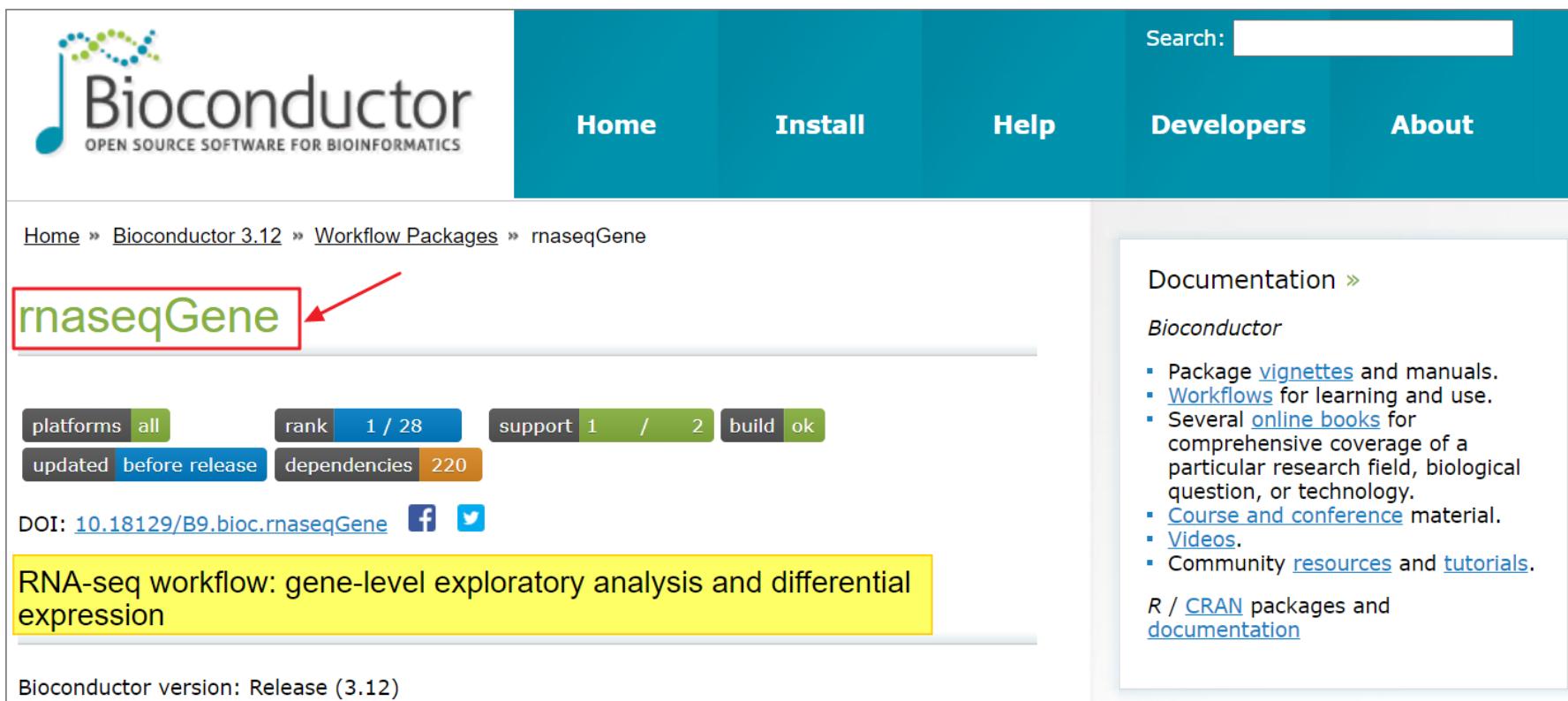
Show All entries Search table:

Package	Maintainer	Title	Rank
rnaseqGene	Michael Love	RNA-seq workflow: gene-level exploratory analysis and differential expression	1 第1名
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	Goledraoui 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

含中文說明

rnaseqGene 套件

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



The screenshot shows the Bioconductor website for the rnaseqGene package. The top navigation bar includes links for Home, Install, Help, Developers, and About. A search bar is also present. The main content area displays the package details for rnaseqGene, including its rank (1 / 28), support (1 / 2), and build status (ok). It also shows that it was updated before release and has 220 dependencies. The DOI is listed as [10.18129/B9.bioc.rnaseqGene](https://doi.org/10.18129/B9.bioc.rnaseqGene). Below this, a yellow box highlights the package's purpose: "RNA-seq workflow: gene-level exploratory analysis and differential expression". The bottom of the page indicates the Bioconductor version is Release (3.12).

rnaseqGene

platforms all rank 1 / 28 support 1 / 2 build ok
updated before release dependencies 220

DOI: [10.18129/B9.bioc.rnaseqGene](https://doi.org/10.18129/B9.bioc.rnaseqGene) [f](#) [t](#)

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

Bioconductor version: Release (3.12)

Documentation »
Bioconductor

- Package [vignettes](#) and manuals.
- [Workflows](#) for learning and use.
- Several [online books](#) for comprehensive coverage of a particular research field, biological question, or technology.
- [Course and conference](#) material.
- [Videos](#).
- Community [resources](#) and [tutorials](#).

R / [CRAN](#) packages and documentation

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
1 >NC_001477.1 Dengue virus 1, complete genome
2 AGTTGTTAGTCTACGTGGACCGACAAGAACAGTTCGAATCGGAAGCTGCTTAACGTAGTTCTAACAGT
3 TTTTTATTAGAGAGCAGATCTCTGATGAACAAACCAACGGAAAAAGACGGGTCGACCGTCTTCATATGC
4 TGAAACGCGCGAGAAACCGCGTGTCAACTGTTCACAGTTGGCGAAGAGATTCTCAAAAGGATTGCTTTC
5 AGGCCAAGGACCCATGAAATTGGTGATGGCTTTATAGCATTCTAACAGATTCTAGCCATACCTCCAACA
6 GCAGGAATTTGGCTAGATGGGCTCATTCAGAAGAACAGGAGGAAAAGATCTGTGACCAGCTCCTCATGCTGCT
7 AAGAAATCTCAAACATGTTAACATAATGAACAGGAGGAAAAGATCTGTGACCAGCTCCTCATGCTGCT
```

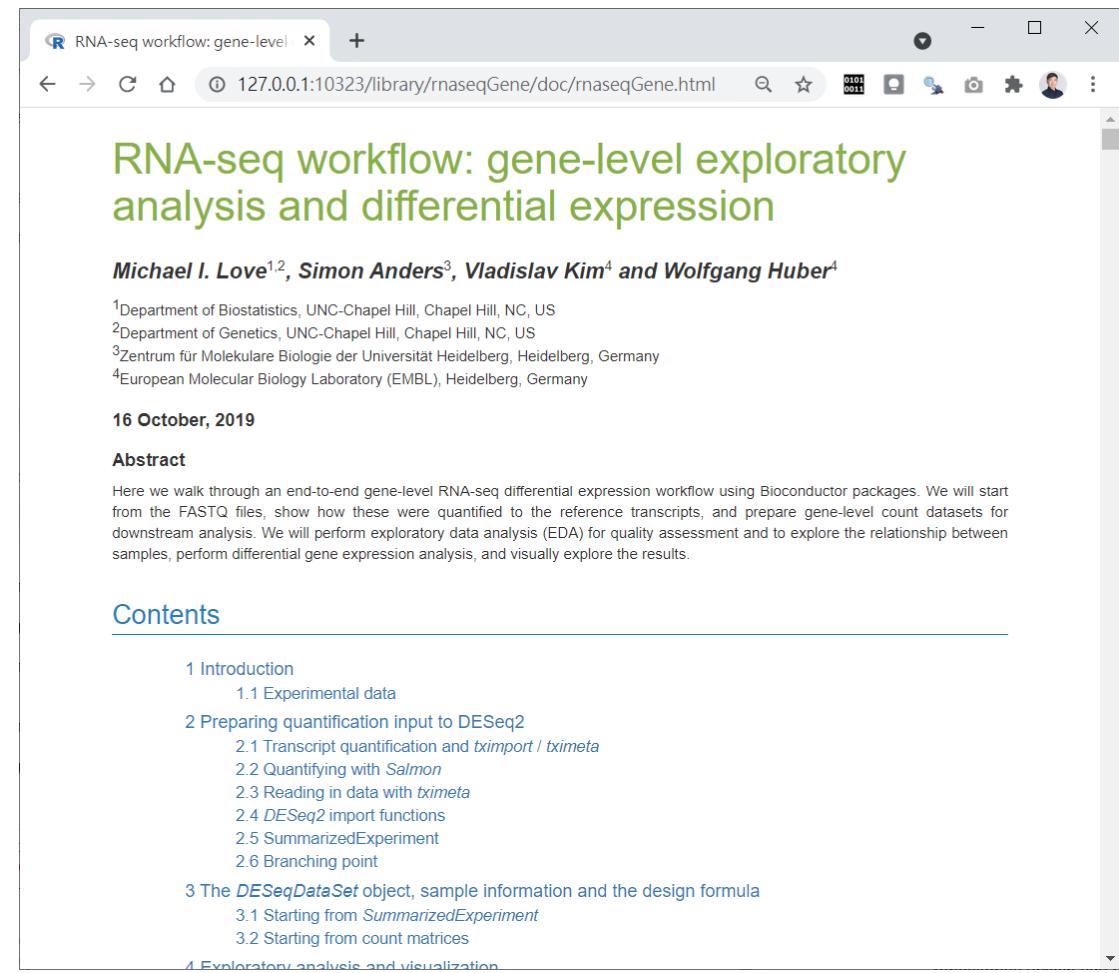
安裝 rnaseqGene 套件

```
> 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', 'lap', 'commonmark', 'bslib', 'htmlwidgets', 'crosstalk', 'formatR', 'checkmate', 'rstudioapi', 'cpp11', 'sysime', 'stringi', 'lazyeval', 'assertthat', 'shiny', 'DT', 'cli', 'utf8', 'lambda.r', 'futile.options', 'numDx', 'mvtnorm', 'colorspace', 'bit', 'cachem', 'Formula', 'data.table', 'htmlTable', 'viridis', 'forcats', 'rjhms', 'prettyunits', 'askpass', 'htmltools', 'xfun', 'tinytex', 'evaluate', 'highr', 'markdown', 'stringr'
```

rnaseqGene 套件 - 線上說明

```
# 線上說明
```

```
browseVignettes("rnaseqGene")
```



The screenshot shows a web browser window with the title "RNA-seq workflow: gene-level". The URL in the address bar is "127.0.0.1:10323/library/rnaseqGene/doc/rnaseqGene.html". The page content is as follows:

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

Michael I. Love^{1,2}, Simon Anders³, Vladislav Kim⁴ and Wolfgang Huber⁴

¹Department of Biostatistics, UNC-Chapel Hill, Chapel Hill, NC, US
²Department of Genetics, UNC-Chapel Hill, Chapel Hill, NC, US
³Zentrum für Molekulare Biologie der Universität Heidelberg, Heidelberg, Germany
⁴European Molecular Biology Laboratory (EMBL), Heidelberg, Germany

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

- 1 Introduction
 - 1.1 Experimental data
- 2 Preparing quantification input to DESeq2
 - 2.1 Transcript quantification and *tximport* / *tximeta*
 - 2.2 Quantifying with *Salmon*
 - 2.3 Reading in data with *tximeta*
 - 2.4 *DESeq2* import functions
 - 2.5 *SummarizedExperiment*
 - 2.6 Branching point
- 3 The *DESeqDataSet* object, sample information and the design formula
 - 3.1 Starting from *SummarizedExperiment*
 - 3.2 Starting from count matrices
- 4 Exploratory analysis and visualization

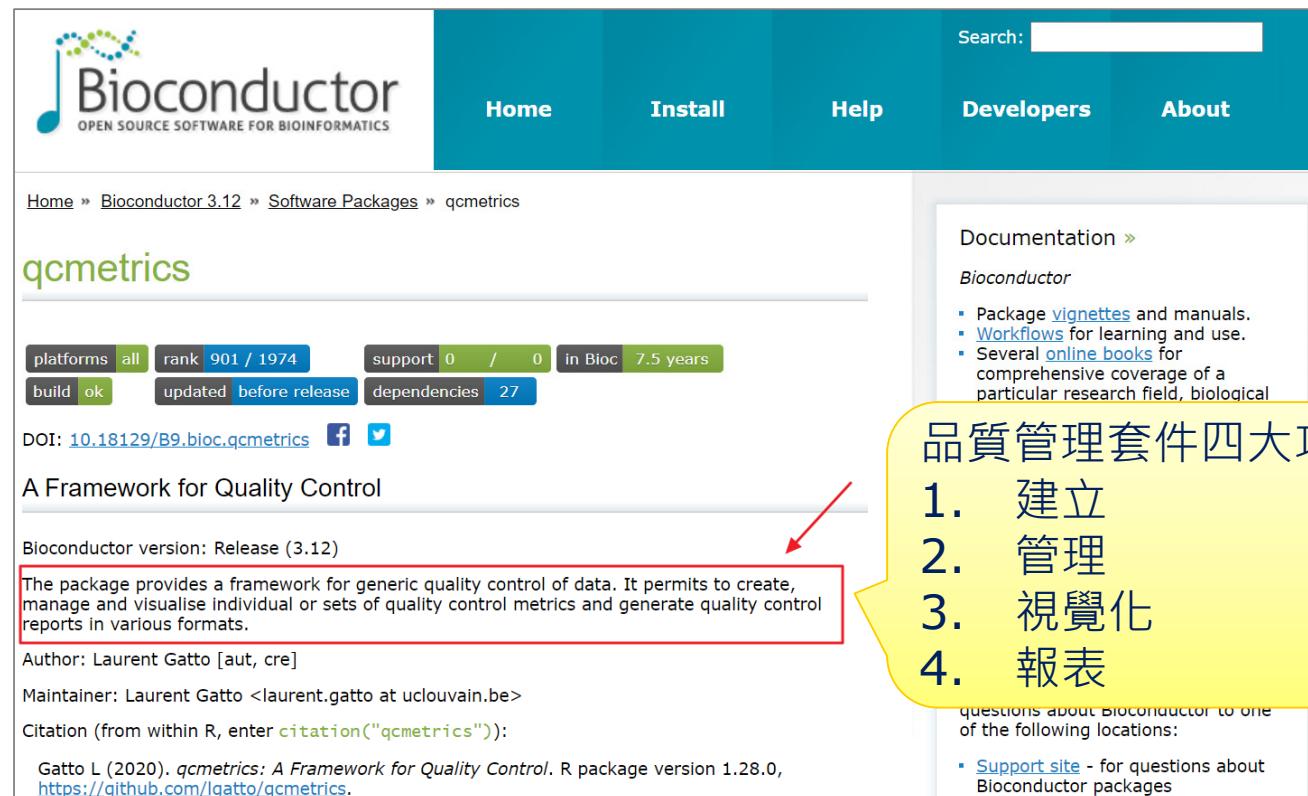
3. 品質控制技術

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>



The screenshot shows the Bioconductor qcmetrics package page. At the top, there's a navigation bar with links for Home, Install, Help, Developers, and About. A search bar is also present. Below the navigation, the package name 'qcmetrics' is displayed in green. The page includes a summary section with metrics like rank (901 / 1974), support (0 / 0), and dependencies (27). It also shows social sharing options (DOI: 10.18129/B9.bioc.qcmetrics, Facebook, Twitter) and a brief description of the package: 'A Framework for Quality Control'. A red box highlights a paragraph about the package's purpose: 'The package provides a framework for generic quality control of data. It permits to create, manage and visualise individual or sets of quality control metrics and generate quality control reports in various formats.' An arrow points from this highlighted text to a yellow callout box containing the '品質管理套件四大功能' (Four major functions of the quality management suite) list. The callout box also contains a link to the Bioconductor documentation.

Documentation »
Bioconductor

- Package [vignettes](#) and manuals.
- [Workflows](#) for learning and use.
- Several [online books](#) for comprehensive coverage of a particular research field, biological

品質管理套件四大功能

1. 建立
2. 管理
3. 視覺化
4. 報表

questions about Bioconductor to one of the following locations:

- [Support site](#) - for questions about Bioconductor packages

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

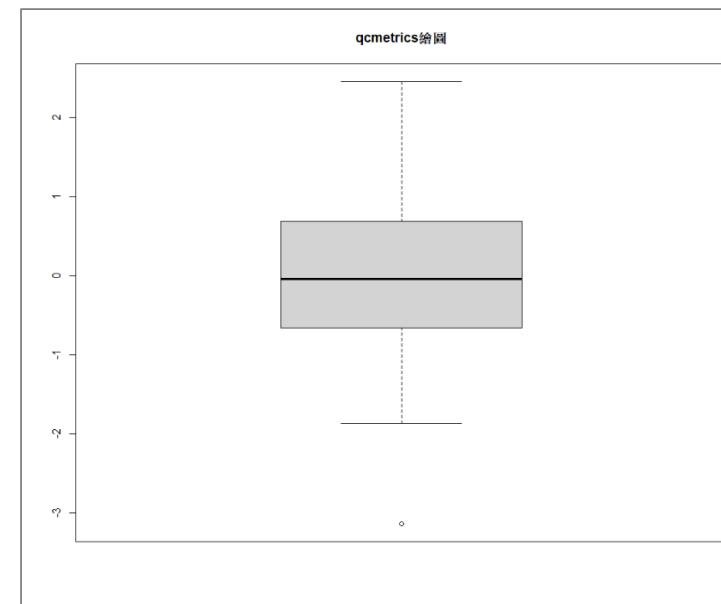
```
> qc
Object of class "QcMetric"
  Name: A test metric
  Status: NA
  Data: x
> show(qc)
Object of class "QcMetric"
  Name: A test metric
  Status: NA
  Data: x
> summary(qcdata(qc, "x"))
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-3.13692 -0.65860 -0.04072  0.01924  0.68710  2.44919
>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

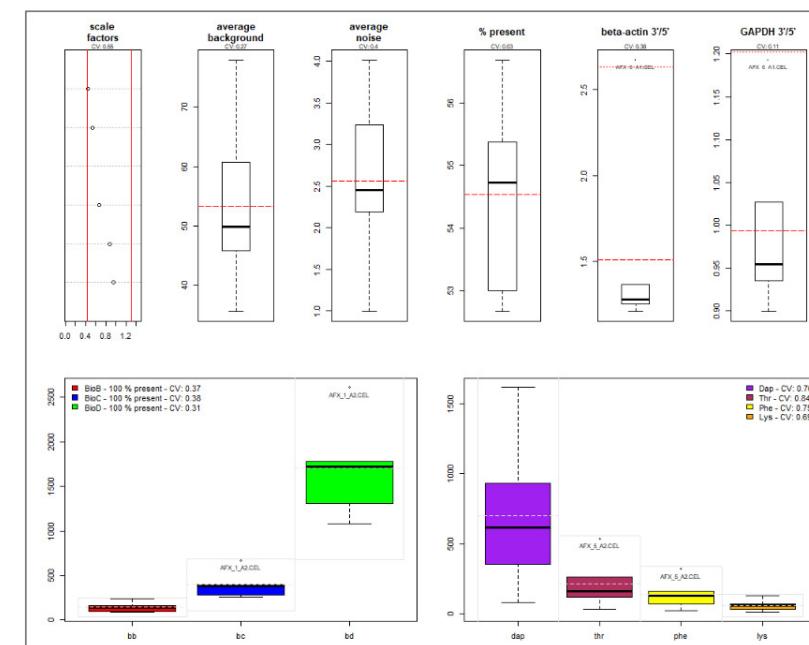
# 計算 RNA degradation
deg <- AffyRNADeg(refA)
deg

# 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

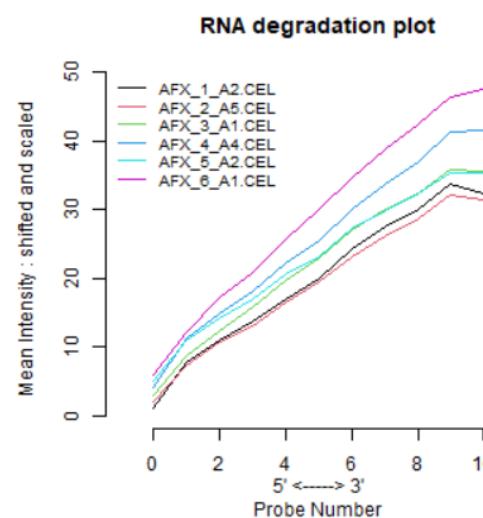
Quality control report generated with qcmetrics

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
```



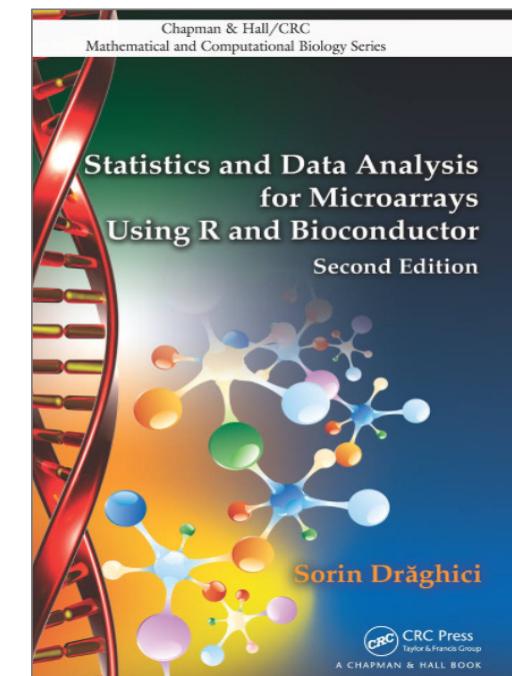
4. 結論與未來展望

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)
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