

Swiss Institute of
Bioinformatics

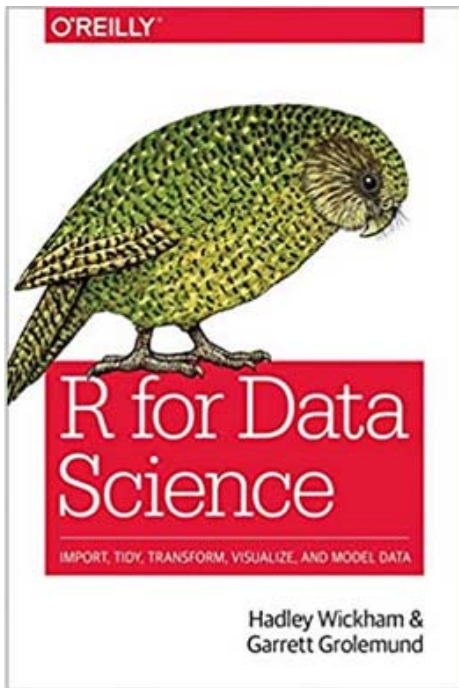
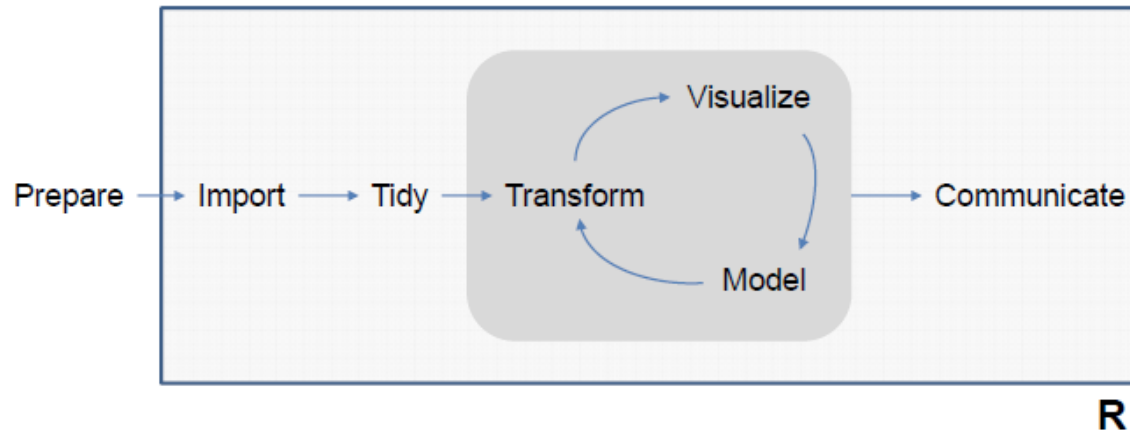
Introduction to Statistics

Isabelle Dupanloup (isabelle.dupanloup@sib.swiss) and Rachel Marcone (rachel.jeitziner@sib.swiss)

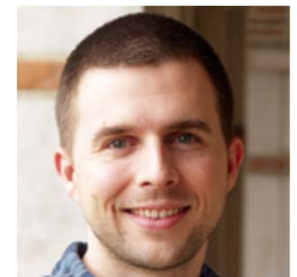
8th-11th February 2021

Data analysis with R: An introduction

Data analysis workflow



Hadley Wickham



Garrett Golemund

Adapted from Hadley Wickham

Prepare: make data available in a specific format

- Database
- Flat file
- Proprietary file

data.xls - LibreOffice Calc

File Edit View Insert Format Tools Data Window Help

Arial 10

AC16

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
1						0	0	1	2	3	4	5	6	8	10	12	14	16	17	18	19	21	22
2		WT																					
3		HFD	HFD	WB no / IH		10-Nov-05	9-Nov-05	16-Nov-05	23-Nov-05	30-Nov-05	7-Dec-05	14-Dec-05	28-Dec-05	11-Jan-06	25-Jan-06	8-Feb-06	23-Feb-06	2-Mar-06	10-Mar-06	17-Mar-06	30-Mar-06	4-Apr-06	
4	1	WT	HFD	224	23.1		23.6	24.4	25.6	25.3	25.1	25.2	26.2	29.1	29.5	29.8	30.7	30.5	31.2	31.5	31.4	31.4	31.9
5	3	WT	HFD	223	21.1		21.3	21.6	22.6	23.2	24	25.4	27.6	29.3	30.9	31.3	33.3	31.6	32.1	32.5	30.4	30.3	
6	5	WT	HFD	229	20.2		22.6	23.7	25.1	25.7	26.2	26.6	27.6	29.0	29.9	29.7	30.1	29.6	30.3	31.5	30.5	30.8	
7	7	WT	HFD	248	18.5		24.6	26.7	29.0	30.7	31.8	33.5	35.8	38.6	40.2	41.3	41.9	43	45	46.4	47.4	47.4	
8	9	WT	HFD	254	17.6		23	27.1	29.5	30.3	30.8	31.8	33.2	35.1	35.7	36.6	37.9	37.4	39.2	39.3	40	40.8	
9	11	WT	HFD	247	17.2		21.7	26.2	27.7	28.8	29.6	30.9	32.2	33.1	34.2	34.4	36.6	37.2	38.8	40.2	39.2	41.6	
10	13	WT	HFD	256	16.4		22.9	25.0	27.0	27.9	29	29.4	30.9	33.4	35.8	37	39.3	39	41.8	43.2	47.1	48.5	
11	15	WT	HFD	240	16.1		21.8	24.1	26.3	28.1	29.4	29.0	34.0	35.8	39.9	41.9	45.1	44.8	46.2	47.9	49.2	49.5	
12	17	WT	HFD	234	15.7		22.8	23.6	25.3	25.6	26.2	26.6	31.0	33.1	34.2	36.5	37.3	36.7	35.8	37.3	38.7	39.7	
13	19	WT	HFD	241	15.4		21.3	22.0	22.8	23.2	24.8	25.9	29.4	30.9	32.0	33.2	34	33.3	35.4	36.2	36.8	37.3	
14	21	WT	HFD	243	15		21.5	23.1	24.6	24.7	26.9	29.2	33.7	36.6	39.1	41	42.4	42.8	41.1	44.4	46.1	47.4	
15	23	WT	HFD	245	14.3		20.3	22.1	23.0	28.1	25.3	26.8	30.9	35.1	37.6	40.8	43.6	43.3	44.9	46.8	48.4	48.4	
16	25	WT	HFD	280		15.5	18.8	18.1	18.9	20.2	20.5	21.1	22.3	24.8	25.6	26.1	28	27.5	28.7	29.5	28.7	29.5	
17	27	WT	HFD	282		19.8	21.3	22.8	24.5	26.7	27.4	28.2	31.8	34.4	36.3	37.7	39.7	40.9	42.4	43.8	44.8	45.9	
18	29	WT	HFD	283		19.6	20.1	20.6	21.2	21.7	23.1	23.4	24.7	27.2	28.4	28.4	30.5	30.6	30.9	32.1	31.1	31.3	
19		WT				0	0	1	2	3	4	5	6	8	10	12	14	16	17	18	19	21	22
20		FEN-HFD		WB no / IH		2-Nov-05	9-Nov-05	16-Nov-05	23-Nov-05	30-Nov-05	7-Dec-05	14-Dec-05	28-Dec-05	11-Jan-06	25-Jan-06	8-Feb-06	23-Feb-06	2-Mar-06	10-Mar-06	17-Mar-06	30-Mar-06	4-Apr-06	
21	1	WT	FEN-HFD	222	23.5		22.4	24.3	26.1	27.8	28.4	29.6	30.7	32	32.6	32.1	33.9	33.4	33.7	33.9	34.5	34.7	
22	3	WT	FEN-HFD	250	21.7		23.5	24.5	25.6	26.8	27.3	28.6	29.9	31.5	32.2	33.0	35	35.4	35.2	36.5	35.5	35.6	
23	5	WT	FEN-HFD	227	20.3		22.2	23.4	24.4	24.9	25.4	26.2	27.4	27.3	28.9	29.0	30.3	30.3	30.3	31.2	30.7	31.1	
24	7	WT	FEN-HFD	226	19.5		21.1	22.6	23	24.1	24.1	24.4	26.8	27.5	29	28.3	28.9	29	27.9	29.5	28.7	27.9	
25	9	WT	FEN-HFD	253	17.6		23.8	25.2	26.2	27.5	28.6	29.6	30.1	32.2	33.5	33.3	34.3	33.9	33.9	34.8	35	35.4	
26	11	WT	FEN-HFD	252	17.5		21.9	23.2	25.2	25.9	26.9	28.9	30.1	33.7	34.9	35.2	36.4	37	38.6	39.1	40.5	39.6	
27	13	WT	FEN-HFD	251	16.5		21.6	22.2	24	25.2	25.7	26.8	28.2	30.5	31.5	32.4	33.5	34.2	34.4	33.8	33.4	33.6	
28	15	WT	FEN-HFD	249	16.3		22.8	24.2	25.6	25.8	27.2	28.2	29	31	31.3	31.3	31.7	33.8	33.7	34.6	35.8	35.9	
29	17	WT	FEN-HFD	242	15.9		21.2	22.6	23.9	23.8	23.8	25.2	26.6	28.9	30.5	32	34	34.2	34.9	35	37.3	37.8	
30	19	WT	FEN-HFD	244	15.7		20.7	22.3	23.1	24.3	25.4	26.5	28.5	31	31.4	32.3	33.3	32.3	33.5	33.3	33.8	33.1	
31	21	WT	FEN-HFD	246	15.2		21	23	25.4	26.6	28.1	29.4	33.4	36.9	39.6	41.2	45.2	46.2	48.1	49.7	50.7	53.1	
32	23	WT	FEN-HFD	236	14.4		19.9	21.7	23.8	24	23.9	24.3	26.5	28.6	29.6	31.2	33.3	32.9	34	34.2	34.9	34.4	
33	25	WT	FEN-HFD	287		14.5	16.7	18.8	21.1	22.3	24	24.7	26.4	28.6	30.5	31.3	32.7	33	33.2	34.3	35.1	35.2	
34	27	WT	FEN-HFD	284		20.2	20.9	21.6	22.2	22.7	23.2	23	25.1	25.2	26.8	27	29	29.2	29.4	29.8	30.1	30.4	
35	29	WT	FEN-HFD	288		18.7	19.6	20.5	22.6	23.7	25.1	25.2	27.8	30.2	31.4	32	32.8	32.4	32.4	33.1	34.1	34.2	
36		KO				0	0	1	2	3	4	5	6	8	10	12	14	16	17	18	19	21	22
37		HFD		WB no / IH		2-Nov-05	9-Nov-05	16-Nov-05	23-Nov-05	30-Nov-05	7-Dec-05	14-Dec-05	28-Dec-05	11-Jan-06	25-Jan-06	8-Feb-06	23-Feb-06	2-Mar-06	10-Mar-06	17-Mar-06	30-Mar-06	4-Apr-06	
38	2	KO	HFD	206	22.2		25.8	26.8	28	29.9	30.8	31.9	33.6	34.2	35.1	36.7	37.1	37.6	38.1	39.8	40.1		
39	4	KO	HFD	201	21.6		25.7	27.8	30.5	31.4	32.4	33.7	36.3	38.7	41.1	42.2	42.2	41.4	45.2	47.1	45.1	44.8	
40	6	KO	HFD	203	21.4		25	26.5	27.6	28.6	29.5	30.2	32	35.4	36.8	37	39.3	41	41.1	38.2	40.9	41.8	

new style BW sheet (2) / July 14 / July 28 / Aug 3 / aug 11 group making / Aug 17 / Aug 22 / Making new groups 31 Aug / Body weights cohort 1 / 4

Sheet 1 / 30 PageStyle_new style BW sheet (2) Sum=0 75%

Which tool to use for data analysis ?

Spreadsheets



Statistical packages



Programming languages

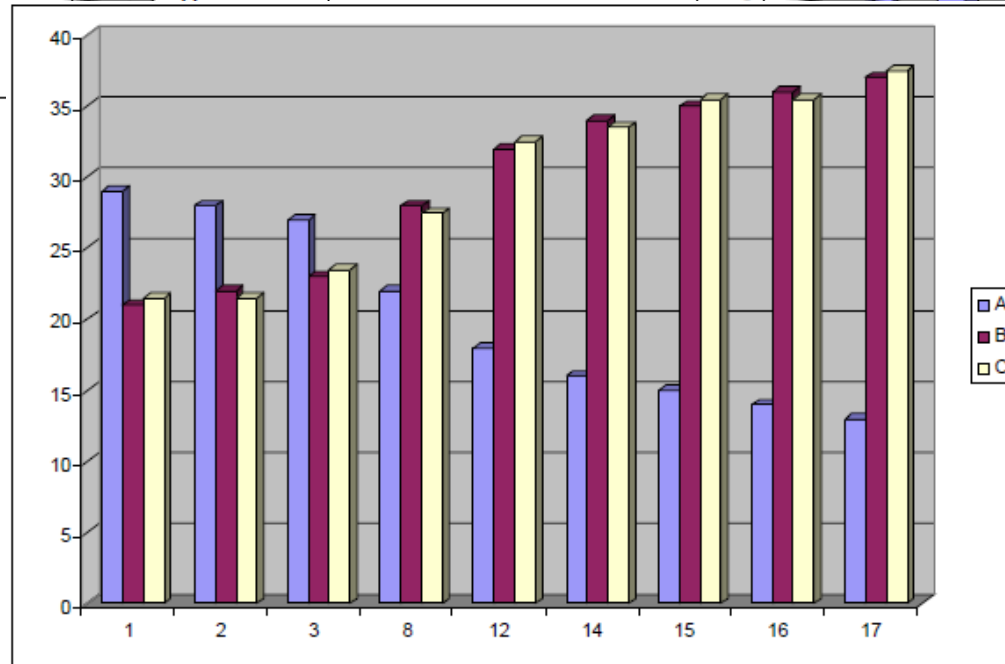
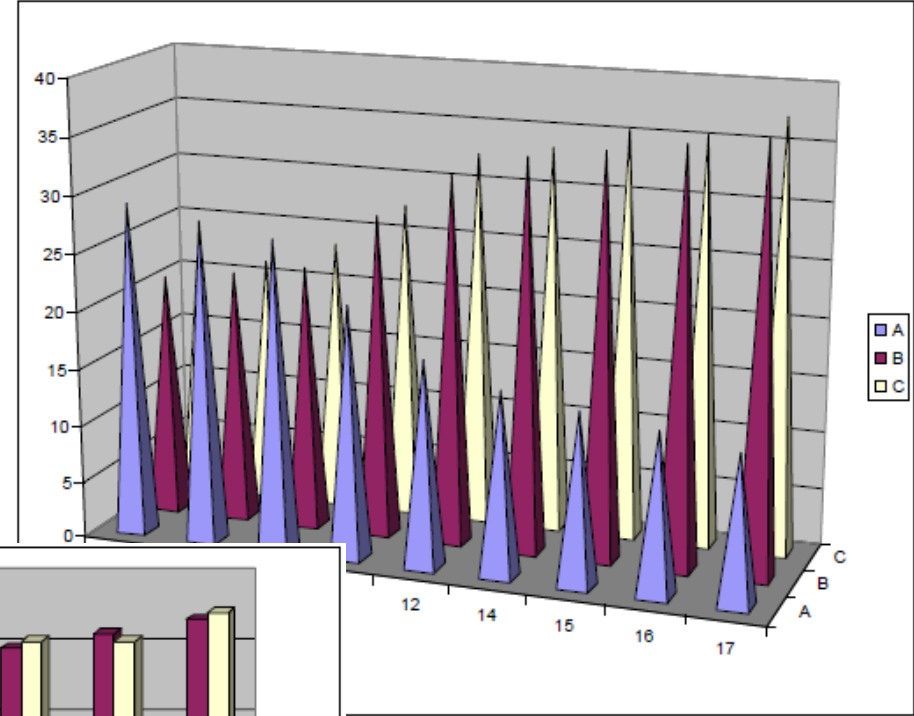
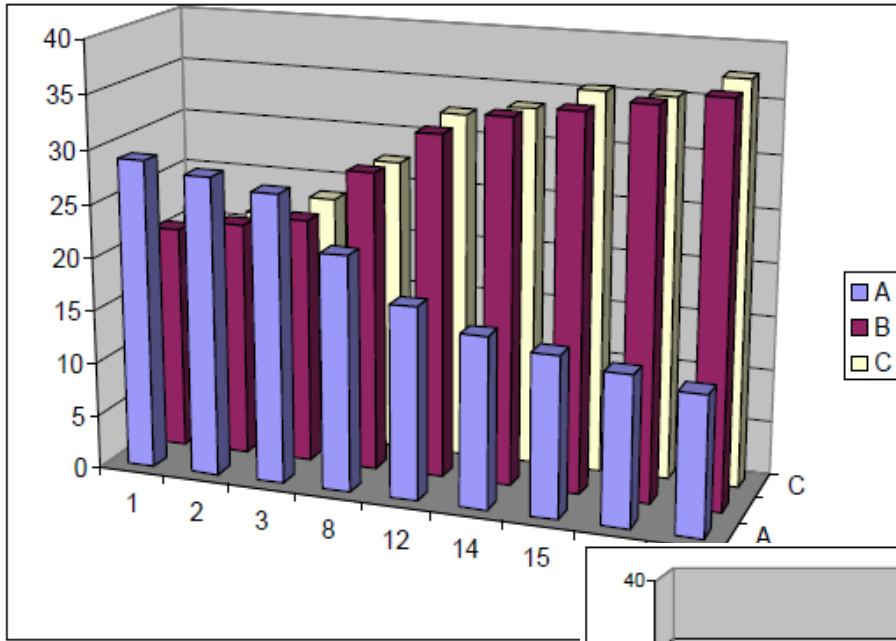


Sample ID	Mouse ID	Genotype	Tumor size	Bcl9 [dCt]	Axin2 [dCt]	Axin2 [dCt]	Axin2 [dCt]	T2
1	S1	WT1	WT	8.7	23	24.5	28.3	25.1
2	S2	WT2	WT	8.4	23.4	24.3	28.4	25.6
3	S3	WT3	WT	7.9	23.5	24.6	28.6	25.3
4	S4	WT4	WT	7.8	23.5	24.3	27.9	24.9
5	S5	WT5	WT	8.2	23.1	24.8	26.3	24.8
6	S6	WT6	WT	7.4	23.6	24.9	25.4	26.1
7	S7	WT7	WT	8.5	22.9	25.1	29.1	25.3
8	S8	WT8	WT	2.5	24	24.3	20.1	23.2
9	S9	WT9	WT	6.1	23.8	24.7	27.4	27.3
10	S10	WT10	WT	3.8	22.8	26.1	28.4	24.3
11	S21	WT1	WT	2.1	23.6	25.1	28.5	26.3
12	S22	WT2	WT	3	23.9	23.2	28.5	25.1
13	S23	WT3	WT	7.9	23.5	24.3	28.9	25.3
14	S24	WT4	WT	2	23.5	22.9	29.1	25.7
15	S25	WT5	WT	7.5	23.7	24.5	28.5	26.1
16	S26	WT6	WT	7.3	23.7	25.7	30.1	24.4
17	S27	WT7	WT	3	23.2	25.2	29.1	24.8
18	S28	WT8	WT	8	23.1	24.9	29.8	23.2
19	S29	WT9	WT	7.7	23.8	24.1	29.9	24.7
20	S30	WT10	WT					
21	S41	WT1	WT					
22	S42	WT2	WT	7.2	22.9	24.7	29.5	26.3
23	S43	WT3	WT	8.2	22.8	24.9	29.7	25.9
24	S44	WT4	WT					

Annoyances with spreadsheets

- Many standard methods in statistics are not available. Other methods only offer basic options (linear regression)
- Different analysis require user to reorganize the data
- Probably ok for simple calculations (basic summary statistics, simple regression)
- Add-ons can be used for missing functions (e.g. StatPlus for Excel)
- Many types of graphics violate standards of good graphics

Sample ID	Mouse ID	Genotype	Tumor size [mm]	Bcl9 [dCt]	Axin2 [dCt]	Axin2 [dCt]	Axin2 [dCt]	T2
2	S1	WT1	WT	8.7	23	24.5	28.3	25.1
3	S2	WT2	WT	8.4	23.4	24.3	28.4	25.6
4	S3	WT3	WT	7.9	23.5	24.6	28.6	25.3
5	S4	WT4	WT	7.8	23.5	24.3	27.9	24.9
6	S5	WT5	WT	8.2	23.1	24.8	26.3	24.8
7	S6	WT6	WT	7.4	23.6	24.9	25.4	26.1
8	S7	WT7	WT	8.5	22.9	25.1	29.1	25.3
9	S8	WT8	WT	2.5	24	24.3	20.1	23.2
10	S9	WT9	WT	6.1	23.8	24.7	27.4	27.3
11	S10	WT10	WT	3.8	22.8	26.1	28.4	24.3
12	S21	WT1	WT	2.1	23.6	25.1	28.5	26.3
13	S22	WT2	WT	3	23.9	23.2	28.5	25.1
14	S23	WT3	WT	7.9	23.5	24.3	28.9	25.3
15	S24	WT4	WT	2	23.5	22.9	29.1	25.7
16	S25	WT5	WT	7.5	23.7	24.5	28.5	26.1
17	S26	WT6	WT	7.3	23.7	25.7	30.1	24.4
18	S27	WT7	WT	3	23.2	25.2	29.1	24.8
19	S28	WT8	WT	8	23.1	24.9	29.8	23.2
20	S29	WT9	WT	7.7	23.8	24.1	29.9	24.7
21	S30	WT10	WT					
22	S41	WT1	WT					
23	S42	WT2	WT	7.2	22.9	24.7	29.5	26.3
24	S43	WT3	WT	8.2	22.8	24.9	29.7	25.9
25	S44	WT4	WT					
26	S45	WT5	WT	8.8	23.4	26.1	28.5	25.1
27	S46	WT6	WT	8.9	23.7	26.1	28.1	24.3
28	S47	WT7	WT	3	23.8	23.1	28.8	26.1
29	S48	WT8	WT					
30	S49	WT9	WT					
31	S50	WT10	WT					
32	S11	KO1	KO	8.4	30.9	26.4	27.6	29.5
33	S12	KO2	KO	8.1	30.5	25.6	28.5	28.4
34	S13	KO3	KO	7.8	32	27.5	28.6	27.5
35	S14	KO4	KO	6.4	33.4	28.5	27.5	26.6
36	S15	KO5	KO	6.4	31.2	28.1	27.4	28.6
37	S16	KO6	KO	7.6	34.2	26.4	28.4	29.1
38	S17	KO7	KO	8.7	33.2	26.7	28.1	30.5



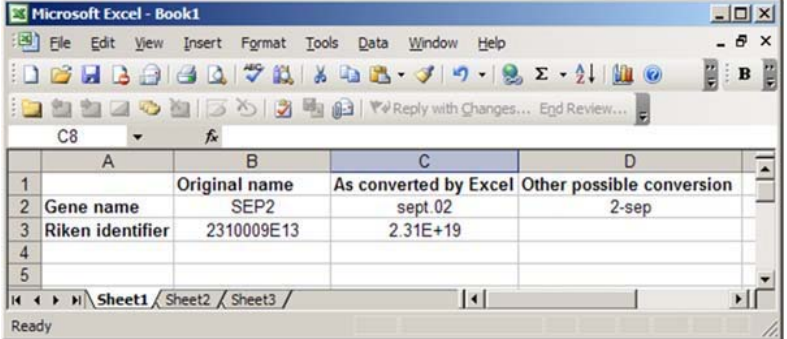
Annoyances with spreadsheets

Mistaken Identifiers: Gene name errors can be introduced inadvertently when using Excel in bioinformatics

[Barry R Zeeberg](#), [Joseph Riss](#), [David W Kane](#), [Kimberly J Bussey](#), [Edward Uchio](#), [W Marston Linehan](#), [J Carl Barrett](#) & [John N Weinstein](#) ✉

BMC Bioinformatics **5**, Article number: 80 (2004) | [Cite this article](#)

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The screenshot shows a Microsoft Excel spreadsheet with the following data:

	A	B	C	D
1		Original name	As converted by Excel	Other possible conversion
2	Gene name	SEP2	sept.02	2-sep
3	Riken identifier	2310009E13	2.31E+19	
4				
5				

“The date conversions affect at least 30 gene names; the floating-point conversions affect at least 2,000 if Riken identifiers are included. These conversions are irreversible; the original gene names cannot be recovered.”

Example of a dataset which is difficult to use with any statistical program

Sample	sample_init	Study_ID	comments	unique patients	1	2	3	4	5	6	7	8	9	10	Age_OP	gender	APFY
2248	MD_2	BE-03		1	0	1	1	0	20	0	50	M	1				
2467	RB_2	BE-04		1	1	1	1	1	12	0	55	M	1				
2468	HB_2	BE-05		1	1	1	1	1	13	1	66	M	1				
2482	WO_2	ZH-01		1	1	1	1	1	7	1	64	M	1				
2484	HW_2	ZH-04		1	1	1	1	1	5	1	50	M	1				
2485	BD_2	ZH-05		1	1	1	1	1	6	0	53	F	1				
2486	BH_2	ZH-06		1	1	1	1	1	9	1	48	F	1				
2487	AW_2	ZH-07		1	1	1	1	1	9	0	53	M	1				
2488	AJN_2	ZH-08		1	1	1	1	1	5	0	35	M	1				
2489	KO_2	ZH-09		1	0	1	1	1	54	0	59	M	1				
2490	BS_2	ZH-11		1	0	1	1	1	150	0	59	M	1				
2491	KPR_3	ZH-12		1	1	1	1	1	5	0	32	M	1				
2492	CB_3	ZH-13		1	0	1	1	0	6	0	37	F	1				
2493	RM_3	ZH-14		1	0	1	1	1	63	0	39	M	1				
2496	BR_2	ZH-17		1	1	1	1	1	5	0	61	F	1				
2497	SP_2_0	2497		1		0	0			1	58	M	1				
2498	NA_2_0	2498		1		0	0			0	54	M	1				
2499	GK_2_0	2499		1		0	0			1	68	M	1				
2500	HIB_2_0	2500		1		0	0			1	62	M	1				
2501	BI_2	2501		1		0	0			0	70	F	1				
2502	VWJ_2	2502		1		0	0			1	59	M	1				
2503	BP_3	2503	autops	1		0	0			0	61	M	1				
2504	UA_2_0	2504		1		0	0			0	35	F	1				
2505	GE_1	2505		0		0	0			1	65	F	1				
2506	TS_2	2506		1		0	0			0	50	M	1				
2507	HV_2_0	2507		1		0	0	2507		0	65	F	1				
2508	TI_3	2508		1		0	0			1	31	F	1				
2509	TI_4_0	2509	Rec 2508	0		0	0			1	31	F	1				
2510	GE_2_0	2510	Rec 2505	1		0	0			1	67	F	0				
2511	SI_2	ZH-18		1	1	1	1	1	5	0	24	F	1				
2512	BH_3	ZH-06.1	Rec 2486	0		1	0			1	50	F	1				
2513	CG_2	2513		1		0	0			0	63	M	1				
1152	NCH1152	NCH1152		Xenograft						1		hXenograft	1				
1154	NCH1154	NCH1154		Xenograft						1		hXenograft	1				
1155	NCH1155	NCH1155		Xenograft						1		hXenograft	1				
1157	NCH1157	NCH1157		Xenograft	1		1		5	1		hXenograft	1				
1159	NCH1159	NCH1159		Xenograft	1		1		5	1		hXenograft	1				
1161	NCH1161	NCH1161		Xenograft	1		1		5	1		hXenograft	1				
BS 153 Control	ctrl BS153	ctrl BS153		Cell line						1		hCell line	0				

Comparison of statistical packages

From Wikipedia, the free encyclopedia

The following tables compare general and technical information for a number of [statistical analysis](#) packages.

Contents [hide]
1 General information
2 Operating system support
3 ANOVA
4 Regression
5 Time series analysis
6 Charts and diagrams
7 Other abilities
8 See also
9 Footnotes
10 References
11 Further reading

General information [\[edit\]](#)

Product	Developer	Latest version	Open source	Software license	Interface	Written in	Scripting languages
ADaMSoft	Marco Scarno	27 April 2015	Yes	GNU GPL	CLI, GUI	Java	
Alteryx	Alteryx Inc.	2019.2 (June 2019)	No	Proprietary	GUI, Python SDK, js SDK	C#, C++, Python, R, js	R, Python
Analyse-it	Analyse-it		No	Proprietary	GUI	C#, C++, Fortran	
ASReml	VSN International	26 March 2014	No	Proprietary	CLI		
BMDP	Statistical Solutions		No	Proprietary			

What is R ?

- R is an open source complete and flexible software environment for statistical computing and graphics.
- It includes :
 - Tools for data import and manipulation
 - Large set of data analysis tools
 - Graphical tools
 - As a programming language, a simple development environment, with a text editor
- R itself is written primarily in C and Fortran, and is an implementation of the statistical language S

Why R ?

- R has become the tool of choice for statistical analysis in several fields, including life sciences
- Two reasons for this success: it is free and many contributed packages are available (can be installed and run directly from R).
- Well-designed publication-quality plots can be produced, including mathematical symbols and formulae where needed.
- Many tools implemented for bioinformatics

Advantages of R

- Advantages of R
 - Availability and compatibility
 - State-of-the-art graphics capabilities
 - Can import files from other (statistical) programs
 - New version every x months
 - Interactive development environments (IDEs) available
 - Large users community
- Advantages of *learning* R
 - Learn to program and do reproducible research
 - Speak the common language

Drawbacks of R

- «Expert friendly»
 - Learn by example
 - Not very (easily) interactive
 - Command-based
 - Documentation sometimes cryptic
-
- (Too) large amount of resources
 - Constantly evolving
 - Memory intensive and slow at times

Downloading and installing R: the R website



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The R Project for Statistical Computing

Getting Started

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](#).

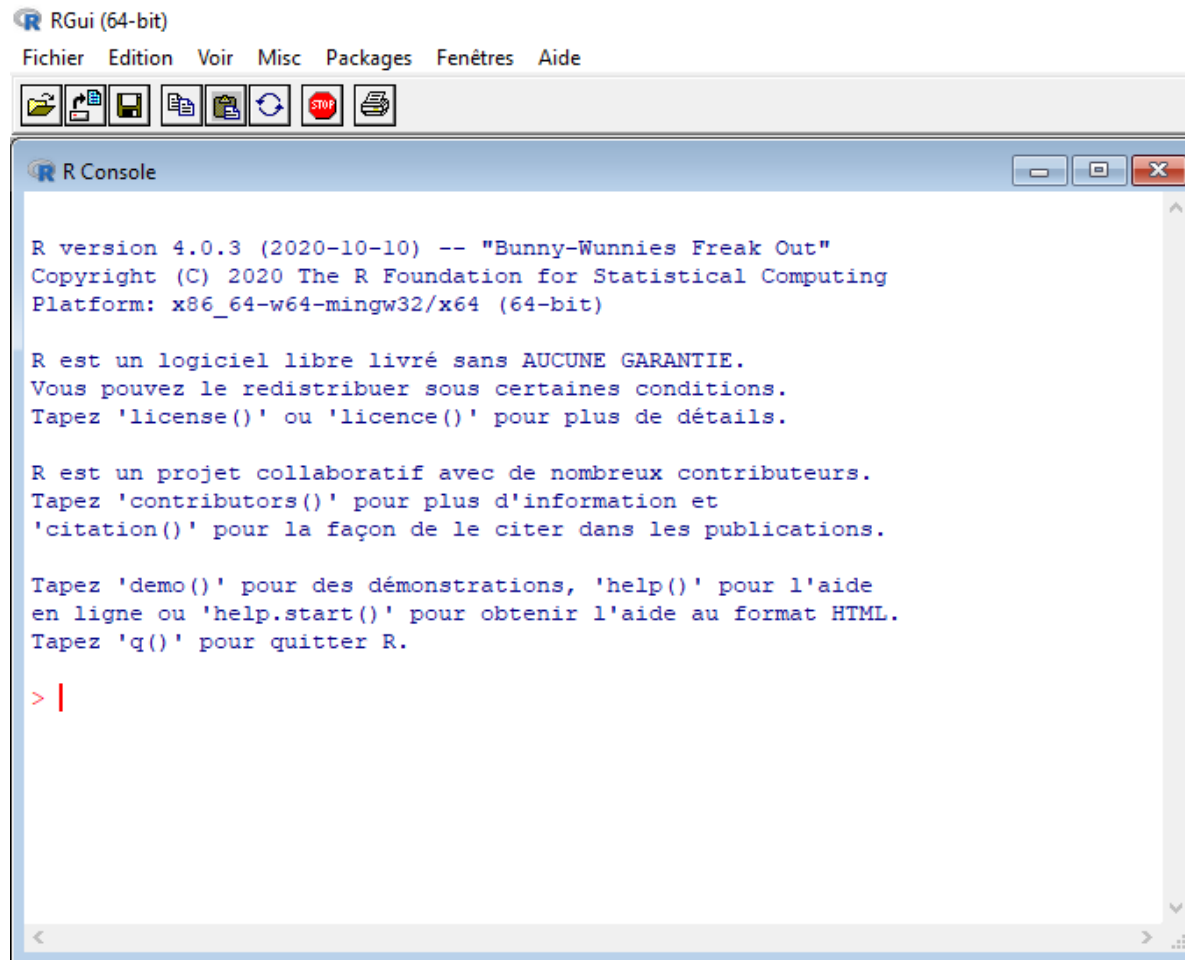
If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

News

- **R version 4.0.4 (Lost Library Book) prerelease versions** will appear starting Friday 2021-02-05. Final release is scheduled for Monday 2021-02-15.
- **R version 4.0.3 (Bunny-Wunnies Freak Out)** has been released on 2020-10-10.
- Thanks to the organisers of useR! 2020 for a successful online conference. Recorded tutorials and talks from the conference are available on the [R Consortium YouTube channel](#).
- **R version 3.6.3 (Holding the Windsock)** was released on 2020-02-29.
- You can support the R Foundation with a renewable subscription as a [supporting member](#)

<https://www.r-project.org/>

R console



```
RGui (64-bit)
Fichier Edition Voir Misc Packages Fenêtres Aide

R Console

R version 4.0.3 (2020-10-10) -- "Bunny-Wunnies Freak Out"
Copyright (C) 2020 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R est un logiciel libre livré sans AUCUNE GARANTIE.
Vous pouvez le redistribuer sous certaines conditions.
Tapez 'license()' ou 'licence()' pour plus de détails.

R est un projet collaboratif avec de nombreux contributeurs.
Tapez 'contributors()' pour plus d'information et
'citation()' pour la façon de le citer dans les publications.

Tapez 'demo()' pour des démonstrations, 'help()' pour l'aide
en ligne ou 'help.start()' pour obtenir l'aide au format HTML.
Tapez 'q()' pour quitter R.

> |
```

The prompt “>” indicates that R is waiting for you to type a command

RStudio interface

The image shows the RStudio interface with four red arrows pointing to specific panels:

- Editor:** Points to the script editor showing R code for a one-sample t-test simulation.
- Console, terminal:** Points to the console window showing the execution of the code and warning messages.
- Workspace, history:** Points to the Environment pane showing the current workspace with variables like `weight`, `mean_weight`, and `sd_weight`.
- File explorer, plots, packages, help:** Points to the Plots pane showing a boxplot of the simulated weight data.

```
13
14
15 # -----
16 # one sample t-test
17 # -----
18
19 # weight <- runif(12, min=26, max=33)
20 weight <- c(31.89381,28.45898,28.18985,30.06679,27.04369,32.30934,
21            31.52805,32.28462,27.25366,29.64034,30.74083,26.88916)
22 weight <- as.data.frame(weight)
23
24 mean_weight <- mean(weight$weight)
25 sd_weight <- sd(weight$weight)
26
27 hist(weight$weight, main="Mice weight at 18 weeks", xlab="")
28
29 ggboxplot(weight$weight, width = 0.5, add = c("mean","jitter"), ylab =
30 weight (g)", xlab = F)
31 identify_outliers(weight)
32
33
```

Environment

Global Environment	
weight	12 obs. of 1 variable
mean_weight	29.6915933333333
sd_weight	2.08078056863429

Plots

Weight (g)

1

R scripts and workspace

- R script (.R file)
 - Very useful instead of typing commands on the console.
 - Allows you to keep track of what you are doing and make any modification easier
 - To actually execute some commands, you can select the lines and run the execution
- Workspace (.Rdata file)
 - The internal memory where R will store the objects you created during the session.
 - To list what is in your workspace: `ls()`
 - To empty the workspace from all objects: `rm(list=ls())`
 - To save only specific R objects: `save(object_name(s), "name_of_file.RData")`
 - To save your entire workspace: `save.image("name_of_file.RData")`
 - To load your workspace: `load("name_of_file.RData")`

R Markdown

- R Markdown provides an authoring framework for data science. You can use a single R Markdown file to both:
 - save and execute code
 - generate high quality reports that can be shared with an audience
- R Markdown documents are fully reproducible and support dozens of static and dynamic output formats



<https://rmarkdown.rstudio.com/lesson-1.html>

A .Rmd file

YAML metadata

```
---  
title: "Topographic Data in R"  
author: "Eric Pante, Benoit Simon-Bouhet and Jean-Olivier Irisson"  
output: html_document  
params:  
  dataset: "Florida"  
---
```

Text

marmap is a package designed for downloading, plotting and manipulating bathymetric and topographic data in R.

Code chunks

```
{r setup}  
library(marmap, warn = FALSE)  
library(ggplot2, warn = FALSE)  
library(viridis, warn = FALSE)  
  
data(list = params$dataset)  
df <- fortify(get(params$dataset))  
  
p <- ggplot(df, aes(x=x, y=y)) +  
  geom_raster(aes(fill=z)) +  
  geom_contour(aes(z=z), colour="white", size=0.1,  
    breaks=c(-100, -200, -500, -1000, -2000, -4000)) +  
  geom_contour(aes(z=z), colour="white", size=0.3, breaks=0) +  
  theme_void() +  
  coord_fixed()  
...
```

Using Topographic Colors

Leaving R

- To leave R, use the `q()` command (or "quit" from the menu in RStudio):

```
> q( )
```

```
Save workspace image? [y/n/c]:
```

Answers:

y save workspace image

n **don't save workspace image**

c cancel quitting

Functions, operators and variables

```
CIhigh <- mean(x) + 1.96*sd(x)/sqrt(n)
```

Variables: objects stored in memory

Functions: always followed by parenthesis

Operators

R syntax

- Case sensitive: A is not a
- Variable names can include A-Z, a-z, 0-9, but can not start with a number
- Commands can be separated by ; or newline

```
> x <- 2; x+2
```

```
[1] 4
```

- # indicates comments:

```
> maxvalue <- 2 # Data above two is not relevant
```

R help

```
> ?sum # equivalent to help(sum)
```

```
sum {base}
```

R Documentation

Sum of Vector Elements

Description

`sum` returns the sum of all the values present in its arguments.

Usage

```
sum(..., na.rm = FALSE)
```

Arguments

`...` numeric or complex or logical vectors.
`na.rm` logical. Should missing values (including `NaN`) be removed?

Using R as a calculator

```
> 2*3
```

```
[1] 6
```

```
> log(6)/2^2
```

```
[1] 0.4479399
```

```
> exp(6)-4
```

```
[1] 399.4288
```

```
> pi-3
```

```
[1] 0.1415927
```

Using R as a programming language

```
> x <- 2.0
```

```
> x
```

```
[1] 2.0
```

```
> y = 3.0 # Equivalent to y <- 3.0
```

```
> y; x
```

```
[1] 3
```

```
[1] 2
```

```
> 1/x
```

```
[1] 0.5
```


Creating vectors using the c() command

```
> x <- c(1.3, 0.32, 10.5, 5.9, 6.3)
```

```
> x
```

```
[1] 1.30 0.32 10.50 5.90 6.30
```

```
> y <- c(x, 1.4, x, x); y
```

```
[1] 1.30 0.32 10.50 5.90 6.30
```

```
[6] 1.40 1.30 0.32 10.50 5.90
```

```
[11] 6.30 1.30 0.32 10.50 5.90
```

```
[16] 6.30
```

Vector operations

Vector operations work element by element:

```
> x <- c(1.3, 0.32, 10.5, 5.9, 6.3)
```

```
> y <- x*2; y
```

```
[1] 2.60 0.64 21.00 11.80 12.60
```

```
> z <- x*y; z
```

```
[1] 3.38 0.21 220.50 69.62 79.38
```

Recycling

- If a vector is too short, R recycles it (reuses it) as needed:

```
> x <- c(1.3, 0.32, 10.5, 5.9)
```

```
> y <- c(2, 10)
```

```
> x*y
```

```
[1] 2.6 3.2 21.0 59.0
```

```
1.3*2 0.32*10 10.5*2 5.9*10
```

- A warning message is displayed if the shortest vector can not be recycled entirely:

```
> x <- c(1.3, 0.32, 10.5, 5.9, 6.3)
```

```
> x*y
```

```
[1] 2.6 3.2 21.0 59.0 12.6
```

Warning message:

In x * y :

longer object length is not a multiple of shorter object length

Generating sequences of numbers

```
> 1:10
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```

This is equivalent to:

```
> c(1,2,3,4,5,6,7,8,9,10)
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```

```
> 10:1
```

```
[1] 10 9 8 7 6 5 4 3 2 1
```

Beware of operator priority

```
> x <- 2*1:10
# equivalent to x <- 2*(1:10)
> x
[1] 2 4 6 8 10 12 14 16 18 20
> n <- 10
> 1:n-1
# equivalent to (1:n)-1
[1] 0 1 2 3 4 5 6 7 8 9
> 1:(n-1)
[1] 1 2 3 4 5 6 7 8 9
```

The seq() function: the same, but more flexible

```
> seq(from=1, to=10)
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```

```
> seq(from=1, to=5, by=0.5)
```

```
[1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
```

```
> x <- seq(from=1, to=5, length=17)
```

```
> x
```

```
[1] 1.00 1.25 1.50 1.75 2.00 2.25 2.50 2.75
```

```
[9] 3.00 3.25 3.50 3.75 4.00 4.25 4.50 4.75
```

```
[17] 5.00
```


Non numeric vectors: boolean (logical) values

```
> x <- seq(from=1, to=5, length=17)
> x
[1] 1.00 1.25 1.50 1.75 2.00 2.25 2.50 2.75
[9] 3.00 3.25 3.50 3.75 4.00 4.25 4.50 4.75
[17] 5.00
> y <- x<5
> y
[1] TRUE TRUE TRUE TRUE TRUE TRUE
[7] TRUE TRUE TRUE TRUE TRUE TRUE
[13] TRUE TRUE FALSE
> sum(x<5)
[1] 16
```

Missing values are designated by NA

```
> z <- c(1:3,NA)
```

```
> z
```

```
[1] 1 2 3 NA
```

```
> is.na(z)
```

```
[1] FALSE FALSE FALSE TRUE
```

```
> mean(z)
```

```
[1] NA
```

```
> mean(z, na.rm=TRUE)
```

```
[1] 2
```

Character strings

```
> char <- c("hello", "world", "!"); char  
[1] "hello" "world" "!"
```

Vectors can not combine numbers and characters:

```
> char <- c("hello", 3:5, "world"); char  
[1] "hello" "3" "4" "5" "world"
```

```
> char <- c(char, NA); char  
[1] "hello" "3" "4" "5" "world" NA
```

Selecting subsets of vectors using []

```
> x <- 10:30
```

```
> x[2]
```

```
[1] 11
```

```
> x[1:5]
```

```
[1] 10 11 12 13 14
```

Selecting subsets of vectors using [] and boolean vectors

```
> x <- 10:30
> x[x>25]
[1] 26 27 28 29 30
> x <-c(seq(from=5, to=10,by=0.5),NA,
seq(from=11,to=15,by=0.5),NA,
seq(from=16,to=20,by=0.5))
> x[!is.na(x)]
[1] 5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5
[9] 9.0 9.5 10.0 11.0 11.5 12.0 12.5 13.0
[17] 13.5 14.0 14.5 15.0 16.0 16.5 17.0 17.5
[25] 18.0 18.5 19.0 19.5 20.0
```

Changing parts of vectors using []

```
> x[32] <- 200
```

```
> x[c(10,29)] <- c(1,100)
```

```
> x[x>15] <- NA
```


Finding the length of a vector

```
> x <- 1:5
```

```
> length(x)
```

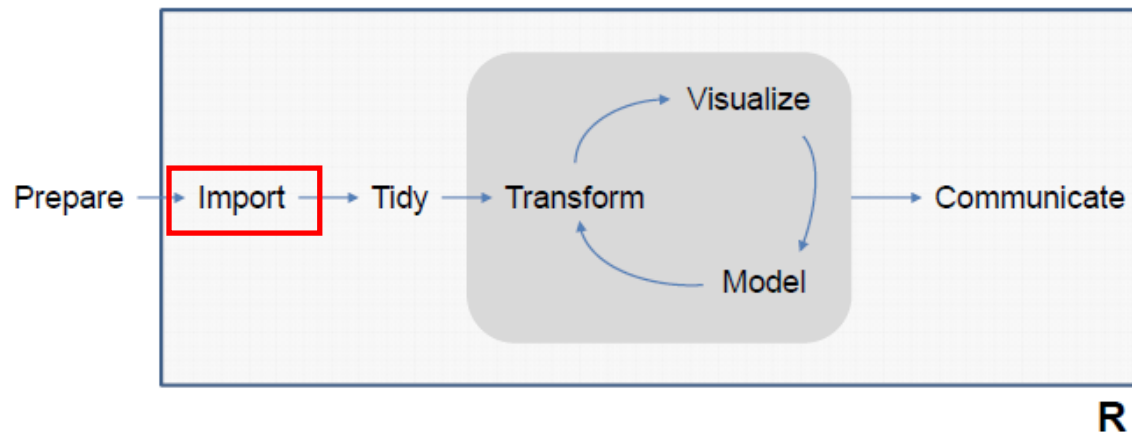
```
[1] 5
```

```
> y <- 1:16
```

```
> len <- length(y) ; len
```

```
[1] 16
```

Data analysis workflow



Adapted from Hadley Wickham

Importing data into R

- R can import flat files using e.g. the commands:

```
read.table()
```

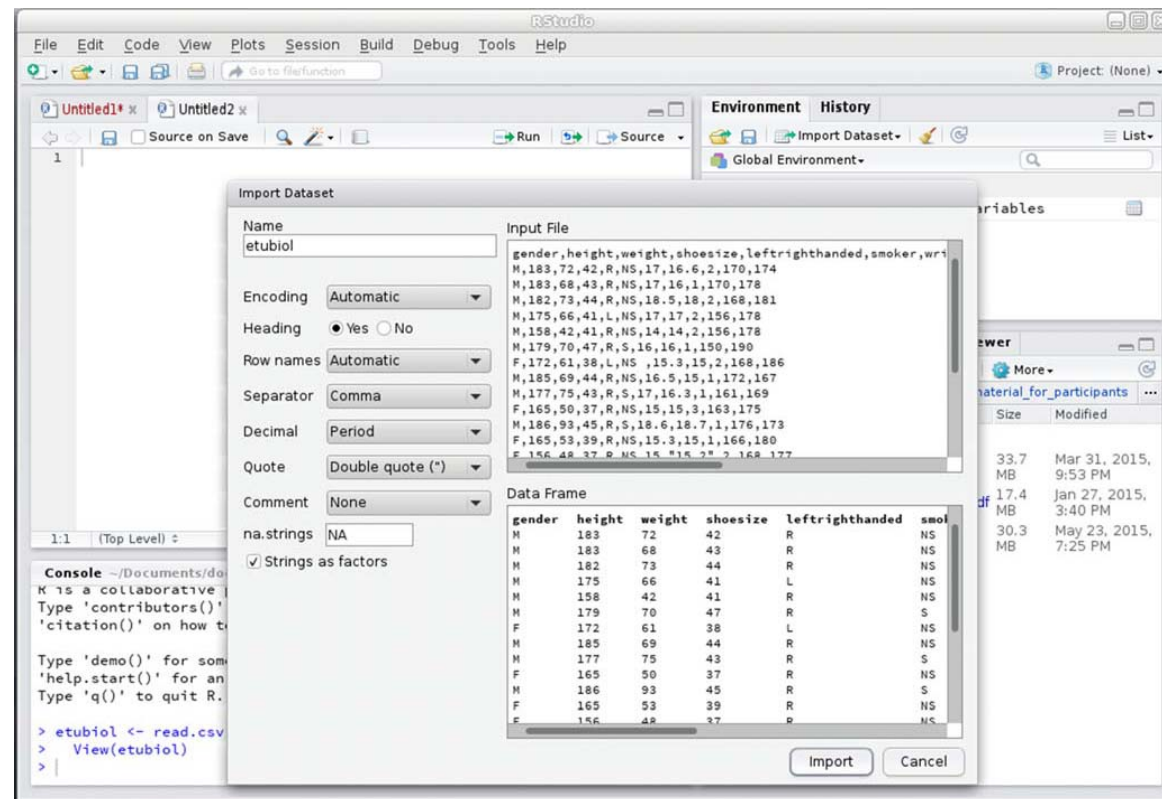
```
read.csv()
```

```
read.delim()
```

(with many options – check the help).

- R can also:

- Read Excel spreadsheets
- Read plenty of other formats
- Directly access databases
- Access files over the web



Data frames

- Data frames are made of columns having all the same number of elements
- They look like matrices, except that the columns can hold different variables types
- They are typically used to store data, with
 - Each row being an experimental unit
 - Each column being a measurement

```
> data[,1] # access first column
```

```
> data[, "data1"] # access column "data1"
```

```
> data$data1 # ... same
```

Creating data frames

```
> x <- 1:10
> y <- seq(from=5,to=10,length=10)
> z <- c("A","B","B","A","A","A","B","A","B","B")
> df <- data.frame(d1=x, d2=y, fact=z)
> df
  d1      d2 fact
1  1  5.000000  A
2  2  5.555556  B
..
> names(df)
[1] "d1" "d2" "fact"
> dim(df)
[1] 10  3
```

Adding new columns

```
> df$d3 <- 10:1
```

```
> df
```

```
  d1      d2 fact d3
1  1  5.000000  A 10
2  2  5.555556  B  9
```

```
...
```

```
> summary(df)
```

d1		d2		fact		d3	
Min.	: 1.00	Min.	: 5.00	Length:	10	Min.	: 1.00
1st Qu.:	3.25	1st Qu.:	6.25	Class	:character	1st Qu.:	3.25
Median	: 5.50	Median	: 7.50	Mode	:character	Median	: 5.50
Mean	: 5.50	Mean	: 7.50			Mean	: 5.50
3rd Qu.:	7.75	3rd Qu.:	8.75			3rd Qu.:	7.75
Max.	:10.00	Max.	:10.00			Max.	:10.00

Select data from a data frame

- Select all values of "d2" for which "fact" is "B"

```
> df[ df$fact == "B", "d2" ]
```

```
[1] 5.555556 6.111111 8.333333 9.444444 10.000000
```

- Select all values of "d1" for which "fact" is "B " and "d2" > 7

```
> df[ (df$fact == "B" & df$d2 > 7), "d1" ]
```

```
[1] 7 9 10
```

- Select all values of "d3" for which "fact" is "A " or "d2" < 6

```
> df[ (df$fact == "A" | df$d2 < 6), "d3" ]
```

```
[1] 10 9 8 4 2 1
```

```
> df
  d1      d2 fact d3
1  1 5.000000  A 10
2  2 5.555556  B  9
3  3 6.111111  B  8
4  4 6.666667  A  7
5  5 7.222222  A  6
6  6 7.777778  A  5
7  7 8.333333  B  4
8  8 8.888889  A  3
9  9 9.444444  B  2
10 10 10.000000 B  1
```