Correctly reporting your clinical trial

- Enhancing transparency and reproducibility

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Vol 435|9 June 2005

COMMENTARY

Scientists behaving badly

To protect the integrity of science, we must look beyond falsification, fabrication and plagiarism, to a wider range of questionable research practices, argue **Brian C. Martinson**, **Melissa S. Anderson** and **Raymond de Vries**.

Table 1 Percentage of scientists who say that they engaged in th previous three years $(n = 3,247)$	e beha	viour listed w	ithin the
Top ten behaviours	All	Mid-career	Early-career
1. Falsifying or 'cooking' research data	0.3	0.2	0.5
2. Ignoring major aspects of human-subject requirements	0.3	0.3	0.4
Not properly disclosing involvement in firms whose products are based on one's own research	0.3	0.4	0.3
 Relationships with students, research subjects or clients that may be interpreted as questionable 	1.4	1.3	1.4
 Using another's ideas without obtaining permission or giving due credit 	1.4	1.7	1.0
 Unauthorized use of confidential information in connection with one's own research 	1.7	2.4	0.8 ***
7. Failling to present data that contradict one's own previous research	6.0	6.5	5.3
8. Circumventing certain minor aspects of human-subject requirements	7.6	9.0	6.0 **
 Overlooking others' use of flawed data or questionable interpretation of data 	12.5	12.2	12.8
 Changing the design, methodology or results of a study in response to pressure from a funding source 	15.5	20.6	9.5***
Other behaviours			
11. Publishing the same data or results in two or more publications	4.7	5.9	3.4**
12. Inappropriately assigning authorship credit	10.0	12.3	7.4 ***
 Withholding details of methodology or results in papers or proposals 	10.8	12.4	8.9 **
14. Using inadequate or inappropriate research designs	13.5	14.6	12.2
15. Dropping observations or data points from analyses based on a gut feeling that they were inaccurate	15.3	14.3	16.5
16. In adequate record keeping related to research projects	27.5	27.7	27.3

241 shades of grey



Contents lists available at SciVerse ScienceDirect

NeuroImage

journal homepage: www.elsevier.com/locate/ynimg



Full Length Articles

The secret lives of experiments: Methods reporting in the fMRI literature

Joshua Carp

University of Michigan, Department of Psychology, 530 Church Street, Ann Arbor, MI, 48109, USA

ARTICLE INFO

Article history: Accepted 3 July 2012 Available online 10 July 2012

Keywords: fMRI Methods reporting Reproducibility Experimental design Analysis methods Statistical power

ABSTRACT

Replication of research findings is critical to the progress of scientific understanding. Accordingly, most scientific journals require authors to report experimental procedures in sufficient detail for independent researchers to replicate their work. To what extent do research reports in the functional neuroimaging literature live up to this standard? The present study evaluated methods reporting and methodological choices across 241 recent fMRI articles. Many studies did not report critical methodological details with regard to experimental design, data acquisition, and analysis. Further, many studies were underpowered to detect any but the largest statistical effects. Finally, data collection and analysis methods were highly flexible across studies, with nearly as many unique analysis pipelines as there were studies in the sample. Because the rate of false positive results is thought to increase with the flexibility of experimental designs, the field of functional neuroimaging may be particularly vulnerable to false positives. In sum, the present study documented significant gaps in methods reporting among fMRI studies. Improved methodological descriptions in research reports would yield significant benefits for the field.

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The key is in the detail



BROWSE

PUBLISH

ABOUT



PERSPECTIVE

Risk of Bias in Reports of In Vivo Research: A Focus for Improvement

Malcolm R. Macleod , Aaron Lawson McLean, Aikaterini Kyriakopoulou, Stylianos Serghiou, Arno de Wilde, Nicki Sherratt, Theo Hirst, Rachel Hemblade, Zsanett Bahor, Cristina Nunes-Fonseca, Aparna Potluru, Andrew Thomson, Julija Baginskitae, [...], Emily S. Sena [view all]

- 1,173 papers assessed
- Only one study did all four of these things
- 68% of studies did not do any of these things

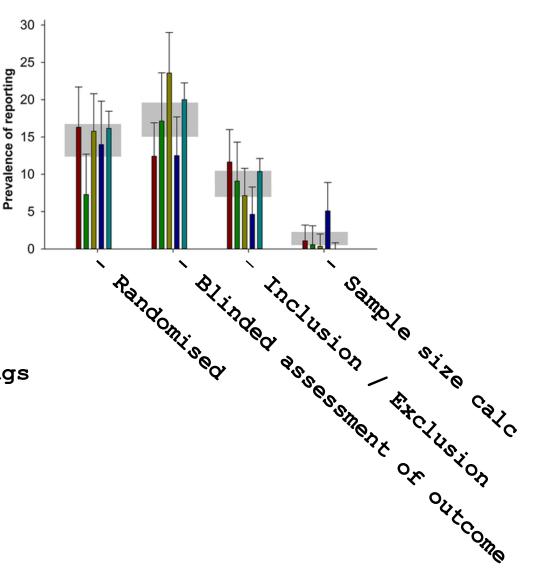


Original Article 🙃 Full Access

1,026 Experimental treatments in acute stroke

Victoria E. O'Collins B.Sci, Malcolm R. Macleod MRCP, PhD, Geoffrey A. Donnan MD, FRACP, Laura L. Horky MD, PhD, Bart H. van der Worp MD, PhD, David W. Howells PhD

▼



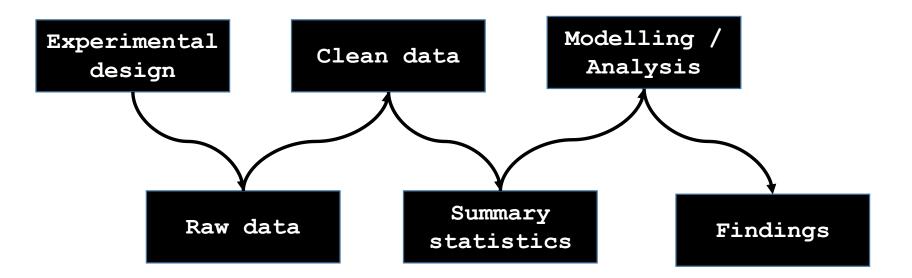
p-values should not define a study

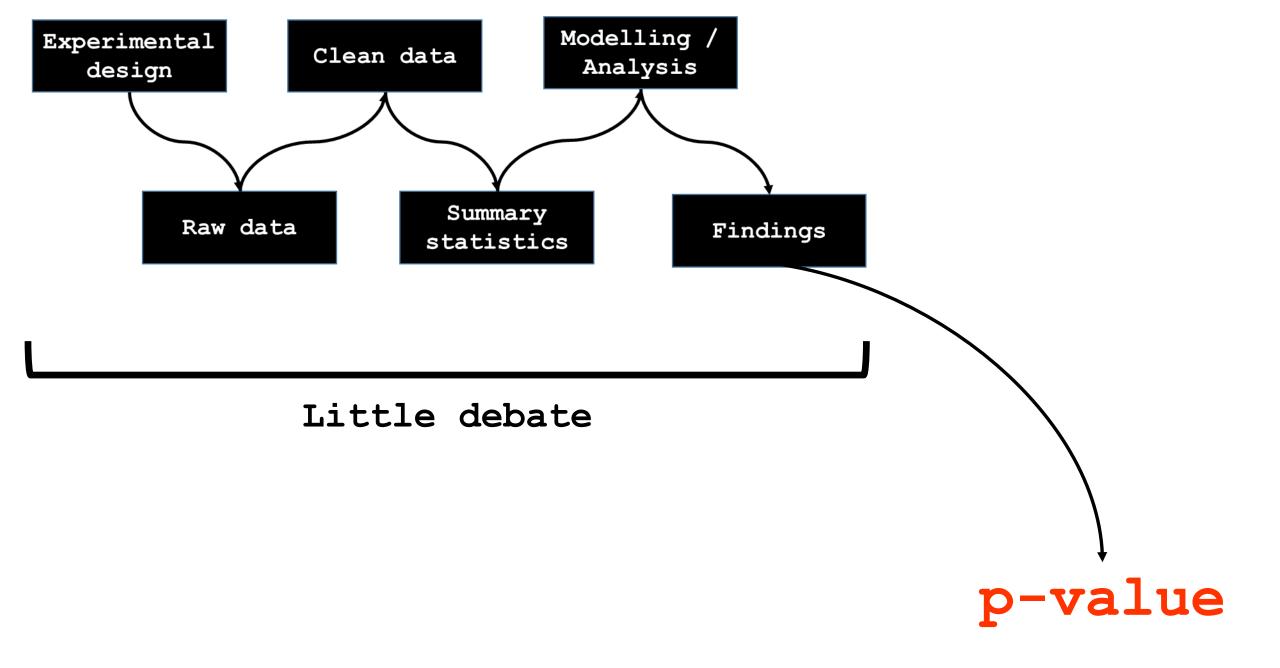


Statistics: P values are just the tip of the iceberg

Jeffrey T. Leek & Roger D. Peng

28 April 2015





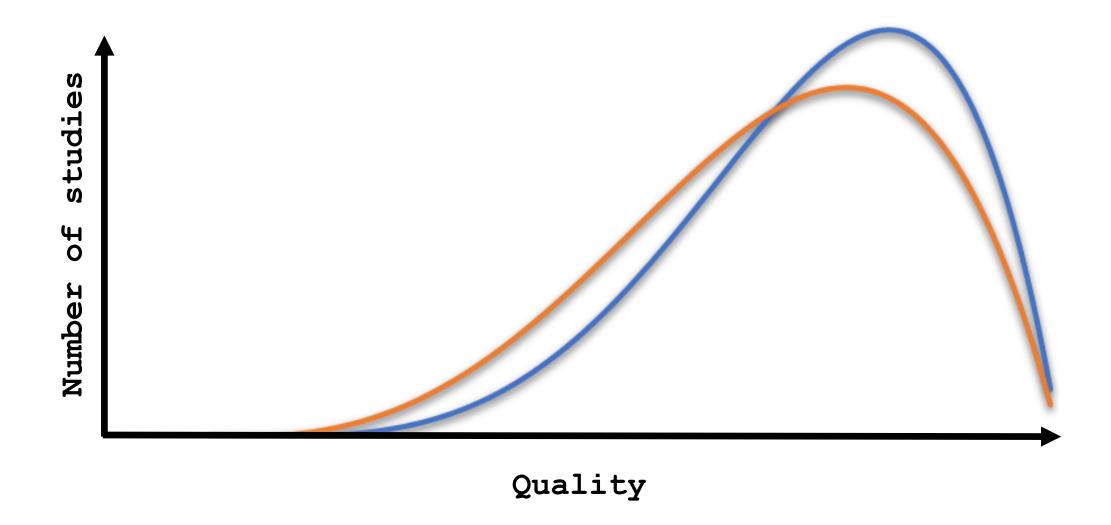
Extreme scrutiny

p-value

Today



Tomorrow



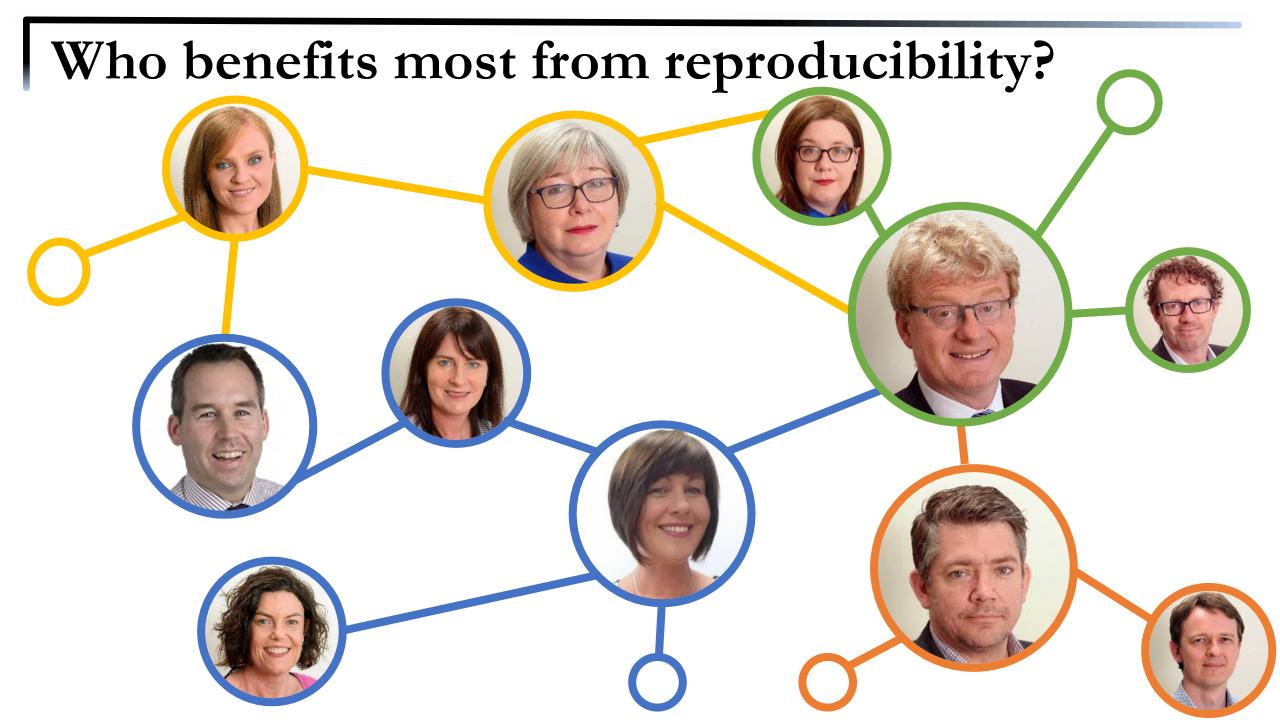
Who benefits most from reproducibility?



Reproducibility is important because the you of 3 months ago is terrible at answering email! - @tracykteal at #2016dssummit

1:17 PM - 26 Oct 2016 from Manhattan, NY



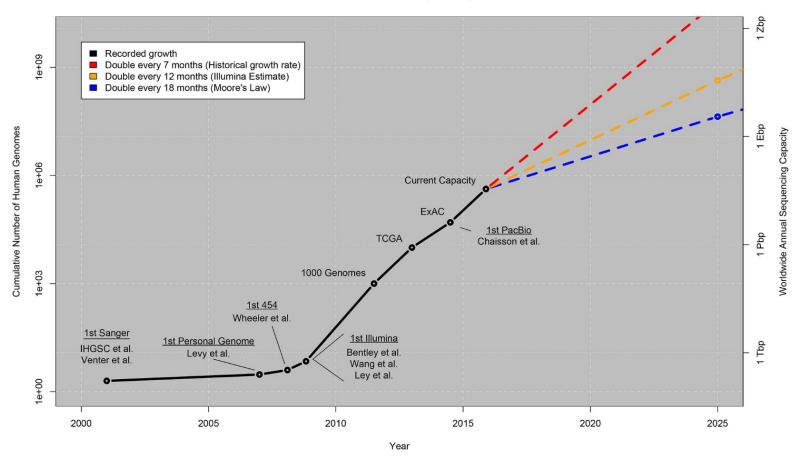


Where to begin...



The challenge

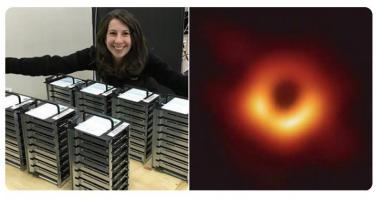
Growth of DNA Sequencing





Follow

Congratulations to Dr Katie Bouman!
This is the woman who created the algorithm to crunch the 5 petabytes of data from 500 kg of hard drives from 8 radio telescopes to make the first image of the #EHTBlackHole #BlackHole



2:55 PM - 10 Apr 2019

Fundamental problem



I'm not in the office at the moment. Send any work to be translated

Beware of default settings

Ziemann et al. Genome Biology (2016) 17:177 DOI 10.1186/s13059-016-1044-7

Genome Biology

COMMENT

Open Access

Gene name errors are widespread in the scientific literature



Mark Ziemann¹, Yotam Eren^{1,2} and Assam El-Osta^{1,3*}

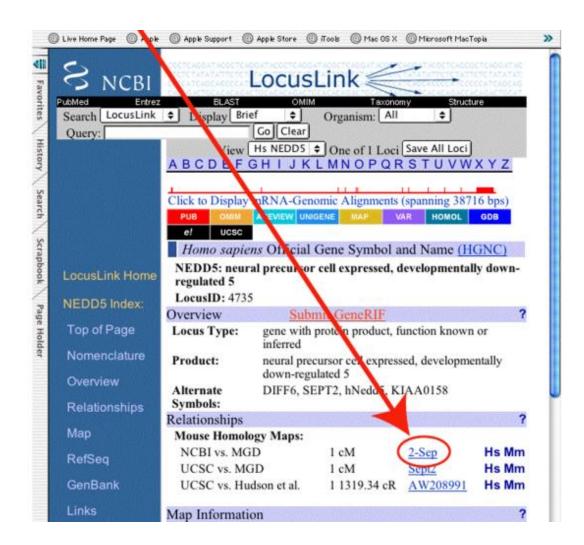
Abstract

conversions.

The spreadsheet software Microsoft Excel, when used with default settings, is known to convert gene names to dates and floating-point numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name

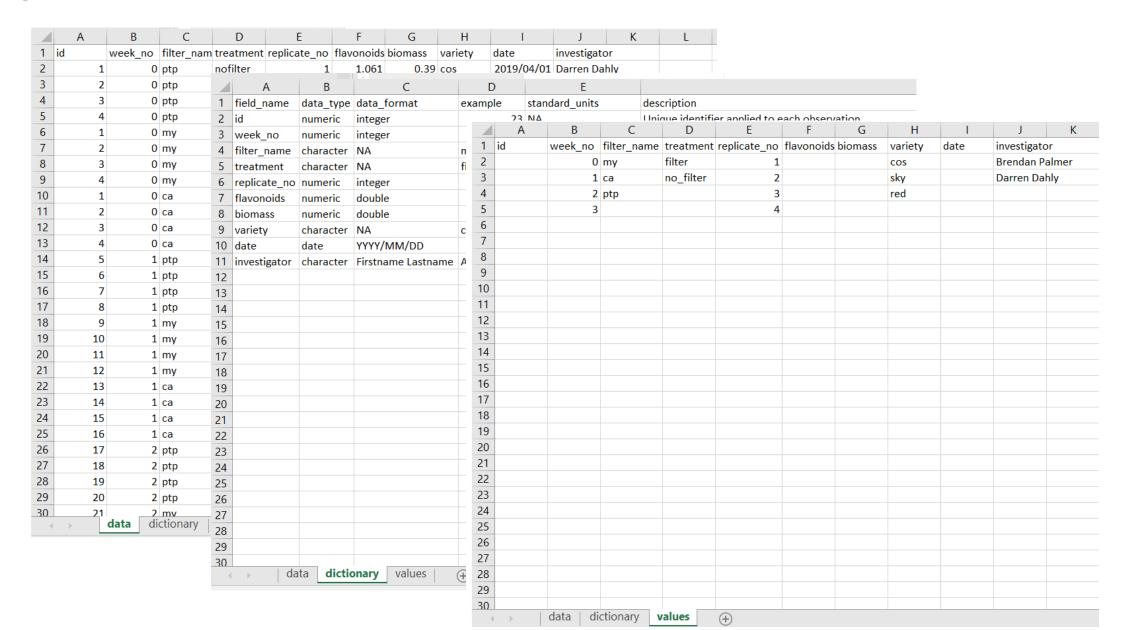
frequently reused. Our aim here is to raise awareness of the problem.

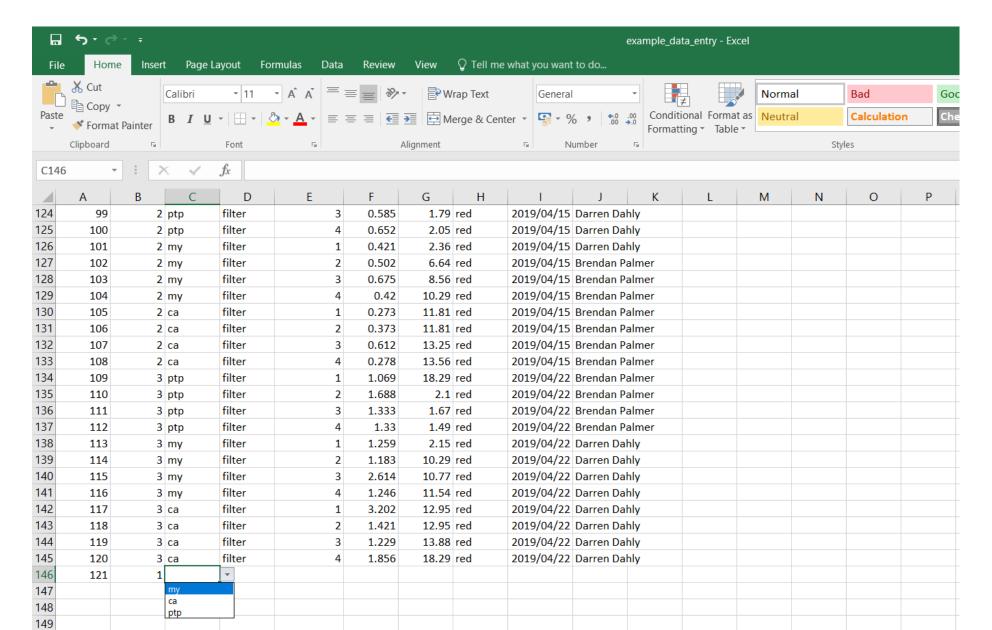
We downloaded and screened supplementary files from 18 journals published between 2005 and 2015 using a suite of shell scripts. Excel files (.xls and.xlsx suffixes) were converted to tabular separated files (tsv) with ssconvert (v1.12.9). Each sheet within the Excel file was converted to a separate tsv file. Each column of data in the tsv file was screened for the presence of gene sym-

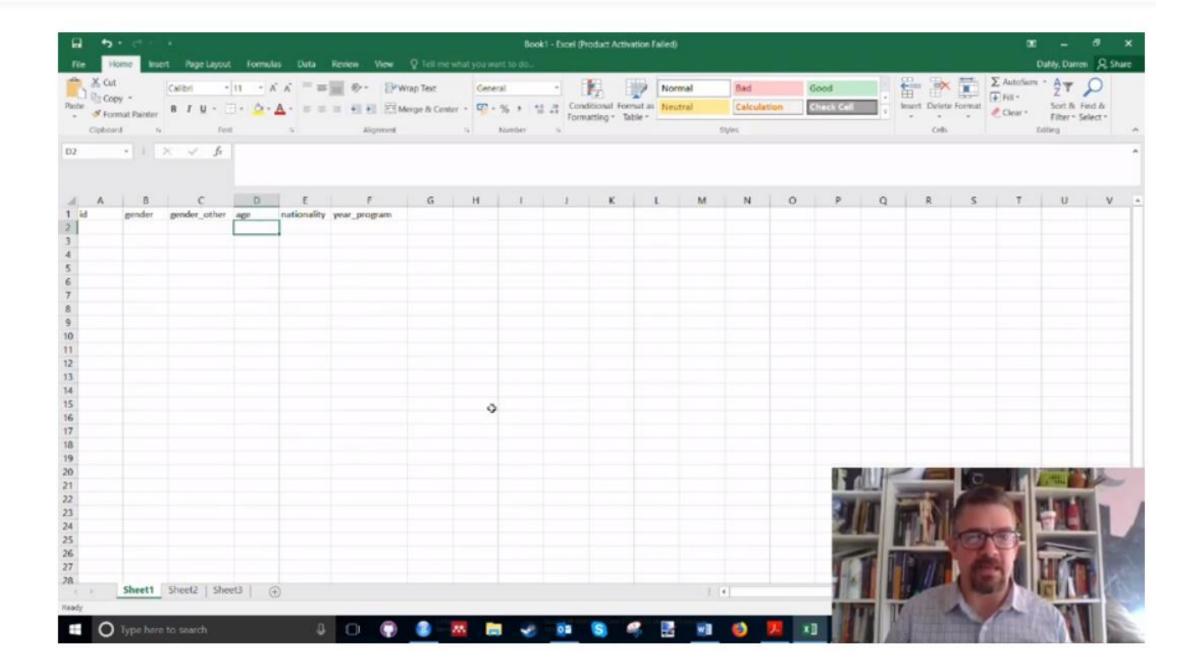


1	Α	В	С	D	Е	F	G	Н	I	J	K	L
1	id	week_no	filter_nam	treatment	replicate_no	flavonoids	biomass	variety	date	investigator		
2	1	0	ptp	nofilter	1	1.061	0.39	cos	2019/04/01	Darren Dahly		
3	2	0	ptp	nofilter	2	1.1805	0.42	cos	2019/04/01	Darren Dahly		
4	3	0	ptp	nofilter	3	1.0345	0.62	cos	2019/04/01	Darren Dahly		
5	4	0	ptp	nofilter	4	1.094	0.63	cos	2019/04/01	Brendan Palm	er	
6	1	0	my	nofilter	1	1.061	0.39	cos	2019/04/01	Brendan Palm	er	
7	2	0	my	nofilter	2	1.1805	0.42	cos	2019/04/01	Brendan Palme	er	
8	3	0	my	nofilter	3	1.0345	0.62	cos	2019/04/01	Brendan Palme	er	
9	4	0	my	nofilter	4	1.094	0.63	cos	2019/04/01	Brendan Palm	er	
10	1	0	ca	nofilter	1	1.061	0.39	cos	2019/04/01	Brendan Palm	er	
11	2	0	ca	nofilter	2	1.1805	0.42	cos	2019/04/01	Brendan Palm	er	
12	3	0	ca	nofilter	3	1.0345	0.62	cos	2019/04/01	Brendan Palme	er	
13	4	0	ca	nofilter	4	1.094	0.63	cos	2019/04/01	Darren Dahly		
14	5	1	ptp	filter	1	0.87	0.76	cos	2019/04/08	Darren Dahly		
15	6	1	ptp	filter	2	0.847	0.95	cos	2019/04/08	Darren Dahly		
16	7	1	ptp	filter	3	1.022	0.95	cos	2019/04/08	Darren Dahly		
17	8	1	ptp	filter	4	0.916	0.95	cos	2019/04/08	Darren Dahly		
18	9	1	my	filter	1	1.119	1.55	cos	2019/04/08	Darren Dahly		
19	10	1	my	filter	2	0.845	3.16	cos	2019/04/08	Darren Dahly		
20	11	1	my	filter	3	1.299	4.9	cos	2019/04/08	Brendan Palme	er	
21	12	1	my	filter	4	1.149	5.5	cos	2019/04/08	Brendan Palme	er	
22	13	1	ca	filter	1	0.716	5.5	cos	2019/04/08	Brendan Palme	er	
23	14	1	ca	filter	2	0.881	7.94	cos	2019/04/08	Brendan Palme	er	
24	15	1	ca	filter	3	0.586	8.71	cos	2019/04/08	Brendan Palme	er	
25	16	1	ca	filter	4	0.561	8.71	cos	2019/04/08	Brendan Palme	er	
26	17	2	ptp	filter	1	0	14.45	cos	2019/04/15	Brendan Palm	er	
27	18	2	ptp	filter	2	1.006	2.14	cos	2019/04/15	Brendan Palm	er	
28	19	2	ptp	filter	3	1.236	1.86	cos	2019/04/15	Brendan Palme	er	
29	20	2	ptp	filter	4	1.206	1.2	cos	2019/04/15	Brendan Palme	er	
30	21		mv	filter	1	1.545	2.45	cos	2019/04/15	Brendan Palm	er	
4		data di	ctionary	values	+							

4	Α		В	С		D		E		F	G		Н	- 1		J	k		L						
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2		1	0	ptp	nof	filter		1		1.061	0.39	cos		2019/	04/01	Darren Da	ahly								
3		2	0	ptp			Α	В		-	С)		Е									
4		3	0	ptp	1	field	name	data_t	ype	data_f	ormat		examp	le	stand	ard_units		desc	riptio	n					
5		4	0	ptp		id		numeri						23	NA			Uniq	ue ide	entifi	er applied to	o each	observat	ion	
6		1	0	my	3	week	_no	numeri	ic	intege	r			1	NA			Wee	k nun	nber,	1 = 7 days e	exposur	e, 2 = 14	days expo	
7		2	0	my	4	filter	name	charac	ter	NA			my		NA			3 filt	er typ	oes; 'p	tp' = polytu	ınnel pl	astic blo	cks all UV I	
8		3	0	my	5	treat	ment	charac	ype data_format ic integer ic integer ter NA ter NA ic integer ic double				filter		NA			Presence or absence of a filter at the time of sampling							
9		4	0	my	6	replic	ate_no	numeri	ic				1 NA				The number of replicates in each treatement								
10		1		ca	7	flavo	noids	numeri	ic	double	,		(0.3421	parts	per millio	n (ppm)	Leaf	disc t	taken	from the ti	p of the	e most m	ature leaf	
11		2	0	ca	8	biom	ass	numeri	ic	double	,				gram	(g)		Abov	ve gro	ound l	oiomass on	the day	of harve	est	
12		3	0	ca	9	varie	ty	charac	ter	NA			cos		NA			3 со	mmer	rical v	arieties of	red lett	uce used	; 'cos' = Co	
13		4	0	ca	10	date		date		ΥΥΥΥ/Ι	MM/DD		2019/	/06/28	ISO 8	601		Expe	erimer	nt dat	:e				
14		5	1	ptp	11	inves	tigator	charac	ter	Firstna	me Lastna	me	Aoife (Coffey	NA			Prim	ary re	esear	her who pe	erforme	ed the ex	periment	
15		6	1	ptp	12																				
16		7	1	ptp	13																				
17		8	1	ptp	14																				
18		9	1	my	15																				
19		10	1	my	16																				
20		11	1	my	17																				
21	:	12	1	my	18																				
22		13	1	ca	19																				
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24		15	1	ca	21																				
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26		17	2	ptp	23																				
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29		20	2	ptp	26																				
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4)		data di	ctionary	28																				
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Beware of default settings

Print



Data and computer code should be made publicly available at an early stage - or else ... esarastudillo

Last week we learned a famous 2010 academic paper, relied on by political big-hitters to

bolster arguments for austerity cuts, contained significant errors; and that those errors came
down to misuse of an Excel spreadsheet.

in LinkedIn

Sadly, these are not the first mistakes of this size and nature when handling data. So what on Earth went wrong, and can we fix it?

Harvard's <u>Carmen Reinhart</u> and <u>Kenneth Rogoff</u> are two of the most respected and influential academic economists active today.

Putting the pieces together

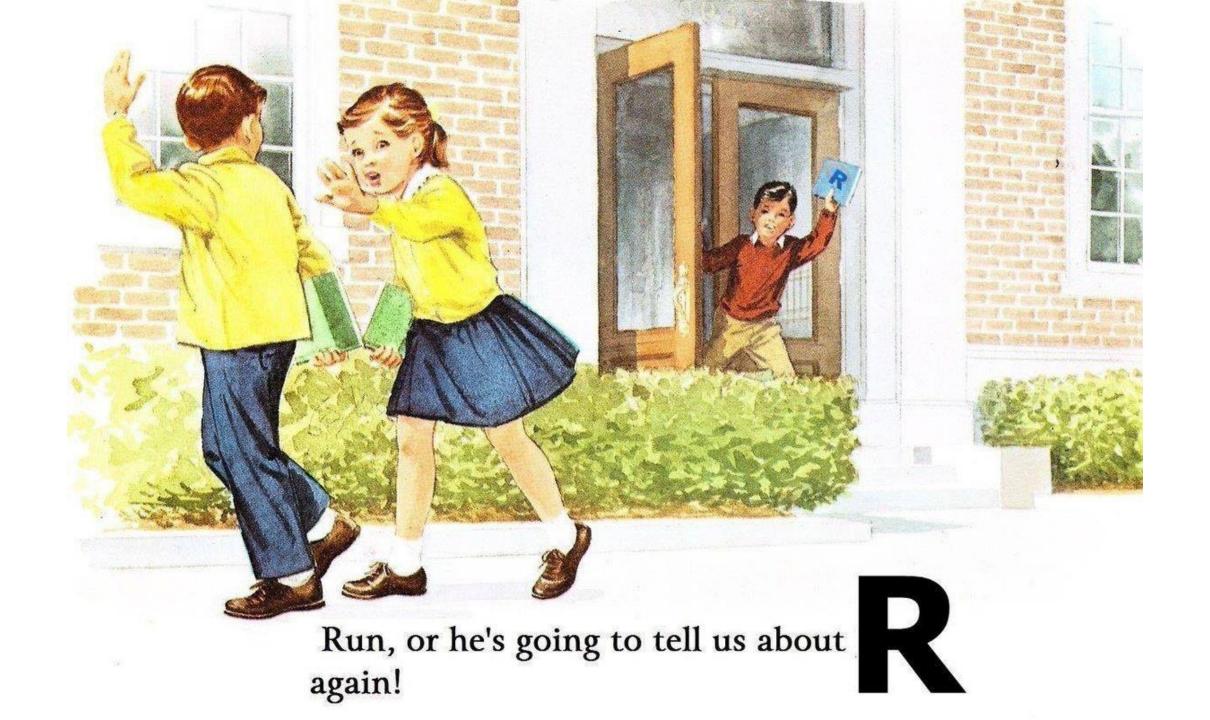
A: Define a project structure

B: Set a naming convention

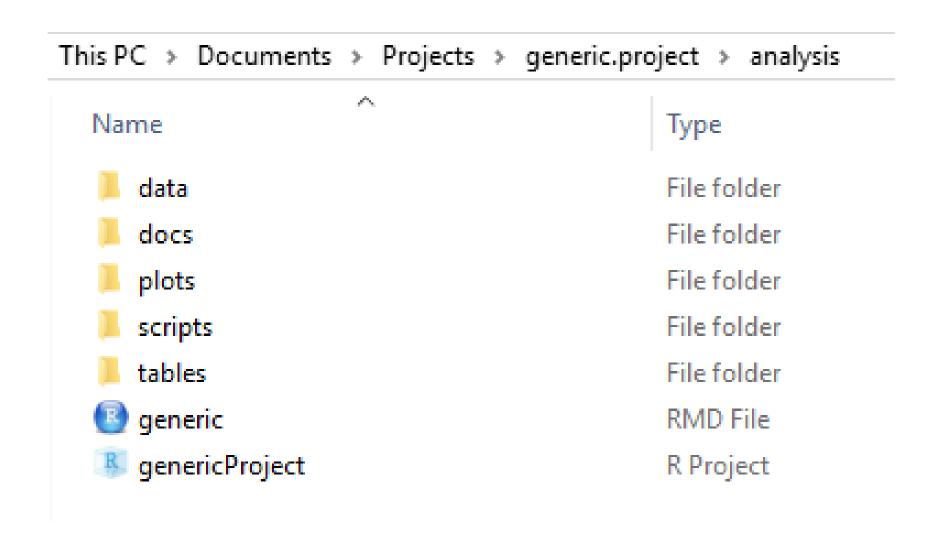
C: Use scripted workflows

D: Digital reports

Reproducible research



A: Define a generic project structure



B: Outline a file naming convention

Machine readable:

- Inherent order
- Avoid spaces
- Avoid punctuation
- Remove case-sensitivity

Human readable:

- Contains info on content
- Avoid spaces
- Avoid punctuation
- Remove case sensitivity

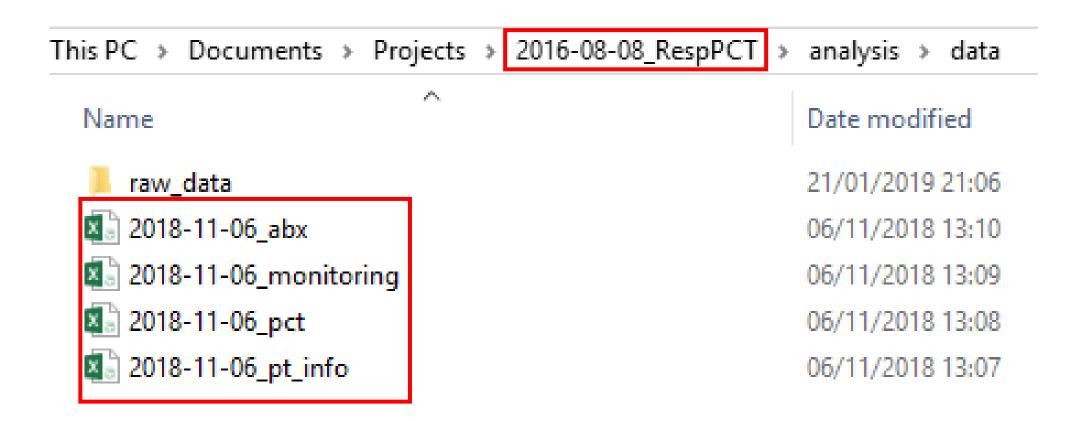
Metadata:

Separate with underscores ("_")

- Avoid punctuation
- Remove case-sensitivity

```
01 marshal-data.r
02 pre-dea-filtering.r
03 dea-with-limma-voom.r
04 explore-dea-results.r
90 limma-model-term-name-fiasco.r
helper01 load-counts.r
helper02_load-exp-des.r
helper03 load-focus-statinf.r
helper04 extract-and-tidy.r
```

B: Give your files and folders informative names



Everything in its right place

- Make your file names:
 - 1. Machine readable
 - 2. Human readable
 - 3. Work with default ordering

NO

Name

- All unique 4a amino acid Sequences (B-N).fas
- All unique 4a amino acid Sequences (B-N).meg
- All_AA_haplotypes.meg
- All_AA_haplotypes_with_clonal_sequences.meg
- BS100_AA_with_clones
- BS100_AA_with_clones.nwk
- BS1000_AA_pyro&clones
- BS1000_AA_pyro&clones.nwk
- BS1000_AA_pyro_only
- BS1000_AA_pyro_only.nwk
- BS1000_Unique_Clonal_AA

Yes

Projects > 2016-08-08_RespPCT > analysis > scripts

Name

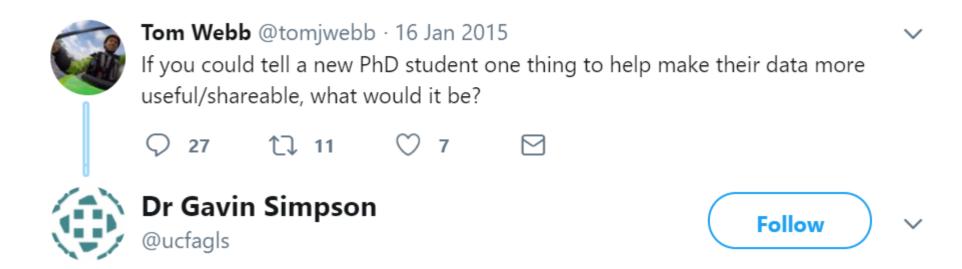
- 01_clean_data
- 02_plots
- 03_tables
- 04_stats_analysis
- 05_post_hoc_stats
- functions
- randomization
- tables

C: Joined up thinking

- The R scripts should also be human readable
 - Annotate the code
 - Break up the scripts into dedicated tasks
 - Interlink to other project scripts

```
1  # Data ----
2  # Eight tibbles returned from the 01_data_import_and_tidying_master_file.R
3  # 1. fgf23_data => FGF23 readings from study centres 01-03
4  # 2. food_level_data => Food diary entries
5  # 3. grouped_data => Dialysis and nondialysis diary entries by component
6  # 4. k_data => Serum potassium
7  # 5. master_data_clean => all the clean master file data if required
8  # 6. p_data => Serum phosphate
9  # 7. pth_data => Parathyroid hormone readings
10  # 8. pulses_nuts_data
11
12 source("scripts/01_data_import_and_tidying_master_file.R")
```

Work from the raw data ALWAYS!!



Replying to @tomjwebb

@tomjwebb don't, not even with a barge pole, not for one second, touch or otherwise edit the raw data files. Do any manipulations in script

D: R Markdown

- R Markdown combines the code you wrote, the output produced and you own comments
- You can view it as a digital lab notebook, where you are both recording what you're doing, and what you were thinking while you were doing it!
- R Markdown outputs can take many forms
 - Word documents, PDFs, slideshows etc.
- Once created the .Rmd file get sent to knitr, which executes the chunks of code and creates a new markdown document
 - this is then processed by pandoc which creates the finished file
 - knitr and pandoc are external websites

R Markdown

YAML header

Chunks of code

Plain text with data outputs from R code

Chunks of code

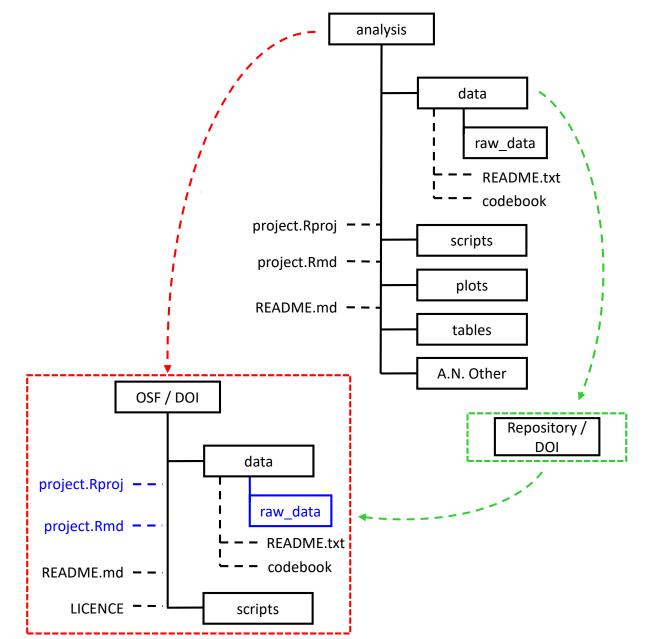
title: "This is a reproducible document" date: 19th June 2019 output: html document {r setup, include = FALSE} library(ggplot2) library(dplyr) smaller <- diamonds %>% filter(carat <= 2.5) We have data about `r nrow(diamonds)` diamonds. Only `r nrow(diamonds) - nrow(smaller) ` are larger than 2.5 carats. The distribution of the remainder is shown below:

{r, echo = FALSE}
smaller %>%
ggplot(aes(carat)) +
geom_freqpoly(binwidth = 0.01)

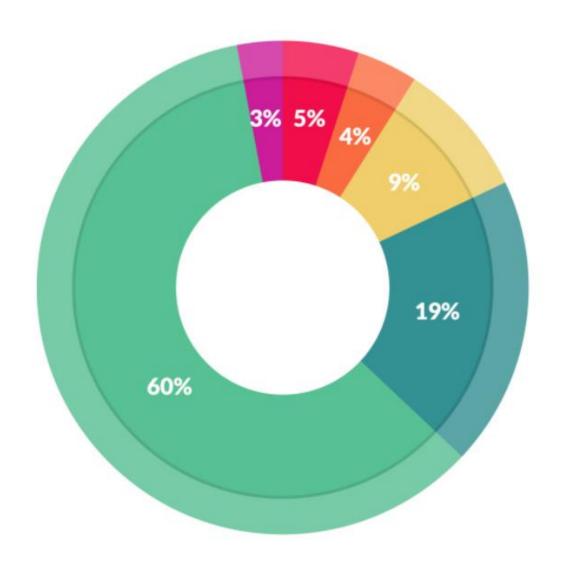
Install the Chrome plugin PubPeer



What does this allow us to do?



It costs a lot of money to run a clinical trial



What data scientists spend the most time doing

- Building training sets: 3%
- Cleaning and organizing data: 60%
- Collecting data sets; 19%
- Mining data for patterns: 9%
- Refining algorithms: 4%
- Other: 5%

The best time to plant a tree was 20 years ago

The second best time is now

