Data Wrangling in R

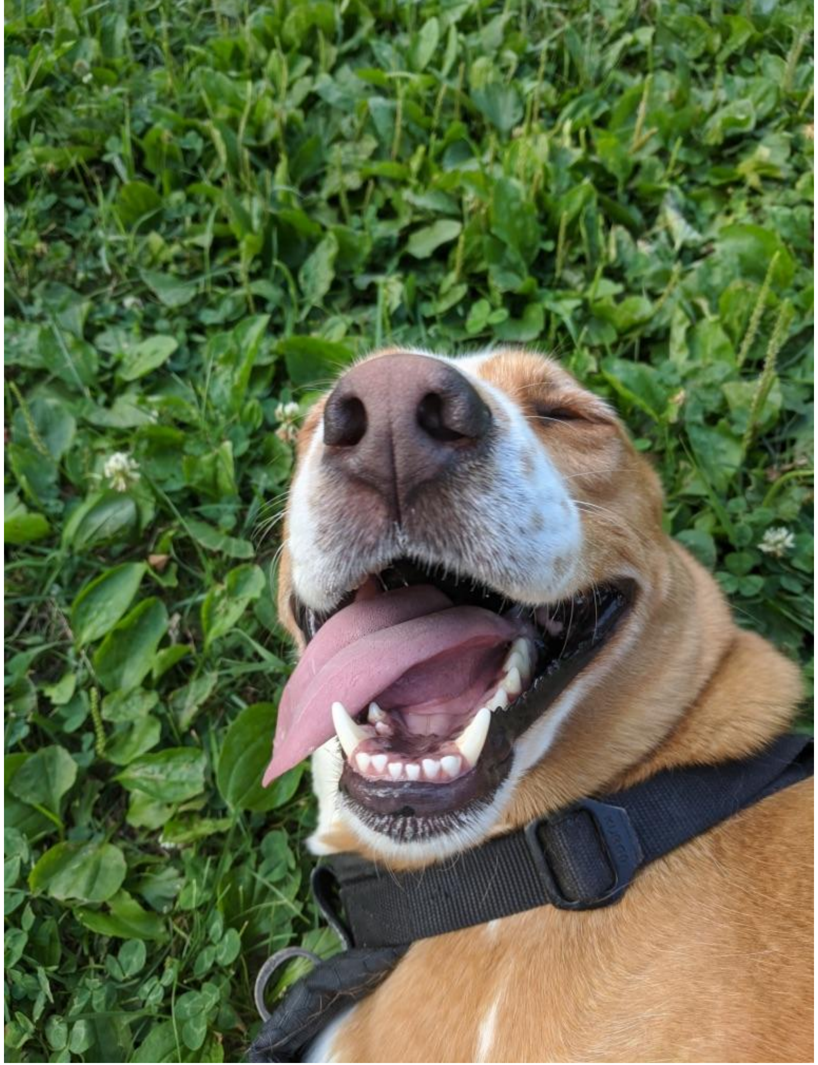
http://sisbid.github.io/Data-Wrangling/

Course Info

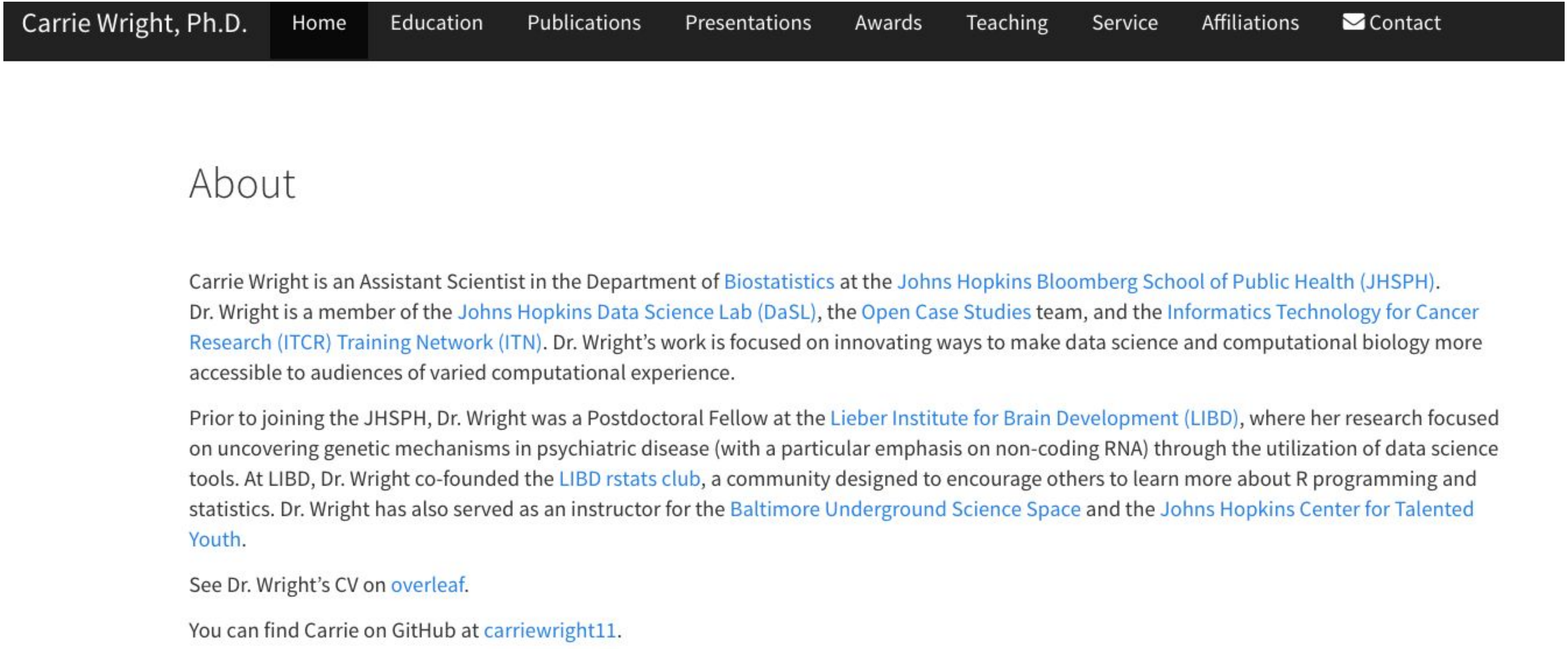
Course name	Data Wrangling in R
Instructors	Carrie Wright and Ava Hoffman
Course website	http://sisbid.github.io/Data-Wrangling/
Goals	Teach you how to get and clean data
Pre-reqs	Hopefully some R programming

How many people feel about data wrangling

How we feel about data wrangling



About us



About

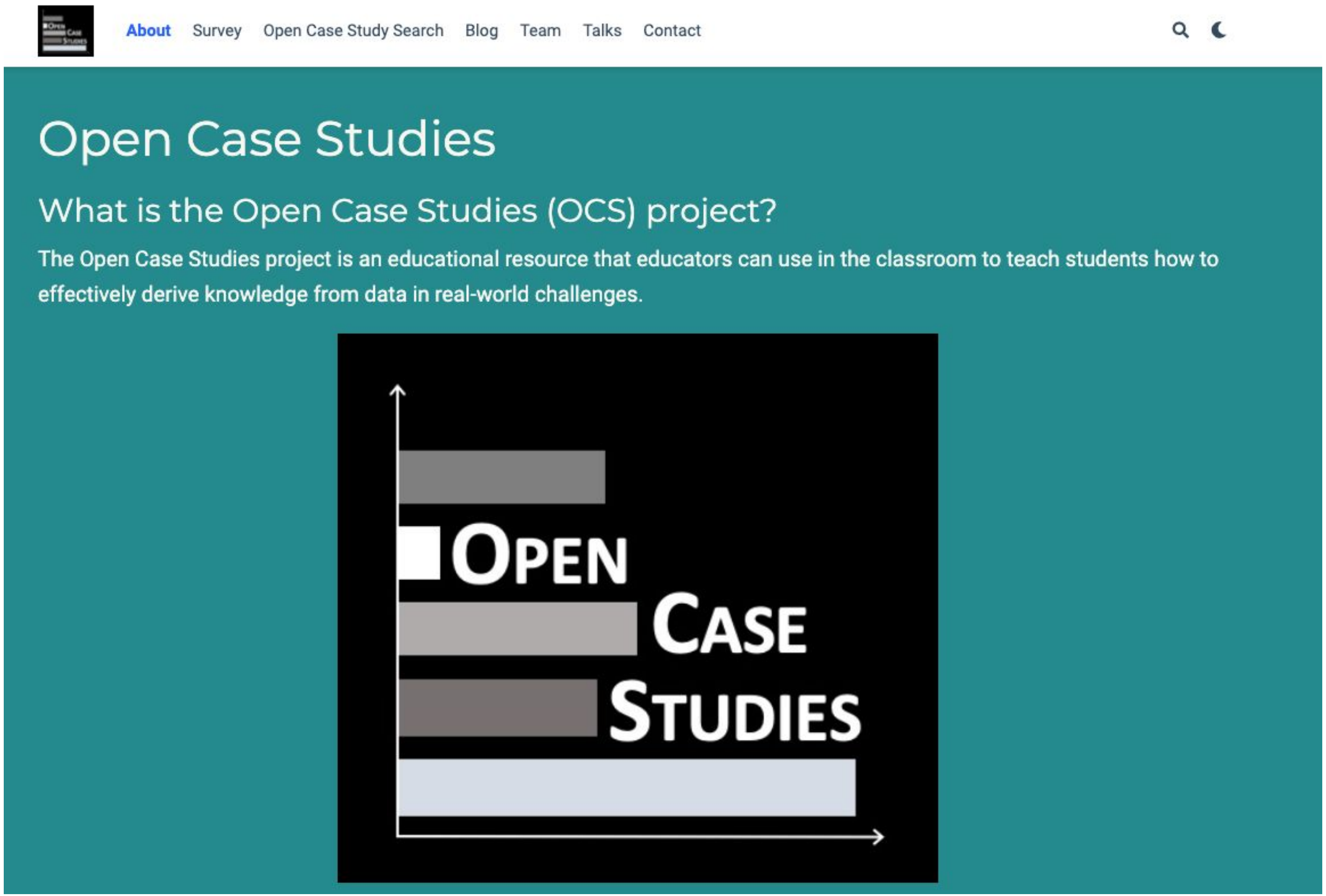
Carrie Wright is an Assistant Scientist in the Department of Biostatistics at the Johns Hopkins Bloomberg School of Public Health (JHSPH). Dr. Wright is a member of the Johns Hopkins Data Science Lab (DaSL), the Open Case Studies team, and the Informatics Technology for Cancer Research (ITCR) Training Network (ITN). Dr. Wright's work is focused on innovating ways to make data science and computational biology more accessible to audiences of varied computational experience.

Prior to joining the JHSPH, Dr. Wright was a Postdoctoral Fellow at the Lieber Institute for Brain Development (LIBD), where her research focused on uncovering genetic mechanisms in psychiatric disease (with a particular emphasis on non-coding RNA) through the utilization of data science tools. At LIBD, Dr. Wright co-founded the LIBD rstats club, a community designed to encourage others to learn more about R programming and statistics. Dr. Wright has also served as an instructor for the Baltimore Underground Science Space and the Johns Hopkins Center for Talented Youth.

See Dr. Wright's CV on overleaf.

You can find Carrie on GitHub at carriewright11.

https://carriewright11.github.io/



Open Case Studies

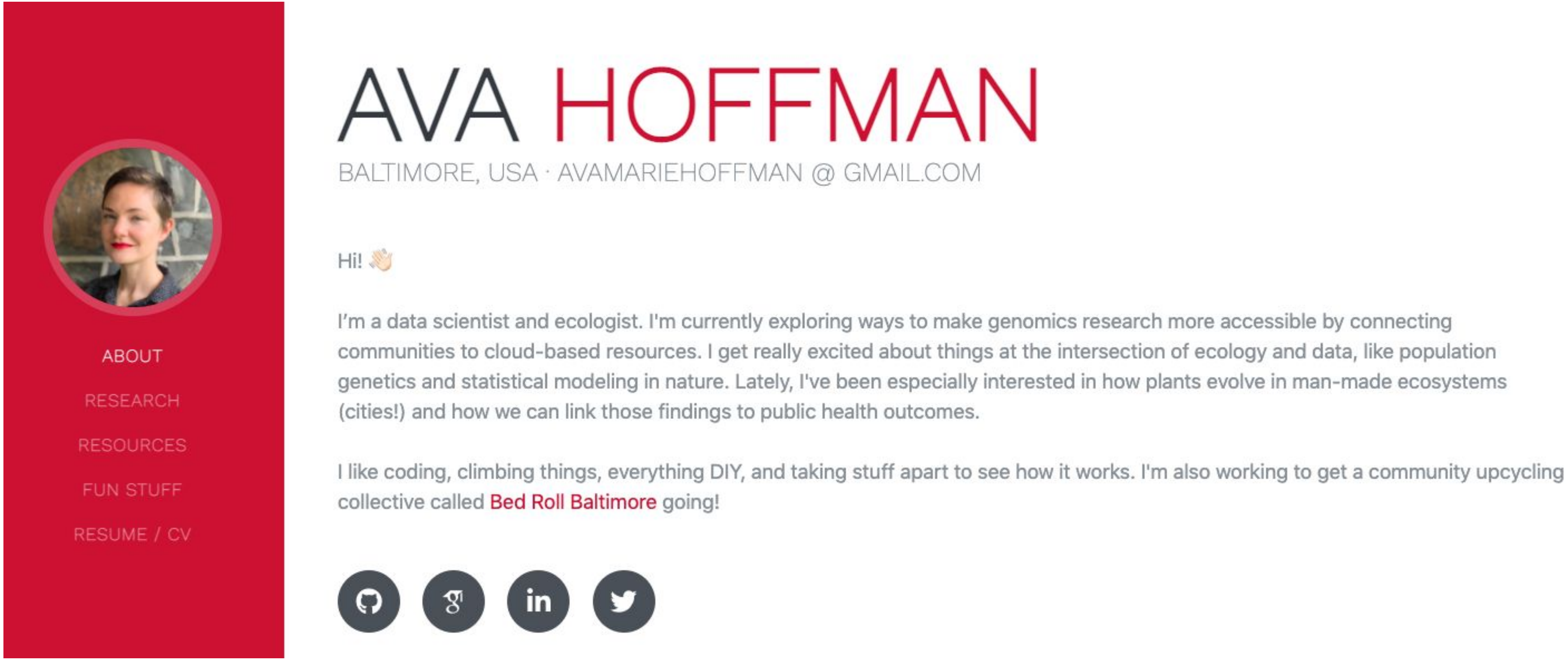
What is the Open Case Studies (OCS) project?

The Open Case Studies project is an educational resource that educators can use in the classroom to teach students how to effectively derive knowledge from data in real-world challenges.

https://www.opencasestudies.org/

About us

(Ava)



AVA HOFFMAN

BALTIMORE, USA · AVAMARIEHOFFMAN @ GMAIL.COM

Hi! 👋

I'm a data scientist and ecologist. I'm currently exploring ways to make genomics research more accessible by connecting communities to cloud-based resources. I get really excited about things at the intersection of ecology and data, like population genetics and statistical modeling in nature. Lately, I've been especially interested in how plants evolve in man-made ecosystems (cities!) and how we can link those findings to public health outcomes.

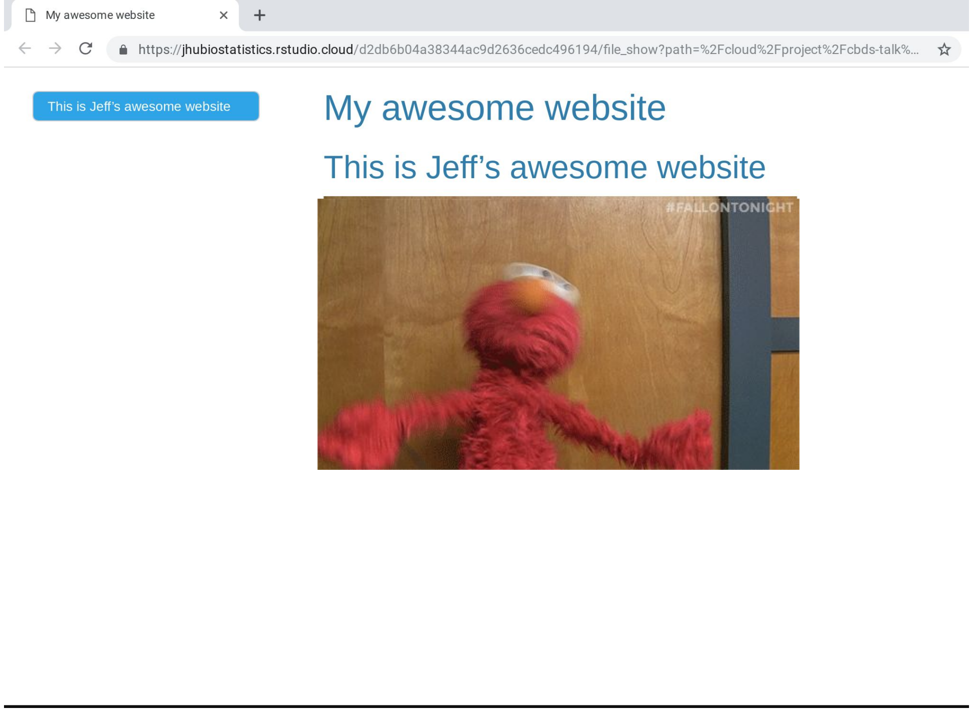
I like coding, climbing things, everything DIY, and taking stuff apart to see how it works. I'm also working to get a community upcycling collective called Bed Roll Baltimore going!

https://www.avahoffman.com/

Why this class

rmarkdown

```
---
title: "My awesome website"
output:
    html_document:
        toc: true
        toc_float: true
        theme: cerulean
---
# This is Jeff's awesome website

![](https://media.giphy.com/media/d
rXGoW1iudhKw/giphy.gif)
```

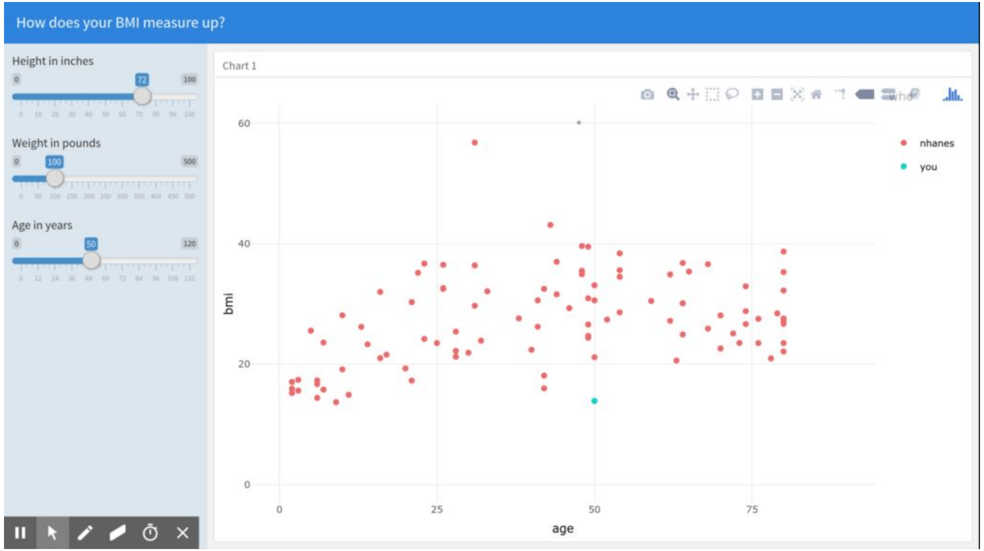


My awesome website

This is Jeff's awesome website

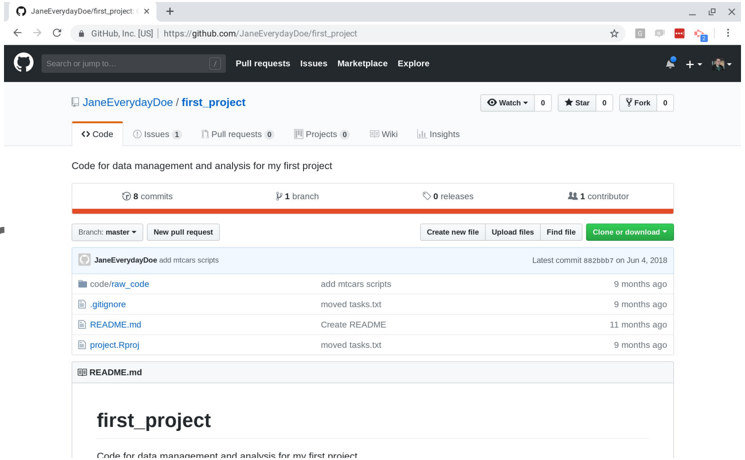
flexdashboard

~~~
---
title: "How does your BMI measure up?"
output: flexdashboard::flex_dashboard
runtime: shiny
---

Inputs {.sidebar}
-------------------------------------

```{r}
library(flexdashboard); library(NHANES); library(plotly);library(dplyr)
sliderInput("height", "Height in inches",0,100,72)
sliderInput("weight", "Weight in pounds",0,500,100)
sliderInput("age", "Age in years",0,120,50)

```

Column
-------------------------------------

### Chart 1

```{r}
nhanes = sample_n(NHANES,100)
renderPlotly({
  df = data.frame(bmi = c(nhanes$BMI,input$weight*0.45/(input$height*0.025)^2),
                  age = c(nhanes$Age,input$age),
                  who = c(rep("nhanes",100),"you"))
  ggplotly(ggplot(df) +
             geom_point(aes(x=age,y=bmi,color=who)) +
             scale_x_continuous(limits=c(0,90)) +
             scale_y_continuous(limits=c(0,60)) +
             theme_minimal()
           )
})
```
~~~



httr

```
library(httr)
library(dplyr)

username = 'janeeverydaydoe'

url_git = 'https://api.github.com/'


api_response =
GET(url = paste0(url_git, 'users/',
username, '/repos'))

content(api_response)[[1]]
```



Code for data management and analysis for my first project

JaneEverydayDoe add mtcars scripts — Latest commit 882bbb7 on Jun 4, 2018

code/raw_code	add mtcars scripts	9 months ago
.gitignore	moved tasks.txt	9 months ago
README.md	Create README	11 months ago
project.Rproj	moved tasks.txt	9 months ago

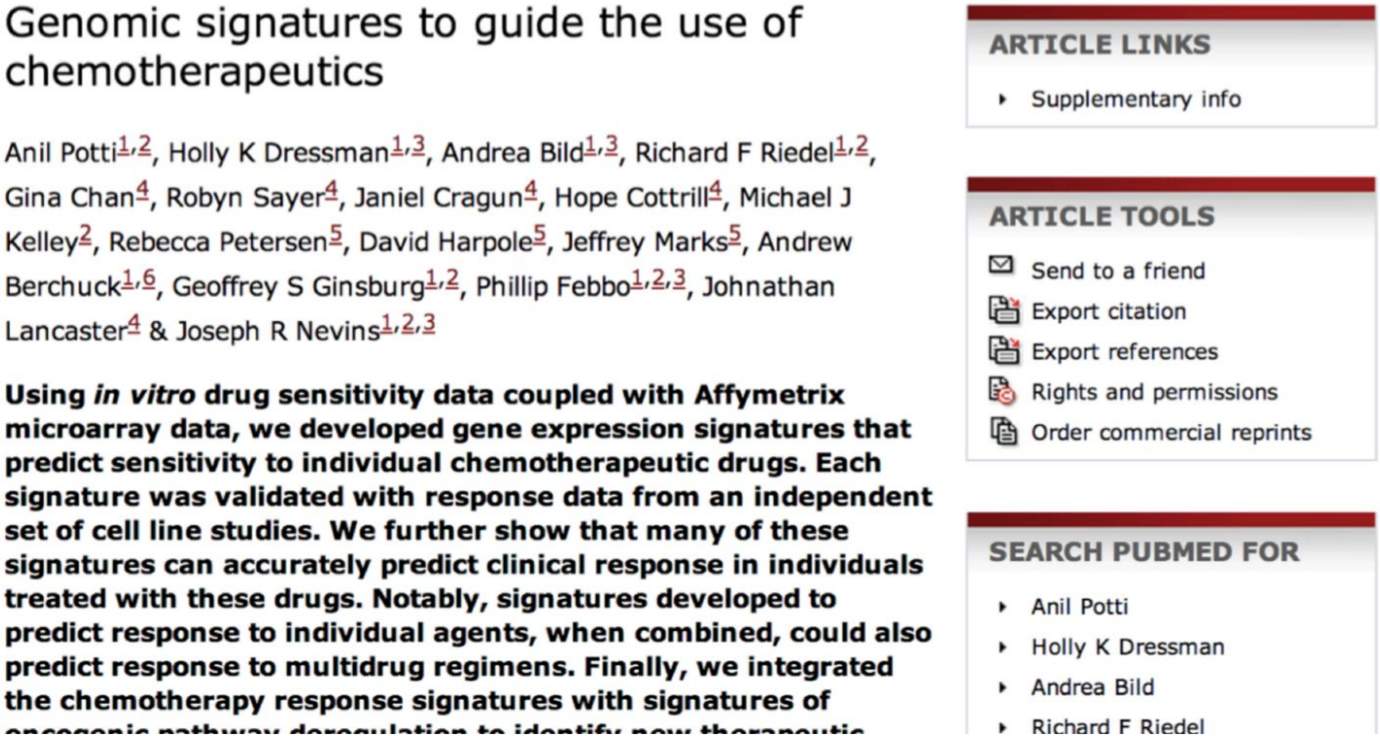
README.md

first_project

Code for data management and analysis for my first project

```
$id
[1] 130377298
$node_id
[1] "MDEwOlJlcG9zaXRvcnkxMzAzNzcyOTg="
$name
[1] "first_project"
$full_name
[1] "JaneEverydayDoe/first_project"
$owner$gravatar_id
[1] ""
$owner$url
[1] "https://api.github.com/users/JaneEverydayDoe"


...
```

But also…



Genomic signatures to guide the use of chemotherapeutics

Anil Potti[1,2], Holly K Dressman[1,3], Andrea Bild[1,3], Richard F Riedel[1,2], Gina Chan[4], Robyn Sayer[4], Janiel Cragun[4], Hope Cottrill[4], Michael J Kelley[2], Rebecca Petersen[5], David Harpole[5], Jeffrey Marks[5], Andrew Berchuck[1,6], Geoffrey S Ginsburg[1,2], Phillip Febbo[1,2,3], Johnathan Lancaster[4] & Joseph R Nevins[1,2,3]

Using *in vitro* drug sensitivity data coupled with Affymetrix microarray data, we developed gene expression signatures that predict sensitivity to individual chemotherapeutic drugs. Each signature was validated with response data from an independent set of cell line studies. We further show that many of these signatures can accurately predict clinical response in individuals treated with these drugs. Notably, signatures developed to predict response to individual agents, when combined, could also predict response to multidrug regimens. Finally, we integrated the chemotherapy response signatures with signatures of oncogenic pathway deregulation to identify new therapeutic

https://doi.org/10.1038/nm1491

Forensic Bioinformatics

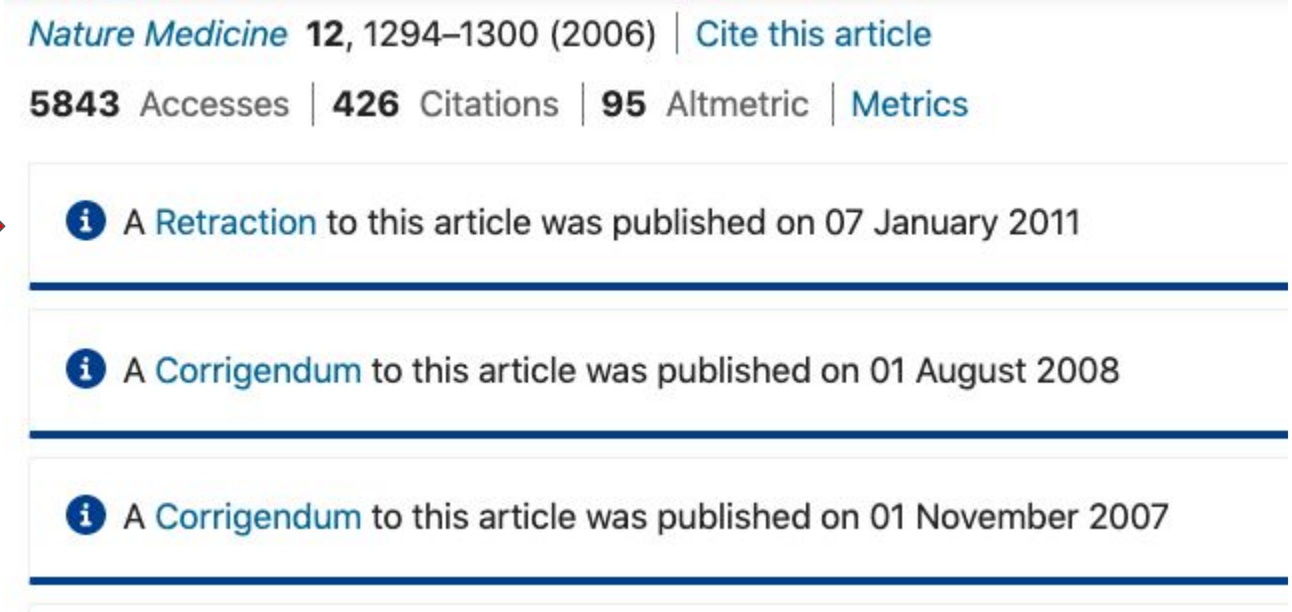
Please watch!!!

When is Reproducibility an Ethical Issue? Genomics, Personalized Medicine, and Human Error

Keith A erly
Bioinformatics and utational Biology
UT M. D. Ande ancer Center
kabagg@mdanderson.org

BIRS Workshop, Aug 14, 2013

http://www.birs.ca/events/2013/5-day-workshops/13w5083/videos/watch/201308141121-Baggerly.mp4



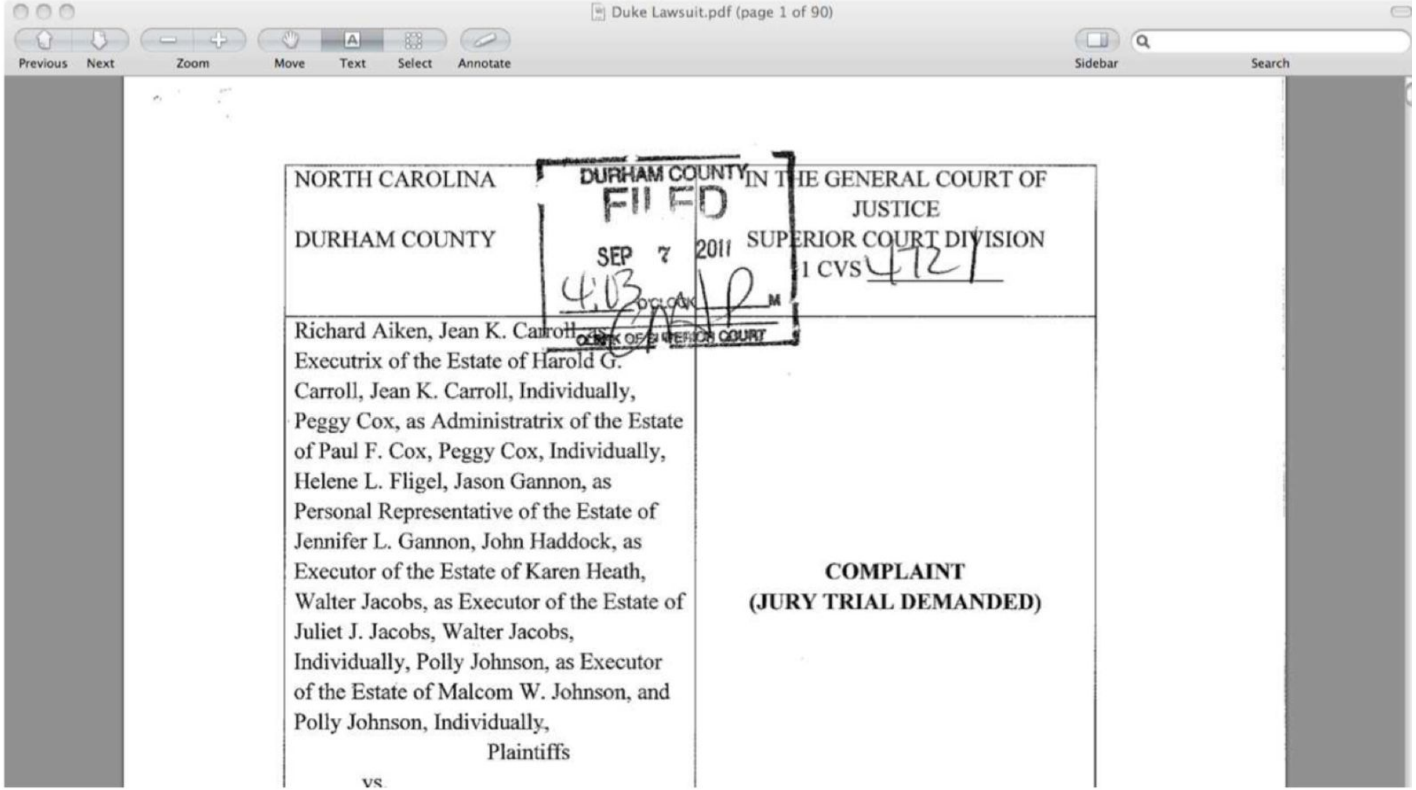
Nature Medicine **12**, 1294–1300 (2006) | Cite this article

5843 Accesses | **426** Citations | **95** Altmetric | Metrics

A Retraction to this article was published on 07 January 2011

A Corrigendum to this article was published on 01 August 2008

A Corrigendum to this article was published on 01 November 2007



NORTH CAROLINA

DURHAM COUNTY

DURHAM COUNTY
FILED
SEP 7 2011
4:13 O'CLOCK P M
CLERK OF SUPERIOR COURT

IN THE GENERAL COURT OF JUSTICE
SUPERIOR COURT DIVISION
1 CVS 4721

Richard Aiken, Jean K. Carroll, as Executrix of the Estate of Harold G. Carroll, Jean K. Carroll, Individually, Peggy Cox, as Administratrix of the Estate of Paul F. Cox, Peggy Cox, Individually, Helene L. Fligel, Jason Gannon, as Personal Representative of the Estate of Jennifer L. Gannon, John Haddock, as Executor of the Estate of Karen Heath, Walter Jacobs, as Executor of the Estate of Juliet J. Jacobs, Walter Jacobs, Individually, Polly Johnson, as Executor of the Estate of Malcom W. Johnson, and Polly Johnson, Individually,

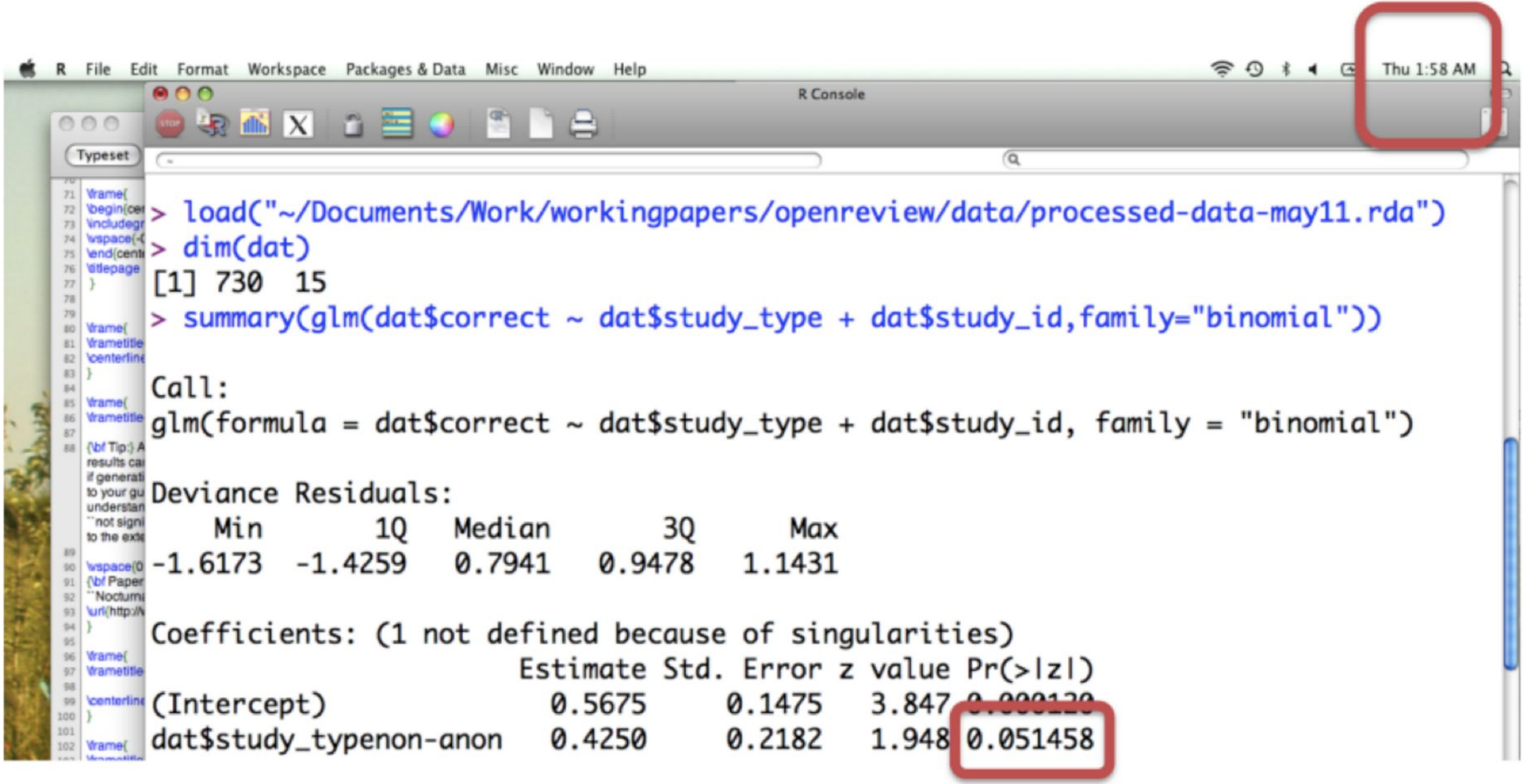
Plaintiffs

vs.

COMPLAINT
(JURY TRIAL DEMANDED)

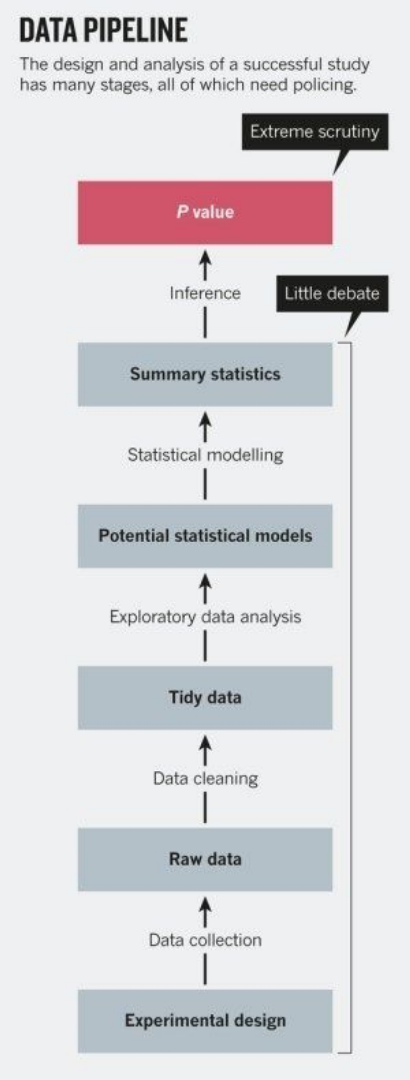
https://www.dukechronicle.com/article/2015/05/duke-lawsuit-involving-cancer-patients-linked-anil-potti-settled

Doesn’t seem that important….



```
> load("~/Documents/Work/workingpapers/openreview/data/processed-data-may11.rda")
> dim(dat)
[1] 730  15
> summary(glm(dat$correct ~ dat$study_type + dat$study_id,family="binomial"))

Call:
glm(formula = dat$correct ~ dat$study_type + dat$study_id, family = "binomial")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6173  -1.4259   0.7941   0.9478   1.1431

Coefficients: (1 not defined because of singularities)
                       Estimate Std. Error z value Pr(>|z|)
(Intercept)              0.5675     0.1475   3.847 0.000120
dat$study_typenon-anon   0.4250     0.2182   1.948 0.051458
```


ON THE ONE HAND...



- Most of the attention is on the last step
- This course is about all the steps that come before
- They are *critical* for getting things rights

Leek and Peng Nature 2015

The garden of forking paths: Why multiple comparisons can be a problem, even when there is no "fishing expedition" or "p-hacking" and the research hypothesis was posited ahead of time*

Andrew Gelman† and Eric Loken‡

14 Nov 2013

> *"I thought of a labyrinth of labyrinths, of one sinuous spreading labyrinth that would encompass the past and the future ... I felt myself to be, for an unknown period of time, an abstract perceiver of the world."* — Borges (1941)

Explorable Multiverse Analyses

Explorable Multiverse Analyses

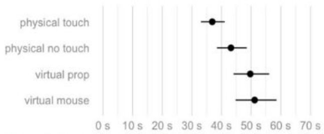
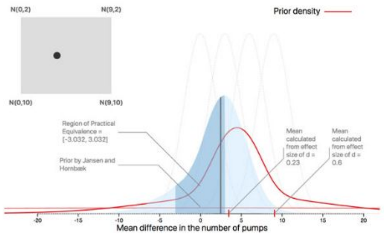
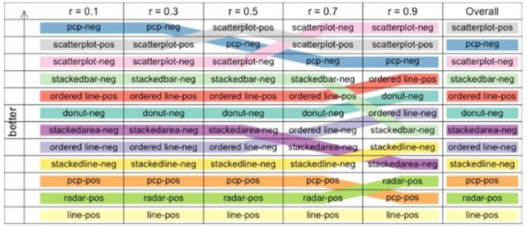


Figure 3. Average task completion time (geometric mean) for each condition. Error bars are 95% t-based CIs.

We focus our analysis on task completion times, reported in Figures 3 and 4. Dots indicate sample means, while error bars are 95% confidence intervals computed on log-transformed data [6] using the t-distribution method. Strictly speaking, all we can assert about each interval is that it comes from a procedure designed to capture the

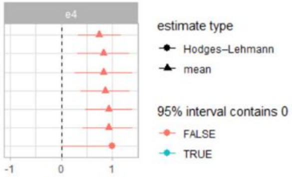
- Skeptical 60% - 40% Optimistic
- Narrow 50% - 50% Wide





r = 0.1	r = 0.3	r = 0.5	r = 0.7	r = 0.9	Overall
pcp-neg	pcp-neg	scatterplot-pos	scatterplot-neg	scatterplot-neg	scatterplot-pos
scatterplot-pos	scatterplot-pos	pcp-neg	scatterplot-pos	scatterplot-pos	pcp-neg
scatterplot-neg	scatterplot-neg	scatterplot-neg	pcp-neg	pcp-neg	scatterplot-neg
stackedbar-neg	stackedbar-neg	stackedbar-neg	stackedbar-neg	ordered line-pos	stackedbar-neg
ordered line-pos	ordered line-pos	ordered line-pos	ordered line-pos	donut-neg	ordered line-pos
donut-neg	donut-neg	donut-neg	donut-neg	ordered line-neg	donut-neg
stackedarea-neg	stackedarea-neg	stackedarea-neg	ordered line-neg	stackedbar-neg	stackedarea-neg
ordered line-neg	ordered line-neg	ordered line-neg	stackedarea-neg	stackedline-neg	ordered line-neg
stackedline-neg	stackedline-neg	stackedline-neg	stackedline-neg	stackedarea-neg	stackedline-neg
pcp-pos	pcp-pos	pcp-pos	pcp-pos	radar-pos	pcp-pos
radar-pos	radar-pos	radar-pos	radar-pos	pcp-pos	radar-pos
line-pos	line-pos	line-pos	line-pos	line-pos	line-pos

Figure 4. Perceptually-driven ranking of visualizations depending on the correlation sign (-neg / -pos), as a function of correlation value (r) and overall (right column).

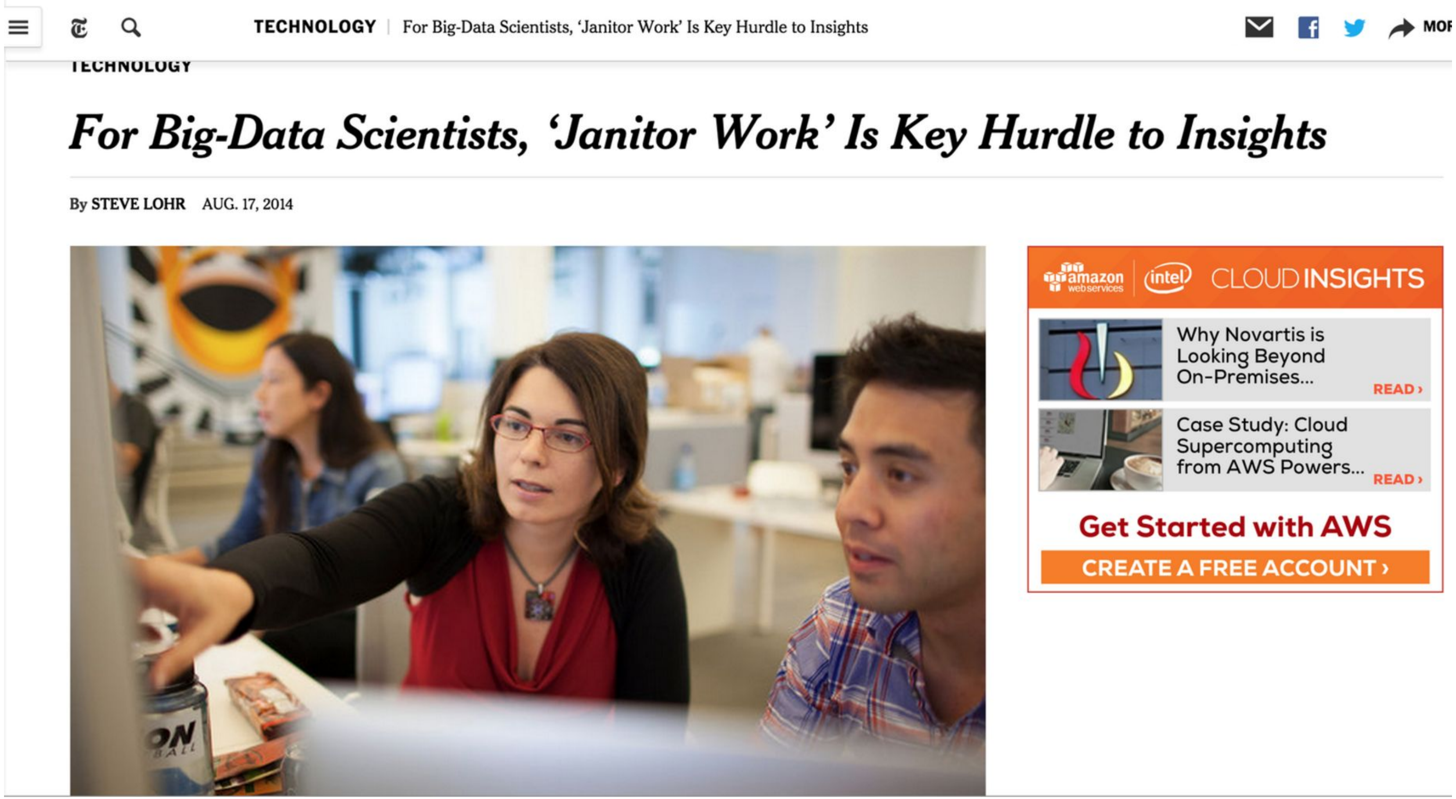


Pierre Dragicevic (Inria), Yvonne Jansen (CNRS - Sorbonne Université), Abhraneel Sarma (University of Michigan)
Matthew Kay (University of Michigan), Fanny Chevalier (University of Toronto)

With **explorable multiverse analysis reports**, readers of research papers can explore alternative analysis options by interacting with the paper itself. This new approach to statistical reporting draws from two recent ideas: multiverse analysis, a philosophy of statistical reporting where paper authors report the outcomes of many different statistical analyses in order to show how fragile or robust their findings are; and explorable explanations, narratives that can be read as normal explanations but where the reader can also become active by dynamically changing some elements of the explanation.

https://explorablemultiverse.github.io/

And so we data wrangle



TECHNOLOGY | For Big-Data Scientists, ‘Janitor Work’ Is Key Hurdle to Insights

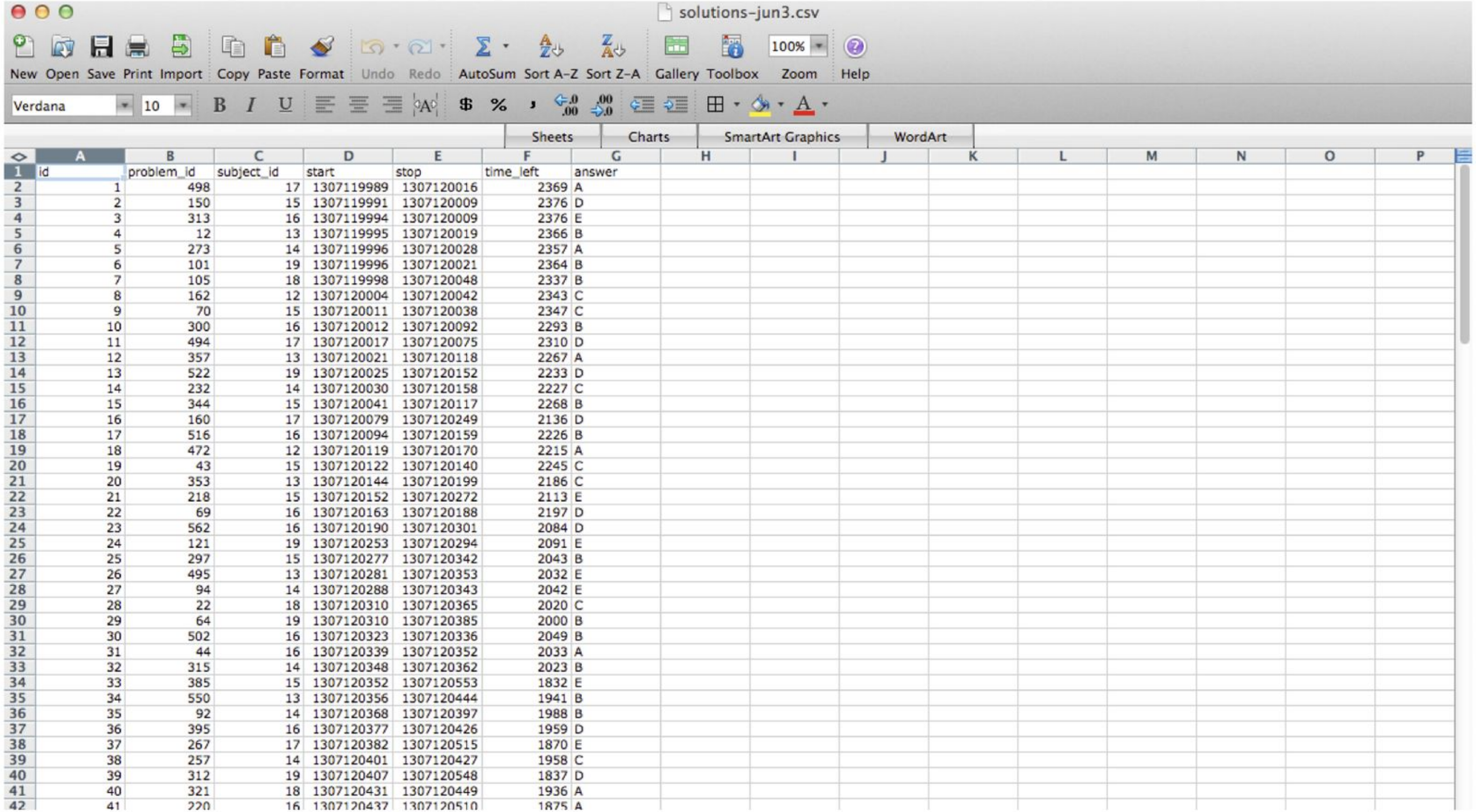
TECHNOLOGY

For Big-Data Scientists, ‘Janitor Work’ Is Key Hurdle to Insights

By **STEVE LOHR** AUG. 17, 2014

http://www.nytimes.com/2014/08/18/technology/for-big-data-scientists-hurdle-to-insights-is-janitor-work.html?_r=0

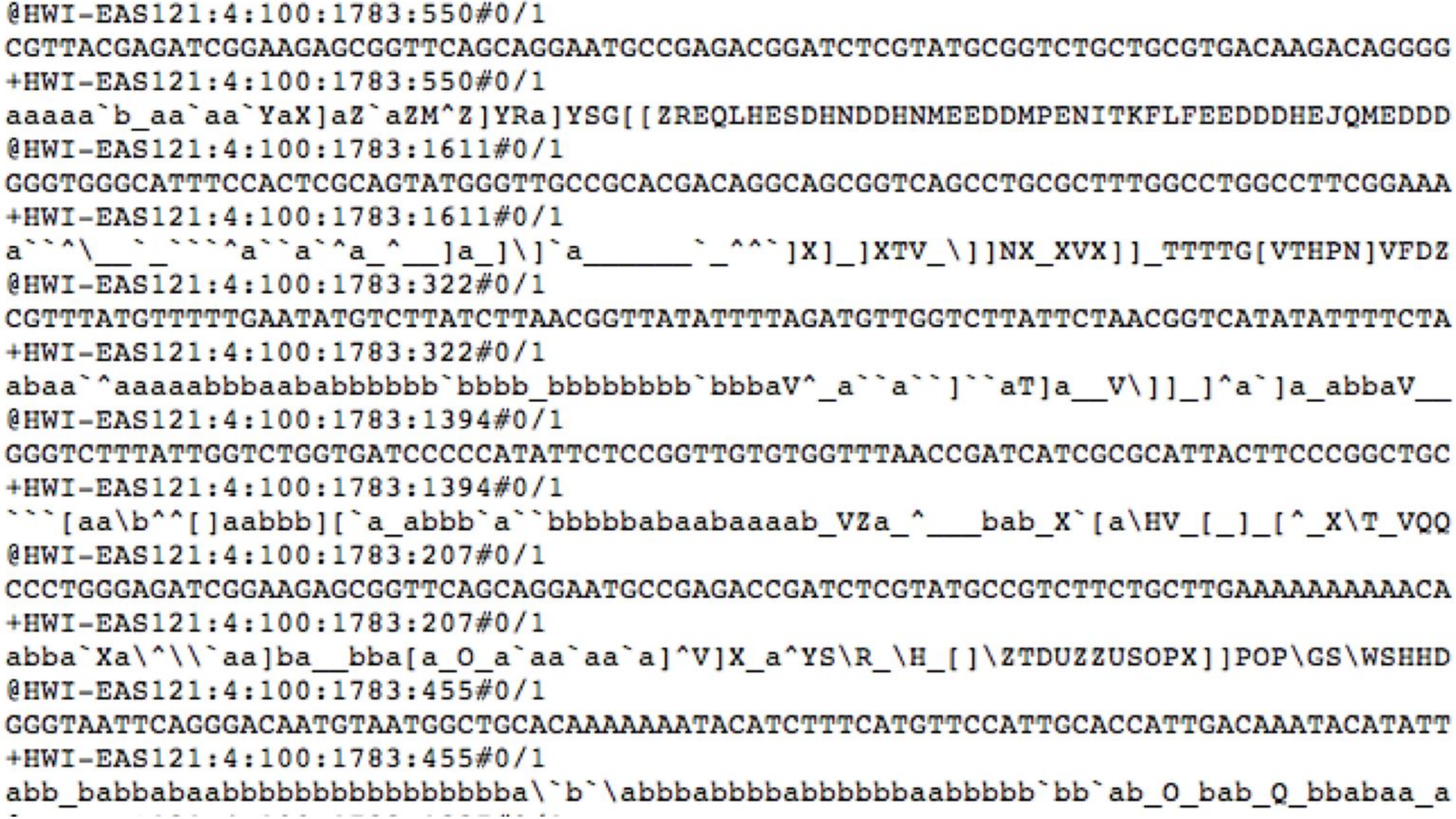
What you wished data looked like



id	problem_id	subject_id	start	stop	time_left	answer
1	498	17	1307119989	1307120016	2369	A
2	150	15	1307119991	1307120009	2376	D
3	313	16	1307119994	1307120009	2376	E
4	12	13	1307119995	1307120019	2366	B
5	273	14	1307119996	1307120028	2357	A
6	101	19	1307119996	1307120021	2364	B
7	105	18	1307119998	1307120048	2337	B
8	162	12	1307120004	1307120042	2343	C
9	70	15	1307120011	1307120038	2347	C
10	300	16	1307120012	1307120092	2293	B
11	494	17	1307120017	1307120075	2310	D
12	357	13	1307120021	1307120118	2267	A
13	522	19	1307120025	1307120152	2233	D
14	232	14	1307120030	1307120158	2227	C
15	344	15	1307120041	1307120117	2268	B
16	160	17	1307120079	1307120249	2136	D
17	516	16	1307120094	1307120159	2226	B
18	472	12	1307120119	1307120170	2215	A
19	43	15	1307120122	1307120140	2245	C
20	353	13	1307120144	1307120199	2186	C
21	218	15	1307120152	1307120272	2113	E
22	69	16	1307120163	1307120188	2197	D
23	562	16	1307120190	1307120301	2084	D
24	121	19	1307120253	1307120294	2091	E
25	297	15	1307120277	1307120342	2043	B
26	495	13	1307120281	1307120353	2032	E
27	94	14	1307120288	1307120343	2042	E
28	22	18	1307120310	1307120365	2020	C
29	64	19	1307120310	1307120385	2000	B
30	502	16	1307120323	1307120336	2049	B
31	44	16	1307120339	1307120352	2033	A
32	315	14	1307120348	1307120362	2023	B
33	385	15	1307120352	1307120553	1832	E
34	550	13	1307120356	1307120444	1941	B
35	92	14	1307120368	1307120397	1988	B
36	395	16	1307120377	1307120426	1959	D
37	267	17	1307120382	1307120515	1870	E
38	257	14	1307120401	1307120427	1958	C
39	312	19	1307120407	1307120548	1837	D
40	321	18	1307120431	1307120449	1936	A
41	220	16	1307120437	1307120510	1875	A

What it actually looks like

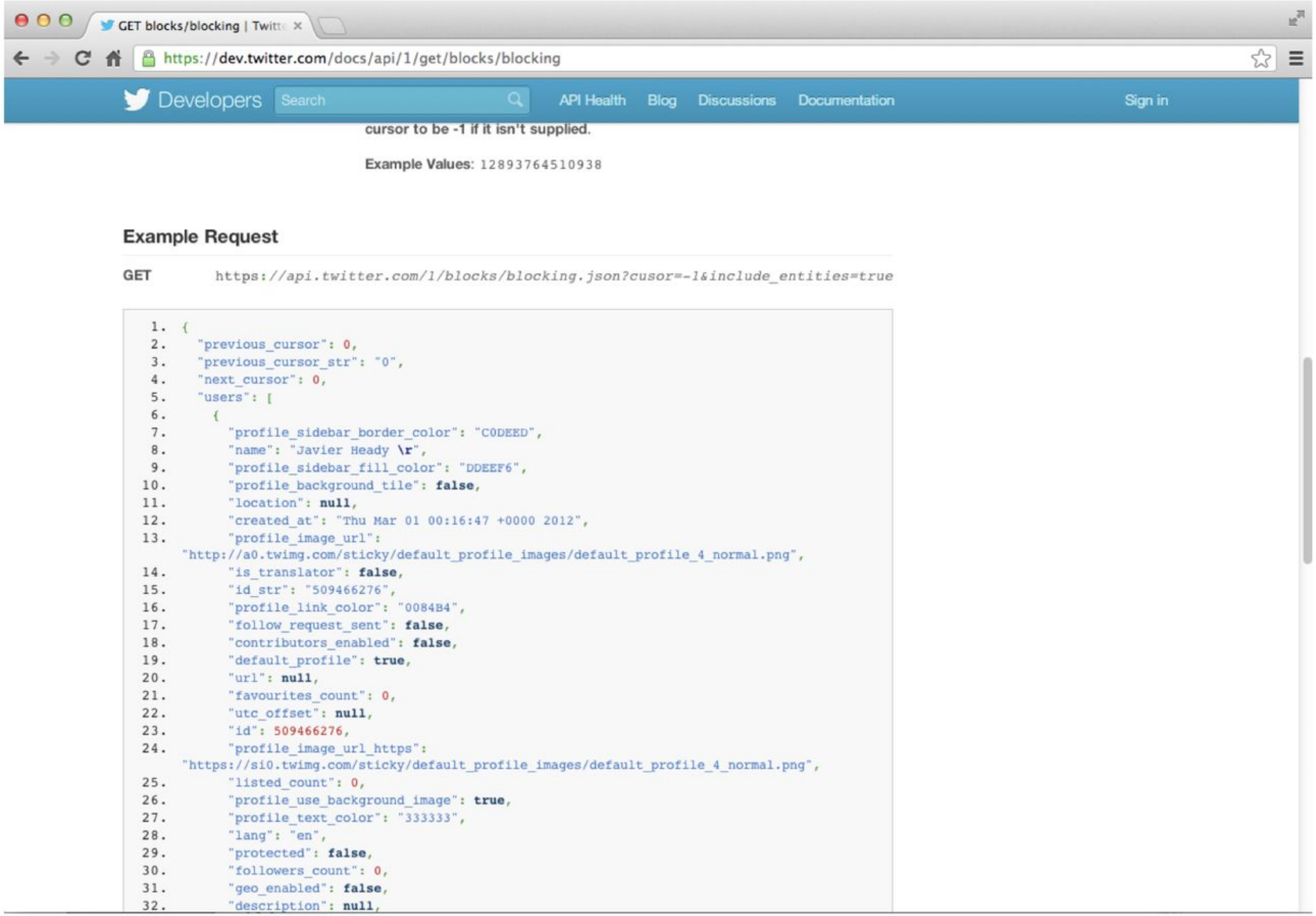
http://healthdesignchallenge.com/



~~~
@HWI-EAS121:4:100:1783:550#0/1
CGTTACGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACGGATCTCGTATGCGGTCTGCTGCGTGACAAGACAGGGG
+HWI-EAS121:4:100:1783:550#0/1
aaaaa`b_aa`aa`YaX]aZ`aZM^Z]YRa]YSG[[ZREQLHESDHNDDHNMEEDDMPENITKFLFEEDDDHEJQMEDDD
@HWI-EAS121:4:100:1783:1611#0/1
GGGTGGGCATTTCCACTCGCAGTATGGGTTGCCGCACGACAGGCAGCGGTCAGCCTGCGCTTTGGCCTGGCCTTCGGAAA
+HWI-EAS121:4:100:1783:1611#0/1
a``^\__`_```^a``a`^a_^__]a_]\]`a______`_^^`]X]_]XTV_\]]NX_XVX]]_TTTTG[VTHPN]VFDZ
@HWI-EAS121:4:100:1783:322#0/1
CGTTTATGTTTTTGAATATGTCTTATCTTAACGGTTATATTTTAGATGTTGGTCTTATTCTAACGGTCATATATTTTCTA
+HWI-EAS121:4:100:1783:322#0/1
abaa`^aaaaabbbaababbbbbb`bbbb_bbbbbbbb`bbbaV^_a``a``]``aT]a__V\]]_]^a`]a_abbaV__
@HWI-EAS121:4:100:1783:1394#0/1
GGGTCTTTATTGGTCTGGTGATCCCCCATATTCTCCGGTTGTGTGGTTTAACCGATCATCGCGCATTACTTCCCGGCTGC
+HWI-EAS121:4:100:1783:1394#0/1
```[aa\b^^[]aabbb][`a_abbb`a``bbbbbabaabaaaab_VZa_^___bab_X`[a\HV_[_]_[^_X\T_VQQ
@HWI-EAS121:4:100:1783:207#0/1
CCCTGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTGAAAAAAAAAACA
+HWI-EAS121:4:100:1783:207#0/1
abba`Xa\^\\`aa]ba__bba[a_O_a`aa`aa`a]^V]X_a^YS\R_\H_[]\ZTDUZZUSOPX]]POP\GS\WSHHD
@HWI-EAS121:4:100:1783:455#0/1
GGGTAATTCAGGGACAATGTAATGGCTGCACAAAAAAATACATCTTTCATGTTCCATTGCACCATTGACAAATACATATT
+HWI-EAS121:4:100:1783:455#0/1
abb_babbabaabbbbbbbbbbbbbbbba\`b`\abbbabbbbabbbbbbaabbbbb`bb`ab_O_bab_Q_bbabaa_a
~~~

What it actually looks like

https://dev.twitter.com/docs/api/1/get/blocks/blocking



cursor to be -1 if it isn't supplied.

Example Values: `12893764510938`

Example Request

GET `https://api.twitter.com/1/blocks/blocking.json?cusor=-1&include_entities=true`

```
{
  "previous_cursor": 0,
  "previous_cursor_str": "0",
  "next_cursor": 0,
  "users": [
    {
      "profile_sidebar_border_color": "C0DEED",
      "name": "Javier Heady \r",
      "profile_sidebar_fill_color": "DDEEF6",
      "profile_background_tile": false,
      "location": null,
      "created_at": "Thu Mar 01 00:16:47 +0000 2012",
      "profile_image_url":
"http://a0.twimg.com/sticky/default_profile_images/default_profile_4_normal.png",
      "is_translator": false,
      "id_str": "509466276",
      "profile_link_color": "0084B4",
      "follow_request_sent": false,
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      "url": null,
      "favourites_count": 0,
      "utc_offset": null,
      "id": 509466276,
      "profile_image_url_https":
"https://si0.twimg.com/sticky/default_profile_images/default_profile_4_normal.png",
      "listed_count": 0,
      "profile_use_background_image": true,
      "profile_text_color": "333333",
      "lang": "en",
      "protected": false,
      "followers_count": 0,
      "geo_enabled": false,
      "description": null,
```
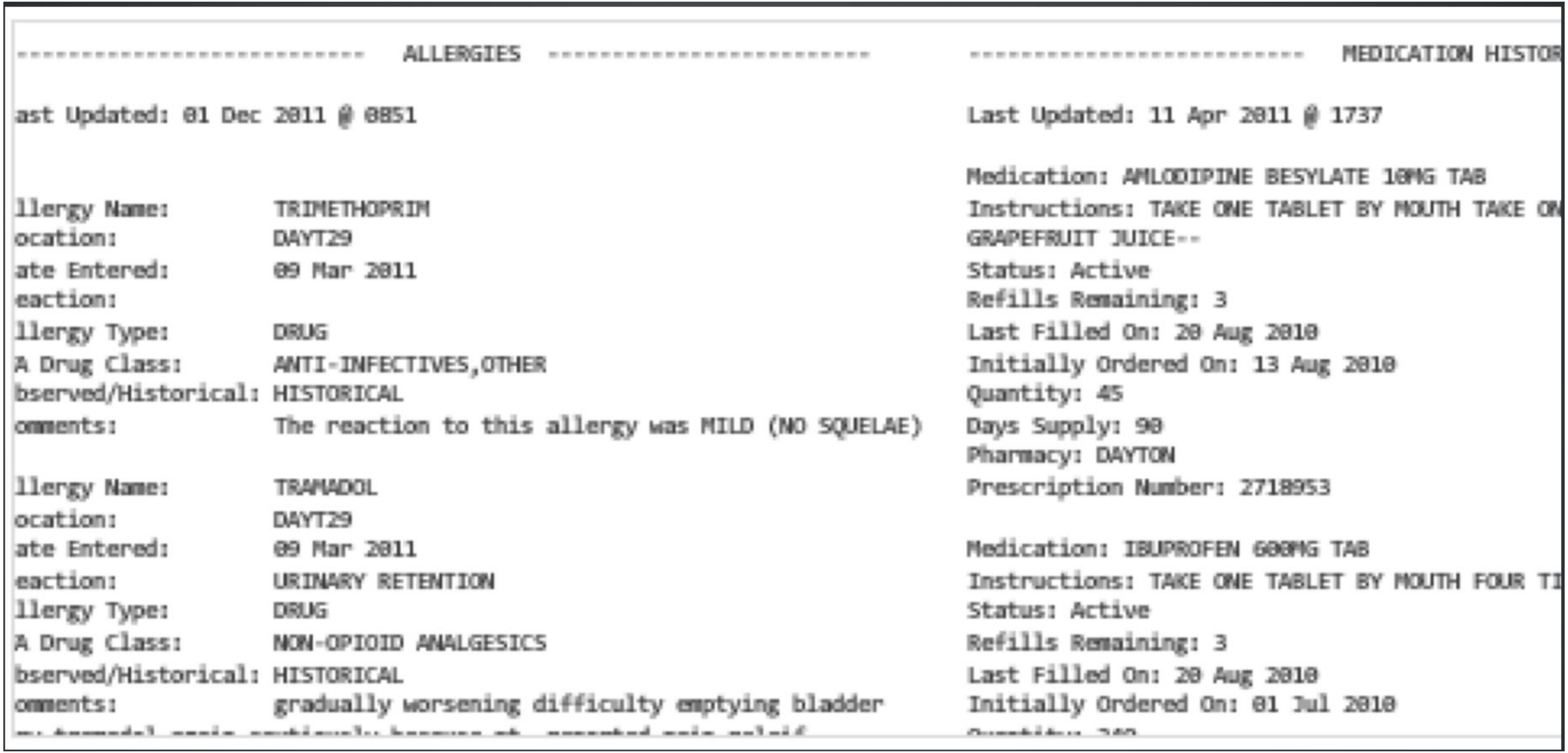
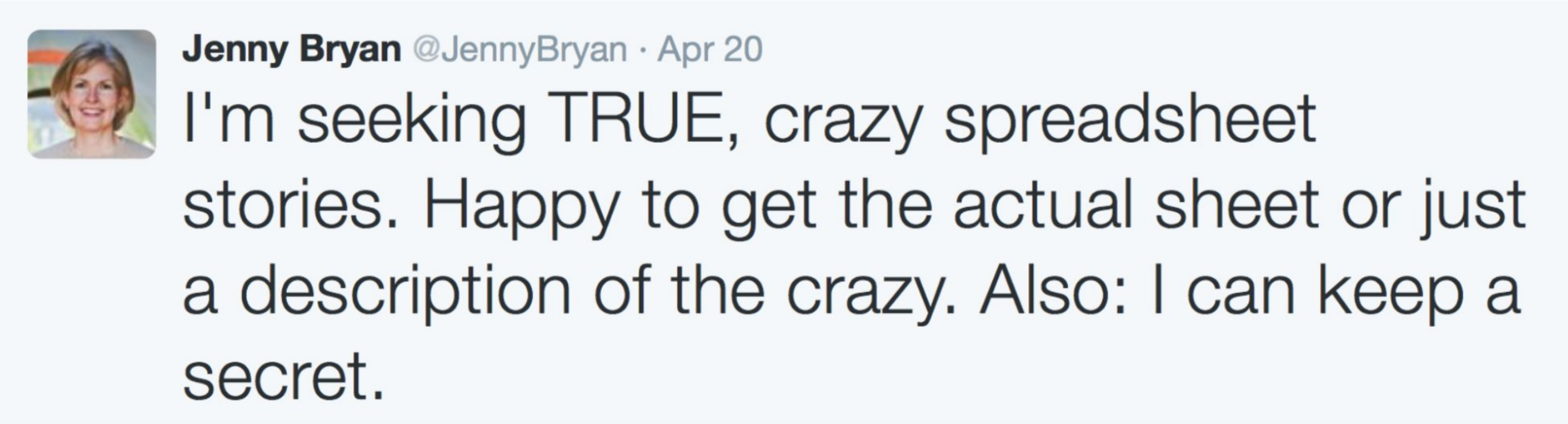

What it actually looks like



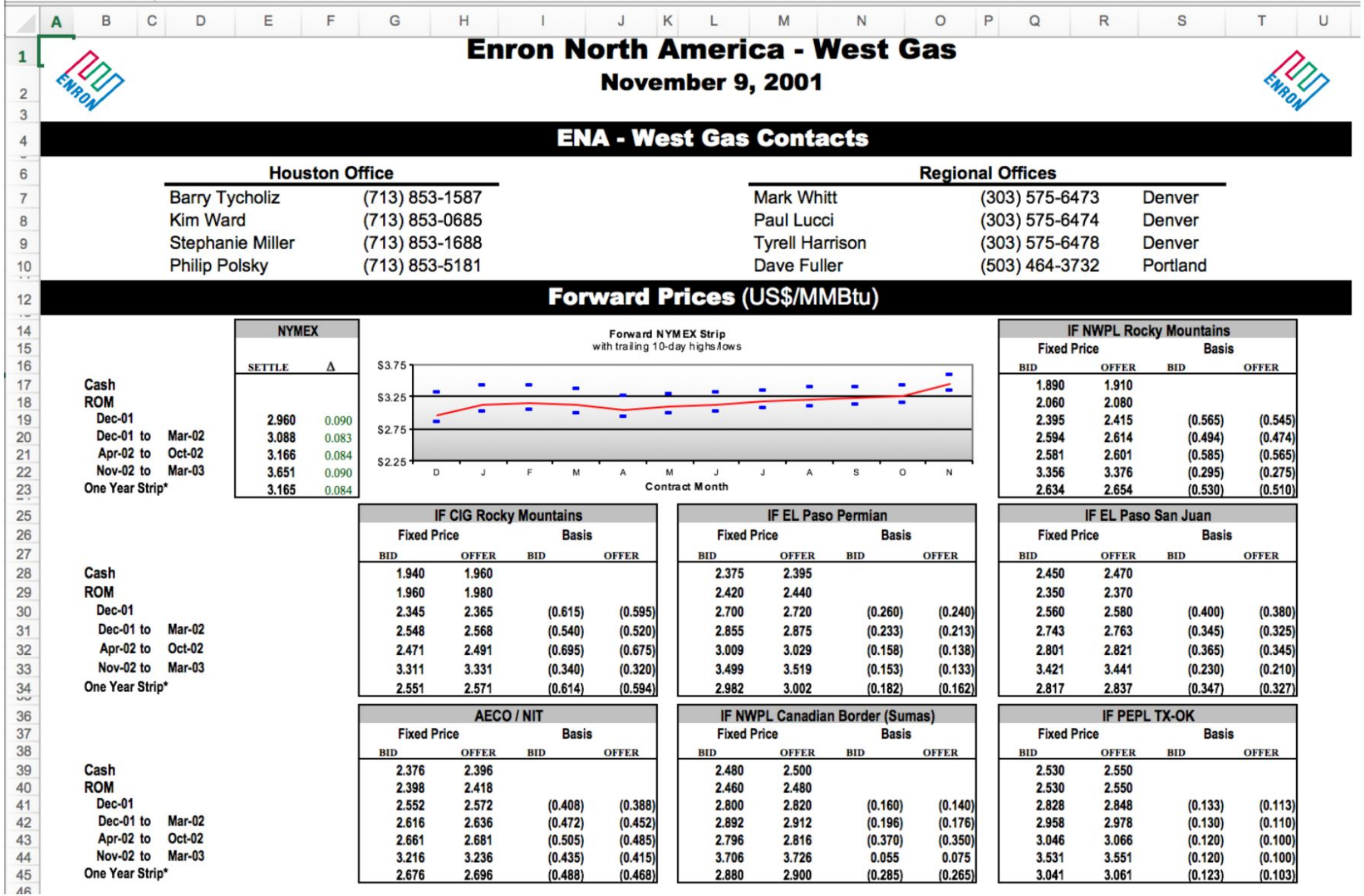
```
-------------------------  ALLERGIES  -----------------------        -------------------------  MEDICATION HISTOR

ast Updated: 01 Dec 2011 @ 0851                                      Last Updated: 11 Apr 2011 @ 1737

                                                                     Medication: AMLODIPINE BESYLATE 10MG TAB
llergy Name:        TRIMETHOPRIM                                     Instructions: TAKE ONE TABLET BY MOUTH TAKE ON
ocation:            DAYT29                                           GRAPEFRUIT JUICE--
ate Entered:        09 Mar 2011                                      Status: Active
eaction:                                                             Refills Remaining: 3
llergy Type:        DRUG                                             Last Filled On: 20 Aug 2010
A Drug Class:       ANTI-INFECTIVES,OTHER                            Initially Ordered On: 13 Aug 2010
bserved/Historical: HISTORICAL                                       Quantity: 45
omments:            The reaction to this allergy was MILD (NO SQUELAE)   Days Supply: 90
                                                                     Pharmacy: DAYTON
llergy Name:        TRAMADOL                                         Prescription Number: 2718953
ocation:            DAYT29
ate Entered:        09 Mar 2011                                      Medication: IBUPROFEN 600MG TAB
eaction:            URINARY RETENTION                                Instructions: TAKE ONE TABLET BY MOUTH FOUR TI
llergy Type:        DRUG                                             Status: Active
A Drug Class:       NON-OPIOID ANALGESICS                            Refills Remaining: 3
bserved/Historical: HISTORICAL                                       Last Filled On: 20 Aug 2010
omments:            gradually worsening difficulty emptying bladder  Initially Ordered On: 01 Jul 2010
```



Jenny Bryan @JennyBryan · Apr 20

I'm seeking TRUE, crazy spreadsheet stories. Happy to get the actual sheet or just a description of the crazy. Also: I can keep a secret.

Slide from Jenny Bryan
(https://github.com/jennybc/2016-06_spreadsheets/blob/master/2016-06_useR-stanford.pdf)



Enron North America - West Gas

November 9, 2001

ENA - West Gas Contacts

Houston Office	
Barry Tycholiz	(713) 853-1587
Kim Ward	(713) 853-0685
Stephanie Miller	(713) 853-1688
Philip Polsky	(713) 853-5181

Regional Offices		
Mark Whitt	(303) 575-6473	Denver
Paul Lucci	(303) 575-6474	Denver
Tyrell Harrison	(303) 575-6478	Denver
Dave Fuller	(503) 464-3732	Portland

Forward Prices (US$/MMBtu)

	NYMEX	
	SETTLE	Δ
Cash		
ROM		
Dec-01	2.960	0.090
Dec-01 to Mar-02	3.088	0.083
Apr-02 to Oct-02	3.166	0.084
Nov-02 to Mar-03	3.651	0.090
One Year Strip*	3.165	0.084

	IF NWPL Rocky Mountains			
	Fixed Price		Basis	
	BID	OFFER	BID	OFFER
Cash	1.890	1.910		
ROM	2.060	2.080		
Dec-01	2.395	2.415	(0.565)	(0.545)
Dec-01 to Mar-02	2.594	2.614	(0.494)	(0.474)
Apr-02 to Oct-02	2.581	2.601	(0.585)	(0.565)
Nov-02 to Mar-03	3.356	3.376	(0.295)	(0.275)
One Year Strip*	2.634	2.654	(0.530)	(0.510)

	IF CIG Rocky Mountains			
	Fixed Price		Basis	
	BID	OFFER	BID	OFFER
Cash	1.940	1.960		
ROM	1.960	1.980		
Dec-01	2.345	2.365	(0.615)	(0.595)
Dec-01 to Mar-02	2.548	2.568	(0.540)	(0.520)
Apr-02 to Oct-02	2.471	2.491	(0.695)	(0.675)
Nov-02 to Mar-03	3.311	3.331	(0.340)	(0.320)
One Year Strip*	2.551	2.571	(0.614)	(0.594)

	IF EL Paso Permian			
	Fixed Price		Basis	
	BID	OFFER	BID	OFFER
Cash	2.375	2.395		
ROM	2.420	2.440		
Dec-01	2.700	2.720	(0.260)	(0.240)
Dec-01 to Mar-02	2.855	2.875	(0.233)	(0.213)
Apr-02 to Oct-02	3.009	3.029	(0.158)	(0.138)
Nov-02 to Mar-03	3.499	3.519	(0.153)	(0.133)
One Year Strip*	2.982	3.002	(0.182)	(0.162)

	IF EL Paso San Juan			
	Fixed Price		Basis	
	BID	OFFER	BID	OFFER
Cash	2.450	2.470		
ROM	2.350	2.370		
Dec-01	2.560	2.580	(0.400)	(0.380)
Dec-01 to Mar-02	2.743	2.763	(0.345)	(0.325)
Apr-02 to Oct-02	2.801	2.821	(0.365)	(0.345)
Nov-02 to Mar-03	3.421	3.441	(0.230)	(0.210)
One Year Strip*	2.817	2.837	(0.347)	(0.327)

	AECO / NIT			
	Fixed Price		Basis	
	BID	OFFER	BID	OFFER
Cash	2.376	2.396		
ROM	2.398	2.418		
Dec-01	2.552	2.572	(0.408)	(0.388)
Dec-01 to Mar-02	2.616	2.636	(0.472)	(0.452)
Apr-02 to Oct-02	2.661	2.681	(0.505)	(0.485)
Nov-02 to Mar-03	3.216	3.236	(0.435)	(0.415)
One Year Strip*	2.676	2.696	(0.488)	(0.468)

	IF NWPL Canadian Border (Sumas)			
	Fixed Price		Basis	
	BID	OFFER	BID	OFFER
Cash	2.480	2.500		
ROM	2.460	2.480		
Dec-01	2.800	2.820	(0.160)	(0.140)
Dec-01 to Mar-02	2.892	2.912	(0.196)	(0.176)
Apr-02 to Oct-02	2.796	2.816	(0.370)	(0.350)
Nov-02 to Mar-03	3.706	3.726	0.055	0.075
One Year Strip*	2.880	2.900	(0.285)	(0.265)

	IF PEPL TX-OK			
	Fixed Price		Basis	
	BID	OFFER	BID	OFFER
Cash	2.530	2.550		
ROM	2.530	2.550		
Dec-01	2.828	2.848	(0.133)	(0.113)
Dec-01 to Mar-02	2.958	2.978	(0.130)	(0.110)
Apr-02 to Oct-02	3.046	3.066	(0.120)	(0.100)
Nov-02 to Mar-03	3.531	3.551	(0.120)	(0.100)
One Year Strip*	3.041	3.061	(0.123)	(0.103)

Slide from Jenny Bryan
(https://github.com/jennybc/2016-06_spreadsheets/blob/master/2016-06_useR-stanford.pdf)

Desiree Narango
@DLNarango

Today's updates on #otherpeoplesdata:

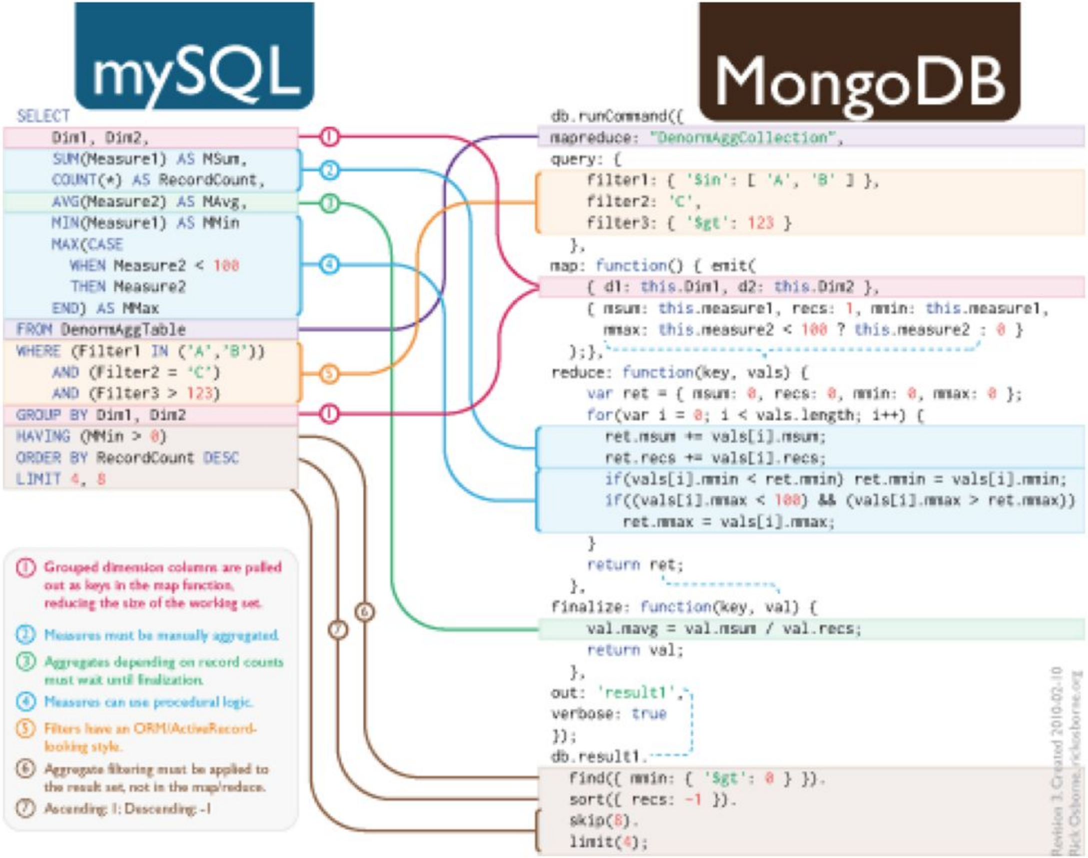
8:56 AM - 22 Oct 2018

1 Like

Where you wish data was

Where data actually is

https://rickosborne.org/blog/2010/02/infographic-migrating-from-sql-to-mapreduce-with-mongodb/



```
SELECT
    Dim1, Dim2,
    SUM(Measure1) AS MSum,
    COUNT(*) AS RecordCount,
    AVG(Measure2) AS MAvg,
    MIN(Measure1) AS MMin
    MAX(CASE
      WHEN Measure2 < 100
      THEN Measure2
    END) AS MMax
FROM DenormAggTable
WHERE (Filter1 IN ('A','B'))
    AND (Filter2 = 'C')
    AND (Filter3 > 123)
GROUP BY Dim1, Dim2
HAVING (MMin > 0)
ORDER BY RecordCount DESC
LIMIT 4, 8
```

```
db.runCommand({
mapreduce: "DenormAggCollection",
query: {
    filter1: { '$in': [ 'A', 'B' ] },
    filter2: 'C',
    filter3: { '$gt': 123 }
  },
map: function() { emit(
    { d1: this.Dim1, d2: this.Dim2 },
    { msum: this.measure1, recs: 1, mmin: this.measure1,
      mmax: this.measure2 < 100 ? this.measure2 : 0 }
  );},
reduce: function(key, vals) {
    var ret = { msum: 0, recs: 0, mmin: 0, mmax: 0 };
    for(var i = 0; i < vals.length; i++) {
      ret.msum += vals[i].msum;
      ret.recs += vals[i].recs;
      if(vals[i].mmin < ret.mmin) ret.mmin = vals[i].mmin;
      if((vals[i].mmax < 100) && (vals[i].mmax > ret.mmax))
        ret.mmax = vals[i].mmax;
    }
    return ret;
  },
finalize: function(key, val) {
    val.mavg = val.msum / val.recs;
    return val;
  },
out: 'result1',
verbose: true
});
db.result1.
  find({ mmin: { '$gt': 0 } }).
  sort({ recs: -1 }).
  skip(8).
  limit(4);
```

① Grouped dimension columns are pulled out as keys in the map function, reducing the size of the working set.

② Measures must be manually aggregated.

③ Aggregates depending on record counts must wait until finalization.

④ Measures can use procedural logic.

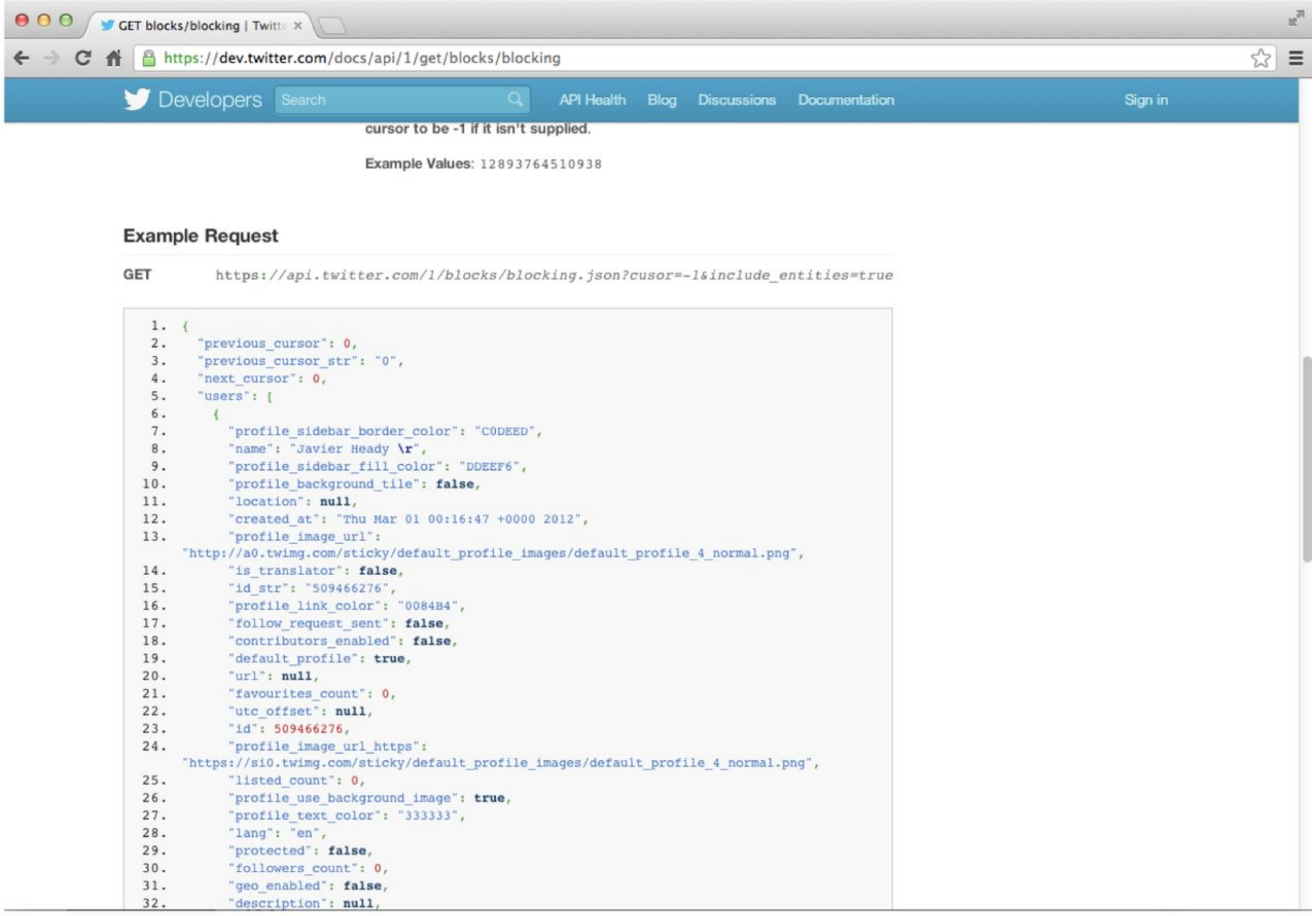
⑤ Filters have an ORM/ActiveRecord-looking style.

⑥ Aggregate filtering must be applied to the result set, not in the map/reduce.

⑦ Ascending: 1; Descending: -1

Where data actually is

https://dev.twitter.com/docs/api/1/get/blocks/blocking



cursor to be -1 if it isn't supplied.

Example Values: `12893764510938`

Example Request

GET `https://api.twitter.com/1/blocks/blocking.json?cusor=-1&include_entities=true`

```
{
  "previous_cursor": 0,
  "previous_cursor_str": "0",
  "next_cursor": 0,
  "users": [
    {
      "profile_sidebar_border_color": "C0DEED",
      "name": "Javier Heady \r",
      "profile_sidebar_fill_color": "DDEEF6",
      "profile_background_tile": false,
      "location": null,
      "created_at": "Thu Mar 01 00:16:47 +0000 2012",
      "profile_image_url":
"http://a0.twimg.com/sticky/default_profile_images/default_profile_4_normal.png",
      "is_translator": false,
      "id_str": "509466276",
      "profile_link_color": "0084B4",
      "follow_request_sent": false,
      "contributors_enabled": false,
      "default_profile": true,
      "url": null,
      "favourites_count": 0,
      "utc_offset": null,
      "id": 509466276,
      "profile_image_url_https":
"https://si0.twimg.com/sticky/default_profile_images/default_profile_4_normal.png",
      "listed_count": 0,
      "profile_use_background_image": true,
      "profile_text_color": "333333",
      "lang": "en",
      "protected": false,
      "followers_count": 0,
      "geo_enabled": false,
      "description": null,
```

Raw & processed data

http://en.wikipedia.org/wiki/Data

> “Data are values of qualitative or quantitative variables, belonging to a set of items.”

http://en.wikipedia.org/wiki/Data

> “Data are values of qualitative or quantitative variables, belonging to a set of items.”

Set of items: Sometimes called the population; the set of objects you are interested in

http://en.wikipedia.org/wiki/Data

> “Data are values of qualitative or quantitative variables, belonging to a set of items.”

Variables: A measurement or characteristic of an item

http://en.wikipedia.org/wiki/Data

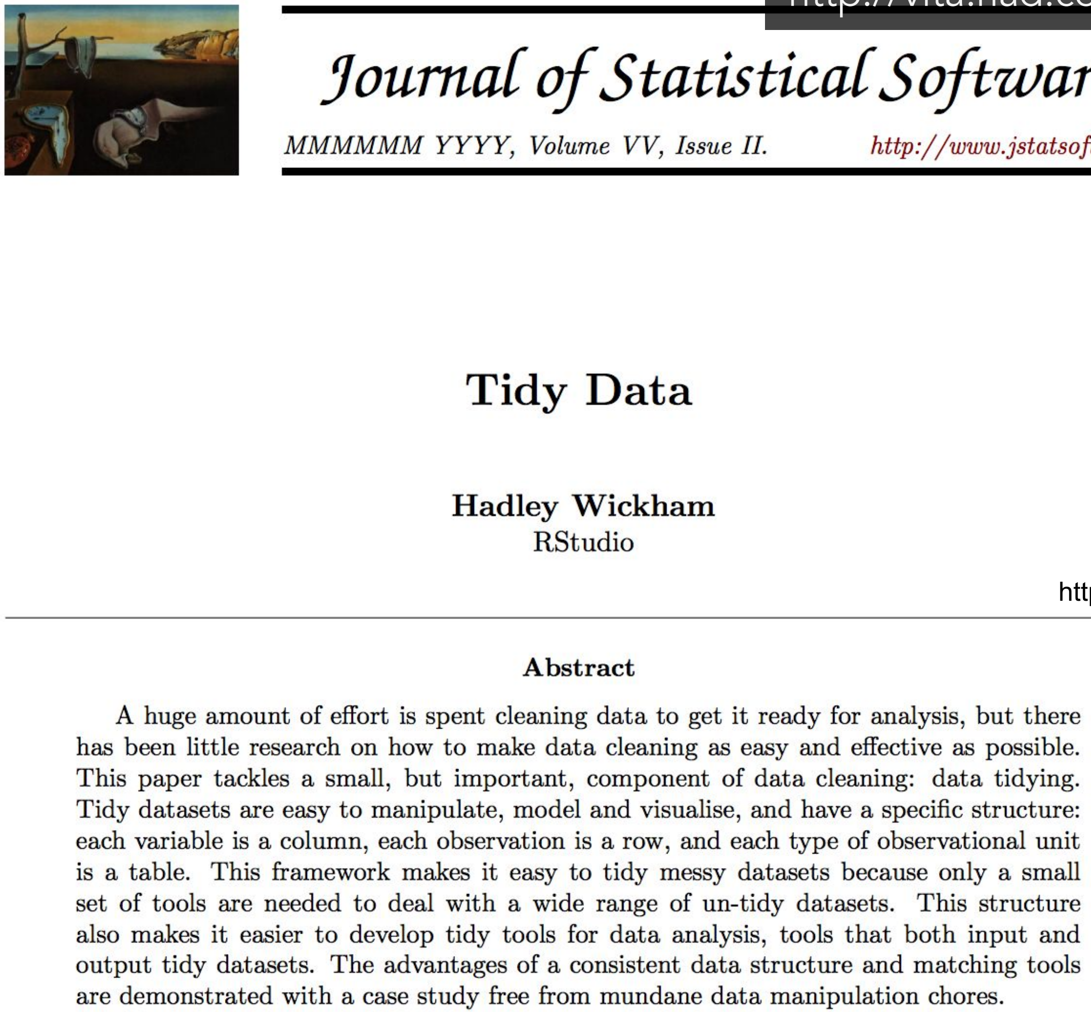
> “Data are values of qualitative or quantitative variables, belonging to a set of items.”

Qualitative: Country of origin, sex, treatment
Quantitative: Height, weight, blood pressure

Data sharing

1. The raw data.
2. A tidy data set
3. A code book describing each variable and its values in the tidy data set.
4. An explicit and exact recipe you used to go from 1 -> 2,3

http://vita.had.co.nz/papers/tidy-data.pdf



Journal of Statistical Software

MMMMMM YYYY, Volume VV, Issue II. http://www.jstatsoft.org/

Tidy Data

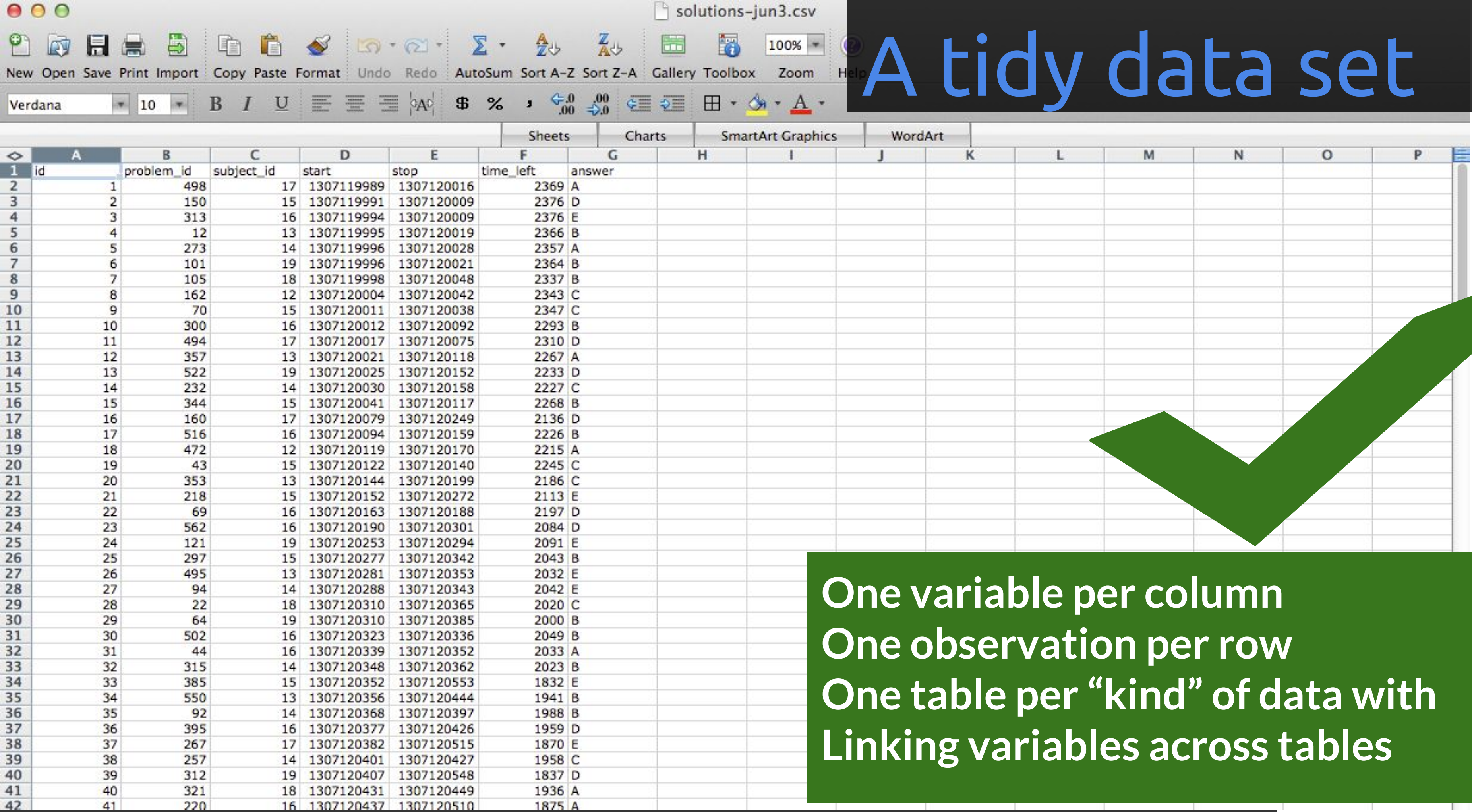
Hadley Wickham
RStudio

https://twitter.com/hadleywickham

Abstract

A huge amount of effort is spent cleaning data to get it ready for analysis, but there has been little research on how to make data cleaning as easy and effective as possible. This paper tackles a small, but important, component of data cleaning: data tidying. Tidy datasets are easy to manipulate, model and visualise, and have a specific structure: each variable is a column, each observation is a row, and each type of observational unit is a table. This framework makes it easy to tidy messy datasets because only a small set of tools are needed to deal with a wide range of un-tidy datasets. This structure also makes it easier to develop tidy tools for data analysis, tools that both input and output tidy datasets. The advantages of a consistent data structure and matching tools are demonstrated with a case study free from mundane data manipulation chores.

A tidy data set



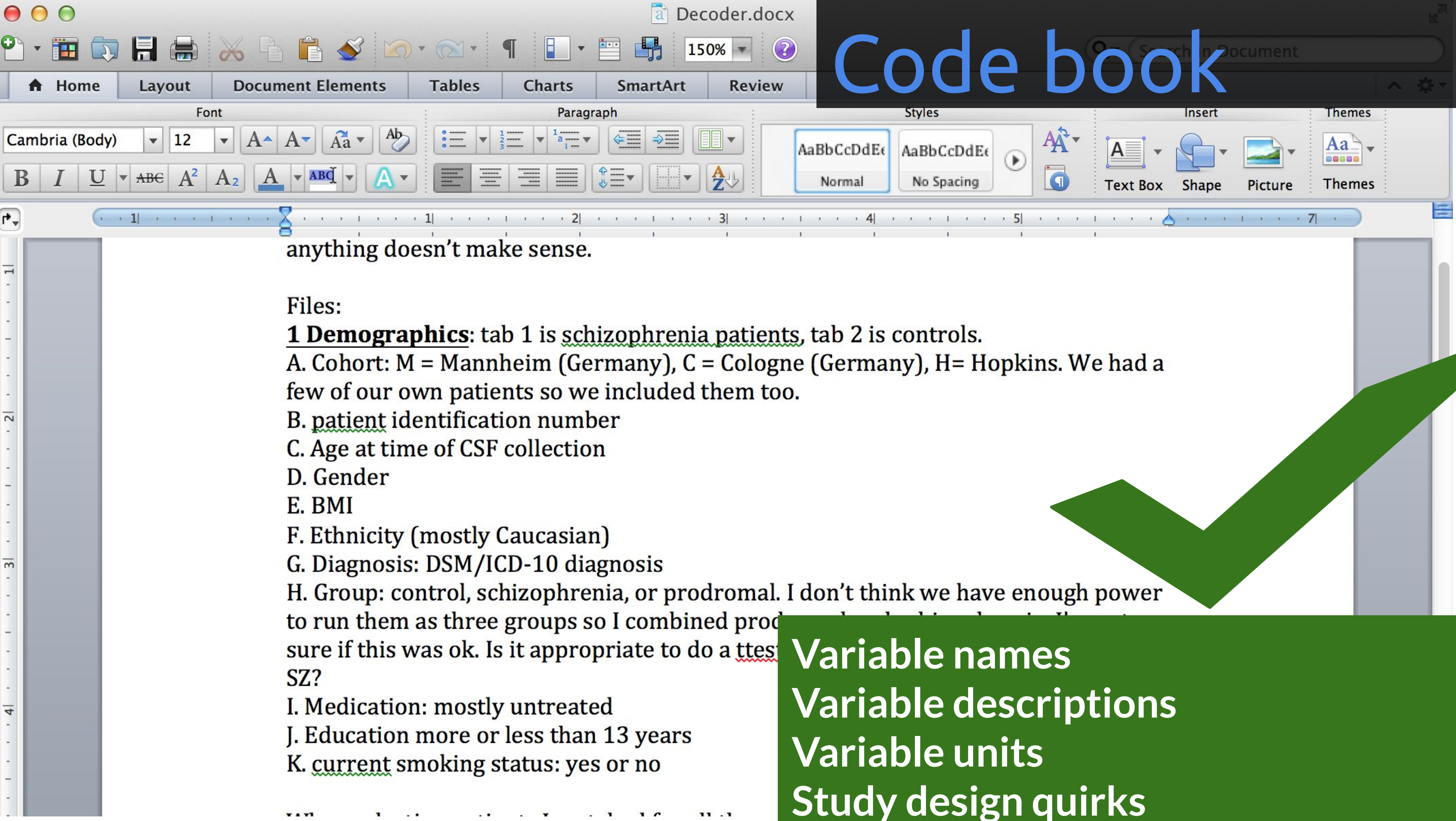
id	problem_id	subject_id	start	stop	time_left	answer
1	498	17	1307119989	1307120016	2369	A
2	150	15	1307119991	1307120009	2376	D
3	313	16	1307119994	1307120009	2376	E
4	12	13	1307119995	1307120019	2366	B
5	273	14	1307119996	1307120028	2357	A
6	101	19	1307119996	1307120021	2364	B
7	105	18	1307119998	1307120048	2337	B
8	162	12	1307120004	1307120042	2343	C
9	70	15	1307120011	1307120038	2347	C
10	300	16	1307120012	1307120092	2293	B
11	494	17	1307120017	1307120075	2310	D
12	357	13	1307120021	1307120118	2267	A
13	522	19	1307120025	1307120152	2233	D
14	232	14	1307120030	1307120158	2227	C
15	344	15	1307120041	1307120117	2268	B
16	160	17	1307120079	1307120249	2136	D
17	516	16	1307120094	1307120159	2226	B
18	472	12	1307120119	1307120170	2215	A
19	43	15	1307120122	1307120140	2245	C
20	353	13	1307120144	1307120199	2186	C
21	218	15	1307120152	1307120272	2113	E
22	69	16	1307120163	1307120188	2197	D
23	562	16	1307120190	1307120301	2084	D
24	121	19	1307120253	1307120294	2091	E
25	297	15	1307120277	1307120342	2043	B
26	495	13	1307120281	1307120353	2032	E
27	94	14	1307120288	1307120343	2042	E
28	22	18	1307120310	1307120365	2020	C
29	64	19	1307120310	1307120385	2000	B
30	502	16	1307120323	1307120336	2049	B
31	44	16	1307120339	1307120352	2033	A
32	315	14	1307120348	1307120362	2023	B
33	385	15	1307120352	1307120553	1832	E
34	550	13	1307120356	1307120444	1941	B
35	92	14	1307120368	1307120397	1988	B
36	395	16	1307120377	1307120426	1959	D
37	267	17	1307120382	1307120515	1870	E
38	257	14	1307120401	1307120427	1958	C
39	312	19	1307120407	1307120548	1837	D
40	321	18	1307120431	1307120449	1936	A
41	220	16	1307120437	1307120510	1875	A

✓

One variable per column
One observation per row
One table per "kind" of data with
Linking variables across tables

Reference: http://brianknaus.com/software/srtoolbox/s_4_1_sequence80.txt

Code book



anything doesn't make sense.

Files:

1 Demographics: tab 1 is schizophrenia patients, tab 2 is controls.

A. Cohort: M = Mannheim (Germany), C = Cologne (Germany), H= Hopkins. We had a few of our own patients so we included them too.

B. patient identification number

C. Age at time of CSF collection

D. Gender

E. BMI

F. Ethnicity (mostly Caucasian)

G. Diagnosis: DSM/ICD-10 diagnosis

H. Group: control, schizophrenia, or prodromal. I don't think we have enough power to run them as three groups so I combined prod
sure if this was ok. Is it appropriate to do a ttest
SZ?

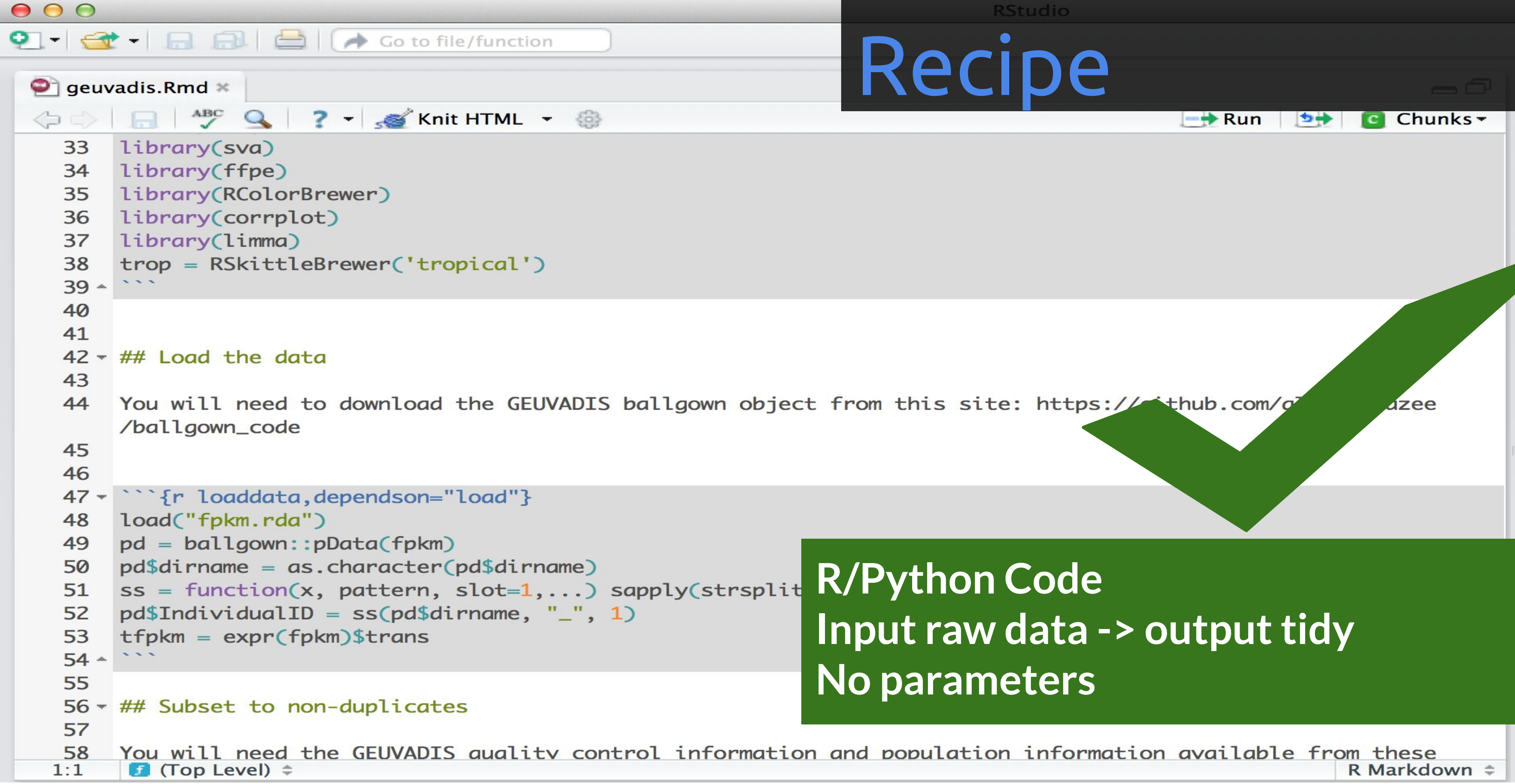
I. Medication: mostly untreated

J. Education more or less than 13 years

K. current smoking status: yes or no

- Variable names
- Variable descriptions
- Variable units
- Study design quirks

Recipe



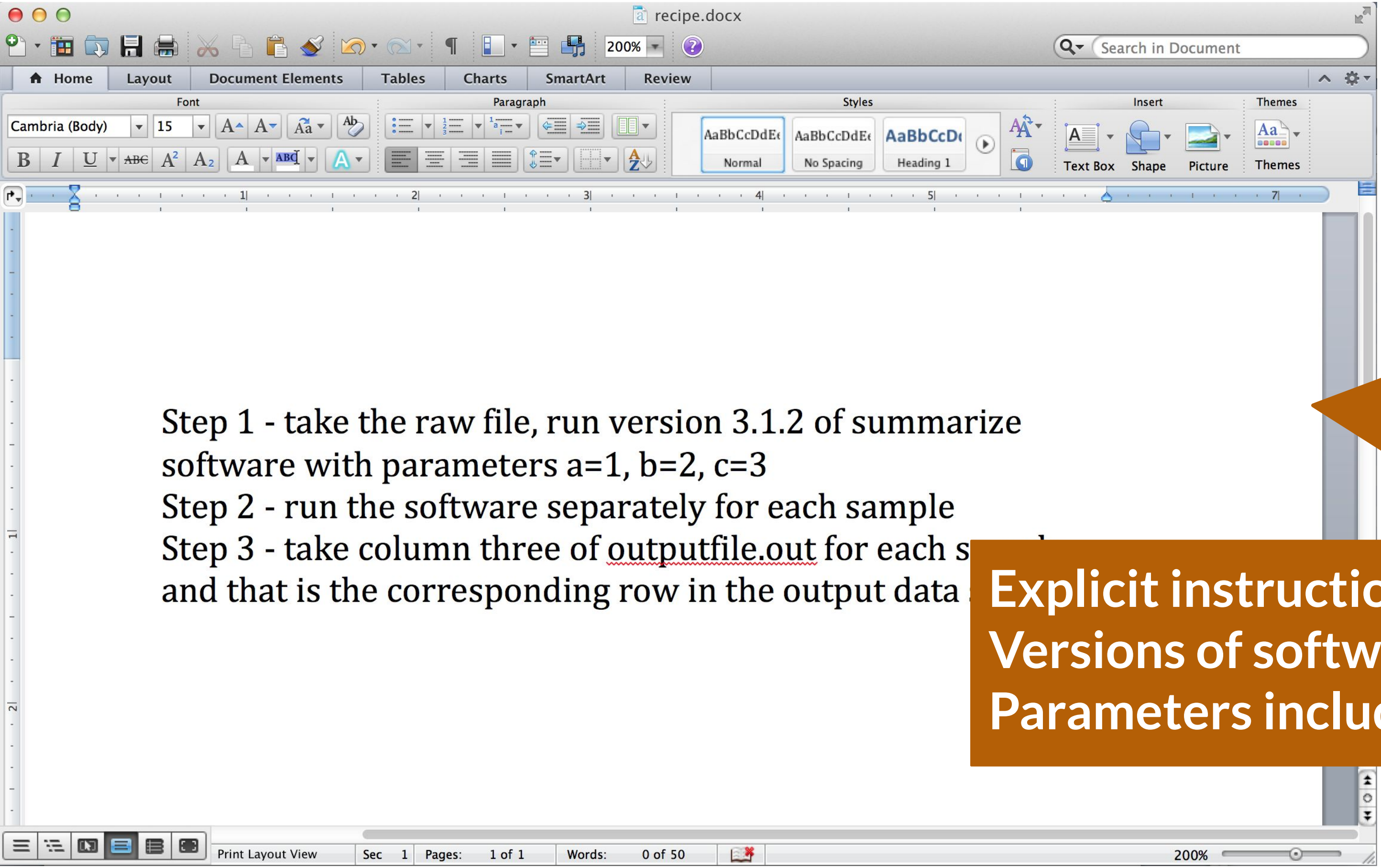
```
library(sva)
library(ffpe)
library(RColorBrewer)
library(corrplot)
library(limma)
trop = RSkittleBrewer('tropical')
```
```

```
## Load the data

You will need to download the GEUVADIS ballgown object from this site: https://  ithub.com/a        dzee
/ballgown_code

```{r loaddata,dependson="load"}
load("fpkm.rda")
pd = ballgown::pData(fpkm)
pd$dirname = as.character(pd$dirname)
ss = function(x, pattern, slot=1,...) sapply(strsplit
pd$IndividualID = ss(pd$dirname, "_", 1)
tfpkm = expr(fpkm)$trans
```

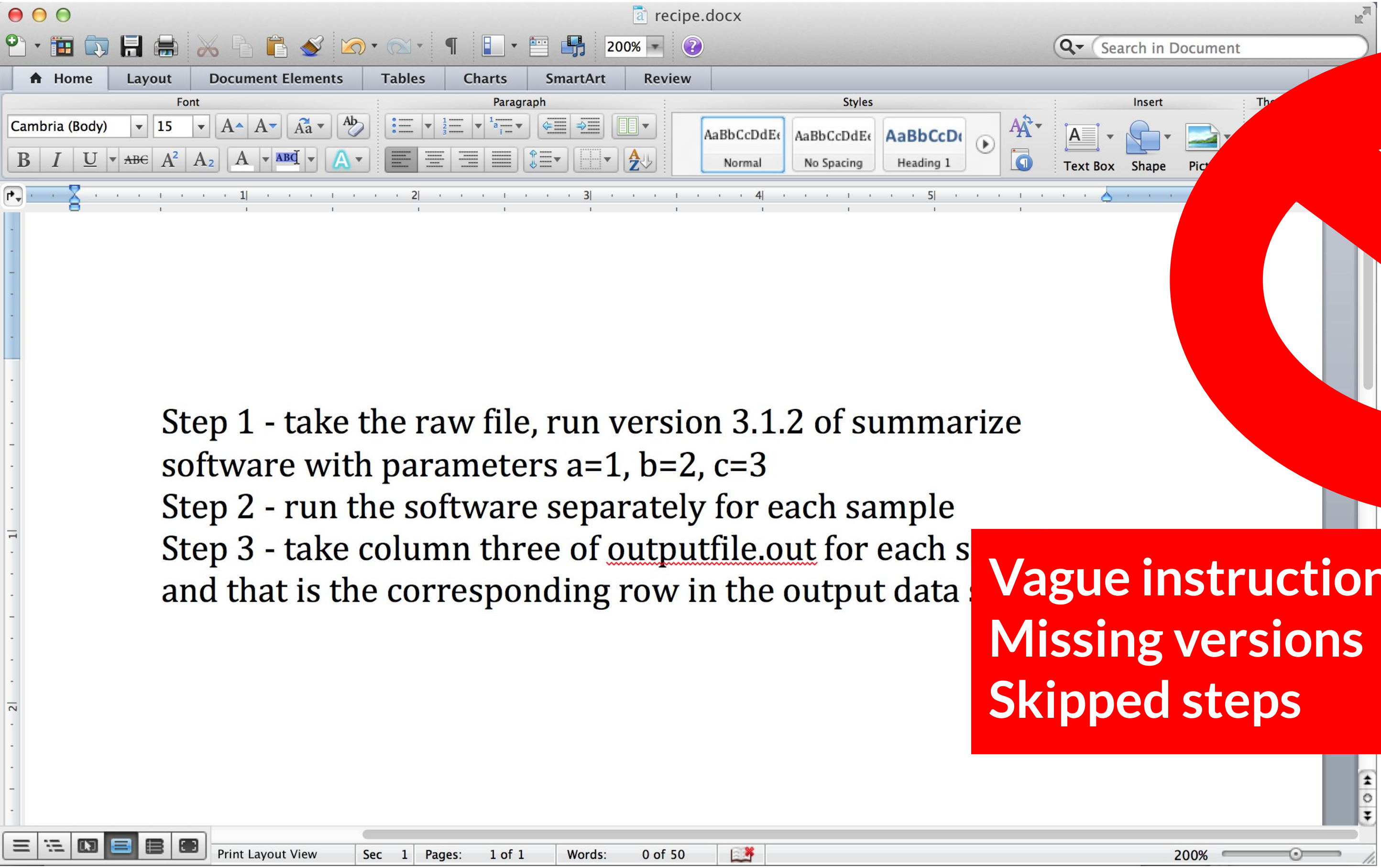
Subset to non-duplicates

You will need the GEUVADIS quality control information and population information available from these
```

R/Python Code

Input raw data -> output tidy

No parameters
```



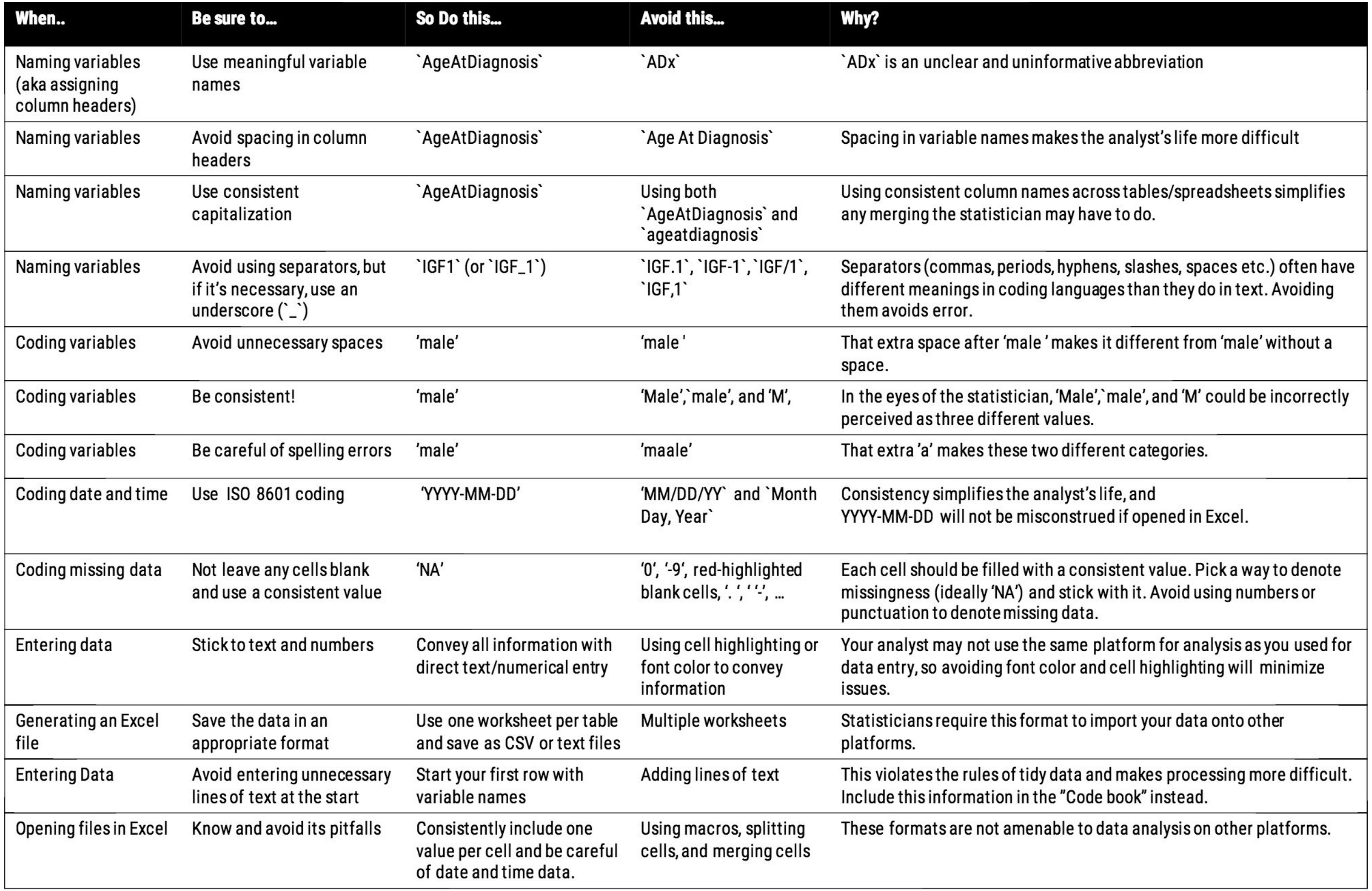
Step 1 - take the raw file, run version 3.1.2 of summarize software with parameters a=1, b=2, c=3
Step 2 - run the software separately for each sample
Step 3 - take column three of outputfile.out for each s
and that is the corresponding row in the output data

Explicit instructions
Versions of software
Parameters included



Step 1 - take the raw file, run version 3.1.2 of summarize software with parameters a=1, b=2, c=3
Step 2 - run the software separately for each sample
Step 3 - take column three of outputfile.out for each s
and that is the corresponding row in the output data

Vague instructions
Missing versions
Skipped steps



| When.. | Be sure to... | So Do this... | Avoid this... | Why? |
|---|---|---|---|---|
| Naming variables (aka assigning column headers) | Use meaningful variable names | `AgeAtDiagnosis` | `ADx` | `ADx` is an unclear and uninformative abbreviation |
| Naming variables | Avoid spacing in column headers | `AgeAtDiagnosis` | `Age At Diagnosis` | Spacing in variable names makes the analyst’s life more difficult |
| Naming variables | Use consistent capitalization | `AgeAtDiagnosis` | Using both `AgeAtDiagnosis` and `ageatdiagnosis` | Using consistent column names across tables/spreadsheets simplifies any merging the statistician may have to do. |
| Naming variables | Avoid using separators, but if it’s necessary, use an underscore (`_`) | `IGF1` (or `IGF_1`) | `IGF.1`, `IGF-1`, `IGF/1`, `IGF,1` | Separators (commas, periods, hyphens, slashes, spaces etc.) often have different meanings in coding languages than they do in text. Avoiding them avoids error. |
| Coding variables | Avoid unnecessary spaces | ‘male’ | ‘male ’ | That extra space after ‘male ’ makes it different from ‘male’ without a space. |
| Coding variables | Be consistent! | ‘male’ | ‘Male’,`male’, and ‘M’, | In the eyes of the statistician, ‘Male’,`male’, and ‘M’ could be incorrectly perceived as three different values. |
| Coding variables | Be careful of spelling errors | ‘male’ | ‘maale’ | That extra ‘a’ makes these two different categories. |
| Coding date and time | Use ISO 8601 coding | ‘YYYY-MM-DD’ | ‘MM/DD/YY` and `Month Day, Year` | Consistency simplifies the analyst’s life, and YYYY-MM-DD will not be misconstrued if opened in Excel. |
| Coding missing data | Not leave any cells blank and use a consistent value | ‘NA’ | ‘0’, ‘-9’, red-highlighted blank cells, ‘. ’, ‘ ‘-’, … | Each cell should be filled with a consistent value. Pick a way to denote missingness (ideally ‘NA’) and stick with it. Avoid using numbers or punctuation to denote missing data. |
| Entering data | Stick to text and numbers | Convey all information with direct text/numerical entry | Using cell highlighting or font color to convey information | Your analyst may not use the same platform for analysis as you used for data entry, so avoiding font color and cell highlighting will minimize issues. |
| Generating an Excel file | Save the data in an appropriate format | Use one worksheet per table and save as CSV or text files | Multiple worksheets | Statisticians require this format to import your data onto other platforms. |
| Entering Data | Avoid entering unnecessary lines of text at the start | Start your first row with variable names | Adding lines of text | This violates the rules of tidy data and makes processing more difficult. Include this information in the ”Code book” instead. |
| Opening files in Excel | Know and avoid its pitfalls | Consistently include one value per cell and be careful of date and time data. | Using macros, splitting cells, and merging cells | These formats are not amenable to data analysis on other platforms. |

Ellis SE, Leek JT. (2017) How to share data for collaboration. *PeerJ Preprints* 5:e3139v5https://doi.org/10.7287/peerj.preprints.3139v5

# Rules for Tidy Spreadsheets

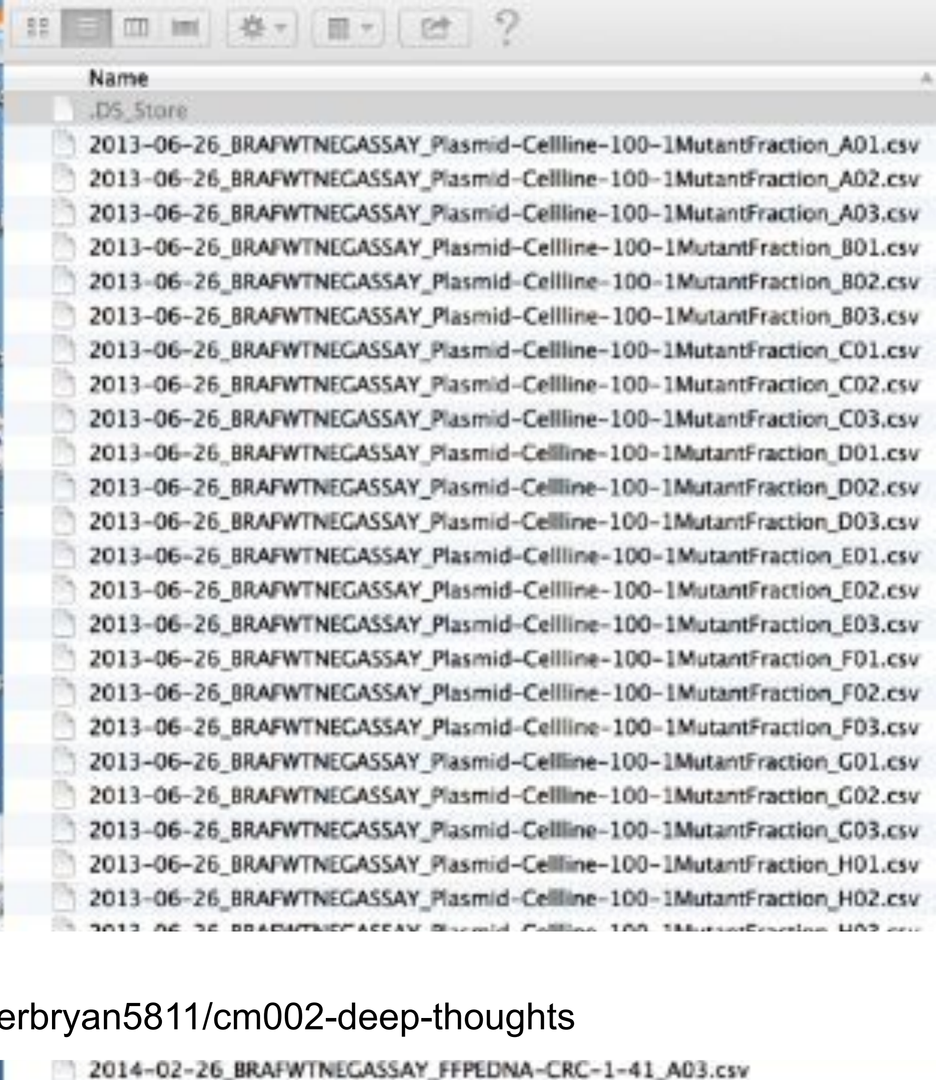
1. Be consistent
2. Choose good names for things
3. Write dates as YYYY-MM-DD
4. No empty cells
5. Put just one thing in a cell
6. Don't use font color or highlighting as data
7. Save the data as plain text files

https://doi.org/10.1080/00031305.2017.1375989

# Organize thyself

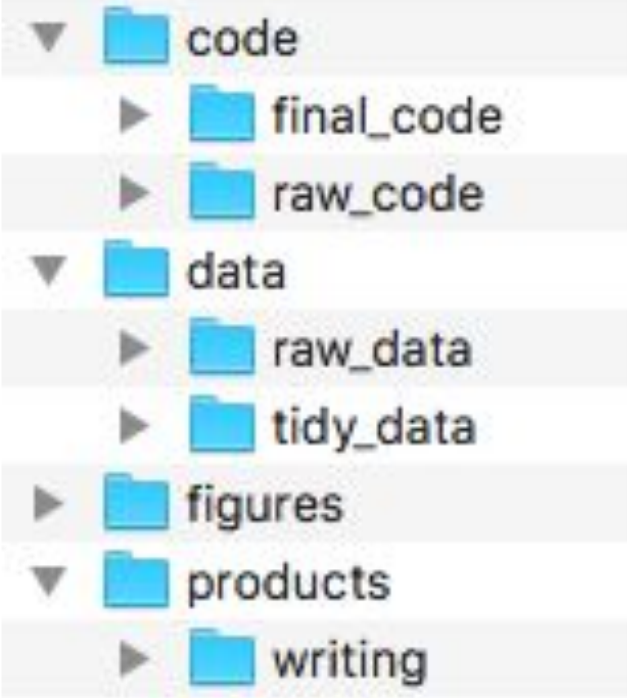
"File organization and naming are powerful weapons against chaos."

- Jenny Bryan



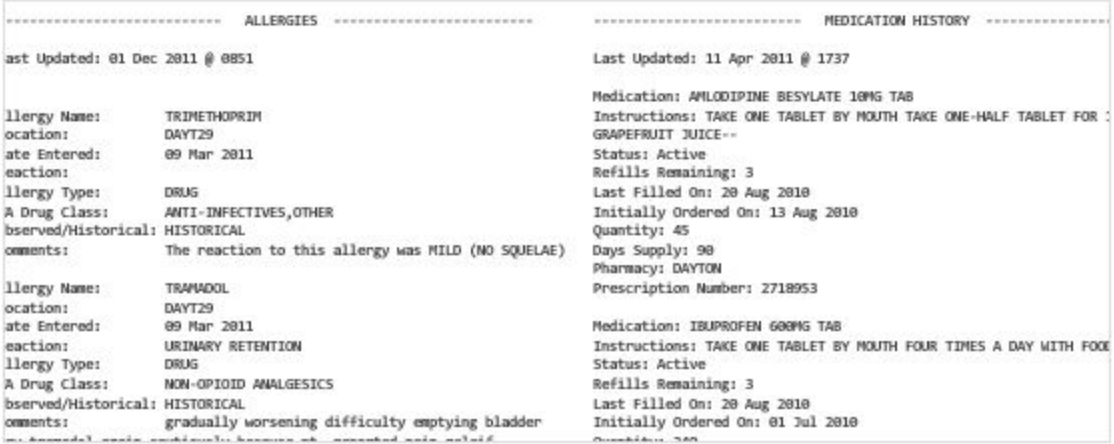
.DS_Store
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_A01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_A02.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_A03.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_B01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_B02.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_B03.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_C01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_C02.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_C03.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_D01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_D02.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_D03.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_E01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_E02.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_E03.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_F01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_F02.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_F03.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_G01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_G02.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_G03.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_H01.csv
2013-06-26_BRAFWTNEGASSAY_Plasmid-Cellline-100-1MutantFraction_H02.csv
2014-02-26_BRAFWTNEGASSAY_FFPEDNA-CRC-1-41_A03.csv

Slide via Jenny Bryan:
http://www.slideshare.net/jenniferbryan5811/cm002-deep-thoughts



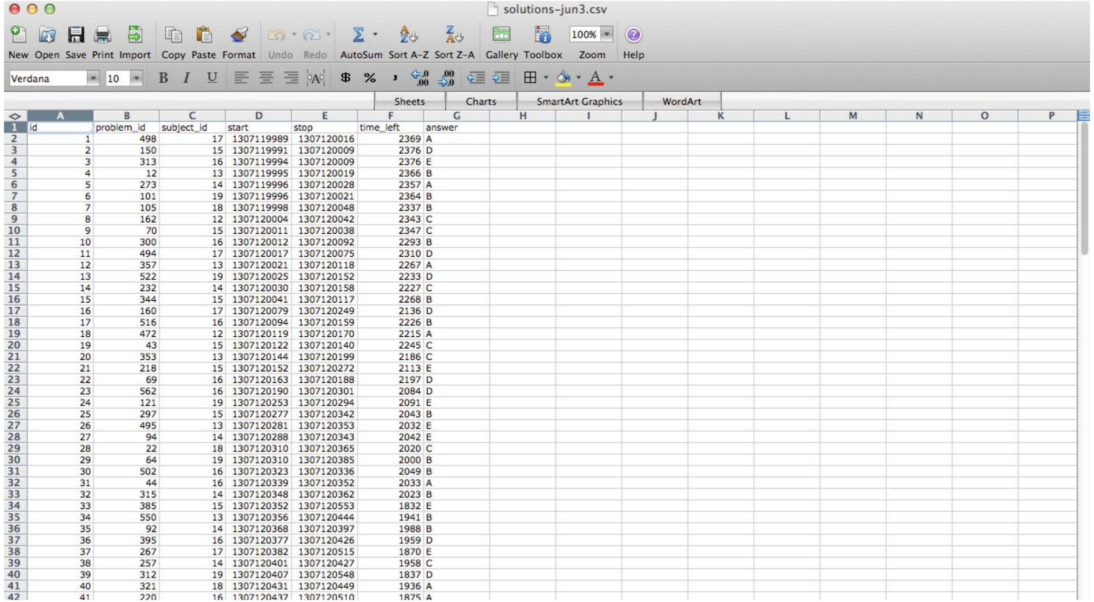
- code
  - final_code
  - raw_code
- data
  - raw_data
  - tidy_data
- figures
- products
  - writing

# Raw data



```
-------------------------   ALLERGIES   -------------------------         -------------------------   MEDICATION HISTORY   ---------------

ast Updated: 01 Dec 2011 @ 0851                                           Last Updated: 11 Apr 2011 @ 1737

                                                                          Medication: AMLODIPINE BESYLATE 10MG TAB
llergy Name:        TRIMETHOPRIM                                          Instructions: TAKE ONE TABLET BY MOUTH TAKE ONE-HALF TABLET FOR
ocation:            DAYT29                                                GRAPEFRUIT JUICE--
ate Entered:        09 Mar 2011                                           Status: Active
eaction:                                                                  Refills Remaining: 3
llergy Type:        DRUG                                                  Last Filled On: 20 Aug 2010
A Drug Class:       ANTI-INFECTIVES,OTHER                                 Initially Ordered On: 13 Aug 2010
bserved/Historical: HISTORICAL                                            Quantity: 45
omments:            The reaction to this allergy was MILD (NO SQUELAE)    Days Supply: 90
                                                                          Pharmacy: DAYTON
llergy Name:        TRAMADOL                                              Prescription Number: 2718953
ocation:            DAYT29
ate Entered:        09 Mar 2011                                           Medication: IBUPROFEN 600MG TAB
eaction:            URINARY RETENTION                                     Instructions: TAKE ONE TABLET BY MOUTH FOUR TIMES A DAY WITH FOO
llergy Type:        DRUG                                                  Status: Active
A Drug Class:       NON-OPIOID ANALGESICS                                 Refills Remaining: 3
bserved/Historical: HISTORICAL                                            Last Filled On: 20 Aug 2010
omments:            gradually worsening difficulty emptying bladder       Initially Ordered On: 01 Jul 2010
```

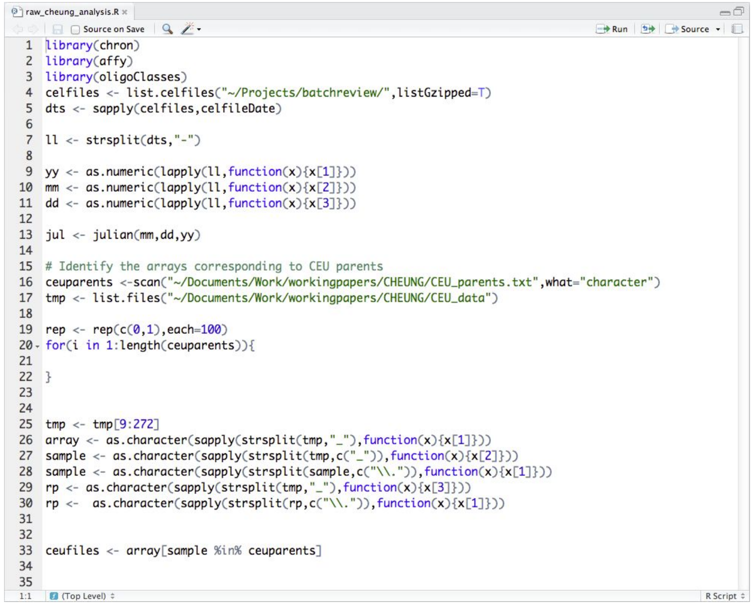
Processed data


solutions-jun3.csv

id	problem_id	subject_id	start	stop	time_left	answer
1	498	17	1307119989	1307120016	2369	A
2	150	15	1307119991	1307120009	2376	D
3	313	16	1307119994	1307120009	2376	E
4	12	13	1307119995	1307120019	2366	B
5	273	14	1307119996	1307120028	2357	A
6	101	19	1307119996	1307120021	2364	B
7	105	18	1307119998	1307120048	2337	B
8	162	12	1307120004	1307120042	2343	C
9	70	15	1307120011	1307120038	2347	C
10	300	16	1307120012	1307120092	2293	B
11	494	17	1307120017	1307120075	2310	D
12	357	13	1307120021	1307120118	2267	A
13	522	19	1307120025	1307120152	2233	D
14	232	14	1307120030	1307120158	2227	C
15	344	15	1307120041	1307120117	2268	B
16	160	17	1307120079	1307120249	2136	D
17	516	16	1307120094	1307120159	2226	B
18	472	12	1307120119	1307120170	2215	A
19	43	15	1307120122	1307120140	2245	C
20	353	13	1307120144	1307120199	2186	C
21	218	15	1307120152	1307120272	2113	E
22	69	16	1307120163	1307120188	2197	D
23	562	16	1307120190	1307120301	2084	D
24	121	19	1307120253	1307120294	2091	E
25	297	15	1307120277	1307120342	2043	B
26	495	13	1307120281	1307120353	2032	E
27	94	14	1307120288	1307120343	2042	E
28	22	18	1307120310	1307120365	2020	C
29	64	19	1307120310	1307120385	2000	B
30	502	16	1307120323	1307120336	2049	B
31	44	16	1307120339	1307120352	2033	A
32	315	14	1307120348	1307120362	2023	B
33	385	15	1307120352	1307120553	1832	E
34	550	13	1307120356	1307120444	1941	B
35	92	14	1307120368	1307120397	1988	B
36	395	16	1307120377	1307120426	1959	D
37	267	17	1307120382	1307120515	1870	E
38	257	14	1307120401	1307120427	1958	C
39	312	19	1307120407	1307120548	1837	D
40	321	18	1307120431	1307120449	1936	A
41	220	16	1307120437	1307120510	1875	A

- Processed data should be named so it is easy to see which script generated the data.
- The processing script - processed data mapping should occur in the README
- Processed data should be tidy

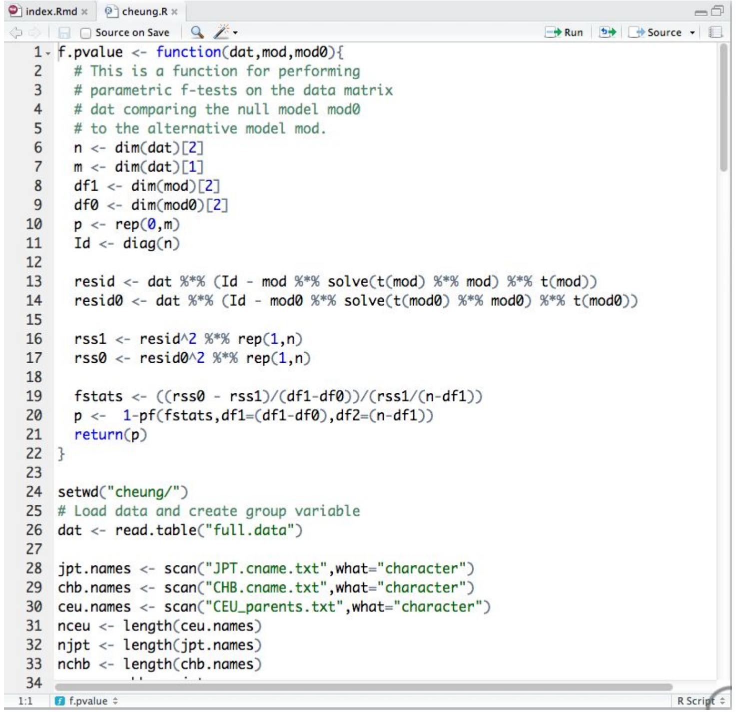
Raw scripts



```r
library(chron)
library(affy)
library(oligoClasses)
celfiles <- list.celfiles("~/Projects/batchreview/",listGzipped=T)
dts <- sapply(celfiles,celfileDate)

ll <- strsplit(dts,"-")

yy <- as.numeric(lapply(ll,function(x){x[1]}))
mm <- as.numeric(lapply(ll,function(x){x[2]}))
dd <- as.numeric(lapply(ll,function(x){x[3]}))

jul <- julian(mm,dd,yy)

# Identify the arrays corresponding to CEU parents
ceuparents <-scan("~/Documents/Work/workingpapers/CHEUNG/CEU_parents.txt",what="character")
tmp <- list.files("~/Documents/Work/workingpapers/CHEUNG/CEU_data")

rep <- rep(c(0,1),each=100)
for(i in 1:length(ceuparents)){

}


tmp <- tmp[9:272]
array <- as.character(sapply(strsplit(tmp,"_"),function(x){x[1]}))
sample <- as.character(sapply(strsplit(tmp,c("_")),function(x){x[2]}))
sample <- as.character(sapply(strsplit(sample,c("\\.")),function(x){x[1]}))
rp <- as.character(sapply(strsplit(tmp,"_"),function(x){x[3]}))
rp <-  as.character(sapply(strsplit(rp,c("\\.")),function(x){x[1]}))


ceufiles <- array[sample %in% ceuparents]


```

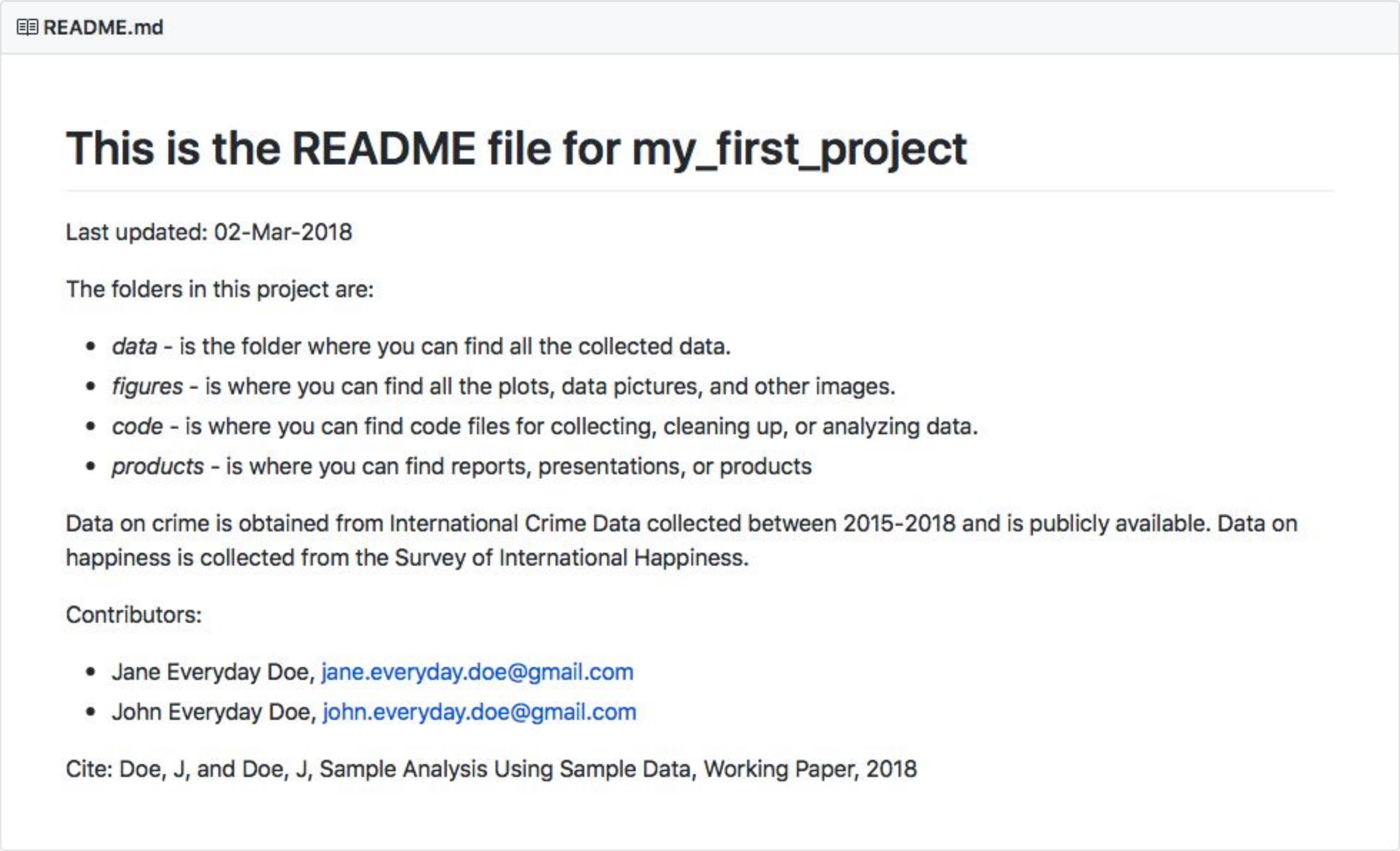
- May be less commented (but comments help you!)
- May be multiple versions
- May include analyses that are later discarded

Final scripts



```
f.pvalue <- function(dat,mod,mod0){
  # This is a function for performing
  # parametric f-tests on the data matrix
  # dat comparing the null model mod0
  # to the alternative model mod.
  n <- dim(dat)[2]
  m <- dim(dat)[1]
  df1 <- dim(mod)[2]
  df0 <- dim(mod0)[2]
  p <- rep(0,m)
  Id <- diag(n)

  resid <- dat %*% (Id - mod %*% solve(t(mod) %*% mod) %*% t(mod))
  resid0 <- dat %*% (Id - mod0 %*% solve(t(mod0) %*% mod0) %*% t(mod0))

  rss1 <- resid^2 %*% rep(1,n)
  rss0 <- resid0^2 %*% rep(1,n)

  fstats <- ((rss0 - rss1)/(df1-df0))/(rss1/(n-df1))
  p <-  1-pf(fstats,df1=(df1-df0),df2=(n-df1))
  return(p)
}

setwd("cheung/")
# Load data and create group variable
dat <- read.table("full.data")

jpt.names <- scan("JPT.cname.txt",what="character")
chb.names <- scan("CHB.cname.txt",what="character")
ceu.names <- scan("CEU_parents.txt",what="character")
nceu <- length(ceu.names)
njpt <- length(jpt.names)
nchb <- length(chb.names)
```

- Clearly commented
  - Small comments liberally - what, when, why, how
  - Bigger commented blocks for whole sections
- Include processing details
- Only analyses that appear in the final write-up



This is the README file for my_first_project

Last updated: 02-Mar-2018

The folders in this project are:

- *data* - is the folder where you can find all the collected data.
- *figures* - is where you can find all the plots, data pictures, and other images.
- *code* - is where you can find code files for collecting, cleaning up, or analyzing data.
- *products* - is where you can find reports, presentations, or products

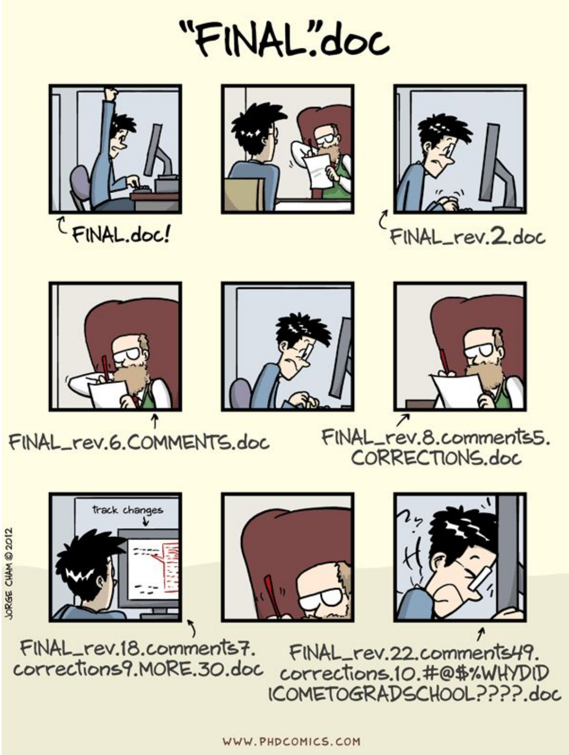
Data on crime is obtained from International Crime Data collected between 2015-2018 and is publicly available. Data on happiness is collected from the Survey of International Happiness.

Contributors:

- Jane Everyday Doe, jane.everyday.doe@gmail.com
- John Everyday Doe, john.everyday.doe@gmail.com

Cite: Doe, J, and Doe, J, Sample Analysis Using Sample Data, Working Paper, 2018

Just no



http://www.phdcomics.com/comics/archive.php?comicid=1531

PROTIP: NEVER LOOK IN SOMEONE ELSE'S DOCUMENTS FOLDER.

https://xkcd.com/1459/

key principles of file naming for data science projects:

- Machine readable
- Human readable
- Be nicely ordered

Source: Jenny Bryan

Bad Naming	Good Naming
2013 my report.md	2013_my_report.md
malik's_report.md	maliks_report.md
01_zoë_report.md	01_zoe_report.md
AdamHooverReport.md	adam-hoover-report.md
executivereportpepsiv1.md	executive_report_pepsi_v1.md

2018_jan_sales_cust001_prod001.md
2017_mar_sales_cust001_prod001.md
2016_may_sales_cust001_prod008.md
2017_jan_sales_cust120_prod007.md
2015_oct_sales_cust034_prod001.md
2015_oct_sales_cust034_prod002.md

Year	Month	Type	Customer ID	Product ID
2018	jan	sales	001	001
2017	mar	sales	001	001
2016	may	sales	001	008
2017	jan	sales	120	007
2015	oct	sales	034	001
2015	oct	sales	034	002

Which one is better?

analysis.R
or
2017-exploratory_analysis_crime.R?

Which one is better?

05-21-2017-analysis-cust001.R
or
2017-05-21-analysis-cust001.R?

Structure of a filename

processed_pvalue_data_from_pubmed_oct24.rda

What did I do to this data

processed_pvalue_data_from_pubmed_oct24.rda

What kind of data is this?

processed_pvalue_data_from_pubmed_oct24.rda

Where did it come from?

processed_pvalue_data_from_pubmed_oct24.rda

When did I get it?

processed_pvalue_data_from_pubmed_oct24.rda

Underscores/slashes not dots/whitespace

processed_pvalue_data_from_pubmed_oct24.rda

Consistency is the main rule

processed_pvalue_data_from_pubmed_oct24.rda
raw_pvalue_data_from_pubmed_oct24.rda

Your closest collaborator is you six months ago, but you don’t reply to emails

- Karl Broman

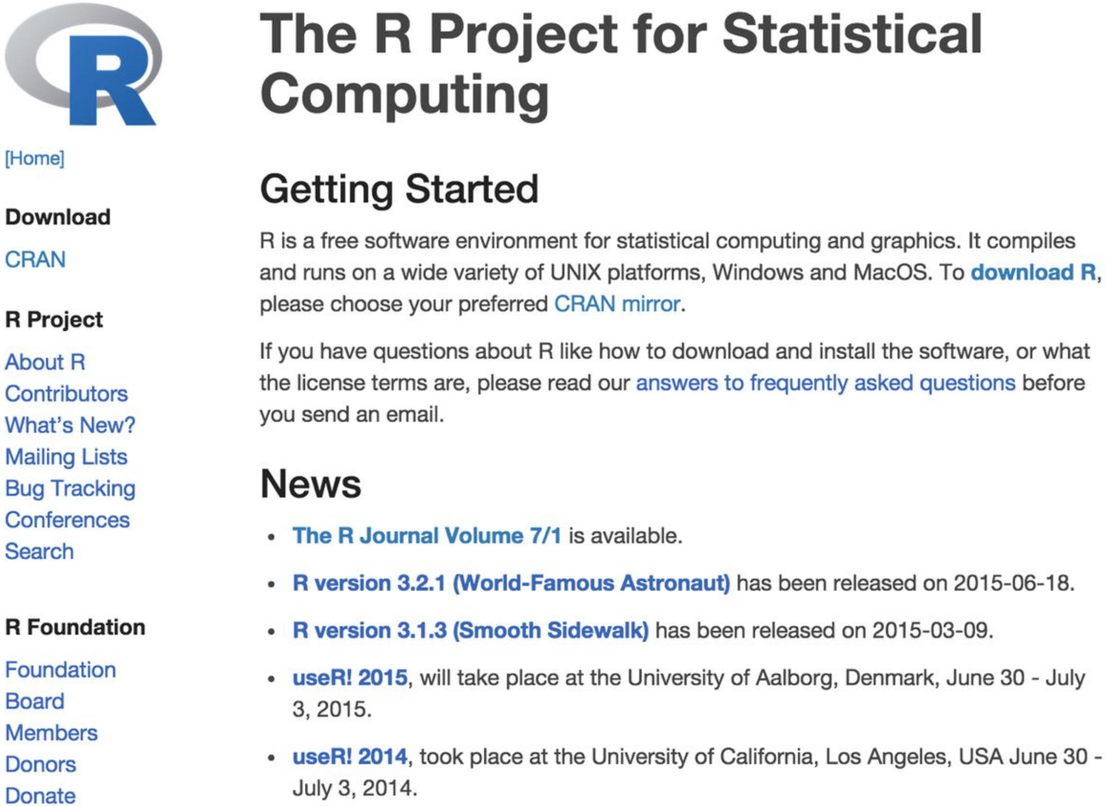
http://kbroman.org/Tools4RR/assets/lectures/06_org_eda.pdf

Step 1: slow down and document.
Step 2: have sympathy for your future self.
Step 3: have a system.

- Karl Broman

http://kbroman.org/Tools4RR/assets/lectures/06_org_eda.pdf

R + RStudio



The R Project for Statistical Computing

Getting Started

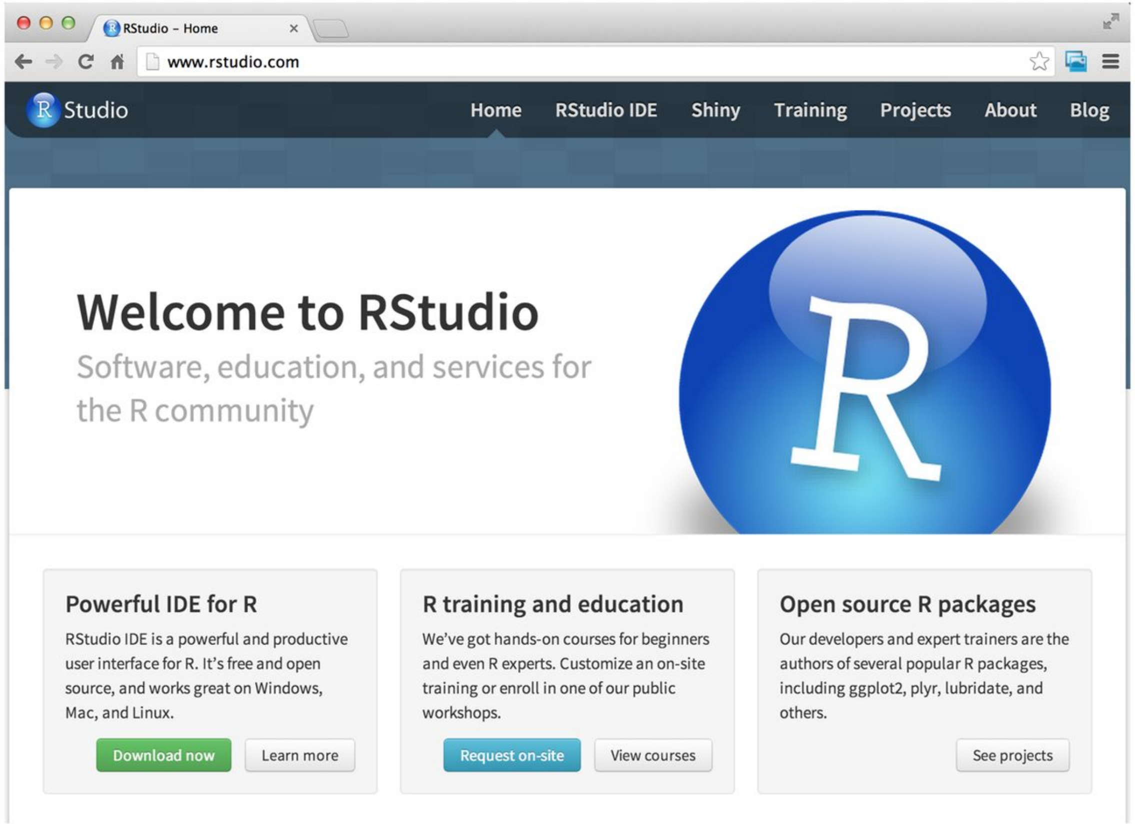
R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To **download R**, please choose your preferred CRAN mirror.

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

- **The R Journal Volume 7/1** is available.
- **R version 3.2.1 (World-Famous Astronaut)** has been released on 2015-06-18.
- **R version 3.1.3 (Smooth Sidewalk)** has been released on 2015-03-09.
- **useR! 2015**, will take place at the University of Aalborg, Denmark, June 30 - July 3, 2015.
- **useR! 2014**, took place at the University of California, Los Angeles, USA June 30 - July 3, 2014.

www.r-project.org



Welcome to RStudio

Software, education, and services for the R community

Powerful IDE for R

RStudio IDE is a powerful and productive user interface for R. It's free and open source, and works great on Windows, Mac, and Linux.

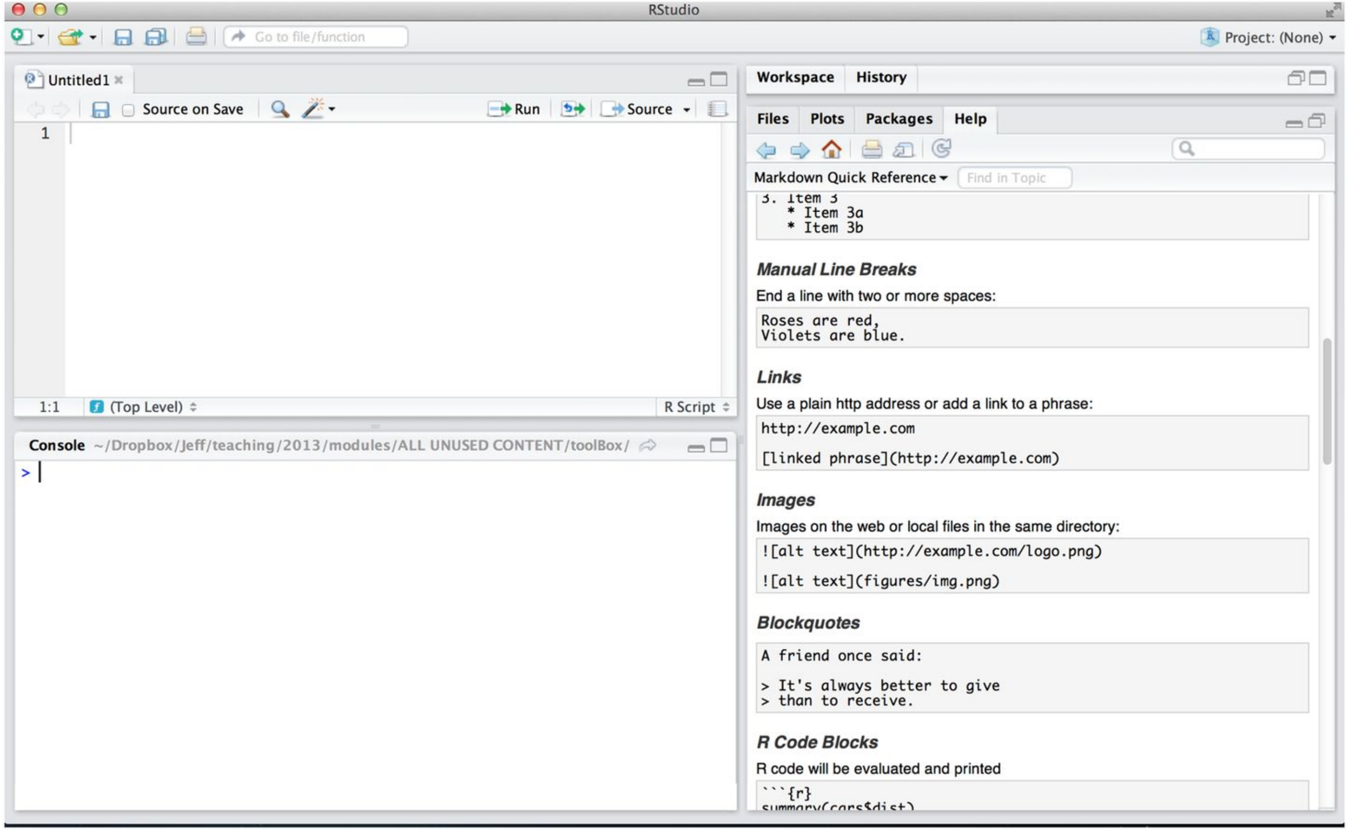
R training and education

We've got hands-on courses for beginners and even R experts. Customize an on-site training or enroll in one of our public workshops.

Open source R packages

Our developers and expert trainers are the authors of several popular R packages, including ggplot2, plyr, lubridate, and others.

https://www.rstudio.com/



```
3. Item 3
  * Item 3a
  * Item 3b
```

Manual Line Breaks

End a line with two or more spaces:

```
Roses are red,
Violets are blue.
```

Links

Use a plain http address or add a link to a phrase:

```
http://example.com

[linked phrase](http://example.com)
```

Images

Images on the web or local files in the same directory:

```
![alt text](http://example.com/logo.png)

![alt text](figures/img.png)
```

Blockquotes

```
A friend once said:

> It's always better to give
> than to receive.
```

R Code Blocks

R code will be evaluated and printed

~~~
```{r}
summary(cars$dist)
~~~

https://www.rstudio.com/

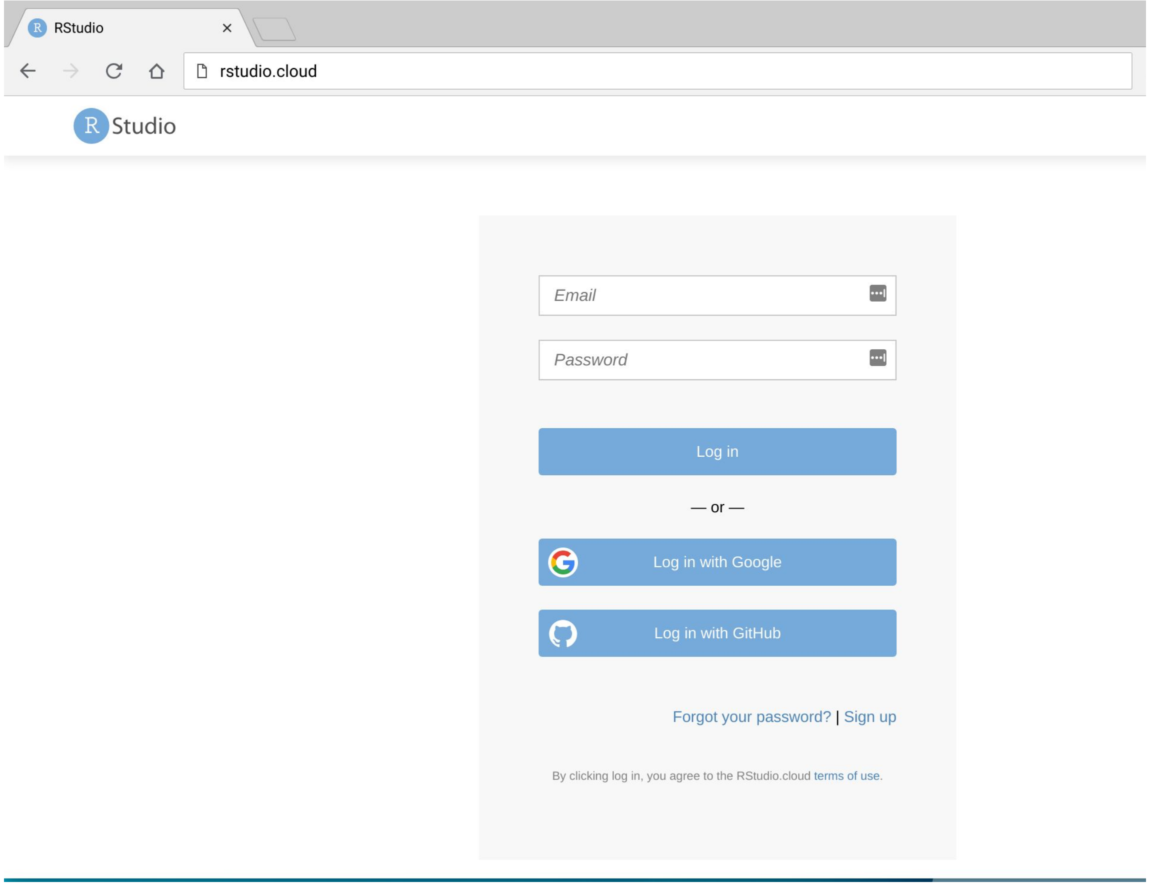
Some useful commands

Cmd + Enter

Ctrl + Enter

Ctrl + 1

Ctrl + 2



By clicking log in, you agree to the RStudio.cloud terms of use.

https://rstudio.cloud

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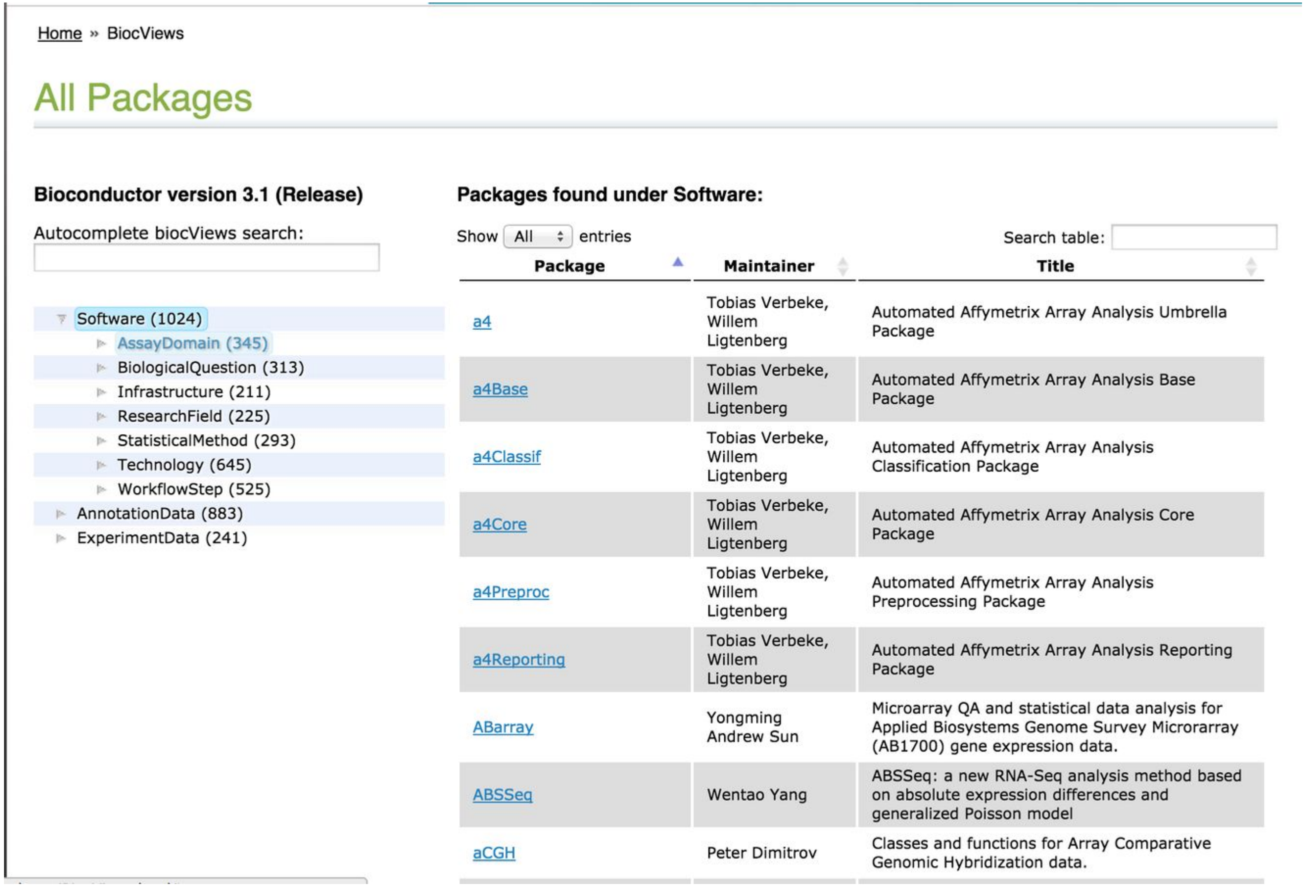
Available CRAN Packages By Name

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

A3	A3: Accurate, Adaptable, and Accessible Error Metrics for Predictive Models
abbyyR	Access to Abbyy Optical Character Recognition (OCR) API
abc	Tools for Approximate Bayesian Computation (ABC)
ABCanalysis	Computed ABC Analysis
abc.data	Data Only: Tools for Approximate Bayesian Computation (ABC)
abcdeFBA	ABCDE_FBA: A-Biologist-Can-Do-Everything of Flux Balance Analysis with this package
ABCoptim	Implementation of Artificial Bee Colony (ABC) Optimization
abctools	Tools for ABC Analyses
abd	The Analysis of Biological Data
abf2	Load Gap-Free Axon ABF2 Files
abind	Combine Multidimensional Arrays
abn	Data Modelling with Additive Bayesian Networks
abundant	Abundant regression and high-dimensional principal fitted components
acc	A Package to Processes Accelerometer Data
accelerometry	Functions for Processing Minute-to-Minute Accelerometer Data
AcceptanceSampling	Creation and evaluation of Acceptance Sampling Plans
ACCLMA	ACC & LMA Graph Plotting
accrual	Bayesian Accrual Prediction
accrued	Data Quality Visualization Tools for Partially Accruing Data
ACD	Categorical data analysis with complete or missing responses
acepack	ace() and avas() for selecting regression transformations

https://cran.rstudio.com/

```r
install.packages("devtools")
install.packages("dplyr")
```



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All Packages

Bioconductor version 3.1 (Release)

Autocomplete biocViews search:

- Software (1024)
  - AssayDomain (345)
  - BiologicalQuestion (313)
  - Infrastructure (211)
  - ResearchField (225)
  - StatisticalMethod (293)
  - Technology (645)
  - WorkflowStep (525)
- AnnotationData (883)
- ExperimentData (241)

Packages found under Software:

Show All entries

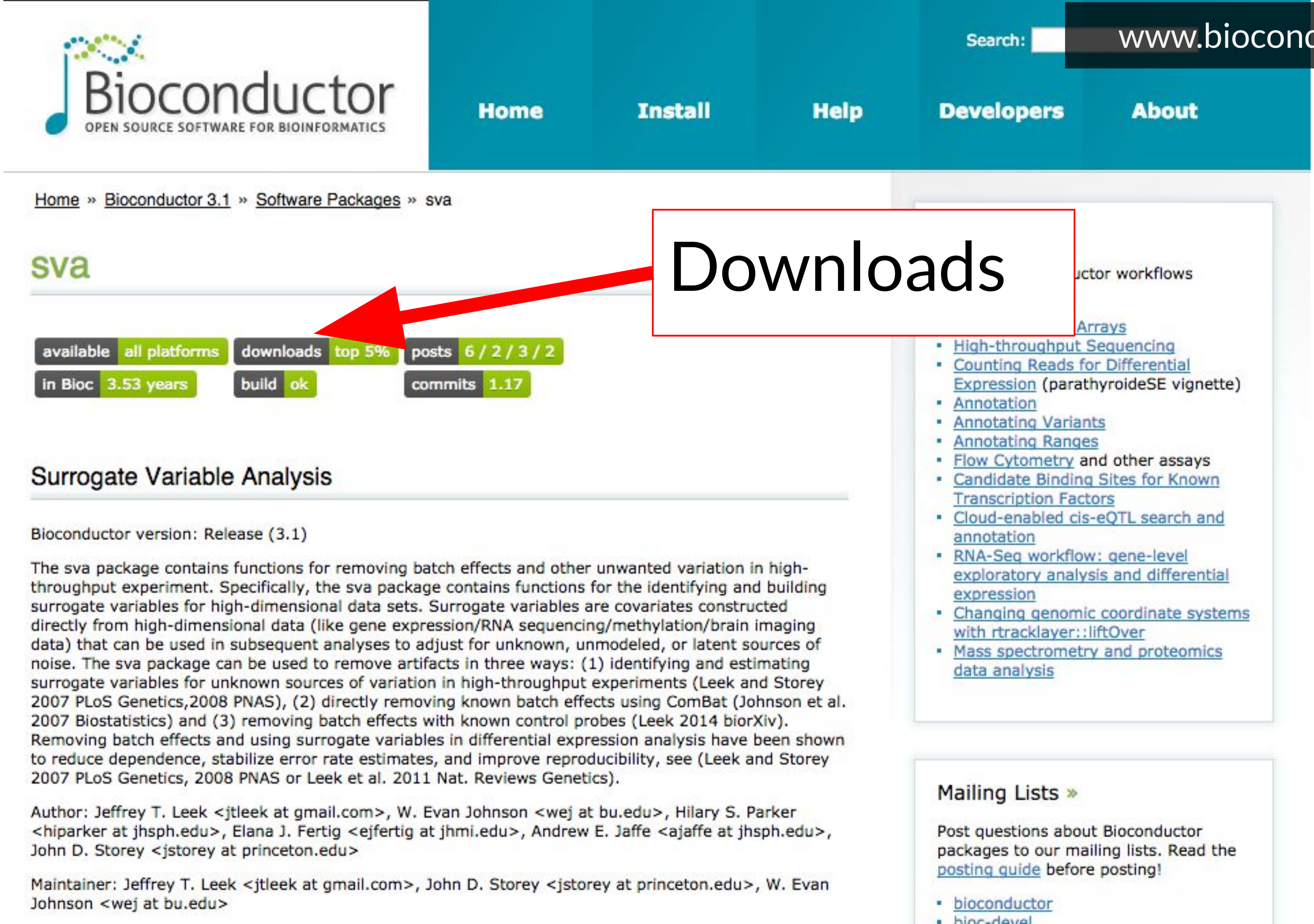
Search table:

Package	Maintainer	Title
a4	Tobias Verbeke, Willem Ligtenberg	Automated Affymetrix Array Analysis Umbrella Package
a4Base	Tobias Verbeke, Willem Ligtenberg	Automated Affymetrix Array Analysis Base Package
a4Classif	Tobias Verbeke, Willem Ligtenberg	Automated Affymetrix Array Analysis Classification Package
a4Core	Tobias Verbeke, Willem Ligtenberg	Automated Affymetrix Array Analysis Core Package
a4Preproc	Tobias Verbeke, Willem Ligtenberg	Automated Affymetrix Array Analysis Preprocessing Package
a4Reporting	Tobias Verbeke, Willem Ligtenberg	Automated Affymetrix Array Analysis Reporting Package
ABarray	Yongming Andrew Sun	Microarray QA and statistical data analysis for Applied Biosystems Genome Survey Microrarray (AB1700) gene expression data.
ABSSeq	Wentao Yang	ABSSeq: a new RNA-Seq analysis method based on absolute expression differences and generalized Poisson model
aCGH	Peter Dimitrov	Classes and functions for Array Comparative Genomic Hybridization data.

http://bioconductor.org/

www.bioconductor.org

Downloads



Home » Bioconductor 3.1 » Software Packages » sva

sva

Surrogate Variable Analysis

Bioconductor version: Release (3.1)

The sva package contains functions for removing batch effects and other unwanted variation in high-throughput experiment. Specifically, the sva package contains functions for the identifying and building surrogate variables for high-dimensional data sets. Surrogate variables are covariates constructed directly from high-dimensional data (like gene expression/RNA sequencing/methylation/brain imaging data) that can be used in subsequent analyses to adjust for unknown, unmodeled, or latent sources of noise. The sva package can be used to remove artifacts in three ways: (1) identifying and estimating surrogate variables for unknown sources of variation in high-throughput experiments (Leek and Storey 2007 PLoS Genetics,2008 PNAS), (2) directly removing known batch effects using ComBat (Johnson et al. 2007 Biostatistics) and (3) removing batch effects with known control probes (Leek 2014 biorXiv). Removing batch effects and using surrogate variables in differential expression analysis have been shown to reduce dependence, stabilize error rate estimates, and improve reproducibility, see (Leek and Storey 2007 PLoS Genetics, 2008 PNAS or Leek et al. 2011 Nat. Reviews Genetics).

Author: Jeffrey T. Leek <jtleek at gmail.com>, W. Evan Johnson <wej at bu.edu>, Hilary S. Parker <hiparker at jhsph.edu>, Elana J. Fertig <ejfertig at jhmi.edu>, Andrew E. Jaffe <ajaffe at jhsph.edu>, John D. Storey <jstorey at princeton.edu>

Maintainer: Jeffrey T. Leek <jtleek at gmail.com>, John D. Storey <jstorey at princeton.edu>, W. Evan Johnson <wej at bu.edu>

ctor workflows

Arrays
- High-throughput Sequencing
- Counting Reads for Differential Expression (parathyroideSE vignette)
- Annotation
- Annotating Variants
- Annotating Ranges
- Flow Cytometry and other assays
- Candidate Binding Sites for Known Transcription Factors
- Cloud-enabled cis-eQTL search and annotation
- RNA-Seq workflow: gene-level exploratory analysis and differential expression
- Changing genomic coordinate systems with rtracklayer::liftOver
- Mass spectrometry and proteomics data analysis

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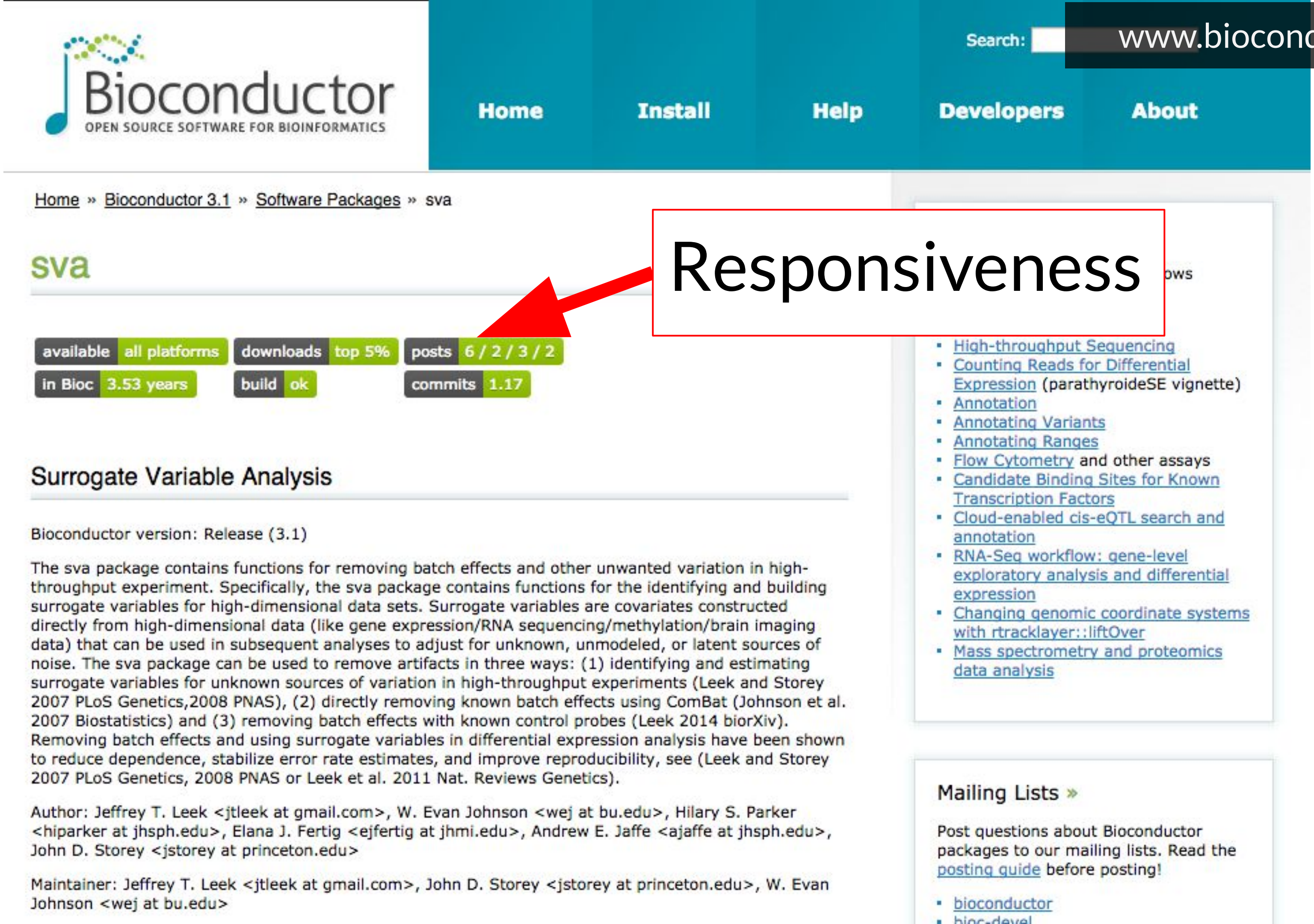
Responsiveness



Home » Bioconductor 3.1 » Software Packages » sva

sva

available	all platforms
downloads	top 5%
posts	6 / 2 / 3 / 2
in Bioc	3.53 years
build	ok
commits	1.17

Surrogate Variable Analysis

Bioconductor version: Release (3.1)

The sva package contains functions for removing batch effects and other unwanted variation in high-throughput experiment. Specifically, the sva package contains functions for the identifying and building surrogate variables for high-dimensional data sets. Surrogate variables are covariates constructed directly from high-dimensional data (like gene expression/RNA sequencing/methylation/brain imaging data) that can be used in subsequent analyses to adjust for unknown, unmodeled, or latent sources of noise. The sva package can be used to remove artifacts in three ways: (1) identifying and estimating surrogate variables for unknown sources of variation in high-throughput experiments (Leek and Storey 2007 PLoS Genetics,2008 PNAS), (2) directly removing known batch effects using ComBat (Johnson et al. 2007 Biostatistics) and (3) removing batch effects with known control probes (Leek 2014 biorXiv). Removing batch effects and using surrogate variables in differential expression analysis have been shown to reduce dependence, stabilize error rate estimates, and improve reproducibility, see (Leek and Storey 2007 PLoS Genetics, 2008 PNAS or Leek et al. 2011 Nat. Reviews Genetics).

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ows

- High-throughput Sequencing
- Counting Reads for Differential Expression (parathyroideSE vignette)
- Annotation
- Annotating Variants
- Annotating Ranges
- Flow Cytometry and other assays
- Candidate Binding Sites for Known Transcription Factors
- Cloud-enabled cis-eQTL search and annotation
- RNA-Seq workflow: gene-level exploratory analysis and differential expression
- Changing genomic coordinate systems with rtracklayer::liftOver
- Mass spectrometry and proteomics data analysis

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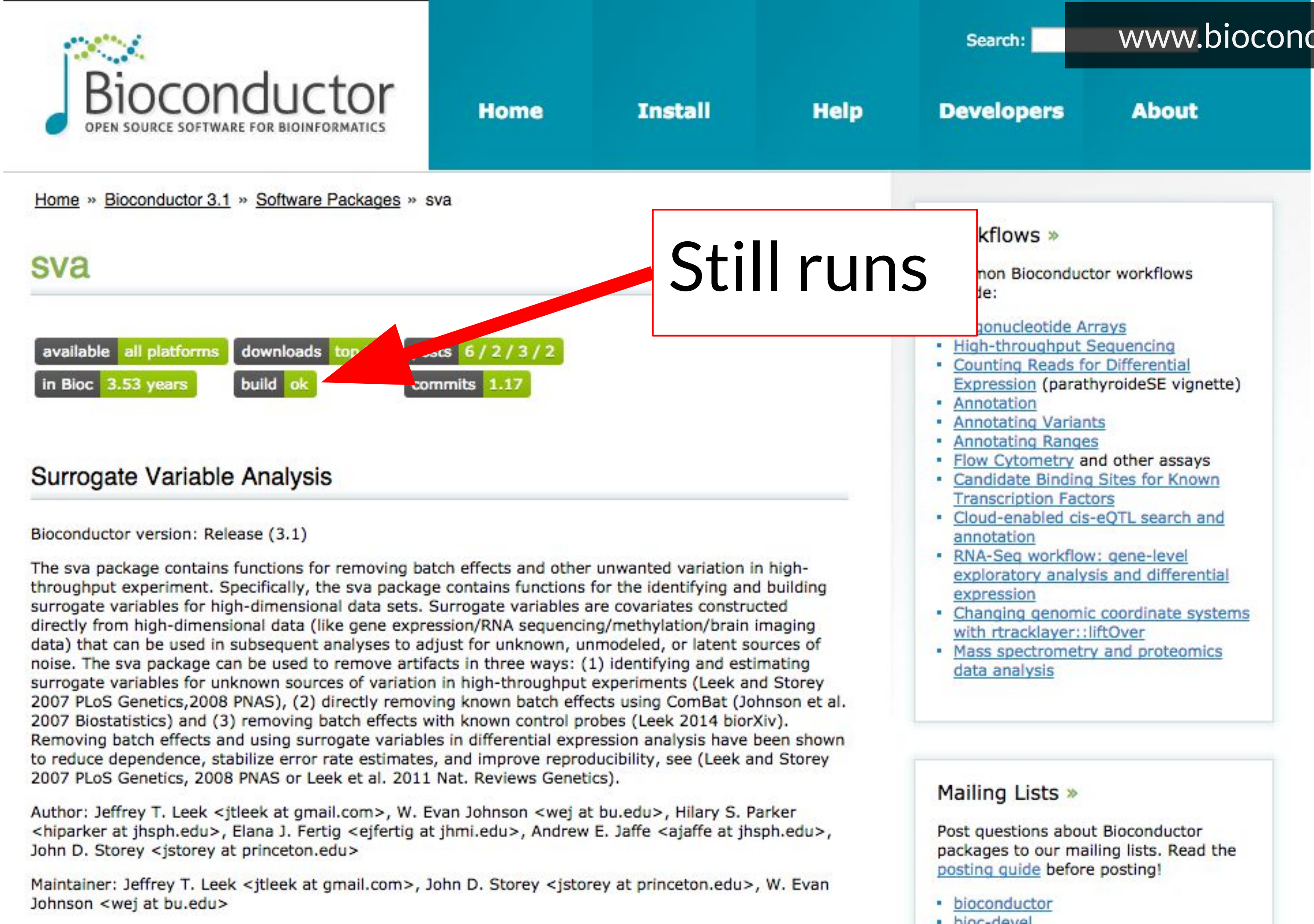

Still runs

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sva

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The sva package contains functions for removing batch effects and other unwanted variation in high-throughput experiment. Specifically, the sva package contains functions for the identifying and building surrogate variables for high-dimensional data sets. Surrogate variables are covariates constructed directly from high-dimensional data (like gene expression/RNA sequencing/methylation/brain imaging data) that can be used in subsequent analyses to adjust for unknown, unmodeled, or latent sources of noise. The sva package can be used to remove artifacts in three ways: (1) identifying and estimating surrogate variables for unknown sources of variation in high-throughput experiments (Leek and Storey 2007 PLoS Genetics,2008 PNAS), (2) directly removing known batch effects using ComBat (Johnson et al. 2007 Biostatistics) and (3) removing batch effects with known control probes (Leek 2014 biorXiv). Removing batch effects and using surrogate variables in differential expression analysis have been shown to reduce dependence, stabilize error rate estimates, and improve reproducibility, see (Leek and Storey 2007 PLoS Genetics, 2008 PNAS or Leek et al. 2011 Nat. Reviews Genetics).

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- gonucleotide Arrays
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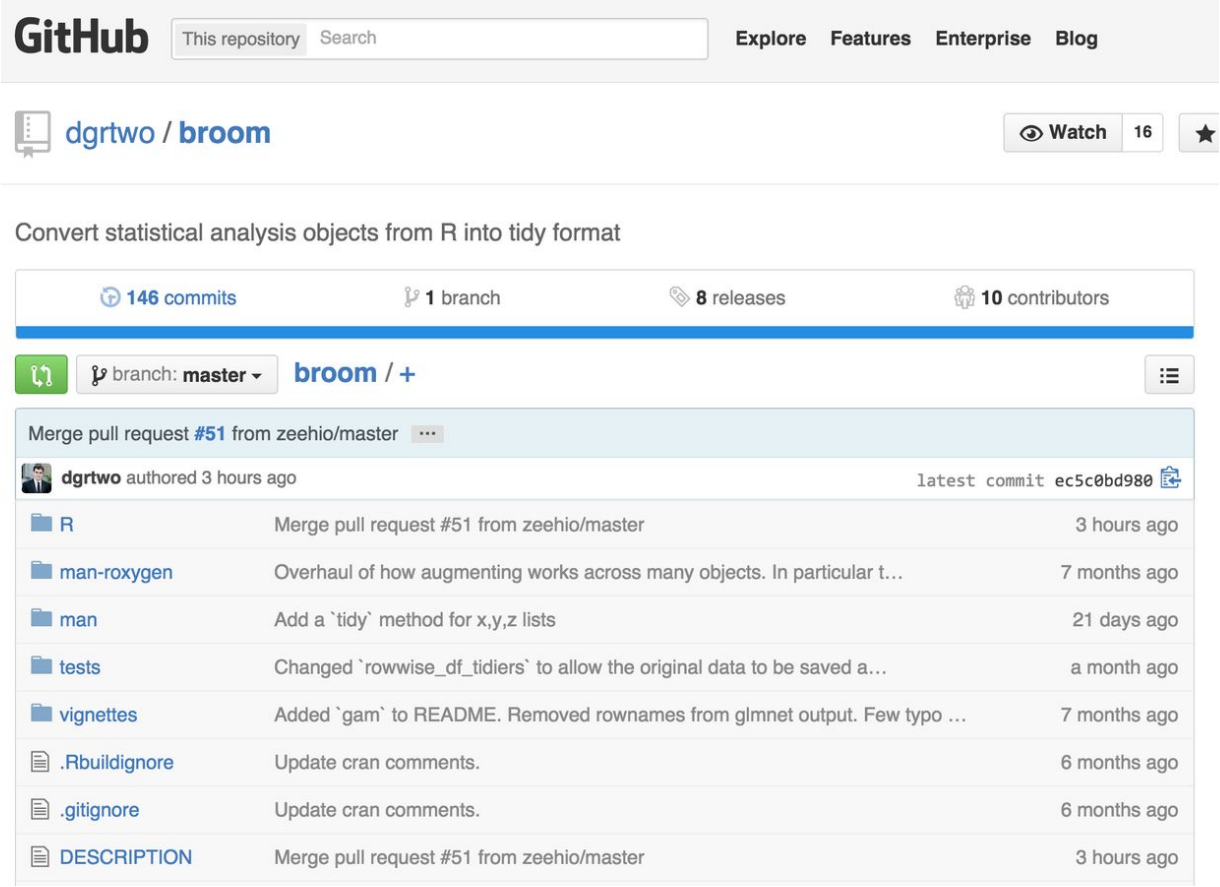
After version 3.6 of R

```
install.packages("BiocManager")
BiocManager::install(c("sva"))
```

Before version 3.6 of R

```
source("http://bioconductor.org/biocLite.R")
biocLite("sva")
```



dgrtwo / **broom**

Convert statistical analysis objects from R into tidy format

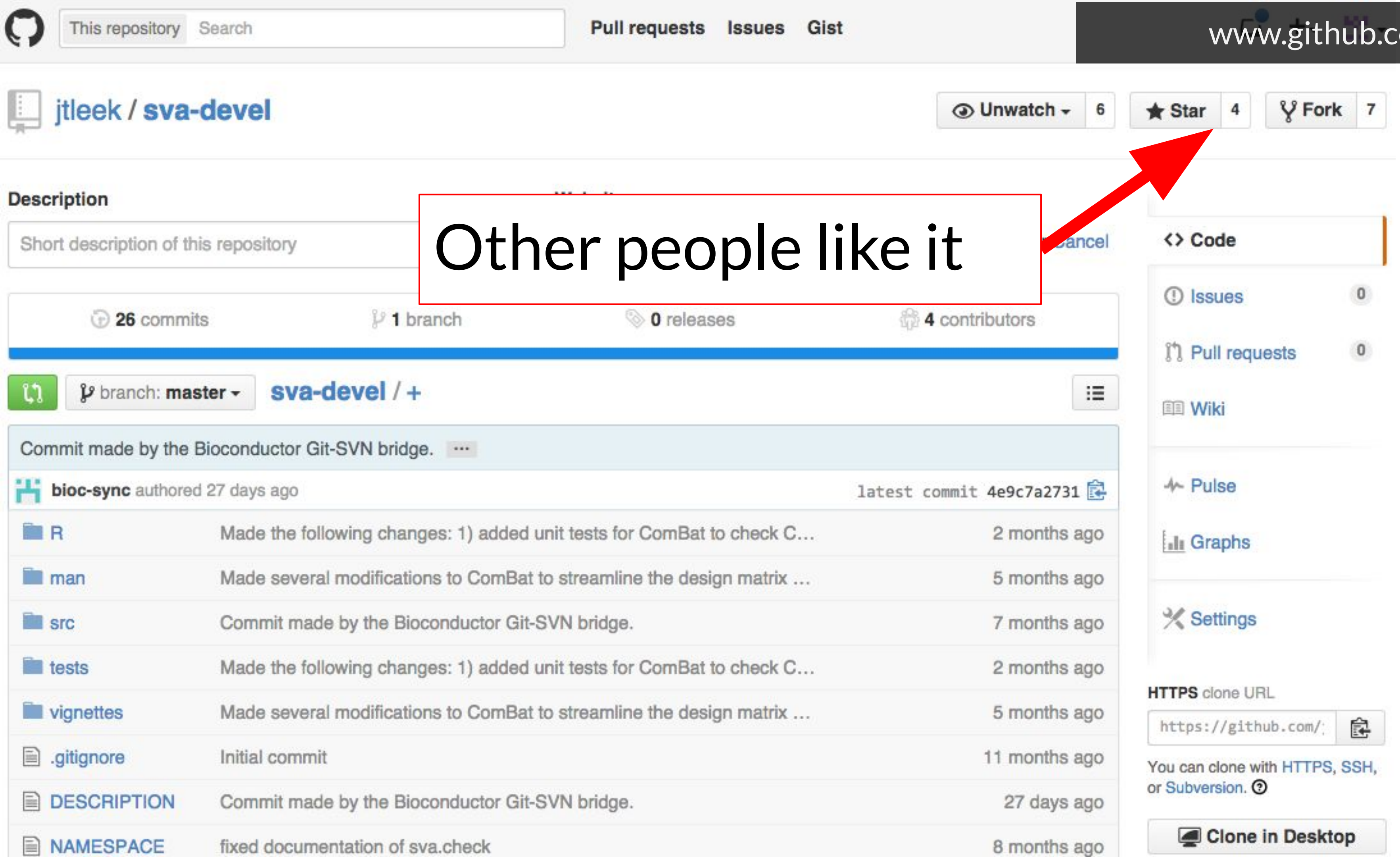
Merge pull request #51 from zeehio/master

dgrtwo authored 3 hours ago — latest commit ec5c0bd980

R	Merge pull request #51 from zeehio/master	3 hours ago
man-roxygen	Overhaul of how augmenting works across many objects. In particular t…	7 months ago
man	Add a `tidy` method for x,y,z lists	21 days ago
tests	Changed `rowwise_df_tidiers` to allow the original data to be saved a…	a month ago
vignettes	Added `gam` to README. Removed rownames from glmnet output. Few typo …	7 months ago
.Rbuildignore	Update cran comments.	6 months ago
.gitignore	Update cran comments.	6 months ago
DESCRIPTION	Merge pull request #51 from zeehio/master	3 hours ago

https://github.com/dgrtwo/broom

www.github.com



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jtleek / **sva-devel**

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Description

Short description of this repository

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26 commits | 1 branch | 0 releases | 4 contributors

branch: master | sva-devel / +

Commit made by the Bioconductor Git-SVN bridge. ...

bioc-sync authored 27 days ago | latest commit 4e9c7a2731

R	Made the following changes: 1) added unit tests for ComBat to check C…	2 months ago
man	Made several modifications to ComBat to streamline the design matrix …	5 months ago
src	Commit made by the Bioconductor Git-SVN bridge.	7 months ago
tests	Made the following changes: 1) added unit tests for ComBat to check C…	2 months ago
vignettes	Made several modifications to ComBat to streamline the design matrix …	5 months ago
.gitignore	Initial commit	11 months ago
DESCRIPTION	Commit made by the Bioconductor Git-SVN bridge.	27 days ago
NAMESPACE	fixed documentation of sva.check	8 months ago

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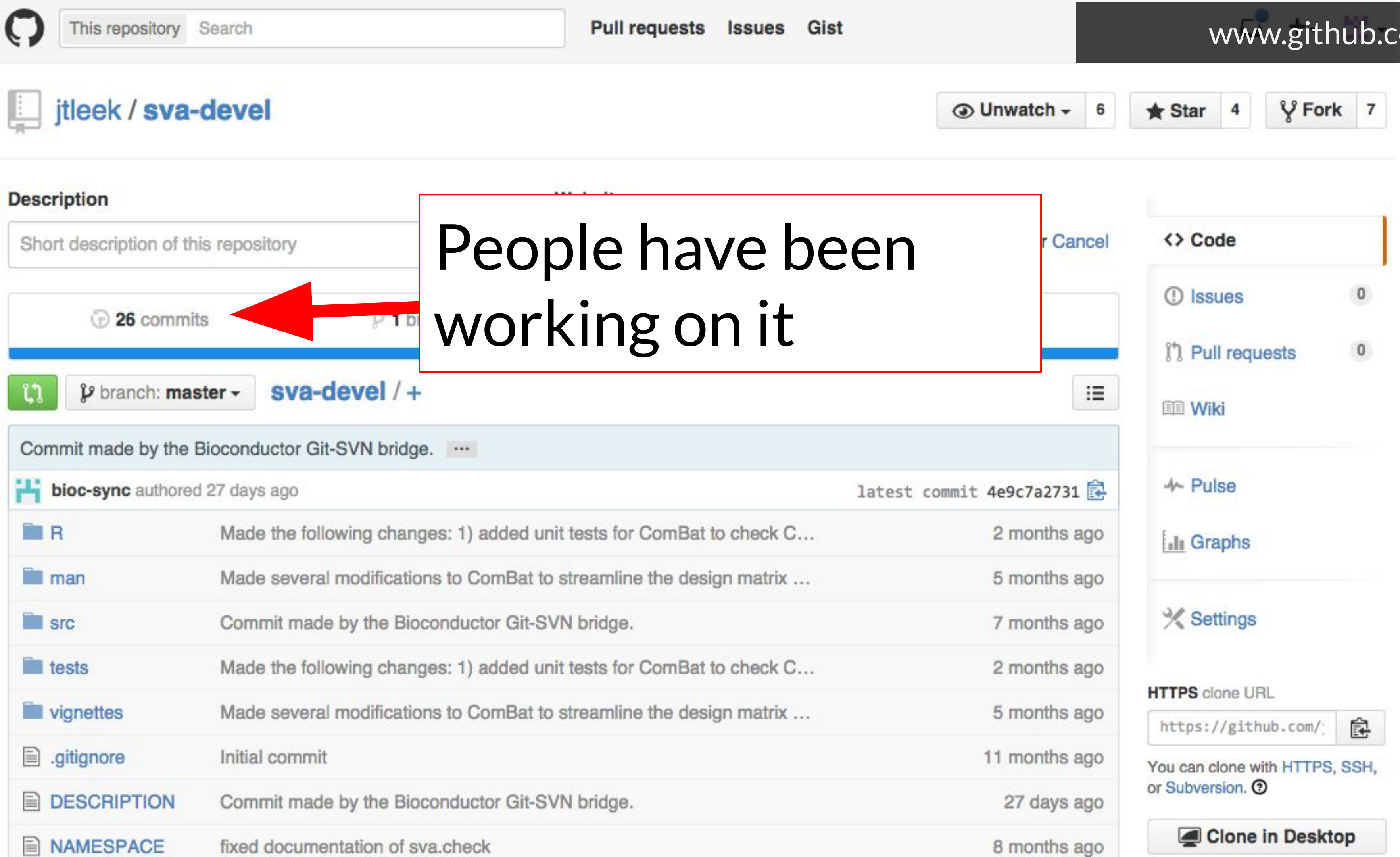

jtleek / **sva-devel**

26 commits

People have been working on it

sva-devel / +

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```r
install.packages("remotes")
library(remotes)
install_github("tidymodels/broom")
```

Average trustworthiness

rstudio.cloud tour

https://rstudio.cloud/spaces/77416/projects