rOpenSci Community Manager Joins Her Community

Learning R by Listening

Stefanie Butland

rOpenSci Community Manager @stefaniebutland @rOpenSci

May 22, 2019 - R-Ladies Seattle



I contain multitudes

- Walt Whitman h/t Ed Yong











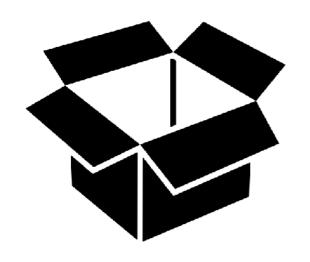






rOpenSci

technical & social infrastructure







Peer review



Community

rOpenSci by the numbers

5 staff

1 postdoc

2 Bioconductor pkgs

192 CRAN pkgs

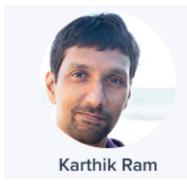
287 total pkgs

~ 500 code contributors

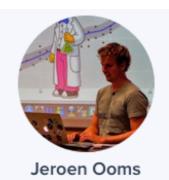
> 500 citations

LOTS! of community members

1 awesome open system for peer review of software

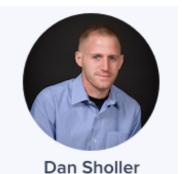




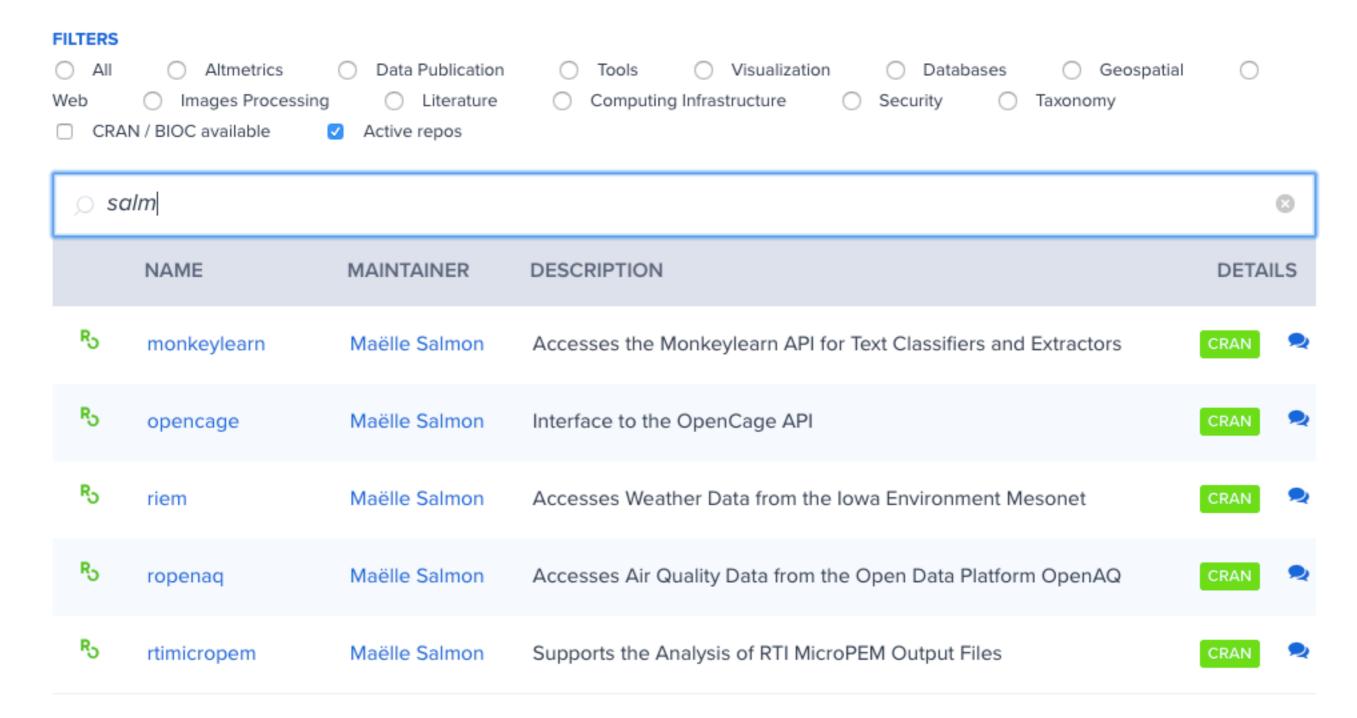








ropensci.org/packages/





4 of 6 new maintainers are women!

- RSelenium: now maintained by Ju Kim
- chromer: now maintained by Paula Andrea
- qualtRics: now maintained by Julia Silge
- rsnps: now maintained by Julia Gustavsen and Sina Rüeger
- rdpla: now maintained by Alyssa Columbus
- webchem: now maintained by Erik Sapper







academic peer review of research publications?

ropensci.github.io/dev_guide/

rOpenSci Packages

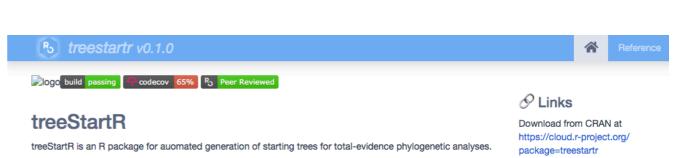
Development, Maintenance, and Peer Review





Software peer review





Phylogenetic trees, and particularly time-scaled phylogenetic trees, are increasingly estimated using parameterrich models of evolution (Lartillot, Lepage, and Blanquart 2009; Wright, Lloyd, and Hillis 2016) and models incorporating macroevoloutionary processes (Heath, Huelsenbeck, and Stadler 2014). Finding a starting tree with a computable likelihood to perform a Bayesian MCMC under these complex models can be a challenge, particularly when when estimation involves many taxa, large datasets, and missing data.

Different phylogenetic estimation packages allow users to find starting trees in different ways, such as estimating a tree under parsimony (Stamatakis (2014)) or neighbor-joining (Bouckaert et al. 2014), randomly adding taxa to the tree (Bouckaert et al. 2014; Stamatakis 2014), or allowing the user to specify the tree. Addition of taxa is usually performed based on data - that is, using an algorithm (such as parsimony or neighbor-joining) to add the tips to the tree. However, in analyses of the fossil record, specimens may be included for which there are no molecular or morphological characters available, but the taxonomy of the

Maril Wright

MIT + file LICENSE

Report a bug at

treeStartR/issues

© License

https://github.com/ropensci/

April Wright

Author, maintainer



Software peer review



July 2018





Generating reasonable starting trees for complex phylogenetic analyses

April Wright

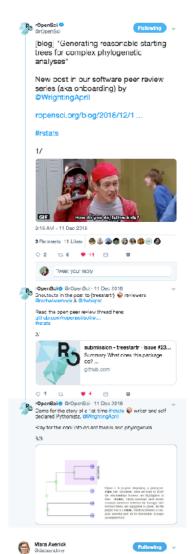
December 11, 2018

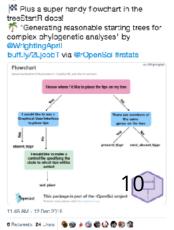
I never really thought I would write an R package. I use R pretty casually. Then, this year, I was invited to participate during the last week of the Analytical Paleobiology short course, an intensive month-long experience in quantitative paleontology. I was thrilled to be invited. But I got a slight sinking feeling in my stomach when I realized all the materials were in R.

And so I, a Pythonista, decided I would spend some of my maternity leave writing R packages to try to blend in with students who had spent the month living and breathing R.









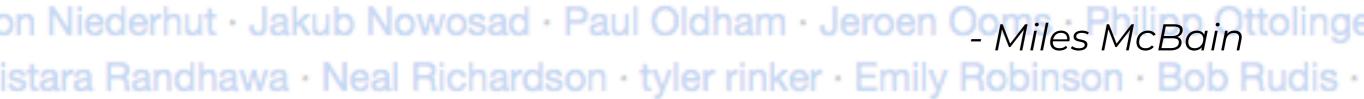
Anderson · Alison Appling · Zebulun Arendsee · Taylor Arnold · Dean Attali · Ma Joëlle Charle US raba · John Baumgartner · Marcus Beck · Gal

ropensci.org/onboarding Christophe Dervie

"As a user, you are qualified as a potential package reviewer if you have some appreciation for what makes your favourite packages useful"

Mark Edmondson · Paul Egeler · Manuel Fernandez · Rich FitzJohn · Robert Flig

rl Ganz · Duncan Garmonsway · Sharla Gelfand · David Gohel · Laura Graham ·



Experience in your midst!



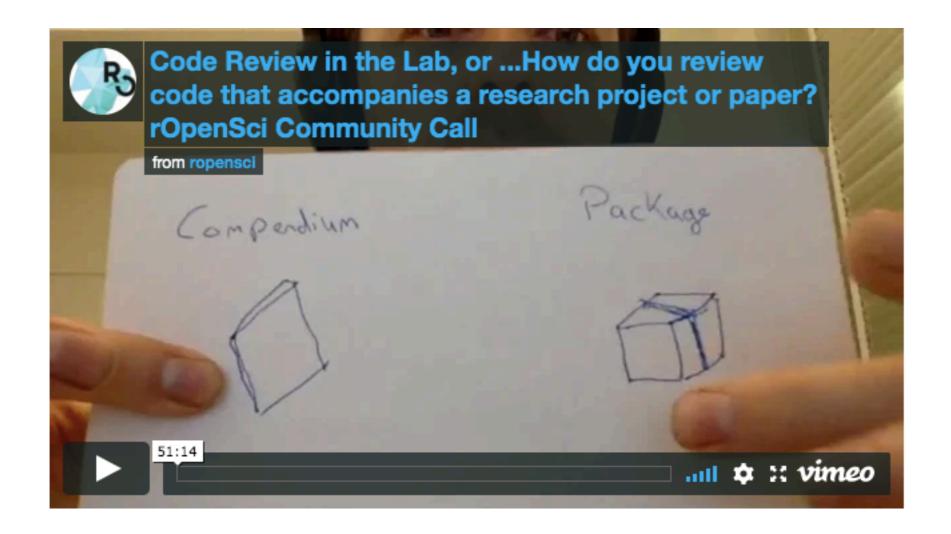
- attended an rOpenSci unconf
- contributed a blog post
- maintain an rOpenSci package
- · reviewed
- · used
- commented in a forum thread
- attended a Community Call
- read a blog post



· V'd or RT'd a tweet

Code review in the lab?

Community Call video, discussion, summary



https://ropensci.org/







/packages

/software-review

/community

I taught myself some R

This is about me ... but really it's about you



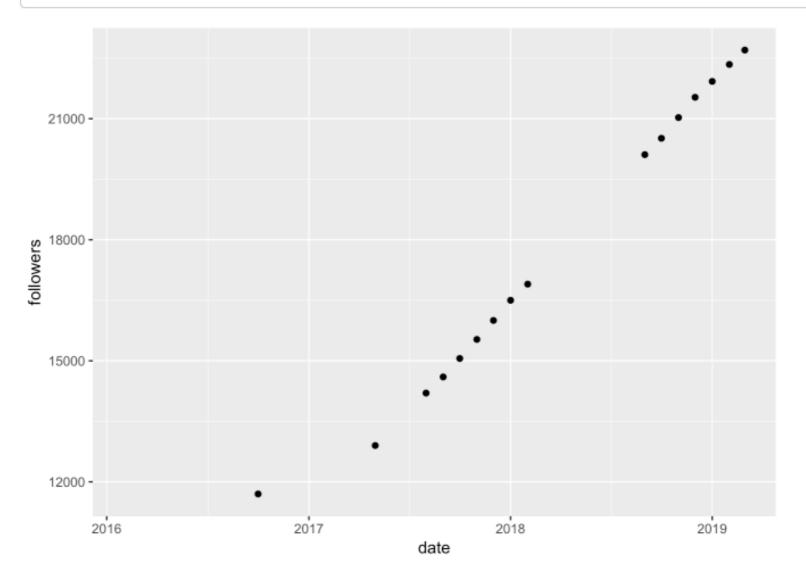


Between January 10th and March 7th, I made an RMarkdown report with the plots I wanted to make...

This is what I came for

```
# use ggplot2 to make point or line plots of date vs tweets, mentions, new followers etc
# followers column is the only one that is not 100% objectve, since it is not archived b
y twitter analytics the way mentions etc are
ggplot(data = metrics, aes(x=date, y=followers)) +
geom_point()
```

Warning: Removed 22 rows containing missing values (geom_point).



...from a csv file with some data I collected and whose date column is formatted correctly, where I understand the provenance of the data...

Read csv of Twitter data

```
# load data from csv -----
# careful: read_csv is tidyverse; read.csv is not
# metrics is an "object"

# > here::here()
# [1] "/Users/stefaniebutland/GitHub/stefaniebutland/twitter_time"

# I learned the hard way that lubridate::here() masked here::here() so need package to avoid errors
```

metrics <- read_csv(here::here("data", "2019-03-02_twitter_metrics_monthly_rOpenSci.csv"))



Display table of Twitter data

knitr::kable(metrics, caption = "Twitter metrics table")

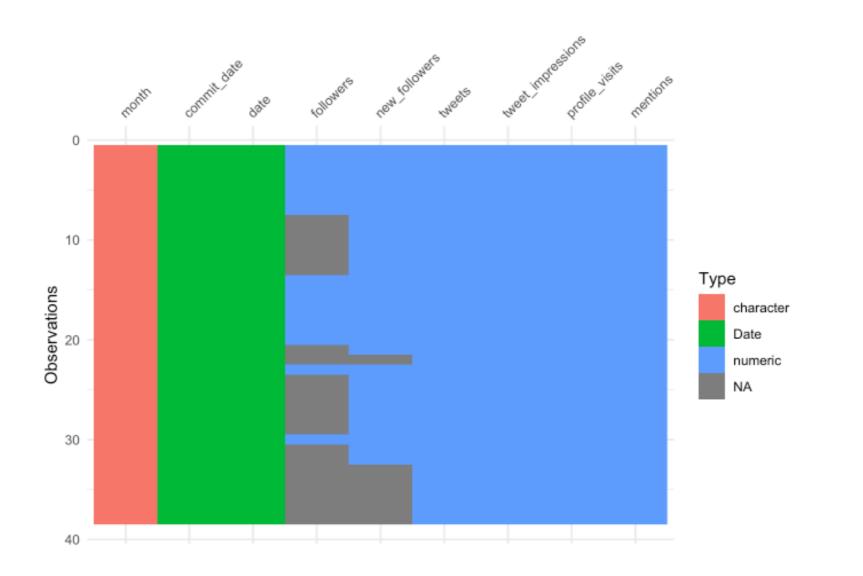
Twitter metrics table

commit_date	date	month	followers	new_followers	tweets	tweet_impressions	profile_visits	mentions
2019-03-01	2019-03-01	Feb	22701	351	20	205000	2327	348
2019-02-01	2019-02-01	Jan	22345	405	26	217000	3603	292
2019-01-02	2019-01-01	Dec	21925	333	28	211000	2369	212
2018-12-02	2018-12-01	Nov	21531	476	38	244000	4104	497

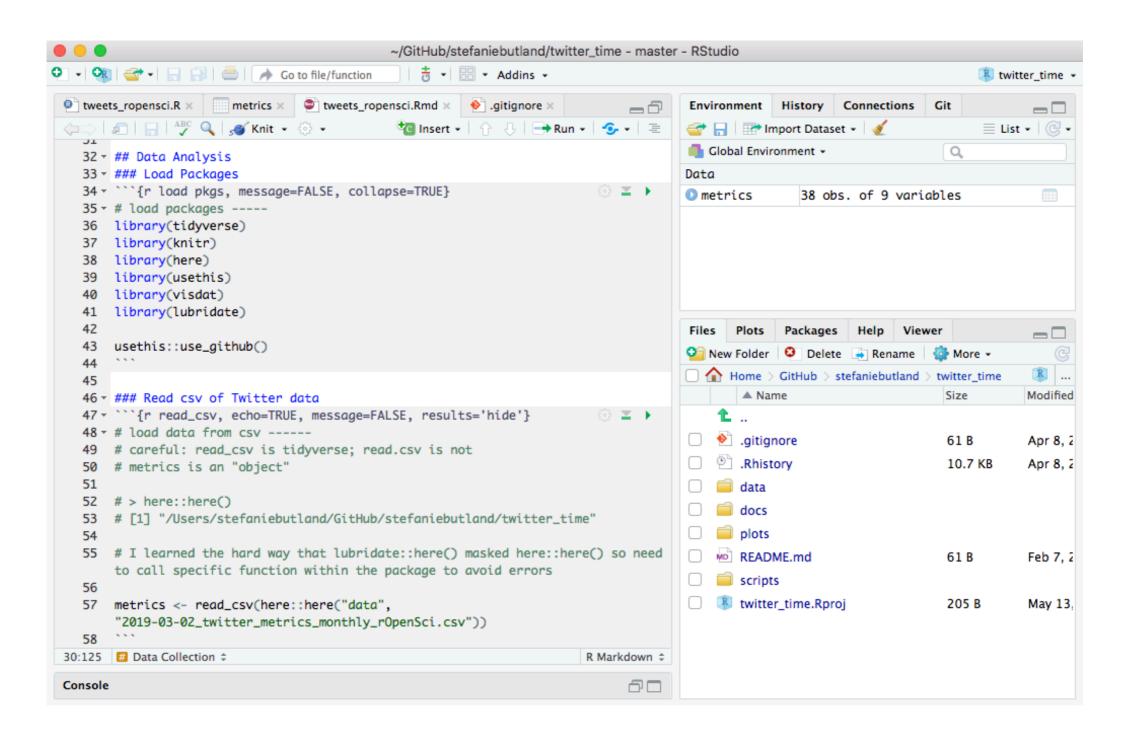
...I tasted the magic of the visdat package and knew where my missing data was...

Try visdat magic

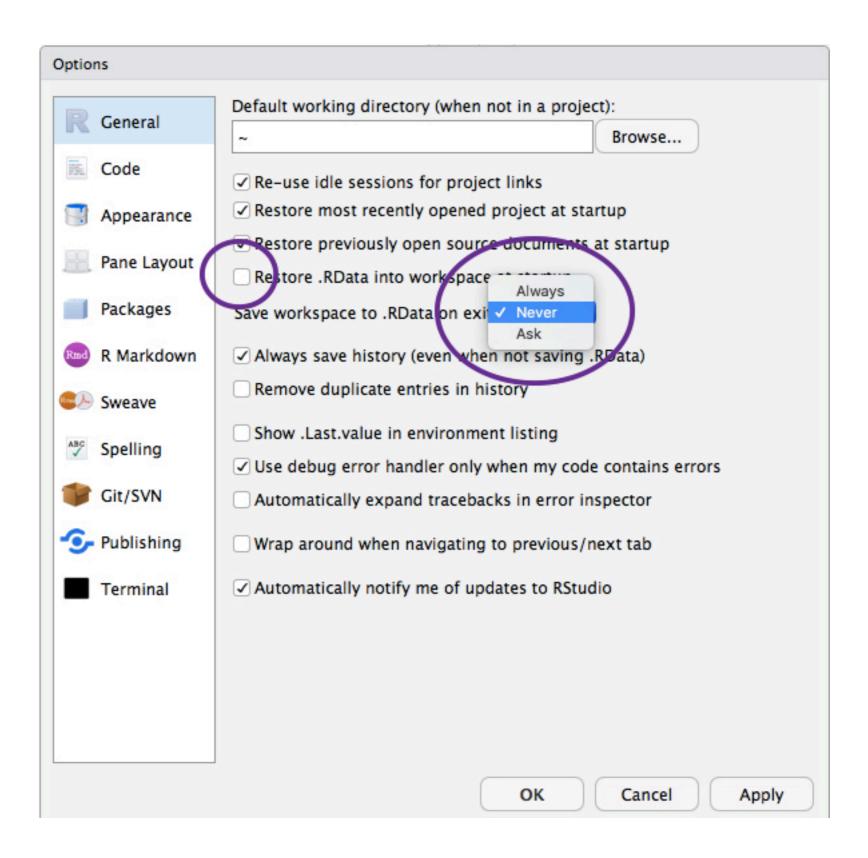
use visdat package to visualize missing data
this was the first package I tried after reading in csv, initially just for fun
vis_dat(metrics)



...and I'm working in RStudio connected to my own public GitHub repository with data and scripts in the right folders...



...never saving my RStudio workspace when I exit...



...using here::here() so I don't hardcode my local file paths so Jenny Bryan doesn't come set my laptop on fire. And once I used "masking the function" and "calling the function from the package" in a sentence!





3 to my (beginner) R success

- · in-person and online trust networks (aka community)
- · a specific modest project
- the "right" tutorials and resources for me



In-person and online trust networks

Omigosh but this community is everything

- Me



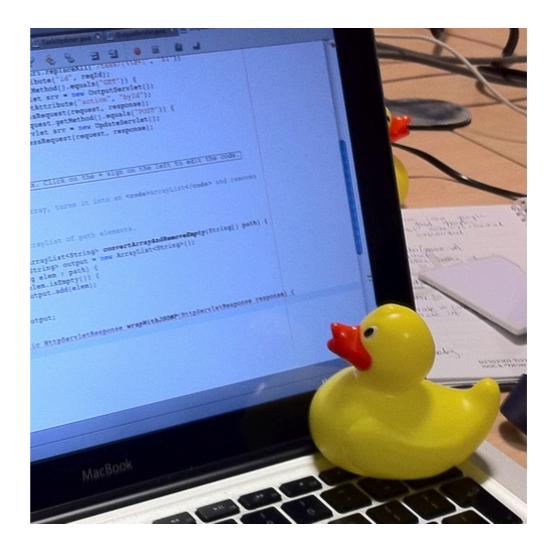




Human rubber duck debuggers

"wait, my x-axis of dates sorted itself alphabetically?!"



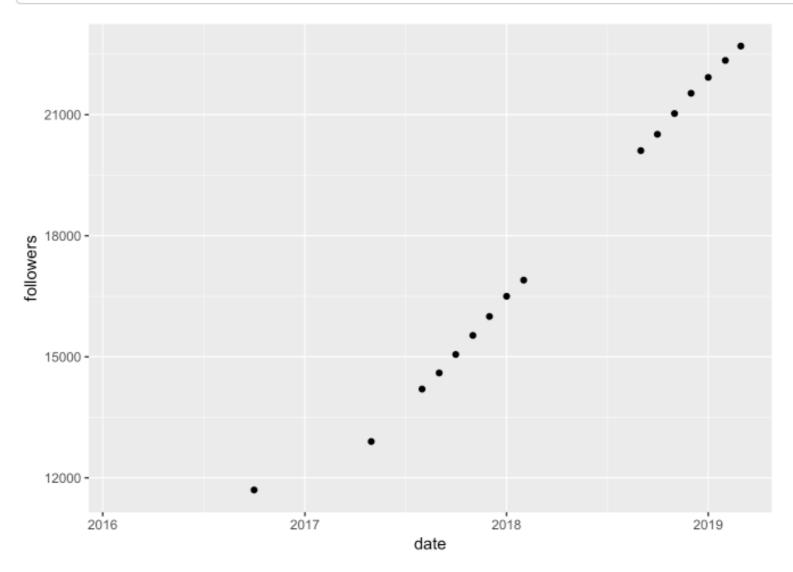


A specific modest project

This is what I came for

```
# use ggplot2 to make point or line plots of date vs tweets, mentions, new followers etc
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```

Warning: Removed 22 rows containing missing values (geom point).



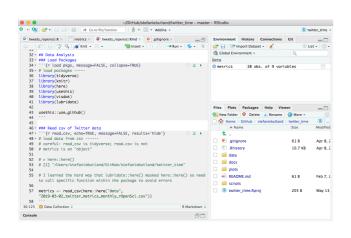
The "right" resources for me

designed by us, for us.
oriented towards R beginners
aims to provide a solid foundation of R skills





never saving my **RStudio** workspace when I exit



working in **RStudio** with data and scripts in the right folders







here::here()

working in RStudio connected to my own public GitHub repository

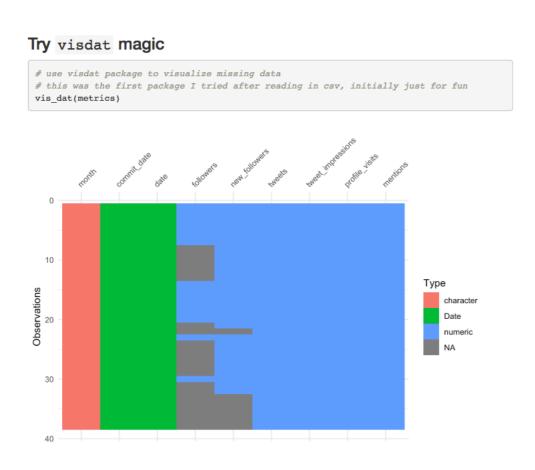
Happy Git and GitHub for the useR

Jenny Bryan, the STAT 545 TAs, Jim Hester

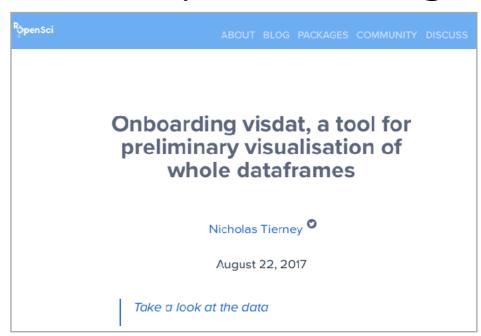
Let's Git started



I knew where my missing data was



The rOpenSci blog!



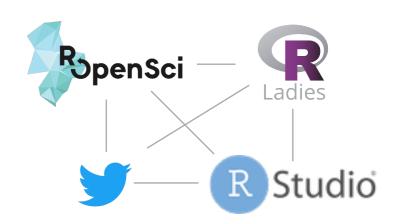
"wait, my x-axis of dates sorted itself alphabetically?!"

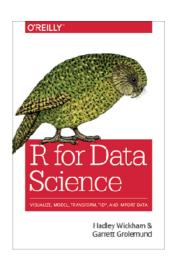
lubridate!

I used "masking the function" and "calling the function from the package" in a sentence



jenny mentioned, you've described the situation as it is.





3 to my success

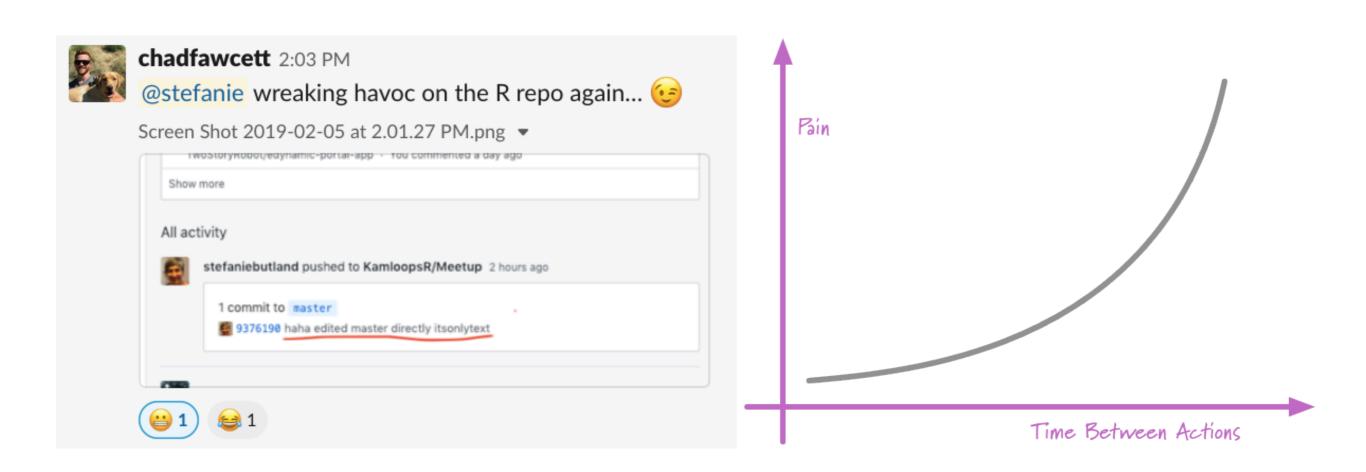
- · in-person and online trust network
- · a specific modest project
- the "right" tutorials and resources for me

"Suck until you don't"

-Pat Schloss

"If it hurts, do it more often"

- Martin Fowler h/t Jenny Bryan



Appreciation

Kara Woo and Monica Gerber for saying this is a talk they'd like to hear

Maëlle Salmon for talk feedback

rOpenSci team for sustaining a values-driven organization

Get Involved!

@rOpenSci - https://ropensci.org/community/

https://ropensci.github.io/dev_guide/

The CSCCE - Community Management

y @StefanieButland