

Steps toward reproducible research

Karl Broman

Biostatistics & Medical Informatics, UW–Madison

`kbroman.org`

`github.com/kbroman`

`@kbroman@rstats.me`

Slides: `kbroman.org/Talk_JAXomics`

This lecture is based on slides for a talk I’ve given a whole bunch of times. This version is for a short course on multiomics analysis, at the Jackson Laboratory.

Source: https://github.com/kbroman/Talk_JAXomics

These slides, with notes:

https://kbroman.org/Talk_JAXomics/repro_research_withnotes.pdf

Full slides without notes: https://kbroman.org/Talk_JAXomics

By “reproducible research,” I’m referring to “computational reproducibility,” by which I mean that the data and code for a project are packaged together in a way that they can be handed to someone else, who can rerun the code and get the same results—the same figures and tables. This is surprisingly hard to do, and it’s even more difficult in the context of a collaboration between two or more data analysts.

Karl -- this is very interesting,
however you used an old version of
the data (n=143 rather than n=226).

I'm really sorry you did all that
work on the incomplete dataset.

Bruce

2

I'm an applied statistician; my goal is to help people make sense of their data. I have a lot of collaborators, and there's nothing I enjoy more than puzzling over their data. So I write a lot of reports, describing what I've done and what I've learned.

This is an email I got from a collaborator, in response to an analysis report that I had sent him. It's always a bit of a shock to get an email like this: what have I done? Why am I working with the wrong data, and where is the right data?

But what he didn't know is that by this point in my life, I'd adopted a reproducible workflow. Because I'd set things up carefully, I could just substitute in the newer dataset, type a single command (“**make**”) to rerun the analyses, and get the revised report.

This is a reproducibility success story. We all make mistakes, but if our projects are reproducible, we can nimbly recover from those mistakes.

There is a second important lesson here: At the start of such reports, I always include a paragraph about our shared goals, along with some brief data summaries. By doing so, he immediately saw that I had an old version of the data. If I hadn't done so, we might never have discovered my error.

The results in Table 1 don't seem to correspond to those in Figure 2.

My computational life is not entirely rosy. This is the sort of email that will freak me out.

Where did we get this data file?

Record the provenance of all data or metadata files.

Why did I omit those samples?

I may decide to omit a few samples. Will I record **why** I omitted those particular samples?

How did I make that figure?

6

Sometimes, in the midst of a bout of exploratory data analysis, I'll create some exciting graph and have a heck of a time reproducing it afterwards.

In what order do I run these scripts?

7

Sometimes the process of data file manipulation and data cleaning gets spread across a bunch of scripts that need to be executed in a particular order. Will I record this information? Is it obvious what script does what?

Reproducible research

organize the data and code in a way
that you can hand them to someone else
and they can re-run the code
and get the same results
(the same figures and tables)

To reiterate my definition of reproducible research: it's about assembling and organizing the data and code so that they can be re-run to give the same results.

Reproducible

vs.

Replicable

9

Computational work is **reproducible** if the data and code are organized in a way that they can be handed to someone else, who can rerun the code and get the same results—the same figures and tables. **Replicable** is more stringent: can someone repeat the experiment and get the same results?

Reproducibility is a minimal standard. That something is reproducible doesn't imply that it is correct. The code may have bugs. The methods may be poorly behaved. There could be experimental artifacts.

(But reproducibility is probably associated with correctness.)

Note that some scientists say replicable for what I call reproducible, and vice versa.

kbroman.org/steps2rr

It was a long, hard process for me to move from my old standard practice to a fully reproducible workflow. In thinking through that process, I wrote down my thoughts on the basic steps to take towards full reproducibility. This forms the basis of what I'll present here.

A little bit reproducible
is better than not reproducible.

A little bit open
is better than not open.

Strive to make each project
a bit better organized than the last.

While it's good to strive for full reproducibility, it can be difficult to achieve. But partially reproducible is better than not-at-all reproducible. Similarly, making data and code partially open is better than nothing.

Don't try to change every aspect of your workflow all at once. Focus on revising one aspect at a time. When you get to the end of a project, you may be dissatisfied with the state of things, but don't give up. Try to make each project a bit better organized and reproducible than the last.

Organize your project

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

(paraphrasing [Mark Holder](#))

The first thing to do is to make your project understandable to others (or yourself, later, when you try to figure out what it was that you did).

Organize your project

```
RawData/           Notes/  
DerivedData/      Refs/  
  
Python/           ReadMe.txt  
R/                ToDo.txt  
Ruby/             Makefile  
  
Analysis/  
Figures/
```

13

Segregate all the materials for a project in one directory/folder on your hard drive.

There will be a lot of files. Organize them in a meaningful way.

This is the way I organize a project directory. The key principles are to put everything related to a project in a common directory, but then to separate data from code and separate raw data from processed data.

Write `ReadMe` files to explain what's what. Make sure they stay current.

Chaos

AimeeNullSims/	Deuterium/	Ping/
AimeeResults/	ExtractData4Gary/	Ping2/
AnnotationFiles/	FromAimee/	Ping3/
Brian/	GoldStandard/	Ping4/
Chr6_extrageno/	HumanGWAS/	Play/
Chr6_segdis/	Insulin/	Prdm9/
ChrisPlaisier/	Int2_for_Mark/	RBM_PlasmaUrine_2012-03-08/
Code4Aimee/	Islet_2011-05/	Slco1a6/
CompAnnot/	MappingProbes/	StudyLineupMethods/
CondScans/	MultiProbes/	kidney_chr6.R
D20_2012-02-14/	NewMap/	pck2_sucla2.R
D20_cellcycle/	Notes/	penalties.txt
D20corr/	NullSims/	transeQTL4Lude/
Data4Aimee/	NullSims_2009-09-10/	
Data4Tram/	PepIns_2012-02-09/	

This is a folder on my hard drive, for the project that led me to reassess my life.

Choose good names for things

```
betw_tissue_corr.R      expr_scatterplot_allprobes.R  gve_similarity_alltissues.R
coatcolor_lod.R        expr_scatterplots_dup.R      gve_similarity.R
colors.R               expr_scatterplots_mix.R      gve_supp.R
cover_fig.R           expr_scatterplots_swap.R     insulin_lod.R
eqtl_counts_10.R      expr_swaps.R                 local_eqtl_locations.R
eqtl_counts.R         func.R                       my_plot_map.R
eve_hist.R            genotype_plates.R           my_plot_scanone.R
eve_scheme.R          gve_hist.R                  sex_vs_X.R
eve_similarity.R       gve_new.R                   xchr_fig.R
eve_similarity_supp.R  gve.R                        xist_and_y.R
expr_corr_dup.R       gve_scheme.R
expr_corr_mix.R       gve_similarity_2ndbest.R
```

15

You'll have a lot of files. In addition to organizing them in subfolders, it's important to choose good names for them.

These names of these files largely explain their contents, but they're also left rather disorganized.

Choose good names for things

fig1.png	fig5.png
fig10.png	fig6.png
fig2.png	fig7.png
fig3.png	fig8.png
fig4.png	fig9.png

These names are well organized, but you have to remember the order of all of the figures to find the one you want.

And note that, alphabetically, figure 10 ends up between figure 1 and figure 2.

Choose good names for things

- ▶ **Machine readable**
 - No spaces
 - No special characters except `_` and `-`
- ▶ **Human readable**
 - Explain the contents
- ▶ **Consistent**
 - Name similar files in a similar way
- ▶ **Make use of computer's sorting**
 - pad numbers with 0's (e.g., 01, 02, ...)
 - start with general grouping, then more specific
 - dates like 2019-05-14

17

You want the names to be easy to handle in software, which generally means no spaces or special characters except for underscore and hyphen (which are useful for separating words).

But you want the names to explain the files' contents, so that you don't have to open the files to figure out what they are.

Consistency is important: if you have a bunch of similar files, you should have some system for naming them.

And make use of the computer's sort of files, by padding numbers with 0's (so that 10 appears after 9 rather than before 2) and organizing the files into groups.

Dates should always be written as 'YYYY-MM-DD', so that when sorted they are in order by date.


PUBLIC SERVICE ANNOUNCEMENT:

OUR DIFFERENT WAYS OF WRITING DATES AS NUMBERS CAN LEAD TO ONLINE CONFUSION. THAT'S WHY IN 1988 ISO SET A GLOBAL STANDARD NUMERIC DATE FORMAT.

THIS IS *THE* CORRECT WAY TO WRITE NUMERIC DATES:

2013-02-27

THE FOLLOWING FORMATS ARE THEREFORE DISCOURAGED:

02/27/2013 02/27/13 27/02/2013 27/02/13
20130227 2013.02.27 27.02.13 27-02-13
27.2.13 2013. II. 27. 2½-13 2013.158904109
MMXIII-II-XXVII M^{LXIII} ^{LXIII} 1330300800
((3+3)×(111+1)-1)×3/3-1/3³ 2013 
10/1101/1101 02/27/20/13 0 1 2 3 4 5 6 7 8

xkcd.com/1179

18

Go with the xkcd format for writing dates, for ease of sorting.

Choose good names for things

```
0_vcf2db.R  
1_prep_genom.R  
2_prep_pheno_clin.R  
2_prep_pheno_otu.R  
3_prep_covar.R  
4_prep_analysis_pheno_clin.R  
4_prep_analysis_pheno_otu.R  
5_scans.R  
6_grab_peaks.R  
7_find_nearby_peaks.R
```

Here's an example to take advantage of the way the computer sorts files: a set of R scripts, which show up in the order they are used.

No “final” in file names



Never include “final” in a file name.

No “final” in file names

```
Deprecated/  
ReadMe.txt  
adipose_int1_final.RData  
adipose_int2_final.RData  
adipose_mlratio_final.RData  
adipose_mlratio_nqrank_final.RData  
adipose_prcomp.RData  
aligned_genome_with_pmap.RData  
batches_final.RData  
batches_raw_final.RData  
cpl_final.RData  
d2o_final.RData  
gastroc_int1_final.RData  
gastroc_int2_final.RData  
gastroc_mlratio_final.RData  
gastroc_mlratio_nqrank_final.RData  
gastroc_prcomp.RData  
hypo_int1_final.RData  
hypo_int2_final.RData  
hypo_mlratio_final.RData  
hypo_mlratio_final_old.RData  
hypo_mlratio_nqrank_final.RData  
hypo_mlratio_nqrank_final_old.RData  
hypo_omit.RData  
hypo_prcomp.RData  
islet_int1_final.RData  
islet_int2_final.RData  
islet_mlratio_final.RData  
islet_mlratio_nqrank_final.RData  
islet_prcomp.RData  
kidney_int1_final.RData  
kidney_int2_final.RData  
kidney_mlratio_final.RData  
kidney_mlratio_nqrank_final.RData  
kidney_prcomp.RData  
lipomics_final_rev2.RData  
liverTG_final.RData  
liver_int1_final.RData  
liver_int2_final.RData  
liver_mlratio_final.RData  
liver_mlratio_nqrank_final.RData  
liver_prcomp.RData  
mirna_final.RData  
necropsy_final_rev2.RData  
plasmaurine_final_rev.RData  
pmark.RData  
rbm_final.RData
```

21

This is an actual directory on my computer. If you include `final` in a file name, there's a risk that you'll end up with `final_rev`, `final_rev2`, and `final_old`.

Another problem here is that the files aren't organized very well.

Choose good names for things

```
batches_raw_v1.rds
batches_v1.rds
clinical_cpl_v2.rds
clinical_d2o_v2.rds
clinical_lipomics_v4.rds
clinical_liverTG_v2.rds
clinical_mirna_v2.rds
clinical_necropsy_v4.rds
clinical_plasmaurine_v3.rds
clinical_rbm_v2.rds
Deprecated/
geneexpr_int1_adipose_v2.rds
geneexpr_int1_gastroc_v2.rds
geneexpr_int1_hypo_v2.rds
geneexpr_int1_islet_v2.rds
geneexpr_int1_kidney_v2.rds
geneexpr_int1_liver_v2.rds
geneexpr_int2_adipose_v2.rds
geneexpr_int2_gastroc_v2.rds
geneexpr_int2_hypo_v2.rds
geneexpr_int2_islet_v2.rds
geneexpr_int2_kidney_v2.rds
geneexpr_int2_liver_v2.rds
geneexpr_mlratio_adipose_v2.rds
geneexpr_mlratio_gastroc_v2.rds
geneexpr_mlratio_hypo_v1.rds
geneexpr_mlratio_hypo_v2.rds
geneexpr_mlratio_islet_v2.rds
geneexpr_mlratio_kidney_v2.rds
geneexpr_mlratio_liver_v2.rds
geneexpr_mlratio_nqrank_adipose_v2.rds
geneexpr_mlratio_nqrank_gastroc_v2.rds
geneexpr_mlratio_nqrank_hypo_v1.rds
geneexpr_mlratio_nqrank_hypo_v2.rds
geneexpr_mlratio_nqrank_islet_v2.rds
geneexpr_mlratio_nqrank_kidney_v2.rds
geneexpr_mlratio_nqrank_liver_v2.rds
geneexpr_omit_hypo.rds
geneexpr_prcomp_adipose_v2.rds
geneexpr_prcomp_gastroc_v2.rds
geneexpr_prcomp_hypo_v2.rds
geneexpr_prcomp_islet_v2.rds
geneexpr_prcomp_kidney_v2.rds
geneexpr_prcomp_liver_v2.rds
geno_aligned_w_pmap.rds
geno_pmark.rds
ReadMe.txt
```

22

This is the same set of files, renamed. Using `clinical_` and `geneexpr_` brings similar files together.

A lot of files, but less forbidding.

Document your work

- ▶ What is all of this stuff?
- ▶ What was your analysis process?

→ ReadMe files

An overall ReadMe file plus an additional such file in each directory.

Well-named files and directories makes everything easier.

Also, keep the documentation current. There's nothing worse than documentation that is out of date and doesn't match the contents.

“What the heck is ‘FAD_NAD SI 8.3_3.3G’?”

24

Sometimes the columns in your data files have meaning only to you.

If the data analyst can't connect to the measurements, they're just columns of numbers.

Metadata

- ▶ **Create a data dictionary**
 - Explain each column
 - Include different versions of the variable names (compact vs descriptive)
 - Units
 - Allowable values
- ▶ **The metadata are data**
 - Make it a spreadsheet

25

Clear metadata is critical for others to be able to understand your data. In particular, make a data dictionary that describes the variables. In addition to a description of each column, I like to have short and longer versions of the names for use in data visualizations, as the column names themselves can be cryptic.

These metadata are data, and so rather than make a Word document describing the data, I personally would prefer to have another data file with the metadata.

Data dictionary

	A	B	C	D
1	name	plot_name	group	description
2	mouse	Mouse	demographic	Animal identifier
3	sex	Sex	demographic	Male (M) or Female (F)
4	sac_date	Date of sac	demographic	Date mouse was sacrificed
5	partial_inflation	Partial inflation	clinical	Indicates if mouse showed partial pancreatic inflation
6	coat_color	Coat color	demographic	Coat color, by visual inspection
7	crumblers	Crumblers	clinical	Indicates if mouse stored food in their bedding
8	diet_days	Days on diet	clinical	Number of days on high-fat diet

Here's an example data dictionary. You might also include units and informationa about possible valid values.

Everything with a script

If you do something once,
you'll do it 1000 times.

27

The most basic principle for reproducible research is: do everything via code.

Downloading data from the web, converting an Excel file to CSV, renaming columns/variables, omitting bad samples or data points...do all of this with scripts.

You may be tempted to open up a data file and hand-edit. But if you get a revised version of that file, you'll need to do it again. And it'll be harder to figure out what it was that you did.

Some things are more cumbersome via code, but in the long run you'll save time.

Small corrections

	A	B	C	D
1	id	Rt Kidney wt	Rt Adipose wt	Liver wt
2	DO-121	294	757	930
3	DO-122	296	583	439
4	DO-123	NA	834	527
5	DO-124	513	808	600
6	DO-125	381	780	493
7	DO-126	225	1.066	355
8	DO-127	262	1.03	512
9	DO-128	231	0.687	497
10	DO-129	263	0.932	580
11	DO-130	266	985	906

Here is a case where a few values were in grams rather than milligrams. You might be tempted to hand-edit the file. It would be better to handle it in your script. Even better would be to go back to your collaborator and have them fix the primary data.

Differing column names

	A	B	C	D	E	
1	id	glucose.mg.dl.0	glucose.mg.dl.5	glucose.mg.dl.15	glucose.mg.dl.30	
2	DO-121	99.165552	349.303552	286.092208	312.047704	
3		A	B	C	D	E
4	1	id	glucose.0	glucose.5	glucose.15	glucose.30
5	2	DO-221	145.742786	206.452638	216.640608	299.55501
6	3	DO-222	138.010378	342.866944	339.836676	276.148802
7	4	DO-223	138.219362	407.443	336.858654	235.501414
8	5	DO-224	100.445504	310.944638	384.97722	308.907044
9	6	DO-225	121.030428	290.41196	345.740474	313.818168
10	7	DO-226	118.418128	189.524934	159.692468	144.488882
11	8	DO-227	117.4777	395.321928	448.612848	310.369932
	9	DO-228	98.773632	149.452252	245.637138	317.423142
	10	DO-229	122.44107	260.63174	231.008258	202.272958

29

Here the column names have been changed between two data files. You again might be tempted to hand-edit the files to match, but if you do that once, you'll be doing that every time the files are updated.

Differing column order

	A	B	C	D	E		
1	id	glucose.mg.dl.0	glucose.mg.dl.5	glucose.mg.dl.15	glucose.mg.dl.30		
2	DO-121	99.165552	349.303552	286.092208	312.047704		
3		A	B	C	D	E	
4	1	id	glucose.0	glucose.5	glucose.15	glucose.30	
5	2	DO-221	145.742786	206.452638	216.640608	299.55501	
6	3		A	B	C	D	E
7	4	1	id	glucose.0	insulin.0	glucose.5	insulin.5
8	5	2	DO-321	66.839405	0.04	246.685995	0.04
9	6	3	DO-322	98.12509	0.51185	246.25574	1.4062
10	7	4	DO-323	94.68305	1.7812	448.1068	1.0248
11	8	5	DO-324	121.051535	0.0882	407.355505	0.63475
	9	6	DO-325	122.95695	0.19155	298.193665	0.6467
	10	7	DO-326	201.447755	0.7454	386.51887	0.6081

30

Now the order of the columns have changed! Again, we need to be able to handle these sorts of changes.

This also emphasizes the importance of relying on the names rather than positions of columns (or rows).

I once had a project where the data were in a 500-worksheet excel file, one sheet per subject. Each sheet had a complex layout where you had to pick out various values from different places. And the order of the rows was different in the middle hundred sheets, versus the other 400 sheets.

Metadata solution

	A	B	C	D	E
1	short_name	file	from_column	id_column	column_offset
2	mouse	wave2_sheet1.csv	mouse #	mouse	0
3	sex	wave2_sheet1.csv	sex	mouse	0
4	sac_date	wave2_sheet1.csv	sac date	mouse	0
5	num_islets	ex_vivo_waves1-3.csv	# islets	mouse	0
6	Ins_per_islet	ex_vivo_waves1-3.csv	IC	mouse	0
7	Glu_0min	gtt2.csv	glucose.mg.dl.0	id	0
8	Ins_0min	gtt2.csv	insulin.ng.ml.0	id	0
9	Glu_tAUC	gtt2.csv	glucose.mg.dl.tAUC	id	0
10	Glu_iAUC	gtt2.csv	glucose.mg.dl.iAUC	id	0
11	Ins_tAUC	gtt2.csv	insulin.ng.ml.tAUC	id	0

My solution to these problems was to create a metadata file that indicated the names of the variables, what files to find them, what their names were in each file, and what the individual IDs names were in those files. I also needed an "offset" column, because in some cases it was like "the column two to the right of the column name _____."

“In what form would you like the data?”

The answer should always be

“In its present form.”

32

To further emphasize here: the data scientist is always in a better position to fix data formatting issues programmatically.

If you're unhappy with the state of your collaborators' data files, don't have them fix them, because they'll likely do so “by hand” at the risk of introducing errors. Rather, deal with the data files as they come, but then work with your collaborators to develop a better system for the future.

Reproducible reports

Gough project diagnostics

Karl Broman, 3 March 2014

Combine genotypes and phenotypes

I've combined the initial genotypes (using the re-clustered genotypes for plates 14-16) with the well-behaved portion of the re-run genotypes. I'm focusing on 36813 markers that are informative (though, as we'll see, there are still a lot of badly behaved and basically non-informative markers that need to be removed). I've combined data on replicate samples, to give one set of genotype calls for each sample.

There are 1497 genotyped mice and 1464 phenotyped mice. All of the mice in the phenotype data have genotypes, but there are 33 genotyped mice with no phenotypes, including 3 Gough mice and 30 F2 progeny.

33

I [love](#) R Markdown for making reproducible reports that document the full details of my analysis. R Markdown mixes Markdown (for light-weight markup of text) and R code chunks; when processed with knitr, the R code is executed and results inserted into the final document.

With these informal reports, I seek to fully capture the entirety of my data explorations and decisions.

Python people should look at [Jupyter](#) notebooks. Many R people have moved to [Quarto](#).

Automate the process (GNU Make)

```
R/analysis.html: R/analysis.Rmd Data/cleandata.csv
  cd R;R -e "rmarkdown::render('analysis.Rmd')"

Data/cleandata.csv: R/prepData.R RawData/rawdata.csv
  cd R;R CMD BATCH prepData.R

RawData/rawdata.csv: Python/xls2csv.py RawData/rawdata.xls
  Python/xls2csv.py RawData/rawdata.xls > RawData/rawdata.csv
```

34

GNU Make is an old (and rather quirky) tool for automating the process of building computer programs. But it's useful much more broadly, and I find it valuable for automating the full process of data file manipulation, data cleaning, and analysis.

In addition to [automating](#) a complex process, it also [documents](#) the process, including the dependencies among data files and scripts.

An alternative is the R package [targets](#). Python people should look at [snakemake](#).

Write modular code

- ▶ Modular code is easier to understand, maintain, and reuse.
- ▶ Turn repeated code into functions
- ▶ Combine useful functions into a package or module

35

Another important step towards reproducibility is to revise your code to make it more clear.

The single most important step towards clear code is to pull out complex or repeated code as a separate function. This makes your code easier to read and maintain.

Next, combine those functions together into a package or module. It's surprisingly easy to create an R package (see https://kbroman.org/pkg_primer) and it's even easier to make a Python module.

When writing functions, try to write them in a somewhat-general way and then pull them out of the project as separate package or module, so that you (and/or others) may reuse them for other purposes.

Keeping track of versions

- ▶ Google drive / Dropbox / Box
- ▶ Version numbers in file names
- ▶ Formal version control (e.g., git/GitHub)
 - Browse changes
 - Try new things without fear of breaking what works
 - Jump to the state of the project at any time point
 - Merge simultaneous changes from multiple people

36

We all struggle to keep track of versions of things.

Shared drives (like google drive, dropbox, and box) often keep track of past versions, but usually there's a time limit (like 30 days or a year).

You can make copies of a file with a version number appended to the name. You might zip up a directory and include the date in the zipped file.

Formal version control has a number of advantages, including easy of browsing the history or jumping to a particular time point. The ability to merge simultaneous changes from multiple users is a key advantage.

git can be hard to learn; it's designed for pretty hard-core programmers. But there are growing learning resources, and the long-term payoff is considerable. For collaborative projects, the payoff is immediate.

Version control (git/GitHub)

PUBLIC kbroman / Talk_MAGIC

Unwatch 1 Star 0 Fork 0

Fix two slight bugs in slides: [Browse code](#)

- 8-way RIL by selfing: map expansion = 1 at k=0
- Slight repair to definition of 3-pt coincidence

master

kbroman authored 4 months ago 1 parent e0e0608 commit 51d4aa9ceb104bf726e0cbe105a5c7f8dc02a832

Showing 2 changed files with 5 additions and 3 deletions. [Show Diff Stats](#)

```
6 R/map_expansion_func.R View file @ 51d4aa9
... @@ -25,8 +25,10 @@ mes1bA4 <- function(k)
25 25 #####
26 26 # Eight-way
27 27 #####
28 -mes1f8 <- function(k)
29 - 4 - (((1)/(2))^(k-2))
+mes1f8 <- function(k) {
+ if(k==0) return(1)
+ 4 - (((1)/(2))^(k-2))
+ }
30 32
31 33 mes1bX8 <- function(k)
32 34 ((14)/(3)) - (((30 + 14*sqrt(5))/(15))) * (((1+sqrt(5))/(4)))^k - (((30 - 14*sqrt(5))/(15))) * (((1-5
```

```
2 magic.tex View file @ 51d4aa9
... @@ -636,7 +636,7 @@
636 636
637 637 \hspace{20mm} {\color{myblue} = \mathsf{Pr}(\text{rec'n in 23} \setminus
638 638 \ \text{rec'n in 12}) /
639 - Pr(\text{rec'n in 12})$}
639 + Pr(\text{rec'n in 23})$}
640 640
641 641 \item
642 642 No interference { \color{myblue} = 1 }
```

git has a steep learning curve, but ultimately I think you'll find it really helpful.

The big selling point is in collaboration: merging changes from collaborators, and keep your work synchronized.

Longer term, there's great value in having the entire history of changes to your project. If something stops working, you can go back to any point in that history to see when it stopped working and why.

With git, you can also work on new features or analyses without fear of breaking the parts that are currently working well.

Backups

- ▶ Multiple places, including off-site
- ▶ Automatic

I can't emphasize enough the importance of backups. And you must have a copy off-site. And if it's not automatic, it won't happen.

License your software

Pick a license, any license

– Jeff Atwood

39

If you don't pick a license for your software, no one else can use it.

So if you want to distribute your code so that others can reproduce your analyses, you need to pick a license, any license.

I choose between the MIT license and the GPL.

Don't use the Creative Commons licenses for code. But feel free to use them for other things.

Share your stuff

▶ Code

- GitHub / BitBucket / Codeberg
- Zenodo (archival, with DOIs)

▶ Data

- Domain-specific repository (e.g., dbGAP)
- General repository (e.g., github, figshare, zenodo, datadryad)
- Institutional repository

40

A reproducible workflow is valuable even if you don't intend to share your work with others.

But if do want to share, it's best to place things at a third-party site. Ideally one that can be trusted as an archive and that provides DOIs.

Place code at GitHub (or the similar site, BitBucket, and many people have moved to Codeberg as Microsoft has taken over GitHub). The only problem is that it can't necessarily be trusted to still be there 5 years from now. There's an easy way to have "releases" archived at zenodo.org automatically, with a DOI. So I recommend that.

For data, it's probably best to use a domain-specific repository, if there is an appropriate one. Otherwise, general repositories github, figshare, zenodo, or datadryad. Again, github is not ideal because it's not archival and doesn't give DOIs.

Summary

1. Organize your project
2. Choose good names for things
3. Document what's what
4. Organize data as a rectangle
5. Metadata is data
6. Everything with a script
7. Even better: reproducible reports
8. Automate the process (GNU Make)
9. Write modular code (functions and packages)
10. Use version control (git/GitHub)
11. License your software
12. Share your data and code

Summaries are always good.

Again, don't try to change everything at once. Reproducibility can be surprisingly hard and requires a daily commitment. And here I'm just thinking about a project with a single data analyst. A collaboration with multiple analysts is yet harder.

Other considerations

- ▶ **Software versions**

will your stuff work when dependencies change?

- ▶ **Testing**

are you getting the right answers?

- ▶ **Large-scale computations**

computation time + dependence on cluster environment

- ▶ **Collaborations**

coordinating who does what and where things live

I've focused on issues for small-scale, single-investigator projects, and even with that limited scope, I've not covered everything.

The most important tool is the **mindset**,
when starting, that the end product
will be reproducible.

– Keith Baggerly

So true. Desire for reproducibility is step one.

Slides: kbroman.org/Talk_JAXomics



kbroman.org

github.com/kbroman

@kbroman@rstats.me

Here's where you can find me, as well as the slides for this talk.