

# Tools for Reproducible Research

Organizing projects; exploratory data analysis

Karl Broman

Biostatistics & Medical Informatics, UW–Madison

`kbroman.org`

`github.com/kbroman`

`@kwbroman`

Course web: [kbroman.org/Tools4RR](https://kbroman.org/Tools4RR)

# Organizing your stuff

```
Code/d3examples/  
  /Others/  
  /PyBroman/  
  /Rbroman/  
  /Rqtl/  
  /Rqtlcharts/  
Docs/Talks/  
  /Meetings/  
  /Others/  
  /Papers/  
  /Resume/  
  /Reviews/  
  /Travel/  
Play/  
Projects/AlanAttie/  
  /BruceTempel/  
  /Hassold_QTL/  
  /Hassold_Age/  
  /Payseur_Gough/  
  /PhyloQTL/  
  /Tar/
```

# Organizing your projects

```
Projects/Hassold_QTL/
```

```
  Data/
```

```
  Notes/
```

```
  R/
```

```
  R/Figs/
```

```
  R/Cache/
```

```
  Rawdata/
```

```
  Refs/
```

```
  Makefile
```

```
  Readme.txt
```

```
  Python/convertGeno.py
```

```
  Python/convertPheno.py
```

```
  Python/combineData.py
```

```
  R/prepData.R
```

```
  R/analysis.R
```

```
  R/diagnostics.Rmd
```

```
  R/ctl_analysis.Rmd
```

# Organizing a paper

```
Docs/Papers/PhyloQTL/
```

```
    Analysis/
```

```
    Data/
```

```
    Figs/
```

```
    Notes/
```

```
    R/
```

```
    SuppFigs/
```

```
    ReadMe.txt
```

```
    Makefile
```

```
    phyloqtl.tex
```

```
    phyloqtl.bib
```

```
    Submitted/
```

```
    Reviews/
```

```
    Revised/
```

```
    Final/
```

```
    Proofs/
```

# Organizing a talk

```
Docs/Talks/SampleMixups/
```

```
  Figs/
```

```
  R/
```

```
  ReadMe.txt
```

```
  Makefile
```

```
  bmi2013.tex
```

```
  Old/
```

# Basic principles

- ▶ Develop your own system
- ▶ Put everything in a common directory
- ▶ Be consistent
  - directory structure; names
- ▶ Separate raw from processed data
- ▶ Separate code from data
- ▶ It should be obvious what code created what files, and what the dependencies are.
- ▶ No hand-editing of data files
- ▶ Don't use spaces in file names
- ▶ Use relative paths, not absolute paths
  - `../blah` not `~/blah` or `/users/blah`

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

Organization takes time.



# Painful bits

- ▶ Coming up with good names for things
  - Code as verbs; data as nouns
- ▶ Stages of data cleaning
- ▶ Going back and redoing stuff
- ▶ Clutter of old stuff that you no longer need
- ▶ Keeping track of the order of things
  - dependencies; what gave rise to what
- ▶ Long, messy Makefiles

# Painful bits

- ▶ Coming up with good names for things
  - Code as verbs; data as nouns
- ▶ Stages of data cleaning
- ▶ Going back and redoing stuff
- ▶ Clutter of old stuff that you no longer need
- ▶ Keeping track of the order of things
  - dependencies; what gave rise to what
- ▶ Long, messy Makefiles

→ Modularity


## 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.  $27\frac{1}{2}$ -13 2013.158904109  
MMXIII-II-XXVII MMXIII  $\frac{LVII}{CCCLXV}$  1330300800  
 $((3+3) \times (111+1) - 1) \times 3 / 3 - 1 / 3^3$  2013  
10/11011/1101 02/27/20/13 01237  MISSS  
2 3 1 4  
5 6 7 8

# Problem: Variations across data files

- ▶ Different files (or parts of files!) may have different formats.
- ▶ Variables (or factor levels) may have different names in different files.
- ▶ The names of files may inconsistent.
- ▶ It's tempting to hand-edit the files. Don't!
- ▶ Create another meta-data file that explains what's what.

# Tidy data

Read Hadley Wickham's [paper on Tidy Data](#).

- ▶ Each variable forms a column.
- ▶ Each observation forms a row.
- ▶ Each type of observational unit forms a table.

Mouse	Treatment	Response
1	control	--
1	ttt	7.4
2	control	3.8
2	ttt	5.2
3	control	5.5
3	ttt	6.6

# Problem: 80 million side projects

```
$ ls ~/Projects/Attie
```

AimeeNullSims/	Deuterium/	Ping/
AimeeResults/	ExtractData4Gary/	Ping2/
AnnotationFiles/	ForFirstPaper/	Ping3/
Brian/	FromAimee/	Ping4/
Chr10adipose/	GoldStandard/	Play/
Chr6_extrageno/	HumanGWAS/	Proteomics/
Chr6hotspot/	Insulin/	R/
ChrisPlaisier/	Islet_2011-05/	RBM_PlasmaUrine/
Code4Aimee/	Lusis/	R_adipose/
CompAnnot/	MappingProbes/	R_islet/
CondScans/	Microarrays/	Rawdata/
D20_2012-02-14/	MultiProbes/	Scans/
D20_Nrm_2012-02-29/	NewMap/	SimsRePower/
D20_cellcycle/	Notes/	Slco1a6/
D20corr/	NullSims/	StudyLineupMethods/
Data4Aimee/	NullSims_2009-09-10/	eQTLPaper/
Data4Tram/	PepIns_2012-02-09/	transeQTL4Lude/

# Saving intermediate results

## R Markdown document with details of data cleaning.

- ▶ Within the `.Rmd` file, periodically `save` the state of things, for further exploratory analysis.
- ▶ Put those intermediate files (which might be large) in a common subdirectory.
- ▶ The subdirectory could be under `separate` version control.
- ▶ But you'll need to `go in there` and commit files.

# Problem: Coordinating with collaborators

- ▶ Where to put data that multiple people will work with?
- ▶ Where to put intermediate/processed data?
- ▶ Where to indicate the code that created those processed data files?
- ▶ How to divvy up tasks and know who did what?
- ▶ Need to agree on directory structure and file naming conventions
- ▶ Consider symbolic links for shared data directories

```
ln -s /z/Proj/blah
```

```
ln -s /z/Proj/blah my_blah
```



Problem: Collaborators who don't use git

Problem: Collaborators who don't use git

Um...

# Problem: Collaborators who don't use git

- ▶ Use git yourself
- ▶ Copy files to/from some shared space
  - Ideally, in an automated way
- ▶ Commit **their** changes.

# Exploratory data analysis

- ▶ what were trying to do?
- ▶ what you're thinking about?
- ▶ what did you observe?
- ▶ what did you conclude, and why?

# Avoid

- ▶ "How did I create this plot?"
- ▶ "Why did I decide to omit those six samples?"
- ▶ "Where (on the web) did I find these data?"
- ▶ "What was that interesting gene?"

# Basic principles

Step 1: slow down and document.

Step 2: have sympathy for your future self.

Step 3: have a system.

# Capturing EDA

- ▶ copy-and-paste from an R file
- ▶ grab code from the `.Rhistory` file
- ▶ Write an informal R Markdown file
- ▶ Write code for use with the KnitR function `spin()`

Comments like `#' This will become text`

Chunk options like so: `#+ chunk_label, echo=FALSE`

# A file to spin()

```
#' This is a simple example of an R file for use with spin().  
  
#' We'll start by setting the seed for the RNG.  
set.seed(53079239)  
  
#' We'll first simulate some data with  $x \sim N(\mu=10, \sigma=5)$  and  
#'  $y = 2x + e$ , where  $e \sim N(\mu=0, \sigma=2)$   
x <- rnorm(100, 10, 5)  
y <- 2*x + rnorm(100, 0, 2)  
  
#' Here's a scatterplot of the data.  
plot(x, y, pch=21, bg="slateblue", las=1)
```



I almost forgot

Backups

I almost forgot

## Backups

Next two weeks: Clear code and R packages