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W04: Pragmatic Reproducible Research for Analysis, Dissemination and Publication

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AMIA 2019 Informatics Summit | March 25, 2019

Instructor Disclosures

Luke Rasmussen - I and my spouse/partner have no relevant relationships with commercial interests to disclose.

Eric Whitley – I and my spouse/partner have no relevant relationships with commercial interests to disclose.

Acknowledgements

This represents joint work with:

- Leah J. Welty, Project Director
- Abigail S. Baldridge, Biostatistician

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The content is solely the responsibility of the instructors and does not necessarily represent the official views of the National Institutes of Health.

We want you to enjoy this workshop!

Let's make sure what you expect to get out of this workshop matches what we're planning to cover.

What you'll learn…

- What is (and isn't) reproducible research
- How to apply the concept of reproducible research to your projects
- How to assess tools, data sets and publication options when planning a reproducible project

What we won't have time to cover…

- Every step needed to clean your data
- All of the tools out there that help with reproducible research *(we will discuss a few)*
- How to master all of the tools we mention *(you will get an idea how a few can be used)*

Agenda

1. Overview of reproducible research (20 minutes)
2. Thinking pragmatically about reproducible research (20 minutes)
3. Exercise: Teams and Data (15 minutes)
4. Use Case – EHR-Based Phenotyping (Part 1) (25 minutes)
5. Exercise: Analysis (10 minutes)
6. Break (30 minutes)
7. Use Case – EHR-Based Phenotyping (Part 2) (25 minutes)
8. Exercise: Documentation (15 minutes)
9. Use Case – EHR-Based Phenotyping (Part 3) (30 minutes)
10. Exercise: Dissemination (15 minutes)
11. Wrap-up (5 minutes)

Exercises

- Goal: Applying the concepts learned
- Methods and Concepts (Primary)
  - Guide – provides questions and prompts to consider
  - Worksheet – spaces to jot down your notes
- Example Software (Secondary)
  - Examples available on GitHub repo

Think of a past / current / future project that you'd like to make reproducible. After each section, think through the prompts in the guide and apply what we covered. Are there new considerations you found that we didn't cover?

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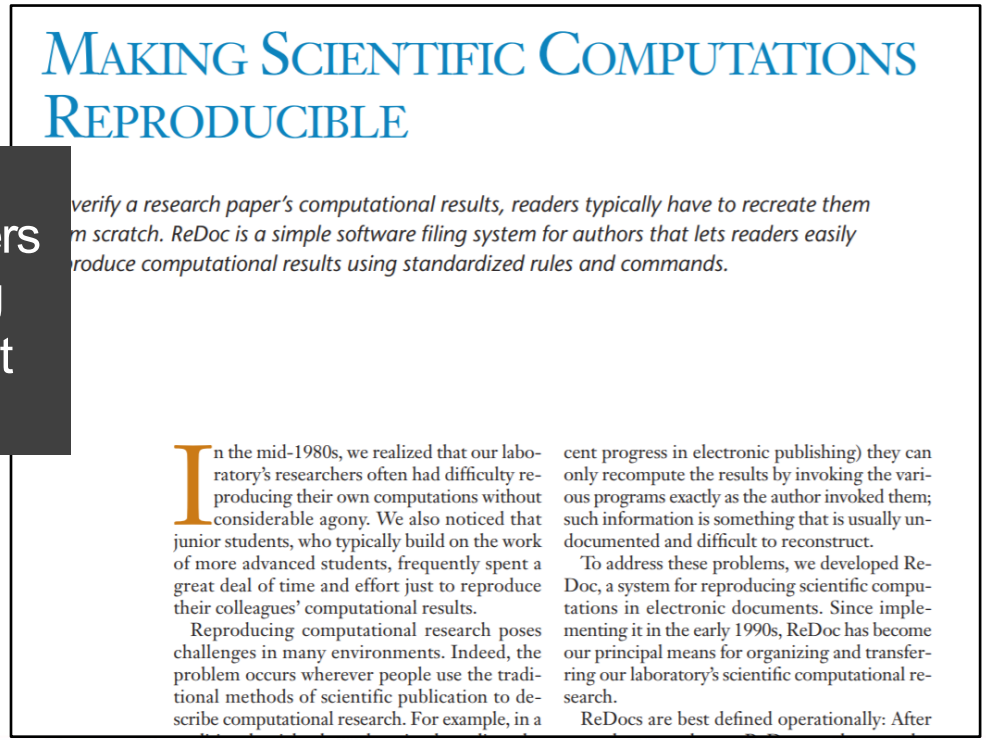
Overview of Reproducible Research

Introduction

Origins lie in the inconvenience of irreproducible research

"In the mid-1980s, we realized that our laboratory's researchers often had difficulty reproducing their own computations without considerable agony."



MAKING SCIENTIFIC COMPUTATIONS REPRODUCIBLE

verify a research paper's computational results, readers typically have to recreate them m scratch. ReDoc is a simple software filing system for authors that lets readers easily roduce computational results using standardized rules and commands.

In the mid-1980s, we realized that our laboratory's researchers often had difficulty reproducing their own computations without considerable agony. We also noticed that junior students, who typically build on the work of more advanced students, frequently spent a great deal of time and effort just to reproduce their colleagues' computational results.

Reproducing computational research poses challenges in many environments. Indeed, the problem occurs wherever people use the traditional methods of scientific publication to describe computational research. For example, in a

cent progress in electronic publishing) they can only recompute the results by invoking the various programs exactly as the author invoked them; such information is something that is usually undocumented and difficult to reconstruct.

To address these problems, we developed ReDoc, a system for reproducing scientific computations in electronic documents. Since implementing it in the early 1990s, ReDoc has become our principal means for organizing and transferring our laboratory's scientific computational research.

ReDocs are best defined operationally: After

Schwab M, Karrenbach M, Claerbout J. "Making Scientific Computations Reproducible". Computing in Science & Engineering 2000 2:6, 61-67

Introduction

Insanity

"doing the same thing over and over and expecting a **different** result”

Irreproducible research

"doing the ‘same’ thing over and over and getting a **different** result”

Reproducible research

"doing the same thing over and over and getting the **same** result”

What Isn't Reproducible Research?

There are many best practices and concepts that can be confused with it:

Open Science

- Open data
- Open source
- Preregistration of studies
- Prepublication servers

Reproducible research can be disseminated openly.

Replication

- "*…the chances other experimenters will achieve a consistent result…*" – Leek & Peng (2015)

Reproducible research can help others replicate your work.

Tools / Software Engineering

- Unit tests
- Bash scripts
- Any specific programming language (Python, C++)
- Any specific tool (Jupyter Notebooks, Docker)

Reproducible research can be automated.

Scientific Rigor

- Are the methods used the right ones?
- Quality of the data collected and used
- "*…invalid reports can do more harm than irreproducible reports*" – Shiffren, Borner & Stigler 2018

Reproducible research can help us evaluate our methods.

Kinds of Reproducible Research

- Computational Reproducibility
  - Have all of the information about the code, software and hardware.
  - Can re-run it on the same data set
- Empirical Reproducibility
  - Able to reproduce the non-computational experiments
  - Requires very clear methods
- Statistical Reproducibility
  - Full details about statistical tests
  - Pre-registration of studies to prevent p-value hacking

Stodden, 2014 - https://www.edge.org/response-detail/25340

The journey to transparency, reproducibility, and replicability FREE

Suzanne Bakken

Journal of the American Medical Informatics Association, Volume 26, Issue 3, 1 March 2019, Pages 185–187, https://doi.org/10.1093/jamia/ocz007
Published: 25 January 2019

Split View PDF Cite Permissions Share ▾

Regardless of the type of biomedical and health informatics research conducted (eg computational, randomized controlled trials, qualitative, mixed methods), transparency, reproducibility, and replicability are crucial to scientific rigor, open science, and advancing the knowledge base of our field and its application across practice domains. These principles are also essential to high-quality publications in *Journal of the American Medical Informatics Asso*
reflected by explicit, clear, and open communi
procedures used to obtain the research results
(ability to repeatedly obtain the same results fr
other investigators to observe the same result
following paragraphs, I summarize key strateg
well as my own thoughts in 4 categories (data,
applicable, describe their relationship to publis
apply across types of research, the relevance of some strategies varies.

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Importance to our field:
- Scientific rigor
- Open science
- Advancing knowledge

Does health informatics have a replication crisis?

Enrico Coiera ✉, Elske Ammenwerth, Andrew Georgiou, Farah Magrabi

Journal of the American Medical Informatics Association, Volume 25, Issue 8, 1 August 2018, Pages 963–968, https://doi.org/10.1093/jamia/ocy028
Published: 13 April 2018 **Article history** ▾

Pragmatic Benefits

- Allows us to go back and know exactly what we did
  - 2015 Luke – “I’ll totally remember where I put that data set”
  - 2019 Luke – ”AGGGH, 2015 LUKE!!!”
- Guides us to being better scientists
  - Forces us to think through parts of the process
  - Still doesn’t guarantee accuracy
- A little can go a long way
  - Not an all-or-nothing endeavor

The Hard Truth

- Up-front investment in time
- Not everyone finds it “fun”
- ROI comes over time
- When you need it, you’ll be happy you did it

Definition For Today

"…the ability to recompute data analytic results given an observed dataset and knowledge of the data analysis pipeline…"

Leek & Peng, PNAS February 10, 2015; 112 (6)
https://doi.org/10.1073/pnas.1421412111

What Could Change?

- People
- Data
- Project-specific analysis code
- Supporting software – statistical package, compiler, interpreter
- Operating system
- Hardware

It is about reducing **variation**

Summary

- Many definitions of “reproducible research” exist
- For today: the ability to recompute results given the data and code
- Goal is reducing variation
- Start small, and work your way up
- It’s okay to do this just for you!

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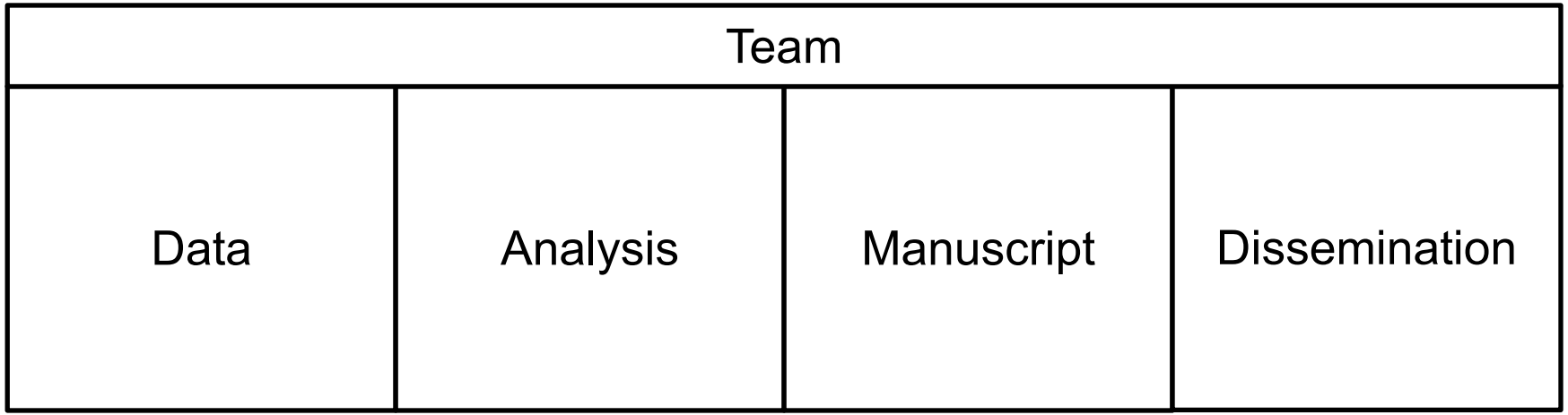
Thinking Pragmatically About Reproducible Research

Assessing and planning for your projects

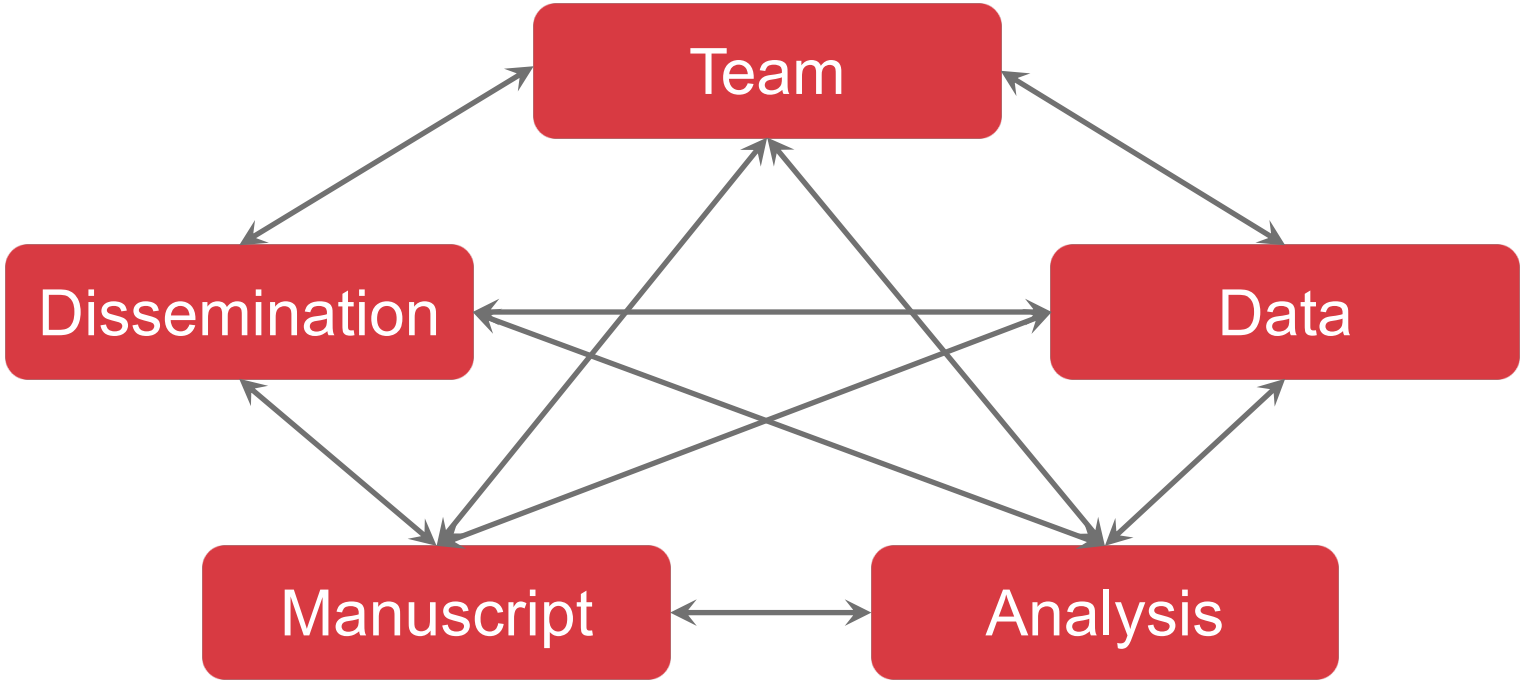
Reproducing the Research Workflow



Tools for reproducible research

Makefiles (Automation), Jupyter Notebook (Electronic Lab Notebook), Git (Source Control), StatTag, R Markdown (Dynamic Documents), Open Science Framework (Documentation)

Thinking Through the Process



Teams

- Who is on the team at any given time can change
  - “Hit by a bus” contingency plan
- Expertise, experience, and willingness to change can differ
  - Preferred tools, technologies, workflow
  - Reproducible research is a cultural change
- Collaboration is great, coordinated collaboration is better
  - Mutual understanding on use of reproducible research
  - Roles and responsibilities
  - Project file structure

Structuring Your Project

Having a central storage location and systematic file/path structure: (1) assists BCC faculty and staff who are collaborating on the same project; (2) protects against transitions in a project team; and (3) provides a long term record of work provided to investigators.

Location:

BCC Project Folders should reside in the following location:

- \\fsmresfiles.fsm.northwestern.edu\fsmresfiles\PrevMed\Projects\BCC\Projects

Project Folder Naming Convention:

Within the above folder, the Project Folder should follow this naming convention:

PILastNameFirstInitial_REDCap Project Number

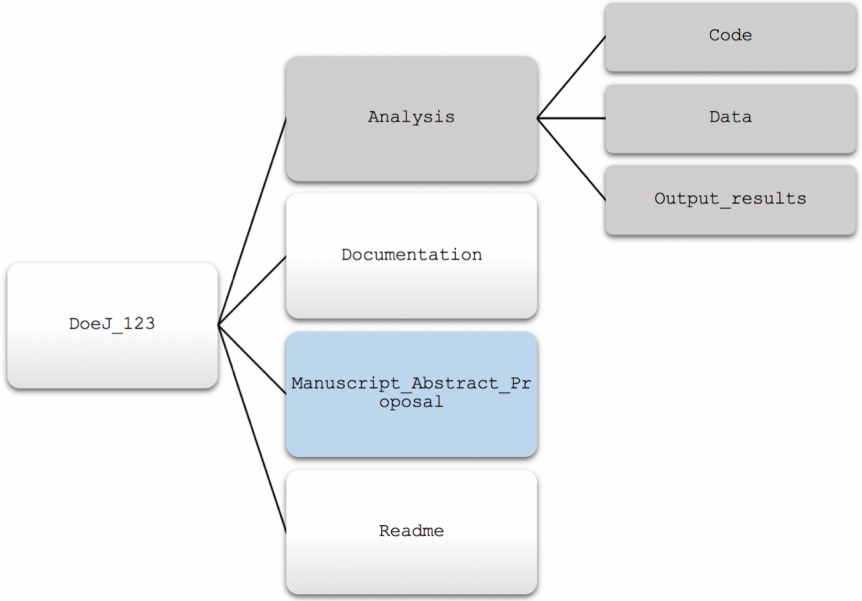
Example: For PI Jane Doe, and REDCap Project Number 123, the file name should be DoeJ_123

- The folder name does not include the project description - this avoids lengthy path/folder names. Project descriptions can be found in the Readme subfolder.
- Do not include leading zeros in the Project Number.

The diagram which follows illustrates the recommended folder structure and substructure. Additional folders may certainly be added as needed.

Date Requirements for Code/Programs/Manuscripts

Code/programs/manuscript files should include date information either inside the programs or as part of the file names. The code header should also include at the minimum the authors' names and the date last updated.



Northwestern Biostatistics Collaborative Core
L. Welty, personal communication, March 21, 2019

Data

- Sensitivity of the data will impact how you approach reproducible research
  - PHI
  - Institutional policies on data handling
  - Considerations for dissemination
- Technology for collecting and storing your data
  - Who can access it?
  - How is it accessed?
    - Flat file export
    - Real-time query / API call

Data Sensitivity
Additional Reference(s):
* NUIT Data Access Policy
** HIPAA Privacy Protected Health Information
*** HIPAA Privacy Limited Data Sets (LDS)

3) Identify the level(s) of data sensitivity that will be collected/maintained during the research. Example categories of sensitivity include HIPAA PHI and/or non-PHI personally identifiable information (PII) <select one or more options>:

_____*Legally/Contractually Restricted (FERPA, Illinois Personal Information Protection Act) Information**

_____*NU Internal Information (see NUIT Data Access Policy*)*

_____*Protected Health Information (HIPAA defined**)*

_____*LDS as a subset of Protected Health Information****

_____*De-identified information***

_____*Public Information**

_____*Other <please explain>*

Source: Northwestern University Feinberg School of Medicine, Central IT Data Security Plan Template v1.4

Data

- Public data sets need consideration too
  - You may not be able to redistribute, but can give instructions on accessing
  - Structure analysis pipeline with a placeholder for the data
- Is the data source changing?
  - e.g., EHR, surveys
- Accessing data in the future
  - Is the data set versioned?
- What version of data did I use?
- How do you know it's the same?
  - Checksum (e.g., MD5 hash)

https://mimic.physionet.org/gettingstarted/access/

Summary

Teams

- Variation – who is on the team at any given time
- Willingness to try reproducible research
  - Even on a large team, you can still make your work reproducible!
  - Project structure may be a place to start

Data

- Variation – what is in the data at any given time
- Consider licenses, agreements, and regulations in storage and sharing
- How can I be reasonably sure each time my data is the “same”?

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Exercise: Applying the Concepts to Your Project

Team and Data

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Use Case – EHR-Based Phenotyping (Part 1)

Technologies we will touch on:

- **Electronic lab notebooks (Jupyter Notebooks)**

Use Case Overview

You want to implement a Type 2 Diabetes Mellitus phenotype at your institution.

Your plan is to approach this in as reproducible a way as you can.

Use Case - The Team & Work

1) Data Warehouse Team
   - Data extraction experts

2) Ontologist
   - Medical terminology expert

3) Data Analyst – focus on phenotyping
   - Loves Python

4) Data Analyst 2 – focus on statistics
   - Loves R

5) Physician – PI
   - Medical expert, but largely non-technical

➡ ***Generate patient data***

➡ ***Map source data to required target standard(s)***

➡ ***Implement phenotype algorithm***

➡ ***Analyze phenotype results***

➡ ***Author paper***

The Tools

1) Data set provided by source system
    1) Synthetic patients generated by MITRE Synthea
2) Data set modified (cleaned)
    1) Mapped from SNOMED CT to ICD-9 where required using UMLS and Python
3) Data set processed (phenotype)
    1) Jupyter Notebook
4) Phenotype-annotated data analyzed
    1) R / R Markdown
5) Paper authored
    1) Microsoft Word

The Tools

1) Data set provided by source system → ***patient_data/*.csv***
    1) Synthetic patients generated by MITRE Synthea
2) Data set modified (cleaned) → ***1_generate_dx_terms.py*** *(UMLS not provided)*
    1) Mapped from SNOMED CT to ICD-9 where required using UMLS and Python
3) Data set processed (phenotype) → ***2_process_algorithm.ipynb***
    1) Jupyter Notebook
4) Phenotype-annotated data analyzed → ***synthea_analysis.rmd***
    1) R / R Markdown
5) Paper authored → ***synthea_paper.docx***
    1) Microsoft Word

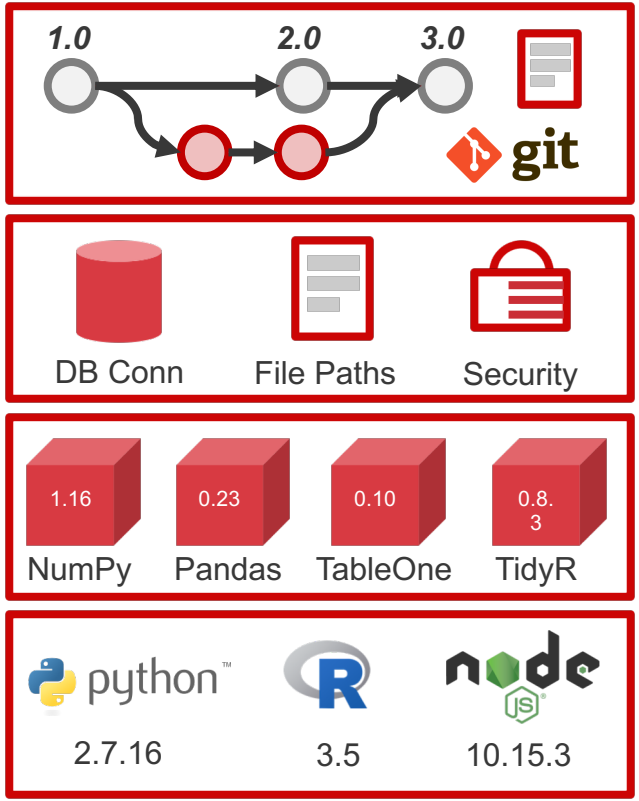
Analysis

Think of your work as a series of **variables**

+ Source code revision
+ System / application / user configuration
+ Module / package versions
+ Language / framework versions

The variables are **combined** to create a single overall computation pipeline

A change to even a *single* variable can influence reproducibility



The Effects of FreeSurfer Version, Workstation Type, and Macintosh Operating System Version on Anatomical Volume and Cortical Thickness Measurements

Ed H. B. M. Gronenschild, Petra Habets, Heidi I. L. Jacobs, Ron Mengelers, Nico Rozendaal, Jim van Os, Machteld Marcelis

Published: June 1, 2012 • https://doi.org/10.1371/journal.pone.0038234

Abstract

FreeSurfer is a popular software package to measure cortical thickness and volume of neuroanatomical structures. However, little if any is known about measurement reliability across various data processing conditions. Using a set of 30 anatomical T1-weighted 3T MRI scans, we investigated the effects of data processing variables such as FreeSurfer version (v4.3.1, v4.5.0, and v5.0.0), workstation (Macintosh and Hewlett-Packard), and Macintosh operating system version (OSX 10.5 and OSX 10.6). Significant differences were revealed between FreeSurfer version v5.0.0 and the two earlier versions. These differences were on average 8.8±6.6% (range 1.3–64.0%) (volume) and 2.8±1.3% (1.1–7.7%) (cortical thickness). About a factor two smaller differences were detected between Macintosh and Hewlett-Packard workstations and between OSX 10.5 and OSX 10.6. The observed differences are similar in magnitude as effect sizes reported in accuracy evaluations and neurodegenerative studies.

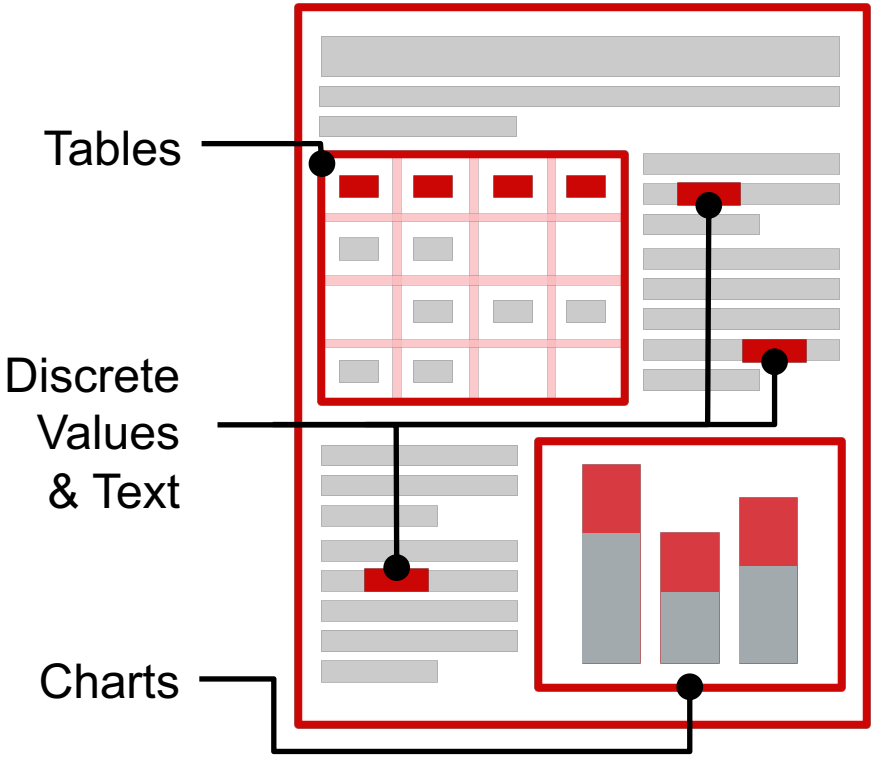
The main conclusion is that in the context of an ongoing study, users are discouraged to update to a new major release of either FreeSurfer or operating system or to switch to a different type of workstation without repeating the analysis; results thus give a quantitative support to successive recommendations stated by FreeSurfer developers over the years. Moreover, in view of the large and significant cross-version differences, it is concluded that formal assessment of the accuracy of FreeSurfer is desirable.

Lab Notebook Platforms

"Weave" code chunks and text into a dynamic document

jupyter & rmarkdown

These tools provide an interactive environment that allows you to run multiple languages in a single session – with several forms of visual output

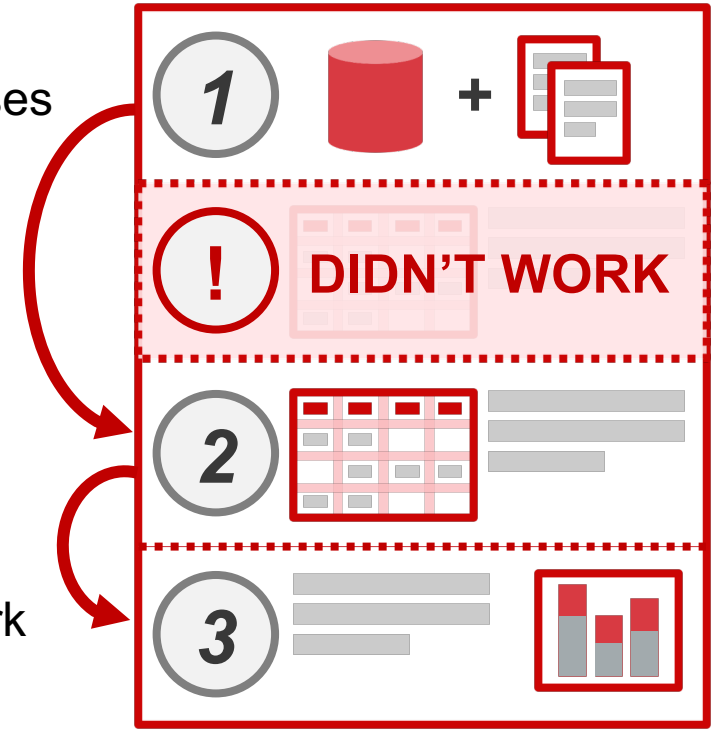


Lab Notebook Platforms

Acts as a Process Pipeline
- Automates & consolidates discrete processes
- Easy to review – highly visual

Shows Provenance
- Trace your work
- See unsuccessful paths
- Trace the ultimate right path

Supports Exploration and Creativity
- Interactive – feedback for faster, easier work
- Doesn't mandate "perfection" – keep *everything* - that's part of the value



Demo

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Exercise: Applying the Concepts to Your Project

Analysis

Break

We will start up again at 10:30

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Use Case – EHR-Based Phenotyping (Part 2)

Technologies we will touch on:

- **R / R Markdown**
- **StatTag**

Manuscripts

- Copy / Paste to bring results into paper
  - Easy to do
  - Time consuming & error prone
- “Weaving” approach can be extended beyond notes to manuscripts
  - Develop code specific to what you need in the manuscript

Dynamic Documents: R Markdown

NHANES Example.Rmd

Knit

```
---
title: 'Association of Education with Anthropometrics in US Adults: National H
  and Nutrition Examination Study 2013-2014'
geometry: margin=.75in
output: html_document
sansfont: Calibri Light
fontsize: 11pt
---

<style type="text/css">
h1.title {
  font-size: 11pt;
  font-weight: bold;
}
</style>

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = FALSE)
setwd("R:/NUCATS/NUCATS_Shared/BERDShared/Analysis Manager/Data and Programs/R
analysis<-read.csv("Analysis.csv")
attach(analysis)
library(tableone)
library(knitr)
options(digits=2)
```

\usepackage[utf8]

Introduction: Education level has been shown to be associated with body ma
metabolic characteristics may alter this association.

Methods: This study included adult ($\geq$ 30 years) participants from the
Examination Study (NHANES). Education and demographic information were assesse
measurements were taken by study personnel. Education was dichotomized based o
Associations were estimated using T-tests or Wilcoxon rank sum tests for conti
data. We examined the association between BMI and education level using multiv

```{r, echo=FALSE}
ps<- table(analysis$PostSecondary)
percents<-100*prop.table(ps)
model <- lm(BMXBMI ~ PostSecondary, data = analysis)
BetaUnivariable <- summary(model)$coefficients[2, 1]
LBUnivariable <- (summary(model)$coefficients[2, 1]) - 1.96 * (summary(model)$
UBUnivariable <- (summary(model)$coefficients[2, 1]) + 1.96 * (summary(model)$
myVars <- c("Gender", "Race", "RIDAGEYR", "Married", "BMXBMI", "LBXTC", "LBXGL
TableOne <- CreateTableOne(data = analysis, vars=myVars, strata= "PostSecondar
```

Association of Education with Anthropometrics in US Adults: National Health and Nutrition Examination Study 2013-2014

Introduction: Education level has been shown to be associated with body mass index (BMI). Gender, race, marital status and metabolic characteristics may alter this association.

Methods: This study included adult (≥ 30 years) participants from the 2013-2014 National Health and Nutrition Examination Study (NHANES). Education and demographic information were assessed by questionnaire and anthropometric measurements were taken by study personnel. Education was dichotomized based on matriculation to post-secondary education. Associations were estimated using T-tests or Wilcoxon rank sum tests for continuous data and chi-squared tests for categorical data. We examined the association between BMI and education level using multivariate linear regression.

Results: Among 4808 participants, 2649 (55.1%) self-reported any post-secondary education. Post-secondary education was associated with lower BMI (Beta: -0.62, 95% CI: -1.03 to -0.21). After adjusting for gender, race, age, marital status, fasting glucose and total cholesterol, post-secondary education was no longer significantly associated with BMI (Beta: -0.19, 95% CI: -0.79 to 0.41).

Table 1. Association of Education with Participant Characteristics among 2013-2014 NHANES Participants

	No Postsecondary	Postsecondary	p
n	2159	2649	
Gender = Male (%)	1079 (50.0)	1208 (45.6)	0.003
Race (%)			<0.001
Mexican American	456 (21.1)	173 (6.5)	
Non-Hispanic Asia	161 (7.5)	411 (15.5)	
```

Demo

Dynamic Documents: R Markdown

NHANES Example.Rmd

Knit

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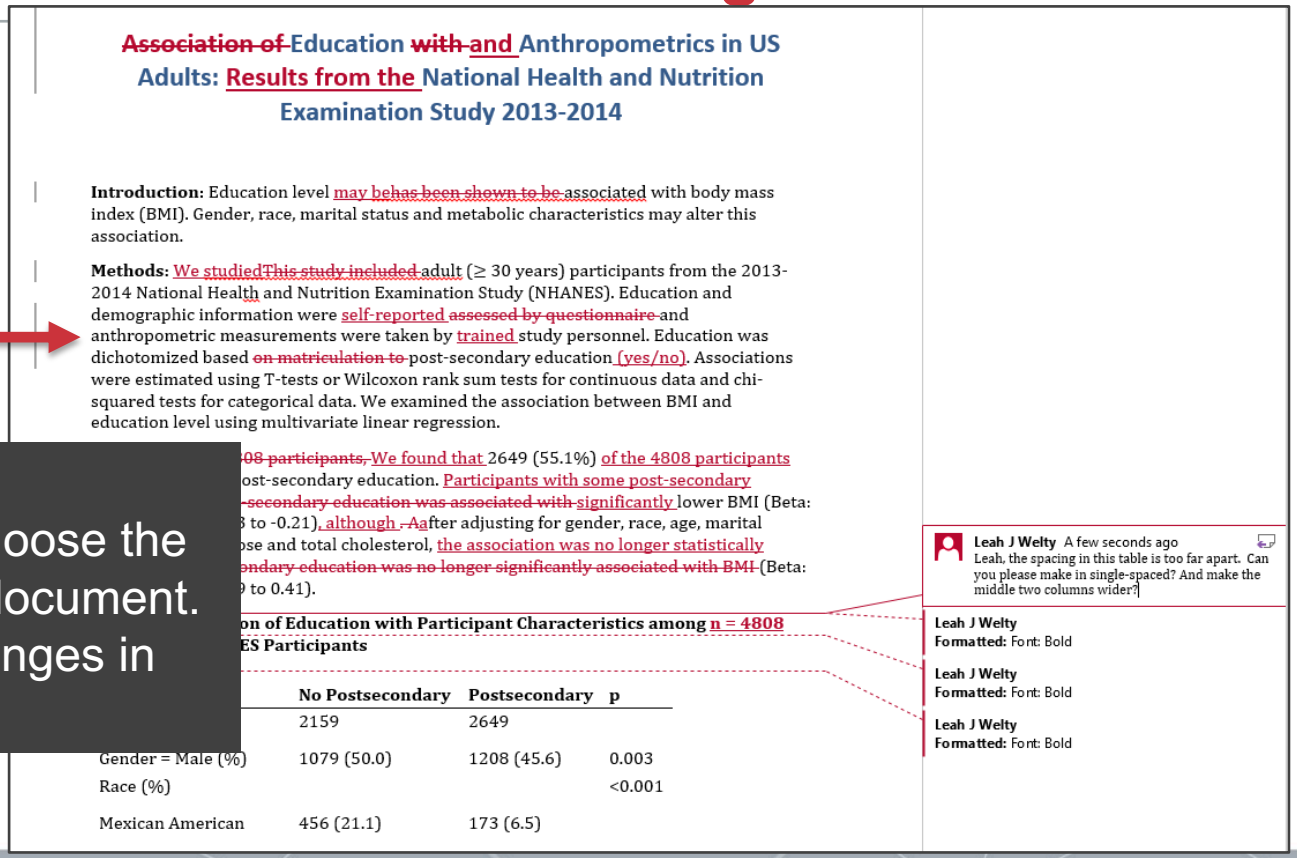
Do you have non-technical collaborators who are willing to work this way? Think of a clinical expert working on a phenotype algorithm paper.

Dynamic Documents and Track Changes

I create a dynamic document, generate the Word file and send it to collaborators.

They send back this

I have two choices:
1. Continue in Word, and loose the dynamic nature of the document.
2. Re-enter all of their changes in my source file.



~~Association of~~ Education ~~with~~ and Anthropometrics in US Adults: Results from the National Health and Nutrition Examination Study 2013-2014

Introduction: Education level may ~~be~~has been shown to be associated with body mass index (BMI). Gender, race, marital status and metabolic characteristics may alter this association.

Methods: We studied~~This study included~~ adult (≥ 30 years) participants from the 2013-2014 National Health and Nutrition Examination Study (NHANES). Education and demographic information were self-reported ~~assessed by questionnaire~~ and anthropometric measurements were taken by trained study personnel. Education was dichotomized based ~~on matriculation to~~ post-secondary education (yes/no). Associations were estimated using T-tests or Wilcoxon rank sum tests for continuous data and chi-squared tests for categorical data. We examined the association between BMI and education level using multivariate linear regression.

~~08 participants,~~ We found that 2649 (55.1%) of the 4808 participants ost-secondary education. Participants with some post-secondary ~~secondary education was associated with~~ significantly lower BMI (Beta: to -0.21), although ~~,Aa~~fter adjusting for gender, race, age, marital se and total cholesterol, the association was no longer statistically ~~ndary education was no longer significantly associated with BMI~~ (Beta: to 0.41).

on of Education with Participant Characteristics among n = 4808 ES Participants

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Mexican American	456 (21.1)	173 (6.5)	

Leah J Welty A few seconds ago
Leah, the spacing in this table is too far apart. Can you please make in single-spaced? And make the middle two columns wider?

Leah J Welty
Formatted: Font: Bold

Leah J Welty
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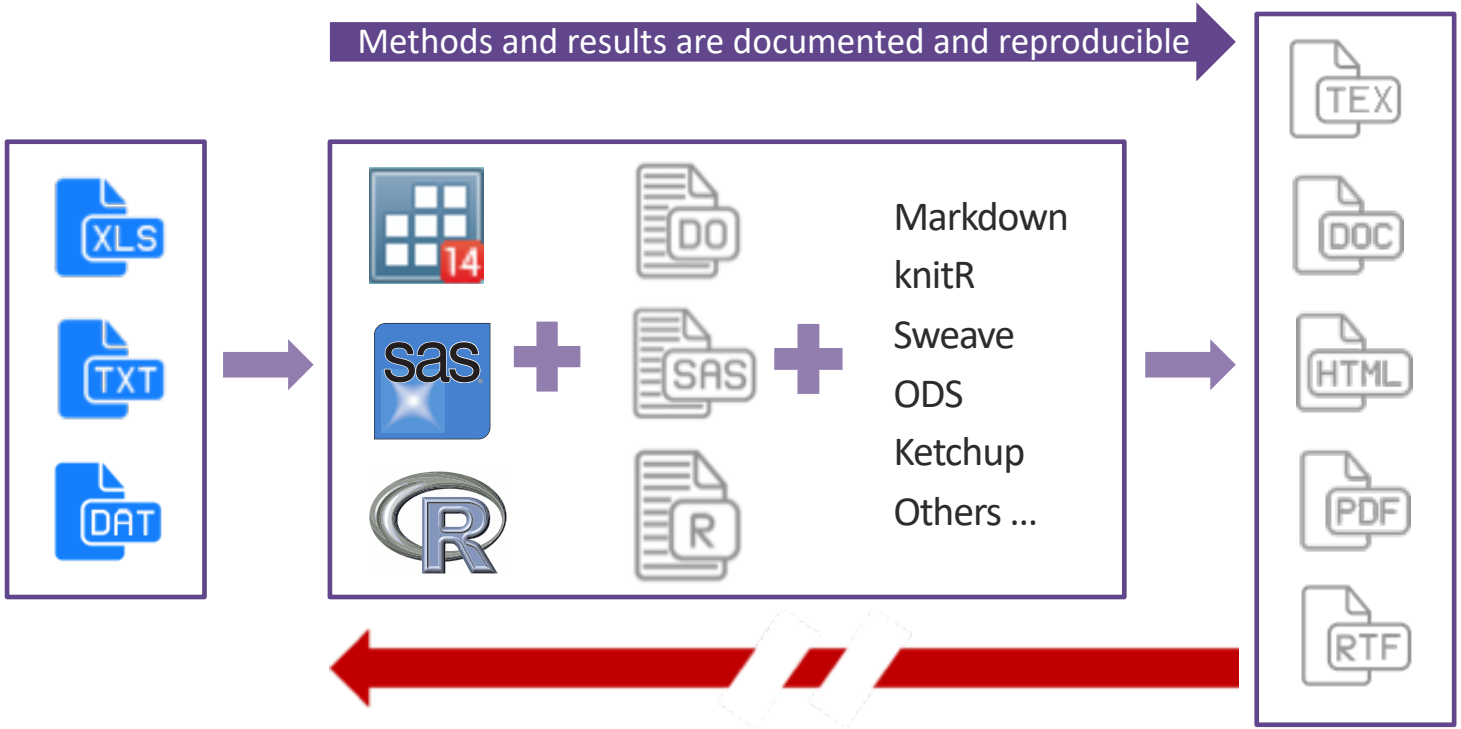
Leah J Welty
Formatted: Font: Bold

Limitations: Unidirectional Flow



Alternative Approach: StatTag

- StatTag creates a link between a statistical code file and a Word document
- Embeds output (values, tables, figures, verbatim) in document
- Can work separately on the code and the Word document but retain link
- Software agnostic: connects Stata, SAS or R code and Word document
- Can connect multiple code files (of different types) to the same document

http://stattag.org

Demo

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Exercise: Applying the Concepts to Your Project

Manuscript

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Use Case – EHR-Based Phenotyping (Part 3)

Technologies we will touch on:

- **Containers (Docker)**

Expanding to NLP

- Expand our phenotype to incorporate natural language processing
- Colleague has some Python 2 code that to calculate frequency distribution of top 50 words (“nltk-freq-dist”)
  - Very specific / curated set of stop words
- Sends you a ZIP containing the Python script and stop word list
- You try to run it on your machine (you’re using Python 3)

```
nltk-freq-dist $ python freq-dist.py
  File "freq-dist.py", line 12
    print "Usage: nltk-freq-dist input-dir/ output-dir/"
                                                       ^
SyntaxError: Missing parentheses in call to 'print'. Did you mean print("Usage:
nltk-freq-dist input-dir/ output-dir/")?
```

Finding the variation

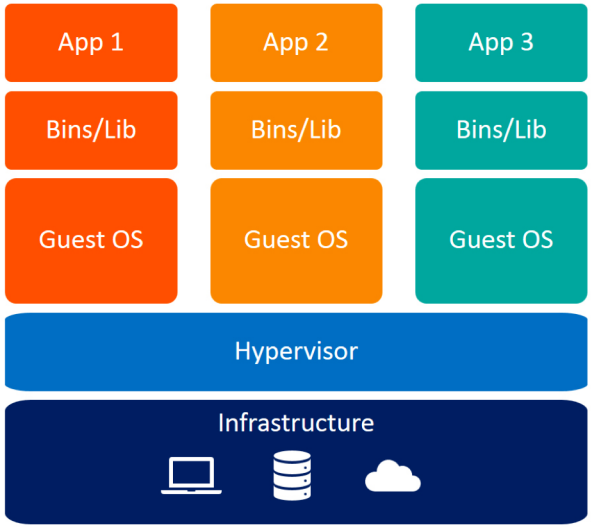
- Differences in Python versions
  - Does this mean you need to install Python 2?
  - Will that mess up any other programs running on your machine?
- How long will Python 2 be available to download?

```
DEPRECATION: Python 2.7 will reach the end of its life on January 1st, 2020. Please upgrade your Python as Python 2.7 won't be maintained after that date. A future version of pip will drop support for Python 2.7.
```

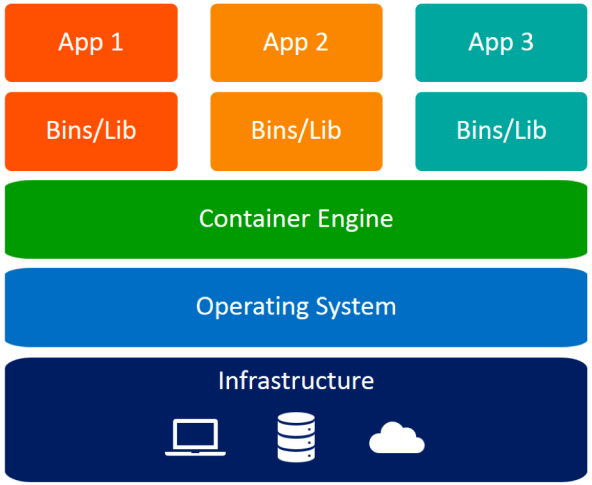
- Same considerations for the underlying dependencies / modules
  - NLTK (https://www.nltk.org/)
- We want to have a snapshot of the environment

Virtual Machines and Containers

Abstractions of physical hardware



Virtual Machines



Containers

Abstractions of software

Source: https://www.bmc.com/blogs/containers-vs-virtual-machines/

Building a Docker image

- The Docker **image** is the actual snapshot of the stack (immutable)
- A running instance of the image is a Docker **container**
  - Mutable when running, but not stateful

- We want to have an image for the program that we can keep and share
- We can't store any of the data in the image – need data to come in
- We want to save the results of the processing – need to preserve state

Collecting the Pieces

nltk-freq-dist	Our source code
NLTK 3.3	Library used by source code
Python 2.7	Language interpreter
Linux	Operating system

Docker image layer cake

For our image, we start with our base, then “do stuff” to add our software and dependencies. When done, it’s a static snapshot of the environment.

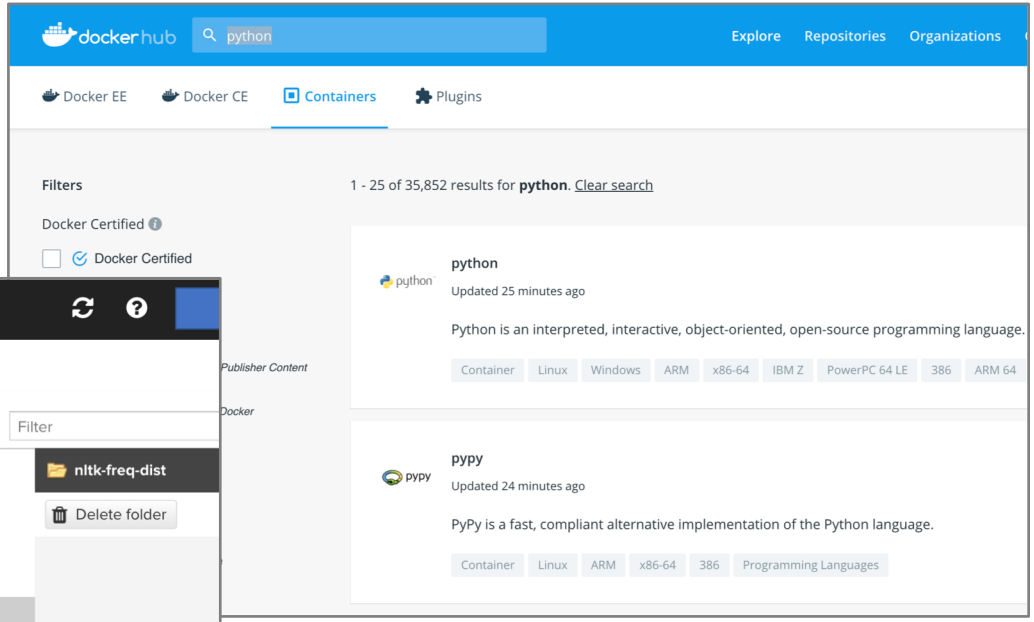
We’ve started with the Python 2.7.16 image as our base. It has the Apline Linux image as its base

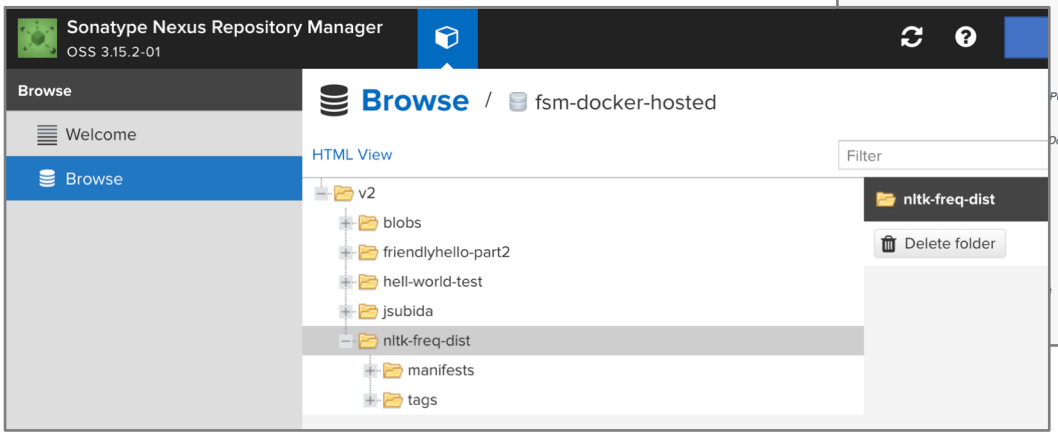
We aren’t particular about the exact OS in this case. We just need it to be consistent.

Demo

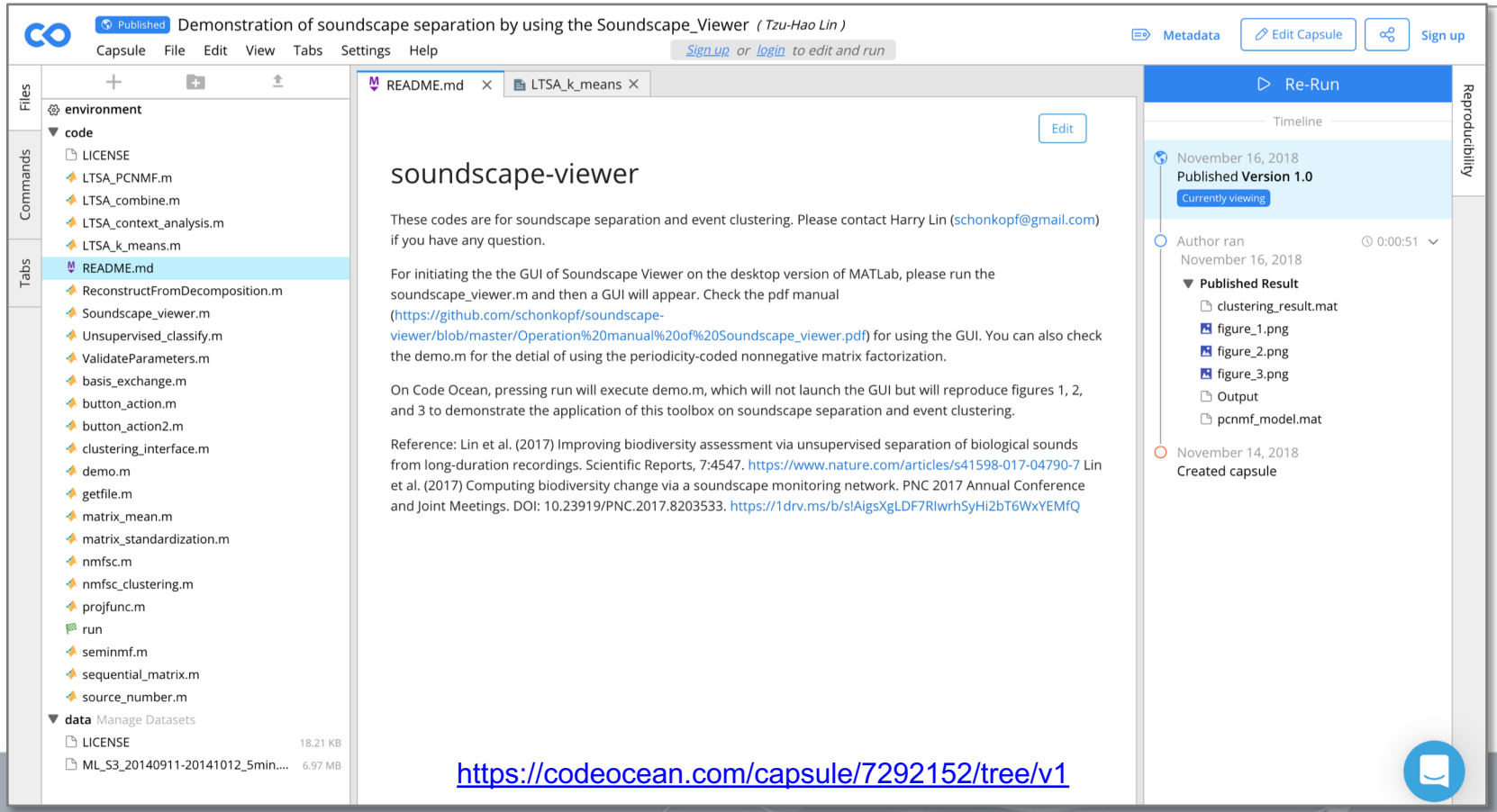
Making Images Available

- Docker Hub - https://hub.docker.com/
  - Public or private
- Internally hosted repos
- Your machine



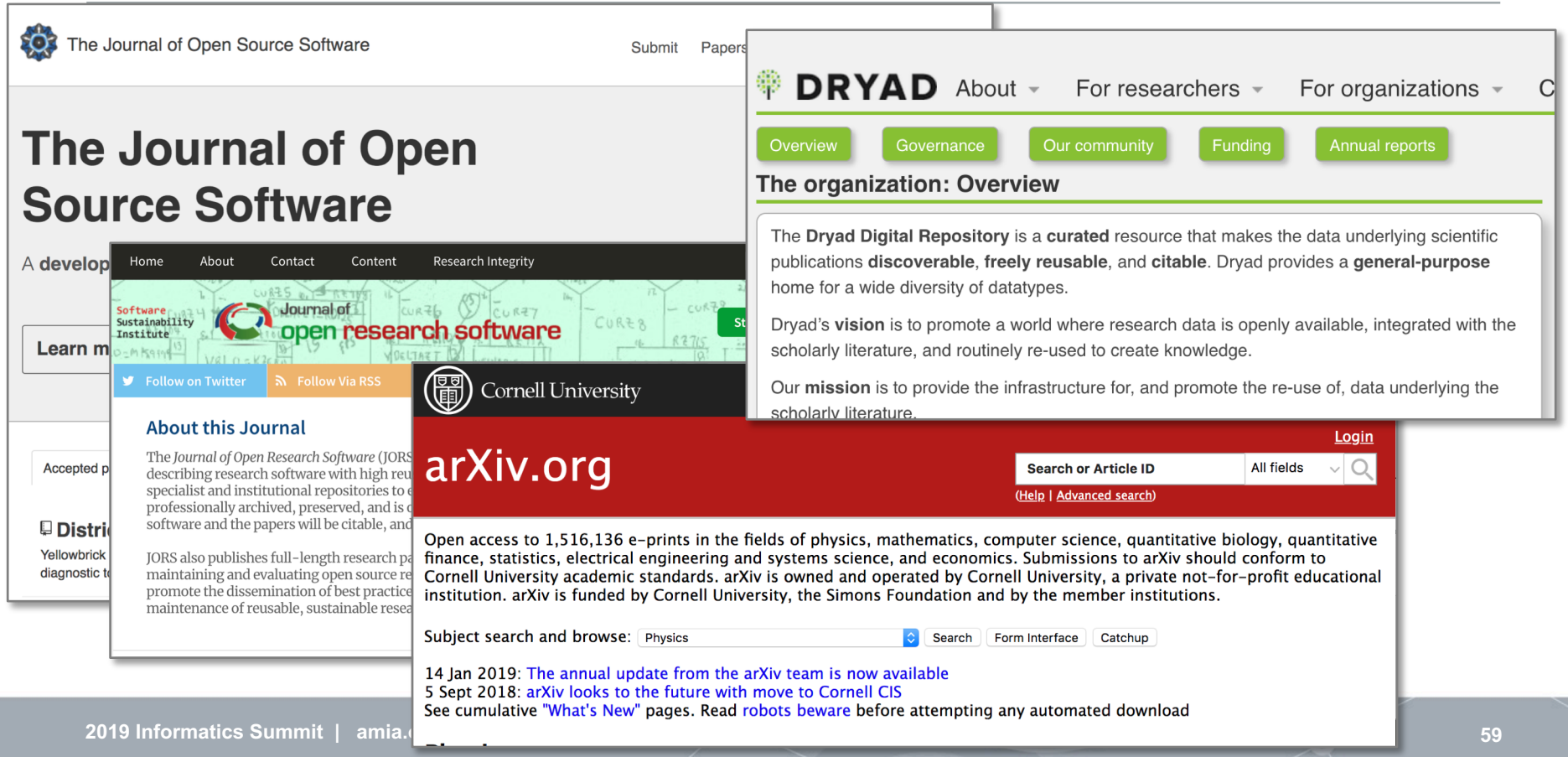


Cloud-Based Solutions



https://codeocean.com/capsule/7292152/tree/v1

Publishing Options



Summary

- Focus on “How I am going to make this available”
- Consider who you want to be able to access this work
  - Just you
  - Internal project team
  - Public
- Think about what you are allowed to share directly
  - Pointers in documentation for things you can’t

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Dissemination

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Wrap-Up

Building on Pragmatism

Focus today was on small steps to get started

Many guides to explore with expanded definitions of reproducible research

- Bakken S. The journey to transparency, reproducibility, and replicability. JAMIA, 26(3) 185-187. https://doi.org/10.1093/jamia/ocz007
- McIntosh LD, et al. Repeat: a framework to assess empirical reproducibility in biomedical research. BMC Medical Research Methodology. 201717:143. https://doi.org/10.1186/s12874-017-0377-6 https://github.com/ripeta/Research_Reproducibility

Continue the Momentum

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

– *Keith Baggerly*

AMIA Workshop Attendee Surveys

AMIA (and ultimately you) benefits from hearing what you thought of this workshop.

If you loved it, hated it, or are even just 'meh', please take a few minutes to fill out the survey when you get it.

Thank you!

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Eric Whitley
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Resources

- Karl Broman – Initial Steps Toward Reproducible Research (https://kbroman.org/steps2rr/)
- Victoria Stodden – Enabling Reproducible Research: Open Licensing for Scientific Innovation (March 3, 2009). International Journal of Communications Law and Policy, Forthcoming. Available at SSRN: https://ssrn.com/abstract=1362040
- Carl Boettiger - An introduction to Docker for reproducible research, with examples from the R environment. (2015) ACM SIGOPS Operating Systems Review, Special Issue on Repeatability and Sharing of Experimental Artifacts. 49(1), 71-79. DOI: 10.1145/2723872.2723882. arXiv:1410.0846 [cs.SE]
- Jeffrey Leek & Richard Peng - Opinion: Reproducible research can still be wrong: Adopting a prevention approach. PNAS February 10, 2015 112 (6) 1645-1646; https://doi.org/10.1073/pnas.1421412111
- Suzanne Bakken - The journey to transparency, reproducibility, and replicability. JAMIA, 26(3) 185-187. https://doi.org/10.1093/jamia/ocz007
- Leslie McIntosh et al., Repeat: a framework to assess empirical reproducibility in biomedical research. BMC Medical Research Methodology. 201717:143. https://doi.org/10.1186/s12874-017-0377-6
- Enrico Coiera et al. Does health informatics have a replication crisis? Journal of the American Medical Informatics Association, Volume 25, Issue 8, 1 August 2018, Pages 963–968, https://doi.org/10.1093/jamia/ocy028

Resources

- Anaconda (https://www.anaconda.com/distribution/)
- Code Ocean (https://codeocean.com/)
- Docker (https://www.docker.com/)
- Dryad (https://datadryad.org/)
- Jupyter Notebook (https://jupyter.org)
- NLM UMLS (https://uts.nlm.nih.gov)
- Natural Language Toolkit (https://www.nltk.org/)
- Python (https://www.python.org)
- R (https://www.r-project.org)
- R Markdown (https://rmarkdown.rstudio.com)
- StatTag (http://stattag.org)