Building a Reproducible Data Analysis Pipeline

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WestGrid Summer School - June 18, 2020

Outline

Background

Key Concepts (theory and code examples)

- Sharing code online
- Writing good documentation
- Code dependencies (Python)
- Reproducing runtime environments (Docker)

Conclusion



Computational Biologist

(Genome Sciences Centre)

- Developing pipelines for tumour characterization
- Work mostly Python, R, CWL, Docker

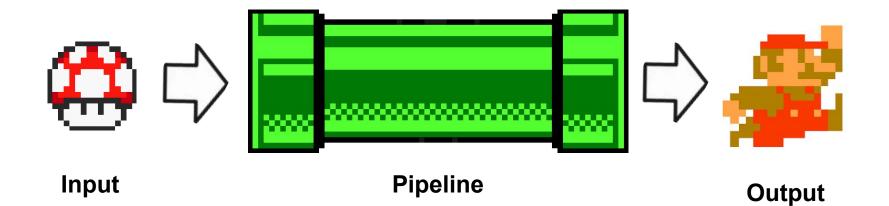
Background in Bio

- B.Sc. Microbiology (University of Victoria)
- M.Sc. Bioinformatics (Simon Fraser University)



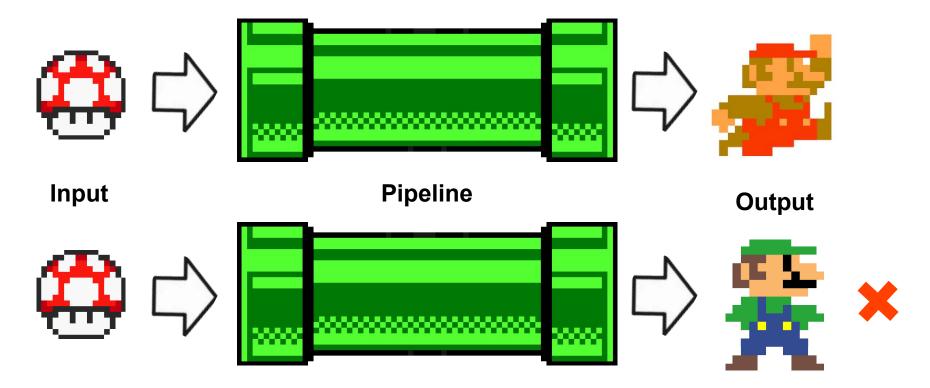


A Data Analysis Pipeline





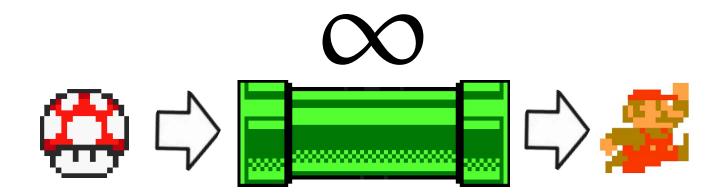
A Data Analysis Pipeline





Reproducibility

obtaining consistent results using the same input data; computational steps/methods/code; and conditions of analysis.

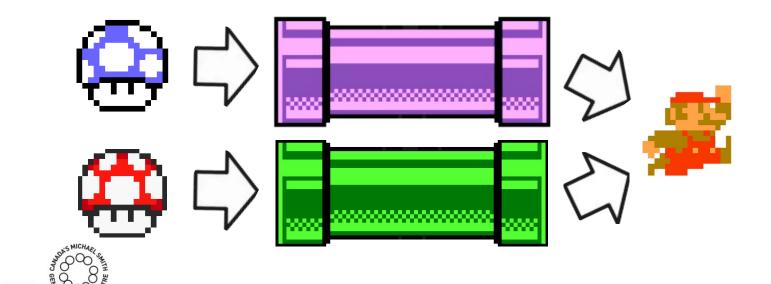




Reproducibility vs. Replicability

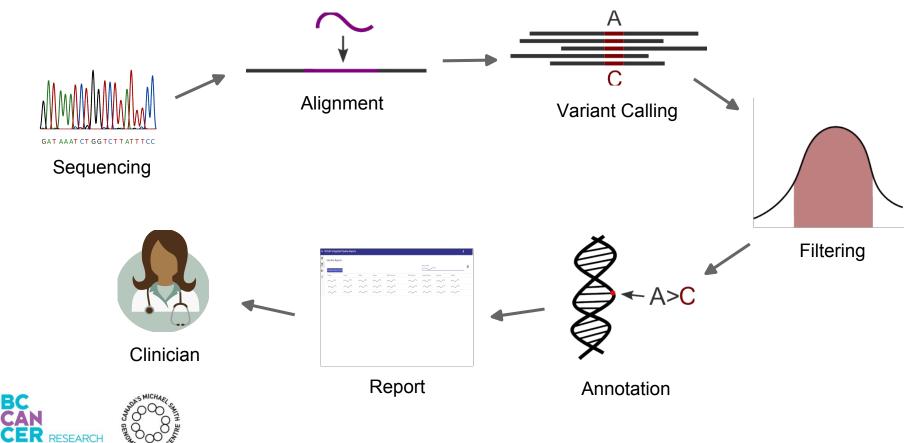
Replicability (Repeatability)

obtaining consistent results using different input data; computational steps/methods/code; or conditions of analysis.



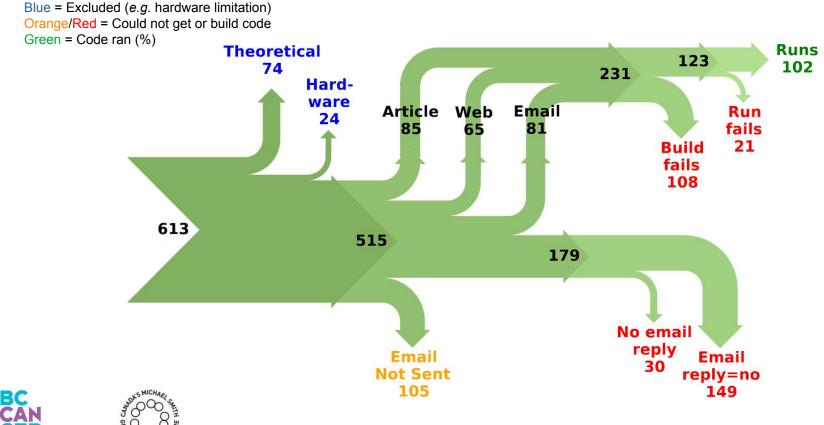
Example Pipeline

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Reproducibility in Data Science

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Most pipelines are built based on good science.

A failure to reproduce a result is often due to how the pipeline is packaged/shared.



Reproducible Pipeline Checklist

Code is available

Good documentation

Dependencies are listed

Runtime environment can be reproduced

The first step in reproducing a bioinformatics result is to obtain the code used to produce the result.



Source Code









Source Code (Human readable)



Binary (Machine readable)





Source Code

```
block = TranslationBlock()
last = i[0][0]
count += 1
for pos, kind in sort_by_type(i[1:]):
    if kind == 0: # if start codon
        block.s_sites.append(pos)
    elif kind == 1: # left splice site
        block.r_sites.append(pos)
    elif kind == 2: # right splice site
        block.l_sites.append(pos)
    elif kind == 3: # if stop codons
        block.start = last + 1
        block.end = pos
        if block.has_splice_site():
            blocks_f[chrom][frame].append(block)
        else:
            empty_blocks_f[chrom][frame].append(block)
            empty_blk += 1
```

Human readable

- Verify
- Improve
- Modify



Machine readable

- Not human readable
- Cannot be verified

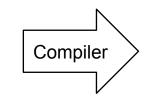
("Black box")

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Binary



```
block = TranslationBlock()
last = i[0][0]
count += 1
for pos, kind in sort_by_type(i[1:]):
    if kind == 0: # if start codon
        block.s_sites.append(pos)
```



00000000	01	00	FF	F.F.	UU	00	00	00	UU	00	UU	00	40	00	CC	80	
00000010	0C	00	00	00	00	00	26	01	8F	00	00	00	00	00	53	00	
00000020	65	00	6C	00	65	00	63	00	74	00	20	00	52	00	75	00	
00000030	6C	00	65	00	00	00	08	00	00	00	00	01	4D	00	53	00	
00000040	20	00	53	00	68	00	65	00	60	00	6C	00	20	00	44	00	
00000050	6C	00	67	00	00	00	00	00	00	00	00	00	00	02	00	00	
00000060	03	01	A1	50	53	00	3A	00	C3	00	36	00	32	25	00	00	
00000070	FF	FF	83	00	00	00	00	00	00	00	00	00	00	00	00	00	
00000080	03	00	01	50	0E	00	56	00	41	. 00	ΟÀ	00	4A	26	00	00	
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Source code

- Need to compile before use*
- May require additional code libraries

*except 'interpreted languages' like Python

Binary

- "Ready to run"
- No need to compile before use
- However, it is limited to the operating system it was compiled for



What form of code should I share with others?





Source Code

- Can be independently verified
- Can be collaborated on
- **K** Less user friendly

Binary Convenient **X** "Black box" *what is the negative of a black box?



How do I share my code with others?

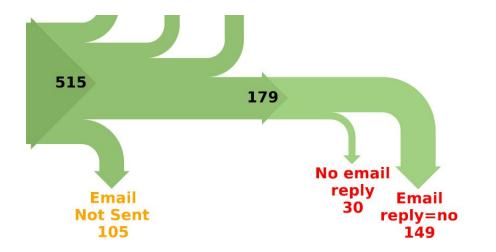


Obtaining Unpublished Code

From: Christian Collberg <ccollberg@gmail.com> first-or-corresponding-author To: Cc: remaining-authors Subject: Your conference-name paper Dear Dr. first-or-corresponding-author, conference-name I've been looking at your paper paper-title and would like to try out the implementation. However, I haven't been able to find it online. Would you please let me know how I can obtain the source code so that I can try to build and run it? Thank you very much for your help! Christian Collberg ccollberg@gmail.com



Obtaining Unpublished Code



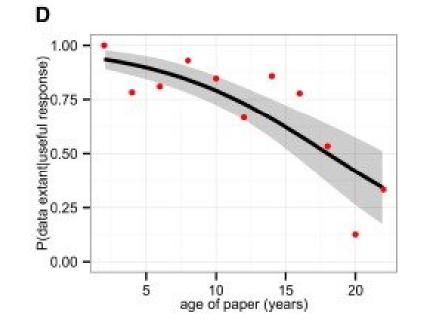
C. Collberg, et al. Measuring Reproducibility in Computer Systems Research. (2014)

- Data gets lost
- Programmer left
- Will be released soon
- No intention to share
- Proprietary
- Will not work outside of <very specific system>
- Broken email addresses



Self-hosted code becomes less available over time.

"Overall, we only received 19.5% [101/512] of the requested data sets..." (Vines, *et al.* 2014)





Vines, T.H., *et al.* The Availability of Research Data Declines Rapidly with Article Age. *Current Biology* **24**, 94-97 (2014).

Public Code Repositories - Version Controlled



Bitbucket

GitLab

- Git repositories (version control)
- Facilitates collaboration!
- Removes the burden of hosting
- Easy sharing



Public Code Repositories - Non-Version Controlled



- Hosting and sharing
- Not version controlled
- Not as easy to collaborate



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Grit is no longer maintained. Check out libgit2/rugged. Grit gives you object oriented read/write access to Git repositories via Ruby. http://grit.rubyforge.org/

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	Brandon Keepe	ers Merge pull request #183 from bke	epers/unmaintained			Late	st commit 5	608567 on Feb 3, 2014	
	examples	Update from GitHub						10 years ago	
	🖿 lib	Fix Tempfile usage	under ruby 1.8.7					7 years ago	
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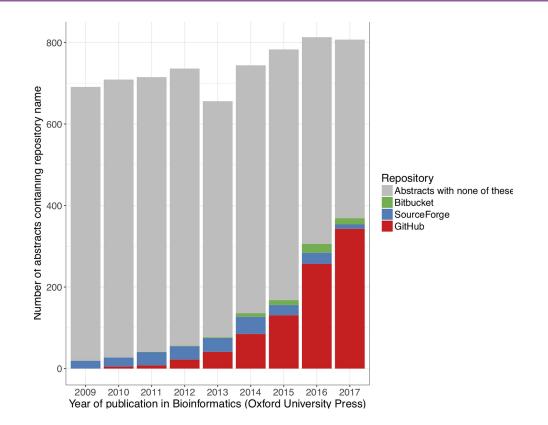
Sourc Code

How Common is Publishing Code?

Public repositories are more widespread in bioinformatics.

Exceptions:

- Not allowed to publish (licensing, *etc.*)
- Published on personal website





Publishing your code online...

- Makes it easy to share your code
- Improves the lifespan of your code
- Facilitates collaboration
- Sometimes required when publishing



Reproducible Pipeline Checklist

Code is available
Good documentation
Dependencies are listed
Runtime environment can be reproduced

You have an awesome pipeline.

How do I use it?



A **README** is a text file that explains your pipeline.

Who is it for?

- Others Explains to others how to install and run
- You Reflect on how the pipeline is structured



C README.md							
This Is	a Bad READM	E					
© 2020 GitHub, Inc. Terms	s Privacy Security Status Help	0	Contact GitHub	Pricing	API Training	Blog	About

	D README.md				
	build failing maven-central v4.1.7.0 license BSD 3-Clause				
	Please see the GATK website, where you can download a precompiled executable, read documentation, ask questions, and receive technical support. For GitHub basics, see here.				
Name	GATK 4				
Description	This repository contains the next generation of the Genome Analysis Toolkit (GATK). The contents of this repository are 100% open source and released under the BSD 3-Clause license (see LICENSE.TXT).				
	GATK4 aims to bring together well-established tools from the GATK and Picard codebases under a streamlined framework, and to enable selected tools to be run in a massively parallel way on local clusters or in the cloud using Apache Spark. It also contains many newly developed tools not present in earlier releases of the toolkit.				
	Table of Contents				
	Requirements				
	Quick Start Guide				
Instruction	Downloading GATK4				
	Building GATK4				
	Running GATK4				
	 Passing JVM options to gatk 				
	 Passing a configuration file to gatk 				
	 Running GATK4 with inputs on Google Cloud Storage 				
	 Running GATK4 Spark tools on a Spark cluster 				
	 Running GATK4 Spark tools on Google Cloud Dataproc 				
	◦ Using R to generate plots				

Name

- Makes your project easier to find
- Lets you be creative
- When in doubt: Acronyms

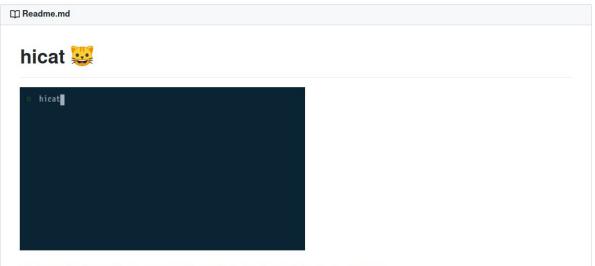
Tutorial On Reproducible Pipelines





Introduction

 A brief description of what your project does



cat with syntax highlighting. The language is auto-detected through the file extension.



How to Install

- All commands
- All dependencies

Installation

\$ npm install -g hicat



How to Use

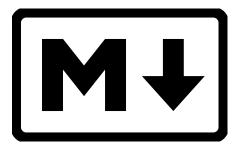
- Examples
- References explaining commands (if helpful)

	cat with syntax highlighting. The language is auto-detected through the file extension.
	hicat index.js
F	Pipe something to hicat. The language will be inferred from the contents.
	curl http://site.com hicat
I	f hicat fails to detect a language, specify it using -1 LANG .
	curl http://site.com hicat -l xml



READMEs are typically written in MarkDown

- Lightweight language for formatting text
- Files have a '.md' (MarkDown) extension
- Commonly seen in Github



MarkDown logo



(i) README.md \times

(1) README.md \times

This is a collection of code used as examples in my tutorial "Building a Reproducible Data Analysis Pipeline".

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 \blacksquare Preview README.md \times

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This is a collection of code used as examples in my tutorial "Building a Reproducible Data Analysis Pipeline".

(i) README.md \times

Reproducible Pipeline Tutorial

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Reproducible Pipeline Tutorial

■ Preview README.md ×

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Reproducible Pipeline Tutorial

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Dependencies

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Reproducible Pipeline Tutorial

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Dependencies

```
File Edit Selection View Go Run Terminal Help
```

(i) README.md \times

Reproducible Pipeline Tutorial

This is a collection of code used as examples in my tutorial "Building a Reproducible Data Analysis Pipeline".

Dependencies

Running the example script requires `python3`.

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Dependencies

Running the example script requires <code>python3</code>.

(i) README.md ×

Reproducible Pipeline Tutorial

This is a collection of code used as examples in my tutorial "Building a Reproducible Data Analysis Pipeline".

```
## Dependencies
```

```
Running the example script requires `python3`.
```

All the necessary Python dependencies can be installed by running:

pip install -r requirements.txt

12

Preview README.md ×

Reproducible Pipeline Tutorial

This is a collection of code used as examples in my tutorial "Building a Reproducible Data Analysis Pipeline".

Dependencies

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Reproducible Pipeline Tutorial

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```
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```

```
Running the example script requires `python3`.
```

9 All the necessary Python dependencies can be installed by running:

```
pip install -r requirements.txt
```

```
12
```

4

```
13
```

.4 The script can also be run inside a Docker container. Instructions on how to install Docker can be found [here](<u>https://docs.docker.</u> com/engine/install/).

15

Reproducible Pipeline Tutorial

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(i) README.md \times

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Dependencies

```
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```

All the necessary Python dependencies can be installed by running:

```
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```

```
12
```

4

```
12
```

The script can also be run inside a Docker container. Instructions on how to install Docker can be found [here] (<u>https://docs.docker.</u> <u>com/engine/install/</u>).

```
## Usage
```

```
Run the example script:
```

```
python3 pipeline.py
```

22 23 Run the example script inside a Docker container:

```
5 docker run mattdoug604/reprodcucible_tutorial
```

23

🖬 Preview README.md imes

Reproducible Pipeline Tutorial

This is a collection of code used as examples in my tutorial "Building a Reproducible Data Analysis Pipeline".

Dependencies

Running the example script requires python3.

All the necessary Python dependencies can be installed by running:

pip install -r requirements.txt

The script can also be run inside a Docker container. Instructions on how to install Docker can be found here.

Usage

Run the example script:

python3 pipeline.py

Run the example script inside a Docker container:

docker run mattdoug604/reprodcucible_tutorial

Documentation is key when writing any sort of software - both for you and others trying to reproduce a result.

A README is a short text file:

- Typically written in MarkDown
- What your project does
- How to install it
- How to run it



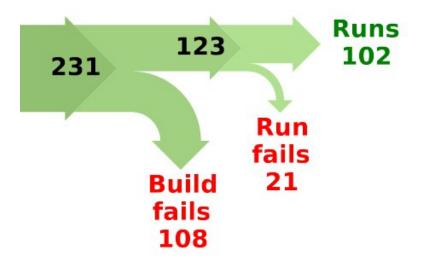
Reproducible Pipeline Checklist

Code is available
Good documentation
Dependencies are listed
Runtime environment can be reproduced

Why is it so Hard to Run Someone's Code?

Up to 50% of published code cannot be run (Collberg, *et al.* 2014).

The most common reason is that the build fails.



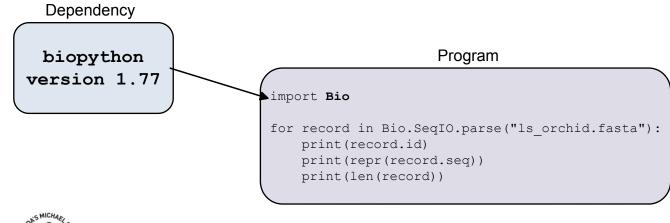
C. Collberg, *et al*. Measuring Reproducibility in Computer Systems Research. (2014)



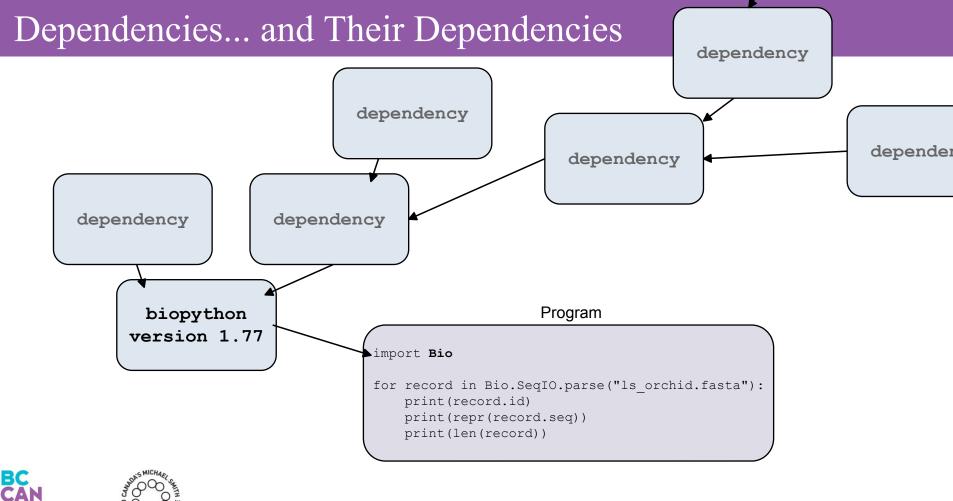
Dependencies...

Dependencies

- Code that is required by a different piece of code
- Often, a specific version of a dependency is required

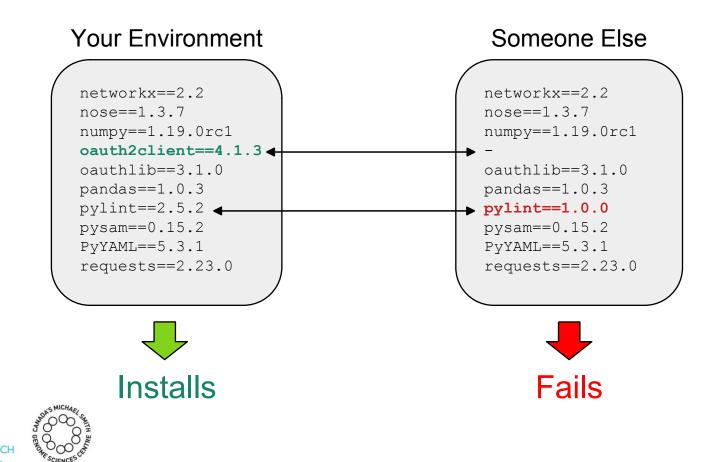






Provincial Health Services Authorit

Dependencies are the Main Cause of Failed Builds



venv

Python virtual environment

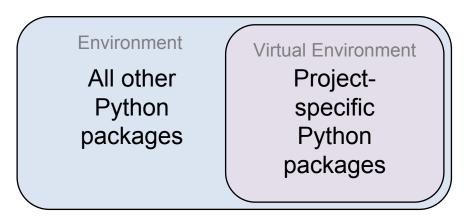
pip

• Python package manager



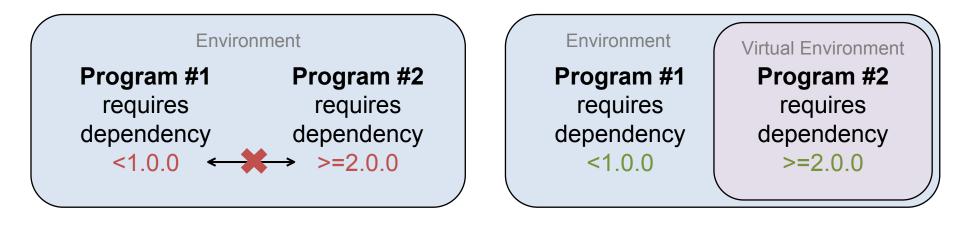
Python Virtual Environments

- Python environment specific to your project
- Libraries and scripts installed into it are isolated from other environments

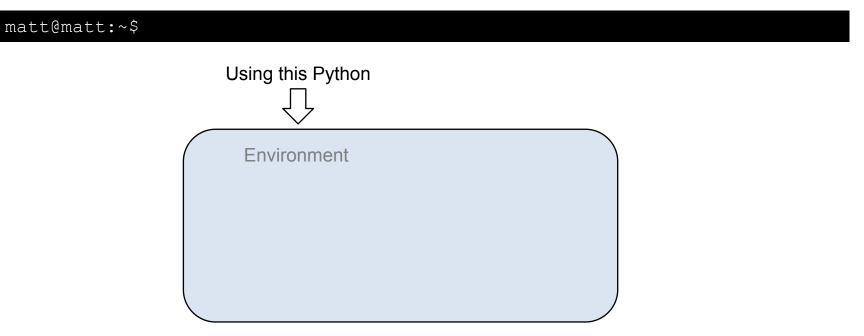




Solves the problem of "this program uses v1.x.x of a package but that program uses v2.x.x"

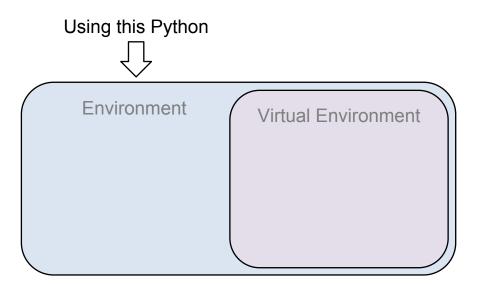






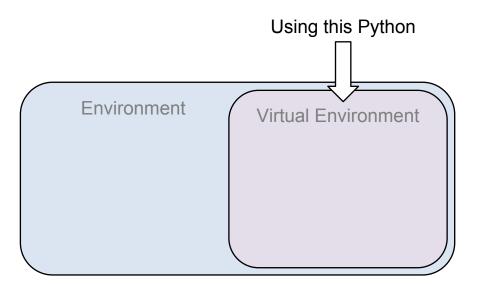


matt@matt:~\$ python3 -m venv my_venv



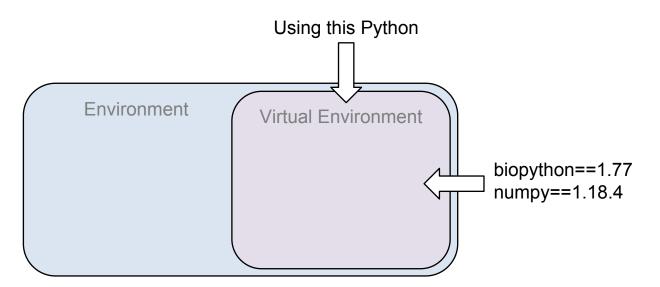


matt@matt:~\$ source my_venv/bin/activate



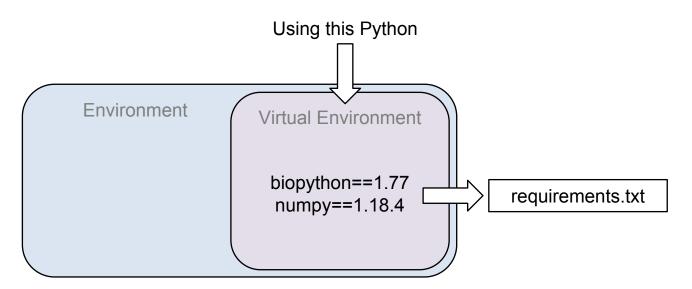


(my_venv) matt@matt:~\$ pip install biopython



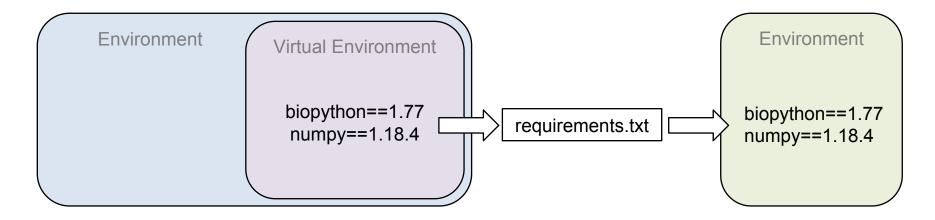


(my_venv) matt@matt:~\$ pip freeze > requirements.txt





(my_venv) matt@matt:~\$ pip install -r requirements.txt









Step 1) Create the virtual environment with the 'venv' python package.

matt@matt:~\$ python3 -m venv my_venv



Step 2) Activate the virtual environment.

matt@matt:~\$ python3 -m venv my_venv matt@matt:~\$ source my_venv/bin/activate (my venv) matt@matt:~\$ pip freeze # nothing prints



Step 3) Install Python dependencies.

matt@matt:~\$ python3 -m venv my_venv matt@matt:~\$ source my_venv/bin/activate (my_venv) matt@matt:~\$ pip freeze # nothing prints (my venv) matt@matt:~\$ pip install biopython



Step 4) List Python dependencies.

```
matt@matt:~$ python3 -m venv my_venv
matt@matt:~$ source my_venv/bin/activate
(my_venv) matt@matt:~$ pip freeze # nothing prints
(my_venv) matt@matt:~$ pip install biopython
(my_venv) matt@matt:~$ pip freeze > requirements.txt
(my_venv) matt@matt:~$ cat requirements.txt
biopython==1.77
numpy==1.18.4
```



Python dependencies can be installed with 'pip install'.

```
matt@matt:~$ python3 -m venv my_venv
matt@matt:~$ source my_venv/bin/activate
(my_venv) matt@matt:~$ pip freeze # nothing prints
(my_venv) matt@matt:~$ pip install biopython
(my_venv) matt@matt:~$ pip freeze > requirements.txt
(my_venv) matt@matt:~$ cat requirements.txt
biopython==1.77
numpy==1.18.4
```

matt@matt:~\$ pip install -r requirements.txt



Everyone should be running the same version of your code.

Dependencies are other pieces of code your software depends on.

Missing or incompatible dependencies prevent others from running your software.

Python dependencies can be managed using:

- 'venv' gives an isolated python environment
- 'pip freeze' lists all the python dependencies of your software



Reproducible Pipeline Checklist

Code is available
 Good documentation
 Dependencies are listed
 Runtime environment can be reproduced

What is a Runtime Environment?

- Operating system
- Environmental variables
- Common libraries
- Network
- Directory structure
- etc...

Everything you need to run a program.





Runtime Environment Can Affect Results

BARD1: P24S ERCC2:D312N PDGFRA:S478P BRCA1:S24P PMS2:P470S TP53:P72R

OS Upgrade

BARD1: P24S ERCC2:D312N PDGFRA:S478P KRAS:P102A PMS2:P470S TP53:P72R



Runtime Environment Can Affect Results

	CentOS 6				CentOS 7		
	Rank	Mutation	Score	Rank	Mutation	Score	
Threshold	98	TP53:P72R	23	98	TP53:P72R	23	
	99	ERCC2:D312N	22	99	ERCC2:D312N	22	
	100	BRCA1:S24P	20	, 100	KRAS:P102A	20	
	101	KRAS:P102A	20	101	BRCA1:S24P	20	
	102	PMS2:P470S	18	102	PMS2:P470S	18	
	103	BARD1:P24S	18	103	BARD1:P24S	18	



Managing Dependencies in Your Runtime Environment

- Able to install and run the pipeline in different runtime environments (different operating systems)
- However, we got inconsistent results between environments
- We cannot expect everyone to have the exact same runtime environment

How do we ensure our pipeline runs the same in any environment?



Containers

Container

- A package of one or more applications and <u>all</u> dependencies
- The environment is isolated from the host OS/infrastructure
- Extremely portable

Docker or Singularity

• An application for running containers

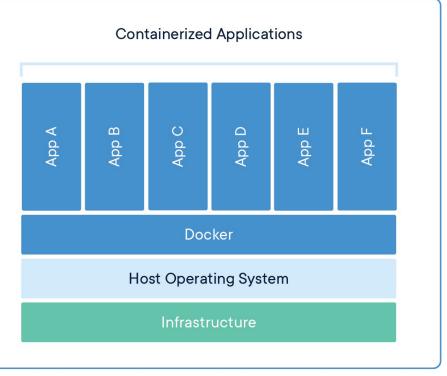
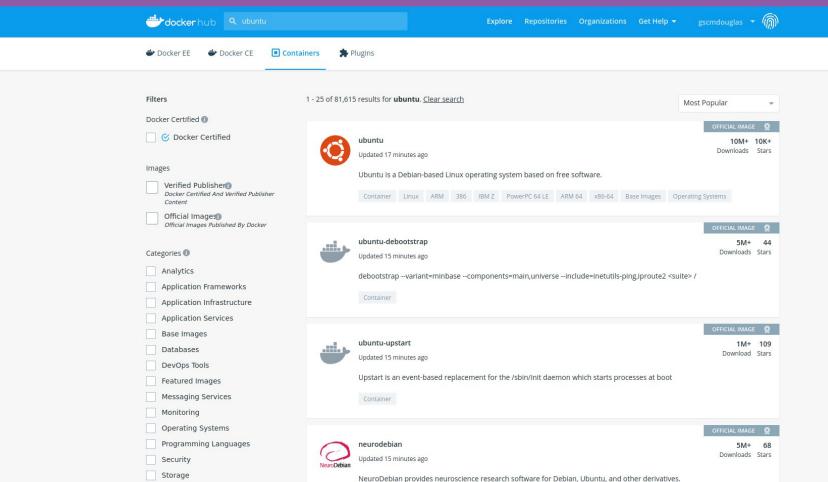


Image: https://www.docker.com/resources/what-container

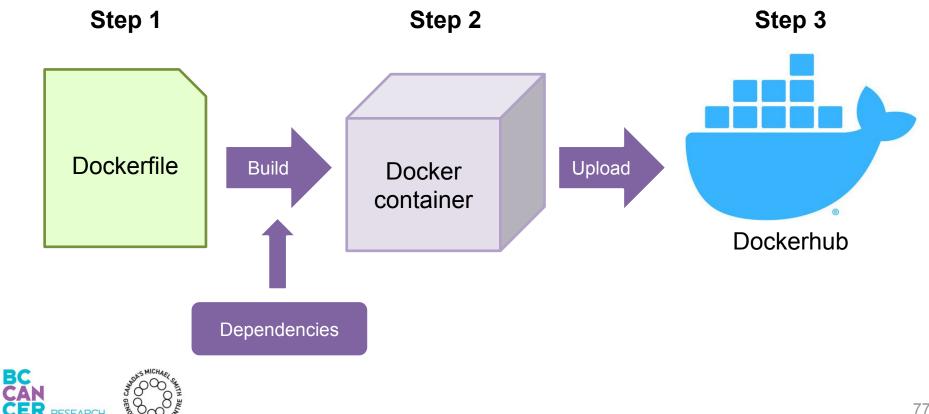


Dockerhub

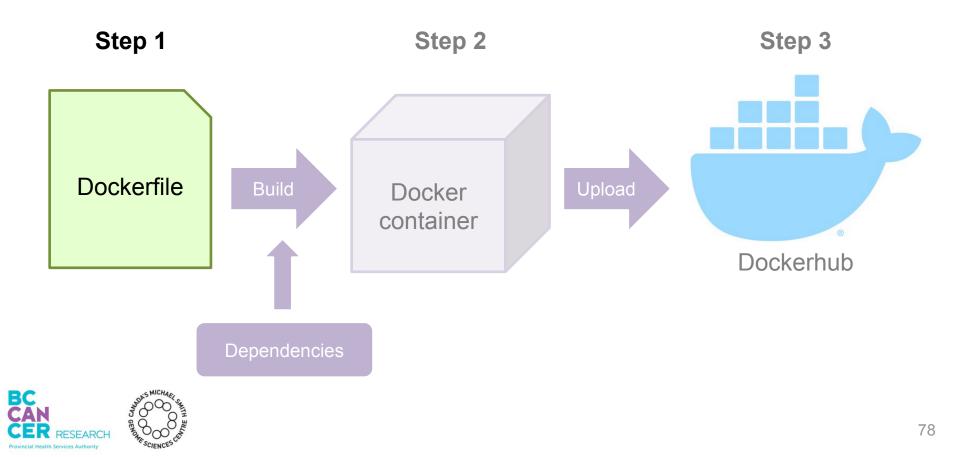


Building a Docker Container

Provincial Health Services Authority



Building a Docker Container



A 'Dockerfile' is a text file.

It is a set of instructions on how to build and run the Docker container.

Contains all the commands the user would run to install and run the pipeline.

matt@matt:~\$ vi Dockerfile



1) Pick a parent image.

Parent image = An existing docker image to base your image on.

Declare a parent image using the FROM keyword.





2) Install your pipeline.

RUN executes the following command when the image is being built.

WORKDIR sets the directory commands will be run in ('cd' in bash).

FROM ubuntu:20.04

RUN git clone https://github.com/mattdoug604/reproducible_tutorial.git WORKDIR reproducible_tutorial RUN pip install -r requirements.txt



3) OPTIONAL: Run a command when the Docker container is started.

Alternative is to run the Docker container "interactively" - behaves essentially the same as the normal command line environment (run commands, navigate directories, etc.).

```
FROM ubuntu:20.04
RUN git clone https://github.com/mattdoug604/reproducible_tutorial.git
WORKDIR reproducible_tutorial
RUN pip install -r requirements.txt
CMD bash run pipeline.sh
```



Building a Docker Container - Version Control

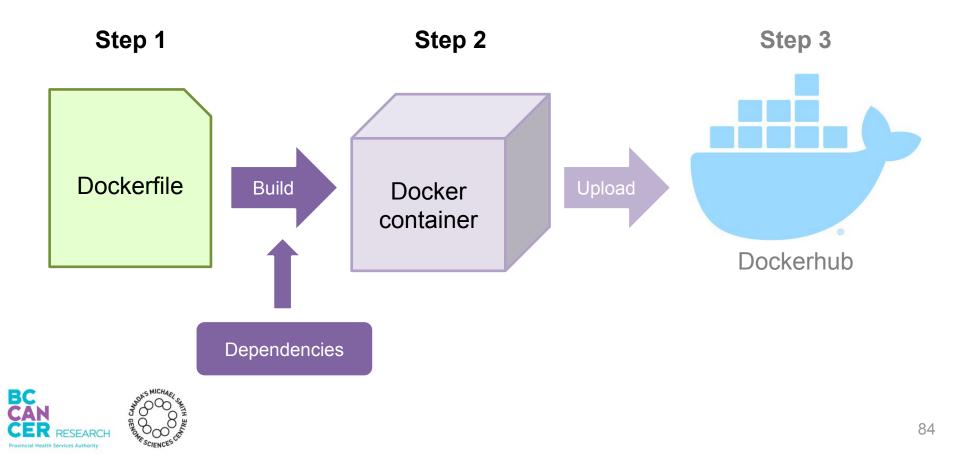
What if we rebuild the docker image and the git repository has changed?

RUN git clone https://github.com/mattdoug604/reproducible_tutorial.git WORKDIR reproducible_tutorial RUN git checkout v1.0.0 RUN pip install -r requirements.txt

Best practice is to control the version of each program included in the image.



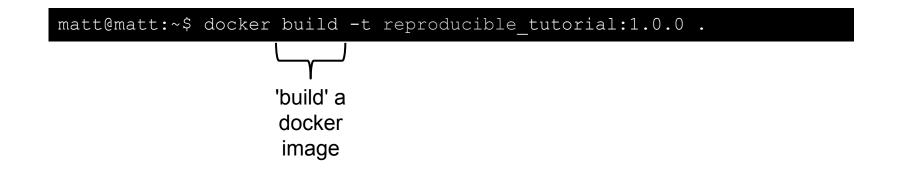
Building a Docker Container



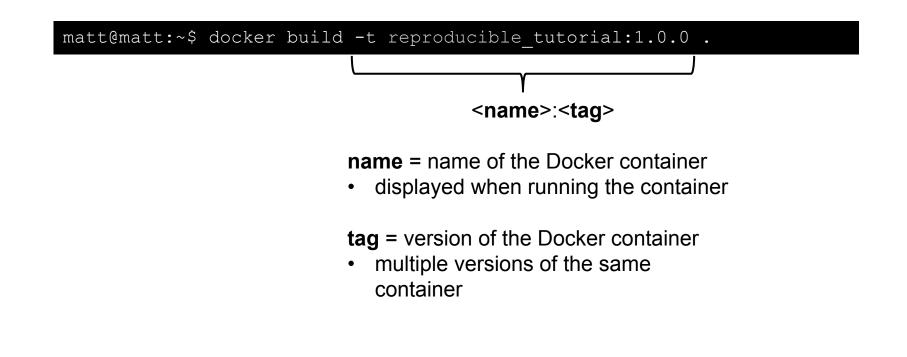




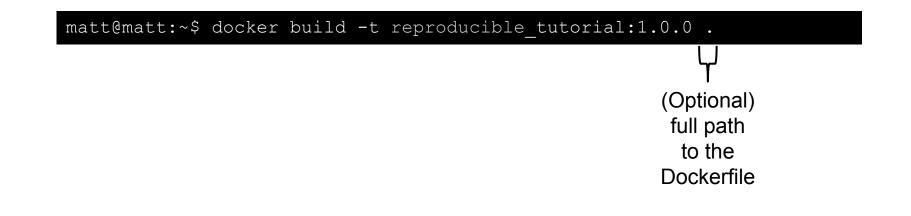








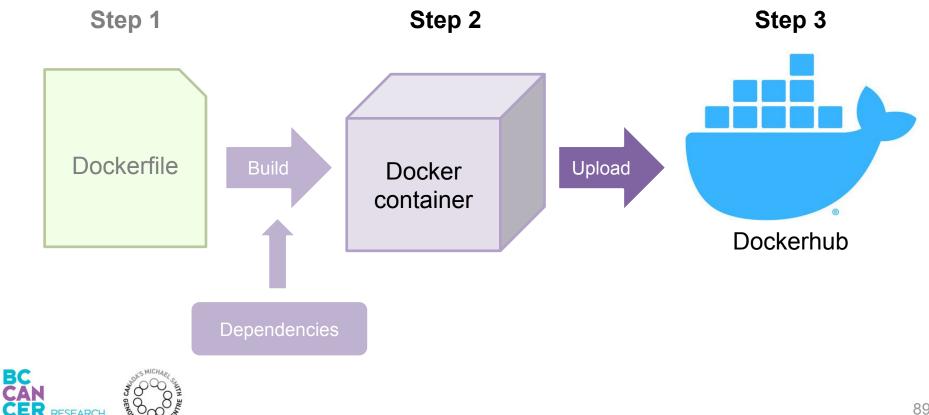






Building a Docker Container

Provincial Health Services Authority

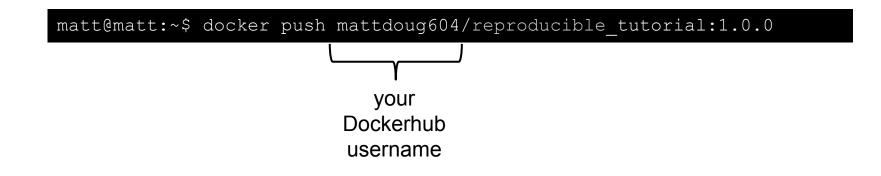




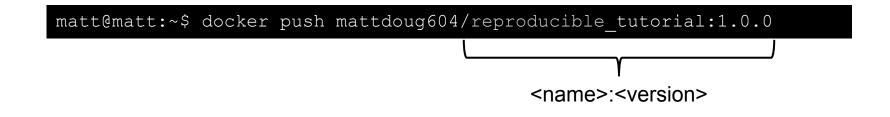














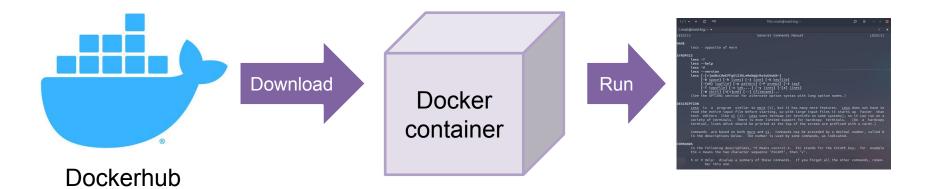
Running a Docker Container

Run the **CMD** we defined in the Dockerfile:

matt@matt:~\$ docker run reproducible_tutorial:1.0.0

OR, run the Dockerfile interactively (-it):

matt@matt:~\$ docker run -it reproducible_tutorial:1.0.0





Installed software should run the same on any machine.

Containers

- Docker or Singularity
- Very portable
- Ensures everyone is running the same code



Reproducible Pipeline Checklist

Code is available
 Good documentation
 Dependencies are listed
 Runtime environment can be reproduced





A failure to reproduce a result is often due to how the pipeline is packaged/shared.



Summary



- Code is easily accessible online
- Github, Sourceforge



- Documentation explains how to obtain, install, and run code
 - READMEs

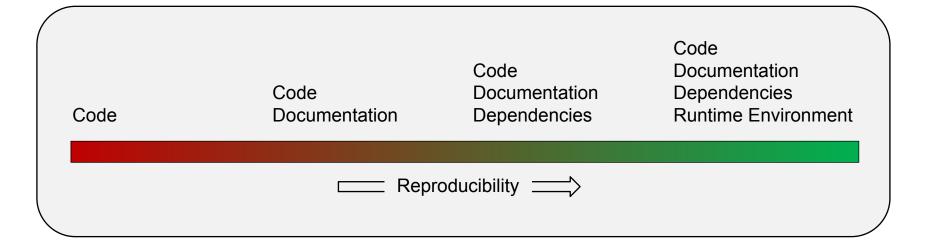


- All dependencies are listed
- 'venv' and 'pip freeze' (Python)



- Runtime environment can be reproduced
 - Containers (Docker, Singularity) contain all dependencies







So much amazing data science software!

Pipelines are not living up to their full potential if they are not accessible.

Making sure a pipeline produces the same output anywhere is not trivial - but is achievable!



Thank You for Listening!