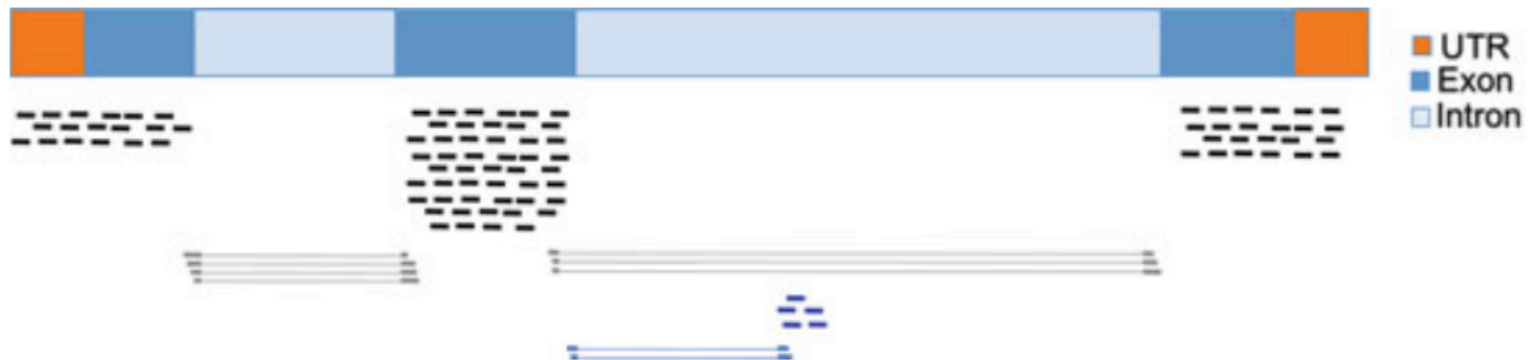


Counting Reads per Gene

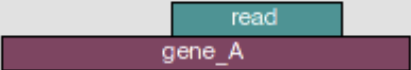
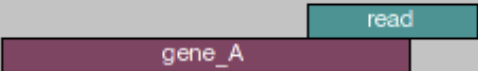




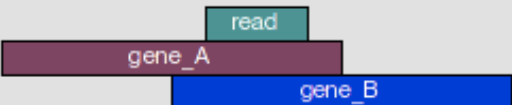
- From read alignments, you next need to summarize the reads into a “table of counts”
- From:



- To:
Gene MLO7 has 100 mapped reads.

HTSeq

- A Python framework to work with high-throughput sequencing data
- Comes with some very useful scripts, including one to count aligned reads
- Allows users to select from a number of counting strategies
- Can select any feature type from a gff3 file to be the “counting unit”
- Categorizes reads:
 - Maps to a feature
 - Does not map to a feature
 - Is ambiguous (could map to more than one feature)
 - Is too low quality
 - Is not aligned at all
 - Alignment is not unique

	union	intersection_strict	intersection_nonempty
	gene_A	gene_A	gene_A
	gene_A	no_feature	gene_A
	gene_A	no_feature	gene_A
	gene_A	gene_A	gene_A
	gene_A	gene_A	gene_A
	ambiguous	gene_A	gene_A
	ambiguous	ambiguous	ambiguous

Reproducible Science (and Scripting)

Reproducibility

- Reproducibility is the ability to duplicate an entire experiment or study, either by the same researcher or by someone else working independently.
- Also called replication
- Reproducibility is one of the main principles of the scientific method.
- Scientific validity = Independent replication of experimental results

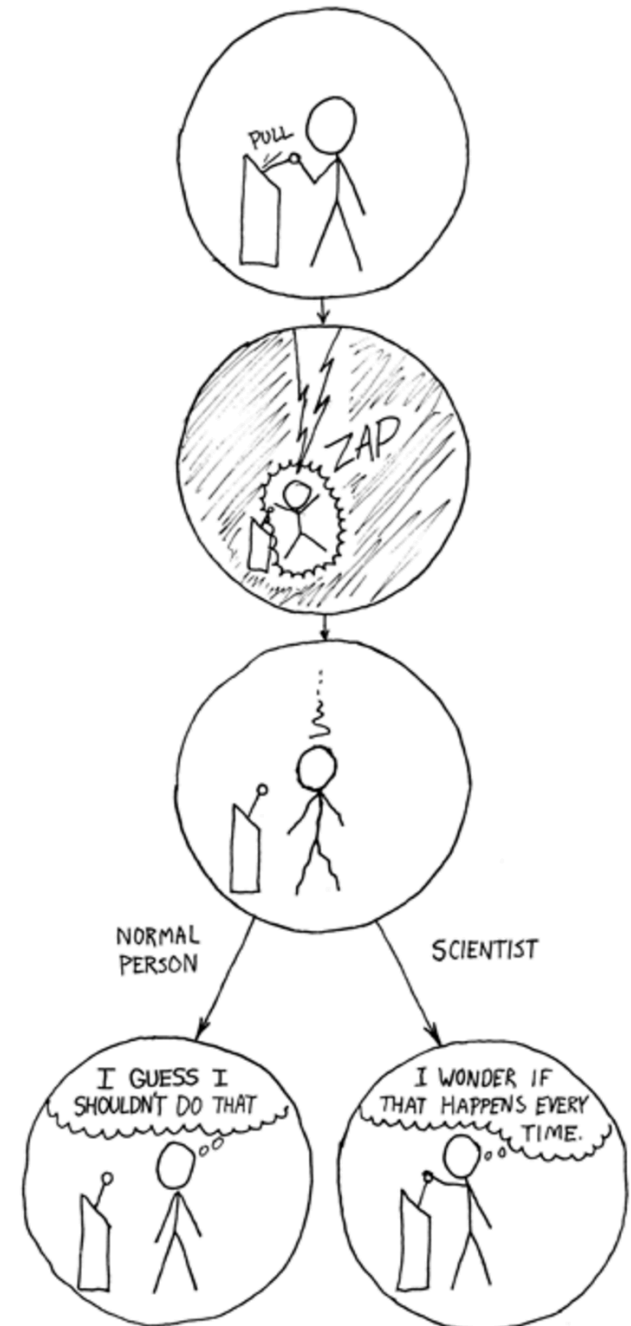


<https://www.technologynetworks.com/informatics/articles/repeatability-vs-reproducibility-317157>

How do I make my analysis reproducible?

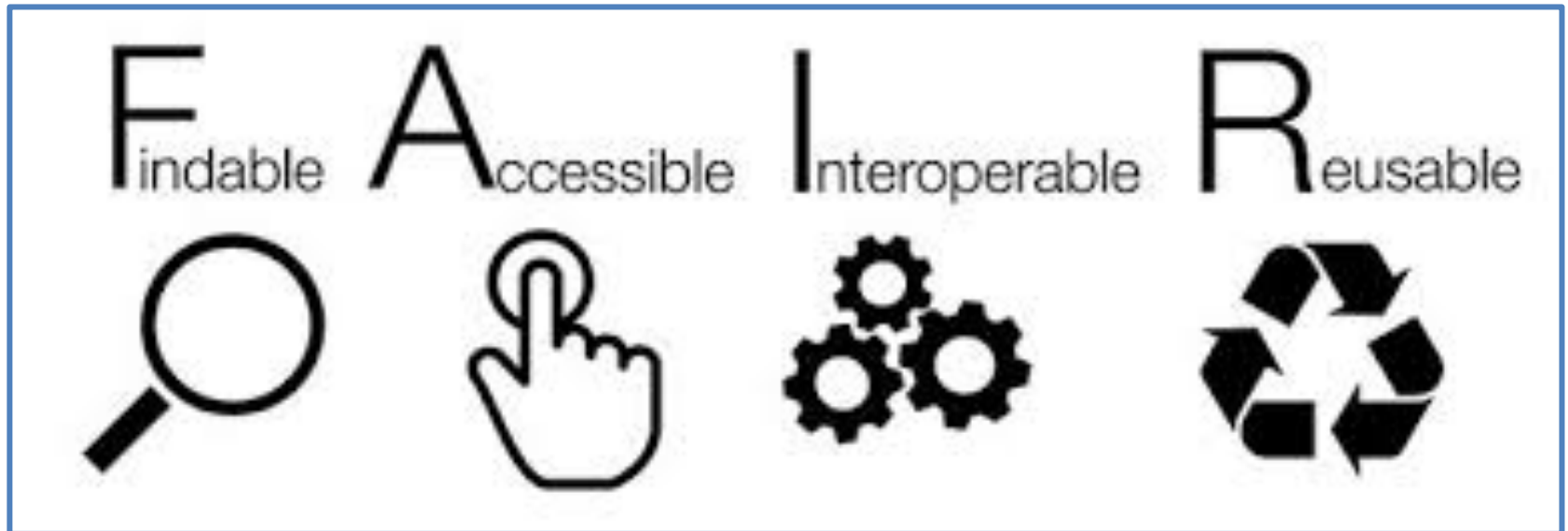
In bioinformatics, this requires sharing code, analysis details and raw data

- Data sharing is almost always required by peer-reviewed journals
- Code/analysis sharing is less standardized, but coming soon



Randall Munroe, xkcd

FAIR Principles



The FAIR Guiding Principles for scientific data management and stewardship

Mark D. Wilkinson, Michel Dumontier [...] Barend Mons [✉](#)

Scientific Data **3**, Article number: 160018 (2016) | [Download Citation](#) [↓](#)

Robustness

- In wet lab research, it is often obvious when an experiment fails.
- This is not always true with computational analysis. Software may not print an error, even when things have gone wrong.
- Fewer users = fewer bug reports
- High dimensional data is complex and difficult to have a priori expectations

Robustness

- Never trust your data or tools – always verify in whatever way possible
- Look at results at each intermediate step
- Visualize output in the most meaningful way possible
- Use good controls and examine them in comparison to treatments often

How do I do reproducible and robust research?

- Record keeping – keep a (preferably online) lab notebook for the dry lab
- Scripting to automate tasks
- Write simple, clear scripts that you and others can read later
- Save raw data
- Publicly release raw data and scripts



What is a script?

- A computer program
- Usually somewhat small and dedicated to a single task or just a few tasks
- Automates the execution of tasks
 - In other words...
 - A person could run each of these commands one by one
 - But instead the commands have been written down and given to the computer to run one by one
- **This is also a great form of documentation!!!**

What is a script?

- Can be in any of many different languages:
 - Python
 - Perl
 - R
 - Bash
- Bash???

Bash

- Bourne Again Shell
- Bash is the terminal program we are using to talk to the ACF
- It also has a simple language
- You've already been learning it! Everything we type on the command line is computer language



More reasons to write scripts!

- Can customize commands and run software with a few key strokes
- Can operate on hundreds to millions of files
- Can have many different jobs running simultaneously across many computers
- Modular workflows and components
 - We can experiment with different pieces of software at each stage of analysis
 - Reuse
 - Examine results at each stage of analysis

Geeks and repetitive tasks

