Data Carpentry Genomics Introduction

- Experimental data
- Workshop overview

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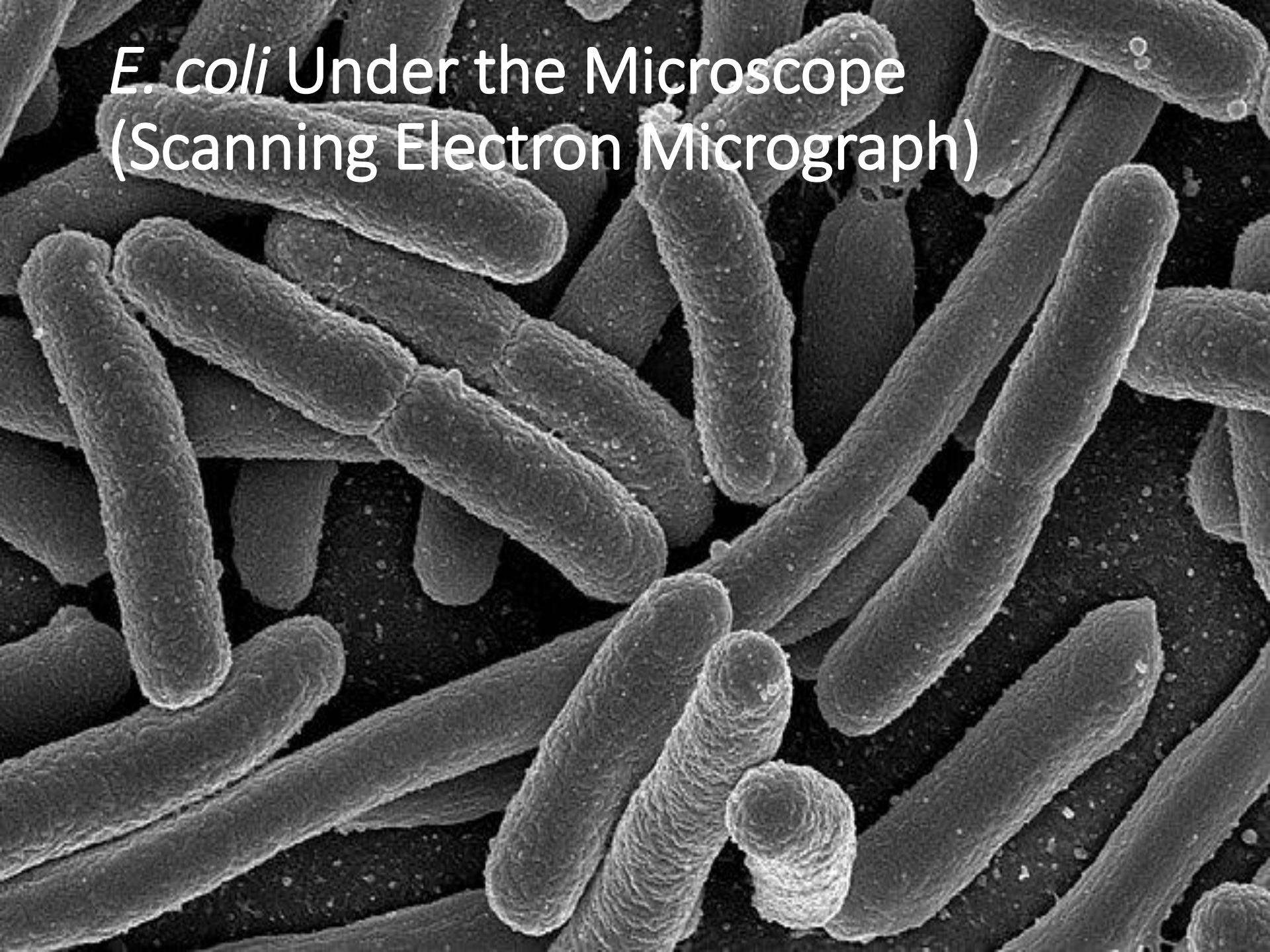
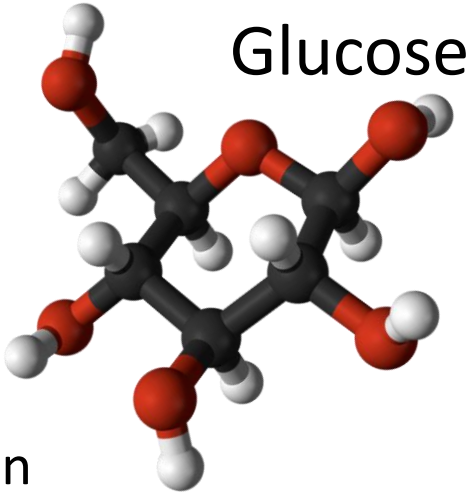
E. coli Under the Microscope (Scanning Electron Micrograph)



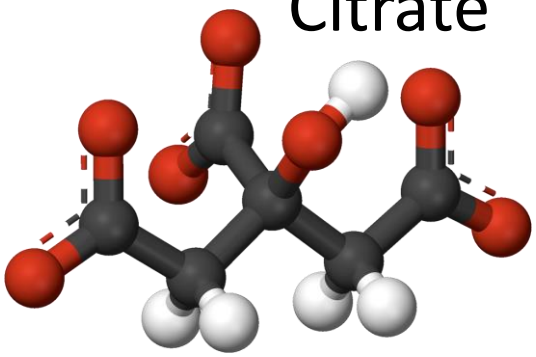
E. coli (*Escherichia coli*)

- **Prokaryotes:** single copy of their circular chromosome per cell
- **Aerobic AND Anaerobic** metabolism:
  - Uses oxygen when available, using the same glycolysis and the citric acid cycle pathways found in eukaryotes to generate energy from carbon-containing molecules like **glucose**.
  - **Citrate** can only be metabolized by *E. coli* in the absence of oxygen.
- **Easy to grow and maintain**
  - Short reproduction time ≈20 min

Glucose



Citrate



E. coli long-term evolution experiment (LTEE)

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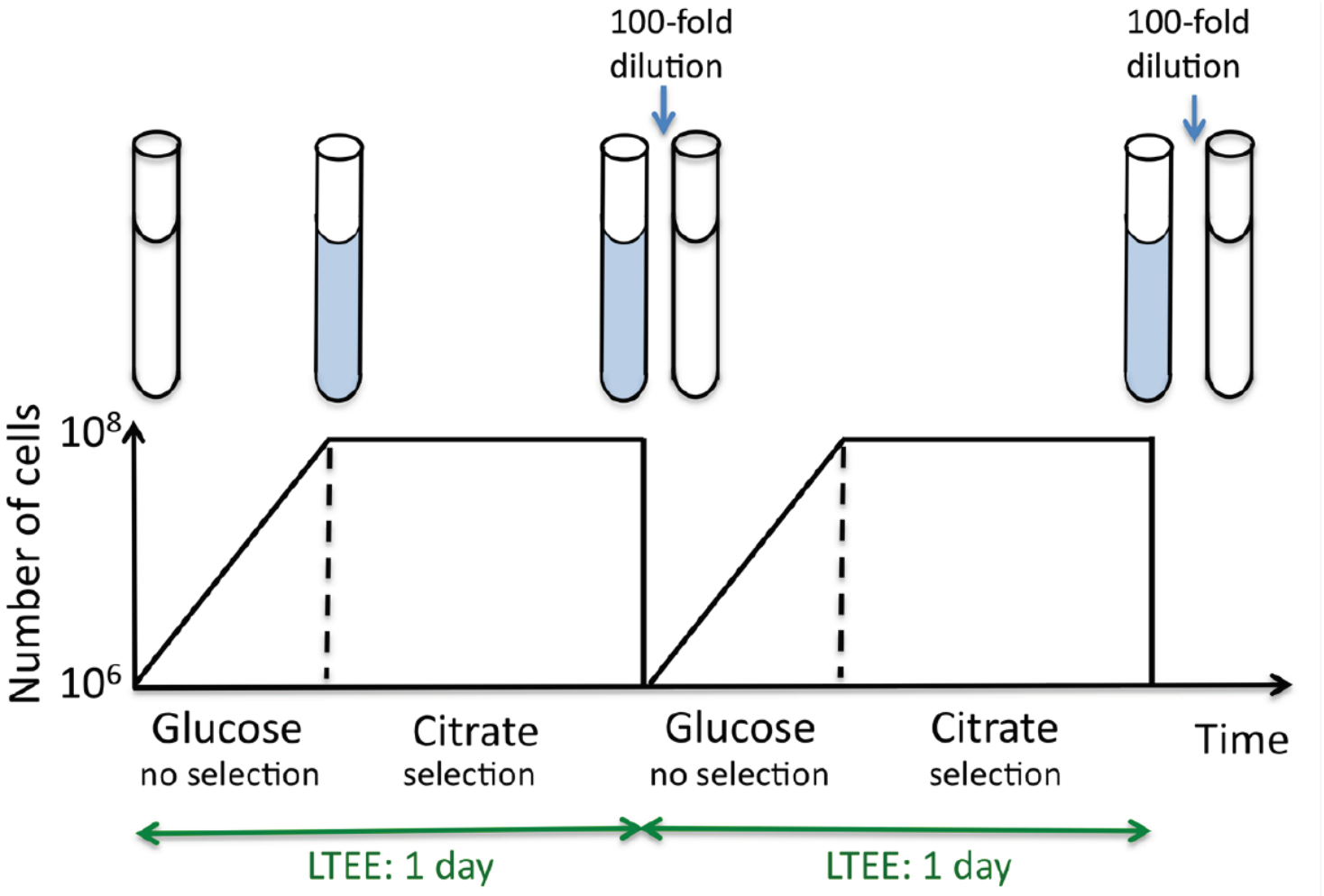
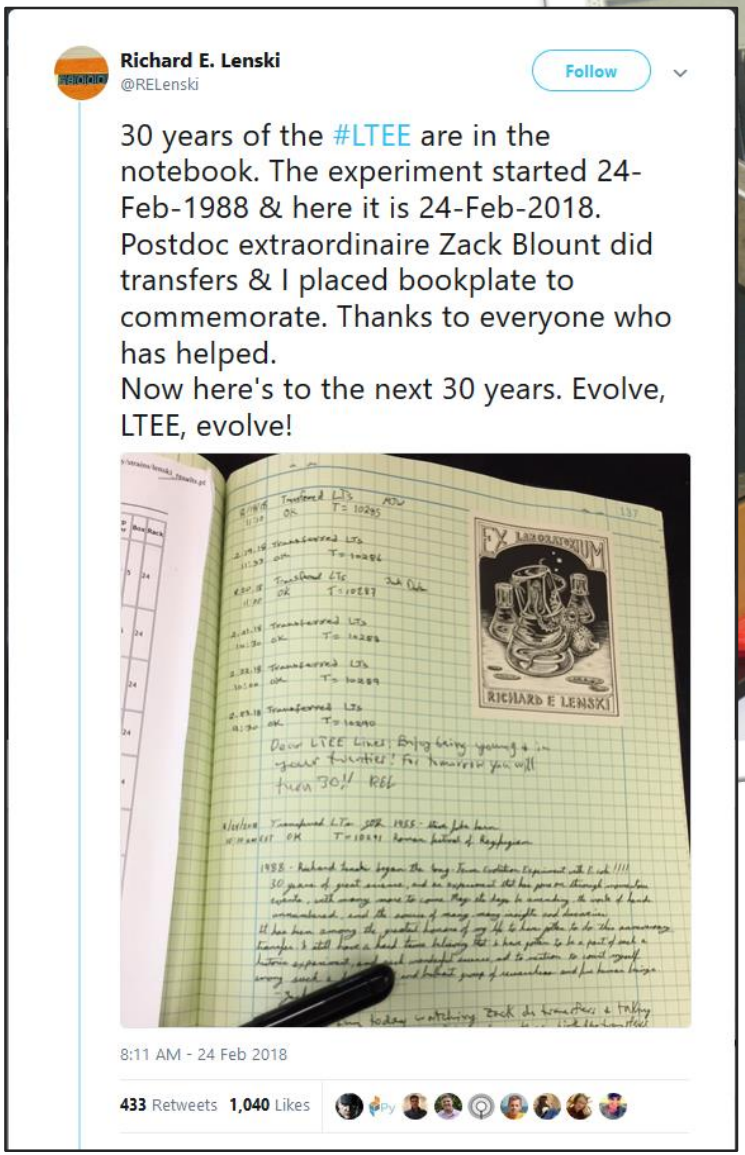
JR Roth et al. *J Bacteriol.* 1009-1012 (2016)





The data in Blount et al. 2012 is restricted to populations from *one* of those initial populations.

E. coli long-term evolution experiment (LTEE)

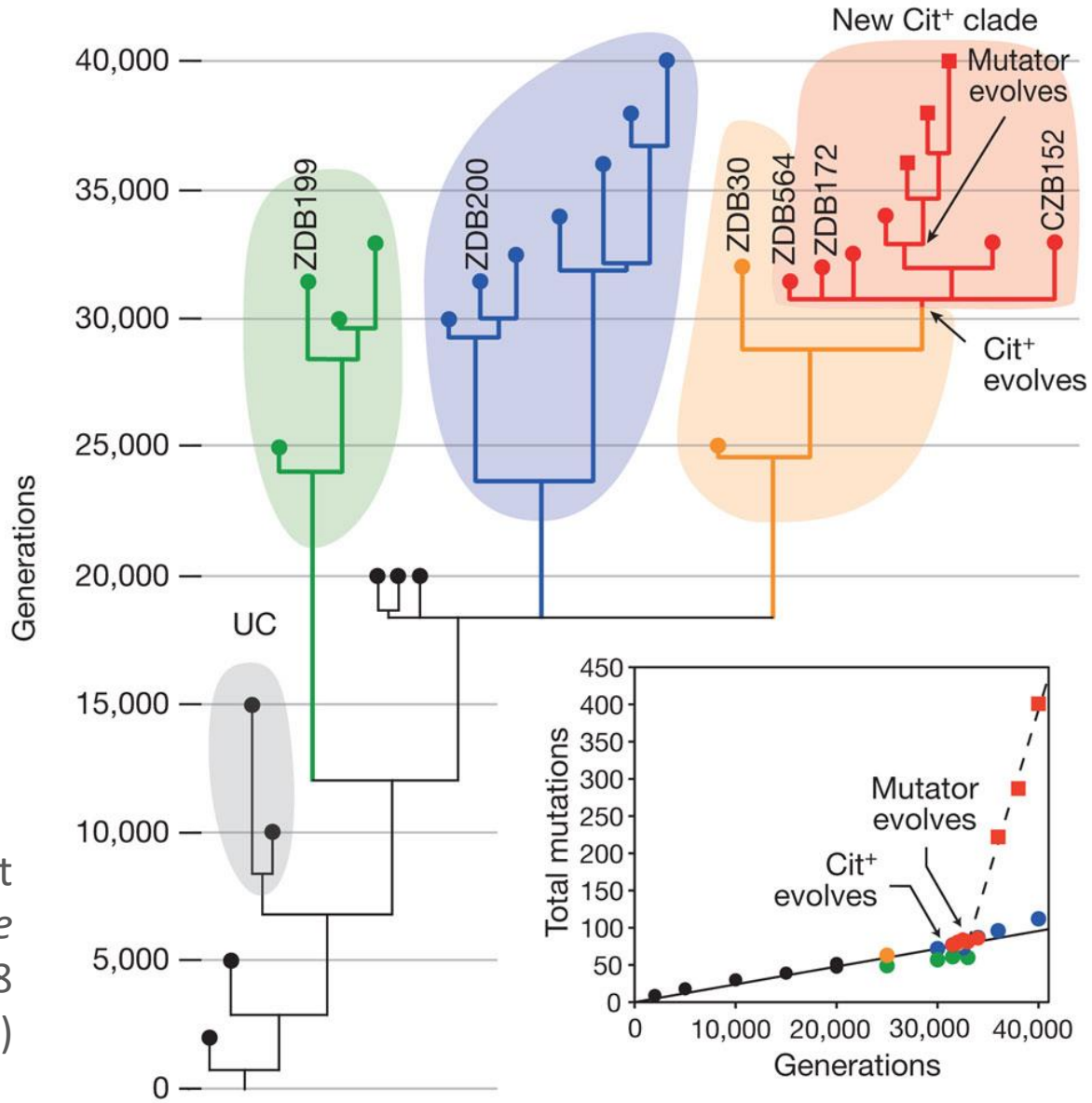
Data Carpentry Genomics data set

- Growth medium contains small amount of glucose (food source) and citrate (helps *E. coli* obtain iron from medium)
- Around 33,000 generations (≈15 years into the experiment!), *E.coli* population could grow aerobically on citrate (Cit^+)
- Remarkable: inability to grow aerobically on citrate (Cit^-) is characteristic of *E. coli* as a species

“Back in 2008, this was really frustrating for those of us who wanted to know the molecular details. I'm sure this was frustrating for Blount and Lenski and their colleagues as well. We had no idea how difficult it would be to sort out the mutations. Now we know, and the photo of Zachary Blount with all his Petri dishes drives home the point.”

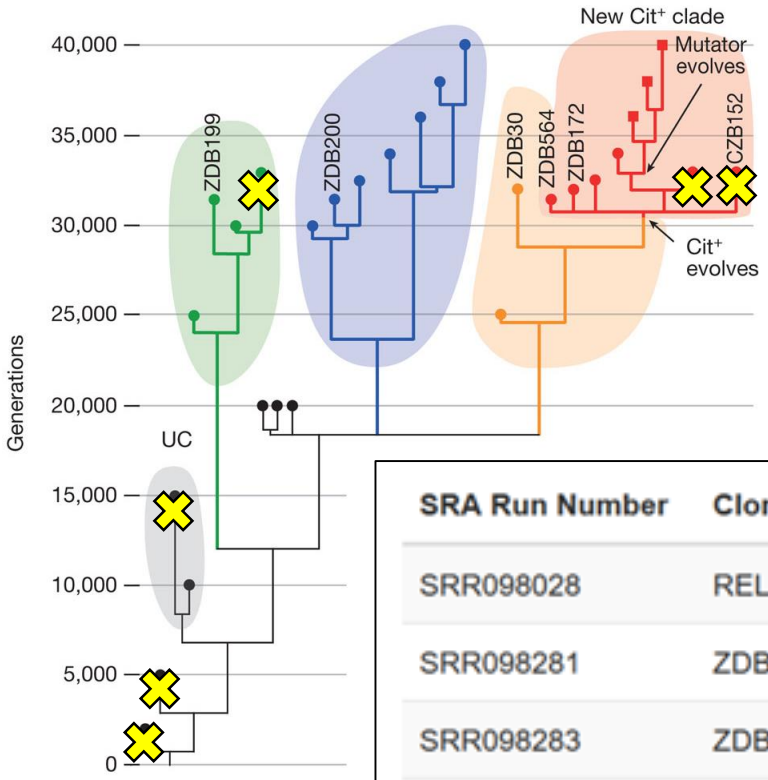
Laurence A. Moran (Professor Emeritus in the Department of Biochemistry at the University of Toronto)

	Clade 1	Clade 2	Clade 3
Cit⁺ replays	2/55	2/97	8/37



ZD Blount et al. *Nature* 489, 513–518 (2012)

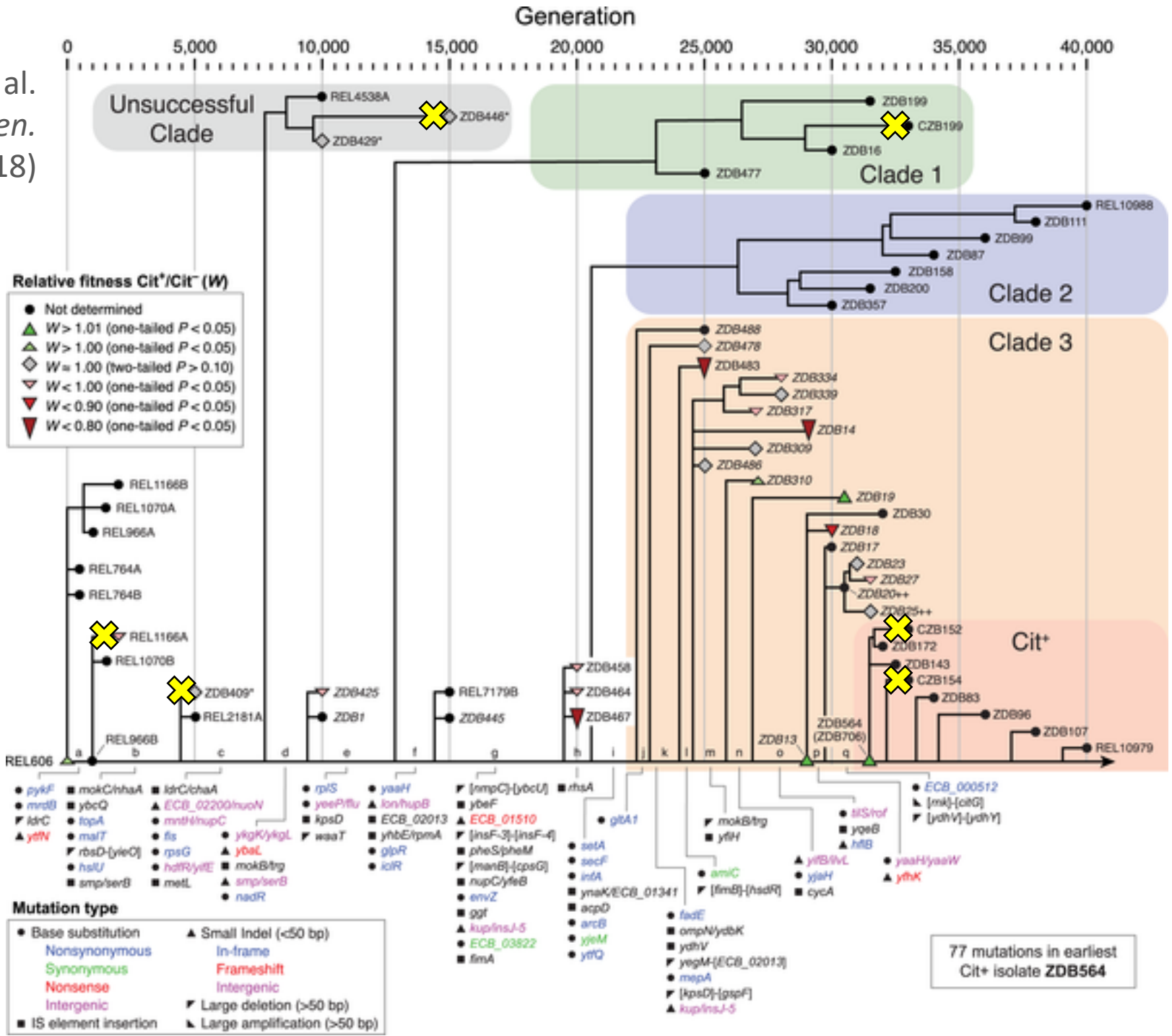
DC Genomics data set



For the purposes of this workshop we're going to be working with 6 of the sequence reads from this experiment. We also made up genome sizes for each of the strains, to look at the relationship between Cit status and genome size. **The genome sizes are not real data!!**

SRA Run Number	Clone	Generation	Cit	GenomeSize
SRR098028	REL1166A	2,000	Unknown	4.63
SRR098281	ZDB409	5,000	Unknown	4.6
SRR098283	ZDB446	15,000	Cit-	4.66
SRR097977	CZB152	33,000	Cit+	4.8
SRR098026	CZB154	33,000	Cit+	4.76
SRR098027	CZB199	33,000	Cit-	4.59

D. Leon et al.
PLOS Gen.
(2018)



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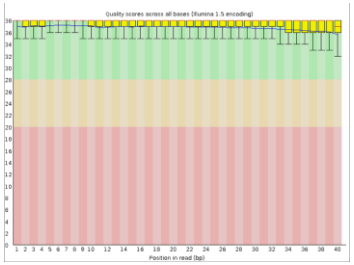
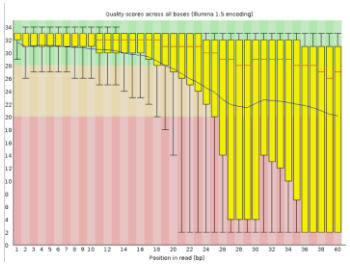
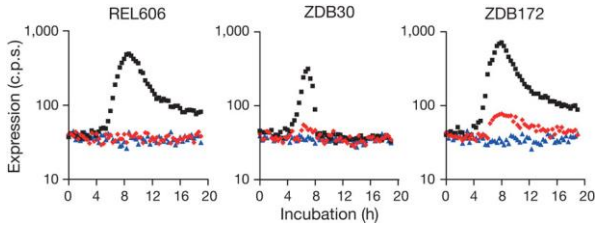
Set up project

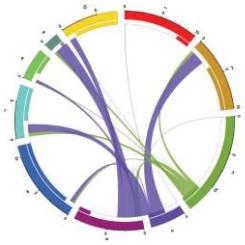
Process data





Analyze & visualize





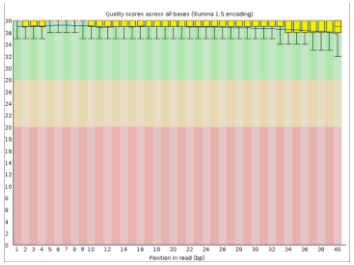
Set up project

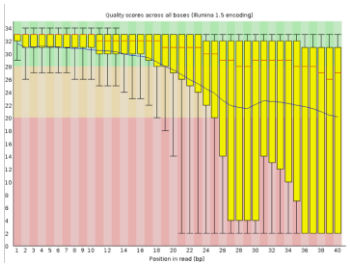
① Tuesday morning:

Project organization

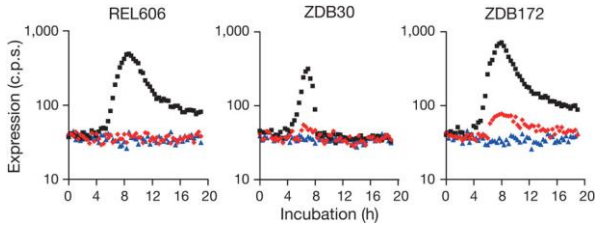
- Metadata files
- Open data

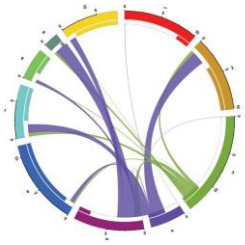
Process data





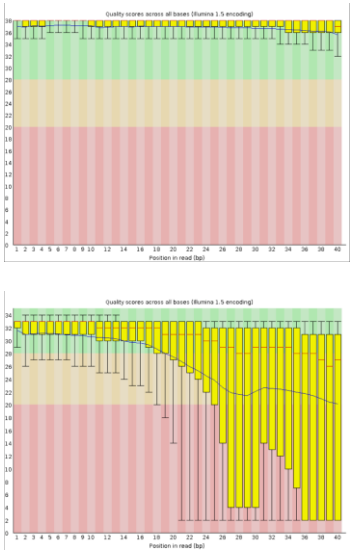
Analyze & visualize



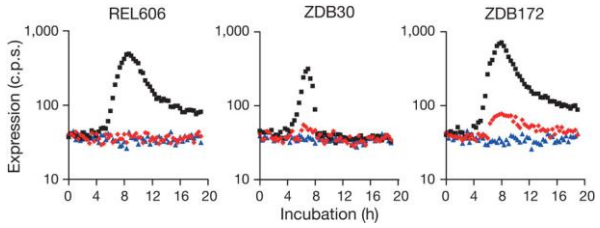


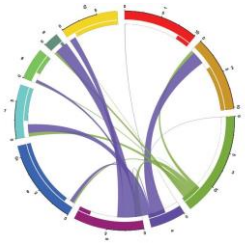
Set up project

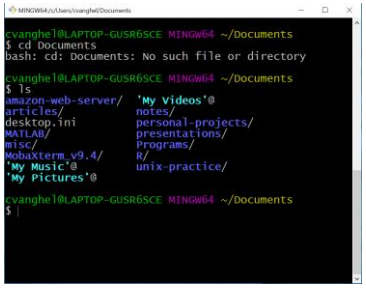
Process data



Analyze & visualize







② Tuesday afternoon:

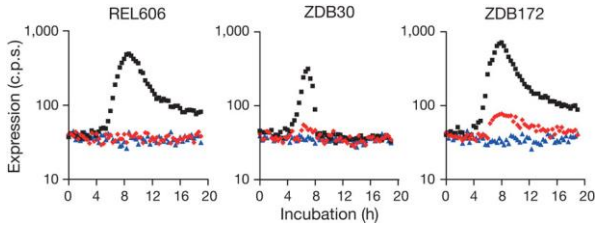
Unix command line

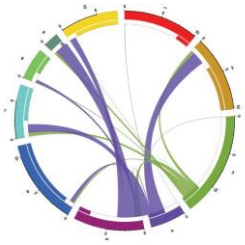
- Fast,
- Repeatable &
- Reproducible data processing

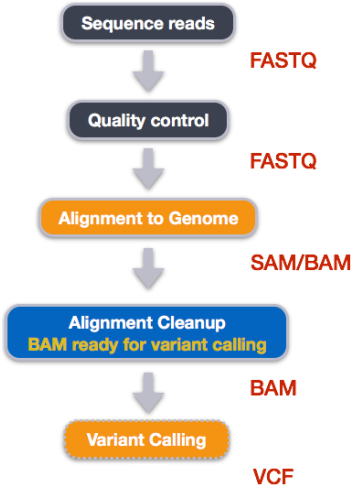
Set up project

Process data

Analyze & visualize







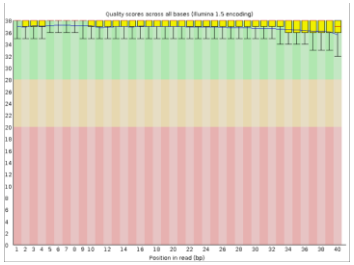
③ Wednesday morning & afternoon:

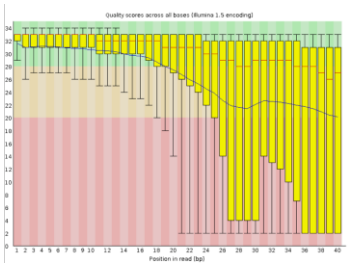
Sequencing pipeline

- Quality control of read data
- Alignment to genome
- Variant calling

Set up project

Process data





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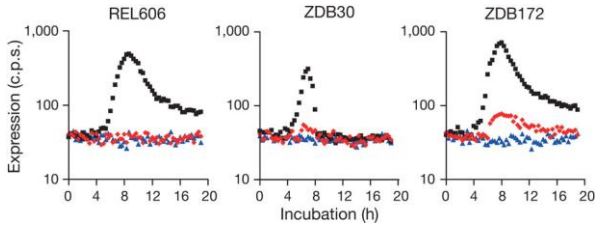
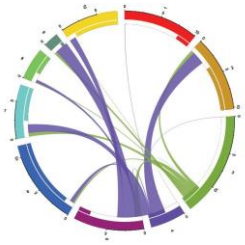


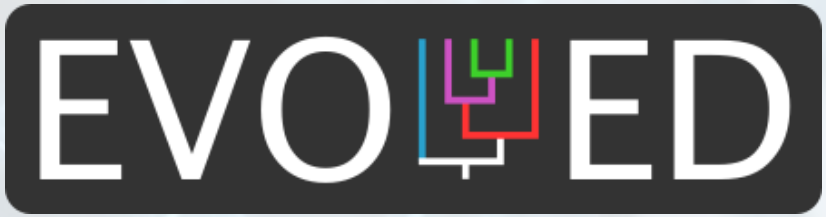


④ Wednesday afternoon:

Data analysis with R

- Manipulate data tables
- ddpyr
- Make plots

References

- 

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