```
library(dplyr)

rladies_global %>%
  filter(city == 'London')
```



Researchers & | Students | Community Launch

@RLadiesLondon
#RLadies

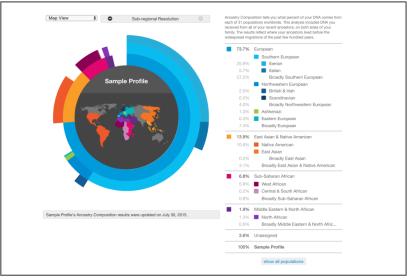
@victoriabutt1

Slack: rladies-london

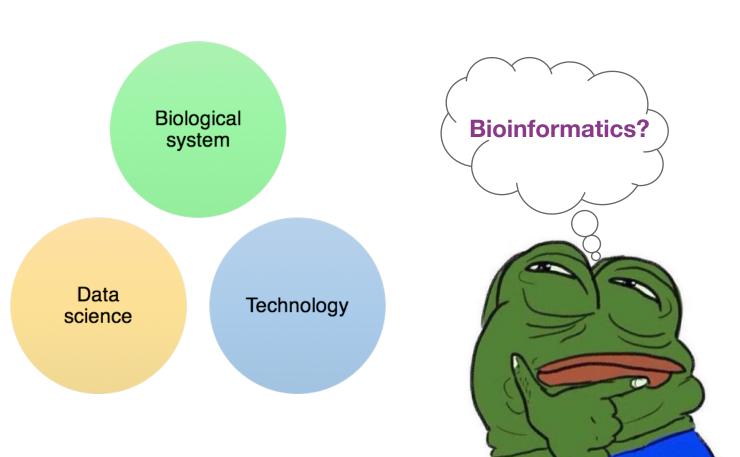


What has bioinformatics done for us?





















Now...





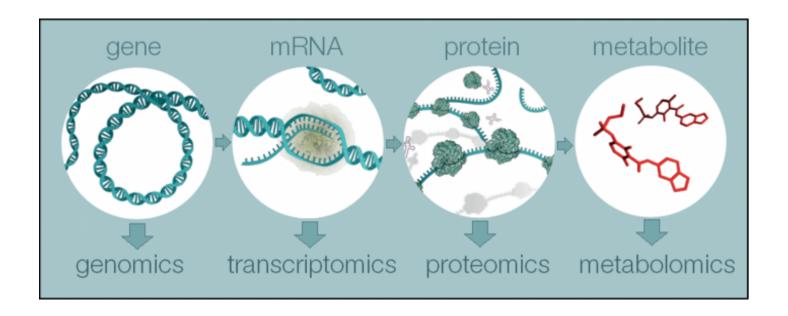
Cheaper and faster

1000s of species...





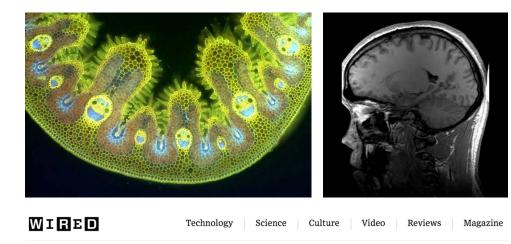
The 'Omics





What else?

Imaging



This AI can spot skin cancer as accurately as a doctor

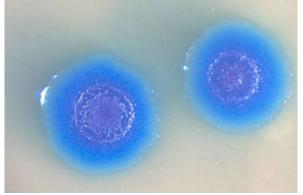
The artificial intelligence was trained on an image database of 129,000 images and performed as well as trained medical professionals



What else?

Synthetic biology







The perks



- Computational biology is now and the future
- Transferrable skills
- Logical thinking
- Fail fast, succeed faster
- Now is the time to learn



Myths?



Coding is hard"

I'm not mathsy enough"

Bioinformaticians have a background in computer science or mathematics"









How do you become a bioinformatician?



Year 1 Physicist







Year 2 Biologist





Lab placement Computational biology



Year 3 Neuroscience







Year 4 Systems Biology







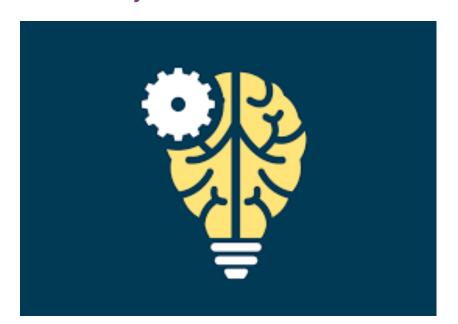
Year 1 PhD



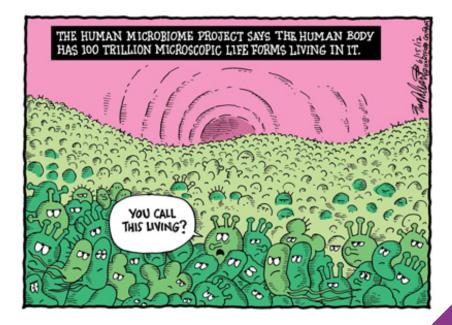
London Interdisciplinary Doctoral Programme @ UCL, KCL, QMUL, Birkbeck, LSHTM, RVC



Project 1 - UCL



Project 2 - KCL





Now it's your turn!

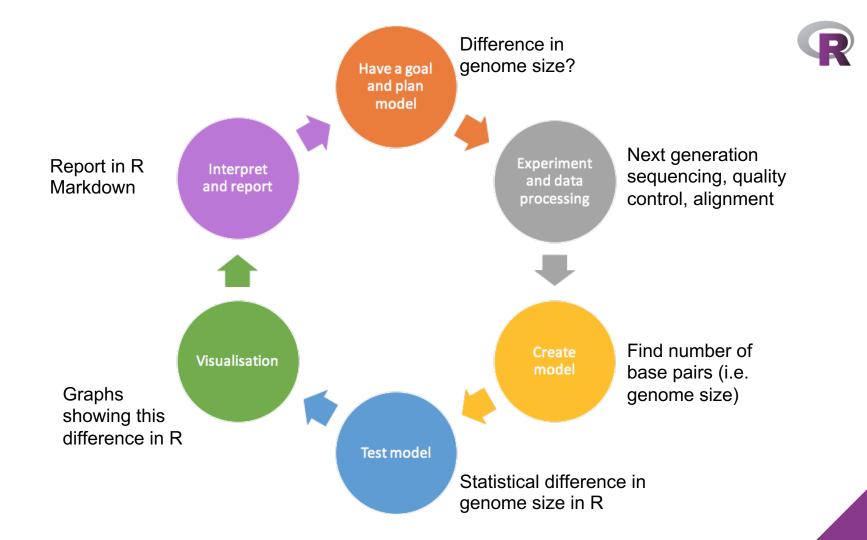


Experiment

We are studying a population of Escherichia coli (Ara-3), which multiplied for more than 40,000 generations in a glucose-limited medium. This medium was supplemented with citrate which E. coli cannot metabolize in the aerobic conditions of the experiment. Sequencing of the populations at regular time points reveals that spontaneous citrate-using mutants (Cit+) appeared at around 31,000 generations.

Goal

Look to see if there is a difference in genome size between citrateusing mutation status of the strain i.e. between Cit- and Cit+





Metadata

Column	Description
sample	clone name
generation	generation when sample frozen
clade	based on parsimony-based tree
strain	ancestral strain
cit	citrate-using mutant status (plus, minus, unknown)
run	Sequence read archive sample ID
genome_size	size in Mbp (mega base pairs)