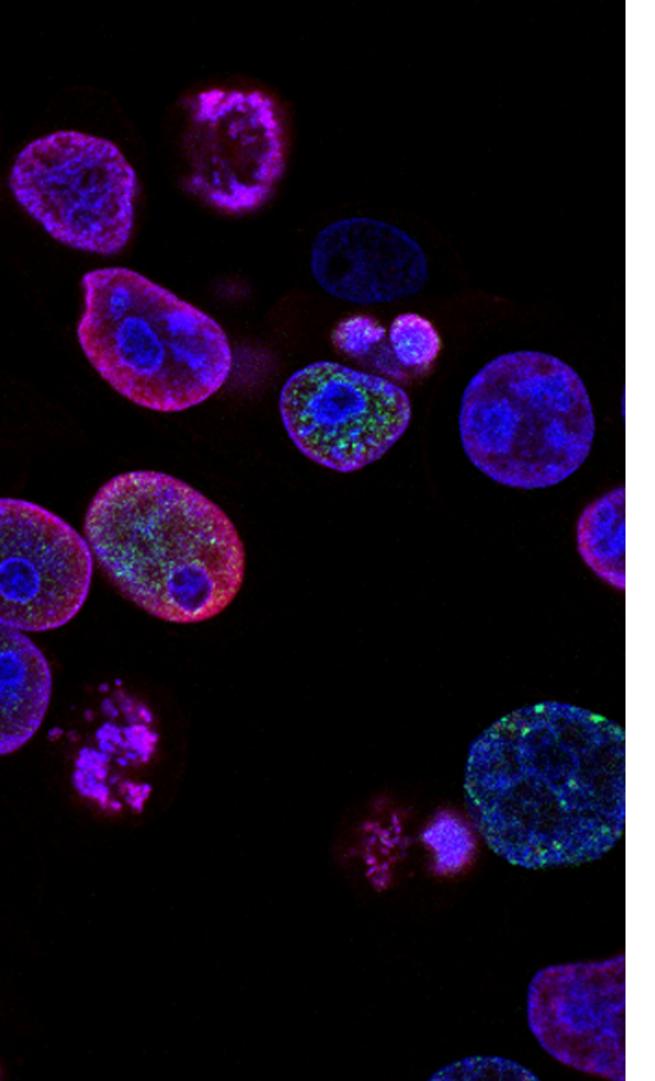
## Machine Learning for Cancer Genomics

Cait Harrigan March 23, 2024

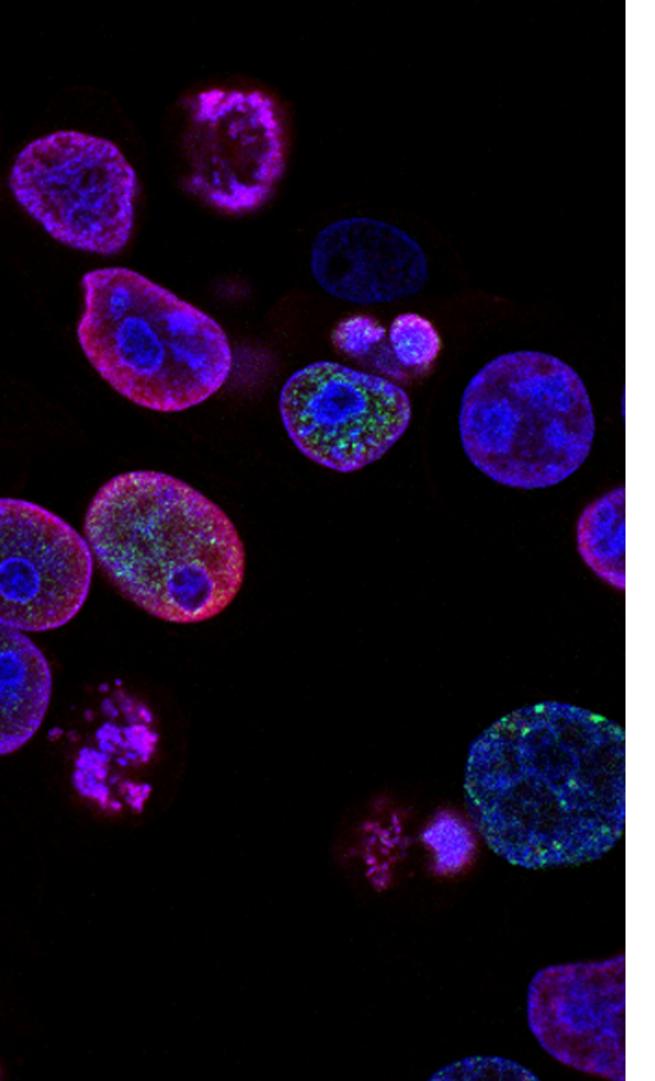
University of Toronto, Vector Institute cait.harrigan@mail.utoronto.ca



### Agenda

# Part 1: Brief overview of the field

Part 2: My research - cancer evolution Part 3: A day in the life of a PhD student

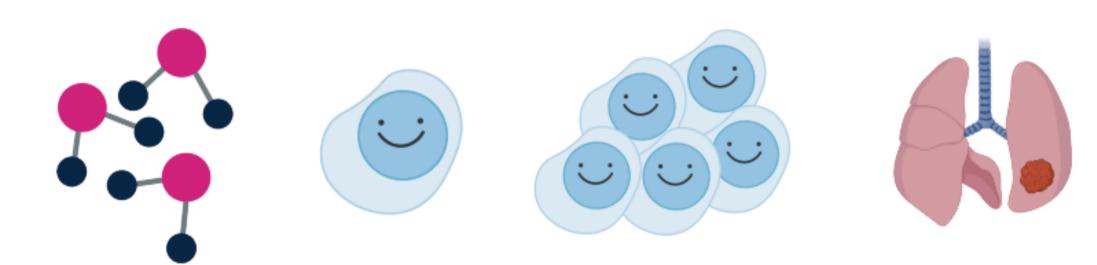


### Agenda

# Part 1: Brief overview of the field

Part 2: My research - cancer evolution Part 3: A day in the life of a PhD student

### **Computational biology**



### **ML for health**





### **Challenges in biomedical ML applications**

- Data size
- Labels are expensive
- Missing "ground truth"
- Generalization
- Interpretability and causal inference

### Two common modelling paradigms



### Two common modelling paradigms

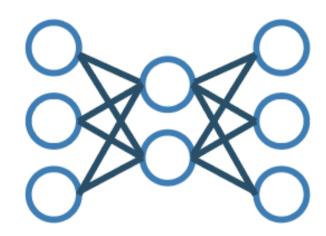
Input

**Training loop** 





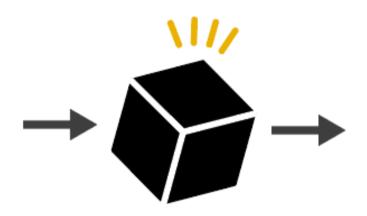
Data



Update weights



### **Final product**



Black box predictor

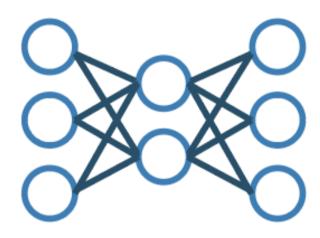
### Two common modelling paradigms

Input

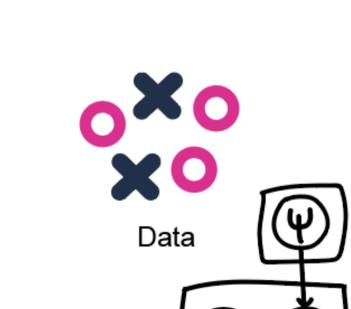
**Training loop** 







Update weights



 $\hat{\Theta}_{i} = U(\hat{\Theta}_{i-1})$ 

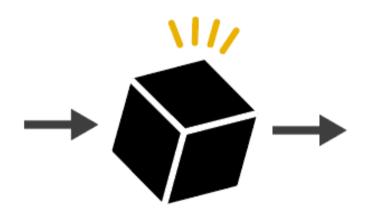
Update parameter estimates

Bayeisan inference

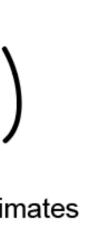
Probabilistic model

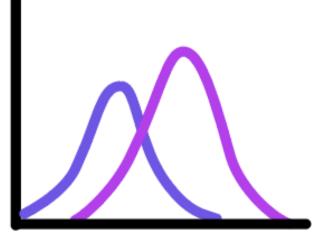


### **Final product**

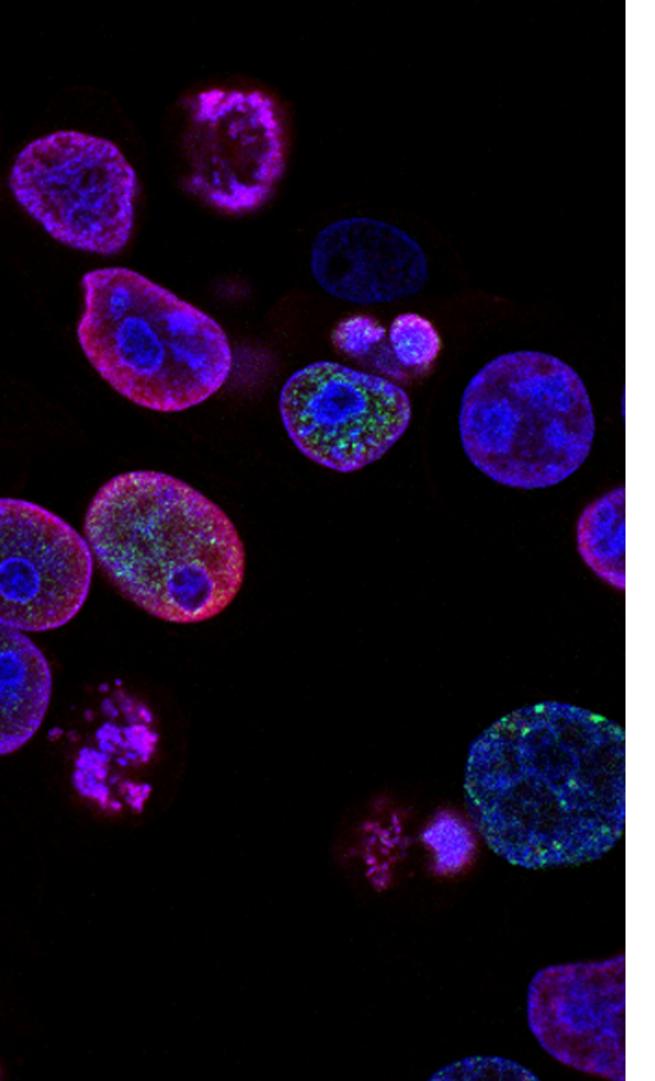


Black box predictor





Posterior distributions

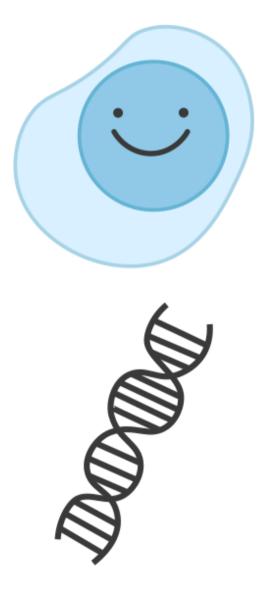


### Agenda

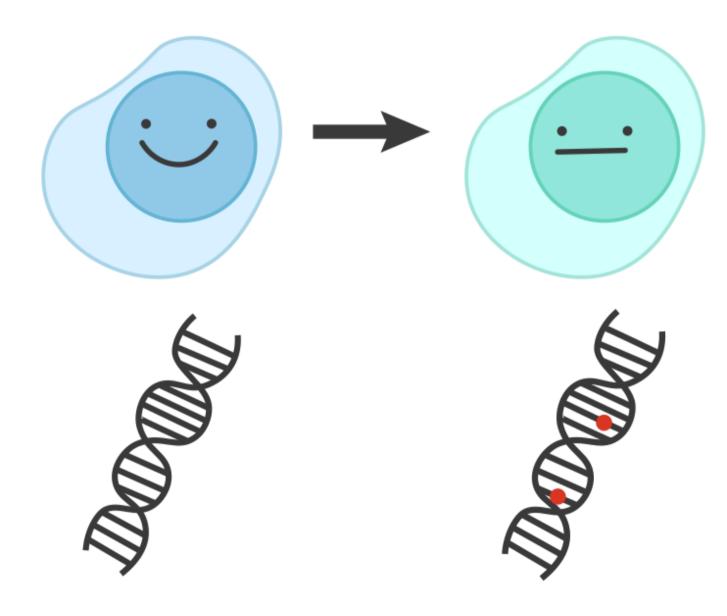
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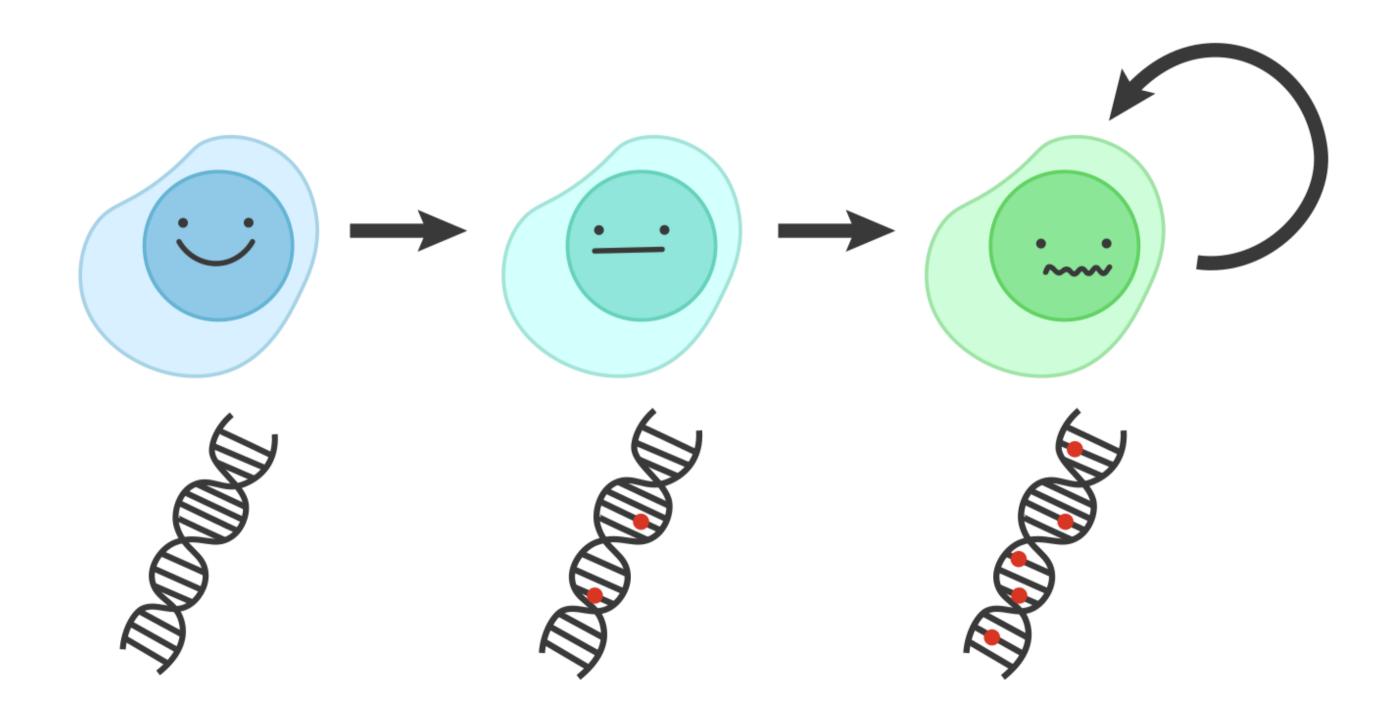
### **DNA = set of instructions which tell a cell what to do**



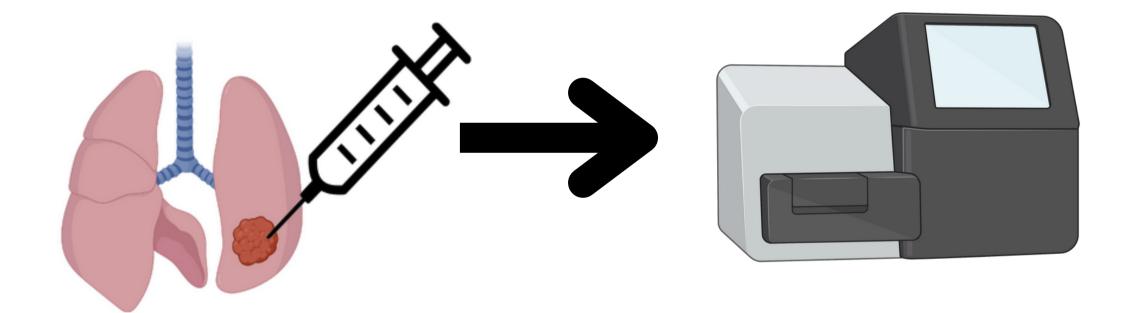
### **DNA = set of instructions which tell a cell what to do**



### **DNA = set of instructions which tell a cell what to do**

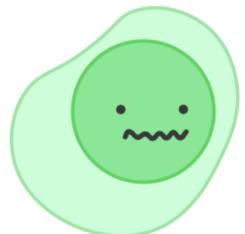


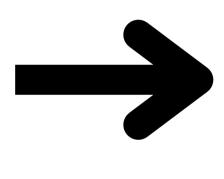
### With whole genome sequencing, get a list of mutations in a sample



### Sample

### **Sequence DNA**







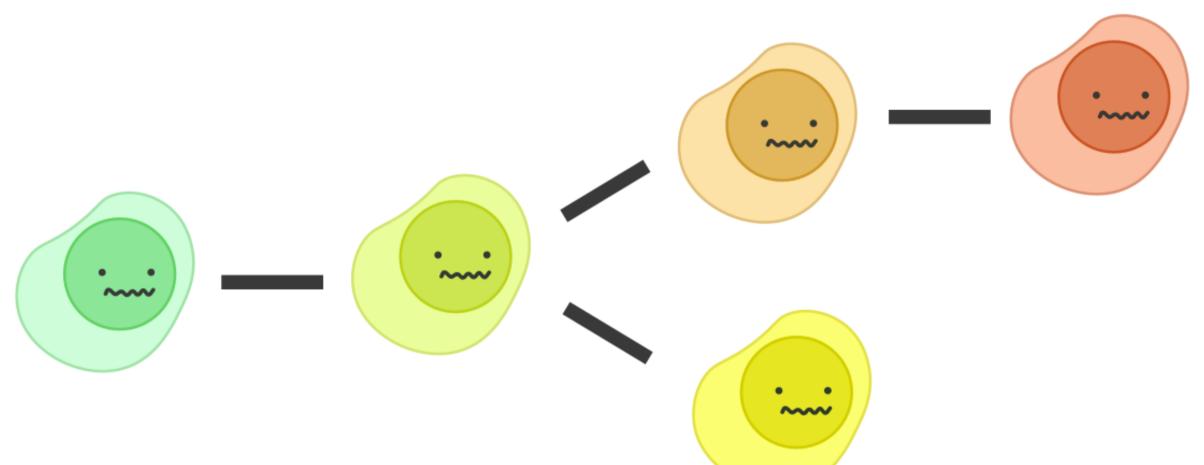


### Identify mutations

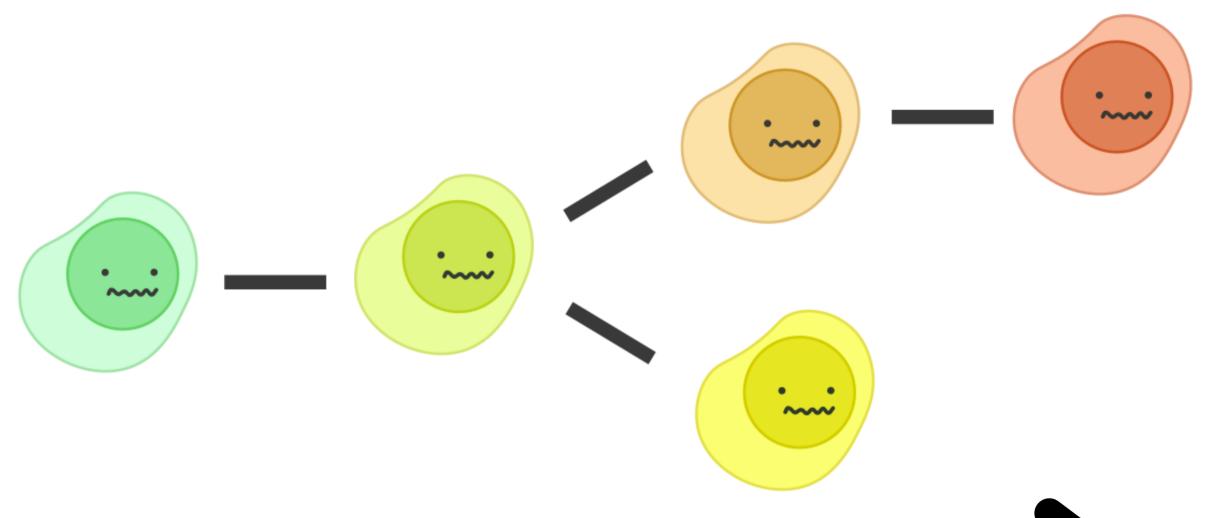
### A tumour sample contains a mixture of cells!



### Cells in a tumour are all related



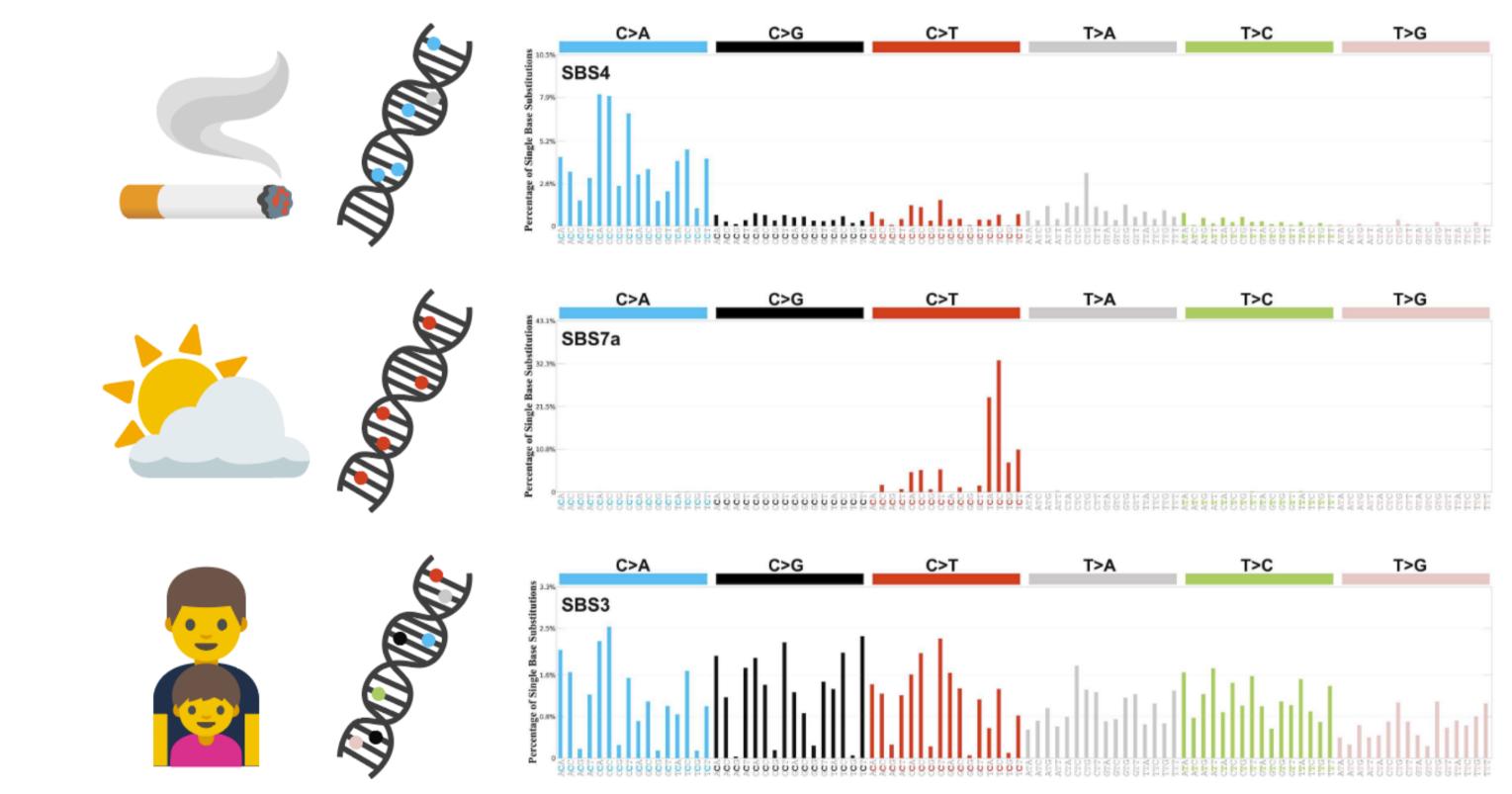
### Cells in a tumour are all related



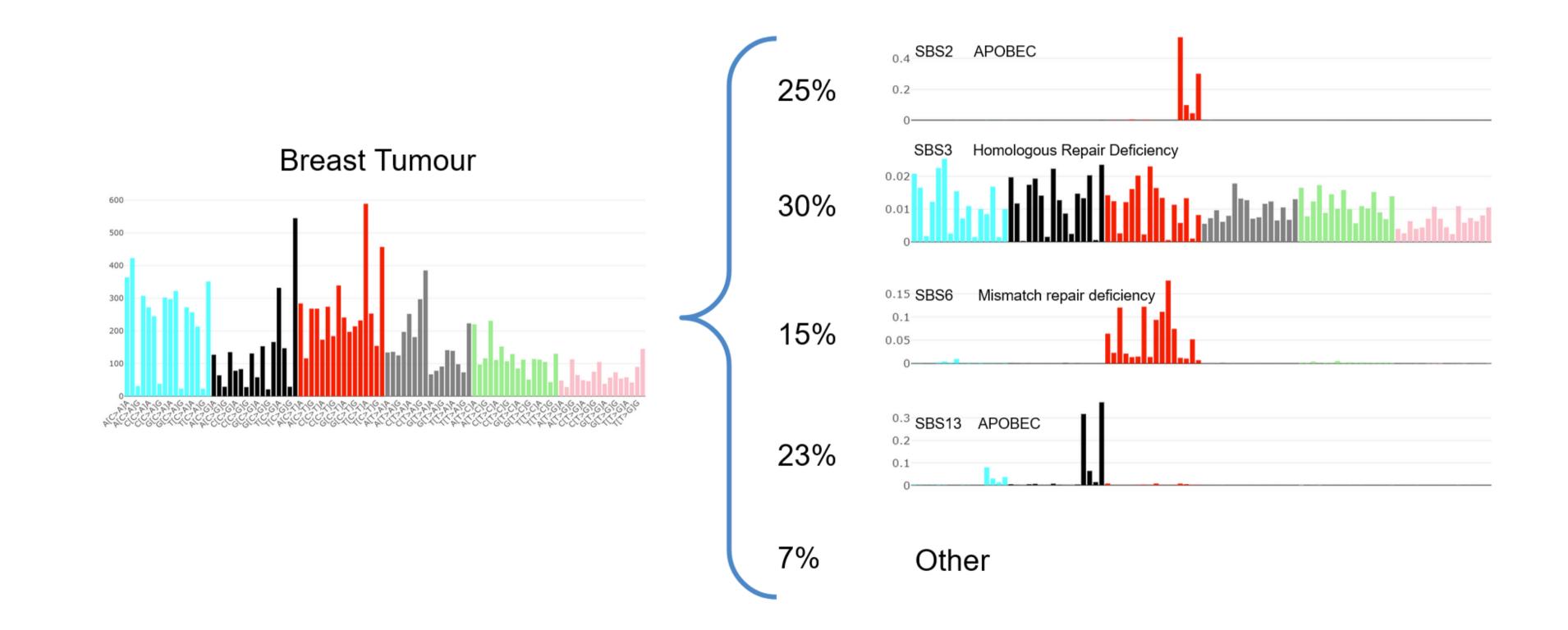
### Time

Mutations act as a "fossil record" of everything that happened to the tumour over its development.

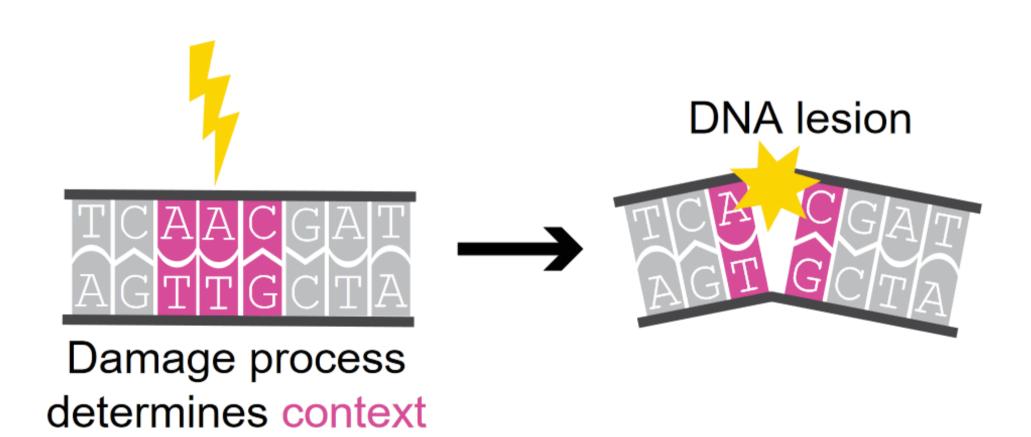
## Mutagens and DNA repair defects can cause distinct patterns of mutations



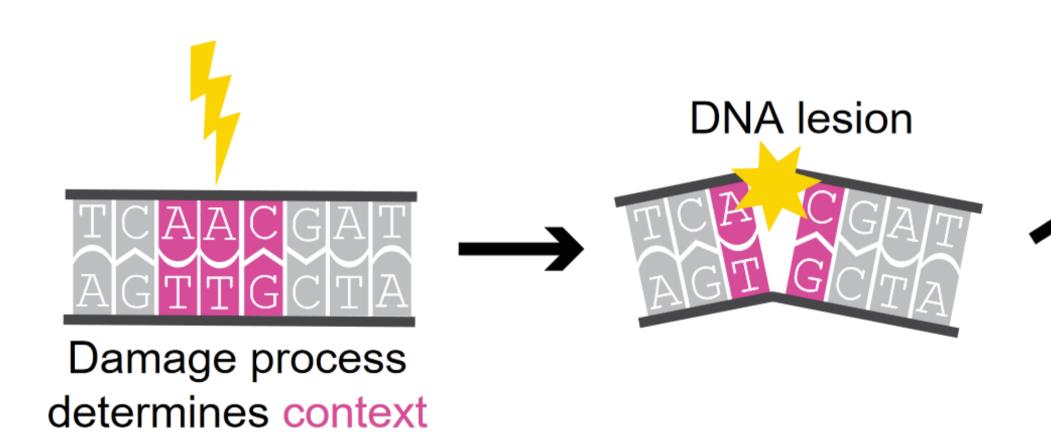
### Mutational signature analysis = identify these patterns



## Problem: current standard model mixes the effects of damage and misrepair processes



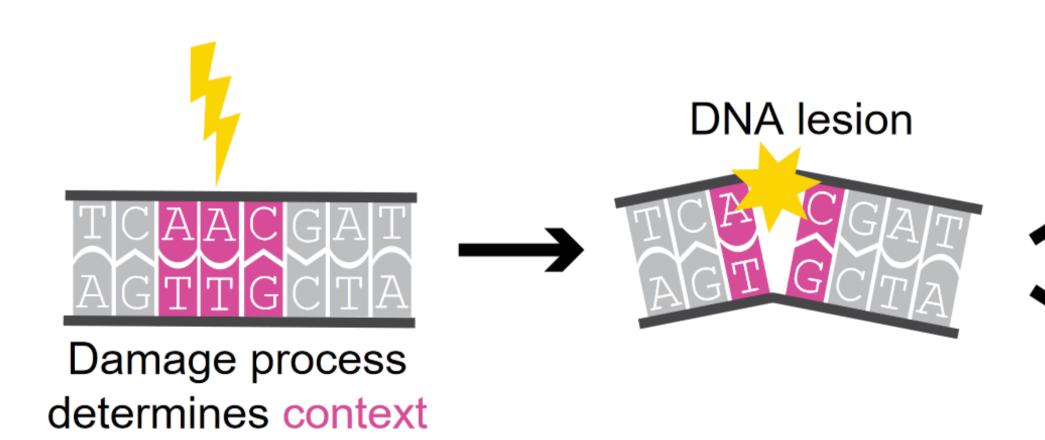
## Problem: current standard model mixes the effects of damage and misrepair processes





Correctly repaired (never detected)

## Problem: current standard model mixes the effects of damage and misrepair processes



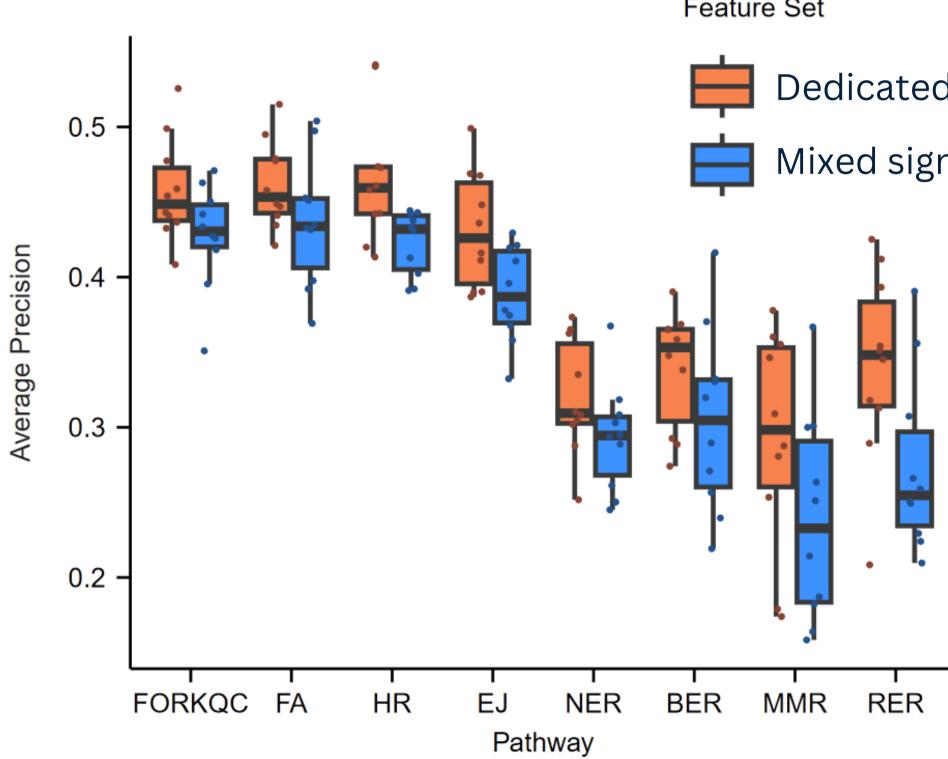


### Correctly repaired (never detected)



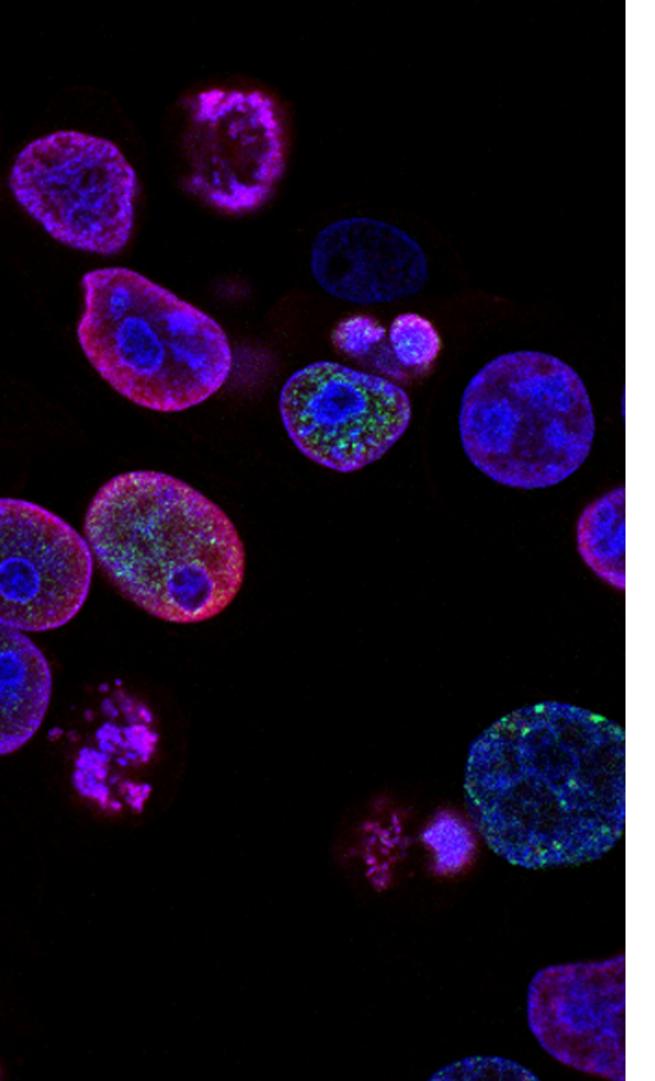
### Base misrepaired substitution observed

### Having dedicated damage and repair signatures helps predict repair deficiencies in cancer



Feature Set

- Dedicated signatures (my work)
  - Mixed signatures (current standard)



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### PhD life

The good: you get to work with amazing people, on problems you think are cool.

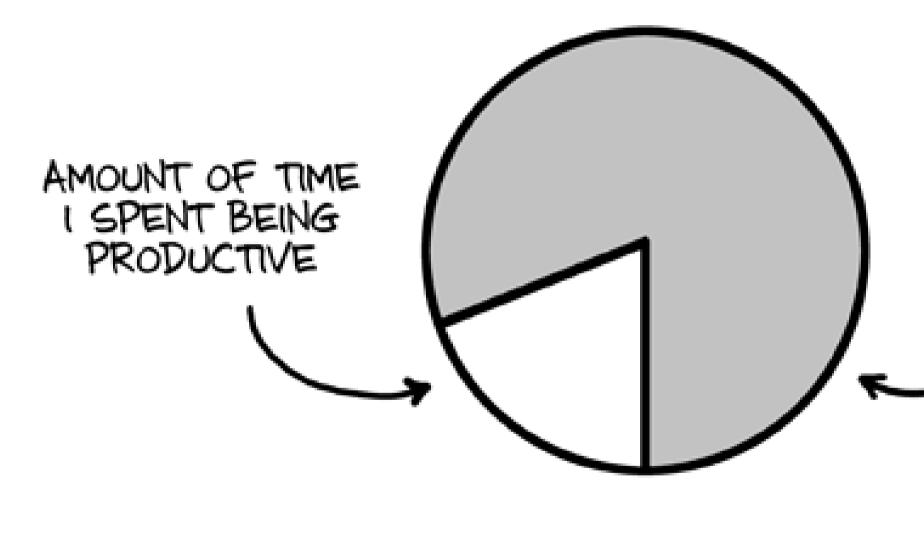
The bad: It can feel like a group project where you're the only one who cares if you get a good grade

The ugly: it takes 4+ years

### How I spend my time

- A lot of reading papers
- Writing code, doing data analysis
- Making plots & figures
- Writing results and scholarship applications
- Talking to other scientists

### HOW MY WEEK WENT:



WWW.PHDCOMICS.COM

JORGE CHAM @ 2014

AMOUNT OF TIME I SPENT DOING THINGS I THOUGHT WOULD MAKE ME MORE PRODUCTIVE.

### Things you can do now to prepare for grad school

- Take a project-based class to get good at working independently
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- Attend talks (ex. monthly meeting of torbug.org)
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### Think about reference letters!

### Email cait.harrigan@mail.utoronto.ca

Web caitharrigan.ca



