Online Report – Bioengineering Outreach Activity

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Bioengineering is a diverse expanding field – this is hard to convey well in schools. The motivation for this outreach activity is to provide a glimpse into this exciting area of science and to motivate students to continue with their STEM courses. My goal is to show hands on how we apply engineering principles in modern biology, and what the future may hold as we all move forth in the postgenomic era.

Collaborating with Emma, she will start us off by giving a run through of basic molecular biology. Here we highlight how fast progress has been in since the discovery of DNA, and the implications it has had on our world now.

Covid-19 has impacted everyone and has created an awareness of molecular biology. I plan to harness this by using the sars-cov2 virus as a path to demonstrate to students how the biology they learn in the classroom has a direct impact on us. This will be done by exploring the genetic sequence variability of the sars-cov2 virus, demonstrating how base changes in the viruses' genetics are the direct drivers for the different variants discussed heavily on the news.

Then I plan to show how to design a PCR covid-19 test using a freely available online software called benching. I think it is easy to view microbiology as an abstract discipline especially when you aren't in the lab conducting research. This recent pandemic has exposed everyone to biology and showing the process of how PCR primers for covid tests are designed will hopefully bring to light how their school studies can be applied.

PLAN FOR WORKSHOP ACTIVITY:

PART 1: Looking at nextstrain.org to see evolution of sars-cov2:

Nextstrain describes itself as : "Nextstrain is an open-source project to harness the scientific and public health potential of pathogen genome data. We provide a continually-updated view of publicly available data alongside powerful analytic and visualization tools for use by the community." By clicking on *Latest Global Analysis – open data* students will be able to view many recorded entries for sars-cov2 sequences in a phylogenic tree to demonstrate the evolutionary behaviour of the virus. Each dot provides further information about the data point, and a link to a genebank entry where sequences can be inspected directly.

1. Go to: nextstrain.org
2. Scroll down and click sars-cov2 (right one)

   Ask students: Do you recognize any of the names?

   Expected answer: Yes, Alpha, Beta, Delta etc. are the variants discussed on the news

3. Click on some of the bubbles (exit a bubble by clicking outside of dark grey)

4. Scroll down and look at the map when pressing the bubble

Ask students: from where in the world are these bubbles located?

Expected answer: all students say different places since they have all chosen a random dot – we all conclude collectively that the information is coming from all over the world

5. Scroll down to the world map and press the play button - watch the animation of the map

   Ask students: What do you notice?

   Expected answer: The timecourse of the pandemic – a new strain appears somewhere and quickly appears everywhere else

6. Click a random bubble and click the *'Genbank accession'* link.

   Ask students: What information do you see?

   Expected answer: Locations, author names, variation etc.

7. Scroll down - do you see long list of letters

   Ask students: what are they for?

   Expected answer: The genetic sequences like Emma discussed earlier

Part 2: Future

After going through this I will conclude with trying to get students about work in the field yet consider the ethical implications and how it is our generation that will be decided how to move forward with these scientific advancements and will have to decide how to use them.

1. Bringing back the mammoth – watch the video from: https://colossal.com/mammoth/

   Ask the students: What do you think of bringing back the mammoth?

   Expected answer: it's cool!

   Ask the students: Who should decide whether we should bring it back?

   Expected answer: diverse set of answers – maybe get a bit of a discussion amongst students

2. 23andMe uses data for studies if participants consent

   Used to improve our understanding of diseases

   Ask the students: What may be the negative effects of sharing genetic information?
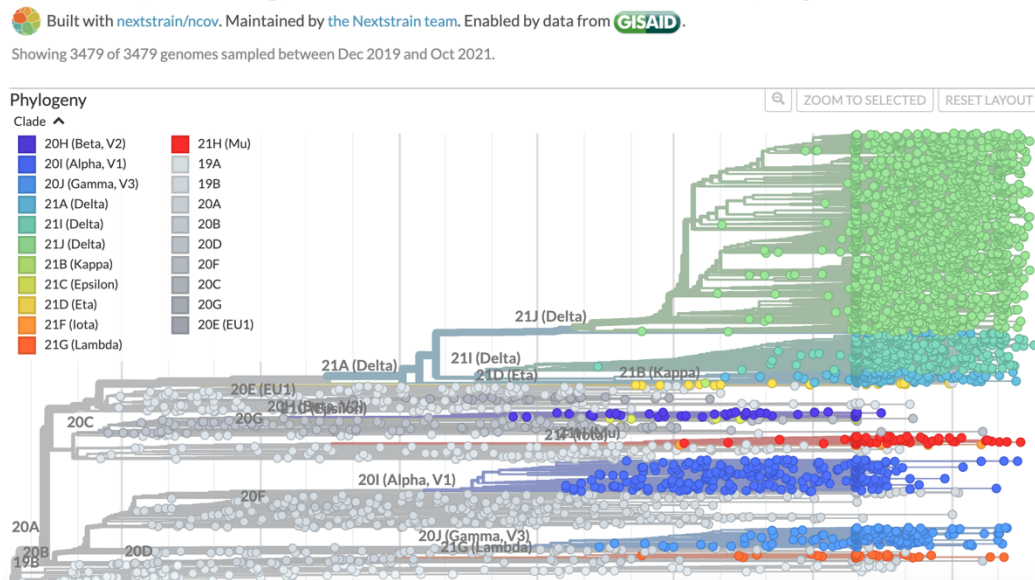
   Expected answers: discrimination

Ask the students: Should we all be giving our genetic information if it may help cure a disease?

Expected answer: diverse set of answers – maybe get a bit of a discussion amongst students

Part 3: Information Engineering in biology

I will walk through code on PCA analysis on gene expression (RNA-Seq) in cancer patients (http://archive.ics.uci.edu/ml/datasets/gene+expression+cancer+RNA-Seq) to show how information engineering is used find genes of interest without understanding the underlying mechanism then provide a modern example: https://doi.org/10.1126/science.abf8683. These will further motivate a discussion on ethics in bioengineering.

Example of looking at nextstrain