**Clinical and Research Genomics Assignment #8**

**Swab analysis**

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**Assignment: Analyze metagenomic data from swabs submitted earlier in the course.**

**Due Date: 5:00PM on May 22nd**

Using the metagenomic classifier or classifiers of your choice (eg. OneCodex from HW4), analyze the data generated by paired end whole genome sequencing of a DNA library for your swab. Submit a report addressing the following questions:

* Where did you swab?
* Do the organisms predicted match what you would expect?
* What is the complexity of the sample?
* Is there evidence for pathogenic microbes? Evaluate the strength of that evidence.
* If your sample did not yield enough DNA or a library, what reasons may have contributed to that?
* Your genome and omes: Given what you have learned in the course, would you want to have your genome sequenced? Why or why not?

(If insufficient data was generated for your sample, answer the same questions, as appropriate, using the undetermined reads. Is there evidence for organisms that you would expect from the environment you swabbed within the undetermined reads?).

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**Please hand in the assignment on the day of the lecture or email beforehand.**

**For any questions, please contact Alexa McIntyre (****abm237@cornell.edu****), Ebrahim Afshinnekoo (****eba2001@med.cornell.edu)****, or Professor Mason (****chm2042@med.cornell.edu****).**