Clinical and Research Genomics Assignment #4

From Lecture_10-11 (April 12th): Genetic Variant Calling

Assignment: Answer questions on genetic variation and clinical genomics.
Due Date: 10:00AM on April 19th

1. Cancer can evolve at the genetic level, but how else does cancer change and evolve?

2. In your answer from #2, what are some of the ways to measure the types of evolution and dynamics of cancer?

3. What is the difference between indels, structural variants (SVs) and copy number variants (CNVs)? And why is this a useful distinction to make for both detection purposes and general biology?

4. What is the difference between precision and accuracy?

5. How do questions of precision and accuracy apply in the case of exome and whole genome sequencing?

6. Explain what you learned regarding false negatives and false positives, and how this relates to sensitivity and specificity for any clinical test such as cancer?

Please hand the assignment on the day of the lecture, or email if you cannot attend.
For any questions, please contact Alexa McIntyre (abm237@cornell.edu), Ebrahim Afshinnekoo (eba2001@med.cornell.edu), Priyanka Vijay (prv2004@med.cornell.edu), or Professor Mason (chm2042@med.cornell.edu).