# Rhodes College

## COMP 342: Bioinformatics

Spring 2020

**Reading Assignment**

"Computational Biology in the 21st Century: Scaling with Compressive Algorithms" by Bonnie Berger, Noah M. Daniels, and Y. William Yu. *Communications of the ACM*, August 2016.

1. What is the difference between Sanger sequencing and next-generation sequencing (NGS)?

2. What is a homology search and what tool is typically used to perform these?

3. What are two data structures mentioned in the article? Provide a definition of each data structure (you may use Wikipedia).  Hint: one is associated with *de novo* assembly and the other with reference-based read mapping.

4. What did you find most interesting about the article?

5. What question(s) do you have after reading the article?