**Anika**: Most of my work was focused on building the python program for building colored De Bruijn graphs, particularly in a format compatible with the frontend visualization application. This process included several iterations of work. I first built a naive uncolored de Bruijn graph adapted for genomic data. I then built a naive colored de Bruijn graph adapted for several strain genomes. I worked on edge reduction techniques for uncompressed colored de Bruijn graphs. In addition, I helped Cindy attempt to implement colored succinct de Bruijn graphs for pangenomic representation. Regarding further work, I developed a method for compression of colored de Bruijn graphs and implemented it. I also implemented a few additional options for graph building use as a part of my graph building Python program, such as the ability to download nodes as fasta files and yield node sequences belonging to particular strains.

**Brian**: I built the majority of the frontend application with React, TypeScript, and the Cosmograph library. I also worked with Anika and Cindy to ensure that the output from their Python application would be compatible with the web-application. I was also responsible for conducting research on how to represent massive graphs in a web browser and experimented with several web-based graph visualization libraries to compare their performance and outputs.

**Cindy**: I focused on building the pangenome and attempted to implement the colored succinct de Bruijn graph for pangenomic application which involved applying the BOSS representation of colored succinct de Bruijn graphs to the algorithms used. I also did validation of Anika's compression method compared to Bifrost output.

**Lambert:** Built the initial python visualization library using NetworkX and Graphviz. This library supported building and visualizing classic de Bruijn graphs, colored de Bruijn Graphs, and Wheeler graphs. Then built a succinct model for representing de Bruijn graphs based on the following. Tested outputs from a number of genome sequences. For the write-up, I worked on the abstract, introduction, past research, and the first section in methods.