# Methods

1. Download genomes
   1. 18,000 contigs: www.ebi.ac.uk
   2. panTro6: ncbi.nlm.nih.gov/datasets/genome/GCF\_002880755.3/
   3. PanTro3.1.1: ncbi.nlm.nih.gov/datasets/genome/GCF\_028858775.1/
   4. GRCh38.p13: ncbi.nlm.nih.gov/genome/guide/human/
   5. T2T: s3-us-west-2.amazonaws.com/human-pangenomics/T2T/CHM13/assemblies/analysis\_set/chm13v2.0.fa.gz
2. Unzip files if necessary. Create .fna files if necessary. Rename sequences in the file if necessary.
3. Create Blast database
   1. Assuming Blast has been installed on your machine (blast.ncbi.nlm.nih.gov/doc/blast-help/downloadblastdata.html). Navigate to the installation directory/bin. The following command starts with an alignment file called input\_fna and creates a database called output\_db. Append directory info to the file names so the data can be found and so the database is placed in the right spot. On my Windows machine, I had to create the output\_db in my root directory (users/.../desktop) and move the files to where I wanted them to be.
   2. > makeblastdb -in "{input\_fna}" -dbtype nucl -out "{output\_db}"
4. Assuming Python is installed on your machine, and all the dependencies, run one of the programs to blast one genome against another, etc.