Lets start by downloading a genome to mine! You can find genome assemblies on www.ncbi.nlm.nih.gov/genome/browse#!/overview/

Lets download the Sloth genome:
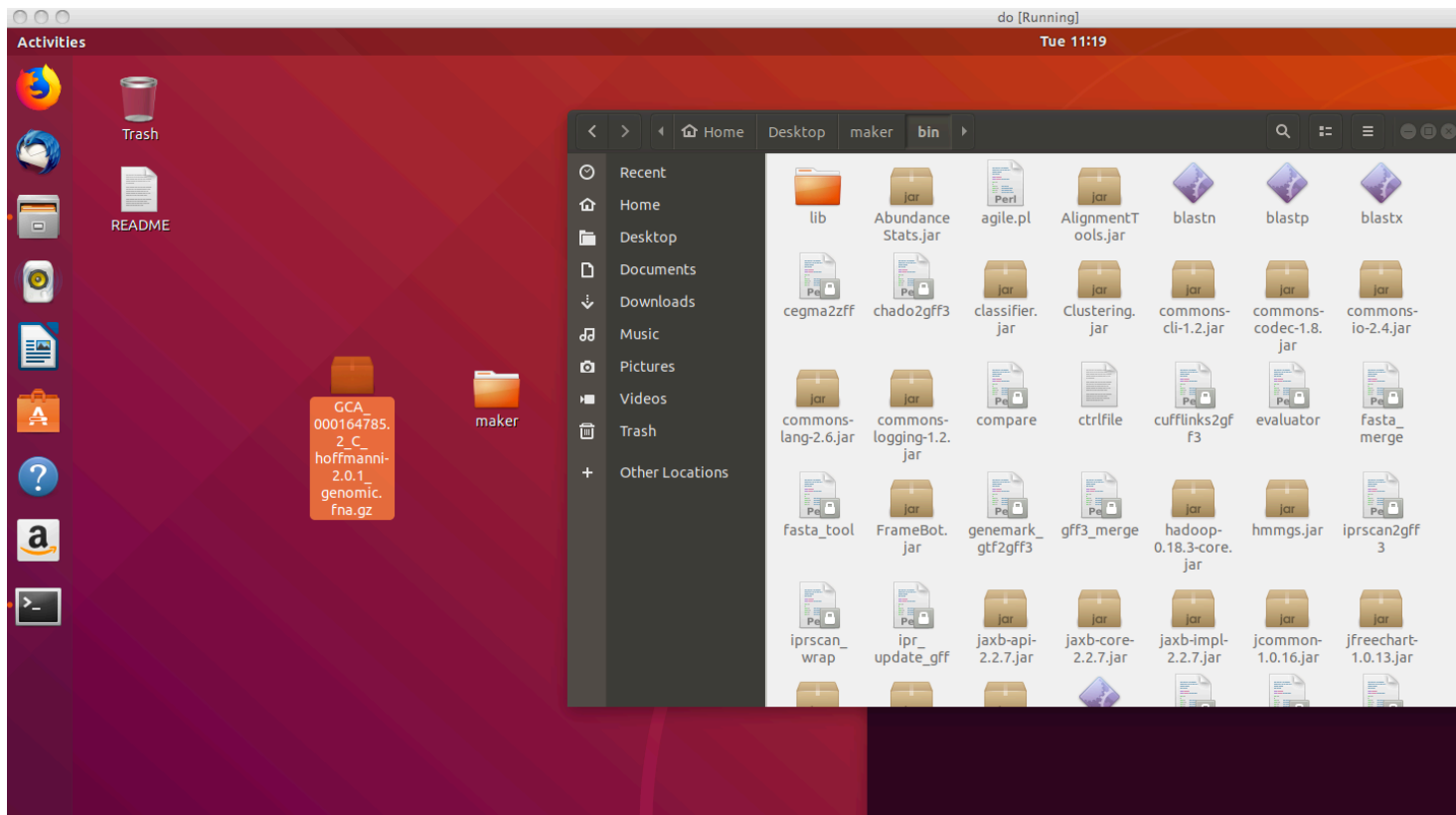
Now lets place the downloaded genome file into the /maker/bin/ directory:

Using terminal, lets move into the /maker/bin/ directory with "cd Desktop/maker/bin/"
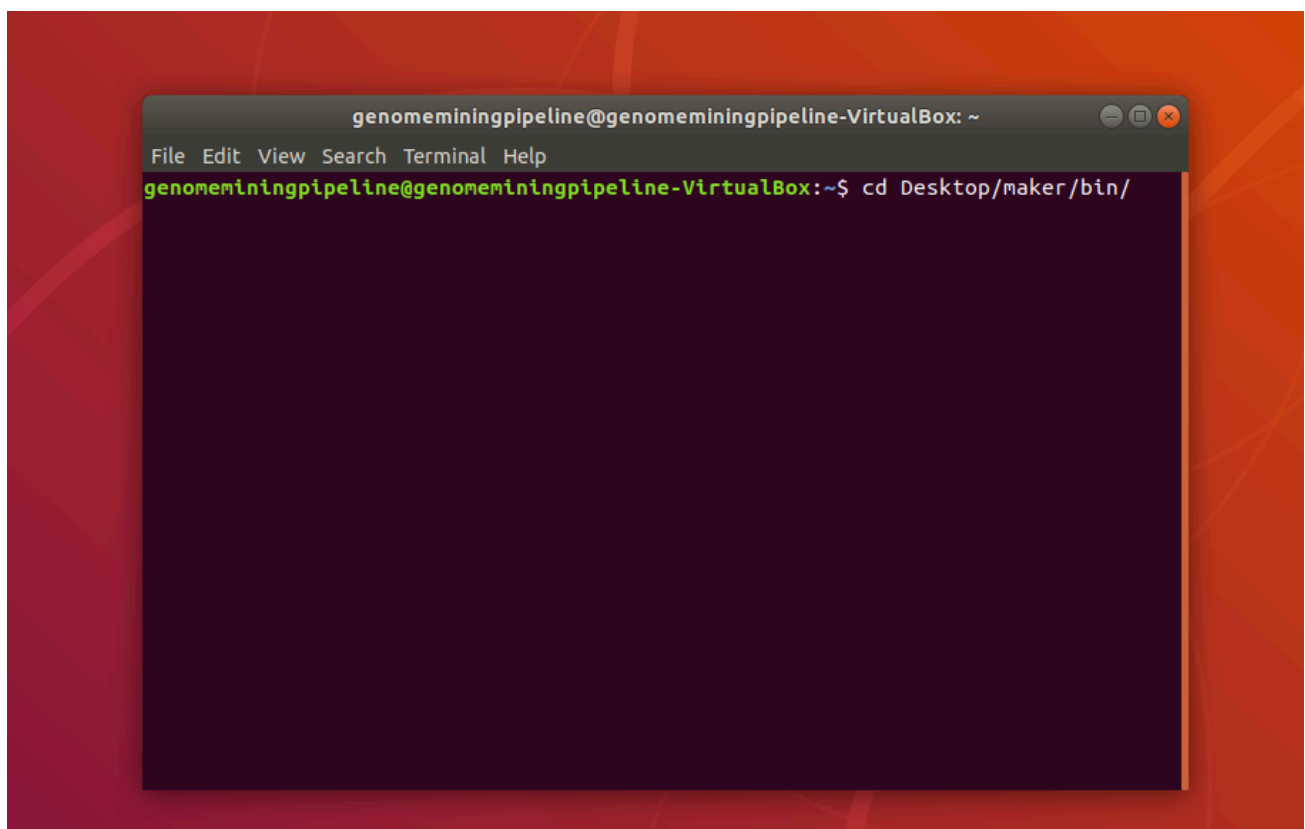
We unzip the genome to mine with "gunzip":

So, we have downloaded our target genome to mine, placed it in the correct directory and unzipped it. Now we need to tell AGILE where to look for all the necessary files.
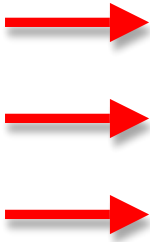
Since all the binaries, including all associated FrameBot files (all .jar files in red), are in the maker/bin/ directory, as EMBOSS matcher, lets point AGILE to the maker/bin/ directory for these. Open the "ctrlfile":
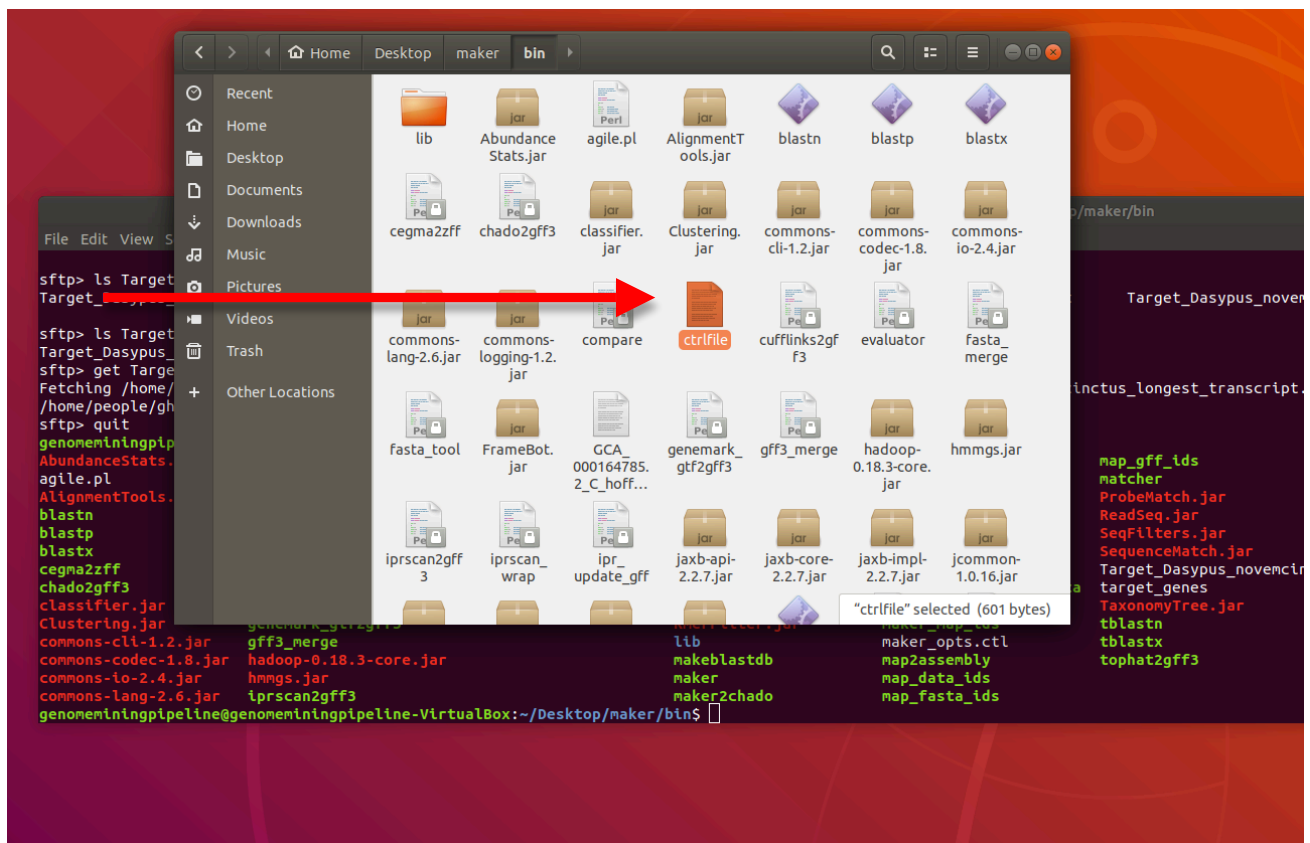
We can get the exact path to our directory using the "pwd" command:

Once opened, we can paste the path as the location of each program binary. We also add the name of the genome file. Note that "Target_genes", "Genome File" and "SisterTaxa" also have names:

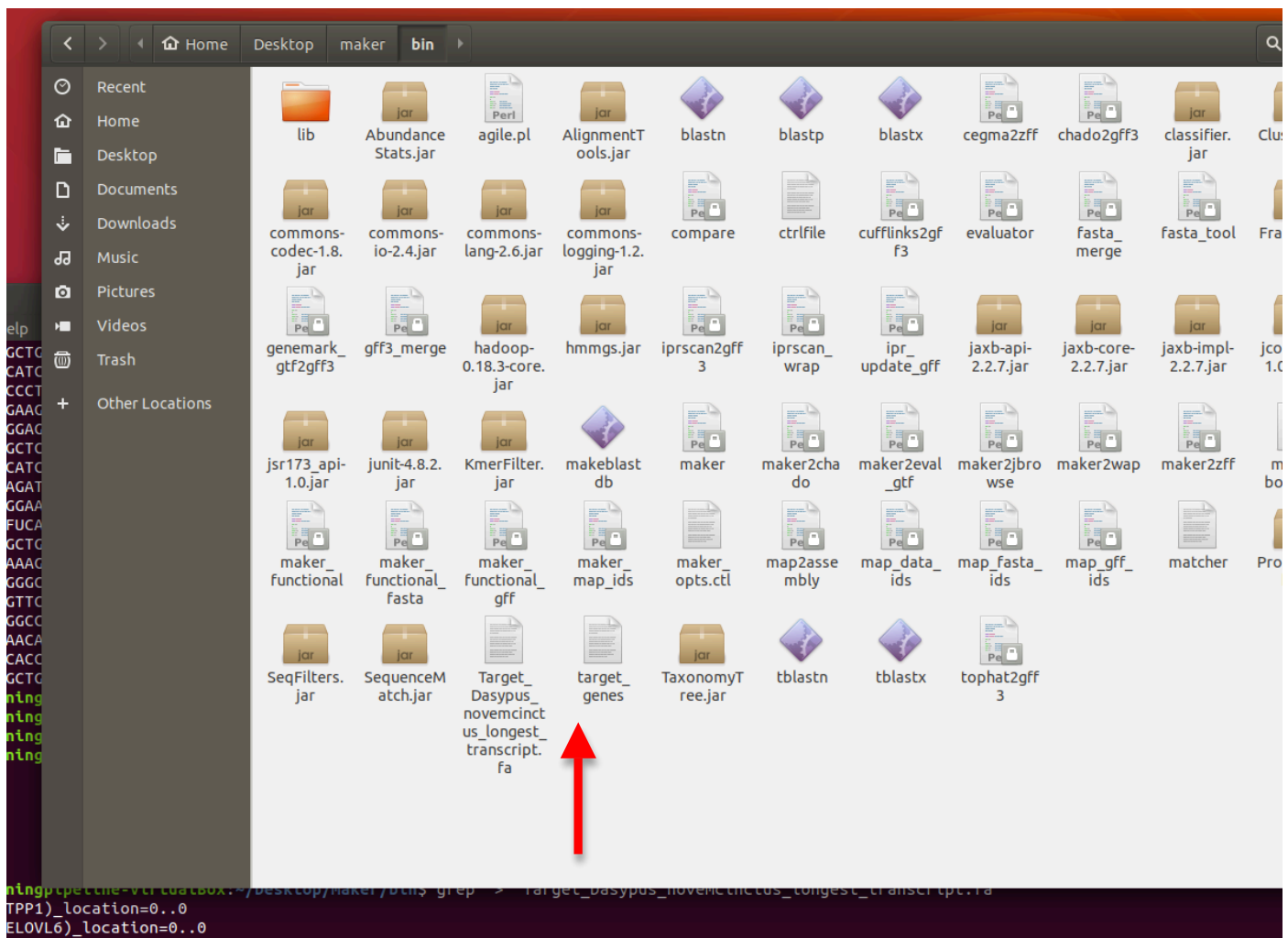Lets create and open a file named "Target_Dasypus_novemcintus_longest_transcripts.fna". We can generate this file using the 'RefSeq_get.pl' script found here: https://github.com/batlabucd/GenomeMining/tree/master/RefSeq_Mining
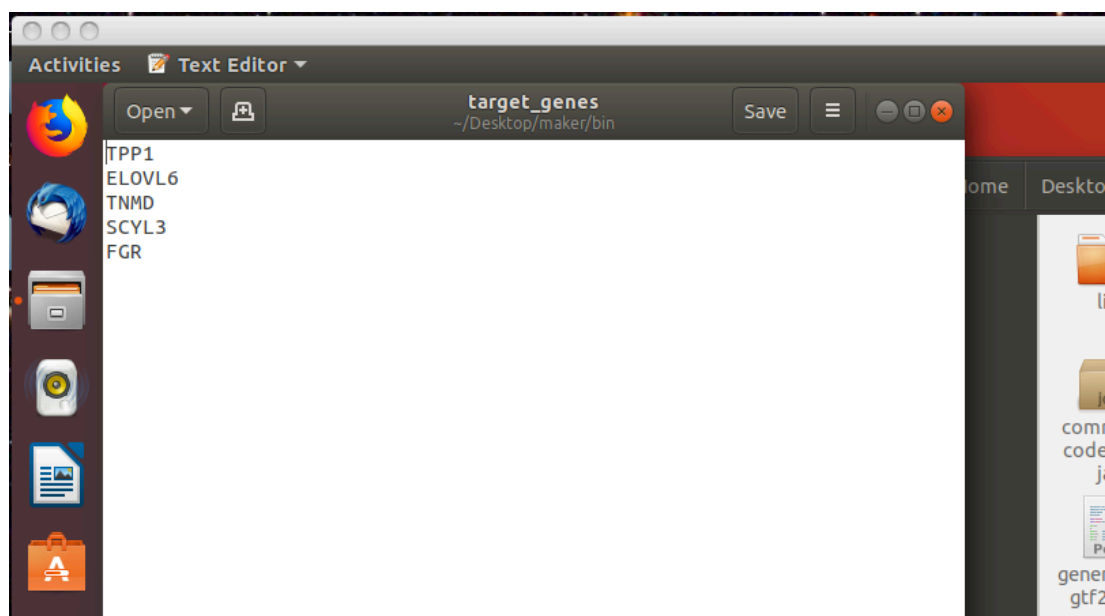
These are the genes we will use as a reference. Note that all fasta headers contain the gene name in the format "(GENE)", eg (TPP1). This is essential as AGILE will look for this format.

Now lets create/modify the "target_genes" file:

We now add a list of all the genes found in the headers of the genes in our reference file:

Lets recap:

-we have downloaded, and unzipped our target genome

-we have placed it into the maker/bin/ directory

-we have modified our ctrlfile to let AGILE know where to look for each program (for convenience, all files are in the same directory)

-we have generated a file with the fasta nucleotide sequence of the genes we want but from a closely related sister taxon to our target genome to mine.

-we have listed all the genes we want in our 'target_gene' file

Now we can run AGILE with "perl agile.pl"

```
genomeminingpipeline@genomeminingpipeline-VirtualBox:~/Desktop/maker/bin$
genomeminingpipeline@genomeminingpipeline-VirtualBox:~/Desktop/maker/bin$
genomeminingpipeline@genomeminingpipeline-VirtualBox:~/Desktop/maker/bin$
genomeminingpipeline@genomeminingpipeline-VirtualBox:~/Desktop/maker/bin$
genomeminingpipeline@genomeminingpipeline-VirtualBox:~/Desktop/maker/bin$ perl agile.pl
```