**Minutes**

10/11/22

* Looked over Google Colab changes.
* Looked at trialled fully connected NN.
  + Discussed fully connected layers and how their connecting edges differ to convolutional layers.
* Identified that the need to transpose one of the matrices implies that my input may not be correct.
  + Reason for transposing was due to working by chance while debugging.
  + Identified mistake is that one amino acid (which is vectorised with 20 rows) is being taken into the first layer (shape 20x10). This is a mistake and is not the behaviour I’m trying to get out of my neural network.
* Mentioned possibly during the pre-processing I would create small text files for each protein sequence (named by ACCESSION\_NO.TXT), and the getitem method would look up the sequence, which could be quicker than requesting the protein sequence using the API for many requests.
  + Advice to pre-process and keep the sequences in the program. There shouldn’t be too many to cause an issue and it will be quicker if they are already in the program.

Goals for this week:

* Have questions prepared about FCN paper.
* Look over conv2D functionality in detail – recommended by Kevin. This applies a 2D convolution.