Program log

**3/07/15** – Finished completing part of the pipeline which aligns individual sequence files, and stores them in folders containing groups of them. Alignment performed using Muscle (m*uscle3.8.31\_i86win32)*. Alignments are in PHYLIP format. Next stage, before these files are run through PartitionFinder, is to setup the configuration file. Will need to consult with others about appropriate data blocks, models and branch lengths on the tree topologies that will be generated for subsets of the final partition.

**14/07/15** – Finished methods for combining sequence alignment files into sample alignment files. But the sample alignment files are not usable by PartitionFinder because of the spaces inbetween each group of 10 sites. I will probably need to combine and concatenate the sequence alignment files using Nexus, and export the result into Phylip format.

**15/07/15** – The partitioning scheme was fine, defining data blocks by columns works. Using some scripts given by Jeremy I was able to convert the fasta alignments into a nexus format, and then into interleaved PHYLIP format. For each sample there’s a mapping file that matches the species names with the names in the PHYLIP alignment file. Pipeline generates configuration files successfully too. Next steps: to include a wrapper function for both PartitionFinder and the RaxML executable into my pipeline.

**17/08/15** - Continuing to put the finishing touches to the pipeline.