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Long term potentiation (LTP) is one the supposed central mechanisms of memory, and it operates in part by strengthening the connections between neurons by increasing the amount of receptors in the post synaptic terminal. When the NMDA, or glutamate, receptor is activated, Ca^{++} flows into the cell, and activates CaMKII. CaMKII is one of the most common proteins in neurons, comprising of about 1-2% of the total proteins in a neuron. It is most commonly expressed in postsynaptic terminals and the surrounding area. Blocking expression of CaMKII has been shown to inhibit LTP. Activation of CaMKII has been shown to not only increase the number of AMPA receptors in the postsynaptic terminal, which mimics the effects of NMDA receptors, but also has been shown after repeated activation to create cytoskeletal changes. Mice with reduced CaMKII activity have also been shown to have reduced levels of hippocampal-dependent memory capacity. In this project, I aligned the CAMKII alpha subunit genes of chicken, rat, and 2 human variants. I wanted to see the differences between species and the extent of the differences between the two recorded variants.

I got the mRNA files from the National Center for Biotechnology Information website changed the names of the files. The program couldn't find them with their normal names for some weird reason. Everything else is purely computational.

I computed all pairs of alignments, found the most similar pair, unceremoniously merged them (gaps = inserting into synthesized sequence), and repeated the process until there were only two sequences left while recording which merged with what.

Human variant one merged with the rat mRNA, and that merged with Human variant2. The chicken was the most distant. The last merging indicator is inaccurate in that it refers to the merged sequence as sequence two, but that's probably because it was so closely related to sequence 2 due to the merging process, which is rather blunt. Human variant 1 mRNA is further away from human variant 2 mRNA than it is from the rat mRNA. This shows that the two variants are very different from each other, and morphological changes in these variants should be analyzed.