Problem Set 4: Genomics

Background

This problem set will introduce you to working hands-on with some introductory genomic tools.

Instructions

1. Download the complete sequence of the GenBank entry with the accession number `NM_000277.2` as a FASTA file.
2. Translate the DNA sequence to amino acids.
3. Using BLAST and the UCSC Genome Browser, align the sequence to the human genome and view the alignment. Take a screenshot of your browser window and attach it to the report.
4. Using PubMed and/or other resources (e.g. The Human Mutation Database), identify at least one disease state of this gene.

The report

Develop a report (I recommend a Word (or other text editor) document) for your problem set that includes answers to all of the questions posed above, showing plots where appropriate. Describe how you translated DNA to amino acids. Provide the amino acid sequence. Where did the sequence align in the human genome? What condition is the sequence associated with? Provide some information on the condition and the association with genetic variants and this condition.

Save your report as a PDF file and submit your report through the course 2GW site.

Due date

Day 7, Week 7