**BINF 732 – Genomics**

**Final Exam**

**Due May 6, 2024**

**Please answer all four questions. Please limit answers to one page per question.**

1. **How were seedless watermelons created? Was this different from the process from the creation of the modern seedless grape? Are these considered genetically modified organisms? Why or why not?**
2. **There are several tools to perform phenotype prediction from the genome sequence. These include standalone tools (SIFT, Polyphen, MutationAssessor, I-Mutant, FatHMM), and consensus tool (Condel, Pon-P, PredictSNP). Consider the amyloid beta protein (UniProtKB - P05067** [**https://www.uniprot.org/uniprot/P05067**](https://www.uniprot.org/uniprot/P05067)**). Choose 8 of the SNP variants and predict pathogenicity. Pick another gene with variants and see how well the tools make predictions. What can you say about the accuracy of standalone vs the consensus-tools? Please note that the PredictSNP can take over a week for output to be returned due to a long queue.**
3. **What is the difference between “junk DNA” and “the dark genome”? Are these reasonable terms? Please justify your answer.**
4. **What is gene editing? Can gene editing be used to treat human disease? Please support your argument with details.**