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Software Design
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Gene Finder Mini-Project Write-up and Reflection

Results:

By using the Protein BLAST or BLAT genome search, I was able to find out more about the output produced from my gene finder program, specifically by taking a few of my output sequences and searching their protein sequences. I also learned about some of the candidate genes I found, SPI-1 type III secretion system protein SpaO [Salmonella enterica subsp. enterica serovar Typhimurium] and SPI-1 type III secretion system protein SpaO [Salmonella enterica]. SPI-1 type III secretion system protein SpaO [Salmonella enterica] (T3SS) is an actual gene that comes from Salmonella pathogenicity island 1 (also referred to as SPI-1). T3SS delivers effector proteins that are referred to as the most vicious factor toward Salmonella as it plays a critical role in the invasion of salmonella into host cells. SPI-1 type III secretion system protein SpaO [Salmonella enterica subsp. enterica serovar Typhimurium] is a pathogenic gene that is a factor in the avian salmonellosis in wild birds, which has caused high mortality rates amongst songbirds and aquatic birds. The transmission of S. Typhimurium is caused by wild birds to people, pets, and livestock.

Reflection:

While I have learned a lot about creating a functional and longer program through this project, I have learned a lot about the impact a program can have on others in real life. For example, the gene finder technology I created could be modified to benefit biologists in their work better convert dna to protein sequences. This could help streamline their daily work. This could also be created to search for sequences that could indicate something about people's genetic makeup which could help give genetic findings to patients about their genetic makeup. As the program stands, there are some limitations. This program specifically takes in a certain dna, and creates a final list of all the larger sequences and converts their code into amino acids. This would mean that there are smaller sequences left out that could be analyzed. This also does not show much about what the sequences actually mean or are. This is a huge downside as there's only so much we can do or know from the output of our program.

In order to adapt the current gene finder program to enable more advanced applications, we could possibly create functions that help read and search through sequences for specific

patterns. This could help search for other diseases, etc. within the dna we are given to do more than just convert the codons to sequences, but rather give tangible information regarding the dna. To do this would require a bit of work, however, it could be beneficial to people in the science field trying to comb through dna to better understand the genetic makeup of people, animals, etc.



