Gene and mRNA Model Viewer

Capstone Project Proposal

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Specifications

The Gene and mRNA Model Viewer will be a program written in C# used for exploring the features of genes and mRNA. The sequence and feature data will first be pulled from the NCBI's Entreaz databases (<http://www.ncbi.nlm.nih.gov/>) from user input into the application. The functions will be made to mimic the Entreaz search and parse functionality of Biopython. The viewer itself will include a visual representation of the sequence with accurately located and sized labeled sections (likely displayed with color) identifying the features. The visual representation will have some sort of navigation (drag and/or zoom) to accommodate long sequences. The features will also be listed as text beside the image; when this text is clicked, the feature will be pointed to on the image with the name of the feature and its location. It may potentially also include either a description or link to an external source which explains what the feature is.

The viewer will be able to search for a new mRNA or gene after the first results have been displayed. Additionally, the results will include links which will trigger a new search for either the mRNA made from the gene currently being examined, or the gene which made the mRNA currently being examined.

Rough Mockup & Timeline

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|  | **First stage:**  Create a general forum and search functions |
| **Second stage:**  Create parse functions and display data in viewer. Error checking. |
| **Third stage:**  Clickable interactions. Testing. Refining. |