

DEVELOPMENT OF A VISUALIZATION APPLICATION FOR GENOMES IN THE ORDER KINETOPLASTIDA

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Genome research, such as prediction of genes, often benefits from the use of visualization tools. There are several such programs in existence, but they suffer from one of two drawbacks. They are either specialized for organisms other than those in the order Kinetoplastida, or are organism definable yet far too elaborate and require significant existing annotation. We thus developed a custom-built web application to aid in our genome research in Kinetoplastids. A multipart CGI script was designed using the Perl programming language, chosen because of its proven versatility and CGI capabilities. The resulting application allows simultaneous multiple users to examine any available Kinetoplastid chromosome. The chromosome data are interactive; thus users can zoom in on regions of interest, view available annotation on predicted and verified genes, and view ORFs and other chromosome features. The application is fully customizable, allowing users to specify which database the features are pulled from and which of those features are to be drawn. Those and several other preferences are then stored client-side via cookies. This application has already been used as a tool in projects such as pattern finding and gene verification in the kinetoplastids.

Anthony would like to present this work as a poster at the Symposium.