VBRC Base By Base: Align entire sequences or subsequence regions

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Abstract

Viral Bioinformatic Resource Centre

- **Provide databases of viral genomic information.**
  - Please check the **_Organisms_** menu to see which viruses we support: we're now focusing on large DNA viruses
  - The VOCs (Virus Orthologous Clusters) database is at the heart of our system.
  - The database links directly to integrated tools for comparative analyses.
  - VOCs sorts genes into ortholog clusters (e.g. RNA polymerase) to simplify data retrieval.
- **Provide easy access to the genes, gene families, and genomes of the different virus families.**
  - via a unique series of powerful Java tools that support multiple computer platforms (see **_VBRC Tools_** menu).
  - design and build software to tackle specific bioinformatics/virology problems, often in collaboration with virologists.
- **Rally the research community to provide expert curation of these viral genomes by:**
  - Adding value to GenBank sequences through enhancing and updating genome annotations
  - Linking to research reviews/papers for the research community.
- **Collaborate with researchers to help on specific bioinformatics problems, e.g.**
  - Custom searches of the databases
  - Building new features into our tools
  - Help with genome annotation

Protocol

Step 1.

To align sequences in BBB, first select the sequences you wish to align (by clicking on their names in the Sequence List; hold down the **CTRL** or **Apple** key to select more then one).

Step 2.

Choose the **"Select"** mouse mode from the toolbar and select the sequence region that you wish to

align.

– Selecting large regions can be done more easily by using the **"Select Region"** tool from the *Edit* menu.

– To select the entire sequence, choose the **"Select Whole Sequence"** option from the *Edit* menu.

Step 3.
Finally, go to **"Align Selection"** under the *Tools* menu; choose the method of alignment (ClustalW, TCoffee, or Muscle (proteins only)) you wish to use.

Step 4.
Adjust the alignment parameters (if necessary) and wait for the alignment to be generated (this may take several minutes or longer for large alignments.)

When the results window appears, click **"Ok"** to accept the alignment