Babraham Bioinformatics

VectorNTI Course Exercises

Licence

Exercise 1 : Starting VNTI and Importing Sequences

- ♦ Launch VNTI Explorer and enter your user details if asked

- ♦ Fetch the nucleotide sequences with the following accessions and save them into your database:

    - ♦ NM_011756

    - ♦ NM_007564

    - ♦ NM_001001806

- ♦ Put all of these sequences into a new subset called Zpf36

- ♦ Change the explorer display to show the descriptions and lengths of the sequences

Exercise 2 : Molecule Display

- ♦ Open NM_011756 into a Vector NTI window

- ♦ Adjust the layout so the graphical display spans the whole top of the window, and resize the molecule to fill this space

- ♦ Create and save a new display profile in which only unique enzyme cuts are shown and in which CDS features are drawn in solid green

- ♦ Use the Edit Picture mode to make some major "adjustments" to your graphic and then save it as a genbank file so these can be preserved for posterity

Exercise 3 : Sequence Editing

- ♦ Fetch the sequence BQ939281 and put it into a new subset

- ♦ Select the region 22-909bp (Note that although this is a complete ORF it is not found by the ORF display tool)

- ♦ Create a CDS feature over this region

- ♦ Trim the 5' end of the sequence so that it starts with the ATG of the CDS, and add a TAA stop codon at the end (Note that the ORF search tool WILL now show you an ORF!)

- ♦ Save the sequence back to the database

Exercise 4 : Analysis

♦ Using the modified BQ939281 sequence from Exercise 3 determine the number and size of restriction fragments generated by TaqI

♦ Add a 3 letter translation to the sequence pane for the CDS of this sequence

♦ Create PCR primers to amplify the TaqI fragment which begins at base 283

Exercise 5 : BLAST Searches

♦ Open up the NM_007564 sequence and perform a blast search just using the CDS. Search the protiein database using an appropriate blast program (nucleotide query vs protein database).

♦ Retrieve the top 11 hits into a new protein subset called "Blast Hits"

Exercise 6 : Sequence Alignment

♦ Create an alignment of the proteins you retrieved from your Blast search.

♦ Save this alignment as both a native AlignX file and an MSF file.

♦ Use the "Broadcast Selection" option from the alignment to highlight a conserved region in a normal VNTI view of one of the molecules.

Exercise 7 : Exporting

♦ Create an archive file containing all of your protein Blast hits

♦ Reopen the molecule you edited in exercise 2 and export the graphic into a PowerPoint presentation or Word document