THE UNIVERSITY *of* EDINBURGH

Bioinformatics 1

Assignment 2

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Contents

1 Question

1.1 Use a BLAST query to find orthologues of your gene. Describe what this query returned, and how you selected potential orthologues.

1.2 Compare your result with a query for homologues, to find these, select 'HomoloGene' in NCBI instead of 'Gene' as search option.

1.3 How well do the results match when you consider e-value, % overlap or score from your BLAST search?

1.4 List those results from your initial query that you think are true orthologues, and explain why.

2 Question

2.1 Now consider the phylogenetic implications of your results. First, create a BLAST tree (using the function 'Distance tree of results').

2.2 Describe the result and its relevance.

2.3 How can this be used to study the disease in another model organism?

2.4 Are there known orthologues in mouse, fruit fly or yeast?

2.5 Using the information under 'General gene information', discuss whether mouse, fruit fly or yeast (or any of these for which an orthologue exists) are suitable models to study the disease.

3 Question

3.1 Select four orthologues, and create a rooted phylogenetic tree using the UPGMA algorithm as shown in class.

3.2 Does it match the BLAST result from Q1/2?

4 Sources

Ensembl genome browser
http://www.ensembl.org/Homo_sapiens/Tools/Blast?db=core

Genetics Home Reference
https://ghr.nlm.nih.gov/condition/huntington-disease

National Center for Biotechnology Information
https://www.ncbi.nlm.nih.gov/

Wikipedia
https://en.wikipedia.org/wiki/Huntington%27s_disease