CSC 314, Methods Write-up

The analysis

Background: The *C. elegans* gene *cep-1* is related to *TP53*, a transcription factor and tumor suppressor gene in humans that regulates the cell cycle. Mutations in *TP53* can result in uncontrolled cell growth, which can result in cancer.

Objective: Identify candidate targets of cep-1, which are genes that have a TP53 binding consensus sequence in their promoters (up to 1000 bp upstream of the gene). Identify all *C. elegans* genes with at least 2 binding sites, and provide a table with the following information: the worm gene name, the number and locations of the binding sites, the human orthologs (if they exist), a summary of the human gene. (You may be asked to identify Gene Ontology (GO) terms at a later date.

The TP53 binding site has the consensus sequence:
G/A, G/A, C, A/T, A/T, G, T/C, T/C

Assignment:

Now that your assignment is complete, you will write up the methods describing your analysis. Although you may continue to work in groups on this assignment, each person must turn in their own write-up to receive credit.

Your write-up should consist of 3 sections, described below:

Methods

Your write-up must describe in detail the methods used in your analysis, including any python libraries or databases used. Your descriptions of the methods should not be at the code level, but should describe the scripts that were written, including their basic purpose, the inputs (types of files read), and outputs, if relevant.

Discussion

In this section, you will discuss the completeness of the project, including comments comments on the accuracy or completeness of the results. If something was not done correctly, you should identify that here, and describe the methodology that should have been used to complete the assignment.

Contributions

Finally, your write-up should end with a *contributions* section, that specifies the contribution of each of the group members.