­­Assignment 2 – Answer sheet

**Configuration file.** After making the requested changes to your configuration file (and sourcing the new file), paste the last five commands from your history here:

**1.i** The number of lines in “structure\_hidden.pdb”:

# of lines:

Relative path command:

Absolute path command:

**1.ii** Lines 4532-4539 of “structure\_hidden.pdb”:

Command:

Content of lines 4532-4539:

**1.iii** Grep command used to display lines 4532-4539 of “structure\_hidden.pdb”:

**1.iv** Grep command using context lines:

**1.iv** The atoms of “structure\_hidden.pdb”:

# of atoms:

Command:

**2.i** Counts of files in “bunchoffiles”:

|  |  |
| --- | --- |
| File extension | # of files |
|  |  |
|  |  |
|  |  |
|  |  |

Commands used:

**2.ii** Commands used to generate “halfthefiles” and move “.txt” files into the new directory:

**2.iii** Command used to concatenate all of the “.txt” files:

**2.iv** Number of lines in “all.txt”: \_\_\_\_\_\_\_\_\_

**2.v** Commands used to delete the “halfthefiles” directory, including all of its content:

**2.vi** Incorrectly named files.

Number of files:

Command used:

**2.vii** Renaming command:

**3.i** Commands used:

**3.ii** Command used:

**3.iv** Sequences in fasta.

Command used:

Number of sequences:

**3.v** Sequences with names that start with “AA”.

Command used:

Number of sequences:

**3.vi** Sequences with names that end with “0”.

Command used:

Number of sequences:

**3.vii** Lines in subset fasta file.

Commands used:

Number of lines: