Homework 1 - Due by 11:00 pm pm Monday, March 10:

All homework must be submitted as an attached file via email. Consider organizing your results into respective subfolders within your “Homework_1” folder. When you are done, compress the “Homework_1” folder into a zip file, “LASTNAME_hw1.zip,” and submit the compressed file via email to leizhou@ufl.edu.

An office hour for homework_1 will be held on March 8th after the class (1-2pm) in CGRC-291.

I.) Web-based bioinformatics resources (20 points):

Identify at least 2 web services (tools) that provide RNA structure prediction.

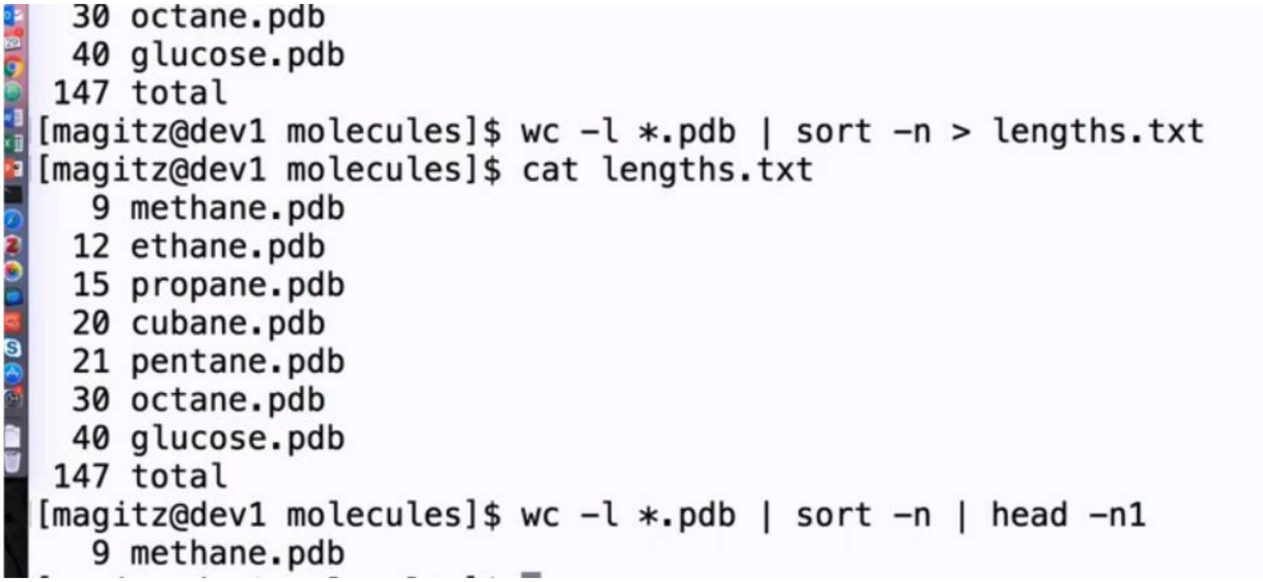
Try out a sample query (any RNA of interest to you) using the two services. Compare the outcome (i.e. Is there any difference?). Turn in the output and your analysis as .pdf or .html file(s).

II.) Functional databases (20 points):

Retrieve the pathway and functional information related to the gene of your interest from the following databases: NCBI/Gene, EBI/UniProt, KEGG, Reactome. Save the search results as either .html/htm or .pdf file.

III.) Log into HiPerGator, navigate to the /blue/gms6014/share/ folder. Make a subfolder with your first name, cd into your subfolder and then follow the practice introduced in the HiPerGator command line tutorial. Submit the “lengths.txt” file or the screen lift image similar as below (30 points).

Example from the tutorial:



```
  30 octane.pdb
  40 glucose.pdb
 147 total
[magitz@dev1 molecules]$ wc -l *.pdb | sort -n > lengths.txt
[magitz@dev1 molecules]$ cat lengths.txt
   9 methane.pdb
  12 ethane.pdb
  15 propane.pdb
  20 cubane.pdb
  21 pentane.pdb
  30 octane.pdb
  40 glucose.pdb
 147 total
[magitz@dev1 molecules]$ wc -l *.pdb | sort -n | head -n1
   9 methane.pdb
```

IV.) Run the command line BLAST on your own computer. Alternatively, you may do so in HiPerGator (30 pts).

For your search, download a **Non-mammalian** genome (predicated cDNAs) from Ensemble FTP ; Search (BLASTP or TBLASTN) the genome with a query sequence of interest to you. **Change the E value** so there are between 1 and 20 hits on your report. Submit the BLAST output as a .html file.

V.) (**Optional**, for extra credits) Download and install Python (http://www.python.org/), Biopython (http://www.biopython.org/). Try an example program from the Tutorial book. Submit the code as well as the result. (20 pts)