**Final Project Submission Deadline: Thursday, May 99th at Midnight**

Final projects may be submitted via email, or flash-drive and should include the following documents:

1. **Final Report** - a publication worthy report of your project. The section outlines detailed below should serve as a guideline of what content belongs in each section – NOT a checklist of the only topics you need to write about. Above all else, your report should clearly and completely describe all aspects of your project. Sections include:
   1. Introduction – your report may reach an audience unfamiliar with the biology or computer science involved in your project, this section should include enough information for a scientist from any discipline to understand your project and why your work is important.
   2. Methods – Describe how the experiment was conducted. This section should answer questions such as: Which genomes were chosen? Where were the genomes downloaded from? Which data sets were scanned? Which programs did you use, and for what purposes?
   3. Results – **(Required) 1 unique figure that directly addresses your experimental question.** Other figures and tables resulting from the Methods should go here as well. Do not interpret your results here, if you calculate a significant number or percentage, simply state it.
   4. Discussion – Interpret every result. Discuss your results in the context of your introduction and experimental question.
   5. Appendix – Do you have a spreadsheet too big to fit in your report? Don’t keep data from your readers! In this section write one quick sentence about the additional files you have made available. You should also mention that these files exist somewhere in your results section.
   6. References – You may cite sources in either MLA or APA. There is no minimum requirement for sources, but you should cite sources wherever they are necessary to a claim. For example:
      1. (no source needed) “Bacteriophages are viruses that infect bacteria”
      2. (source needed) “Bacteriophages are the most abundant biological entities on the planet with an estimated 1031 infectious particles globally”
2. **.bam and .m8 files** – These files took a large amount of time, energy, and computational power to generate, yet they are quite small in size. Please download and submit these files alongside your final report. To download these files:

FROM A TERMINAL ON YOUR COMPUTER (before you ssh into your Jetstream IP)

scp username@jetstreamip:~/bam\_scripts/Input/BAM\_files/\* /path/on/your/computer/

1. **One Unique Figure** – In addition to including this figure in your paper, please submit the figure separate from your report. If you have more than 1 awesome figure, please include them as well.
2. **SraAccList.txt** – If you used more than 5 SRA Runs in your experiment, do not individually list them in your Methods section – especially if you used hundreds or thousands - instead, mention this file in your report and appendix. Every student should submit this file with their project.
3. **“hits” and “stats” CSV files –** If you ran a “make (sam/protein)\_stats” or “make (sam/protein)\_hits”, then you probably have a CSV file too large to display in your report and had to use a smaller set of that data; include the full files with your submission and mention them in your report and appendix.