

# WVU GENOMIC DATA ANALYSIS – FINAL REPORT FORMAT AND CRITERIA

## Report Format

Your final report should be 3-5 pages, single-spaced, with 1 inch margins. Pay attention to spelling, grammar, and punctuation – glaring errors will reflect poorly on your grade for this element of the project. Please include the following sections in your report:

**1. Introduction** (*0.5 page*). Give a brief overview of the project scope, significance, and goals. You may use your proposal document as a guide.

**1. Changes from Proposal** (*0.5 page*). Include a brief, point-by-point discussion of any changes that you made to your project since the proposal stage (e.g., different assembler, different data set, etc.). Note what changed, and why it was changed. If you did not change anything, simply state that.

**2. Results** (*1-2 pages*). Present the results of each step of your project (i.e., data retrieval, QC, processing, post-processing). Include all steps – even if a step was unsuccessful or you were not able to complete it. You are encouraged to include up to 3 figures and/or tables to help present your results.

**3. Discussion** (*1-1.5 pages*). Briefly discuss your results, especially where they do not align with your expected outcomes. Also include lessons learned from this project that you may carry forward to the next. Identify significant challenges that you encountered and solutions that you devised during the project.

**4. Pipeline code** (*not included in page limit*). Include **all of the code** used to generate your final product. For each command or group of commands, indicate briefly (using comment lines) the task that is being addressed.

Turn in your final report as a Word file by pushing it to the appropriate “final\_reports\_#” directory on the class github repository. Please include your first name in the file name, and in the file itself. See **Pipeline and Report Scoring** for more information about how your report will be assessed.

## Pipeline and Report Scoring

Your final report will include the code that comprises your pipeline. The following three criteria will be used to assess your report and pipeline code:

- 1. Does the code run?** For full credit, your code\* must be properly formatted with the correct arguments.
- 2. Does the code complete all the required tasks?** For full credit, your pipeline must include code to address each step in the process that used a script or code (data acquisition, QC, processing, and post-processing).
- 3. Does the report conform to the posted guidelines?** For full credit, please submit your report on time with proper grammar, syntax, page limits, font sizes, etc. Also, figures and tables should be numbered, titled, explained with a brief caption or legend, and called out appropriately in the text.
- 4. Is the report well-organized with a logical flow?** For full credit, your report should be well-organized and readable. The use of section headers is encouraged. Colored text, bold, and underlining are also useful mechanisms for highlighting important information when used in moderation.
- 5. Were any lessons learned?** For full credit, identify significant challenges that you encountered and solutions that you devised during the project, plus any fundamental lessons that you took away from the experience.

\*Note that your pipeline requires human feedback at various points (e.g., after QC). As a result, it is understood that your entire pipeline will not be able to run sequentially. However, each line or block of code should be syntactically correct.