CMEE Masters: Computing Coursework Assessment

Assignment Objectives: To work on a series of computing/programming exercises and problems in a coherent, modular, reproducible workflow under version control.

Note that:

- The overall assessment will typically have significantly lesser marks than a simple weighted average of each week's points because the overall assessment is based on not just the "Computing Coursework Assessment Criteria", but also the the "Marking Criteria for Exams, Essays and Coursework". Both sets of marking criteria are in the Assessment Appendix of the online TheMulQuaBio notes and git repository.
- In your 1:1 post-assessment feedback session, we will discuss where you gained or lost marks, and what you could have improved further. To the extent possible, please come with questions about specific scripts based upon the overall and weekly feedback you have received. This may require you to compare your code with the solution code in many cases.

Student's Name: Eamonn Murphy

1 Specific feedback

1.1 The Good (what you did well!)

- 1. Found all the core CMEE weekly directories in your parent directory.
- 2. Your code and repo are cleanly and logically organised.
- 3. Your Git repo size when I checked week 7 was about 3 MB nicely compact! This suggests you correctly suppressed unnecessary files from version control, and did not commit excessively. It could also mean that you did not commit enough, and/or somehow along the the way lost parts of your git history but we don't check these possibilities!
- 4. Generally a very good job with the coding, just be careful to check for details like loading packages and ensuring that data files on which your scripts rely are included in your repo!
- 5. Your Python is generally very nicely modular this is excellent and very Pythonic!
- 6. Good job with your docstrings, all of which were present where needed, and nicely informative.
- 7. You have included both overall and week-specific readme files. These are comprehensive, well-organised, and you have even included things like dependencies (with version numbers!) for each one. This is excellent practise, so well done. Also check out this resource: https://github.com/jehna/readme-best-practices. As you become a seasoned programmer, you will learn to make the readme file descriptions even more informative yet succinct.
- 8. Your Groupwork practicals were all in order, and your group did well in collaborating on it. More feedback on this in the 1:1 sessions.

1.2 The Bad (errors, missing files, etc)

1. align_seqs_better.py and align_seqs_fasta.py tried to load data from data/seq1.fasta and data/seq2.fasta, but these two files were not included in your repo, causing a fatal

error in the execution of these scripts.

2. MyBars.R, Girko.R and plotLin.R threw fatal errors because you forgot to load the

ggplot2 library at the start of the script.

1.3 The Ugly (niggling issues like commenting, cosmetics, complexity of

code, etc)

1. Nothing aesthetic to complain about!

2 Overall Assessment

Very good job overall, despite the data and package errors. With a bit more attention to detail these style of errors are easily fixed. Your coding style is clear and your documentation spot on.

These are a strong foundation on which to build from here onwards!

Provisional Mark: 69%

Signed: Alexander Kier Christensen & Samraat Pawar

March 23, 2022

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