CMSC423: Wrapup

UNIVERSITY OF
MARYLAND

End of Semester FAQ

1. When is the final?

   - Wed. Dec 13 (8-10AM). **NOTE:** Next Tues (Dec 12) is reading day — there is no class next Tues!

2. Where is the final?

   - In this room (IRB 2207)

3. What content will be on the final?

   - The final is *comprehensive*, and so you should be prepared to see content from throughout the course. That being said, there will be a *focus* in the final on (a) new material and (b) material proportional to how long we spent on it in class. So, you should expect a question on de Bruijn graphs, full-text indexing, RNA-seq, dynamic programming, etc.

4. What will the format of the exam be?

   - Same as the midterms; True/False & fill-in-the-blank and short answer "thinking" questions. The final is longer (2 hours), and so the final exam will be a little bit longer than the midterms, but probably not proportionally so. So, you'll likely have a bit more time per question.

5. How can I prepare for the final?

   - Go over the lectures (slides and videos), *go over your projects*, go over the midterm exams and make sure you understand where you lost points and what the correct answers were. Reach out on piazza (public discussions where possible, please), and look for additional resources on material you still feel you don't understand.

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6. What grade will I get?

- I don't know (yet) – the final grades will be scaled up (if necessary) and so it's not possible to know even approximate grade cutoffs when 25% of the credit is yet to be obtained.

- There is still time to get extra credit via the picomap project. Remember, it is worth 4 total points on your final grade, and it is not all or nothing (you get whatever fraction of that your project gets on Gradescope).

7.Course Survey: https://confluence.umd.edu/display/courseexperiences/

- Please consider taking the "Course Experiences" survey for this class

8. Other questions?

What we didn’t cover in this class

Most of bioinformatics and computational biology!

- All of “long read” technology and method development
- Metagenomics
- Details of phylogenomics and related statistical methods
    - Consider registering for CMSC498Y (Statistical Inference & Machine Learning Methods for Genomics Data)
- Biological network analysis
- “Systems” biology (e.g. regulatory inference)
- Biostatistics and statistical interpretation of genomics results
- Modern approaches of machine learning in bioinformatics (Deep learning, Transformers, Foundation Models in Genomics)
- Even in “algorithmic genomics” where we focused, we didn’t have time to go into the details about *how* many of the data structures we covered should be implemented in practice (e.g. succinct data structure primitives, minimal perfect hashing, etc.)
- Much, much more.