

CS4330: Combinatorial Methods in Bioinformatics
Course Briefing

Wong Limsoon



NUS
National University
of Singapore

National University of Singapore

Pre-requisites

Completed modules on

Programming

Algorithms

Basic molecular biology

ST2334 Probability & Statistics

CS2220 Introduction to Computational Biology

Objective

Exposure to computational methods for genome sequencing, assembly, and analysis

About me

Wong Limsoon



Professor in Computing & Medicine

ACM Fellow

Research interests

Database theory: Intensional expressive power

Computational biology: Batch effects

Data science: Justifiability, mistakes

Time Table

Lecture

Thursday @ 2-4pm

COM3-02-60

Office hours

Friday @ 2-3.30pm, except 9 Feb, 1 Mar, 29 Mar

COM2-03-57

Email

wongls@comp.nus.edu.sg

Course Syllabus

Overview of genome sequencing & assembly

Read mapping

Reference-based genome assembly

De novo genome assembly

Quality of genome assembly

Polyploid genome assembly

Long-read & hybrid genome assembly

Variant calling

Teaching Style

Need to learn a lot of material by yourself

Reading papers

Consult “AI” ... but beware that they are like “B students”

Try exercises

Practise on your own

Don't expect to be told everything

Assignments, Project, & Exam

Assignments (30-40% of marks)

2 to 3 assignments

Project (20-30% of marks)

Based on a case study in the class

8-10 pages of report / ppt slides expected

Exam (40-50% of marks)

1 final open-book exam

Be Honest

Exam

Absence w/o good cause results in ZERO mark

Cheating results in ZERO mark

Discussion on assignments & project is allowed

Blatant plagiarism is not allowed

Offenders get ZERO mark for assignment or exam, for those who copied AND those who were copied

SOC's academic honesty guidelines

<https://www.comp.nus.edu.sg/cug/plagiarism/>

Background Readings

Every lecture will be accompanied by a small set of “must-read” and “good-to-read” articles

The “must-read” articles are considered lecture notes and are examinable