

Academic Org: Div of Computer Science & Engg – Subject: Computer Science

Course: CSCI5050 **Course ID:** 009700 **Eff Date:** 2022-07-01 **Crse Status:** Active **Apprv. Status:** Approved **【Course Rev】**
Bioinformatics and Computational Biology 生物資訊及計算生物學

This course introduces several core topics in bioinformatics and computational biology. Each topic will be discussed from three aspects: 1) motivation and concepts, 2) computational problems and methods, and 3) available tools and data. The topics include basics in molecular biology, high-throughput experiments and data preprocessing, sequencing and alignment, motifs and domains, ontology and functional enrichment, biological networks and data mining, secondary and tertiary structures, and other latest developments in this research area.

本科介紹生物資訊和計算生物學數個重要的課題。就每一項課題，我們將從三方面作出討論：1)動機和理論、2)計算問題和方法、3)現有的工具和數據。課題包括：分子生物學基礎、高速實驗和數據整理、序列的產生和排序、基序和模體、譜系和功能分析、生物網絡和數據開採、二級和三級結構，以及這研究範疇的其他最新進展。

Grade Descriptor:

A

EXCELLENT – exceptionally good performance and far exceeding expectation in all or most of the course learning outcomes; demonstration of superior understanding of the subject matter, the ability to analyze problems and apply extensive knowledge, and skillful use of concepts and materials to derive proper solutions.

有關等級說明的資料，請參閱英文版本。

B

GOOD – good performance in all course learning outcomes and exceeding expectation in some of them; demonstration of good understanding of the subject matter and the ability to use proper concepts and materials to solve most of the problems encountered.

有關等級說明的資料，請參閱英文版本。

C

FAIR – adequate performance and meeting expectation in all course learning outcomes; demonstration of adequate understanding of the subject matter and the ability to solve simple problems.

有關等級說明的資料，請參閱英文版本。

D

MARGINAL – performance barely meets the expectation in the essential course learning outcomes; demonstration of partial understanding of the subject matter and the ability to solve simple problems.

有關等級說明的資料，請參閱英文版本。

F

FAILURE – performance does not meet the expectation in the essential course learning outcomes; demonstration of serious deficiencies and the need to retake the course.

有關等級說明的資料，請參閱英文版本。

Equivalent Offering:

Units: 3 (Min) / 3 (Max) / 3 (Acad Progress)

Grading Basis: Graded

Repeat for Credit: N

Multiple Enroll: N

Course Attributes: MSc Computer Science
MPhil-PhD Computer Sci & Erg

Topics:

COURSE OUTCOMES

Learning Outcomes:

- At the end of the course of studies, students will have acquired the ability to
1. explain the concepts and basic methods related to a broad range of topics in bioinformatics;
 2. apply what they have learned based on hands-on experience in using existing tools and locating; processing and analyzing some available data
 3. work and research in bioinformatics-related areas.

Course Syllabus:

This course introduces several core topics in bioinformatics and computational biology. Each topic will be discussed from three aspects: 1) motivation and concepts, 2) computational problems and methods, and 3) available tools and data. The topics include basics in molecular biology, high-throughput experiments and data preprocessing, sequencing and alignment, motifs and domains, ontology and functional enrichment, biological networks and data mining, secondary and tertiary structures, and other latest developments in this research area.

Assessment Type:

Essay test or exam	: 30%
Others	: 40%
Presentation	: 30%

Feedback for Evaluation:

- 1.Course evaluation and questionnaire
- 2.Reflection of teachers
- 3.Question-and-answer sessions during class
- 4.Student consultation during office hours or online

Required Readings:

To be provided by course teacher.

Recommended Readings:

This course does not have any text book. Students will read some latest research papers for class discussions and course project. Here is a list of papers used before. The exact list to be used will be revised every year.

- 1.Flicek and Birney, Sense from Sequence Reads: Methods for Alignment and Assembly. Nature Methods 6(11s):S6-S12, (2009)
- 2.Ernst et al., Mapping and Analysis of Chromatin State Dynamics in Nine Human Cell Types. Nature 473(7345):43-49, (2011)
- 3.Lawrence et al., Detecting Subtle Sequence Signals: A Gibbs Sampling Strategy for Mult Align. Science 262(5131):208-214, (1993)
- 4.Marioni et al., RNA-seq: An Assessment of Technical Reproducibility and Comparison with Gene Expression Arrays.
- 5.Rhee et al., Use and Misuse of the Gene Ontology Annotations. Nature Reviews Genetics 9(7):509-515, (2008)
- 6.Jansen et al., A Bayesian Networks Approach for Predicting Protein-Protein Interactions from Genomic Data. Science (2003)

OFFERINGS

1. CSCI5050	Acad Organization=CSEGV; Acad Career=RPG
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COMPONENTS

LEC : Size=30; Final Exam=Y; Contact=3
TUT : Size=30; Final Exam=N; Contact=1

ENROLMENT REQUIREMENTS

1. CSCI5050	Enrollment Requirement Group:
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For students in MSc Computer Science; or
For students in MPhil-PhD Computer Science & Engineering; or
For students in UG Computer Science; or
For students in UG Computer Engineering

CAF

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