The Chinese University of Hong Kong
Faculty of Science
Science Academy for Young Talent

Summer Courses 2024
Course Outline

CUSA1063 Bioinformatics for secondary school students
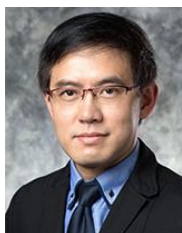*生物信息學*

Introduction:	In the past decade, high-throughput sequencing (HTS) has revolutionized scientific discoveries and breakthroughs. The sheer volume of sequencing data, consisting of just four nucleotide bases (A, T, G, and C), holds an immense wealth of information yet hidden in plain sight. Bioinformatics has emerged as an indispensable field, playing a pivotal role in managing, processing, and analyzing this vast amount of data. By leveraging computational algorithms and their design, bioinformatics addresses complex problems in biology and related disciplines. Furthermore, the development of pipelines and implementations (tools) is integral to computational biology – a field closely linked with bioinformatics. Together, these disciplines play a crucial role in transforming plain data to valuable biological insights by deciphering the information in nucleotide (DNA or RNA) sequences. While we have yet to realize the full potential of HTS and bioinformatics, their application has been widely and clearly demonstrated during the COVID-19 pandemic. For instance, the epidemiological surveillance of SARS-CoV-2 and the emergence of its variants were made possible with bioinformatics and computational biology – raising public awareness that science is indispensable and has important and practical roles in our society. While bioinformatics can be abstract and conceptual, its understanding and appreciation require practical implementation through dexterity. This course is designed to introduce bioinformatics to secondary school students as a practical science with theories and concepts largely anchored on general biology and chemistry. The concept of sequence alignment will be leveraged as a core component emphasizing on how it can be used to tackle different problems in biology such as mutations and evolution among others. The course will be implemented as lectures supplemented with hands-on drills (pen-and-paper exercise or tool-based exercise) as follow-through to provide concrete demonstrations or illustrations of relevant concepts.

在過去的十年，高通量測序技術（HTS）徹底改變了科學的發現和突破。僅由四個核苷酸鹼基（A、T、G 和 C）組成的大量測序數據蘊藏著巨大的信息，然而這些信息卻隱藏在明顯的視野之中。生物信息學在管理、處理和分析這大量數據方面發揮著關鍵作用，已經成為一個不可或缺的領域。利用計算演算法及其設計，生物信息學解決了生物學和相關學科中的複雜問題。此外，流程的設計和工具的開發對於計算生物學來說至關重要，它是與生物信息學密切相關的一個領域。通過解讀核苷酸（DNA 或 RNA）序列中的信息，這兩個學科共同在將平淡的數據轉化為有價值的生物學見解方面扮演著重要的角色。儘管我們尚未完全實現 HTS 及生物信息學的全部潛力，但在 COVID-19 大流行期間，它們的應用已經得到了廣泛而明確的證明。例如，基於生物信息學和計算生物學的流行病學監測使我們能夠追蹤 SARS-CoV-2 及其變異體的出現，提高公眾對科學的認識，了解科學的不可或缺性及其在社會中扮演重要且實際的角色。雖然生物信息學可能抽象和概念化，但通過靈巧的操作便能理解和欣賞它。本課程旨在向中學生介紹生物信息學，一個將理論和概念主要依托於一般生物學和化學的實用科學。序列比對的概念將作為本課程的核心部分，強調它在解決生物學中的不同問題，如突變和進化等方面的應用。該課程將以講座形式進行，並輔以實際演練，具體演示或說明生物信息學的相關概念。

Medium of Instruction:	English supplemented with Cantonese 英語輔以粵語
Organising Unit:	School of Life Sciences, Faculty of Science, CUHK
Teachers:	**Professor CHAN Ting Fung** Associate Professor School of Life Sciences, Faculty of Science, CUHK Rm 177, Science Centre South Block, CUHK E-mail: tf.chan@cuhk.edu.hk

Course Content:

13 August 2024 (Tuesday) 10:00 am – 12:30 pm	**Lecture 1**
	• Introduction to Genomics and Bioinformatics
	    • DNA Structure and the Canonical Watson-Crick Base Pairing
	    • The Central Dogma of Molecular Biology
	    • Bioinformatics: Computational Analysis of Biological Sequences
	• Research Paradigms: Hypothesis-driven and Data-driven Approach
	Lab 1: Pen-and-paper Exercise: Central Dogma of Molecular Biology
	Case Discussion 1: Exceptions to the Central Dogma of Molecular Biology
	Assessment 1: Short-answer exercise

15 August 2024 (Thursday) 10:00 am – 1:00 pm	**Lecture 2** • Computational Infrastructure: Hardware and Software (Tools) • Biological Databases • Knowledge Discovery in Databases (KDD) • Types of Biological Databases Based on Contents **Lab 2** • Accessing Biological Database/s (NCBI) • Exploring Its Features: Features Most Relevant to Life Sciences • Retrieval of Information: DNA/Protein Sequence/s **Case Discussion 2** • A Specialized Database on SARS-CoV-2 (COVID-19): NCBI Virus DB • Bioinformatics Tools Developed During the Pandemic (Non-exhaustive list): What are the motivations for their design and development? **Web-based teaching 2:** Lab-based/hands-on workshop (*Lab 2*) **Assessment 2:** Short-answer exercise

20 August 2024 (Tuesday) 10:00 am – 1:00 pm	**Lecture 3**
	• Sequence Alignment: Pairwise and Multiple Sequence Alignment
	• Applications of Sequence Alignment: Detecting Variations, Types, and Implications
	• Are all variations bad?
	    • How does nature leverage variations?
	    • How does bioinformatics leverage variations?
	Lab 3: Online Sequence Alignment: DNA, DNA-to-Protein Translation
	Case Discussion 3: Special Case of Alignment: Structural Alignment (e.g., proteins)
	Web-based teaching 3: Lab-based/hands-on activity (*Lab 3*)
	Assessment 3: Short-answer exercise

22 August 2024 (Thursday) 10:00 am – 1:00 pm	**Lecture 4:** Phylogenetics and Molecular Evolution and Their Applications **Lab 4** • Pen-and-paper Exercise: Sequence-based Distance and Phylogeny • Using Online Phylogenetics Tool to Infer Phylogeny • Supplemented with *Case Discussion 4* on SARS-CoV-2 Variants **Case Discussion 4:** What are SARS-Cov-2 variants? How did the World Health Organization (WHO) come up with this classification? **Web-based teaching 4:** Lab-based/hands-on activity (*Lab 4*) **Assessment 4:** Short-answer exercise
27 August 2024 (Tuesday) 10:00 am – 12:30 pm	**Lecture 5** • Debriefing and Integration of Concepts • Bioinformatics: Its Past, Present and Future • Q&A
29 August 2024 (Thursday) 10:00 am – 1:00 pm	Make-up Class

Date	13, 15, 20, 22, 27, 29* August 2024 (14 hours)
Time	10:00 am – 12:30 pm/1:00 pm
Teaching Mode	Face-to-Face (The Chinese University of Hong Kong)
Enrolment	25 – 30
Expected Applicants	Students who are advancing to or studying S4 – S6
Tuition Fee	HKD 3,140.00
Credit	1 Academy Unit(s) *Students can accumulate credits which will be regarded as "Other Learning Experience" when applying University.*

Grading Methods		*Certificate*	*Assessment*	*Attendance*	*Credit(s)*
	Distinction	*Certificate of Distinction*	*Pass*	*>75%*	*1*
	Pass	*Certificate of Merit*	*Pass*	*>75%*	*1*
	Attended	*Certificate of Attendance*	*Fail*	*>75%*	*0*
	Fail	*N/A*	*Fail*	*N/A*	*0*

Remarks:	**Students are requested to bring laptops/notebooks or tablets with them for this course.**

* This date is reserved for make-up classes in case there is any cancellation of classes due to unexpected circumstances.