

Course Title/Code:	Practical Bioinformatics (MMPH6005)
Department:	School of Biomedical Science
Objective:	To provide students with the basic understanding of the principles and latest developments/tools in bioinformatics.
Content:	<ul style="list-style-type: none"> • Biological databases • Gene prediction • Information retrieval: entrez and SRS • Introduction - Essential concepts on gene structure and sequence, protein structure and function • Multiple sequence alignment • Pair-wise sequence alignment I: dot plot • Pair-wise sequence alignment II: dynamic programming • Phylogenetic prediction • Sequence database searches: BLAST, FASTA • Substitution matrices
Learning outcomes:	<p>On completion of this course, the students will be able to:</p> <ul style="list-style-type: none"> • demonstrate a solid knowledge of DNA and protein sequence analysis and how to use public database and web servers to solve biological problems with bioinformatic approaches. • analyse, evaluate and interpret data of dot plots, local and global sequence alignments. • explain the principles for using different substitution matrices. • analyse and interpret BLAST search and understand the statistical rationale behind it. • describe the principles and methods for gene prediction and phylogeny.
Prerequisite:	None
Duration:	1 semester; 2 hours/week; 24 contact hours
Continuous assessment/ examination ratio:	In-course assessment (40%) and Final Examinatin (60%)
Examination method/ duration:	Written examination / 2 hours
Remarks:	Also offered to RPg from other Faculties at HKU