

Subject Description Form

Subject Code	ABCT4115
Subject Title	Bioinformatics
Credit Value	3
Level	4
Pre-requisite	DNA Technology
Co-requisite	NIL
Objectives	The subject introduces students to basic principles of bioinformatics, paying particular attention to practical aspects. Students will be able to learn how to use common software for database searching and sequence analysis. In addition, the latest topics like genome project, DNA chip and proteomics will also be covered.
Intended Learning Outcomes	<p>Upon completion of the subject, students will be able to:</p> <ol style="list-style-type: none"> a. integrate the basic concepts of bioinformatics including the pairwise alignment, phylogeny and its application in database searching of GenBank, SWISS-PROT, PDB, dbEST and PROSITE. b. use appropriate software to investigate gene and protein functions. c. identify recent development of genomics, proteomics, metabolomics and post-genomic research and appreciate their significance on biological research. d. Understand essential statistics in bioinformatics such as multivariate analysis with PCA or PLS-DA. Brief understanding of programming in Bioinformatics analysis. e. be aware of the impact of bioinformatics developments and trends on science, humanity and society.
Subject Synopsis/ Indicative Syllabus	<p>Pairwise alignment, Multiple Sequence Alignment, Local Alignment, and Gap Penalties: FASTA3, BLAST, PSI/PHI-BLAST, CLUSTALW</p> <p>Databases : DNA, protein, 3-D structure, EST, protein domain GenBank, SWISS-PROT, PDB, dbEST, PROSITE</p> <p>Genome and proteome projects overview</p> <p>Domain searches: PROSITE, PRODOM, Pfam Transmembrane domain prediction: TMHMM Secondary structure prediction: GenePredict Gene finding and prediction:</p> <p>✓ DNA Chips: Microarray, Affymetrix chip principles and application</p> <p>Proteomics: 2D-PAGE, mass spectrometry principles, MS-FIT, multivariate analysis and introduction of programming in Bioinformatics. Use of integrated molecular biology software: EMBOSS, EXPASY, Protein Prospector, and others.</p>

Teaching/Learning Methodology	Lectures will be used as the major content-delivery tool. Students will be able to learn software by practice. A self-learning component will be included to write a term paper on an interesting application of bioinformatics. For tutorials, students will participate in small group discussions. Reference materials will be distributed in class, from library and from Internet where software is constantly updated. Computer lab practicals will be used to learn how to perform database searching and gene/protein function analysis.						
Assessment Methods in Alignment with Intended Learning Outcomes	Specific assessment methods/tasks	% weighting	Intended subject learning outcomes to be assessed (Please tick as appropriate)				
			a	b	c	d	
1. Attendance	5%						
2. Quizzes	40%	✓	✓	✓	✓		
3. Term paper	10%			✓	✓		
4. Seminar presentation	10%			✓	✓		
5. Practical	35%	✓	✓				
<p>Explanation of the appropriateness of the assessment methods in assessing the intended learning outcomes:</p> <p>Quizzes are used to gauge how much students have learned in the basic concepts of bioinformatics, genomics, and proteomics. Writing skills will be assessed in all the assessment tasks and methods. Term paper and seminar presentation are used to assess whether students can identify recent developments in bioinformatics. The practicals and lab reports demand students to demonstrate their competence in using software and in the interpretation and analysis of data.</p> <p>Students are required to attend at least 75% of scheduled sessions for the subject. Students fail to fulfill the attendance requirement will lose the 5% attendance score.</p>							
Student Study Effort Expected	Class contact:						
	Lectures		22 Hrs.				
	Tutorials		5 Hrs.				
	Practical (computer applications)		12 Hrs.				
	Other student study effort:						
	Self-study		60 Hrs.				
	Total student study effort		99 Hrs.				
Reading List and References	Supplementary www.ncbi.nlm.nih.gov						