一、課程說明(Course Description)

"Throughout the foreseeable future, research in medicine, molecular biology, and biotechnology will be dominated by scientific advancements resulting form the Human Genome Project. Knowledge of genomes will elucidate disease patterns and promises improved and personalized treatments. Food and drug development will be revolutionized by the focused manipulated of genes and biochemical process."

– by Prof. Eberhard O. Voit.

本課程兼重學理與實作,藉由習題與範例,使學員能熟悉網路上各種生物資訊之取得及應用,並針對各種常用生物資料庫作概略性的介紹,包括 NCBI, Protein Data Bank (PDB)、 KEGG、ExPasy 等生物資料庫。 課程中將連線上網,實際操作、演練各種輔助軟體 (Browser, viewer, molecular displayer...)。

部分內容需具有生科系本科生大二基礎,建議大三以上(含)修讀,學習效果較佳。

二、參考書籍(References)

1. Bioinformatics: a practical guide to the analysis of genes and proteins, Third Edition (http://as.wiley.com/WileyCDA/WileyTitle/productCd-0471478784.html)
The reference is for Gene Module.

三、教學方式(Teaching Method)

在電腦教室上課,課堂講解示範與學生實地操做並行。

四、成績考核(Evaluation)

總成績算法 ─ Homework 50% / Midterm and final Exam. 30% / Projects 20%
Homework 遲交一天扣該次 homework 成績 10%,遲交三天視同未交。
請勿遲到,遲到兩次以曠課一次論,曠課一次扣總成績十分,曠課三次以不及格論。

五、可連結之網頁位址

NTHU E-Learning System
http://alpha.life.nthu.edu.tw/

六、教學進度(Syllabus)

Week	Topic	Exercises – server, program	Instructor
Gene Module			
1	Introduction to bioinformatics	Open account, Life Science Alpha Server, NCBI	Chuang
2	Network and pathway modeling tool	CellDesigner, CGAP	Chuang
3	Biological database mining	NCBI, BLAST, (Primer Design)	Chuang
4	Genomic databases	Ensemble, CLUSTALW, Major Model Organism Sites	Chuang
5	Predictive methods using primary sequences	GeneID, TRANSFAC, (RE analysis)	Chuang
6	Phylogenetic analysis	PHYLIP, Harvester, Expasy	Chuang
7	Gene expression profiling	SMD, GeneCard, DAVID (BandScan)	Chuang
8	SNP and genotyping	NCBI-SNP, HapMap	Chuang
9	**Midterm Exam**		TA
Protein Module			
10	Protein analysis and prediction	ExPASy	Lyu
11	Protein structure database Structural classification	PDB SCOP	Lyu
12	Protein structure visualization	Rasmol & Chime	Lyu
13	Protein structure modeling & prediction	SWISS-MODEL	Lyu
14	Molecular Docking	AutoDock; Molegro	Lyu
15	Structural comparison	VAST; CE ; Swiss-PdbViewer; SARST	Lyu
16	Biology Server and Metabolic Pathways	KEGG	Lyu
17	**Final Exam**		TA
18	**Final Week**		