

NEW COURSE PROPOSAL

PROGRAM AREA BIOLOGY**1. Catalog Description of the Course.**

BIOL 502 TECHNIQUES IN GENOMICS/PROTEOMICS (2)

Six hours of laboratory per week

Prerequisite BIOL 401 or permission of instructor

This laboratory course introduces students to the current techniques and methodologies in the fields of comparative and functional genomics and proteomics. Topics and techniques covered include genome sequencing, micorarrays, mutagenesis, transgenic plants and animals, single nucleotide polymorphism (SNP) discovery and analysis. Students will gain hands-on lab bench experience and will make on-site visits to high volume regional biotechnology facilities.

2. Mode of Instruction.

	Units	Hours per Unit	Benchmark Enrollment
Lecture	_____	_____	_____
Seminar	_____	_____	_____
Laboratory	<u>2</u>	<u>3</u>	<u>15</u>
Activity	_____	_____	_____

3. Justification and Learning Objectives for the Course. (Indicate whether required or elective, and whether it meets University Writing, and/or Language requirements) *[Use as much space as necessary]*

This course is a required element of the core curriculum for the proposed Professional Science Masters degree in Bioinformatics

Upon completion of this course, students will be able to:

- Generate, edit and annotate a genomic DNA sequence
- Use Clustal to align several DNA sequences
- Compare and contrast the major techniques used in transcriptome profiling
- Use the xProfiler at NCBI online
- Perform and interpret a northern blot
- Interpret a DNA fingerprint and explain the fundamental populations genetics that underlie the data
- Navigate and interpret a QTL map

4. Is this a General Education Course NO

If Yes, indicate GE category:

A (English Language, Communication, Critical Thinking)	
B (Mathematics & Sciences)	
C (Fine Arts, Literature, Languages & Cultures)	
D (Social Perspectives)	
E (Human Psychological and Physiological Perspectives)	

5. Course Content in Outline Form. *[Be as brief as possible, but use as much space as necessary]*

Genome sequencing and annotation (automated DNA sequencing, high-throughput sequencing, contig assembly, hierarchical and shotgun sequencing, EST sequencing)

Analysis of gene expression (cDNA microarrays, oligonucleotide microarrays, microbeads, SAGE, differential display, quantitative PCR)

Protein methods (2D-PAGE, protein microarrays)

Functional genomics (reverse genetics, transgenic plants and animals, fingerprinting, fine-structure genetics)

SNPs (QTL mapping, linkage disequilibrium mapping, SNP detection via hybridization, Invader assays)

6. References. *[Provide 3 - 5 references on which this course is based and/or support it.]*

Ewing B, Hillier L, Wendl M, Green P: Basecalling of automated sequencer traces using phred. I. Accuracy assessment. *Genome Research* 8, 175-185 (1998).

Stephen P. Hunt, Frederick J. Livesey, F. M. Livesey, Rick Livesey. (2001). *Functional Genomics: A Practical Approach* (Practical Approach Series). Oxford University Press