Master Course Syllabus
Kennedy King College
One of the City Colleges of Chicago
Biotechnology
Semester/Academic Year (20__ - 20__)

Course Prefix and Number: Biotech 245

Course Title: Bioinformatics for Biotechnology

Length of Course: 16 weeks

PCS Code: 1.2

IAI Code:

Semester Credit Hours: 3.0
Contact Hours (minutes): 5 (4000 minutes)

Lecture Hours (minutes): 1 (800 minutes)

Lab Hours (minutes): 4 (3200 minutes)

Method of Delivery (mark all that apply): Face to Face __X__ Online _X___ Hybrid __X__

Course Catalog Description:
This course will cover a range of bioinformatics research and concepts using a case-based and problem-solving approach. This course will consist of a combined lecture and computer laboratory format to provide hands on approach in applying bioinformatics to a variety of research problems include genome analysis, DNA microanalysis, phylogenetics, three-dimensional structure prediction and proteomics. Special attention will be paid to ethical, legal, and personal concerns in the practice of bioinformatics. Writing assignments, as appropriate to the discipline, are part of the course.

Prerequisites: Biotechnology 225, Biotech 230 with a grade of C or better, or Consent of Department Chairperson. Corequisite CIS 103 (Python)

Course Objectives:
This course covers:

- How students can predict the consequences of mutations, and how to identify and distinguish between missense, nonsense, and frameshift mutations.
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- How students can understand the effects of mutations, and why they must understand translation and reading frames.
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- What are the different kinds of bonds that amino acids form and the different types of molecular interactions they can undergo.
- How to identify a sequence and pick the correct database and the different BLAST algorithms and how they work.
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- How to locate information at the National Center for Biotechnology Information (NCBI).

Student Learning Outcomes:

Upon successful completion of the course, students will be able to:

1. Choose appropriate biological databases (e.g., National Center for Biotechnology Information) and perform a search (Simple and Advanced).
2. Analyze database fields and indices to count the number of items within a particular database that match a description (e. g. the number of exons in the gene database).
3. Distinguish between amino acids and nucleotides in a molecular structure.
4. Determine the net charge and whether it is hydrophobic or hydrophilic for an amino acid or nucleotide using molecular modeling software.
5. Analyze biomolecules using molecular modeling software to determine the type of chemical bond or interaction it undergoes (e.g., disulfide, hydrogen, hydrophobic, ionic, metal).
6. Compare molecular models to identify differences and make predictions about the impact of the different structures on function.
7. Analyze sequence analysis software (e.g., BLAST and sequence homology) to determine how to repurpose existing drugs to treat new diseases.
8. Interpret and use the information from a genetic map to understand the size of a gene, the location of control elements, and the location and number of exons and introns.
9. Select the appropriate multiple alignment software to align sequences and create a phylogenetic tree to visualize relationships and identify amino acids that are important for protein function.
10. Apply DNA barcoding techniques to a DNA sample to correctly identify a particular species.
11. Analyze a DNA sequence for mutations, using sequence analysis software (e.g., BLAST) to determine whether a frame shift or non-sense mutation is created.
12. Determine what changes to the protein structure are caused by mutations in the gene and evaluate the changes in the proteins function using molecular modeling software.

Suggested Topical Outline					
Class Units (# of units is dependent on course – adjust accordingly)	Topic (Required)	Content (Optional - provide details)	Lab Information	Desired Outcome(s)	Suggested Assessment Method(s)
Unit 1	Part I Databases: Simple database searches	Discussion 1	Learning guide 1: Orientation & databases	1, 2, 3	A1 orientation
Unit 2	Part I Databases: More complicated searches, using query builder, and Boolean terms	Discussion 2	Learning Guide 2: Databases	1, 2, 3	A2 databases
Unit 3	Part II Molecular Structures: Proteins, nucleic acids, amino acids, and nucleotides	Discussions D3 Major & minor grooves 2. D4 Nucleotides and amino acids 3. D5 Amino acids & charge 4. D6 Amino acids & hydrophobicity	Learning Guide 3: Molecular structures: proteins, nucleic acids and their building blocks	5, 6, 7,	A3 Amino acids and nucleotides
Unit 4	Part II Molecular Structures: Identifying chemical bonds, levels of protein structure	Discussions: 1. D7 covalent bonds 2. D8 disulfide bonds 3. D9 metal bonds	Learning Guide 4: Chemical bonds	5, 6, 7, 8	A4 Chemical bonds in biological polymers and levels of protein structure
Unit 5	Part II Molecular Structures: Investigating levels of protein structure, levels of protein structure	Discussions: 1. D10 ionic interactions 2. D11 hydrophobic interactions 3. D12 hydrogen bonds	Learning Guide 4: Chemical bonds	5, 6, 7, 8, 11	A4 Chemical bonds in biological polymers and levels of protein structure Exam 1
Unit 6	Part II Molecular Structures: Comparing drug sensitive (normal) and drug resistant (mutant) structures	D13 Influenza and drug resistance	Learning Guide 5: Comparing molecular structures and reviewing bonds	8, 9, 10	A5 Influenza and chemical bonds
Unit 7	Part III Molecular Sequences: Experimenting with blastn - the effect of word size and algorithm		Learning Guide 6: nucleotide blast, and word size	8, 9, 10	Assignment 6: Blasting the flu

Unit 8	Part III Molecular Sequences: Drug discovery and alignments		Learning Guide 7: Molecular Sequences, protein blast & drug discovery	8, 9, 10	A7 Drug discovery & Zika virus
Unit 9	Part III Molecular Sequences: Multiple alignments, simple phylogenetic trees, why are some residues conserved through evolution?	D14 Molecular Murder Mystery	Learning Guide 8: Multiple alignments and evolution	11, 12	A8 Multiple alignments, phylogenetic trees, and sequence conservation
Unit 10	Part III Molecular Sequences: Understanding gene maps - the relationship between sequence and structure		Learning Guide 9: Molecular Sequences and genetic maps	1, 2, 12, 14	A9 Gene structure and using genetic m Exam 2
Unit 11	Spring Break				
Unit 12	Part III Molecular Sequences: Using primer BLAST to pick PCR primers		Learning Guide 10: BLAST and PCR, primer blast, blastn, reading maps	1, 2, 12, 14	Assignment 10 Using blast to pick PCR primers
Unit 13	Part IV Genetic Variation: Identifying and understanding small mutations	Discussions: D15 Stop codon mutations D16 Frameshift mutations	Learning Guide 11: Mutations and translation	1, 2, 12, 13, 14	A11 Mutations - Identifying variants Identify and map mutations
Unit 14	Part IV Genetic Variation: Identifying and understanding the impact of mutations on protein structure	D17 Frameshift models	Learning Guide 11: Mutations and translation	15, 16	A11 part 2 Modeling frameshift variants Model the impact of a frameshift mutation on protein structure and predict the effect on activity
Unit 15	Part IV Genetic Variation: Final project - investigating the effect of a clinically relevant mutation		Learning Guide 12: Missense variants and variants of unknown significance	14, 15, 16	A12 Genetic variants and disease

Unit 16	Part IV Genetic Variation: Final project - investigating the effect of a clinically relevant mutation		Learning Guide 12: Missense variants and variants of unknown significance	1, ,2, 14, 15, 16	A12 Genetic variants and disease Final Exam

Students Course Is Expected to Serve: Students who are pursuing an Associates of Applied Science degree in Biotechnology.

Suggested Texts, Materials, and Resources:

Text: Exploring Molecular Structures: Bioinformatics for Biology Students by Sandra Porter, Digital World Biology, LLC
Materials:
Resources: various Internet resources
Supplies:

Suggested Methods of Instruction: We will utilize lectures, discussions, and computer-based activities.

Suggested Methods of Assessment and Evaluation:
(Formative and Summative): We will utilize quizzes, exams, homework and papers to assess students in this course.

Suggested Grading Scale:

Assignments:	Grade Distribution:
	90 % to 100 % = A 80 % to 89% = B 70 % to 79 % = C 60 % to 69 % = D Below 60% = F

Suggested Exit Assessment/Competencies (as applicable):

Processing Validation (To be completed by College)

Add – Effective Term/Year: ___________ Reactivate – Effective Term/Year: ___________
Inactivate – End Term/Year: ___________ Withdraw – End Term/Year: ___________

Approved College(s):

DA: ___ HW: ___ KK:_X_ MX:___ OH:___ TR:___ WR:___

Syllabus Preparer/Advocate: _______________________Clifford Wilson, III_____________________

Title of Advocate: ______________________Assistant Professor_______________________

College of Advocate: _________________________Kennedy King College________________

ICCB Submission Date: (/ /)
ICCB Approval Date: (/ /)
IAI Submission Date: (/ /) IAI Panel: ___________
IAI Approval Date: (if applicable) (/ /) IAI Code: ___________

PACC Master Course Syllabus Template –August 2020