### SYLLABUS

05/2018
24.0101
02/2013
Introduction to Bioinformatics
BIOL-0291
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**PREREQUISITE**: Familiarity with using the Internet.

**REQUIRED TEXT AND MATERIALS**: See bookstore for current textbook.

#### **COURSE DESCRIPTION:**

This course will provide an introduction to the field of bioinformatics. This will include a brief survey of genes and genomics, hands-on experiences with some simple DNA sequencing activities, and manipulation of data using currently available programs for computational analysis of nucleic acids and protein sequences. This course is very active and although skills will be taught in class, the student will need to be able to take skills acquired in class and finish projects on their own time. This is a competency-based course and will be graded as such.

**METHOD OF INSTRUCTION:** A variety of instructional methods may be used depending on content area. These include but are not limited to: lecture, multimedia, cooperative/collaborative learning, labs and demonstrations, projects and presentations, speeches, debates, and panels, conferencing, performances, and learning experiences outside the classroom. Methodology will be selected to best meet student needs.

**Online Sections:** Online courses rely on the use of the Internet and a course management system for content delivery. Courses are accessible both on campus and from most remote sites. Specific information regarding computer skills and system requirements can be found at <u>http://helpdesk.kckcc.edu/helpdesk/</u>

**Honors Sections:** An honors section of this course provides a non-traditional environment for learning that incorporates active student participation, critical reflection, use of primary sources and innovative teaching methods. Classes are designated as honors on the transcript. Enrollment in the honors section of this class requires the permission of the Director of Honors Education

## **COURSE OUTLINE:**

- I. Biology review
  - A. Cell structure
  - B. The nucleus, nucleotides, DNA, RNA
  - C. The gene
  - D. The Human Genome Project
  - E. Proteins
- II. Internet usage.
  - A. Cut and paste functions
  - B. Multiple windows
  - C. Navigating through the Internet
- III. Bioinformatics defined
  - A. What is bioinformatics?
  - B. When is bioinformatics used?
  - C. What are the goals for bioinformatics?
  - D. Terminology
  - E. Applications
- IV. BLAST
  - A. BLAST defined
  - B. BLAST tutorial
  - C. BLAST activities
  - D. BLAST project
  - E. PSI-BLAST
  - F. Gapped BLAST
- V. NCBI/NLM
  - A. Resources
  - B. ENTREZ
  - C. Boolean logic
  - D. Using ENTREZ to search several linked databases
  - E. Using ENTREZ to retrieve scientific articles through PubMed
  - F. Using ENTREZ to search Genbank (nucleotide sequence database
  - G. Using ENTREZ to search Protein sequence database
  - H. Other possibilities using ENTREZ
- VI. Principles of DNA sequencing
  - A. Recognizing autoradiograms
  - B. Interpretation of autoradiograms
- VII. DNA informatics application
  - A. Read X-rays containing DNA sequences
  - B. Using the Internet, identify the gene product and other closely related proteins.

- VIII. Impact of Automated DNA Sequencing on Bioethics
  - A. Examine actual data representing important genes from automated DNA Sequences.
  - B. Compare and extrapolate database information
  - C. Identify the gene product and other closely related proteins
  - D. Discuss data within bioethical parameters
- IX. Restriction Enzyme Mapping
  - A. Electrophoresis explained
  - B. Restriction enzyme description
  - C. Cleaving of the plasmid DNA
  - D. Running a gel electrophoresis
  - E. Determining fragment size
  - F. Determining the relative positions of the restriction sites
- X. Independent Research Project
  - A. Define project
  - B. Outline procedures
  - C. Do project
  - D. Write report
  - E. Present project and report to class

**EXPECTED LEARNER OUTCOMES**: At the end of this course the student will be able to take data given to them, identify which data bases to use and perform a search using the appropriate databases to identify genes, compare protein and nucleic acid sequences an compare alignments. They also will have a working knowledge of how the data was acquired.

# **COURSE COMPETENCIES:**

- 1. The student will be able to explain what a gene is.
- 2. The student will be able to tell where genes are found.
- 3. The student will be able to relate the significance of the Human Genome Project.
- 4. The student will be able to define what a genome is.
- 5. The student will be able to define nucleotides.
- 6. The student will be able to name the four nucleotides.
- 7. The student will be able to cut and paste information.
- 8. The student will be able to use multiple windows.
- 9. The student will be able to navigate through the Internet.
- 10. The student will be able to perform scientific literature searches using various browsers.
- 11. The student will be able to define Bioinformatics.
- 12. The student will be able to describe in what capacity a bioinformatics search might be used.
- 13. The student will be able to describe the goals for bioinformatics.
- 14. The student will be able to describe what the P-value is.
- 15. The student will be able to explain what an E-value is.
- 16. The student will be able to define what an optimal alignment is.
- 17. The student will be able to explain the significance of homology.
- 18. The student will be able to finish the BLAST tutorial.
- 19. The student will be able to describe what BLAST is.

- 20. The student will be able to set parameters for a BLAST search.
- 21. The student will be able to explain what BLAST is doing.
- 22. The student will be able to explain what FASTA is.
- 23. The student will be able to decipher BLAST results.
- 24. The student will be able to explain what the BLAST scoring system is based on.
- 25. The student will be able to participate in the various BLAST activities.
- 26. The student will be able to develop a BLAST query.
- 27. The student will be able to enter sequence data into BLAST.
- 28. The student will be able to explain the difference between local alignment and global alignment.
- 29. The student will be able to search for nucleotide sequences using BLAST.
- 30. The student will be able to set up a protein query for BLAST.
- 31. The student will be able to describe what a sequence similarity search is.
- 32. The student will be able to perform a sequence similarity search.
- 33. The student will be able to search using ENTREZ.
- 34. The student will be able to use the history function in ENTREZ.
- 35. The student will be able to use ENTREZ to research for articles in PubMed.
- 36. The student will be able to navigate through the NCBI databases.
- 37. The student will be able to retrieve articles using PubMed.
- 38. The student will be able to use PSI-BLAST.
- 39. The student will be able to read scientific literature for relevancy.
- 40. The student will be able to survey Gapped BLAST.
- 41. The student will be able to relate what one might choose to use the FASTA format.
- 42. The student will be able to use ENTREZ to maneuver through several databases.
- 43. The student will be able to use ENTREZ to search Genbank.
- 44. The student will be able to use ENTREZ to search protein sequence database.
- 45. The student will be able to explore ENTREZ for other uses.
- 46. The student will be able to explain identity.
- 47. The student will be able to explain why the E-value is relevant.
- 48. The student will be able to explain what E-value is acceptable for similarity.
- 49. The student will be able to define motif.
- 50. The student will be able to define Gap.
- 51. The student will be able to define H.
- 52. The student will be able to read X-rays containing DNA sequences.
- 53. The student will be able to run an experiment in restriction enzyme mapping.
- 54. The student will be able to assess data for quality.
- 55. The student will be able to identify the sequence of genes using data acquired in lab and the bioinformatics databases.
- 56. The student will be able to explain what gel electrophoresis is.
- 57. The student will be able to explore GenBank.
- 58. The student will be able to relate the control of gene expression (i.e. under what circumstances proteins are transcribed from DNA).
- 59. The student will be able to explain the relationship between the amino acid sequence of proteins and their structures.
- 60. The student will be able to explain what SNP's are.(single nucleotide polymorphisms)
- 61. The student will be able to explain the significance of SNP's
- 62. The student will be able to write searches using Boolean logic.

## ASSESSMENT OF LEARNER OUTCOMES:

Student assessment is evaluated by means of analysis of competencies which will be addressed in exams, projects, reports, and assignments. The following grading scale will be used with the points earned being divided by points possible times 100.

## **SPECIAL NOTES:**

This syllabus is subject to change at the discretion of the instructor. Material included is intended to provide an outline of the course and rules that the instructor will adhere to in evaluating the student's progress. However, this syllabus is not intended to be a legal contract. Questions regarding the syllabus are welcome any time.

Kansas City Kansas Community College is committed to an appreciation of diversity with respect for the differences among the diverse groups comprising our students, faculty, and staff that is free of bigotry and discrimination. Kansas City Kansas Community College is committed to providing a multicultural education and environment that reflects and respects diversity and that seeks to increase understanding.

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All enrolled students at Kansas City Kansas Community College are subject to follow all rules, conditions, policies and procedures as described in both the Student Code of Conduct as well as the Student Handbook. All Students are expected to review both of these documents and to understand their responsibilities with regard to academic conduct and policies. The Student Code of Conduct and the Student Handbook can be found on the KCKCC website.