# Applications of Bioinformatics and Genomics/ Proteomics.

The University of Toledo BRIM Program in Bioinformatics & Proteomics/ Genomics BIPG6400/8400, Application of Bioinformatics

### COURSE/ CATALOG DESCRIPTION

Lab Location: Lab Day/Time: Credit Hours:

127 HEB

Wed/Fri, 10:00-11:30 am 3cr hr

Delivery: All procedures related to current COVID-19 requirements will be engaged. Currently, no conventional

seminars/lectures are allowed by UT Administration. Thus, all teaching activities will be provided via online Blå6døSarsitø/abc/i@elladoCatlabbhatéddilitite£acOitiliese @ottimese/seuniesassrwithbre wilditgeV@ednje&daginæsdayfidaagn@rt@rt@ag</mark> am till 11:30 am. from 10:00 am till 11:30 am.

#### COURSE OVERVIEW

In this course, students will be familiarized with the most advanced computational techniques, programs and databases used at the frontiers of biomedical sciences. Advanced applications will be covered in four broad areas: new bioinformatics tools, genomics, proteomics, and RNomics/transcriptomics. The course is team-taught by faculty from The University of Toledo and Bowling Green State University.

- Assignment and/or <u>quiz</u> will be given after each session. Students will have ten days to complete an assignment and upload it into Blackboard. At the end of first half of the course there will be a <u>mid-term</u> take-home exam. At the end of the course there will be a <u>final exam</u>.
- < <u>Grading principles:</u> Homework/projects and quizzes= 55%; Mid-term exam = 15%; Final exam = 20%; Class and labs activity = 10%.
- < <u>Office hours</u> will be held every Monday and Wednesday from 2:00-3:00 PM in Dr. Fedorov's office, room 308, Health Science Building.

## STUDENT LEARNING OUTCOMES

Successful students WILL BE ABLE TO:

- Understand and perform RNAseq gene expression investigation starting from raw Fastq datafiles to the expression matrices.
- Be able to perform large-scale SNP analysis of individual human genome based on initial SNP microarray chip or Next Generation Sequencing datasets.
- Understand whole-genome sequencing data from FASTQ, BAM, SAM, and VCF formatted files
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- Appreciate organization and structure of the Human genome, and use RepeatMasker program for finding and characterization of DNA repeats.
- Be familiarized with Artificial Intelligence and Machine Learning approaches in Bioinformatics, with concentration on Data Mining in Bioinformatics; Cluster Analysis; Pattern Recognition; and Gene Regulatory Networks.
- Gain experience in Advanced Molecular Phylogenetics.
- Grasp insights into epigenetic control of activation and silencing genes.
- Comprehend the roles of Biomarkers in modern Biomedical Sciences
- Analyze various non-coding RNA molecules using online tools.
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All assignments, quizzes, video-lectures, and supporting materials will be available through UT Blackboard portal.

## TECHNOLOGY REQUIREMENTS

Due to COVID restrictions, this term the computer lab will not be available. For this reason, to participate in the course you will need to have your own laptop or desk top computer.

### UNIVERSITY POLICIES