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| Subject Code and Title | BI6190: Special Topic: Current problems in bioinformatics |
| Details of Subject | <p>Rationale for introducing this topic Need to introduce more relevant and current electives to enrich the M.Sc. BI program with real-world complexity of contemporary genomics & proteomics datasets, analytical and computational methods.</p> <p>BI6190 is designed for students who wish to catch up with the latest developments in Bioinformatics, computational biology and systems biology research, to apply their programming skills to solving actual biological problems, and to become proficient in answering key biological questions in-silico.</p> <p>Aims and Objectives It is imperative for computer scientists to maintain relevance to real-world biology. It is equally imperative for biologists in the post-genomic era to be highly competent users of publicly available bioinformatics and computational tools. It is no less important for both camps to be aware of trend-setting current developments in bioinformatics and computational tools in systems biology. BI6190 is designed to address these issues. Students will catch up with the latest developments in mentioned fields: new sequencing technologies, discovering biomolecular functions through protein sequence analysis, statistical methods for micro-array data analysis, current transcription regulation paradigms and models shifting in our understanding of gene and genome structures and functions, Monte Carlo strategies in Statistical bioinformatics, methods in computational imaging of biological objects, 3-D molecular simulation methods and popular bioinformatics software. Students will have an opportunity to apply their programming skills to solving actual computational and biological problems, and</p> |

learn how to obtain answers to key biological questions in-silico through skillful use of bioinformatics and computational tools and database resources in the public domain. BI6190 is strongly recommended as an elective course for all students pursuing an M.Sc. in Bioinformatics by coursework.

Coordinator: *prof. Vladimir Kuznetsov*

Syllabus

- 1. Discovering biomolecular functions through protein sequence analysis. *Frank Eisenhaber & Sebastian Maurer-Stroh*
- 2. Analysis Genome structures and genome complexity using integrative bioinformatics databases. Structures and function of Sense-antisense gene pairs in the human genome. *Vladimir Kuznetsov. & P. Jengaroipun&O. Grinchuk.*
- 3. Monte Carlo Strategies in Statistical bioinformatics. Basic theory. Lee Hwee Kuan
- 4. Lee Hwee Kuan. Monte Carlo Strategies in Statistical bioinformatics. Sequential Importance Sampling. *Lee Hwee Kuan*
- 5. Methods to model 3D structures of proteins. Sequence-sequence & sequence-structure alignments. *Madhusudhan Mallur Srivatsan*
- 6. Methods to model 3D structures of proteins Homology & Ab initio modeling. *Madhusudhan Mallur Srivatsan .*
- 7. Introduction to current molecular simulation methods. *Shubhra GHOSH DASTIDAR*
- 8. Molecular simulations and its application in biology. *Chandra Verma*
- 9. Understanding Transcription Factor-DNA interactome via Statistical & Computational Analyses of massive sequencing data sets

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| | <p>(Chip-seq, Chip-PET). <i>V. Kuznetsov</i> .</p> <ul style="list-style-type: none"> • 10. Statistical methods and computational algorithms for analysis of expression data and clinical information. <i>Efthimios Motakis&V. Kuznetsov</i>. • 11. Genome-wide expression data analysis for genetic classification of cancer subtypes clinical prediction. Applications of computational bio-statistical methods, data mining, machine learning feature selection software, sampling approaches in cancer biology. Integrative bioinformatics medicine informatics approaches and computational tools. Gene signatures. Gene expression networks. Disease-essential genes. New Gene prediction. <i>V. Kuznetsov</i> • 12. Prediction of short protein sequence motifs for posttranslational modifications and targeting signals. <i>Sebastian Maurer-Stroh & Brigit Eisenhaber</i> • 13. Popular software in bioinformatics and computational biology. Overview of the purpose, scope and usage outline of the software most commonly used in bioinformatics and computational biology in the academic and corporate setting. <i>Ivana MIHALEK</i> |
| Assignment | 4 - 6 Assignments |
| Hours of Contact /Location/A Us | 3 hours a week. Location: 30 Biopolis Street #07-01, BII/A-STAR 3 AU |
| Offered with effect from | Semester 2 of AY 2008-2009 |
| Maximum Class Size: | 20 |
| Modes of Teaching and Learning | Lectures (major), problem-based assignment and laboratory sessions with instructors using standard bioinformatics software and some programming and analytical presentations and discussions. |