

**Department of Computer and Electrical Engineering and Computer Science
Florida Atlantic University
Course Syllabus**

1. Course title/number, number of credit hours	
COT 6930 – Computational Models in Genomics	3 credit hours
2. Course prerequisites, corequisites, and where the course fits in the program of study	
<i>Prerequisites:</i> Graduate students in bioengineering/ computer science / computer engineering/Electrical engineering. Programming background in any language (R/Python/Java/C/C++). BME 6930 – 'Genomics Analysis' is not a prerequisite to this course. Biology concepts will be covered as appropriate.	
3. Course logistics	
<i>Term:</i> Fall 2019 This is a course with live and distance learning sections. Lectures will be videotaped and made available via Canvas LMS. <i>Class location and time:</i> TBA	
4. Instructor contact information	
<i>Instructor's name</i> <i>Office address</i> <i>Office Hours</i> <i>Contact telephone number</i> <i>Email address</i>	Ravi Shankar, Professor Engineering East (EE) Bldg., Room 513 TBA 561-297-3470 shankar@fau.edu
5. TA contact information	
<i>TA's name</i> <i>Office address</i> <i>Office Hours</i> <i>Contact telephone number</i> <i>Email address</i>	NA
6. Course description	
<p>GWAS, a study of SNPs (Single Nucleotide Polymorphisms, i.e., variations at the level of single bases in the 3 billion long human genome), has advanced mapping of genome to pathology. Population (or public) health studies (with twins, families, ancestral and ethnic groups) have estimated heritability at 40 to 60 % for various common chronic diseases; yet, GWAS has only uncovered less than 10 % heritability through GWAS studies of the genome itself. Studies so far have focused on high MAF (minor allele frequency) of >5 % for SNPs because of statistical power restrictions and reasonable size of cohorts (300,000 subjects or less). Identifying more SNPs with lower MAF, gene-to-gene interactions (epistasis), and tissue-specific variations (epigenetics) will require millions of cohorts. This faces the reality of high cost of logistics, sequencing, and bioinformatics. Genomics is also beset with a steep learning curve. Building biological pathway models for each disease is needed to lower the barrier and enhance participation of biomedical professionals. This course uses state-of-the-art tools and databases to help build such models and tools to further the field. The team project can be among students taking this course or collaboration with other engineering students who are doing DIS (directed independent study) or taking another course with this professor. Discuss with the professor and decide by the 7th week. The former type will involve using a visualization tool to build a specific biological pathway. For the latter, the interested students will work with computer engineering students to build an executable biological path module, albeit of lower complexity. Either way, the professor will help.</p>	
7. Course objectives/student learning outcomes/program outcomes	
<i>Course objectives</i>	Build executable biological pathway modules for genomic analysis

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8. Course evaluation method	
Five assignments: 30%; Mid-term exam: 30%; and Project (on Biological pathway model) 30%. Class community service (bonus): 10%. No final exam Assignment topics: Choose a specific biological pathway. Review; Use SBML/ BioPax to document the model; Use mEPN to build a model. Execute and discuss; Build a more abstract model in any programming language. Simulate and verify earlier results; and Develop a mixed level model. Project (report): A research paper that combines work in the assignments into a publishable conference paper. Professors from biology, engineering, and medicine will help (edit/review).	<i>Note: The minimum grade required to pass the course is C.</i>
9. Course grading scale	
Proposed Grading Scale: 90-100 for "A" and "A-"; 80-89 for "B+", "B", or "B-"; 70-79 for "C+", "C", or "C-"; 60-69 for "D+", "D", or "D-"; 59 and below: "F"	
10. Policy on makeup tests, late work, and incompletes	
<i>All assignments and exams are online and open-book and open notes. Late assignments will be accepted with a 10% penalty per week for 2 weeks. The Project assignment is due before the reading day.</i>	
11. Special course requirements	
12. Classroom etiquette policy	
University policy requires that in order to enhance and maintain a productive atmosphere for education, personal communication devices, such as cellular phones and laptops, are to be disabled in class sessions. High level well behavior and class discipline are expected.	
13. Disability policy statement	
In compliance with the Americans with Disabilities Act (ADA), students who require special accommodations due to a disability to properly execute coursework must register with the Office for Students with Disabilities (OSD) located in Boca Raton campus, SU 133 (561) 297-3880 and follow all OSD procedures.	
14. Honor code policy	
Students at Florida Atlantic University are expected to maintain the highest ethical standards. Academic dishonesty is considered a serious breach of these ethical standards, because it interferes with the university mission to provide a high quality education in which no student enjoys unfair advantage over any other. Academic dishonesty is also destructive of the university community, which is grounded in a system of mutual trust and place high value on personal integrity and individual responsibility. Harsh penalties are associated with academic dishonesty. See University Regulation 4.001 at www.fau.edu/regulations/chapter4/4.001_Code_of_Academic_Integrity.pdf	
15. Required texts/reading	
A collection of recent (2012-2018) papers, tools, and websites on GWAS (its benefits and challenges) and biological pathway modules. Some specific ones are listed below: (Journal articles listed are accessible through the FAU library): 1. US Federal Government Resources: https://www.genome.gov/10000375/online-research-	

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[resources/](#)

2. KEGG (Kyoto Encyclopedia of Genes and Genomes) database: <https://www.genome.jp/kegg/>
3. O'Hara, et al., Modelling the Structure and Dynamics of Biological Pathways (2016): <http://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.1002530>. This introduces mEPN
4. Pathguide- The pathway resource list: <http://www.pathguide.org/>
5. Zuk, et al., The mystery of missing heritability: Genetic interactions create phantom heritability (2011): <https://www.ncbi.nlm.nih.gov/pubmed/22223662>

16. Supplementary/recommended readings

(1) Genome-Wide Association Studies: From Polymorphism to Personalized Medicine, by K. Appasani (Ed), Cambridge Univ. Press, 2016. Additional reading: (2) The genetics of obesity, S. Grant (Ed), 2014, Springer.

17. Course topical outline, including dates for exams/quizzes, papers, completion of reading

(lectures are 75 minutes long)

1. Introduction to Genetics and the Human Genome: 5 lectures
2. Introduction to sequencing and analysis tools for genomic analysis: 5 lectures
3. KEGG (Kyoto Encyclopedia of Genes and Genomes) database resource: 5 lectures
4. Case study of cardiovascular diseases – Before and after GWAS, and statistical aspects: 3 lectures
5. Biological pathways with mEPN (modified Edinburgh Pathway Notation) and Petri Nets: 5 lectures
6. Structure and dynamics of biological pathways with mEPN, a visualization tool: 3 lectures
7. Team project (6 week long): Model a biological pathway (different for each team). Submit for publication
8. Challenges and proposed solutions (potential thesis topics): Missing and phantom heritability, Copy Number Variants, Statistics, Computational Speedup, and Scaling up of GWAS studies: 2 lectures