

COMPUTATIONAL GENOMICS – BIOL 7210 A – Spring 2017

Professor: **I. King Jordan** and T.A.: **Lu Wang**

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Course summary: The science of genomics involves the intersection of experimentation and computation. Computers are quite obviously required to handle the massive amount of data produced by genome sequencing projects. More importantly however, genome sequencing efforts yield 'information' alone, which can only be converted into 'knowledge' through the use of computers. In this class, the students will convert raw genomic information (*i.e.* sequence reads) into knowledge through the use of computational genomics tools and applications. The class will be provided with unassembled genome sequence data from the Centers for Disease Control and Prevention (CDC) and will proceed through five distinct stages of analysis and interpretation of that data: **1-genome assembly, 2-gene prediction, 3-functional annotation, 4-comparative genomics** and 5-production of a **genome browser**. This course will be entirely practical in nature. Students will learn to do the actual work of computational genomics. Expert guest lecturers will be brought in to provide information on state-of-the-art computational genomics tools. Based on this information, other class lectures and their own research, students will be solely responsible for choosing which tools (e.g. programs and/or databases) to use, how to implement them and for producing and thoroughly documenting their final results. All results will be integrated into a publicly available genome browser.

This class meets on Mondays and Wednesdays from 10:35 to 11:55 am in Klaus Advanced Computing Building 1447. There is no textbook. Required and recommended readings will be made available on the course Wiki page - <http://compgenomics2017.biology.gatech.edu/> along with any lecture material. Students are required to use online databases and the scientific literature to inform their choice of computational tools to be used. Since there is no textbook and many of the sessions involve class discussion and lab activities rather than formal lecture, attendance and class participation are absolutely mandatory.

Evaluation:

Class participation	12.5%
Group presentation I	12.5%
Group presentation II & Lab	12.5%
Group presentation III & Demo	12.5%
Final Results & Documentation	50%

Class attendance and participation are mandatory. **Class participation** will be judged by the degree to which each student participates in class lectures and discussions (by asking questions, answering questions, offering ideas and opinions), during group presentations (by asking questions during others' presentations, by engaging the audience during their own presentation, by connecting their presentation to previous class discussions, by working successfully in a small group), and during computer laboratory activities (by performing analyses and working with other students). Students who show up late or miss class will lose 10% of their class participation grade each time.

Each group will give a series presentations and laboratories/demos. **Group presentations and labs/demos** will be judged by the depth of analysis presented, the clarity of presentation, the utility of the exercises, the appropriateness and justification of the choices made, the validity and robustness of the results and the thoroughness of the documentation. In addition to presentations, results and documentation should be presented on the class Wiki site. Specific requirements for the presentations will be provided during class sessions. Contributions of each individual student to the overall group effort must be meticulously detailed and documented.

Please see www.honor.gatech.edu for Georgia Tech's Academic Honor Code, which you are required to uphold.

Date	Topic	Presenter(s)
Mon 1/9/2017	Introduction & Logistics	King Jordan & Lu Wang Georgia Tech
Wed 1/11/2017	Class groups & Wiki	King Jordan & Lu Wang Georgia Tech
Wed 1/18/2017	CDC Enteric Diseases Laboratory Branch & PulseNet	Heather Carleton-Romer CDC
Mon 1/23/2017	Bioinformatics on the Cloud	King Jordan & Lu Wang Georgia Tech
Wed 1/25/2017	Genome Based Methods for Molecular Typing	King Jordan Georgia Tech
Mon 1/30/2017	Genome Assembly	Lee Katz CDC
Wed 2/1/2017	Bioinformatics at the CDC	Scott Sammons CDC
Mon 2/6/2017	Genome Assembly Background & Strategy	Students - Genome Assembly Group
Wed 2/8/2017	Bioinformatics with Amazon Web Services (AWS)	Ahsan Huda Booz Allen Hamilton
Mon 2/13/2017	Genome Assembly Lab & Preliminary Results	Students - Genome Assembly Group
Wed 2/15/2017	Gene Prediction with GeneMark	Mark Borodovsky Georgia Tech
Mon 2/20/2017	Functional Annotation at NCBI	Leonardo Mariño-Ramírez NCBI
Wed 2/22/2017	Gene Prediction Background & Strategy	Students - Gene Prediction Group
Mon 2/27/2017	Functional Annotation & Comparative Genomics	Lu Wang Georgia Tech
Wed 3/1/2017	Gene Prediction Lab & Preliminary Results	Students - Gene Prediction Group
Mon 3/6/2017	Genome Assembly Results, Protocol & Demo	Students - Genome Assembly Group
Wed 3/8/2017	Functional Annotation Background & Strategy	Students - Functional Annotation Group
Mon 3/13/2017	Salmonella comparative genomics and objectives	Sung Im CDC
Wed 3/15/2017	Functional Annotation Lab & Preliminary Results	Students - Functional Annotation Group
Mon 3/27/2017	Gene Prediction Results, Protocol & Demo	Students - Gene Prediction Group
Wed 3/29/2017	Comparative Genomics Background & Strategy	Students - Comparative Genomics Group
Mon 4/3/2017	Comparative Genomics Lab & Preliminary Results	Students - Comparative Genomics Group
Wed 4/5/2015	Generic Model Organism Database	Lavanya Rishishwar Georgia Tech
Mon 4/10/2017	Functional Annotation Results, Protocol & Demo	Students - Functional Annotation Group
Wed 4/12/2017	Database Background & Strategy	Students - Genome Database Group
Mon 4/17/2017	Database Lab & Preliminary Results	Students - Genome Database Group
Wed 4/19/2017	Comparative Genomics Results, Protocol & Demo	Students - Comparative Genomics Group
Mon 4/24/2017	Final presentation of the Project / Database	Students - Group representatives