

UNC CHARLOTTE

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COMPUTING and INFORMATICS

The College of Computing and Informatics (CCI) is one of the few such stand-alone colleges in the US. CCI is a leading participant in interdisciplinary projects, placing particular emphasis on connecting fundamental research to critical scientific, societal and defense challenges. CCI is committed to being a recognized leader in education, by training competitive, innovative, entrepreneurial individuals able to meet the needs of our society in the 21st century. CCI fosters research excellence across its departments, focusing on trend-setting approaches to the most challenging research problems in both national and international areas.

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UNC CHARLOTTE

College of Computing and Informatics

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WINGS

WORKSHOP IN
NEXT GENERATION
SEQUENCING



Department of
Bioinformatics
and **Genomics**



UNC CHARLOTTE
College of Computing and Informatics

SCHEDULE

DAY 1

Thursday May 17

THE BIOLOGICAL SYSTEMS

Primary Venue: Room 105 (spillover in 104, 217)

MORNING

- 10 - 11** **Registration** – Bioinformatics Building, Room 303
- 11 - 12** **Lunch** – Atrium (catered)

AFTERNOON

- 12 - 12:15** Welcome, Dr. Larry Mays, BiG chairman
- 12:15 - 1** Dr. Anthony Fodor (UNC Charlotte)
“Analyzing human – associated microbial communities with next-generation sequencing of 16S rRNA amplicons.”
- 1 - 1:45** Dr. Huidong Shi (Georgia Health Sci Uni)
“Genome – wide bisulfite sequencing analysis reveals novel epigenetic changes in prognostic subsets of chronic lymphocytic leukemia”
- 1:45 - 2:30** Dr. Cory Brouwer (UNC Charlotte)
“Preprocessing and Quality Control of Next-Generation Sequencing Data”
- 2:30 - 3** **Break** – Atrium (beverages, snacks)
- 3 - 3:45** Dr. Ann Loraine (UNC Charlotte)
“Visualizing RNA – Seq data using the Integrated Genome Browser”
- 3:45 - 4:30** Dr. Jeremy Goecks (Emory Uni.) “Expression Dynamics of Human XBP1 Revealed using an Integrative Approach and Galaxy”
- 4 :30 - 5:15** Dr. Mark Wilson (Western Carolina Uni)
“An evaluation of the Roche GS – Junior pyrosequencer to detect minor variants in mixed human mitochondrial DNA amplicons”
- 5:15 - 6** **Break**
- 6 - 8:00** **Workshop Dinner** – Atrium (catered)

DAY 2

Friday May 18

HANDS-ON SESSIONS

Two sessions will be held concurrently, so attendees will be able to sign up for at most 3 sessions.

MORNING

7 - 8

Breakfast – Atrium (catered)

SESSION 1

8 - 10

Workshop 1A: Room 104

Detecting minor sequence variants in amplicons. Session leaders: Dr. Mark Wilson, Dr. Shannon Schlueter.

Workshop 1B: Room 105

Splice detection in Arabidopsis transcripts. Session Leader: Dr. Ann Loraine.

10 - 10:30

Break – Atrium (coffee, snacks)

SESSION 2

10:30 - 12:30PM

Workshop 2A: Room 104

Mapping BiS (methylation) sequencing reads. Session Leader: Dr. Justin Choi.

Workshop 2B: Room 105

Cleansing short-read sequence data. Session Leaders: Dr. Ra'ad Gharaibeh and Dr. Cory Brouwer.

AFTERNOON

12:30 - 2

Lunch – Atrium (catered)

SESSION 3

2 - 4

Workshop 3A: Room 104

Processing 16S rRNA amplicons from a mixed source. Leader: Dr. Anthony Fodor.

Workshop 3B: Room 105

Using Galaxy to establish an NGS workflow. Leader: Dr. Jeremy Goecks.

4 - 4:30

Final remarks, departure



WINGS

WORKSHOP IN NEXT GENERATION SEQUENCING

Transforming your data to information: processing the high-throughput sequencing data from your epigenetic, metagenomic, SNP amplicon, or transcriptome project.

High-throughput sequencing platforms are becoming the expected method for acquiring DNA and RNA data in many biological experiments, as the technology becomes inexpensive and routine. The data challenges are significant given the size, and platform idiosyncracies affect data cleansing choices. Experimental design also has a large impact on the choice of algorithms and pipelines. Workshop attendees will receive expert advice about processing pipeline choices, hands-on experience in operating the software, and an opportunity to network.



Department of Bioinformatics and Genomics

The Department of Bioinformatics and Genomics (BiG) was established within the College of Computing and Informatics in 2009 to foster research and education in Bioinformatics and Computational Biology. Located in the Bioinformatics Building on UNC Charlotte's CRI Campus, the Department offers a Ph.D. in Bioinformatics and Computational Biology, a Professional Science Master's in Bioinformatics, and an undergraduate Minor in Bioinformatics and Genomics. The building has both wet and dry laboratories, and includes core facilities for molecular biology, genomics, and high-performance computing. Currently, the Department has 14 full-time faculty, 24 Ph.D. students, 25 Master's students, and a professional staff of 12.

The Department also operates a Bioinformatics Services Division on the North Carolina Research Campus, a billion-dollar, 350-acre research park in nearby Kannapolis. The focus of this group is the development and application of novel analytical methods for knowledge discovery involving large biological datasets.

Presenters and Workshop Session Leaders

Dr. Ann Loraine is an Associate Professor in the UNC Charlotte Bioinformatics and Genomics Department. Previously she has worked in the Biotech industry as well as at UAB. Her current studies focus on alternative splicing in *A. thaliana* for which her lab has developed and continues to extend the Integrated Genome Browser (IGB), software designed to visualize genomic data.

<http://bioviz.org/igb/>

Dr. Anthony Fodor is an Assistant Professor in the UNC Charlotte Bioinformatics and Genomics Department. In addition to initiating and participating in numerous studies that have linked the state of the human microbial community to health and disease, he has been an active participant in the data analysis team of the Human Microbiome Project.

<http://fodorlab.uncc.edu/>

Dr. Cory Brouwer is the Director of the Bioinformatics Services Division (BiSD) and Associate Professor of Bioinformatics and Genomics at UNC Charlotte. Prior to his appointment at UNCC, he led a global computational biology group for the pharmaceutical company Pfizer. Dr. Brouwer and his team provide a wide range of bioinformatics and computational biology services to the NCRC, UNC Charlotte and surrounding area life sciences community.

<http://bigscience.uncc.edu/directory/cbrouwer>

Dr. Ra'ad Gharaibeh is a Research Associate Scientist at the Bioinformatics Services Division (BiSD) in the Dept. of Bioinformatics and Genomics at UNC Charlotte. Dr. Gharaibeh holds a Ph. D. in Bioinformatics from UNC Charlotte. His PhD research involved the influence of biophysical molecular properties on microarray data analysis. He is involved in several NGS projects ranging from de novo assembly to Cancer Genomics.

<http://bigscience.uncc.edu/directory/rgharaib>

Dr. Huidong Shi is an Associate Professor of Biochemistry and Molecular Biology in the Georgia Health Science University, where he is a member of the Molecular Oncology Program at GHSU Cancer Center. Dr. Shi's research interests are in the area of epigenomics, and most of his work focuses on developing high-throughput technologies for dissecting the complex epigenetic regulation in normal and cancer cells. Dr. Shi's laboratory is currently interested in developing genome-wide bisulfite sequencing methods based on the next-generation sequencing platform. <http://www.georgiahealth.edu/cancer/people/hshi.html>

Dr. Justin Choi is an Assistant Professor of Biostatistics in the Georgia Health Science University, where he is a member of the Molecular Oncology Program at GHSU Cancer Center. Prior to moving to the Medical College of Georgia in 2011, he was an associate director of Bioinformatics at The Center for Genomics and Bioinformatics, Indiana University, Bloomington. Dr. Choi's work focuses on developing computational algorithms and pipelines to analyze NGS data for various biological applications. Currently his lab focus is on computational approaches for genome-wide bisulfite sequencing methods.

<http://www.georgiahealth.edu/cancer/people/jchoi.html>

Dr. Shannon Schlueter is an Assistant Professor in the UNC Charlotte Bioinformatics and Genomics Department. He has been a major contributor to the PlantGDB and xGDB projects. His major interests are the application of data mining and computational pattern recognition in the field of genome informatics. This research includes algorithm and software development for genome annotation as well as predictive modeling of biomolecule function and involvement in transcriptional gene regulation.

<http://bigscience.uncc.edu/directory/sschluet>

Dr. Jeremy Goecks is a Postdoctoral Fellow in the Departments of Biology and Math & Computer Science at Emory University. His research interests include (a) computational methods and infrastructure for biomedical research and (b) integrative analyses to understand genomic regulation dynamics. He is a core member of the Galaxy team, a Web-based platform for performing accessible, reproducible, and transparent computational biomedical research.

<http://bx.mathcs.emory.edu/people/jeremy/>

Dr. Mark Wilson is the Director of the Forensic Science Program at Western Carolina University in Cullowhee, N.C. Dr. Wilson spent 23 years as a Special Agent and Supervisory Special Agent in the F.B.I. Most of this time was spent working in DNA analysis in the Laboratory Division. Dr. Wilson was heavily involved in the development, validation, and eventual acceptance of human mitochondrial DNA in forensic science.

<http://www.wcu.edu/6699.asp>

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