Statistical Modeling and Analysis of Whole Genome Methylation and Chromatin Interaction (Epigenetics)

March 9-10, 2015

SCHEDULE

Monday March 9th

8:00 Shuttle to SAMSI

8:30-8:50 Registration

8:50-9:00 Opening Remarks – **Sujit Ghosh**, SAMSI, **Shili Lin**, Ohio State University

9:00-10:30 Session 1: Epigenetics and Statistical Methods for Analyzing Epigenetic Data
Chair: **Shili Lin**, Ohio State University

Bob Schmitz, University of Georgia
"Challenges and Biases Associated with Whole-Genome Bisulfite Sequencing Data"

Michael Zhang, University of Texas, Dallas
"Computational Advances in ChIP-seq and ChIA-PET Data Analysis"

10:30-11:00 Break

11:00-12:30 Session 2: DNA Methylation I
Chair: **Yong Seok Park**, University of Pittsburgh

Peng Jin, Emory University
"Dynamic Cytosine Modifcation in Human Diseases"

Maureen Sartor, University of Michigan
"Analysis Tool for Combined DNA Methylation and 5-Hydroxymethylcytosine Data"

Hao Wu, Emory University
"Differential Methylation Analysis from Whole Genome Bisulfite Sequencing: a Matter of Spatial Correlation, Coverage Dept, and Biological Variance"

12:30-2:00 Lunch (SAMSI, 2nd Floor Lounge)

2:00 - 3:00 Session 3: Modeling of Long-range Chromatin Interaction I
Chair: **Ming Hu**, New York University

Inkyung Jung, University of California, San Diego
“Deciphering Dynamic Chromatin 3D Organization: from Structure to Gene Regulation”

Liang Niu, University of Cincinnati
“Statistical Modeling and Analysis of ChIA -PET Data”

3:00-3:30 Break

3:30-5:00 Session 4: Contributed Talks
Chair: **Victor Jin**, University of Texas, San Antonio Health Science Center

Eric Lock, University of Minnesota
“Bayesian Screening for Group Differences in Methylation Array Data”

Deepak Ayyala, Ohio State University
“Faster and Efficient Tests for Detection of Differentially Methylated Region from MethylCap-seq Data”

Oswaldo Lozoya, NIH/NIEHS
“The Impact of Mitochondrial Dysfunction on the Epigenome”

Chenchen Zou, Jackson Laboratory for Genomic Medicine
“Multi-track Structure Inference Model for Genome-wide Chromatin Conformation-capturing Data”

5:00-7:00 Poster Session/Reception (SAMSI, 2nd Floor Lounge)
(The board dimensions are 4 ft. wide by 3 ft. high. They are tri-fold with each side being 1 ft. wide and the center 2 ft. wide. Please make sure your poster fits the board. The boards can accommodate up to 16 pages of paper measuring 8.5 inches by 11 inches.)

7:00 Shuttle to Hotel

Tuesday, March 10th

8:00 Shuttle to SAMSI

8:45-9:00 Registration and Announcements, **Shili Lin**, Ohio State University

9:00-10:30 Session 5: DNA Methylation II
Chair: **Steve Qin**, Emory University

Pearlly Yan, Ohio State University
“DNA Methylation Profiling in Cancer: Perspectives from a Genomics/Computation Group”

Yong Seok Park, University of Pittsburgh
"Statistical Analysis of DNA Methylation using Within-Fragment Information"

Karen Conneely, Emory University
"DNA Methylation, Gene Expression, and Aging: What Can We Learn from Cross-Sectional Microarray Data?"

10:30-11:00 Break

11:00-12:30 Session 6: Modeling of Long-Range Chromatin Interaction II
Chair: **Hao Wu**, Emory University

Miriam Huntley, Harvard University
"How the 3D Genome Folds - Now in the Loop"

Ming Hu, New York University
"A Hidden Markov Random Field Based Bayesian Method for the Detection of Long-Range Chromosomal Interactions in Hi-C Data"

Victor Jin, University of Texas, San Antonio Health Science Center
"Genomic Analysis of Three-Dimensional Data Identifies Functional Enhancer-Mediated Looping"

12:30-2:00 Box Lunch and Adjourn