Center for Minimally Invasive Therapeutics

## **Seminar series**



University of California, Los Angeles (UCLA), U.S.A. Monday, March 4<sup>th</sup>, 2019 at 1:00pm-2:00pm 4101 Engineering V Hosted by Prof. Ali Khademhosseini

## "Predictive Algorithms & Cyberinfrastructures for Precision Medicine"

## Abstract:

Precision medicine emphasizes the way in which health and disease vary in every single individual or in cohorts of individuals. This is because the health of an individual is a function of her genome, epigenome, and metagenome. Every cell of the human body has the same genome. How then is a brain cell distinct from a heart cell? How does a cancer cell bypass the checks and balances of the immune system? This is where the cell's epigenome offers a distinct "symphony" to diverse cellular states in varied contexts (level of maturity, pathogenicity, etc.). Driven by the exabytes of sequencing data being generated, there is an increasing need to analyze genomic big data to interpret and stratify disease for personalized therapies. How can this "genomical" big data enable the strides of precision medicine? What kinds of algorithms can deal with the inherent heterogeneity, the noise, and the high-dimensionality of this kind of data? Are there recurrent kernels or motifs in these algorithms that can be identified to speed up development of new algorithms? Can these efforts result in precise data-driven medicine? In this talk, I will answer some of the above questions through our ML algorithmic suite—Avishkar. First, in our Avishkar suite, we uncover the non-canonical signatures of small regulatory RNA (e.g., microRNA, miRNA for short) targets. Regulatory miRNA-gene interactions are known to control a vast swath of cellular processes and can be leveraged to design precise and effective nucleotidebased therapeutics. Using our suite of predictive algorithms (SVM and ANN variants), we are able to predict miRNA targets in a data-driven manner. Then, I will present a few examples of context-aware interactions that can uncover combinatorial regulatory effects whereby multiple miRNAs together regulate expression of individual genes or clusters of genes dependent on the cellular context. Our modular and distributed implementations of the models are effective both from the standpoint of speed and for biological relevance, say for example varied gene regulatory interactions in a healthy person, distinct from a person in the throes of an anomaly. Finally, I will present our work on federated cyberinfrastructures for genomics. This is in the context of the MG-RAST repository, the largest metagenomics portal and analysis pipeline and hosted by the US Department of Energy.

## **Biography:**

Dr. Somali Chaterji is an Assistant Professor in the Department of Agricultural and Biological Engineering at Purdue University. She works in the areas of data science and engineering for digital agriculture and genomics and in building cyberinfrastructures for these domains. She is a part of the WHIN (Wabash Heartland Innovation Network) leadership team working to bring IoT to advance agriculture. Data is power! She believes in leveraging the power of big data by drawing actionable insights from diverse agricultural sensing data to make agricultural practices high-throughput and sustainable. As a second thrust of her work, Prof. Chaterji is extracting insights from epigenomic data for predictive and personalized healthcare, one in which health and vitality is the focus. To accomplish her goals, Prof. Chaterji develops algorithms and statistical models for precision medicine, and more recently, in digital agriculture with an eye toward sustainability. She got her PhD in Biomedical Engineering from Purdue University, winning the Chorafas International Award (2010), College of Engineering Best Dissertation Award (2010), and the Future Faculty Fellowship Award (2009). She did her Post-doctoral Fellowship at the University of Texas at Austin in the Department of Biomedical Engineering, where her work was supported by an American Heart Association (AHA) award. She has won the best paper award at the ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (BCB) in 2015. Dr. Chaterji is also a lab-to-bedside commercialization enthusiast and is a scientific advisor to the IC2 Institute at the University of Texas at Austin since 2014. Dr. Chaterji won Purdue's Seed-for-Success Award in 2016 for winning a research grant of more than \$1M (NIH R01).

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