17th Annual LBRN Meeting - 2019

Invited Talk - January 19th, 2019 – 9:00 to 9:30 AM
Learning biology as a data science - the future of bioinformatics in the lab

Elia Brodsky
CEO Pine Biotech

Abstract: Advances in molecular biology are driving innovation in computing, including data processing, analysis and integration. This field of bioinformatics "speaks" a different language of statistics, computer code and "megaflops". In this talk, Elia Brodsky from Pine Biotech will speak about these two worlds and the future of biomedical research in Louisiana depending on the adoption of bioinformatics as a language among students, biologists and the broader public. Data science literacy and inclusion are the key to growing our capacity for cutting edge biomedical research. Working together with LBRN, Pine Biotech has been developing tools and training materials to lower the barrier for students, biologists, biotechnologist and lab technicians to learn biology as a data science and leverage bioinformatics in biomedical research.

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Keynote Talk - January 19th, 2019 - 8:15 to 9:00 AM
Comprehensive Solution to Characterize and Treat Disease

Ram Samudrala PhD
Professor and Chief, Division of Bioinformatics
Department of Biomedical Informatics
Jacobs School of Medicine & Biomedical Sciences

Abstract: Discovery and development of small molecule compounds into therapeutics is time and resource intensive, a process that can be made more efficient by computational drug repurposing. We have developed the Computational Analysis of Novel Drug Opportunities (CANDO) platform for shotgun drug repurposing, i.e., screen and rank every existing human use drug or compound for every disease/indication. The modeling pipeline in CANDO predicts interactions between every compound and every protein structure present in corresponding curated libraries to generate compound-proteome interaction signatures that are then analysed and compared to identify similar drug behavior. For each drug, CANDO produces a ranked list relative to every other compound based on the similarity of their interaction signatures. The performance of CANDO is evaluated based on its ability to recover drugs approved for each indication within a particular cutoff of the corresponding ranked compound similarity lists; top ranked compounds other than the known approved drugs are hypothesized to be novel putative therapeutics for that indication. We have added new ligand-based virtual screening, data fusion, and decision tree pipelines, as well as made improvements to existing pipelines, to better understand drug behavior and improve benchmarking performance. The presentation will address the latest improvements to the CANDO platform and its potential to substantially increase drug recovery accuracy via the integration of multiple pipelines to determine similarity of compound behavior, thereby increasing our confidence in generating putative therapeutic repurposing candidates.

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Keynote Talk - January 18th, 2019 – 5:00 to 5:30 PM
IDeA Program and Community: Priorities and Opportunities

Ming Lei, Ph. D.
Director
Division for Research Capacity Building
National Institute of General Medical Sciences

Ming Lei, Ph.D., is Director of the Division for Research Capacity Building. He oversees the Institute's capacity-building programs, which include the Institutional Development Award (IDeA), Support of Competitive Research (SCORE), and Native American Research Centers for Health (NARCH), as well as the Science Education Partnerships Awards (SEPA).

Dr. Lei joined NIGMS in 2018 from the National Cancer Institute (NCI), where he was deputy director of the Center for Cancer Training and chief of the Cancer Training Branch. Prior to joining NCI as a program director in 2008, Lei was leader of the Genes and Genome Cluster in the Division of Molecular and Cellular Biosciences at the National Science Foundation from 2006-2008

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