“Frameworks for multidimensional data integration in complex human diseases”

Large-scale projects are generating multidimensional genomic data sets on a variety of diseases with the goal of improving disease diagnosis, prognosis, and treatment efficacy. However, integration of these data, both across assay types and diseases, is a challenge that will become increasingly difficult as data sets grow. This is particularly true given the high ratio of individual genomic measurements to samples and systematic biological and technical correlations among those measurements. Here I will address the critical need to develop analytical frameworks that can leverage the overlapping and unique information captured by different genomic assays in order to advance large-scale genomic study designs, facilitate systems biology approaches to disease, and improve clinically-relevant biomarker performance. An emphasis will be placed on cancer research including inferring molecular signatures from genomic data sets and characterizing feature set enrichment, building multi-omics classifiers with machine learning, and developing computational tools for integrating multidimensional data sets to promote reproducibility and accelerate future research.

Friday, 10/13/2017 at 10:00am

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