Statistical methods in Systems Medicine

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Abstract

Discovery of prognostic and diagnostic biomarker signatures for diseases, such as cancer, is seen as a major step towards a better personalized medicine. During the last decade various methods have been proposed for inferring such signatures from high dimensional molecular data (e.g. genomics, transcriptomics, proteomics and metabolomics profiles). However, one important obstacle for making molecular signatures a standard tool in clinical diagnosis is the typical low reproducibility of these signatures combined with the difficulty to achieve a clear biological interpretation. For that purpose in the last years there has been a growing interest in approaches that employ biological background knowledge. In addition, the increasing availability of different –omics profiles for the same patient now raises the question on how to integrate these data.

The purpose of this course is to shed light on current integrative modeling efforts that combine different -omics entities and/or biological background knowledge in order to achieve higher robustness, stability and interpretability of molecular biomarker signatures.

Prerequisites for participants: Experience with classification and regression methods for high dimensional data

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