FASSBERG
Seminar Series

**Tuesday
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Data Mining in the Life Sciences: Combinatorial Association Mapping

Despite all advances in large-scale genotyping, phenotyping and genome-wide association mapping, the problem of predicting complex disease phenotypes from an individual's genotype remains largely unsolved. One possible explanation is that the vast majority of current statistical methods ignores any trait-related interactions between genetic loci. The difficulty in discovering these interactions stems from the combinatorial explosion of the candidate space, which grows exponentially with the number of interacting loci. This leads both to an enormous computational efficiency problem and a severe multiple testing problem. Ignoring this multiple testing problem may lead to millions of false positive associations; accounting for it may lead to a complete loss of statistical power. For this reason, statistically sound and efficient *Combinatorial Association Mapping* was long deemed an unsolvable problem.

In this talk, we will present our recent solutions to this problem of Combinatorial Association Mapping through the development of novel Data Mining algorithms and the results of their first applications to genome-wide association mapping. We will conclude with an outlook on the future role of Data Mining in Genetics and, more generally, the Life Sciences.

Host: Patrick Cramer

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