Detecting Dense and Sparse Signals in Omics Studies

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Abstract: In omics studies, there is a common scenario when we are interested in testing whether there exists any signal of unknown proportion in a dataset that contains tremendous amount of noise. For example, in chromosome copy number detection problem, the goal is to detect the unknown proportion of carriers of certain copy number change among non-carriers; and in GWAS, we are interested in detecting an unknown proportion of SNPs in a SNP set that may associate with a certain disease. In this talk, I will propose a novel approach that adaptively combines statistical tests to detect both dense and sparse signals in high dimensional data. Simulation will be used to explore the properties of this approach around the theoretical detection boundary. I will also discuss the application of this new approach in SNP set analysis and microbial community analysis.