

# Statistical Analysis of Somatic Mutations in Cancer Genomes

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**Abstract:** Somatic mutations drive the growth of tumor cells and are pivotal biomarkers for many cancer treatments. In contrast to germline mutations, somatic mutations may occur in a subset of tumor cells (intra-tumor heterogeneity) and calling somatic mutations often have non-ignorable false positive rate and/or false negative rate. I will present our recent on association analysis using somatic mutations, while accounting for somatic mutation calling uncertainty, and association analysis for intra-tumor heterogeneity.