# Efficient algorithms for resampling-based hypothesis testing in genomic data analysis

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**Abstract:** Resampling-based hypothesis testing procedures such as bootstrapping and permutations tests are widely used in genomic data analysis when the distribution of the test statistic is analytically intractable. However, these test procedures are often computationally intensive, especially when the dataset is large, the desired significant level is very small or there are many tests to perform, all of which are commonly encountered scenarios in modern genomic studies. In this talk, I will discuss several computational methods for accelerating such testing procedures while having theoretical justification and empirical evidence of achieving substantial speedup and high accuracy. The methods will be demonstrated with both simulated and real data experiments in genomics.