

## “On Control of False Discovery Rate under Dependence”

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### Abstract

It has been shown that the Benjamini-Hochberg method of controlling false discovery rate remains valid under various dependence structures. It is also often assumed that the p-values are known and the number of true alternative hypothesis is of the same order as the number of tests. However, this idealized assumption is hard to meet in practice because the population distribution is usually unknown and the signals in many applications may be sparse. In this talk we propose a robust control of false discovery rate under dependence. It not only allows the sparse alternatives but also is robust against the tails of the underlying distributions and the dependence structure. Only finite fourth moment of the null distribution is required to achieve asymptotic-level accuracy of large scale tests in the ultra high dimension.

The method is applied to gene selection, shape analysis of brain structures and periodic patterns in gene expression data. The method also shares favorable numerical performance on both the simulated data and a real breast cancer data.

To get a more accurate approximation for the null distribution, a computation efficient bootstrap procedure is also developed.