Yu, Wei; Xu, Wangli; Zhu, Lixing
Estimating the number of equal components for two high-dimensional mean vectors. (English) Zbl 07532160
Summary: In this article, we propose a new method for estimating the number of equal components $m_0$ of two $m$-dimensional population means when $m$ is large. The proposed method can be used to estimate the number of equally expressed or differentially expressed genes in DNA microarray studies. It can also be applied in the step of estimating $m_0$ in adaptive false discovery rate controlling procedures. Simulation results show that the bias of the moment estimator is very small for both normal and non normal data. It has higher precision than existing methods in most cases. It has more evident advantage under non normal data.

MSC: 62-XX Statistics

Keywords: multiple hypothesis testing; high-dimensional data; DNA microarray analysis; false discovery rate

Full Text: DOI

References:


This reference list is based on information provided by the publisher or from digital mathematics libraries. Its items are heuristically matched to zbMATH identifiers and may contain data conversion errors. It attempts to reflect the references listed in the original paper as accurately as possible without claiming the completeness or perfect precision of the matching.