



MAXIMIN EFFICIENCY ROBUST TEST FOR MULTIPLE NUISANCE PARAMETERS AND ITS STATISTICAL PROPERTIES*



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Abstract We propose the maximin efficiency robust test (MERT) for multiple nuisance parameters based on theories about the maximin efficiency robust test for only one nuisance parameter and investigate some theoretical properties about this robust test. We explore some theoretical properties about the power of the MERT for multiple nuisance parameters in a specified scenario intuitively further more. We also propose a meaningful example from statistical genetic field to which the MERT for multiple nuisance parameters can be well applied. Extensive simulation studies are conducted to testify the robustness of the MERT for multiple nuisance parameters.

Key words maximin efficiency robust; multiple nuisance parameters; score test; statistical power

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1 Introduction

A definition of asymptotic relative efficiency (ARE) [1] in non-parameter inference was proposed by Statistician Pitman, which is of great importance in robust nonparametric tests.

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[2] investigated a very meaningful theorem about ARE. [3, 4] proposed one type of robust test named the maximum efficiency robust test (MERT) when investigating rank tests based on distribution-free methods. In general, denote parameter space $\Lambda = [0, 1]$. For any known $\lambda \in \Lambda$, let $z(\lambda)$ be a test statistic. We need to note that λ may be an unknown parameter. If $\lambda^* \in \Lambda$ is the true value, dealing with hypothesis test problems, Pitman's ARE (see [3, 4]) of $z(\lambda)$ relative to $z(\lambda^*)$ is given by

$$e(z(\lambda), z(\lambda^*)) = \rho_{\lambda, \lambda^*}^2, \quad (1.1)$$

where $\rho_{\lambda, \lambda^*}$ is the asymptotic null correlation of $z(\lambda)$ and $z(\lambda^*)$. Denote $T_0 = \{z(\lambda) : \lambda \in [0, 1]\}$. Let T_1 be a set of all convex linear combinations of T_0 . One can specify $z(\lambda)$ when confronting specific statistical problem, for an example, Zheng et. al. [5] displayed a expression about $z(\lambda)$ when analyzing genetic association with complex diseases. According to [3, 4, 6], the MERT, denoted by z_{MERT} is defined as a test satisfying

$$\inf_{\lambda \in \Lambda} e(z_{\text{MERT}}, z(\lambda)) = \sup_{z \in T_1} \inf_{\lambda \in \Lambda} e(z, z(\lambda)). \quad (1.2)$$

If z_{MERT} exists, it is also called a test with the most efficiency robustness in T_1 . In general, it is not easy to gain the MERT in T_1 . [4] found a close form for MERT under some regular conditions. [4] called $(z(\lambda_L), z(\lambda_U))$ the extreme pair of T_0 if $\rho_{\lambda_L, \lambda_U} > 0$ is the minimum of any pair-wise correlation of two tests in T_0 . If $(z(\lambda_L), z(\lambda_U))$ is the extreme pair of T_0 and for any $\lambda \in \Lambda$ satisfying

$$\rho_{\lambda_L, \lambda} + \rho_{\lambda, \lambda_U} \geq 1 + \rho_{\lambda_L, \lambda_U}, \quad (1.3)$$

[4] also proved that the MERT in T_1 exists, is unique, and has a simple expression given by

$$z_{\text{MERT}} = \frac{z(\lambda_L) + z(\lambda_U)}{\sqrt{2(1 + \rho_{\lambda_L, \lambda_U})}}. \quad (1.4)$$

Obviously, the MERT proposed by [3, 4, 6], is only suitable for only one nuisance parameter. The MERT for only one nuisance parameter can be applied in extensive fields such as genome-wide association analysis (GWAS) from genetic epidemiology. GWAS, also known as whole genome association study or common-variant association study (CVAS), is an examination of many common genetic variants in different individuals to see if any variant is associated with a trait. GWAS typically focus on associations between single-nucleotide polymorphisms (SNPs) and traits like major diseases. [5] investigated the MERT when testing the association between the trait and only one marker in a chromosome. [5] also explored some statistical properties of the MERT and applied it to the analysis of an example described by [7] (p.109). [8] derived the MERT and applied it to case-parents trios data. [9] derived the MERT and applied it to case-control data. [10] applied the MERT to other genetic studies when analyzing quantitative traits. [11] applied the MERT to other genetic studies when analyzing family-based association.

We can see from the above applications that all the test theories are suitable for only one nuisance parameter. We may encounter score tests including multiple (≥ 2) nuisance parameters. When genetic models for all SNPs are uncertain in GWAS, the ordinary score tests may include multiple nuisance parameters, the common MERT does not fit this scenario. In this article, we aim to extend the MERT for only one nuisance parameter to the MERT for multiple nuisance parameters. We also aim to investigate some theoretical properties of the MERT for

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