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Parametric methods for confidence interval estimation of overlap coefficients

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ARTICLE INFO

Article history: Received 5 January 2016 Received in revised form 12 August 2016 Accepted 19 August 2016 Available online xxxx

Keywords: High-throughput platforms Genomic biomarker Overlap coefficient Generalized inference Parametric bootstrapping Mixture Gaussian *EM* algorithm

ABSTRACT

Overlap coefficient (*OVL*), the proportion of overlap area between two probability distributions, is a direct measure of similarity between two distributions. It is useful in microarray analysis for the purpose of identifying differentially expressed biomarkers, especially when data follow multimodal distribution which cannot be transformed to normal. However, the inference methods about *OVL* are quite sparse. This article proposes two methods, a generalized inference (*GI*) approach and a parametric bootstrapping (*PB*) method, are proposed to construct confidence intervals of *OVL* under the assumption of normality. In conjunction with the *EM* algorithms, these methods are evaluated empirically under a variety of distributions including normal, gamma and mixture Gaussian. At last, the proposed approaches are applied to a published microarray dataset from a gene expression study of three most prevalent adult lymphoid malignancies.

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1. Introduction

Let X_1 and X_2 denote the continuous response variables for two user-defined groups (e.g. case and control) respectively, and let f_{X_1} and f_{X_2} be the corresponding probability densities. The overlap area under the curves of f_{X_1} and f_{X_2} (denoted as *OVL*) is

$$OVL = \int_{-\infty}^{\infty} \min[f_{X_1}(x|\Theta_1), f_{X_2}(x|\Theta_2)]dx,$$

where Θ_1 and Θ_2 stand for parameter spaces for $f_{X_1}(X_1, \Theta_1)$ and $f_{X_2}(X_2, \Theta_2)$, respectively. If the distributions are discrete, *OVL* can be calculated by replacing the integral with a summation. The *OVL* is scaleless with value ranging from 0 (i.e. two distributions being completely distinct) to 1 (i.e. two distributions being identical). *OVL* directly measures the similarity (or difference) between two distributions. Hence, it can serve as a diagnostic measure which is sensitive to any differences between two distributions despite the structures of the underlying distributions.

The concept of *OVL* was first proposed by Weitzman (1970), and it was generalized to *n* dimensions by Bradley et al. (1982). Since then, *OVL* has been widely used in various practical applications, such as quantitative ecology (Gastwirth, 1975), cluster analysis in mathematical geology (Sneath, 1977), stress–strength models of reliability analysis (Ichikawa, 1993),

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http://dx.doi.org/10.1016/j.csda.2016.08.013 0167-9473/© 2016 Elsevier B.V. All rights reserved.



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electromyographic assessment of muscular asymmetry (Ferrario et al., 2000), and treatment assessment in clinical trials
 (Mizuno et al., 2005).

Recently, OVL was introduced to genomic study by Silva-Fortes et al. (2012). The resurgence of OVL in genomic studies is 3 attributable to the fact that it is a more convenient and proper diagnostic measure compared to other traditional diagnostic 4 measures, such as AUC (area under receiver operating curve). High-throughput technologies such as microarray have 5 revolutionized genomic studies in the past decade and the massive amount of data generated by these high-throughput 6 methods poses a variety of challenges to existing statistical methods. Since a major goal of genomics is to identify genes 7 significantly differentially expressed in diseased versus healthy groups, it is of paramount significance to find a diagnostic 8 index which is sensitive to any differences between diseased and healthy groups. However, traditional diagnostic indices q such as AUC mainly focus on examining the difference of means between groups, and fail to capture other possible 10 differences, e.g. shapes between two distributions. For instance, bimodal or multimodal gene expression data commonly 11 exist in genomic studies due to differing molecular subtypes or unknown subclasses within a population of cells. For such 12 data, the diseased and healthy groups can differ dramatically, while having the same mean (Silva-Fortes et al., 2012; Parodi 13 et al., 2008). Regardless of the underlying distributions, OVL serves as a convenient and proper measure of the diagnostic 14 ability of biomarkers while traditional diagnostic indices such as AUC might fail. More details about OVL versus AUC can be 15 found in Appendix A. 16

The reason that OVL has not been widely used as a diagnostic measure is partially due to the lack of methods for confidence 17 interval estimation of OVL. Currently, both existing parametric and nonparametric methods for OVL inference have certain 18 limitations. Parametric methods (Al-Saidy et al., 2005; Al-Saleh and Samawi, 2007; Samawi and Al-Saleh, 2008; Chaubey 19 et al., 2008; Helu and Samawi, 2011; Reiser and Faraggi, 1999; Mulekar and Mishra, 2000; Mizuno et al., 2005) have not yet 20 been applied to general Gaussian (i.e. without equal mean or equal variance condition) or mixture Gaussian distributions, 21 and non-parametric methods only focused on the point estimator for the cases with large sample sizes (Clemons and Bradley, 22 2000; Mizuno et al., 2005; Schmid and Schmidt, 2006; Anderson et al., 2012). To popularize OVL as a diagnostic index, it is 23 important to develop methods for estimating the confidence intervals of OVL. 24

The goal of this paper is to propose methods for confidence interval estimation of OVL under a variety of distributions, 25 including normal, normal transformed and multimodal distributions. In Section 2, we propose a generalized inference (GI)26 method and parametric bootstrapping (PB) method to construct the confidence interval estimation of OVL under normality 27 for original and transformed data. Section 3 deals with mixture normal distributions by combining EM algorithms with the 28 GI and PB methods. Section 4 presents the details of simulation study to check the performance of the proposed method. In 29 Section 5, the proposed methods are applied to a published microarray dataset from a gene expression study of three most 30 prevalent adult lymphoid malignancies. Section 6 concludes the paper with a discussion. Appendix A presents a brief review 31 of AUC as well as a comparison between OVL and AUC. 32

2. Under normality: original and transformed data

This section presents two parametric approaches, i.e. a generalized inference approach (*GI*) and a parametric bootstrapping approach (*PB*) for confidence interval estimation based on normality. Let $X_{11}, X_{12}, \ldots, X_{1n_1}$ and $X_{21}, X_{22}, \ldots, X_{2n_2}$ denote the n_1 and n_2 observations for the control (X_1) and case (X_2) groups, respectively. Assume X_{ij} ($i = 1, 2; j = 1, 2, \ldots, n_i$) follow normal distribution with mean μ_i and variance σ_i^2 . The parameter space Θ_i in formula (1) is (μ_i, σ_i^2) where i = 1, 2. Hence *OVL* can be calculated as

$$OVL = \int \min[f_{X_1}(x|\mu_1, \sigma_1^2), f_{X_2}(x|\mu_2, \sigma_2^2)] dx.$$
(2)

When normality cannot be justified for original data but can be achieved via a monotonic transformation such as Box–Cox transformation (Box and Cox, 1964), the proposed methods can be applied to the transformed data due to the fact that *OVL* is invariant under monotonic transformation. This approach has been found to be useful in *ROC* analysis for a wide variety of scenarios (Molodianovitch et al., 2006; Fluss et al., 2005; Zou and Hall, 2000; Faraggi and Reiser, 2002; Schisterman et al., 2004). To be specific, a power transformation of the Box–Cox type is

$$X_i^{(\lambda)} = egin{cases} X_i^{\lambda} - 1 & \lambda
eq 0 \ \lambda & \log(X_i) & \lambda = 0, \end{cases}$$

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where it is assumed that $X_i^{(\lambda)} \sim N(\mu_i, \sigma_i^2)$. For the transformed data, the appropriate likelihood function can be constructed as follows:

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$$l(\mu_1, \mu_2, \sigma_1, \sigma_2, \lambda | X_1, X_2) = l(\mu_1, \sigma_1, \lambda | X_1) + l(\mu_2, \sigma_2, \lambda | X_2),$$

where $l(\mu_i, \sigma_i, \lambda | X_i) = -\frac{1}{2} \log(2\pi \sigma_i^2) - \sum_{j=1}^{n_i} \frac{X_{ij}^{\lambda} - \mu_i}{2\sigma_i^2} + (\lambda - 1)(\sum_{j=1}^{n_i} \log(X_{ij}))$. The parameters $(\lambda, \mu_1, \sigma_1^2, \mu_2, \sigma_2^2)$ can be estimated using the maximum likelihood estimation procedure, and the transformed data will be used for confidence interval estimation of *OVL*.

Please cite this article in press as: Wang, D., Tian, L., Parametric methods for confidence interval estimation of overlap coefficients. Computational Statistics and Data Analysis (2016), http://dx.doi.org/10.1016/j.csda.2016.08.013

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