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Editorial

New Advances in Biostatistics

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Biostatistics deals with data arising from biomedical research. It remains a very active research area with complicated time-to-event data and missing data emerging in application areas including medicine, genetics, neuroscience, and engineering. Recent advances in biomedical research have created new challenges and opportunities for statisticians and data scientists. For example, big data analysis, precision medicine, artificial intelligence, causal inference, and other new research fields have inspired data scientists to develop modern statistical methods and innovative inference procedures.

The present special issue presents statistical research and new advances in contemporary biostatistics. It provides one review article and seven research articles contributed by some of the leading experts in the field. The review article contained in this issue gives an overview of the current development in biostatistics, while each of the seven research articles addresses new challenges in contemporary biostatistics, as summarized below.

In the review paper "Mixed Effects Models with Censored Covariates, with Applications in HIV/AIDS Studies," by L. Wu and H. Zhang, the authors focus on the problem of censored time-dependent covariates in regression analysis of longitudinal data and time-to-event data. They review the two-step method and the joint likelihood method and describe examples from HIV/AIDS studies to illustrate the problem and applications of the methods.

The research article entitled "A Comparison of Mean-Based and Quantile Regression Methods for Analyzing Self-Report Dietary Intake Data," by M. L. Vidoni et al., compares the traditional mean-based linear regression with quantile regression in terms of investigating the relationship between health behavior intervention and eating indices. The authors found that only the quantile regression, through modeling the coefficients across distributions of the outcome, can fully describe the effect of intervention on healthy and unhealthy eating indices between intervention and standard care groups. The results can help develop more effective behavioral intervention trails with heterogeneous populations.

The research article entitled "Atrial Fibrillation Detection by the Combination of Recurrence Complex Network and Convolution Neural Network," by X. Wei et al., proposes an R wave peak interval independent atrial fibrillation detection algorithm on the basis of analyzing the synchronization features of the electrocardiogram signal by a deep neural network. Results show that the sensitivity, specificity, and accuracy of the algorithm are all around 95%, and the algorithm is more effective than the traditional algorithms in terms of detecting individual variation in the atrial fibrillation.

The research paper entitled "A Note on the Adaptive LASSO for Zero-Inflated Poisson Regression," by P. Banerjee et al., proposes a flexible variable selection approach to efficiently identify correlated features in a zero-inflated Poisson (ZIP) regression model. The existing approach for variable selection in a ZIP regression model which satisfies the oracle property is the EM adaptive LASSO (EM AL), which generates suboptimal results when the features are correlated. The proposed approach is able to identify the true model consistently, and the resulting estimator is as efficient as oracle.

The past decade has seen extensive development of statistical methodology for designing phase I clinical trials for drug combinations including designs allowing individualized maximum tolerable dose (MTD) determination in single agent cancer phase I trials. In the research article "A Bayesian Adaptive Design in Cancer Phase I Trials Using Dose Combinations in the Presence of a Baseline Covariate," by M. A. Diniz et al., the authors describe a Bayesian adaptive design for dose finding of a combination of two drugs in cancer phase I clinical trials. The method takes into account patients' heterogeneity possibly related to treatment susceptibility. The authors accomplish this using escalation with overdose control principle, and the proposed method gives a smaller pointwise average bias and a higher percent of MTD recommendation.

In the research paper "Improved Small Sample Inference on the Ratio of Two Coefficients of Variation of Two Independent Lognormal Distributions," by A. Wong and L. Jiang, the authors study the two-sample inference for the ratio of two coefficients of variation where the data is sampled from lognormal distributions. They propose a simulated likelihood ratio method that outperforms existing methods with small samples in simulation studies.

In the research article "Detecting Spatial Clusters via a Mixture of Dirichlet Processes," by M. A. Ray et al., the authors propose an approach able to detect spatial clusters with skewed or irregular distributions. A mixture of Dirichlet processes is used to describe spatial distribution patterns. The effects of different batches of data collection efforts are also modeled with a Dirichlet process. Inferences of parameters including clustering are drawn under a Bayesian framework.

The research article entitled "On the Use of Min-Max Combination of Biomarkers to Maximize the Partial Area under the ROC Curve," by H. Ma et al., adopts and extends the min-max method to the estimation of the pAUC when multiple continuous scaled biomarkers are available and compare the performances of the proposed approach with existing approaches via simulations. The extensive simulation results demonstrate that the proposed method provides the largest pAUC estimates. The proposed method is robust, and it is encouraged to use this approach in the estimation of the pAUC for many practical scenarios.

As the editors of this special issue, we hope that readers of this special issue will find these articles representative of the contributions of the contemporary biostatistics, in terms of statistical procedures and practical applications. We hope that the special issue provides new methods and novel applications motivated by biomedical examples in the broad areas of biostatistics and stimulate new interests in contemporary biostatistics.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

We would like to express our appreciations to the authors and reviewers for their excellent contributions to this special issue. We also thank the Journal of Probability and Statistics for the professional service, which makes this special issue possible.

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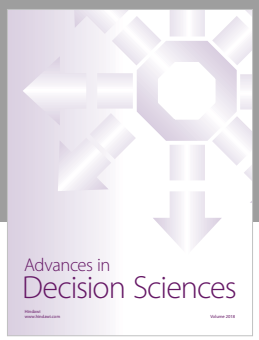

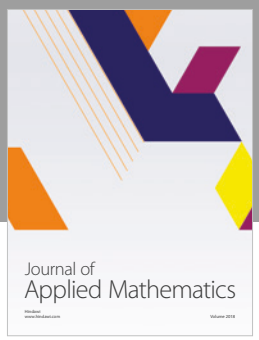

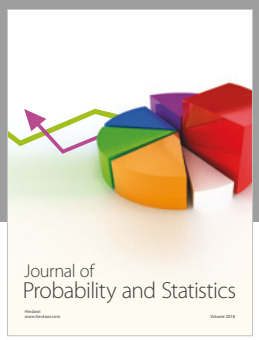

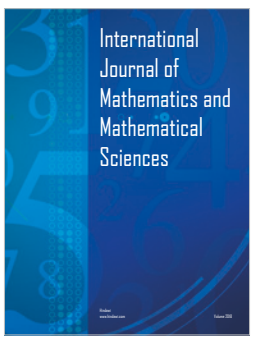

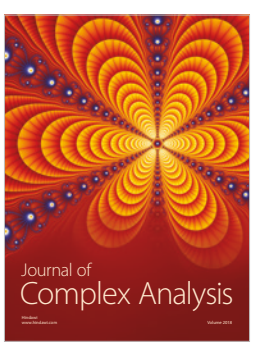

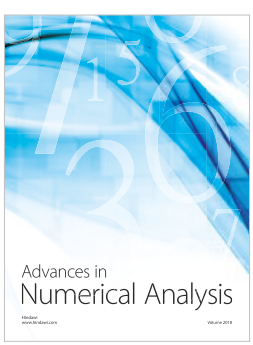

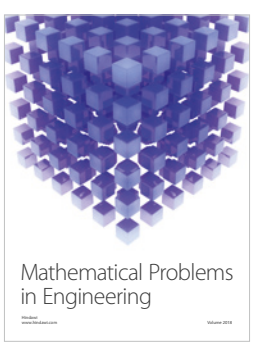

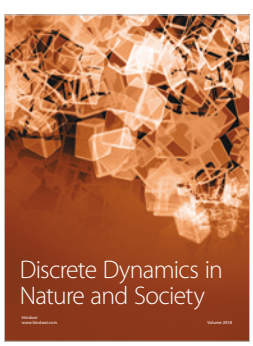

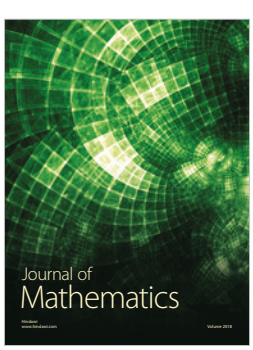

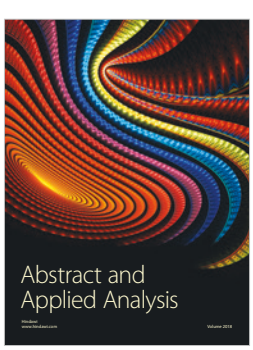

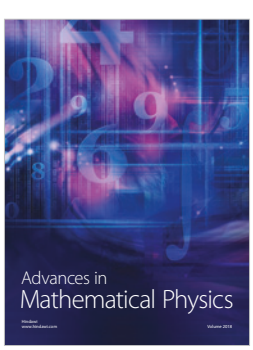

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