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Second Issue, 2017

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EDITORIAL FOREWORD

Second Issue, 2017

After the successful publication of the first issue of *Statistical Theory and Related Fields* in August, we are very happy to see the second issue in print. We would like to take this opportunity to express our sincere gratitude to all the supporters of this journal.

Following the first issue, *Statistical Theory and Related Fields* continues to publish significant and original articles in modern statistical theory and applications in natural, economical, medical and social sciences.

The first article in the second issue by Li, Fine and Pencina is a review paper for the statistical analysis of diagnostic accuracy in a multi-category classification task. The paper reviews important statistical concepts for multi-category classification accuracy and their utilities, demonstrated with real medical examples and problem-based R code.

The next three papers are in precision medicine and personalised medical treatments. Zhou, Dai, Zheng and Cai applied a non-parametric inverse probabilityweighted kernel estimating equation to provide accurate and dynamic age-specific risk prediction in precision medicine. Their approach facilitates the utilisation of predictors varying over an individual's lifetime, and allows borrowing information across individuals of similar ages. Xiong, Yu and Shao proposed a single-index contrast function model for treatment recommendation in personalised medicine. They adopted a non-parametric kernel method to construct treatment rules that are asymptotically optimal. The short communication by Luo is an abstract of the author's PhD thesis in the problem of finding a solution to the treatment assignment when there are multiple treatments.

The next four articles are in the general area of Bayesian analysis. Cao's article provided a Bayesian functional enrichment analysis of high-throughput experiment results to identify genes or proteins with certain characteristics, gain more insights into the underlying biology, and provide functional interpretation for the identified genes or proteins. Jha, Li and Guha developed a cost-effective Markov chain Monte Carlo strategy for censored outcomes in a semiparametric Bayesian analysis, motivated by the study of breast cancer mortality rates in New Mexico. The results offered insights into differences in breast cancer mortality rates between ethnic groups, tumour grade and spatial effect of counties. The next article by Liang, Habiger and Min focused on the influence of a misspecified covariance structure on false discovery

rate for the large-scale multiple testing problem. They evaluated the influence on the marginal distribution of local false discovery rate statistics related to Bayesian posterior probabilities, under both correctly specified and incorrectly specified models. Tang, Liu and Xu studied Bayesian and maximum-likelihood estimation based on data augmentation method in a zero-and-one-

inflated Poisson model. The method was illustrated by the analyses of data-sets from Legionnaires' disease in Singapore and from accidental rates data in Detroit, Michigan.

Partially linear or partially nonlinear models are important extensions of the traditional linear mod-

important extensions of the traditional linear models in studying relationship between a response and some covariates. Que, Huang and Zhang in their article applied the generalised least square estimation and B-splines method to estimate the link function and variance components related to random effects. Both theoretical and empirical results were derived. The paper by Li, Li and Tong proposed a sequential profile lasso method for screening the linear predictors in an ultrahigh-dimensional partially linear model. The proposed procedure can detect all relevant predictors with probability tending to one, regardless of whether the ultrahigh model involves a non-parametric part or not. An extended Bayesian information criterion was also added to select the best model among the models generated by the sequential profile lasso method.

High-dimensional issue is also addressed in the next paper by Marino and Li in factor analysis of correlation matrices based on contemporary data for biomedical studies, disease surveillance and genetics, in which the number of variables may be much larger than the sample size. Motivated by the study of annual cancer mortality rate in the United States, the authors developed an approach based on group sequential theory to estimate the number of relevant factors to be extracted. To facilitate interpretation of the extracted factors, they used a Bayesian information criterion to produce a sparse factor loading representation.

The Current Population Survey is the oldest household sample survey in the United States conducted monthly to provide estimates of employment, unemployment and other characteristics of the non-institutionalised civilian population 16 years of age and older. In the paper by Cheng, Shao and Yu, they derived an estimation procedure that improves the currently used composite type estimator for monthly population total in terms of the mean-squared error of estimators.

Their proposed method involves the use of historical data and a data replication technique.

Finally, the last article is a book review of a recently published new edition of a popular book in pharmaceutical industry for the calculation of sample sizes in clinical and pharmaceutical developments.

Like in the first issue, the articles in this issue provide interesting and diversified results to the readers. We welcome submissions of high-quality articles in statistical theory and related fields, and are confident that we can together build a great journal for statisticians and scientists analysing various types of data.

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