Biostatisitcs 2017

6th International Conference on

BIOSTATISTICS AND BIOINFORMATICS

November 13-14, 2017 | Atlanta, USA

Keynote Forum

Day 1

En-Bing Lin, J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-004

En-Bing Lin
Central Michigan University, USA

Big data analysis in bioinformatics

With the increasing use of advanced technology and the exploding amount of data in bioinformatics, it is imperative to introduce effective and efficient methods to handle Big data using the distributed and parallel computing technologies. Big data analytics can examine large data sets, analyze and correlate genomic and proteomic information. In this presentation, we begin with an overview of Big data and Big data analytics, we then address several challenging and important tasks in bioinformatics such as analyzing coding, noncoding regions and finding similarities for coding and noncoding regions as well as many other issues. We further study mutual information-based gene or feature selection method where features are wavelet-based; the bootstrap techniques employed to obtain an accurate estimate of the mutual information and other new methods to analyze data. Given the multi-scale structure of most biological data, several methods will be presented to achieve improvements in the quality of mathematical or statistical analysis of such data. In a DNA strand, it is essential to find sequences, which can be transcribed to complementary parts of the DNA strand. We will mention several methods to identify protein coding regions. We also use some special variance and entropy to analyze similarities among coding and noncoding regions of several DNA sequences respectively and compare the resulting data. We will address the use of big data analytics in many phases of the bioinformatics analysis pipeline.

Biography

En-Bing Lin is a Professor of Mathematics at Central Michigan University, USA. He has been associated with several institutions including Massachusetts Institute of Technology, University of Wisconsin-Milwaukee, University of California, Riverside, University of Toledo, UCLA, and University of Illinois at Chicago. He has received his PhD from Johns Hopkins University. His research interests include Data Analysis, Applied and Computational Mathematics, and Mathematical Physics. He has Supervised a number of graduate and undergraduate students. He serves on the Editorial Boards of several journals. He has organized several special sessions at regional IEEE conferences and many other professional meetings.

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Notes:

Abdel-Salam Gomaa, J Biom Biostat 2017, 8:5 (Suppl)
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Abdel-Salam Gomaa

Qatar University, Qatar

Model robust profile monitoring for the generalized linear mixed model for phase I analysis

There are so many applications for detecting the changes in the relationship between the response variable and explanatory variable (s) may be the most important consideration rather than detecting the changes in univariate or multivariate quality characteristics. This relationship between the response variable and one or more explanatory variables is called a profile. The act of using various techniques to statistically monitor the process or product profiles is known as profile monitoring. The study introduces two mixed model methods to monitor profiles from the exponential family: a nonparametric (NP) regression method based on the penalized spline regression technique and a semi-parametric (SP) method (Model robust profile monitoring for the generalized linear mixed model (MRGLMM)) which combines the advantages of both the parametric and nonparametric methods. A correctly specified parametric (P) model will have the most power in detecting the profile shift, while a NP method can give improved performance for any type of profile. The MRGLMM method gives results similar to the P method when P model is correctly specified and it gives results similar to the NP method if the proposed P model is badly misspecified. The MRGLMM method gives results that are superior to either the P method or the NP method if the P model provides some useful information regarding profile behavior. Thus, the MRGLMM method is robust to model misspecification. The performances of P, NP and MRGLMM methods are compared through a simulation study using binary data.

Biography

Abdel-Salam Gomaa holds BS and MS (2004) degrees in Statistics from Cairo University and MS (2006) and PhD (2009) degrees in Statistics from Virginia Polytechnic Institute and State University (Virginia Tech, USA). Prior to joining Qatar University as an Assistant Professor and a Coordinator of the Statistical Consulting Unit and Coordinator for the Statistics Programs, he taught at Faculty of Economics and Political Science (Cairo University), Virginia Tech, and Oklahoma State University. Also, he worked at JPMorgan Chase Co. as Assistant Vice President in Mortgage Banking and Business Banking Risk Management Sectors. He has published several research papers and delivered numerous talks and workshops. He has awarded couples of the highest prestige awards such as Teaching Excellence from Virginia Tech, Academic Excellence Award, Freud International Award, and Mary G Natrella Scholarship from American Statistical Association (ASA) and American Society for Quality (ASQ), for outstanding graduate study of the theory and application of Quality Control, Quality Assurance, Quality Improvement, and Total Quality Management. He is a Member of the ASQ and ASA.

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Hong Lin, J Biom Biostat 2017, 8:5 (Suppl)
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Hong Lin

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Information technologies: Opportunities and challenges in personal healthcare systems

The well-being of a person consists of 2 aspects: The physical body well-being and the mind well-being (the perception or the feeling of well-being). Technology development makes it possible to massively produce cheap sensors for personal use. The data collected, if being properly analyzed, can provide objective and comprehensive personal health information. The information helps us to understand the well-being of the person and then further offers the opportunity to develop a high quality personal healthcare system for the well-being of the person. In this talk, I will report our preliminary findings in applying modern information technology to personal healthcare systems. We construct a brain activity level model by using EEG signals to objectively measure the effectiveness of meditation, detect mental fatigue and boredom, and comprehend human emotions. Also, we have used accelerometer and GPS data to assess sports performance and training enhancement, leg muscle injury prevention and recovery monitoring, and fall prevention for aged people. In addition, the ubiquitous nature of accelerometer and GPS technology make it possible to deliver personal healthcare services for people in physical excise. Then, we exploit the potential of Kinect device in monitoring the movements of aged persons in their houses to prevent falls. Finally, we point out some remaining challenges and possible opportunities in using information technologies to deliver personal health care.

Biography

Hong Lin was a Postdoctoral Research Associate at Purdue University; an Assistant Research Officer at the National Research Council, Canada, and a Software Engineer at Nokia, Inc. He is currently a Professor with UHD. His research interests include human-centered computing, parallel/distributed computing, grid computing, multi-agent systems, and high level computational models. He is a Co-supervisor of the Grid Computing Lab at UHD.

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Day 2

Mikhail Moshkov, J Biom Biostat 2017, 8:5 (Suppl)
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Mikhail Moshkov

King Abdullah University of Science and Technology, Saudi Arabia

Multi-stage optimization of decision trees: Two applications

Multi-stage optimization of decision trees is one of the extensions of dynamic programming. It allows us to optimize decision trees sequentially relative to a number of cost functions. We will discuss two applications of this technique: finding of minimum average depth of a decision tree for sorting eight elements and creation of an algorithm for reduct minimization. The question about minimum average depth of a decision tree for sorting of eight elements was open since 1968 and was considered by D Knuth in his famous book *The Art of Computer Programming*, Volume 3, Sorting and Searching. Reduct is a minimal set of conditional attributes in a decision table which gives the same information about decision attribute as the whole set of conditional attributes. The problem of reduct minimization is closely connected with the feature selection. The end of the presentation is devoted to the introduction to KAUST.

Biography

Mikhail Moshkov is Professor in the CEMSE Division at King Abdullah University of Science and Technology, Saudi Arabia since October 1, 2008. He has earned his Master's degree from Nizhni Novgorod State University, received his Doctorate from Saratov State University, and habilitation from Moscow State University. From 1977 to 2004, He was with Nizhni Novgorod State University. Since 2003, he has worked in Poland in the Institute of Computer Science, University of Silesia, and since 2006, also in the Katowice Institute of Information Technologies. His main areas of research are complexity of algorithms, combinatorial optimization, and data mining. He is the author or coauthor of five research monographs published by Springer.

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Herman Ray, J Biom Biostat 2017, 8:5 (Suppl)
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Herman Ray

Kennesaw State University, USA

Unbiased estimation after phase II clinical trials involving multiple endpoints

The single arm, two-stage clinical trial design is a popular methodology to evaluate oncology treatments in the phase II setting. The designs are typically augmented with an ad hoc toxicity monitoring rule which is imposed outside of the formal two-stage design but there are also several designs that formally incorporate both endpoints simultaneously. There are many problems that prevent the designs from being used in practice which includes point estimation after the execution of the study. We will examine an unbiased estimator that accounts for both endpoints simultaneously along with the correlation between the endpoints. The behavior of the estimate is examined through simulation studies. It is compared to the maximum likelihood estimator.

Biography

Herman Ray has received his PhD from the University of Louisville, where he has conducted research at the JG Brown Cancer Center. He currently has several manuscripts published in clinical trial design and bioinformatics as well as STEM education policy in the secondary education system. He is now an Associate Professor of Statistics at Kennesaw State University as well as the Director of the Center for Statistics and Analytical Research which is housed within the new Analytics and Data Science Institute.

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