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BIOSTATISTICS AND BIOINFORMATICS

November 13-14, 2017 | Atlanta, USA



Exhibitor

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Scientific Program

Biostatisitcs 2017

Day 1 November 13, 2017

09:00-09:20 Registrations

Majestic-1

conferenceseries.com 09:20-09:50

Opening Ceremony

Keynote Forum

Introduction

09:50-10:35 **Title: Big data analysis in bioinformatics**

En Bing Lin, Central Michigan University, USA

Panel Discussion

Networking and Refreshment Break 10:35-10:55 @ Piedmont Prefunction

Group Photo @ 10:55-11:05

11:05-11:50 **Title: Model robust profile monitoring for the generalized linear mixed model for phase I analysis**

Abdel-Salam Gomaa, Qatar University, Qatar

11:50-12:35 **Title: Information technologies: Opportunities and challenges in personal healthcare systems**

Hong Lin, University of Houston-Downtown, USA

Sessions:
Clinical Biostatistics | Statistical Methods | Bayesian statistics | Biostatistics applications | Big Data Analytics | Structural Bioinformatics | Systems Biology in Bioinformatics | Regression Analysis

Session Chair: Abdel-Salam Gomaa, Qatar University, Qatar
Session Co-chair: Meenakshi Nadimpalli, Reliable Software Resources Inc., USA

Session Introduction

12:35-13:05 **Title: Complex activity recognition with multi-modal multi-positional body sensing**

Pratool Bharti, University of South Florida, Tampa

Panel Discussion

Lunch Break 13:05-13:55 @ Ballroom Prefunction

13:55-14:25 **Title: Cost analysis of metastatic non-small cell lung cancer (NSCLC) after completion of chemotherapy with the introduction of erlotinib**

Rashid Ahmed, University of North Dakota, USA

14:25-14:55 **Title: Spatio-temporal quantile interval regression using R-INLA with applications to childhood overweight and obesity in Sub-Saharan Africa**

Owen P L Mtambo, Namibia University of Science and Technology, Namibia

14:55-15:25 **Title: New entropy measures for censored data**

Abdul Basit, State Bank of Pakistan, Pakistan

15:25-15:55 **Title: Integrated quadrbly reduced additive weighted mixture poisson distribution**

Mohamed Yusuf Hassan, UAE University, UAE

Panel Discussion

Networking & Refreshment Break 15:55-16:15 @ Ballroom Prefunction

Video Presentation

16:15-16:45 **Title: Statistical methodologies for handling ordinal longitudinal responses with monotone dropout patterns using multiple imputation**

Aluko O S, University of KwaZulu-Natal, South Africa

Panel Discussion

Day 2 November 14, 2017

Majestic-1

Keynote Forum

09:15-10:00 **Title: Multi-stage optimization of decision trees: Two applications**
Mikhail Moshkov, King Abdullah University of Science and Technology, Saudi Arabia

10:00-10:45 **Title: Unbiased estimation after phase II clinical trials involving multiple endpoints**
Herman Ray, Kennesaw State University, USA

Panel Discussion

Networking and Refreshment Break 10:45-11:05 @ Piedmont Prefunction

Workshop

11:05-13:00 **Title: Parametric regression analysis for Biostatisticians**
Abdel-Salam Gomaa, Qatar University, Qatar

Panel Discussion

Lunch Break 13:00-13:50 @ Ballroom Prefunction

Poster Presentations

13:50-14:20 **Title: 3D heat maps of cancer mutations in the mitochondrial electron transport system to identify driver domain candidates**
Estella Chen-Quin, Kennesaw State University, USA

Sessions:
Clinical Biostatistics | Statistical Methods | Regression Analysis | Systems Biology in Bioinformatics | Biostatistics applications | Biometric security | Big Data Analytics | Modern data analysis

Session Chair: Yedidi Narasimha Murty, BI Solutions Architect, USA
Session Co-chair: Meenakshi Nadimpalli, Reliable Software Resources Inc., USA

Session Introduction

14:20-14:50 **Title: Exponential behavior of health indicators of Pakistan**
Anam Riaz, National College of Business Administration and Economics, Pakistan

14:50-15:20 **Title: Examining the effect of climate variability on malaria transmission using a dynamic mosquito-human malaria model**
Gbenga J Abiodun, Foundation for Professional Development, South Africa

15:20-15:50 **Title: Recent journey through the analyzes of oncology trial data**
Revathy Duvedi, ICON plc, USA

Panel Discussion

Networking and Refreshment Break 15:50-16:10 @ Ballroom Prefunction

16:10-16:40 **Title: Covariate rank weighting is a powerful method for prioritizing hypothesis tests in high throughput data**
Mohamad S Hasan, University of Georgia, USA

Panel Discussion

Awards & Closing Ceremony

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Supporting Journals

Supporting Journals

Journal of Biometrics & Biostatistics
Journal of Proteomics & Bioinformatics
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Dec 04-06, 2017 Sao Paulo, Brazil

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Dec 11-12, 2017 Dubai, UAE

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Dec 04-05, 2017 Sao Paulo, Brazil

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14th International Conference on
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Dec 06-07, 2017 Sao Paulo, Brazil

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Dec 04-05, 2017 Dubai, UAE

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Dec 04-05, 2017 Dubai, UAE

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Nov 16-17, 2017 Vienna, Austria

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Neurology and Neuro Surgery
Nov 27-28, 2017 Dubai, UAE

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46th Global Nursing and Healthcare Conference
Dec 06-07, 2017 Sao Paulo, Brazil

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Nursing Pharmacology and Nursing Education
Nov 20-21, 2017 Melbourne, Australia

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16th International conference and Exhibition on
Obesity & Weight Management
Nov16-17, 2017 Atlanta, USA

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Nov 16-17, 2017 Atlanta, USA

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World Cancer Convention
Nov 27-28, 2017 Dubai, UAE

International Conference on **Cancer Diagnostics**
Nov 27-28, 2017 Dubai, UAE

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20th World Ophthalmology Summit
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18th European Ophthalmology Congress
Dec 07-09, 2017 Madrid, Spain

17th Global Ophthalmology and Glaucoma Conference
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Dec 04-06, 2017 Madrid, Spain

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6th International Conference on
Physiotherapy
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International Conference on
High Energy Physics
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PSYCHIATRY

International Conference on
Psychiatry and Mental Health
Nov 20-21, 2017 Melbourne, Australia

10th World Psychiatrists Meet
Dec 07-08, 2017 Dubai, UAE

VACCINES

29th Global Vaccines & Vaccination Summit And Expo
Nov 30-Dec 1, 2017 Dubai, UAE

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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)
DOI: 10.4172/2155-6180-C1-004



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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Notes:

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



Hong Lin

University of Houston-Downtown, USA

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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Notes:

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Scientific Tracks & Abstracts

Day 1

Sessions

Clinical Biostatistics | Statistical Methods | Bayesian statistics | Biostatistics applications | Big Data Analytics | Structural Bioinformatics | Systems Biology in Bioinformatics | Regression Analysis

Session Chair
Abdel-Salam Gomaa
Qatar University, Qatar

Session Co-Chair
Meenakshi Nadimpalli
Reliable Software Resources Inc., USA

Session Introduction

Title: **Complex activity recognition with multi-modal multi-positional body sensing**
Pratool Bharti, University of South Florida, Tampa

Title: **Cost analysis of metastatic non-small cell lung cancer (NSCLC) after completion of chemotherapy with the introduction of Erlotinib**
Rashid Ahmed, University of North Dakota, USA

Title: **Spatio-temporal quantile interval regression using R-INLA with applications to childhood overweight and obesity in sub-Saharan Africa**
Owen P L Mtambo, Namibia University of Science and Technology, Namibia

Title: **New entropy measures for censored data**
Abdul Basit, State Bank of Pakistan, Pakistan

Title: **Integrated quadrbly reduced additive weighted mixture poisson distribution**
Mohamed Yusuf Hassan, UAE University, UAE

Pratool Bharti, J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-005

Complex activity recognition with multi-modal multi-positional body sensing

Pratool Bharti
University of South Florida, USA

Current state-of-the-art systems in the literature using wearables are not capable of distinguishing many fine-grained and/or complex human activities, which may appear similar but with vital differences in context, such as lying on floor vs. lying on bed vs. lying on sofa. This paper fills this gap by proposing a novel system, called HuMAn, that recognizes and classifies complex at-home activities of humans with wearable sensing. Specifically, HuMAn makes such classifications feasible by leveraging selective multi-modal sensor suites from wearable devices, and enhances the richness of sensed information for activity classification by carefully leveraging placement of the wearable devices across multiple positions on the human body. The HuMAn system consists of the following components: Practical feature set extraction from specifically selected multi-modal sensor suites; a novel two-level structured classification algorithm that improves accuracy by leveraging sensors in multiple body positions; and improved refinement in classification of complex activities with minimal external infrastructure support (e.g., only a few Bluetooth beacons used for location context). The proposed system is evaluated with 10 users in real home environments. Experimental results demonstrate that the HuMAn can detect a total of 21 complex at-home activities with high degree of accuracy. For same-user evaluation strategy, the average activity classification accuracy is as high as 97% over all the 21 activities. For the case of 10-fold cross- validation evaluation strategy, the average classification accuracy is 94%, and for the case of leave-one-out cross-validation strategy, the average classification accuracy is 76%.

Biography

Pratool Bharti is pursuing his PhD at University of South Florida, Tampa. He is also a Graduate Student Ambassador for artificial intelligence at Intel corp. He has completed his undergraduate in Computer Science and Engineering from Kalyani Government Engineering College, India in 2010. Before starting his PhD in 2014, he has worked 4 years as Software Developer in machine learning. His current research is in finding pervasive solution for healthcare problems in society. He has published multiple journals and conference papers on activity recognition and smart healthcare.

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Notes:

Rashid Ahmed, J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-005

Cost analysis of metastatic non-small cell lung cancer (NSCLC) after completion of chemotherapy with the introduction of Erlotinib

Rashid Ahmed
University of North Dakota, USA

Erlotinib has been funded for use as a second and third line treatment of advanced NSCLC since 2006 in Manitoba, Canada. Prior research examined, the cost effectiveness of Erlotinib across various countries, yet results may not be generalizable to the healthcare system within Canada. The present paper outlines the cost effectiveness of Erlotinib by examining population-based total costs, service utilization, and clinical outcomes of patients with metastatic NSCLC receiving Erlotinib were explored from the time they completed chemotherapy till the end of follow-up date (31 Dec 2012), death, or relocation. Metastatic NSCLC patients, who were approved for Erlotinib in Manitoba between June 2006 and 31 Dec 2012, were selected. The Manitoba Cancer Registry (MCR) and chart review were used to capture the information on treatment and clinical outcome. Service utilization information and direct cost information were extracted from the electronic health records known as ARIA, the Physicians Claims, the Hospital Discharge database, and the Drug Program Information Network. Survival rate, using the Kaplan-Meier method, was calculated from the date of the Erlotinib approval date till end of follow-up date, Dec 31, 2012, or death. The median survival rate was 40.1 weeks. The average cost per patient was CA$ 30,503 and CA$ 987 per patient-week for patients who received Erlotinib. Ninety percent of the cost was accounted for by hospital stays and drug costs. General demographic patterns per cost suggested that current smokers tended to incur higher costs compared to non-smokers. The results of this study appear to replicate patterns of other studies examining the cost effectiveness such that Erlotinib appears to have a high survival rate paired with lower costs related to side effect management.

Biography

Rashid Ahmed has completed his PhD in Bio-Statistics from University of Waterloo; ON; Canada. He has strong background in epidemiology and biostatistics and has experience in the development of statistical methods for the design of community-based interventions and the analysis of longitudinal health data. Currently, he is developing diagnostic measures for joint models for longitudinal and survival data in the presence of non-ignorable missing data. Currently, he is working as an Associate Dean for Research with the College of Nursing and Professional Disciplines at the University of North Dakota. He has published more than 30 papers in reputed journals and has been serving as reviewer of several journals.

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Notes:

Owen P L Mtambo, J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-005

Spatio-temporal quantile interval regression using R-INLA with applications to childhood overweight and obesity in sub-Saharan Africa

Owen P L Mtambo
Namibia University of Science and Technology, Namibia

Childhood malnutrition has serious adverse effects on a child, a family and the development of a country. It leads to more than 30% of deaths in children below five years in sub-Saharan African countries. A malnourished child is more likely to be sick and die. Malnutrition can lead to stunted growth, overweight and obesity, impaired cognitive and behavior development, poor school performance, lower working capacity and lower income. It can slow down economic growth and increase level of poverty. Furthermore, it can prevent a society or a nation from meeting its full potential through loss in productivity, cognitive capacity and increased cost in health care. The indicators of malnutrition range from stunting, wasting and underweight to overweight and obesity. In the past, childhood undernutrition was used to be the most malnutrition burden over the past two decades across the sub-Saharan Africa and is still remaining a burden to date. Doubly surprising, childhood overnutrition is alarmingly becoming the most prevalent parallel to still existing undernutrition burden in sub-Saharan Africa. Overweight and obesity rates are reaching epic proportions in sub-Saharan Africa. The prevalence of childhood overweight and obesity in sub-Saharan Africa was 8.5% in 2010 and is expected to reach 12.7% by 2020. The consequences of overnutrition can be more devastating than those for undernutrition because it leads to chronic failure problems which in turn lead to increased medical expenditure. For this reason, only childhood overweight and obesity were analyzed in this study, in order to assess socio-demographic and socio-economic determinants of childhood overweight and obesity in sub-Saharan Africa. This study also assessed the geographical variation of childhood overweight and obesity in sub-Saharan Africa with more emphasis on both spatial and spatio-temporal effects. All available Demographic and Health Survey (DHS) datasets since 2000 were used and the statistical inference was fully Bayesian using R-INLA package in the selected countries. Almost all studies on spatial quantile modelling of childhood overweight and obesity have emphasized on selecting only one specific response quantile level of interest and report the recommendations based on the only chosen response quantile. Unlike mean response modelling, quantile regression yields model estimates which are stochastic functions of quantile levels such that. This implies that quantile regression modelling using estimates based on only one chosen quantile level might be inefficient and not robust enough. $0 < < 1$. In this study, we used weighted mean estimates based on all quantiles in the quantile interval which corresponded to modelling childhood overweight and obesity. We found out that the significant $= 0.90 \pm 0.05$ determinants of childhood overweight and obesity ranged from socio-demographic factors such as type of residence to $= [0.85, 0.95]$ child and maternal factors such as child age, duration of breastfeeding and maternal BMI. We also observed significant positive structured spatial effects on childhood overweight and obesity mostly in the regions in the center of Namibia.

Biography

Owen P L Mtambo is a Lecturer in Statistics at Namibia University of Science and Technology since March 2014. He was a Lecturer in Statistics at University of Malawi from July 2007 to March 2014. He was Secondary School Teacher in Mathematics and Physics from January 2002 to June 2007. He holds an MSc (Biostatistics) with credit (2012), a BSc (Mathematical Sciences) with distinction (2007), and a DipEdu (Sciences) with distinction (2001); all obtained from University of Malawi. He has more than 8 publications. Currently, he is pursuing his PhD in Statistics at University of South Africa (UNISA) since February 2016.

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Notes:

Abdul Basit et al., J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-005

New entropy measures for censored data

Abdul Basit, Anam Riaz, Zafar Iqbal, Munir Ahmad
State Bank of Pakistan, Pakistan

Survival function and hazard rate are very informative and reliable characteristics of any distribution. Entropy is a tool to measure the maximum information of any distribution. In this study, we use the hazard function to develop a new entropy measure. We also introduce the modified forms of Renyi, Tsallis and Havrda and Charvat entropy. The main properties and characteristics and applications associated with these modified entropies are established. We made a comparison between modified entropies by applying them on health indicators Infants Mortality Rate, Crude Death Rate and Life Expectancy of Pakistan. New entropy measures are very useful for censored data. We also introduced a new methodology for the comparison of entropy measures.

Biography

Abdul Basit is the PhD Research Scholar in the discipline of Statistics in National College of Business Administration and Economics Lahore, Pakistan. He has completed his MS in Social Sciences from SZABIST Karachi, Pakistan in 2014. Currently, he is serving as Deputy Director in Research Cluster of State Bank of Pakistan. He has published 07 research papers in journals and many articles were presented in national and international conferences.

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Notes:

Mohamed Yusuf Hassan, J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-005

Integrated quadrbly reduced additive weighted mixture poisson distribution

Mohamed Yusuf Hassan
UAE University, UAE

We propose a new family of probability distributions derived from the mixtures of weighted Poisson probability distributions. This family of distributions will overcome some of the potential limitations suffered by the existing dominant distributions including lack of modeling over-dispersion, under-dispersion and bimodality. The family is flexible and could be applied to a variety of problems from different disciplines like business, finance, medicine and reliability in engineering. To construct this family, a baseline Poisson distribution and a number of reasonable weights are chosen to get weighted versions of the baseline distribution. These distributions are combined into a mixture format that sums up to a single component probability distribution in a closed form. The resulted density function will be parsimonious and flexible and will be able to capture the nature of many count data patterns. Real count data will be used and goodness-of-fit statistical techniques will be developed to compare its performance with the other existing competing models.

Biography

Mohamed Yusuf Hassan has completed his PhD from University of California, Riverside. He is the first Author of bivarivarite Mixture Transition Distribution and the Bimodal Skew-Symmetric Normal.

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Video Presentation

Day 1

Aluko O S et al., J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-005

Statistical methodologies for handling ordinal longitudinal responses with monotone dropout patterns using multiple imputation

Aluko O S and **Mwambi H**
University of KwaZulu-Natal, South Africa

Missing data are common challenge in any longitudinal clinical trials. Multiple imputation is one of the modern methods of handling incomplete data. This approach is applicable to different missing data patterns but sometimes faced with complexity of the type of variables to be imputed and the mechanism underlying the missing values. In this study, we compare the performance of three methods under multiple imputation, namely expectation maximization, fully conditional specification and multivariate normal imputation in the presence of ordinal responses with monotone dropout. We proposed and demonstrated the usefulness of the ordinal negative binomial distribution for ordinal data generation through simulation studies and implementation. However, the real dataset application and simulation studies reveal that the three methods perform equivalently well, thus any of the methods can be recommended for use.

Biography

Aluko O S is pursuing his PhD at the University of KwaZulu-Natal, South Africa. Three of his papers are in review under reputable journals and the fourth paper is about to be sent to another journal for publication. As a matter of fact, he use and write codes in both R and SAS softwares conveniently.

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Keynote Forum

Day 2

Mikhail Moshkov, J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-004



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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Notes:

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

Day 2

Abdel-Salam Gomaa, J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-005



Abdel-Salam Gomaa

Qatar University, Qatar

Parametric regression analysis for Biostatisticians

This short course is designed to provide some of the advanced and common statistical techniques for researches and practitioners. The short course will demonstrate the parametric simple and multiple linear regression models, Logistic regression, Poisson regression, ZIP Poisson regression models and their applications in Biostatistics, Medical, Biology, Business, Mass Communication, Engineering, public health, Epidemiology, pharmaceutical and biomedical fields. These examples and case-studies will be implemented using the SPSS and SAS. Attendees will learn concepts, techniques and some secrets about the followings: How to use the F-test to determine if your predictor variables have a statistically significant relationship with your outcome/response variable? What are the assumptions for linear regression analysis and what you should do to meet these assumptions? Why adjusted R2 is smaller than R2 and what these numbers mean when comparing between several models? For which predictors are the regression coefficients significantly different than zero and how can you select the significant variables? What is the difference between regression and ANOVA and when are they equivalent? When and how to use the Generalized Linear Models with some examples? How to select the best model? What is the general strategy to approach any modeling problem? How to report the results in your research paper/report?.

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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Scientific Tracks & Abstracts

Day 2

Clinical Biostatistics | Statistical Methods | Regression Analysis | Systems Biology in Bioinformatics | Biostatistics applications | Biometric security | Big Data Analytics | Modern data analysis

Session Chair
Yedidi Narasimha Murty
BI Solutions Architect, USA

Session Co-Chair
Meenakshi Nadimpalli
Reliable Software Resources Inc., USA

Session Introduction

Title: **Exponential behavior of health indicators of Pakistan**
Anam Riaz, National College of Business Administration and Economics, Pakistan

Title: **Examining the effect of climate variability on malaria transmission using a dynamic mosquito-human malaria model**
Gbenga J Abiodun, Foundation for Professional Development, South Africa

Title: **Recent journey through the analyzes of oncology trial data**
Revathy Duvedi, ICON, USA

Title: **Covariate rank weighting is a powerful method for prioritizing hypothesis tests in high throughput data**
Mohamad S Hasan, University of Georgia, USA

Anam Riaz et al., J Biom Biostat 2017, 8:5 (Suppl)
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Exponential behavior of health indicators of Pakistan

Anam Riaz, Abdul Basit, Zafar Iqbal and **Munir Ahmad**
National College of Business Administration and Economics Lahore, Pakistan

The study is being to describe the relationship of Basic Medical Staff (BMS) and Life Expectancy (LE) of Pakistan. Another relationship has been developed between Infrastructure (INF) of health sector and Life Expectancy. A bivariate exponential distribution has been developed using the hazard rate and found the correlation coefficients of the BMS and LE and INF and LE. The properties and different characteristics have been derived for new bivariate exponential distribution. Empirical study of new bivariate distribution has been found using the Crude Death Rate, Infant Mortality Rate, Life Expectancy, Medical Staff and Infrastructure of Pakistan.

Biography

Anam Riaz is PhD Research Scholar in the discipline of Statistics in National College of Business Administration and Economics Lahore, Pakistan. Higher Education Commission (HEC) of Pakistan awarded her scholarship for PhD. She has published 02 research papers in journals and many articles were presented in national and international conferences.

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Gbenga J Abiodun, J Biom Biostat 2017, 8:5 (Suppl)
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Examining the effect of climate variability on malaria transmission using a dynamic mosquito-human malaria model

Gbenga J Abiodun
Foundation for Professional Development, South Africa

The reasons for malaria resurgence mostly in Africa are yet to be well understood. Although the causes are often linked to regional climate change, it is important to understand the impact of climate variability on the dynamics of the disease. However, this is difficult due to the unavailability of long-term malaria data over the study areas. In this study, we develop a climate-based mosquito-human malaria model to study malaria dynamics in the human population over KwaZulu-Natal, one of the epidemic provinces in South Africa, from 1970-2005. We compare the model output with available observed monthly malaria cases over the province from September 1999 to December 2003. We further use the model outputs to explore the relationship between the climate variables (rainfall and temperature) and malaria incidence over the province using principal component analysis, wavelet power spectrum and wavelet coherence analysis. The model produces a reasonable fit with the observed data and it captures all the spikes in malaria prevalence. Our results highlight the importance of climate factors on malaria transmission and show the seasonality of malaria epidemics over the province. Results from the principal component analyzes further suggest that, there are two principal factors associated with climates variables and the model outputs. One of the factors indicate high loadings on Susceptible, Exposed and Infected human, while the other is more correlated with Susceptible and Recovered humans. However, both factors reveal the inverse correlation between Susceptible-Infected and Susceptible-Recovered humans respectively. Through the spectrum analysis, we notice a strong annual cycle of malaria incidence over the province and ascertain a dominant of one-year periodicity. Consequently, our findings indicate that an average of 0 to 120-day lag is generally noted over the study period, but the 120-day lag is more associated with temperature than rainfall. This is consistence with other results obtained from our analyses that malaria transmission is more tightly coupled with temperature than with rainfall in KwaZulu-Natal province.

Biography

Gbenga J Abiodun is a young Scientist whose research interest focuses on biomathematics, epidemiology and mathematical modelling of the impacts of climate (variability and change) on vector-borne and infectious diseases. He has completed his Masters and Doctoral degrees in Mathematics at the University of the Western Cape (UWC) in 2012 and 2016, respectively. He has worked extensively on infectious diseases and published peer-reviewed papers in high-profile international journals.

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Notes:

Revathy Duvedi et al., J Biom Biostat 2017, 8:5 (Suppl)
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Recent journey through the analyzes of oncology trial data

Revathy Duvedi and **Dilip Nalla**
ICON plc, USA

The purpose of the paper is to share methods and nuances of how to analyze clinical trial data in oncology. The following will be shared: Kaplan-Meier analyses, handling of missing data, competing risks related to overall survival, issues related to proportional hazards model assumption violations, interval censoring and recurrence event analyses. SAS codes and Macros will also be shared. Typically these topics are spread out in various papers. We will provide a consolidated paper documenting all the issues and methods. The intention is for the paper to be used as a roadmap or blueprint on how to approach analyses in oncology trials covering a variety of indications.

Biography

Revathy Duvedi has been in the Pharma/Biotech industry for more than 26 years and have been Icon for more than 10 years. She has been focusing primarily on Oncology therapeutic area for more than 10 years.

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Notes:

Mohamad S Hasan et al., J Biom Biostat 2017, 8:5 (Suppl)
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Covariate rank weighting is a powerful method for prioritizing hypothesis tests in high throughput data

Mohamad S Hasan and **Paul Schliekelman**
University of Georgia, USA

The large scale multiple testing inherent to high throughput biological data necessitates very high statistical stringency and thus true effects in data are difficult to detect unless they have high effect sizes. One solution to this problem is to use independent information to prioritize the most promising features of the data and thus increase the power to detect them. Weighted p-values provide a general framework for doing this in a statistically rigorous fashion. However, calculating weights that incorporate the independent information and optimize statistical power remains a challenging problem despite recent advances in this area. Existing methods tend to perform poorly in the common situation that true positive features are rare and of low effect size. We introduce Covariate Rank Weighting a method for calculating approximate optimal weights conditioned on the ranking of tests by an external covariate. This approach uses the probabilistic relationship between covariate ranking and test effect size to calculate more informative weights that are not diluted by null effects as is common with group-based methods. This relationship can be calculated theoretically for normally distributed covariates or estimated empirically in other cases. We show via simulations and applications to data that this method outperforms existing methods by a large margin in the rare/low effect size scenario and has at least comparable performance in all scenarios.

Biography

Mohamad S Hasan is a PhD candidate in Statistics at the University of Georgia. He has completed his Masters in Statistical Computing from the University of Central Florida. He intends to start his job career as an Assistant Professor in Statistics, Biostatistics, and Bioinformatics.

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Poster Abstracts/ Presentations

Estella Chen-Quin et al., J Biom Biostat 2017, 8:5 (Suppl)
DOI: 10.4172/2155-6180-C1-006

3D heat maps of cancer mutations in the mitochondrial electron transport system to identify driver domain candidates

Estella Chen-Quin and **Trang Dang**
Kennesaw State University, USA

A link between tumorigenesis and mutations in the mitochondrial genes of the electron transport system (ETS) has long been posited, due to the high prevalence of mitochondrial mutations in all tumors. However, whether mitochondrial mutations play a causal role in cancer is unknown. Here, we analyze somatic mutations of ETS complex II (Succinate Dehydrogenase; SDH). People with inherited (germline) mutations in SDH have a known cancer predisposition; however, the path from inherited predisposition to cancer-causing lesions is not understood. Mutational lesions in the ETS disrupt the normal flow of electrons, increasing levels of reactive oxygen species (ROS) and creating a mutagenic source. Increased levels of ROS stabilize the mitogenic factor HIF-1□. To identify and visualize which SDH protein domains are selected for somatic missense mutations during tumorigenesis, we created the 3D protein heatmap to identify potential cancer driver domains. A structural analysis via homology modeling allows us to highlight cancer-associated mutations on the ETS protein structure. This may identify areas of the mitochondrial proteins that promote cancer when altered and inform on the cellular mechanisms involved. Mutations are scored for their predicted protein effect using Polyphen2; and potential driver domains are identified by their mean Polyphen2 score. Cancer data is taken from the Cancer Genome Atlas; control data is from the 1000 Genomes Project. We use Pymol and the porcine crystal protein structure to create the 3D protein heatmaps, providing comparative analysis between the control and cancer set..

Biography

Estella Chen-Quin is an Associate Professor in the Department of Molecular and Cellular Biology at Kennesaw State University. She investigates the cancer genetics of mitochondrial lesions during tumor formation. She has completed her PhD at Yale University and Postdoctoral studies at Emory University

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e-Posters

G Sh Tsitsiashvili et al., J Biom Biostat 2017, 8:5 (Suppl)
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Factorization of directed graph describing protein network using for research of plants stability to drought and extreme temperatures

G Sh Tsitsiashvili, V P Bulgakov and **A S Losev**
Far Eastern Federal University, Russia

In this paper, a sequential algorithm of graph nodes classification and their partial order definition are applying to protein network using for a study of the key players required for connecting ABA signaling and ABA-mediated drought and thermo tolerance. Suggested classification procedure allows finding in the network using for research of plants stability to drought and extreme temperatures proteins, the most important clusters for thermo stability and impacts to provide them conditions that are more convenient. It is possible to allocate output proteins DREB2C, ABA receptors PYLs, which are the most important for thermo stability of plants by their biochemical characteristics. In the network, there are only two multi node clusters and only one of them has edges connected with allocated output proteins. Details of this multi node cluster with allocated output proteins are analyzing.

Biography

G Sh Tsitsiashvili is is professor of the chair of Algebra, Geometry and Analysis at Far Eastern Federal University. 68 years since the birth of Tsitsiashvili Gurami Shalvovich (19 December, 1948), doctor of physical-mathematical sciences, Professor, main scientific researcher of Institute for Applied Mathematics Far Eastern Branch of RAS

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Accepted Abstracts

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Method development for the analysis of pooled biomarker data

Molin Wang
Harvard T H Chan School of Public Health, USA

For many health outcomes, it has become increasingly common to aggregate data from multiple studies to obtain increased sample sizes. The enhanced sample size of the pooled data allows investigators to perform subgroup analyses, evaluate the dose-response relationship over a broad range of exposures, and provide robust estimates of the biomarker-disease association. However, study-specific calibration processes must be incorporated in the statistical analyses to address between-study variability in the biomarker measurements. We introduce methods for evaluating the biomarker-disease relationship that validly account for the calibration process. We consider both internal and external calibration studies in the context of nested case-control studies. We then illustrate the utility of these estimators using simulations and an application to a pooling project of 25(OH)D and colorectal cancer.

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The role of allele specific expression (ASE) in genomic evolution

Sergei Bombin
The University of Alabama, USA

Evolutionary adaptation to abiotic stresses is essential for the survival of living organisms. Previous studies have tested the evolutionary adaptation and phenotypic response of populations of the nematode worm *Caenorhabditis remanei* to heat stress. Genes responsible for growth, metabolism and development showed higher expression rates in populations under constant heat stress when compared with the control group. However, transcriptional expression in the evolved groups did not show significant differences in comparison with the ancestral population. These results suggest that processes other than transcriptional regulation may be responsible for rapid evolutionary adaptation. However, because neither the overall genes' expression rate nor the expression level of the heat stress response genes changed, changes in the allele frequencies, which resulted in structural and functional changes in stress response proteins, and/or alteration in the other stress response pathways may be responsible for the observed adaptation to environmental stress. This hypothesis is supported by a separate study of allelic expression in barley, which found that gene expression could be altered during adaptation to drought stress. The main goal of my current project is to analyze transcriptomic data of ancestral and stress-evolved populations of *C. remanei* and evaluate the role of ASE in the evolution of stress response, which will be presented during the poster session.

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Utility of signal processing theories and practices in data processing

Gahangir Hossain
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Data vs. signal is just like the yoghurt vs. curd. Data is considered as the basic form of information in the age of big data. Data can be in the form of numbers, letters, or a set of characters and often collected through measurements. Data processing represents data in a form of structure, such as table, data tree, a data graph, etc. Signal is the term often used by electrical engineers to represent electronic form of data. For, data to be transferred electronically, it must first be converted into electromagnetic signals. In signal processing, signals are considered either as analog (a continuous stream of data) or digital (discreate states, binary codes). Furthermore, the analog signals can have infinite number of values in range, whereas digital can have only a limited number of values. In this way, the data processing and the signal processing are related. The main goal of this study is to explore some useful theories and best practices in signal processing vs. data processing to utilize in big data challenges. The study will connect the dots among wide range of research from bio-signal processing to bio-statistics.

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The emergence of FOG computing which has originated from cloud computing; what does their coexistence looks like?

Ihssan Alkadi
Louisiana State University, USA

The need for a much more improved traffic control and management, aka intelligent transportation systems, better massive storage, more accurate problem solving and computations, and effective network communication and performance across the nation prompted and motivated the cloud and computer experts to conceptually design "FOG" computing. The unique and brilliant design of FOG computing will enable each sector (governmental, private, and academic) to: Make software distribution and licensing easier since it is founded on the Cloud innovative technologies. It improves and make the process of data analytics more potent and prompt in delivering results on time. It has time critical 5G applications (which run on Mobile devices run faster with the FOG) will be faster, accurate, and most importantly more readily available all the time and hence reliable and productive. Efficiency is key here. Fog computing is invented for that reason. Improve battery life for devices as well as energy use and lessening of its depletion. Fog computing also uses a unique and powerful "delay in utilization" technique to control and saves the life of batteries and energy in various important and sensitive devices. Bandwidth of networks by using 5G technologies solving the inadequacy of IoT and lack of efficiency problems. Traffic congestions and road bottlenecks can be predicted better and ultimately the use and utilization of FOG computing will resolve congestions and improve road management by applying and implementing better and more effective queueing algorithms. It helps in work and load balancing which is a carryover form the cloud computing paradigm. By having multiple instances of CPUs and virtualized hosts via multiple and different operating systems, enables FOG computing to furnish better work load completion in optimal and desired time as well as balancing the load across all connected serves on the FOG network. Motion control of devices is optimized via the application of effective motion analysis methods and techniques which reside in FOG computing servers in any network on any sector (governmental, private, and academic).

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Using machine learning to forecast local epidemics of dengue fever in Latin America

Anna Kiefer
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Statement of the Problem: Dengue fever is a mosquito-borne disease that occurs in tropical and sub-tropical parts of the world. As many as 400 million people are infected yearly. In mild cases, symptoms are fever, rash, and muscle and joint pain, while in severe cases, dengue fever can cause severe bleeding, low blood pressure, and even death (in fact, the first death of dengue fever this year in Hanoi, Vietnam was just reported today, May 22, 2017). Because, it is carried by mosquitoes. The transmission of dengue is related to climate variables such as temperature and precipitation. A growing number of scientists argue that climate change is likely to produce distributional shifts that may cause an increase in the outbreaks of dengue fever and have significant public health implications worldwide. The increased risk of dengue augments the need for accurate models to predict the time, location, and severity of dengue outbreaks in Latin America.

Methodology & Theoretical Orientation: This study builds a predictive statistical model using logistic regression, classification, and cluster analysis machine learning algorithms to forecast dengue fever outbreaks. It utilizes training data from NOAA's Global Historical Climatology Network temperature data, PERSIANN satellite precipitation measurements, NOAA's NCEP climate forecast system reanalysis precipitation measurements, and NOAA's satellite vegetation index for two cities prone to dengue, San Juan, PR and Iquitos, Peru.

Potential Recommendations: This study will help inform health care workers, local communities, and NGO-led efforts to combat dengue fever outbreaks. Accurate dengue outbreak prediction will also inform effective resource allocation and health and social policies. Recommendations for additional climate training data and/or data from other Latin American cities to increase the model's accuracy will also be included.

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Big data techniques for extracting insight from data arising out of demonetization, digitization and cashless economy initiatives of India

Ajit Kumar Roy
Central Agricultural University, India

The digital economy is rapidly developing worldwide as the largest driver of innovation, competition, and growth. Even though many people have been excluded, tremendous opportunities are available for the digital economy to support financial inclusion for sustainable economic development. India could see a boost of $700 billion, an 11.8% increase by 2025. This additional GDP could create up to 21 million jobs. McKinsey has estimated that Indians lose more than $2 billion a year in forgone income simply because of the time it takes travelling to and from a bank. India aims to create a cleaner, more transparent economy via digitalization that will lead to an improved climate for foreign investment, boost economic growth. Goldman Sachs predicts that India - comprising 15% of the world population, with a growth rate of 7 to 8%, could be the second largest economy by 2030. India's new leadership considers the digital economy as a major growth enabler. When Prime Minister strategically listed "Digital India" among the top priorities for the new central government launching a major drive for financial inclusion in terms of opening Jan Dhan Accounts, giving a statutory basis for Aadhaar, implementation of Directs Benefits Transfer, introduction of RuPay Cards and Voluntary Disclosure Scheme for unaccounted money. Demonetization of 500 and 1000 Rs. notes on 8th November 2016 was another important milestone in this endeavour. Following demonetization, there has been a spurt in the digital payments across the country leading towards a cashless society. Since demonetization, the government has taken many steps to encourage people to use digital platforms like mobile wallets, BHIM, Unified Payment Interface (UPI) to pay for their daily needs. The government has set a target of 2,500 crore digital transactions for FY 2017-18 through UPI, Aadhaar, IMPS and debit cards in the Budget 2017. Economic digitization also enhanced taxation systems. In the process of digitization, huge data is generated. Presently data is considered as a new oil of the economy and Big Data is the fuel of the digital economy. Its value increases with every use and it brings about a change in paradigms. Therefore, it is time for extracting insights and innovation from data and to develop the ability to gather and mine varied types of related public data, and deploy more specialized techniques such as machine learning and neural networks.

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Bayesian generalized linear mixed modeling of breast cancer in Nigeria

Ropo Ebenezer Ogunsakin and **Siaka Lougue**
University of Kwazulu Natal, South Africa

Breast cancer treatment strategies in Nigeria need urgent strengthening to reduce the growth of the disease. Two main classes of approach have been developed for modeling modality of breast cancer treatment in the setting of generalized linear mixed models: classical statistics approach and Bayesian approach. This study compares the Bayesian approach with the exact conditional inference procedures for selection of predictor variables that are associated with modality of treatment given to breast cancer patients. In this paper, we introduce a Bayesian multilevel model that combines the random and fixed effect models. We investigate its performance as well as that of exact conditional inference approach in the setting of generalized linear mixed models with binary outcomes. We apply the techniques to breast cancer datasets and conduct Markov Chain Monte Carlo (MCMC) simulations. Simulation results indicate that Bayesian approach helps in selecting the more significant factors associated with modality of breast cancer treatment in Western Nigeria, as compared to the classical statistics approach. The result of Bayesian with non-informative prior is very similar to that of classical statistics and it can be superior for data with very small random effects.

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Detection and Interpretation of weak signals from big data for a strategic decision: Pre-adoption of new technology

Ali Fouladkar
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Big Data, the energy of the 21st century, the seed of innovative companies. The explosion of the volume of data and the emergence of Big Data drastically modify the decision-making process, particularly the strategic decision. Our research proposes a managerial approach to Big Data through qualitative studies based on the Organizational Vision model (Swanson and Ramilier 1997). Our research analyzes the media and the scientific discourse surrounding Big Data with the objective to define an inter-organizational grid of the pre-adoption of new technologies used to detect weak signals and support the strategic decision. The objective of this research is to identify the Organizing Vision Communities that influence the decision of adoption of new Big Data Technologies to detect Weak Signal from huge amount of data to help decision makers opting the best possible strategic decisions and to study how the discourse of the organizing vision influences the pre-adoption decision of these new technologies? Our research mainly investigates five sectors: health, financial markets, marketing, energy and security. Hence, our research question is: Which communities of the organizing vision influence the decision of adoption of Big Data technologies to detect weak signals and support strategic decision? Our research based on three studies. The first study analyzes the professional media discourse around the concepts of Big Data, weak signal and strategic decision. The second analyze the systematic literature review on Big Data concepts, weak signal and strategic decision. The third study based on interviews with users, expert and professionals of Big Data, is interested in understanding how and why some Big Data technologies are adopted to detect weak signals and support strategic decision and not others. This research study the influence of different communities of organizing vision specifically on the decision of adoption of new technologies and the contributions of these technologies to detect weak signals and support strategic decision (helps to detect fragmented, ambiguous but essential information).

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Biometric security, E-health care: Indian context

Ch Sanjay
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The advances in Medical Sciences and ICT (Information and Communication Technologies) are offering wide opportunities for improved health care. Electronic health is a new and efficient method for providing health care services to the society. ICT is playing a crucial role in improving the performance of health care system in the developing countries. A Biometric device is a security identification and authentication device, such devices use automated methods of verifying or recognizing the identity of a living person based on a physiological or behavioral characteristic. Novel systems, methods and apparatus are disclosed for enabling the standardization of healthcare delivery, which provides a simple, convenient and paperless experience for the patient. In an embodiment, ubiquitous standardization of communication nationwide and internationally at point-of-care is initiated and implemented via patient mobile device. The integration of mobile device biometrics improves the privacy and security of patients and the incorporation of NFC technology effectuates the simple transfer of information from patient data to electronic transactions allowing the patient and healthcare industry to instinctively interact with their healthcare electronic environment.

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