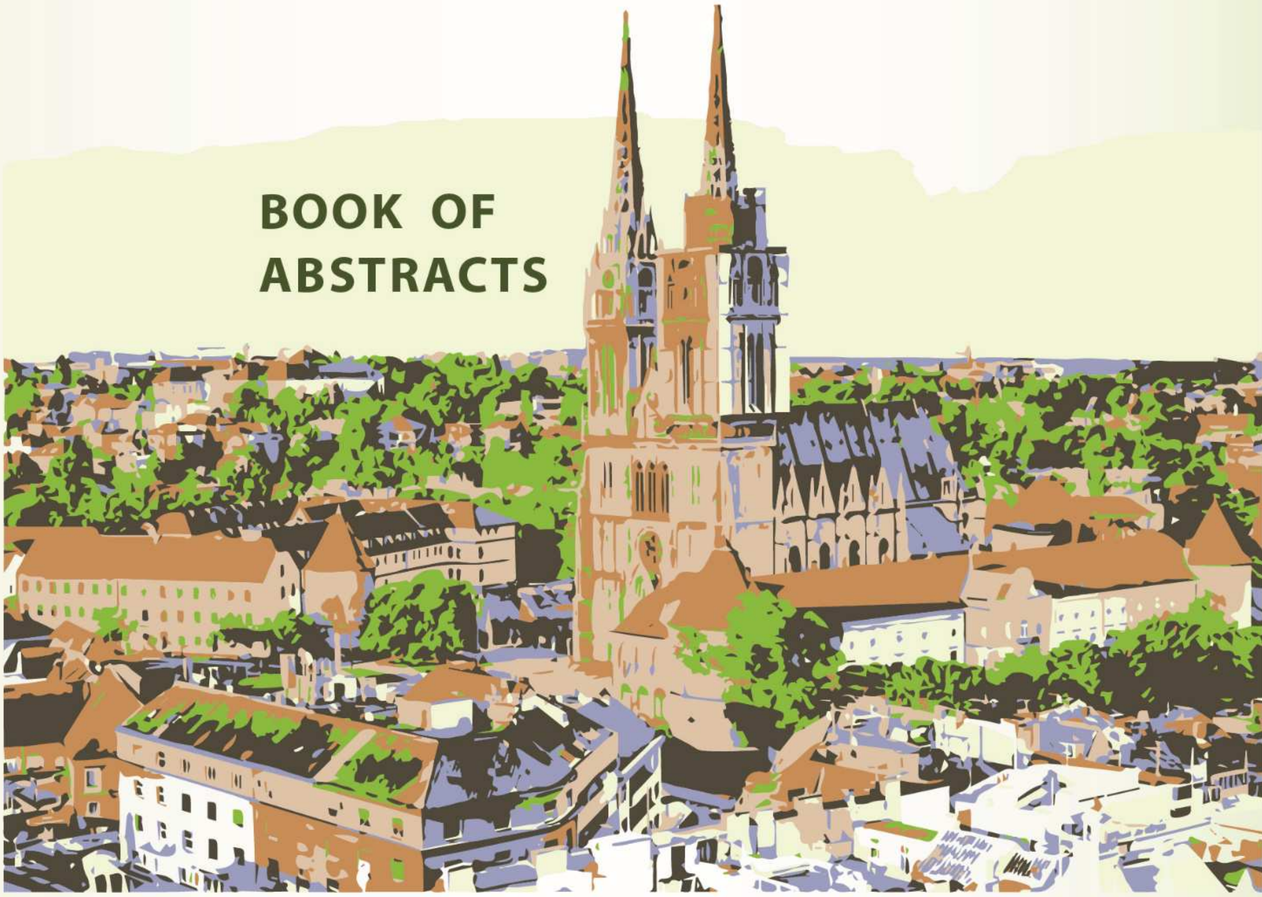
# BIOSTAT 2019

HRVATSKO BIOMETRIJSKO DRUŠTVO - ZAGREB -

UNIVERSITAS STUDIORUM ZAGRABIENSIS MDCLXIX

## 24th International Scientific Symposium on Biometrics

ZAGREB, CROATIA, **5 - 8 JUNE 2019**



## BOOK OF ABSTRACTS

**EDITED BY:** Anamarija Jazbec
Marija Pecina
Zdenko Sonicki
Diana Šimić
Mislav Vedriš
Slavica Sović

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BOOK OF ABSTRACTS

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## EDITORS:

Anamarija Jazbec
Marija Pecina
Zdenko Sonicki
Diana Šimić
Mislav Vedriš
Slavica Sović

Zagreb, 2019.

# IMPRESSUM

# BIOSTAT 2019

24th International Scientific Symposium on Biometrics

Zagreb, Croatia, 5 - 8 June 2019

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Croatian Biometric Society

## CO-ORGANISER

University of Zagreb

School of Medicine

Andrija Štampar School of Public Health

Škola narodnog zdravlja „Andrija Štampar"

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of the Croatian Academy of Sciences and Arts

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## 22nd SCHOOL OF BIOMETRICS

**Andrew B. Lawson**
Medical University of South Carolina, USA

## KEYNOTE SPEAKERS

**Andrea Berghold**
Medical University of Graz

**Lavoslav Čaklović**
University of Zagreb

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BIOSTAT 2019

24th International Scientific Symposium on Biometrics
Zagreb, Croatia, 5 - 8 June 2019

ABSTRACTS

# PREFACE

BIOSTAT 2019

24th International Scientific Symposium on Biometrics
Zagreb, Croatia, 5 - 8 June 2019

Welcome to the Book of Abstracts of BIOSTAT 2019 – The 24th International Scientific Symposium on Biometrics organized by the Croatian Biometric Society and co-organized by the School of Public Health "Andrija Štampar", School of Medicine, University of Zagreb – held in Zagreb, Croatia, June 5-8, 2019.

BIOSTAT Symposium is held under the auspices of the Croatian Academy of Sciences and Arts.

The symposium is an intrinsically interdisciplinary meeting accepting papers from a wide array of research disciplines at the intersection of data sciences and life sciences as evidenced by this Book of Abstract. BIOSTAT 2019 comprises 22nd School of Biometrics, keynote lectures, and contributed papers. This brochure contains 23 (3 students) abstracts written by 62 authors from 9 countries – Austria, Bosnia and Hercegovina, Croatia, Italy, North Macedonia, Slovenia, Spain, United Kindom and United States of America.

Symposium is taking place at the "Andrija Štampar" School of Public Health, School of Medicine, University of Zagreb. The School was founded in 1927, owing to the initiative of a group led by Dr. Andrija Štampar (the first president of the World Health Assembly, the decision making body of the World Health Organization) and with a financial support of the Rockefeller Foundation. Schools's activities were guided by the principle of medicine as an integrated discipline, encompassing both prevention and treatment. Education at all levels from the general population to the postgraduate level was always an important aspect of prevention, and we hope that this Symposium will contribute to the rich portfolio of knowledge sharing events at the School. The choice of venue for this year's Symposium is also symbolic, as Croatian Biometric Society was established at the "Andrija Štampar" School of Public Health in 1989, and this year we celebrate our 30th anniversary.

We are continuing this year with our traditional 22nd School of Biometrics. Our guest lecturer this year is professor **Andrew B. Lawson** from the Department of Public Health, Medical University of South Carolina, USA, with the topic of "Spatial Analysis for Biomedical and Related Fields".

This year keynote speakers are professor **Andrea Berghold** (Institute for Medical Informatics, Statistics, and Documentation, Medical University of Graz, Austria) with a lecture on "Randomization Techniques - Theory and Practice", and professor **Lavoslav Čaklović** (Department of Mathematics, Faculty of Science, University of Zagreb) with a lecture on "Network Choice Theory".

There are few novelties on BIOSTAT from this year: 1. we introduce awards for the best presentation for Students and for Scientists and 2. we encourage BS and MS students to participate in Symposium with or without abstracts (presentations) with a popular registration fee of 0 € (0 kn).

We are looking forward to sharing with you pleasant moments, lively discussions, and successful networking, and to forging new partnerships and friendships. We believe that our exchange of ideas and interchange of knowledge will contribute to the progress of Biometric science.

Editors:
Anamarija Jazbec, Marija Pecina, Zdenko Sonicki, Diana Šimić, Mislav Vedriš and Slavica Sović
Zagreb, June, 2019

BIOSTAT 2019

24th International Scientific Symposium on Biometrics
Zagreb, Croatia, 5 - 8 June 2019

## SYMPOSIUM PROGRAM at Glance

| | | | |
|---|---|---|---|
| June, 5 | 19:00 | Registration &<br>Welcome Cocktail | |
| | 20:00 | | |
| Thursday, June, 6 | 9:00 – 9:30 | Opening ceremony | Zdenko Sonicki, HBMD President<br>Mirjana Kujundžić Tiljak, University of Zagreb School of Medicine, "Andrija Štampar" School of Public Health, Director<br>Anamarija Jazbec, BIOSTAT OC President |
| | 9:30 – 11:00 | *Chair: Zdenko Sonicki* | School of Biometrics – *Part I*<br>**Andrew B. Lawson**:<br>Spatial Analysis for Biomedical and Related Fields |
| | 11:00 – 11:30 | COFFEE BREAK | |
| | 11:30 – 13:00 | *Chair: Zdenko Sonicki* | School of Biometrics – *Part II*<br>**Andrew B. Lawson**:<br>Spatial Analysis for Biomedical and Related Fields |
| | 13:00 – 14:00 | LUNCH BREAK | |
| | 14:00 - 15:30 | *Chair: Diana Šimić* | Contributed session |
| | 15:30 – 16:00 | COFFEE BREAK | |
| | 16:00 – 17:20 | *Chair: Karina Gibert* | Contributed session |
| | 18:00 | Zagreb sightseeing | |
| Friday, June, 7 | 9:00 - 10:40 | *Chair: John Vena* | Contributed session |
| | 10:40 – 11:10 | COFFEE BREAK | |
| | 11:10 – 12:00 | *Chair: Marija Pecina* | Keynote Lecture: **Andrea Berghold**<br>Randomization techniques – theory and practice |
| | 12:00 – 13:00 | *Chair: Slavica Sović* | Contributed session |
| | 13:00 – 14:00 | LUNCH BREAK | |
| | 14:00 – 14:30 | ISPC Meeting | |
| | | COFFEE BREAK | |
| | 14:30 – 24:00 | Excursion | |
| Saturday, June 8 | 9:00 – 10:40 | *Chair: Janez Stare* | Contributed session |
| | 10:40 – 11:10 | COFFEE BREAK | |
| | 11:10 – 12:00 | *Chair: Mislav Vedriš* | Keynote Lecture: **Lavoslav Čaklović**<br>Network choice theory |
| | 12:00 – 13: 00 | *Chair: Anamarija Jazbec* | STUDENTS SESSION |
| | 13:00 – 14:00 | LUNCH BREAK | |
| | 14:00 – 14:30 | Closing ceremony | |
| | 14:30 – 15:00 | Farewell COFFEE | |

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# PROGRAM

BIOSTAT 2019
24th International Scientific Symposium on Biometrics
Zagreb, Croatia, 5 - 8 June 2019

## SYMPOSIUM PROGRAM in Detail

| | | | |
|---|---|---|---|
| June, 5 | 19:00<br>20:00 | Registration &<br>Welcome Cocktail | |
| Thursday, June, 6 | 9:00 – 9:30 | Opening ceremony | Zdenko Sonicki, HBMD President<br>Mirjana Kujundžić Tiljak, University of Zagreb School of Medicine, “Andrija Štampar” School of Public Health, Director<br>Anamarija Jazbec, BIOSTAT OC President |
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| | 13:00 – 14:00 | LUNCH BREAK | |
| | 14:00 - 15:30 | *Chair: Diana Šimić* | Contributed session # |
| | | AUTHOR | TITLE |
| | | Ana Martinčić Špoljarić, Ivica Rubelj, Miljenko Huzak | A Mathematical Model of Telomere Shortening |
| | | Janez Stare, Nina Ružić Gorenjec, Robin Henderson | Estimating the probability of random cancers |
| | | Karina Gibert, Miquel Sánchez-Marrè, Beatriz Sevilla | An intelligent recommender for personalized diets considering health and life style |
| | | Gloria Gheno | A new algorithm to determine sleep quality |
| | 15:30 – 16:00 | COFFEE BREAK | |
| | 16:00 – 17:00 | *Chair: Karina Gibert* | Contributed session # |
| | | AUTHOR | TITLE |
| | | Andrew R. Barron, Lidija Jakobek, Mirta Benšić, Petra Matić | Statistical fitting of adsorption isotherms |
| | | Lavoslav Čaklović | Sparse propensity matching |
| | | Milan Rimac, Tonka Vuksevic, Jelena Roganovic, Zdenko Sonicki | Global geographic clustering of childhood cancer in Croatia |
| | 18:00 | Zagreb sightseeing | |
| Friday, June, 7 | 9:00 - 10:40 | *Chair: John Vena* | Contributed session # |
| | | AUTHOR | TITLE |
| | | Želimir Kurtanjek | Statistical propensity analysis of *Triticum aestivum* DaRT genome profiles |
| | | Matthew Bozigar, Erik Svendsen, John Pearce, Kathryn Cristaldi, John Vena | Methodological considerations in constructing a space-time model of disease risk: an applied case study of asthma in South Carolina 1999-2015 |
| | | Yuko Y. Palesch | Is alpha=0.05 a “one-size-fits-all” criterion in clinical trials? |
| | | Mulugeta Gebregziabher, Carter Allen, Daniel Baer, Aastha Khatiwada, Virginia Shipes, Abeba A Teklehaimanot, Philip S. Insel | A Multivariate Generalized Linear Mixed Model for Joint Modeling of Cognitive and Neuroimaging Outcomes |

|  |  |  |  |
|---|---|---|---|
|  |  | Paul A. Thompson and Norm Matloff | Improving the reproducibility of image manipulation: Using journaling to track the process |
|  | 10:40 – 11:10 | COFFEE BREAK |  |
|  | 11:10 – 12:00 | *Chair: Marija Pecina* | Keynote Lecture: **Andrea Berghold**<br>Randomization techniques – theory and practice |
|  | 12:00 – 13:00 | *Chair: Slavica Sović* | Contributed session # |
|  |  | AUTHOR | TITLE |
|  |  | Borut Bosančić, Marija Pecina | Meta-analysis in agricultural sciences: Guidelines with novel ME-MetaPCA |
|  |  | Diana Šimić, Jelena Gusić | Do We Influence Students' Attitudes toward Statistics? |
|  |  | Marijana Žunić, Krunoslav Teslak | My forest for me is...? Building private forest owners objectives network |
|  | 13:00 – 14:00 | LUNCH BREAK |  |
|  | 14:00 – 14:30 | ISPC Meeting |  |
|  |  | COFFEE BREAK |  |
|  | 14:30 – 24:00 | Excursion |  |
| Saturday, June 8 | 9:00 – 10:40 | *Chair: Janez Stare* | Contributed session # |
|  |  | AUTHOR | TITLE |
|  |  | Tamara Jurina, Adela Šain, Davor Valinger, Jasenka Gajdoš Kljusurić, Maja Benković, Ana Jurinjak Tušek, Želimir Kurtanjek, Vesna Antoška Knights | Principal component regression vs. partial linear squares regression in prediction modelling |
|  |  | Jasminka Dobša | Capturing clustering structure of the data in cross-language representation of textual documents |
|  |  | Martina Đodan, Sanja Perić | Comparison of different sessile oak planting techniques after windthrow in Norway spruce artificial stands |
|  |  | Maja Buhin Pandur, Jasminka Dobša | Classification of dentists in Slovenia based on their availability |
|  |  | Roberto Mužić, Slavica Sović, Zdenko Sonicki | Frequency phobia vs. probability blindness |
|  | 10:40 – 11:10 | COFFEE BREAK |  |
|  | 11:10 – 12:00 | *Chair: Mislav Vedriš* | Keynote Lecture: **Lavoslav Čaklović**<br>Network choice theory |
|  | 12:00 – 13: 00 | *Chair: Anamarija Jazbec* | STUDENTS SESSION # |
|  |  | AUTHOR | TITLE |
|  |  | Lara Rajković | Overview Of Methods For Meta-analysis |
|  |  | Igor Radanović, Deni Rkman, Kristian Dominik Rudež, Igor Milovčić, Ivan Horvat, Robert Likić | Heatmap analysis of emergency patients flow at the University Hospital Centre Zagreb |
|  |  | Kristina Stamenković, Katarina Skopljak | Evaluation of mental health workshops in a sample of Croatian secondary-school adolescents |
|  | 13:00 – 14:00 | LUNCH BREAK |  |
|  | 14:00 – 14:30 | Closing ceremony |  |
|  | 14:30 – 15:00 | Farewell COFFEE |  |

**# Note:** Time for each title is 20 minutes - 15 for presentation followed by 5 minutes for questions and discussion

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# 22nd SCHOOL OF BIOMETRICS

## 22nd SCHOOL OF BIOMETRICS

**Andrew B. Lawson**
Department of Public Health Sciences
Medical University of South Carolina, USA
Email: lawsonab@musc.edu

Dr Lawson is Professor of Biostatistics in the Division of Biostatistics and Bioinformatics, Department of Public Health Sciences, College of Medicine, MUSC and is an MUSC Distinguished Professor and ASA Fellow. He was previously a Professor of Biostatistics in the Department of Epidemiology & Biostatistics, University of South Carolina, SC. His PhD is from the University of St. Andrews, UK and was in Spatial Statistics.

He has over 160 journal papers on the subject of spatial epidemiology, spatial statistics and related areas. In addition to a number of book chapters, he is the author of 10 books in areas related to spatial epidemiology and health surveillance. The most recent of these is Lawson, A.B. et al (eds) (2016) *Handbook of Spatial Epidemiology*. CRC Press, New York, and in 2018 a 3rd edition of *Bayesian Disease Mapping; hierarchical modeling in spatial epidemiology* CRC Press. As well as associate editorships on a variety of journals, he is an advisor in disease mapping and risk assessment for the World Health Organization (WHO). He is founding editor of the Elsevier journal Spatial and Spatiotemporal Epidemiology. Dr Lawson has delivered many short courses in different locations over the last 15 years on Bayesian Disease Mapping with OpenBUGS and INLA, Spatial Epidemiology and disease Clustering.
Web site: http://academicdepartments.musc.edu/phs/research/lawson/

Topic:

# Spatial Analysis for Biomedical and Related Fields

## Statistical and Epidemiological Issues in Small Area Health Analysis: disease mapping, clustering, and surveillance

Abstract:

The spatial analysis of health outcome data has seen a major expansion in the last few years. Many studies now routinely incorporate geo-referencing to allow for contextual effects. Spatial contextual effects could take a variety of forms: ‘neighborhood’ effects, census region or postal district effects or more directly environmental effects such as measured air pollution, radiation or water quality. In this talk I will discuss the basic statistical and epidemiological issues affecting small area analysis of health outcomes. A major focus will be on cancer and disease mapping and cluster detection. A secondary focus will be on online health surveillance. I will look at case event and count data and discuss modeling these different types of outcome. Focus will be on lip and respiratory cancer as well as surveillance of respiratory infections.

# KEYNOTE LECTURE

## KEYNOTE SPEAKER

**Andrea Berghold**
Medical University of Graz,
Institute for Medical Informatics, Statistics and
Documentation,
Graz, Austria

Email: andrea.berghold@medunigraz.at
Web site: https://www.medunigraz.at/imi/en/index.php

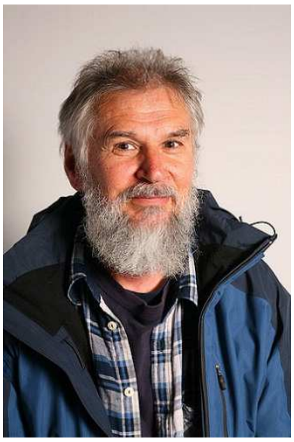
Topic:

# Randomization techniques – theory and practice

Abstract:

The ICH E9 statistical principles for clinical trial guideline states that “the most important design techniques for avoiding bias in clinical trials are blinding and randomization”. Thus, using adequate randomization techniques is an important prerequisite in conducting a clinical trial. Over the years various restricted randomization techniques such as permuted block design, biased coin design, urn design or big stick design have been proposed as well as covariate-adaptive and response-adaptive randomization. In this talk, I will discuss the performance of different restricted randomization techniques regarding their treatment balance behavior and allocation randomness. However, it is not only important to have different techniques available but also to have suitable software to allow use of these techniques in practice. I will present a web-based randomization tool for multi-centre clinical studies (“Randomizer” – www.randomizer.at) which was developed by the Institute for Medical Informatics, Statistics and Documentation, Medical University of Graz, Austria. This tool facilitates efficient management of the randomization process including allocation concealment, stratification, audit trails etc. and can also be used for simulation of different randomization designs.

## KEYNOTE SPEAKER



**Lavoslav Čaklović**
University of Zagreb
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Department of Mathematics
Zagreb, Croatia

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Web site: https://www.pmf.unizg.hr/math/lavoslav.caklovic

Topic:

# Network choice theory

Abstract:

The problem of single choice repetition from the finite set of objects {A, B, C, …} has a long story. The classical choice theory, binomial and multinomial, are based on the random utility which captures the uncertainty of choosing one object among offered two or all of them. This theory depends upon the choice axiom of Luce (1959) which asserts that the probability of choosing an element does not depend upon the context of choosing. Network choice theory describes what happens when this axiom is not satisfied.

The simplest version of the individual choice network model represents the objects as the nodes in the graph and the oriented edges capture the frequency of choosing the elements from the offered pair. For instance, if A:B = 3:2 is the relative ratio of probabilities of choosing A and B when {A,B} is offered, this ratio generates a multi-graph with parallel edges: one from B to A with weight 3, and the other one from A to B with weight 2. The situation may be more complicated if the ratios of A:B:C or A:B:C:D are offered. Even in the case of sparse network the probability distribution may be calculated.

Potential method (PM), developed by the author, gives the probability of choosing each element after solving Laplace equation of the given graph. The graph is consistent if and only if the axiom of Luce is satisfied. Some examples of the choice network will be presented and solved by the PM-software.

Group networks may be analysed by cluster analysis after defining a suitable distance of the individual networks.

Possible applications with a little modification are: consumption, survey analysis, social sciences.

# CONTRIBUTED SESSIONS

Title:

# A Mathematical Model of Telomere Shortening

Authors:

**Ana Martinčić Špoljarić, Ivica Rubelj, Miljenko Huzak**

Affiliation:

University of Zagreb, Croatia

Abstract:

In 1961 Moorhead and Hayflick first described the molecular mechanisms that control the limited number of human cell divisions, i.e., the limited growth capacity of the cell. Numerous studies point to the telomeres , the end of chromosomes ,as the underlying cause of the cellular (or replicative) senescence, which is considered to be the basis of organismal aging. During cell division, telomeres shorten until the telomere length falls below a critical level, causing the cell to cease proliferation and enter the replicative senescence. Hayflicks experiments during the late '60s and early '70s demonstrated a large variation of *in vitro* lifespan among cell cultures and among lifespans of individual clones selected from the same cell culture, proving that dynamics by which individual cells enter senescence exhibits stochastic behaviour.

In 1980 Smith and Whitney conducted the experiment in which they described the heterogenity in proliferative potential of a single clone of normal human fibroblast. They also showed that the degree of difference in doubling potential between two sister cells coming from the same mitosis event may vary significantly. The model presented here continues the work of Rubelj and Vondraček, who described the concept of telomere abrupt shortening for the first time. In this research we propose advanced model of telomere controlled cell senescence considering both modes of telomere shortening – gradual (by incomplete replication) and abrupt shortening (introducing the region that is hotspot for recombination). In order to investigate how the stochastic behaviour of telomeres affects the cell with time, we derive, from the discrete model, continuous model and we check our theory by computational simulations of telomere dynamics. By simulating Smith and Whitney's original experiments we demonstrate that this research sets a valid biological and mathematical model that is able to explain stochastic nature of cell aging.

| | |
|---|---|
| Title: | **Estimating the probability of random cancers** |
| Authors: | **Janez Stare, Nina Ružić Gorenjec, Robin Henderson** |
| Affiliation: | University of Ljubljana, Newcastle University |
| Abstract: | Estimating the probability of random cancer has become a topic of interest in the last few years. The term random is used rather loosely in the sense that cancers are called random if they cannot be avoided.<br>In this talk we present methodology to estimate upper limits of probabilities of random cancers. For illustration, we presents our results for some cancer sites and compare them with other estimates in the literature. Our approach is completely data driven, meaning that it relies on the quality of the data. |

Title:

# An intelligent recommender for personalized diets considering health and life style

Authors:

**Karina Gibert, Miquel Sánchez-Marrè, Beatriz Sevilla**

Affiliation:

Intelligent Data Science and Artificial Intelligence Research Center
Universitat Politècnica de Catalunya-BarcelonaTech, Catalonia, Spain

Abstract:

The system Diet4You is presented in the paper. It is an intelligent recommender for personalized diets oriented to play a central role in the new paradigm of health life styles and personalized medicine.

Indeed healthy life-styles have become a keystone of the modern health approach, according to its relationship with prevention of development of some chronic diseases and maintaining, or even improve, the quality of life. Following the proper diet is becoming essential from the health point of view. However, the current state of the art in nutrition is based on diets designed by nutritionists on the specific needs of each person, using their accumulated experience and some basic tools like tables of food decomposition.

Well-formalized mechanisms supporting specific diet design are still limited. The project Diet4You proposes an intelligent decision support system oriented to the adaptive and dynamic preparation of personalized diets fitting nutritional prescriptions and adapted to specific health situation of a person, including genomics, personal habits and food preferences, cultural context, the prescription of the nutritionist and allergies or restricted foods for health reasons. Diet4You is a hybrid system with a complex integration of artificial intelligence, specific nutritional knowledge, and data science components, able to compose complete personalized menus, for a certain period of time. The Personal Menu Planner (PMP) is the specific component choosing the dishes to be proposed in the solution.

In the paper a global perspective of the system functionalities and performance is provided, together with the results of a preliminary evaluation for some real case studies developed in the project

ACK: Diet4You has been financed by the Spanish Government Research Plan under project TIN2014-60557-R

| | |
|---|---|
| Title: | **A new algorithm to determine sleep quality** |
| Authors: | **Gheno Gloria** |
| Affiliation: | Innovative data analysis (Italy) |
| Abstract: | With the extension of life the attempt to improve its quality is more and more prevailing. A third of life is spent sleeping, so the analysis about the nature of sleep and about its incisiveness on people's health status, in particular about the complications caused by the various types of insomnia, is of primary importance. Indeed, the researchers found a relationship between neurodegenerative diseases, such as Parkinson disease and Lewy body dementia, and REM sleep behavior disorders. Currently, some methods have been developed to correctly assess the quality of sleep, such as polysomnography, a test used to determine sleep disorders, and the examination of data collected by sensors, which can be applied to the monitored subject, to the bed or to both simultaneously. The use of sensors is inexpensive, it does not require hospitalization in specific facilities, it can be done at home and it easily provides sleep parameters, using various methods depending on the positioning of the sensors. Sleep can be evaluated by applying to the obtained parameters the appropriate index, which, however, has the limit of being deterministic. The new stochastic index, introduced by me, and specific statistical tests, which determine its goodness and highlight its eventual anomalous values, remove its deterministic limitation. The construction of this index implies the creation of a new algorithm applicable to the simple data collected by the sensors to obtain the sleep parameters. Having obtained these, I build a new modified version of the index by inserting other variables of interest. For example, a difference between the index proposed in the literature and the new one consists of the use of the sleep stages. The first separates only the REM stage, distinguishable by the random and rapid movements of the eyes, by the lower muscle tone and by the propensity to vivid dreams, from the other 4 stages, defined as non-REM, while the second considers the 5 stages of sleep separately . The new variables added improve sleep monitoring and establish, with more specific precision, any parasomnias and dyssomnias. I demonstrate the goodness of the new index by applying it to real cases and additionally by comparing them to each other. |

Title:

# STATISTICAL FITTING OF ADSORPTION ISOTHERMS

Authors:

**Andrew R. Barron[1], Lidija Jakobek[2], Mirta Benšić[3], Petra Matić[2]**

Affiliation:

[1] Yale University, Department of Statistics and Data Science, USA
[2] J. J. Strossmayer University of Osijek, Faculty of Food Technology
[3] J. J. Strossmayer University of Osijek, Department of Mathematics

Abstract:

Adsorption processes can be studied in food science to understand the proportions of specified bioactive molecules (such as polyphenols) that are adsorbed onto larger molecules present in food, which impact their bioaccessibility. These processes are analyzed with nonlinear mathematical expressions called adsorption isotherms. For given physiological conditions (e.g. temperature, acidity and amount of adsorbent), an adsorption isotherm relates the amount of the bioactive molecules that are adsorbed $q_e$ to the concentration not adsorbed $c_e$, in equilibrium, for each of several experimentally-specified initial amounts. Traditional fitting of adsorption isotherms by nonlinear regression (minimizing sums of squares of the vertical error at each $c_e$) suffers from a statistical inconsistency that we overcome. Proper statistical fitting in this setting relates the observed amounts adsorbed to that unique value on the adsorption isotherm that corresponds to the specified initial amount. Theoretical considerations are followed up with exhaustive simulations confirming them.

| | |
|---|---|
| Title: | **Statistical propensity analysis of *Triticum aestivum* DaRT genome profiles** |
| Authors: | **Želimir Kurtanjek** |
| Affiliation: | University of Zagreb, Faculty of Food Technology and biotechnology*<br>Zagreb, Croatia |
| Abstract: | Proposed are statistical propensity models of *Triticum aestivum* (common wheat) based on genome typization by Diversity Array Technology (DaRT). Applied is the data set of single nucleotide perturbations (SNP) obtained from CIMMYT International Maize and Wheat Improvement center. Analyzed are 30 000 DaRT profiles of 600 landrace varieties cultivated under controlled test fields located at 4 different climate regions. Each of the varieties are characterized by the following traits: days to heading (DTH), days of maturity (DTM), thousand kernel weight (TKW), test weight (TW), grain hardness (GH), grain protein (GP), grain length (GL), sedimentation (SDS), grain width (GW), and plant height (PHT). All of the trait values are transformed into corresponding standardized *z* values. Histogram plots of the data indicate underlaying normal probability density functions. Autocorrelation heat maps of DaRT profiles show insignificant collinearity ($r < 0.1$) among corresponding gene SPS perturbations. The data are classified into quartiles and focus of analysis is to elucidate SNP profiles for functional causality to maximum grain protein content and optimal protein production per hectare. In order to determine propensity for optimal protein yield the quartile classification are also transformed to dichotomous data sets with positive responses $X = 1$ for the first quartile, while $X = 0$ are assigned to quartiles 2-4. The trait predictors are derived by linear regularization model using the Least Absolute Shrinkage and Selection Operator (LASSO). The predictors are evaluated by 10 fold validation yielding average prediction accuracy of 85 %. Based on LASSO model coefficients the SNP-s responsible for the most positive and inhibition trait effects are determined. To obtain propensity scores of SNP-s for maximal protein production applied is logistic regression model. The regularized data set is matched to account for effects of unobservable confounders, such as variable soil properties and especially for uncontrolled climate fluctuations. Obtained are propensity score probability distributions for prediction of optimal protein yield. The results are applicable for programs of wheat cultivar improved by deliberate interbreeding, and more importantly by use of molecular CRISP-cas9 technology.<br>*retired |

Title:

# Sparse propensity matching

Authors:

**Lavoslav Čaklović**

Affiliation:

PMF-MO, University of Zagreb

Abstract:

Propensity scoring is a well known approach for calculating the treatment effect in controlled and observed experiments based on Logistic Regression (LR). Here we investigate a possibility of using the Potential Method (PM) as a base method for scale construction before matching.

A testing example is *lalonde* (dataset from the R-package Matching), an observational data with 297 treated and 15992 controlled items. The idea is to make approximative matching (using treated items profiles), to construct some scale (potential) and in the second stage to make matching (hungarian algorithm) using this scale instead of items profiles. In the second stage a few of the treated items are also removed from the table.

The second phase matching is done on each strata and the overall effect is calculated after that. Some strata effect is negative which needs some social explanations, but the overall effect is even higher than the same one calculated using propensity score with different matching algorithm.

The parse propensity matching works in the same way. In the first step the approximative matching is done without exact matching and the potential scoring works with incomplete data as well.

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| Title: | **Global geographic clustering of childhood cancer in Croatia** |
| Authors: | Milan Rimac, MD, MSc[1*]; Tonka Vuksevic, MD[2]; Jelena Roganovic, MD, PhD[3]; Zdenko Sonicki, MD, PhD[4] |
| Affiliation: | [1]Health Care Centers of Istrian County, Health Care Center Labin; [2]Emergency Medicine Institute of Zadar County; [3]Clinical Hospital Center Rijeka, University of Rijeka School of Medicine, [4]'Andrija Stampar' School of Public Health, University of Zagreb School of Medicine; *Presenter |
| Abstract: | Childhood cancer is second leading cause of death in children 1-14 years of age in developed countries. Mortality rates, high treatment-related morbidity and its considerable social and financial impact make childhood malignancy important public health issue. Furthermore, its unknown etiology makes it even more fearful disease causing concern in public perception.<br>In order to contribute to the clarification of childhood cancer occurrence in Croatia we conducted nationwide clinical data survey of childhood cancer cases registered at pediatric oncology departments in 2001-2015 and examined spatial epidemiology at the county level. For disease mapping we used spatial data from Central register of spatial units (State geodetic administration). Population under risk in investigated period has been estimated by linear interpolation/extrapolation of 2001 and 2011 population censuses data (Croatian bureau of statistics). Global and regional age-specific incidence rates, age-standardized rates and standardized incidence ratios were calculated.<br>ArcGIS Desktop 10.5 software has been used for creation of initial maps of diseases and data aggregation by spatial units. Exploratory spatial data analysis has been performed by GeoDa 1.12 software tool. Presence of global clustering has been examined by Pearson's chi square and Potthoff-Whittinghill statistics as implemented in DCluster 0.2-7 package for R.<br>Results suggested possibility of global clustering of embryonal tumors in Croatia and necessity of higher resolution investigation of childhood cancer incidence. |

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| Title: | **Methodological considerations in constructing a space-time model of disease risk: an applied case study of asthma in South Carolina 1999-2015** |
| Authors: | **Matthew Bozigar, Erik Svendsen, John Pearce, Kathryn Cristaldi, John Vena** |
| Affiliation: | Medical University of South Carolina, Centers for Disease Control and Prevention (CDC) |
| Abstract: | Disparities in health outcomes can be difficult to investigate using existing data and methods. Utilization of a geographic information system (GIS) to create spatially-explicit measures can improve knowledge of potential drivers of health outcomes, yet more advanced spatio-temporal methods can further improve understanding. Applying a Bayesian Hierarchical Model (BHM) that allows for estimation of parameters can be advantageous for improving the utility of population-wide hospitalization data. Numerous methodological issues arise when using hospitalization data that are aggregated to spatial units for analysis. These include spatio-temporally-explicit measures, spatio-temporal confounding, missing geographic information, variable selection, and calculated expected counts of disease, among others. Researchers can control for spatio-temporal confounding and stabilize risk exceedance probability estimates by including correlated and uncorrelated spatial, temporal, and spatio-temporal random effects. Geographic imputation of missing geographic information can be conducted by stochastically imputing small area identifiers (e.g., census tracts) within known larger areas (e.g., ZIP codes) using areal proportions as probabilities of assignment. Employing entry parameters with prior distributions on prospective social, environmental, and interaction variables can assist in important variable selection. Sensitivity of variable selection results and coefficient estimates to expected counts calculated using a single average areal ED visit rate over the study period contrasted with an annually-varying rate can be assessed. Each of these issues are addressed in an applied case study by building a space-time model of census tract risk for emergency department (ED) visits due to asthma among South Carolina children from 1999 to 2015 in a Bayesian framework. Results showed that controlling for spatio-temporal confounding, imputing missing geographic information, all-at-once variable selection, and using a single statewide rate to calculate expected counts were preferred for accurately detailing asthma risk disparities. This methodology could be applied to numerous health outcomes. |

Title:

# Is alpha=0.05 a “one-size-fits-all” criterion in clinical trials?

Authors:

**Yuko Y. Palesch, PhD**

Affiliation:

Medical University of South Carolina
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Abstract:

Attaining study results with a p-value less than 0.05 is a very much desired outcome in biomedical research. But why 0.05? Many papers have been published on the interpretation of p-values, and more recently, on the merits of reliance on p-values. In particular, in March 2016, the American Statistical Association issued a statement on this topic with guidance on the use of p-values to “improve conduct and interpretation of quantitative sciences.” With this in the background, situations arise under which alpha level of 0.05 may not be the best criterion under certain superiority, non-inferiority, and futility designs in clinical trials. While in all cases, the rejection of the null hypothesis is the desired outcome to make definitive claims on the inference from the study data, these designs differ in the practical interpretation of the type I (alpha) and II (beta) error probabilities due to their specific research aims, and consequently, their null and alternative hypothesis statements.

In the familiar superiority design, in its simplest case, the purpose is to ascertain that the treatment of interest (TX) is better than the control treatment (e.g., placebo or another available treatment). Hence, we place that statement in the alternative, and the null hypothesis statement is that there is no difference between the treatments. In the non-inferiority design, which is often used in the phase III or IV comparative effectiveness trials, the purpose is to show that the TX is no worse than the active treatment currently in use (e.g., standard of care; same drug but in a different formulation). Hence, the null hypothesis states that the TX performs worse than the comparator. For the futility design, which is generally applied in the phase II stage of the TX development, the alternative statement reflects that the TX does *not* show sufficiently large treatment effect over the other (e.g., placebo or another available treatment) such that it would be futile to continue its development. The failure to reject the null hypothesis infers that the TX *may* have some promise.

The rejection of the null hypothesis under a superiority or non-inferiority design is a positive outcome for the TX and negative in a futility design but that which the study aims to show. Regardless, the choice of the alpha level must take into account the interpretation of what it stands for, and 0.05 may not necessarily be the best criterion. Concurrently, the choice of the beta level requires similar attention. The presentation will elaborate on some different scenarios that may lead to considerations of alpha levels that may or should not be 0.05.

Title:

# A Multivariate Generalized Linear Mixed Model for Joint Modeling of Cognitive and Neuroimaging Outcomes

Authors:

**Mulugeta Gebregziabher[1], Carter Allen, Daniel Baer, Aastha Khatiwada, Virginia Shipes, Abeba A Teklehaimanot, Philip S. Insel**

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Abstract:

The Alzheimer's Disease Neuroimaging Initiative (ADNI) captures longitudinal multivariate cognitive and imaging data of inherent complexity (between outcome correlations and within subject correlation of longitudinal measurements taken at subject-specific time intervals). However, a common method to analyze these types of data is to fit each outcome separately using a generalized linear mixed model (sGLMM), which ignores these between outcome correlations – a characteristic inherent to cognitive and imaging data. To address the limitations in existing methods, we propose a multivariate generalized linear mixed model (mGLMM) and assess its performance. We demonstrate a novel application of mGLMM in modeling multiple longitudinal outcomes (mix of cognitive and neuroimaging) from ADNI to study the difference in the trajectory of these outcomes by patient apolipoprotein epsilon 4 allele *APOE(*ε4) and amyloid beta (Aβ) negativity status adjusting for age, sex, and education. We use eight outcomes that were measured longitudinally at baseline and every 4-6 months at 8 consecutive visits. To discern the optimal specification of the mGLMM, we vary its specification to include either independent, shared or separate random effects across outcomes, as well as either conditional independence or a dependence covariance structure within outcomes either homogeneously or heterogeneously specified across all eight outcomes. Model fitting was performed using a novel application of the GLIMMIX procedure included in SAS 9.4, and model performance was determined on the basis of a variety of information criteria. Multiple imputation was performed to address missingness in these data, and parameter estimates were combined across imputations using standard procedures. We found that the mGLMM with shared random intercepts and a heterogeneous dependence covariance structure across outcomes fit our data best according to all available fit statistics. Furthermore, we found that the only exposure effect that was consistently significant across our mGLMM model variants was the main effect of Aβ negativity status. We failed to detect a significant interaction between Aβ negativity and *APOE(*ε4) status. Thus, we conclude that the sharing of random effects across outcomes in the mGLMM framework is advantageous in modeling these ADNI data, and that Aβ negativity status (irrespective of time and *APOE(*ε4) status) is significantly associated with ADNI patient cognitive status. Our proposed methods are applicable to a wide variety of multivariate longitudinal settings.

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| Title: | **Improving the reproducibility of image manipulation: Using journaling to track the process** |
| Authors: | **Paul A. Thompson and Norm Matloff** |
| Affiliation: | University of South Dakota (Sioux Falls, SD, USA) and<br>University of California (Davis, CA, USA) |
| Abstract: | The reproducibility of scientific research is a key component of science. Reproducibility reduces fraud, increases efficiency, and improves scientific rigor. In analysis of data, reproducibility is achieved by the use of written programs for data analysis, rather than the use of interactive tools. In image manipulation, this has been traditionally less available. Interactive tools (i.e., GIMP, Photoshop, Lightroom) are generally used, and the process is done interactively. This leads to image fraud and to the lack of reproducibility. Several years ago, a small grant was awarded from the Office of Research Integrity, a component of NIH (National Institutes of Health). The outcome of the grant will be discussed, the methods will be demonstrated, and the successful conclusion of the grant discussed. |

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| Title: | **Meta-analysis in agricultural sciences: Guidelines with novel ME-MetaPCA** |
| Authors: | **Borut Bosancic[1], Marija Pecina[2]** |
| Affiliation: | [1]Faculty of Agriculture University of Banja Luka<br>[2]Faculty of Agriculture University of Zagreb |
| Abstract: | Usefulness and validity of meta-analysis largely depends both on data quality as well as on following specific rules and procedures which ensures the high quality output. Although there are continuously developing up-to-date guidelines for fields of medical and environmental sciences, there is a scarce amount of studies conducted and published in this field for the agricultural sciences. There are series of obligatory steps that have to be made in order to conduct a valid meta-analysis. Those steps and procedures are drawn in combination from literature sources and practical expertise of meta-analysis in agriculture. Numerous literature sources from developed scientific fields are used as the basis while practical expertise and experience is drown from a number of meta-analysis in field of agriculture that were practically conducted with both simulated and real research data. There are following key elements to every published meta-analysis – structure and procedure. In this study both are developed to suit agricultural research and researchers with their typical data. Specific effort is made to explain novel multivariate technique of Main Effects Meta Principal Components Analysis (ME MetaPCA) as a tool of choice for analysis of complex but for agricultural research typical high dimensional multivariate dataset with multilayer variability consisted of multiple characteristics in multiple varieties measured across multiple scales. We are aware that no guidelines are either exhaustive or final. With that in mind here they are presented comprehensively as a part of the pioneering effort in the direction of unbiased systematic structured reviewing of agricultural experimentation results as an invaluable part of the decision making process. |

Title:

# Do We Influence Students' Attitudes toward Statistics?

Authors:

**Šimić Diana, Gusić Jelena**

Affiliation:

University of Zagreb, Faculty of Organization and Informatics
Pavlinska 2, HR-42000 Varaždin, Croatia

Abstract:

Students' responses to Survey of Attitudes Toward Statistics (SATS-36, Schau, 2003) were collected during the first and the last week of the course Statistical Data Analysis at graduate study of Economics of Entrepreneurship at the Faculty of Organization and Informatics, University of Zagreb during the academic year 2018/19. There were 55 students enrolled in the course, and 51 responded to both pre- and post- survey.

Students' feeling toward statistics (*Affect*) were positive at the beginning of the course, and significantly decreased at the end of the course.

Students' attitudes about their intellectual knowledge and skills (*Cognitive Competences*) were also positive at the beginning, but they did not change after the course.

Attitudes toward *Value* of statistics started neutral and significantly increased at the end of the course.

Attitudes toward Difficulty were highly positive (students expected statistics to be easy), but decreased significantly at the end of the course.

At the beginning of the course, students' level of *Interest* in statistics was low, but it increased significantly at the end of the course.

Students' attitude toward amount of work (*Effort*) was positive at the beginning of the course, and still increased significantly at the end of the course.

Only attitude about *Cognitive Competence* did not change during the course. *Affect* and *Difficulty* decreased, while *Value*, *Interest*, and *Effort* increased.

References

Schau C, Emmioğlu E (2012) Do introductory statistics courses in the United States improve students' attitudes? Statistics Education Research Journal 11(2): 86-94. Retrieved from http://iase-web.org/documents/SERJ/SERJ11(2)_Schau.pdf.

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| Title: | **My forest for me is…? Building private forest owners′ objectives network** |
| Authors: | **Marijana Žunić,** PhD<br>Assistant Professor **Krunoslav Teslak** |
| Affiliation: | Faculty of Forestry, Department of Forest Inventory and Management |
| Abstract: | The general hypothesis is that private forest owners (PFO) are multiobjective favouring both monetary and amenity values toward their forest property. Hence, this study examined how multiple PFO objectives are interrelated in a network and how they mutually interact. Network analysis offers a different conceptual interpretation of data via direct relationships between observed variables. Firstly, PFO were randomly surveyed in Forestry Advisory Services around Croatia and a sample of 442 responses was achieved. The structured face-to-face interview was chosen as the most suitable method for obtaining the informations about meanings that PFO attach to ownership. They were provided with 22 different objectives for ownership and asked to rate the importance for each item on a scale from 1 (not important at all) to 5 (very important). Secondly, undirected network structure was estimated by computing Gaussian graphical model (GGM) with LASSO regularization. After network visualisation, inference methods like edge weights and centrality indices (betweenness, closeness and strength) were assessed. Also, community analysis examined if the network contains clusters. The network robustness were checked by non-parametric bootstrapping (edge weight bootstrap and subset bootstrap). All statistical analysis were performed in R programming software within the corresponding packages *qgraph, bootnet, EGA* and *lasso*. Lastly, results showed a strongly connected network of PFO objectives. A community analysis revealed three larger clusters of strongly related items which were labeled as conservation and recreation, economic interests and family heritage. Also, clusters are connected by bridges implying a strong global connectivity of the PFO objectives network. Bootstrap analysis confirmed that centrality measures for betweenness and closeness are not stable under subsetting cases, while order of nodes strength are interpretable ($r > 0.5$). Therefore, bearing in mind strength centrality, the most central node is: *My forest is an object for nature protection and conservation*. This study provides a new insight into a complex nature of PFO objectives representing them within a strongly connected network structure. |

Title:

# Principal component regression vs. partial linear squares regression in prediction modelling

Authors:

**Tamara Jurina[1], Adela Šain[1], Davor Valinger[1], Jasenka Gajdoš Kljusurić[1], Maja Benković[1], Ana Jurinjak Tušek[1], Želimir Kurtanjek[1], Vesna Antoška Knights[2]**

Affiliation:

1 University of Zagreb, Faculty of Food Technology and Biotechnology, Croatia
2 University St. Kliment Ohridski, Faculty of Technology and Technical Sciences, Bitola, Macedonia

Abstract:

Principal component regression (PCR) and partial least squares regression (PLSR) are mostly used multivariate analysis tools in the chemometrics. Challenge is to analyse superiority of one over another. As example herbal extract of melissa was used in this study. On melissa extract samples spectra analysis (Ultraviolet–visible spectroscopy, UV-VIS and near infrared spectroscopy, NIR) and the content of total phenols (TP) were performed.

The UV and NIR absorbance spectra of the aqueous extracts were gathered at three temperatures (T = 40, 60 and 80°C) in time interval from 0.5 to 90 min and were subject of PCR and PLS models. Models were tested for UV spectra range, for NIR spectra range and for the UV+NIR spectra range and the models refinement procedure and validation was performed by cross-validation. For the model efficiency analysis parameters as R-squared, root mean squared error of prediction RMSE, adjusted R2, Ratio of standard error of Performance to standard Deviation (RPD) and the Range Error Ratio (RER) were used. R2is describing how well the experimental data fit the statistical model. RMSEP is used as the measure of the average accuracy of the prediction. The accuracy of the model is also compared on the basis of adjusted R2 in order to regulate the number of model parameters for the available spectra. The R2, RER and RPD are dimensionless, meaning that they can be compared on the same basis between models for different constituents/properties allowing model efficiency assessment. Higher RPD and RER values suggest more accurate models. Values of RPD and RER less then 3 and 10, respectively, are an indication of qualitative models; while models with higher values are considered even to be used in quantitative prediction.

When the selected wavelength region of UV-VIS and NIR were used separately, the PLS produced slightly better results (R2UV-VIS=0.973, RPDUV-VIS=6.123, RERUV-VIS=22.236) with RMSE=4.800. For the combined spectral range of UV-VIS and NIR (325-1699 nm) the PCR model produced better results (R2=0.999, RPD=3.138, RER=13.200 with the RMSE=11,877). To comment the superiority of one model over another is not an easy task, because the dimensionless parameters and error(s), RMSE, did not show exactly the same trend. The R2was higher for the model with higher RMSE. The major difference between PLSR and PCR was in obtaining the higher number of factors for PCR, which is not a significant problem.

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| Title: | **Capturing clustering structure of the data in cross-language representation of textual documents** |
| Authors: | **Jasminka Dobša** |
| Affiliation: | Faculty of Organization and Informatics, University of Zagreb |
| Abstract: | Here we propose a new approach for representation of textual documents in lower-dimensional space. Approach aims at capturing clustering structure of the data in the goal of further application for cross-language classification of textual documents. The proposed approach is based on factorization of a term-document matrix by an iterative method of Reduced *k*-means clustering. Method of Reduced *k*-means aims at simultaneous reduction of objects (documents) and variables (index terms). Proposed method is compared to standard machine learning techniques of cross-language representation of textual documents by usage of latent semantic indexing and canonical correlation analysis. |

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| Title: | **Comparison of different sessile oak planting techniques after windthrow in Norway spruce artificial stands** |
| Authors: | **Đodan Martina, Perić Sanja** |
| Affiliation: | Croatian Forest Research Institute |
| Abstract: | Damages caused by negative forcing of diverse biotic and abiotic influences (e.g. bark beetles, ice loads, windthrow) in artificial Norway spruce (Picea abies /L./ Karst.) stands constantly increase. In addition, it is predicted that they will even increase in the forthcoming decades. Direct consequences for forest management are significant financial and ecological losses, which makes the management of these forests complex and demanding. Taking into account the fact that ecological degradation starts soon after canopy cover is lost, the post-disturbance areas should be reforestated immediately after disturbance takes place. Unsuccessful reforestation, besides further commercial losses, results with site degradation in such matter that further reforestation would be restricted to the use of less desired tree species and more challenging silvicultural methods (e.g. higher cost of tending activities). Despite the fact that there are early successional tree species which can provide fast and efficient reforestation (e.g. birch, sycamore maple), their commercial and biological value is lower than those of late successional and commercially more interesting tree species. Such important native tree species, which is crucial part of natural species composition of hilly areas of Central Croatia is sessile oak. Thus, there was a need to study the post-planting success of Sessile oak seedlings. The trial plots are set on locality in central Croatia in a Latin square research design. Three different planting methods are studied (control treatment, moulding and removal of litter). Seedlings were marked individually and measured in four consecutive years after planting (2010 – 2013) and again in seventh year (2017) after planting. Data were analysed using Statistica soft. Repeated measures ANOVA showed significant differences both in terms of treatments and interaction treatments x years. Data analysis revealed that selection of planting method has important influence on post-planting growth and development. The best method was moulding, followed by removal of accumulated litter, so these methods are strongly advised to be used in reforestation practices in Central Croatia in the future. |

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| Title: | **Classification of dentists in Slovenia based on their availability** |
| Authors: | **Maja Buhin Pandur, Jasminka Dobša** |
| Affiliation: | Faculty of Organisation and Informatics, Varaždin |
| Abstract: | Human resource management is crucial for the organisation of the health care system. This research aims at a prediction of availability of the dentists in regions of Slovenia. The data for analysis is collected from the Health insurance institute of Slovenia (ZZZS), which publishes a list of active dentists, and the Statistical Office of the Republic of Slovenia. A dentist who has a contract with the ZZZS and meets the conditions for the selected dentist is obligated to accept every insured person who chooses him/her as a dentist. Insured persons can be rejected when the number of patients for a chosen dentist exceeds allowed number of patients by 10% (index is higher than 110). The allowed number of patients is defined by ZZZS for a local unit where the business is based. In this research, we are dealing with problematic of predicting the availability of dentists based on the variables of the number of patients per dentist, regions of Slovenia, type of health care activity and patients age. For the prediction, we will use methods of logistic regression and decision tree. |

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| Title: | **Frequency phobia *vs*. probability blindness** |
| Authors: | **Roberto Mužić, Slavica Sović, Zdenko Sonicki** |
| Affiliation: | School of Medicine University of Zagreb, Croatia |
| Abstract: | |

# STUDENT SESSION

Title:

# Overview Of Methods For Meta-analysis

Authors:

**Lara Rajković**

Affiliation:

Faculty of Science - Mathematics, University of Zagreb
Graduate study of Mathematical Statistics

Abstract:

Meta-analysis is commonly used statistical technique for combining the results from multiple studies with the same objective. The estimate obtained by meta-analysis should be more precise than the estimates in the individual studies and the statistical power should be increased. Quality of the meta-analysis depends on the careful planning and data collection but also on the adequate statistical methods. The researchers can do aggregate data (AD) meta-analysis or individual participant data approach (IPD). IPD meta-analysis is considered to be 'gold standard', but it costs more and usually takes longer so AD meta-analysis is more common. The models that can be used in AD meta-analysis are fixed-effects model and random-effects model. The original DerSimonian and Laird random-effects model is the most widely used, but alternative random-effects models are being provided. In this overview the difference between fixed-effects and random-effects model is explained with examples and some random-effects models are given and explained. Incorporating heterogeneity of different studies into the model, one of the issues of meta-analysis, is discussed.

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| Title: | **Heatmap analysis of emergency patients flow at the University Hospital Centre Zagreb** |
| Authors: | **Igor Radanović[1], Deni Rkman[1], Kristian Dominik Rudež[1], Igor Milovčić[2], Ivan Horvat[2], Robert Likić[1,2]** |
| Affiliation: | [1] – School of Medicine, University of Zagreb<br>[2] – University Hospital Centre Zagreb |
| Abstract: | **INTRODUCTION:** There is an ever-increasing burden on Emergency Departments (ED), regarding the patient demand and insufficient staff members, but also because of the present lack of financial resources. The patterns of patient arrival differ throughout the day and have seasonal variations as well, thus spotting and analysing patterns of demand can be very valuable in assisting clinical managers and hospital administration so that resources can be allocated more efficiently. We aimed to develop a descriptive heatmap analysis and investigate patterns of patient flow at the Department of Emergency Medicine of the University Hospital Centre Zagreb (UHC Zagreb), the largest health institution and university hospital in the Republic of Croatia.<br>**METHODS:** Anonymized administrative data was obtained from the UHC Zagreb ED registries from January 2013 to March 2019 and analysed with Tableau software. The outcome of interest was monthly average number of ED visits per hour and average number of visits per day of the week. Group of underage patients was analysed independently in order to detect differences in arrival times compared to adult patients.<br>**RESULTS:** Heatmap for the average monthly number of adult ED arrivals per hour showed an increase in patient arrival rate between 08.00 and 20.00 hours, with the maximum peak between 9.00 and 11.00 (average of 18.9 arrivals per hour). Arrival rate was stable during night periods, while most adult ED arrivals occurred on Monday, with an average of 282 patients. Significantly less visits happened during the weekends. On the other hand, heatmap for the average monthly number of underage ED arrivals showed a gradual rise between 10.00 and 22.00, with highest numbers of arrivals happening between 17.00 and 21.00 hours, except in July and August. Additionally, seasonal variations were also present in adult population, with fewer patient arrivals during the months of July and August. Finally, in contrast to adults, most underage ED arrivals happened on Sunday, followed by Saturday.<br>**CONCLUSION:** The heatmap analysis allowed patterns of patient arrival in ED to be spotted and analysed more efficiently. There are daily and seasonal variations of ED visits, both for underage and adult population, with some distinct variations between the two. Furthermore, heatmap analyses that incorporate not only the arrival rate, but also the length of patient stay in ED should be used more frequently for improved resource allocation and appropriate staffing during the periods with higher activity. |

Title:

# Evaluation of mental health workshops in a sample of Croatian secondary-school adolescents

Authors:

**Kristina Stamenković[1], Katarina Skopljak[2]**

Affiliation:

[1] School of Medicine University of Zagreb, Croatia
[2] Psychiatric Hospital „Sveti Ivan“, Zagreb, Croatia

Abstract:

Introduction: In order to take an active role in improvement of youth mental health care Croatian Medical Students’ Association in collaboration with City Office for Health in Zagreb and Regional Health Center Zagreb - West started a project on mental health promotion. Project is based on peer education, with previously educated students conducting workshops in high schools, in order to emphasize the importance of early prevention and mental health promotion.

Methods: As a part of the project prospective multicenter one-group pre-post evaluation study was performed on the cluster sample of Croatian secondary-school adolescents who underwent the series of 8 workshops. The primary outcome measure was the change of ratio of private and public self-consciousness measured using the Private self-consciousness scale (Huic, 2009). Secondary outcomes were private self-consciousness scales focus on emotions, cognitions and body.

Results: Two thirds, 174 (38.2%) of enrolled pupils were boys, and 365 (78.8%) were in the 3rd class with the median age of 17 years. After the adjustment for gender, school and class, the change of ratio to private self-consciousness after the workshops was not significant ($\Delta=0.11$; $CI_{95\%}$ 0.05-0.20; $p=0.720$). However, we observed the significant changes of particular sub-scales results. Private self-consciousness increased for 4 ($CI_{95\%}$ 2-5) percentage points ($\eta^2=0.02$; $p_{corrected}=0.020$), emotions private self-consciousness for 5 ($CI_{95\%}$ 3-6) percentage points ($\eta^2=0.02$; $p_{corrected}=0.015$), cognitions private self-consciousness for 3 ($CI_{95\%}$ 2-5) percentage points ($\eta^2=0.02$; $p_{corrected}=0.015$), and body private self-consciousness for 5 ($CI_{95\%}$ 3-7) percentage points ($\eta^2=0.01$; $p_{corrected}=0.038$). Increase of ≥10% in the overall private self-consciousness was experienced by 164 (35.4%; $CI_{95\%}$ 30.9%-39.7%) of participants. Subjective evaluation of the workshops was good: 82.2% ($CI_{95\%}$ 81.0%-83.6%) of participants were “mostly” or “very satisfied”, and 78.5% ($CI_{95\%}$ 77.1%-79.9%) though they were “mostly” or “very useful”.

Conclusion: Our evaluation indicated good outcomes of the peer workshops in a sample of Croatian secondary-school adolescents, and the participant's satisfaction, showing that peer education should be considered as a powerful framework for active involvement in improvement of youth mental health care, in collaboration with mental health services and efforts from teachers and parents. However, we need to employ the outcome measures of better metric characteristics, collect more data and control a numerous possible confounders in the next wave of workshops.