# BIOSTAT 2014

## 21st International Scientific Symposium on Biometrics

## BOOK OF ABSTRACTS

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

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osnovano 1989.

BOOK OF ABSTRACTS

# BIOSTAT 2014

**21st International Scientific Symposium on Biometrics**

Dubrovnik, Croatia, **11 - 14 June 2014**

**EDITORS:**


Anamarija Jazbec
Marija Pecina
Zdenko Sonicki
Diana Šimić
Mislav Vedriš



Zagreb, 2014.

IMPRESSUM

# BIOSTAT 2014

## 21st International Scientific Symposium on Biometrics

Dubrovnik, Croatia, **11 - 14 June 2014**

ORGANISER
Croatian Biometric Society

UNDER THE AUSPICES of the
University of Zagreb

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### 19th SCHOOL OF BIOMETRICS

Kent Eskridge
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### KEYNOTE LECTURES

Ingram Olkin
Stanford University, USA

Amanda L. Golbeck
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### PUBLISHER:

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# BIOSTAT 2014

**21st International Scientific Symposium on Biometrics**

Dubrovnik, Croatia, **11 - 14 June 2014**

Welcome to the Book of Abstracts of BIOSTAT 2014 – The 21st International Scientific Symposium on Biometrics organized by the Croatian Biometric Society in Dubrovnik, Croatia, June 11 – 14, 2014.

BIOSTAT 2014 comprises keynote lectures, 19th School of Biometrics, contributed papers and software presentations. This brochure contains 21 abstracts written by 44 authors from five countries – Bosnia and Herzegovina, Croatia, Slovenia, Sweden and United States of America.

Symposium is organized under the auspices of the University of Zagreb in its Centre for Advanced Academic Studies (CAAS) in Dubrovnik.

This year marks the 25th anniversary of the Croatian Biometric Society. After organizing 18 Schools and 20 BIOSTATs within ITI – International Conference on Information Technology Interfaces – we have come of age and this is the first year in which BIOSTAT and the School are held as independent events. We appreciate the support and hosting provided to the Symposium and the School by the University Computing Centre of the University of Zagreb. Without the ITI's stimulating environment BIOSTAT and the School of Biometrics would not have become what they are now.

Topic of the 19th School of Biometrics is:

Causal Modeling presented by the invited lecturer
Professor Kent Eskridge (University of Nebraska – Lincoln, USA).

This year we have two keynote lectures:

Professor Emeritus Ingram Olkin (Stanford University, USA):
Multivariate Analysis Meta-Analysis (MAMA)

Professor Amanda L. Golbeck (University of Montana, USA):
Statistician Elizabeth L. Scott's Advocacy Leadership for Social Change

We thank Ministry of Science, Education and Sports of the Republic of Croatia and Hrvatske šume d.o.o. for financial support and SAS Institute Inc. for silver sponsorship.

We hope to share with you pleasant moments, lively discussions, successful networking and forge new partnerships and friendships.

Editors:
Anamarija Jazbec, Marija Pecina, Zdenko Sonicki, Diana Šimić and Mislav Vedriš
Zagreb, June, 2014

# BIOSTAT 2014

## 21st International Scientific Symposium on Biometrics

Dubrovnik, Croatia, **11 - 14 June 2014**

## SYMPOSIUM PROGRAM At Glance

| hour | Wednesday, June 11 | Thursday, June 12 | Friday, June 13 | Saturday, June 14 |
|---|---|---|---|---|
| 9:00 – 10:30 | | School of Biometrics<br><br>Kent Eskridge<br>„Causal Modeling“<br><br>Chair: Marija Pecina | Contributed session<br>Group 2<br><br>Chair: Diana Šimić | Contributed session<br>Group 4<br><br>Chair: Marija Pecina |
| 10:30 – 11:00 | | COFFEE BREAK | COFFEE BREAK | COFFEE BREAK |
| 11:00 – 12:00 | | School of Biometrics<br><br>Kent Eskridge<br>„Causal Modeling“<br><br>Continuation | Keynote Lecture<br><br>Ingram Olkin<br>„Multivaria te Analysis<br>Meta-Analysis (MAMA)“<br><br>Chair: Diana Šimić | Contributed session<br>Group 5<br><br>Chair: Katarina Košmelj |
| 12:00 – 12:45 | | Chair: Marija Pecina | Keynote Lecture<br>Amanda L. Golbeck<br>„Statistician<br>Elizabeth L. Scott[1]s<br>Advocacy Leadership for<br>Social Change“<br><br>Chair: Anamarija Jazbec | Closing Ceremony |
| 12:45 – 13:00 | | Vesna Lužar-Stiffler<br>SAS presentation | | |
| 13:00 – 14:00 | | LUNCH BREAK | LUNCH BREAK | |
| 14:00 – 15:30 | | Contributed session<br>Group 1<br><br>Chair: Zdenko Sonicki | Contributed session<br>Group 3<br><br>Chair: Nancy Flournoy | |
| 15:30 – 16:00 | | COFFEE BREAK | COFFEE BREAK | |
| 16:00 – 17:00 | | ISPC Meeting | HBMD 25th Anniversary ceremony | |
| 17:00 | Registration | | HBMD Silver Anniversary Dinner | |
| 18:00 | Opening Ceremony<br>Welcome Cocktail | | | |

Presentation time (with discussion): 15 + 5 min.

# BIOSTAT 2014

## 21st International Scientific Symposium on Biometrics

Dubrovnik, Croatia, **11 - 14 June 2014**

## SYMPOSIUM PROGRAM In Detail

| | | | |
|---|---|---|---|
| Wednesday June, 11 | 17:00 | Registration | |
| | 18:00 | Opening Ceremony<br>Welcome Cocktail | |
| Thursday, June, 12 | 9:00 – 10:30 | Chair: Marija Pecina<br><br>Kent Eskridge | School of Biometrics:<br><br>Causal Modeling<br>Part 1 |
| | 10:30 – 11:00 | COFFEE BREAK | |
| | 11:00 – 12:45 | Chair: Marija Pecina<br><br>Kent Eskridge | School of Biometrics:<br><br>Causal Modeling<br>Part 2 |
| | 12:45 – 13:00 | Vesna Lužar-Stiffler | Silver Sponsor Presentation:<br>SAS |
| | 13:00 – 14:00 | LUNCH BREAK | |
| | 14:00 - 15:30 | Chair: Zdenko Sonicki | Contributed session: GROUP 1 |
| | | AUTHOR | TITLE |
| | | Bethany J. Wolf, Sybil Prince-Nelson, Viswanathan Ramakrishnan | C.Logic: A Statistical Algorithm for Discovering Interactions that Lead to Disease Susceptibility |
| | | Viswanathan Ramakrishnan, Jessica M. Ketchum | A Within Subjects Normal-Mixture Model with Random Effects |
| | | Patrik Waldmann | SIS-BEN: an efficient two-stage approach for high dimensional analysis of correlated data |
| | | Paul J Nietert | The Art of Biostatistical Collaboration in the Era of Team Science |
| | 15:30 – 16:00 | COFFEE BREAK | |
| | 16:00 – 17:00 | ISPC Meeting | |
| Friday, June, 13 | 9:00 - 10:30 | Chair: Diana Šimić | Contributed session: GROUP 2 |
| | | AUTHOR | TITLE |
| | | Biserka Kolarec | Denying the bell curve |
| | | Želimir Franjo Kurtanjek, D. Horvat, G. Drezner, D. Magdić | Statistical estimators of Croatian wheat cultivar properties |
| | | Janez Stare, Nataša Kejžar | On bias of measures of explained variation in survival analysis |
| | | Nancy Flournoy | Sequential Dose-finding Designs for Binary Responses for Bioassays and Clinical Trials |
| | 10:30 – 11:00 | COFFEE BREAK | |
| | 11:00 – 12:00 | Chair: Diana Šimić<br><br>Ingram Olkin | Keynote Lecture:<br>Multivariate Analysis Meta -Analysis (MAMA) |
| | 12:00 – 13:00 | Chair: Anamarija Jazbec<br><br>Amanda L. Golbeck | Keynote Lecture:<br>Statistician Elizabeth L. Scott[1]s Advocacy Leadership for Social Change |
| | 13:00 – 14:00 | LUNCH BREAK | |

| | | | |
|---|---|---|---|
| Friday, June, 13 | 14:00 - 15:30 | Chair: Nancy Flournoy | Contributed session: GROUP 3 |
| | | AUTHOR | TITLE |
| | | Ksenija Baždarić, Martina Mavrinac, Vanja Pupovac, Lidija Bilić-Zulle, Gordana Brumini, Mladen Petrovečki | Measuring Prevalence and Characteristics of Scientific Plagiarism: Design of the Study |
| | | Tomislav Meštrović, Zdenko Sonicki, Ivica Premužić Meštrović, Mladen Petrunić | Data mining methods for predictive modelling based on small samples in surgery |
| | | Ivan Kovač, Jasminka Dobša, Jelena Gusić | Modeling of nitrate concentrations in alluvial groundwater aquifer |
| | | Lavoslav Čaklović | Early recognition of Alzheimer Disease |
| | 15:30 – 16:00 | COFFEE BREAK | |
| | 16:00 – 17:00 | HBMD 25th Anniversary Ceremony | |
| | 17:00 | HBMD Silver Anniversary Dinner | |
| | | | |
| Saturday, June, 14 | 9:00 - 10:30 | Chair: Marija Pecina | Contributed session: GROUP 4 |
| | | AUTHOR | TITLE |
| | | Vesna Lužar-Stiffler | Procedures for Assessing Population Bioequivalence Modified to be One-Sided with Respect to Mean Comparison |
| | | Lavoslav Čaklović | Structure Equation Model of the Heptathlon |
| | | Andrijana Rebekić, Zdenko Lončarić, Sonja Petrović, Sonja Marić | Comparison of Pearson's and Spearman's correlation coefficients for grain cadmium concentration and agronomic traits in winter wheat genotypes |
| | | Nikola Mićić, Jasmin Komić, Borut Bosančić | Biometrical analysis in between the descriptive and the inferential mathematical-statistical approach |
| | 10:30 – 11:00 | COFFEE BREAK | |
| | 11:00 – 12:00 | Chair: Katarina Košmelj | Contributed session: GROUP 5 |
| | | AUTHOR | TITLE |
| | | Sanja Perić, Martina Tijardović | Structural parameters analysis of forest cultures in Croatia |
| | | Anamarija Jazbec, Damir Ugarković, Mislav Vedriš | Analysis of defoliation using logistic regression model with ordinal response |
| | 12:00 – 13:00 | Closing Ceremony | |
| | | | |

See you next year on

BIOSTAT 2015

**22nd International Scientific Symposium on Biometrics**

Dubrovnik, Croatia, **28 - 30 June 2015**

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BIOSTAT 2014

**21st International Scientific Symposium on Biometrics**

Dubrovnik, Croatia, **11 - 14 June 2014**

# 19th SCHOOL OF BIOMETRICS

## 19th SCHOOL OF BIOMETRICS

**Kent Eskridge**

University of Nebraska - Lincoln, USA

http://statistics.unl.edu/people/staff/faculty/eskridge.shtml

Topic:

# Causal Modeling

Abstract:

Interest in modeling causal structures has grown in recent years simulated primarily by increasing data availability. One of the most important contributions of modern statistics is the randomized trial which has had an enormous scientific impact in establishing causal relationships. However, application of randomized trials is limited to situations where the researcher has control over the experimental factors and the primary focus is how the factors affect a single response variable.

Statistical methods have not been as successful when either the researcher does not have control over the "treatment" factors and/or there are multiple response variables with likely causal relationships. The purpose of this work will be to present some recent developments applicable under one or both of these situations.

Specifically, I will

(1) discuss the identification and analysis of causal structures when the response variables are causally related and

(2) describe methods useful when the researcher does not have control over the factors of interest and must rely on observational data.

I will illustrate the approaches with actual data and present software that will aid with the application of these methods.

BIOSTAT 2014

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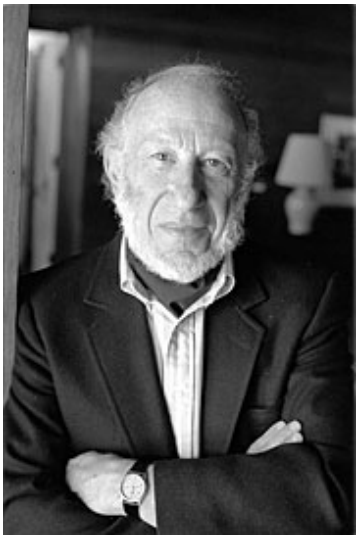
Dubrovnik, Croatia, **11 - 14 June 2014**

# KEYNOTE LECTURES

## KEYNOTE LECTURE



**Ingram Olkin**

Stanford University, USA

http://arxiv.org/pdf/0802.0557.pdf

Topic:

# Multivariate Analysis Meta-Analysis (MAMA)

Abstract:

Meta-analysis refers to the methodology for combining the results of independent studies. Historically this goes back to R.A. Fisher who provided a method for combining p-values. Later the methodology turned to combining other metrics such as proportions, standardized mean differences, regressions, correlations to mention but a few. The early models were simple two-arm comparisons of treatment and control.

However, as data has become more extensive and available, the models and their analyses have become more complex. One current general model is that of a network meta-analysis in which there are multiple comparators. We can think of this as an analysis of the various anti-depressants in which various comparisons have been made. Another thrust is that of multivariate models in which there are multiple outcomes that are related. In this talk I will try to walk through the history of these models with examples and methods for analyzing multivariate meta-analyses.

## KEYNOTE LECTURE

**Amanda L. Golbeck**

University of Montana, USA

http://publichealth.health.umt.edu/Faculty/Faculty%20and%20Staff.php?ID=2898

Topic:

# Statistician Elizabeth L. Scott's Advocacy Leadership for Social Change

Abstract:

Statistics leaders advance the quality of research methods or outcomes in a broad spectrum of disciplines from medicine to astronomy to economics, make others better as a result of their presence, and make sure their positive impact on both people and science lasts in their absence. University of California - Berkeley Statistics Professor Elizabeth L. Scott (1917-1988) was a statistics leader by this definition. Her legacy continues in the form of the Elizabeth L. Scott Award, administered by the Committee of Presidents of Statistical Societies (COPSS). While Scott at times led from within titled positions in the university or professional associations, she was at her best when she exercised natural leadership based on pure influence toward solving societal problems, especially problems surrounding the status of women in academe. In this talk I will explore some of the qualities and behaviors of Scott that made her an effective natural leader and prominent role model for future generations, and I will note the potential for all statisticians to develop their leadership and increase their positive impact in their workplaces and communities.

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# CONTRIBUTED SESSIONS

| | |
|---|---|
| Title: | C.Logic: A Statistical Algorithm for Discovering Interactions that Lead to Disease Susceptibility. |
| Authors: | Bethany J. Wolf, Sybil Prince -Nelson, Viswanathan Ramakrishnan |
| Affiliation: | Medical University of South Carolina, Department of Public Health Sciences |
| Abstract: | Predicting patients' disease risk, disease severity, or response to treatment often necessitates modeling complex interactions among genetic and environmental factors. Traditional statistical methods such as logistic regression require specifying interactions a prior making it difficult to identify higher-order interactions such as those that might describe disease status. Additionally sufficient sample size must be available to model interactions and their main effects. Classification and Regression Trees (CART), a non-parametric tree-based method, is capable of modeling complex interactions among predictors. However, CART is biased towards inclusion of continuous predictors in the model. Logic regression (LR) is an alternative tree-based method capable of modeling disease status using Boolean combinations of binary predictors. In scenarios where all predictor variable are binary, LR exhibits superior ability to correctly identify interactions associated with an outcome relative CART. However, LR as currently implemented cannot incorporate continuous predictors in the model. We extend LR to allow for incorporation of continuous covariates by identifying appropriate cut points for all continuous covariates and then applying LR to the fully dichotomized data. The resulting method is called C.Logic. We conduct a simulation study comparing the ability of C.Logic and CART to correctly identify interactions among binary and continuous predictors associated with a binary outcome. Our simulation results indicate that C.Logic is superior to CART for identification of interactions between binary and continuous variables. C.Logic is also applied to data from a study to determine associations between genetic and health factors with periodontal disease. |

| | |
|---|---|
| Title: | A Within Subjects Normal-Mixture Model with Random Effects |
| Authors: | V. Ramakrishnan and Jessica M. Ketchum |
| Affiliation: | Medical University of South Carolina and Virginia Commonwealth University |
| Abstract: | Data on Heart Rate Variability (HRV) have been used extensively to indirectly assess the autonomic control of the heart. The distributions of HRV measures, such as the RR-interval, often exhibit a bimodality, which is not adequately accounted for in current statistical analyses, especially in models that include random effects. In this presentation, a mixed-effects modeling approach under the assumption of a two-component normal-mixture distribution for the within-subject observations is proposed. Traditional normal-mixture models impose the mixture normality on the random effects. In our formulation of the mixed effects model the errors (R-side rather than G-side) are assumed to be normal-mixtures. Estimation of the parameters of the model can be performed through an application of the EM algorithm, which extends the traditional EM application for the normal-mixture distributions. An application of this method is presented and the results from a simulation study will be discussed. |

| | |
|---|---|
| Title: | SIS-BEN: an efficient two-stage approach for high dimensional analysis of correlated data |
| Authors: | Patrik Waldmann |
| Affiliation: | Division of Statistics, Department of Computer and Information Science, Linköping University, SE-58183 Linköping, Sweden |
| Abstract: | High dimensional data analysis has become a major issue in a range of different scientific fields. Genomic data is often characterized by a huge number of predictor variables measured on a limited number of individuals. Moreover, variables are often correlated following complicated patterns. In these situations, it turns out to be difficult to find a method that provides an optimum between few computational operations and high statistical reliability. Tuning of hyper-parameters in regularized regression tends to be difficult in the frequentist paradigm, and Bayesian methods are often computationally intractable because of the need to iteratively cycle through a large number of variables. A two-stage approach that is computationally efficient and provides very low error rates regarding variable selection is here presented. The first stage is based on the Sure Independence Screening (SIS) technique, which is both fast and well-suited for correlated data. The second stage consist of the Bayesian Elastic Net (BEN) with adaptive regularization parameters. The method is tested on large scale simulated data, and real data from a genome-wide association study. |

Jazbec A, Pecina M, Sonicki Z, Šimić D, Vedriš M, eds. (2014) Book of Abstracts BIOSTAT 2014 – 21st International Scientific Symposium on Biometrics, Dubrovnik 11-14 June 2014. Zagreb: Croatian Biometric Society. ISSN 1849-434X

| | |
|---|---|
| Title: | The Art of Biostatistical Collaboration in the Era of Team Science |
| Authors: | Nietert, Paul J |
| Affiliation: | Medical University of South Carolina |
| Abstract: | Biostatistics is, by definition, interdisciplinary. Successful careers in biostatistics are often built around strong collaborations with clinical investigators. These types of working relationships are being recognized more frequently, now that we are officially in a scientific era in which "team science" is being emphasized. In working with other researchers, however, there is often a tension that arises due the biostatistician being perceived (rightly or wrongly) as a "consultant" instead of a true "collaborator". Consulting tends to involve statistical support with limited interactions between an investigator and a biostatistician to find a solution to a specific problem, whereas collaboration implies a longer term, more mature relationship between the parties. There are strategies that biostatisticians can use to prevent these types of perceptions from occurring and ensure that he/she is a full team member. Pillars of strong collaboration, for example, include having excellent communication skills, developing mutually clear expectations, earning respect and trust, and being productive. There are also means by which leaders of biostatistics departments (or other organizational units) can and should ensure that their faculty members progress within inter-disciplinary research teams, such as recognizing the different career paths of biostatisticians, developing career progression maps (grids), and communicating with other departments about these distinctions. The future of biostatistics is bright, and in becoming stronger collaborators, biostatisticians have excellent opportunities for advancing biomedical science. |

| | |
|---|---|
| Title: | Denaying the bell curve |
| Authors: | Biserka Kolarec |
| Affiliation: | Faculty of Agriculture, University of Zagreb, Croatia |
| Abstract: | Because IQ is distributed roughly normally, most educators expect grades to conform to the normal distribution. But, does the normal distribution of scores indicates that a good job of grading was done? Here we argue that the nature of the bell curve is invalid for grading. We reject norm-referenced approach to grading and speak in favor of criterion-referenced approach instead. Based on our experience in teaching statistics at the Faculty of Agriculture, University of Zagreb we suggest that in fact skewness to the left must be the goal of any educational process. |

| | |
|---|---|
| Title: | Statistical estimators of Croatian wheat cultivar properties |
| Authors: | Želimir Kurtanjek*, Daniela Horvat**, Georg Drezner**, Damir Magdić*** |
| Affiliation: | * University of Zagreb, Faculty of Food Technology and Biotechnology , Pierottijeva 6, Zagreb, Croatia, zkurt@pbf.hr<br>** Agricultural Institute Osijek, Osijek, Južno pregradje 17, Osijek, Croatia<br>***Faculty of Food Technology, Univ. of J.J. Strossmayer, F. Kuhača 17, Osijek, Croatia |
| Abstract: | This study is focused on comprehensive and comparative linear and nonlinear analysis of various classes of statistical predictors of Croatioan wheat cultivar properties. Included are 28 Croatian winter cultivars from the experimental fields of Agricultural Institute Osijek, Croatia , 2 cultivars were selected at Zagreb BC Institute for Breeding and Production of Field Crops in Zagreb, 2 cultivars by the Jošt-Seed Križevci, Croatia, and 4 foreign cultivars from Russia, Hungary, Austria and France which are included into Croatian source of germplasm [1-2]. The cultivars were characterized by several sets of properties, from biochemical level to technological properties and baking quality tests. Measured are chemical quality parameters of flour and grain, farinographic and extensographic parameters, flour yield, bread quality parameters, wheat HPLC gliadins content, SDS-PAGE HMW-GS composition, and GLU-1 score. Tested are statistical predictors based on inputs determined by HPLC data of gliadins content in wheat samples and SDS-PAGE determined high molecular HMW-GS content. Compared are principal component based linear multivariate predictors: principal component regression (PCR) with partial least squares regression (PLS); nonlinear (quadratic) PCR and PLS, decision tree models (DT) and random forest (RF) predictors, artificial neural networks (ANN), Kohonen self organizing map, and the linear algorithm of machine learning vector support machine (SVM). The predictors are tested as regressors of physical dough and technological baking properties, and also as classifiers of cultivars to discriminate between Croatia (Osijek, Zagreb, Križevci) and the foreign cultivars. The predictors are compared based on predicted residual sum of square errors (PRESS) calculated as the sum of squares of the model prediction residuals for experimental observations (for continuous function properties and discrete classifications). Applied is ten fold validation algorithm. Statistical properties of the model residuals are tested in order to evaluate their random character or potentially presence of the model biased predictions. Besides the model error analysis, important attention is focused on the predictor variables global sensitivities and their relative variable importance (VIP) analysis. for dough technological properties and the baking quality indicators. The long term goal of this study is to test and compare different statistical predictors based on biochemical properties for their possible application in improvement in the program of Croatian wheat selection and breeding in the early (pre mass production stage) stage.<br>[1] Ž. Kurtanjek, D. Horvat, G. Drezner, D. Magdić, Acta Alimentaria 42(4 )609-617(2014)<br>[2] D. Horvat, Ž. Kurtanjek, G. Drezner, G. Šimić, D. Magdić, Food Technol. Biotechnol. 47(3) 253-259(2009) |

| | |
|---|---|
| Title: | ON BIAS OF MEASURES OF EXPLAINED VARIATION IN SURVIVAL ANALYSIS |
| Authors: | Janez Stare, Nataša Kejžar |
| Affiliation: | University of Ljubljana, Slovenia |
| Abstract: | Papers comparing measures of explained variation in survival analysis invariably see bias under censoring, or independence of censoring, as the most important criterion for choosing among them. As a result, measures which do not allow for effects and covariates changing in time end up being promoted as best. Obviously, such measures are useless for practitioners who will routinely find changes in time in their data. We will show that independence of censoring is in fact misunderstood. And that the property of independence comes from the measures inherently assuming that the fitted model holds everywhere (and thus paying the price of not allowing for time dependency). If measures, seemingly inferior to those promoted, are allowed to make the same assumption, in fact a lesser one, they are easily corrected to fit the independence criterion, with all their flexibility remaining. At the end, we will list criteria which we believe should play the main role in choosing between measures of explained variation in survival analysis. |

| | |
|---|---|
| Title: | Sequential Dose-finding Designs for Binary Responses for Bioassays and Clinical Trials |
| Authors: | Nancy Flournoy |
| Affiliation: | University of Missouri |
| Abstract: | We consider two simple situations that apply widely. First, toxicity increases with dose. Second, in addition, one considers efficacy, and assumes efficacy also increases with dose – so except at the extremes, the probability of efficacy without toxicity (success) will increase up to a point at which the toxicity is great enough to cause it to turn down. In the first situation, one typically seeks to identify a dose with a prescribed toxicity rate; in the second situation, one seeks to identify the dose that maximizes the probability of success. These goals can be posed in terms of estimation or dose selection, as a finite sample space of doses is typically required. Three classes of procedures that differ in many fundamental ways are described and contrasted: up-and-down, adaptive optimal designs and best intention designs. |

| | |
|---|---|
| Title: | Measuring Prevalence and Characteristics of Scientific Plagiarism: Design of the Study |
| Authors: | Ksenija Baždarić, Martina Mavrinac, Vanja Pupovac, Lidija Bilić-Zulle, Gordana Brumini, Mladen Petrovečki |
| Affiliation: | Department of Medical Informatics, Rijeka University School of Medicine, Croatia |
| Abstract: | Research integrity is fundamental value of both scientists and science, medical especially, because results usually have immediate impact on human health. Thus, integrity and honesty of scientific work are its inherent characteristics that define the meaning of science, whilst dishonesty and fraud restrain it. Plagiarism is a form of dishonesty, “illegitimate appropriation of intellectual property, ideas, methods, results, text, speech or thought for the purpose of displaying as its own.” Plagiarism does not enlarge human knowledge at all, but brings to perpetrator (author) undeserved credits. The problem has been recognized worldwide, as well as at the Rijeka University by the Forum for Ethics and Development of Science and Higher Education by expressing the view that plagiarism is a "sign of universal prostitution in which cheating becomes legitimate way to earn money." Act of plagiarizing has been explored by our team from the Department of Medical Informatics for the past fifteen years. Following our previous research we set three-year study with three main objectives: to measure attitude of scientists towards plagiarism and identify factors that determine it, in parallel by measuring personality characteristics, to research the prevalence of plagiarism in three Croatian biomedical journals (Croatian Medical Journal, Biochemia Medica, and Acta Stomatologica Croatica), and to determine the characteristics of scientific plagiarism in overall international scientific community by systematic review and meta-analysis of published scientific studies that measure the prevalence of plagiarism using questionnaires or computer programs to detect plagiarism. Design of the study will be presented with expected research objectives, methodology and proposed statistical analysis of data. (Study is supported by the project 13.06.1.2.29 of the Rijeka University.) |

| | |
|---|---|
| Title: | Data mining methods for predictive modelling based on small samples in surgery |
| Authors: | Meštrović Tomislav, Sonicki Zdenko, Premužić Meštrović Ivica, Petrunić Mladen |
| Affiliation: | University of Zagreb, School of Medicine, Šalata 3, Zagreb, Croatia |
| Abstract: | Prediction of outcome has long been a matter of interest in surgery. Established models for prediction of perioperative mortality have traditionally been based on logistic regression. However, retrospective analyses of clinical data have been hampered by availability of small samples with many highly correlated predicting variables, and lots of missing values. On the other hand, quality of logistic regression models is limited by the sample size and requires at least ten events for each predictor variable in the resulting model. One way of overcoming those obstacles is to use stepwise logistic regression, but this is prone to overfitting. Data mining techniques, especially used in «ensembles», offer a potential resolution to this problem. This research is investigating possible values of using data mining methods, such as induction rules, decision trees, random forests and multivariate visualization techniques, for prediction modelling in surgical domains. |

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|---|---|
| Title: | Modeling of nitrate concentrations in alluvial aquifer |
| Authors: | Ivan Kovač (a), Jasminka Dobša (b), Jelena Gusić (b) |
| Affiliation: | (a) Faculty of Geotehnical Engineering, University of Zagreb;<br>(b) Faculty of Organization and Informatics, University of Zagreb |
| Abstract: | In the water supply of the city of Varazdin for many years there was a problem of too high nitrate concentrations in drinking water . The problem was solved in a way that well field where the nitrate concentration in groundwater was greatest was closed. At the same time new well fields were opened, so that today the wider area of the city of Varazdin groundwater pumped is in two locations: Vinokovščak and Bartolovec .In both well fields groundwater is pumped from alluvial strata of Quaternary age that are constructed mainly of sand and gravel . However , although the hydro geological conditions at both sites are equal, at the well field of Vinokovščak the nitrate concentrations were almost constantly increasing over the last ten years and have exceeded the maximum concentration recommended by the EU nitrate directive . Here we are modeling the annual average concentration of nitrate in groundwater at the well field Vinokovščak by polynomial functions of the first, second and third degree and by few nonlinear growth functions: general growth model, logistic function, Gompertz function and Richardson function. Since there are great oscilations in time series of nitrate concentrations, the time series is smoothed by method of moving average. Our hypothesis was that time series is going to be well adjusted to an increasing function that has asymptotic behaviour. |

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|---|---|
| Title: | Early recognition of Alzheimer Disease |
| Authors: | Lavoslav Čaklović |
| Affiliation: | Faculty of Natural Sciences, Mathematical Department |
| Abstract: | On the basis of a measurement results of the nineteen participants A1–A19 subjected to four psychological tests: Mental Status Exam (MSE), Rey-Osterrieth complex figure test (REY), Performance IQ test (IQprf), Verbal IQ test (IQver), and two Magnetoencephalography (MEG) tests: let us call them for the moment: Frq and Rare. The fact is that some participants are healthy, some of them have Mild Cognitive Impairment diagnosis (MCI),which is seen as a risk factor for Alzheimer's disease (AD) and the others seems to have AD already. The aim of this analysis is: to find out a relationship between psychological and MEG variables, more precisely, between the categorical values: Healthy, MCI, AD, suggested by both type of variables. The first insight to the data suggests 2 (two) clusters of the 'psychological participants' while 'MEG participants' are divided into 3 evident clusters. In both clusterizations AD-participants are correctly identified. Three methods are tested to split non-AD 'psychological participants' into 2 clusters. (1) Brut force method, (2) Canonical Correspondence Analysis and (3) Multicriteria Decision Analysis approach. All of them suggests 3 clusters of the 'psychological participants'. The results should be clinically improved (or disapproved). |

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| Title: | Procedures for Assessing Population Bioequivalence Modified to be One-Sided with Respect to Mean Comparison |
| Authors: | Vesna Luzar-Stiffler |
| Affiliation: | CAIR-Centar d.o.o., "The House of Statistics"Zagreb, Croatia,<br>vesna.luzar-stiffler@cair-center.hr |
| Abstract: | Regulatory agencies (such as the FDA in the US or EMA in the EU) require that pharmaceutical companies intending to submit an investigational new drug application (IND), a new drug application (NDA), or an abbreviated new drug application (ANDA) use equivalence criteria in analyzing in vivo and/or in vitro bioequivalence (BE) study data. For data from nonreplicated crossover or parallel designs, two alternative approaches for BE analyses are recommended: average bioequivalence (ABE), required by the EMA, or population bioequivalence, commonly suggested by the FDA.While average bioequivalence is based on the comparison of test to reference geometric mean ratio using the 90% confidence intervals and average bioequivalence limits, with the population bioequivalence approach both test to reference means and variance are compared using the upper 95% confidence bounds for two linearized criteria and the regulatory constants for population bioequivalence. The 95% confidence bounds for the two population bioequivalence linearized criteria were developed by Hyslop T, et.al. [2] and described in Chow S-C, et.al. [1], and Hsu JC, et.al. [3]. However, in one of the FDA guidances it is required that (for one of the BE parameters) a procedure for population bioequivalence be modified to be one-sided with respect with the mean comparison. In this presentation we propose and compare three methods for population bioequivalence analysis modified to be one-sided with respect with the mean comparison. Two of the proposed approaches use aggregate criteria, and one uses disagreggate moment-based criteria. One of the methods uses the bootstrap percentile method for the estimation of the upper 95% confidence bound for the population bioequivalence criteria, while for the other two approaches, analytical procedures for calculating the 95% confidence bounds are proposed.References:[1] Chow S-C, J. Shao and H.Wang. "In Vitro Bioequivalence Testing". Statistics in Medicine. 2003. 22. 55-68.[2] Hyslop T, Hsuan F, Holder DJ. A small sample confidence interval approach to assess individual bioequivalence. Statistics in Medicine 2000; 19:2885–2897.[3]Hsu JC, Hwang JTG, Liu HK, Ruberg SJ. Confidence intervals associated with tests for bioequivalence. Biometrika 1994:81(1); 103-14. |

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|---|---|
| Title: | Structure Equation Model of the Heptathlon |
| Authors: | Lavoslav Čaklović |
| Affiliation: | Faculty of Natural Sciences, Mathematical Department |
| Abstract: | Women's heptathlon is the combined event which consists of the following events: 100 meters hurdles, High jump, Shot put, 200 meters, Long jump, Javelin throw and 800 meters. Understanding he interrelationship between the disciplines may have implications for training optimization and competition as well. One approach to understand this relationships can be addressed through multivariate statistical analysis, defined as structural equation modeling and path analysis (Heazlewood (2011)). Mackenzie (2007) has attempted to assign relative conceptual weights for each event with constructs of aerobic endurance, gross strength skill, relative strength, running speed, mobility, explosive strength-power, speed endurance and strength endurance that are believed to underpin each event (motoric skills). The template of Mackenzie is a starting point for our approach based on simple Multicriteria Decision Analysis procedures. The aim of the analysis is to use the heptathlon event results (OI London 2012) as the measurement process for the motoric skills, and to suggest eventually a new scoring system which is different from the current IAAF system. |

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|---|---|
| Title: | Comparison of Pearson's and Spearman's correlation coefficients for grain cadmium concentration and agronomictraits in winter wheat genotypes |
| Authors: | Andrijana Rebekić, Zdenko Lončarić, Sonja Petrović, Sonja Marić |
| Affiliation: | Josip Juraj Strossmayer University of Osijek, Faculty of Agriculture in Osijek, Kralja Petra Svačića 1d, 31000 Osijek |
| Abstract: | Winter wheat (Triticum aestivum L.) is staple crop in human nutrition and therefore lots of resources is invested in wheat research resulting in tens of thousands publications covering results obtained from wheat research annualy. In many publications Pearson's correlation coefficient is reported for variables that are, by its nature or by high number of outliers, non-normally distributed. The aim of this paper is to compare Pearson's product-moment correlation coefficient (r) and Spearman's rank correlation coefficient (rs) in examination of relation between grain cadmium (Cd) concentration (mg kg-1) and grain Zn (Zn) concentration (mg kg-1), plant height (cm), plant weight (g), number of spikelets per spike and 1000 kernel weight (g) in 51 winter wheat genotype. Experiment was set up in semi-controlled conditions, 40 wheat grains was sown in plastic containers containing 12 kg of Cd contaminated soil (20 mg Cd kg-1 soil) or uncontaminated soil (0 mg Cd kg-1 soil). Experimental design was completely randomized design with four replicates. Statistical analyses were done using SAS 9.3. Software for Windows, Copyright © 2012 by SAS Institute Inc., Cary, NC, USA, SAS Enterprise Guide 5.1 and SAS JMP® 9.0.2. Distribution of variables was tested using Shapiro-Wilk test and non-normally distributed variables were log transformed to assess normality. Homoscedasticity was checked with scatterplot of the residuals versus predicted values. Original data (prior to removal of outliers and log transformation) were correlated and r and rs coefficients were compared. Pearson's correlation coefficient is a measure of strength of linear relationship, so higher r coefficient in compare to rs indicating linear rather that monotonic relationship. On uncontaminated soil, correlation analysis of original data yielded similar r and rs coefficients for correlation between grain Cd and grain Zn, plant weight and number of spikelets per spike. These three dependent variables were normally distributed according to Shapiro-Wilk test of normality, and that is a probable reason for similar values of these two coefficients. On uncontaminated soil, variable plant height was non-normally distributed ($p = 0.002$) even after log transformation ($p = 0.021$). The r coefficient for grain Cd concentration versus plant height, was non-significant ($r = -0.22$; $p = 0.108$) while Spearman's correlation coefficient was marginally significant ($rs = -0.28$; $p = 0.04$) although both correlation coefficients indicated very poor correlation. After log transformation and outlier removal (only one outlier) correlation coefficients increased, $r = -0.31$; $p = 0.030$ and $rs = -0.32$; $p = 0.023$, and both were significant at significance level of 95%. Correlation between grain Zn and Cd concentration on Cd contaminated soil was marginally significant according to rs while r obtained non-significant correlation between these variables. After log transformation of grain Zn concentration, correlation coefficients remain very low, with rs still obtaining marginally significant relation. This result indicating that relation between grain Cd and Zn concentration is probably monotonic rather than linear. Choosing appropriate measure of correlations is crucial for assessing true nature of relationship between variables. Normally distributed, homoscedastic variables, measured on interval scale are appropriate for Pearson correlation, while ordinal, non-normally distributed variables will perform better with Spearman's correlation coefficient. |

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|---|---|
| Title: | Biometrical analysis in between the descriptive and the inferential mathematical-statistical approach |
| Authors: | Nikola Mićić*, Jasmin Komić**, Borut Bosančić* |
| Affiliation: | *Faculty of Agriculture University of Banja Luka<br>**Faculty of Economics University of Banja Luka |
| Abstract: | Biometrics as the methodology of the scientific research integrates experimental and instrumental methods and the logical-mathematical argumentation of the research results. However, in biometrics the issue of sample is methodologically always opened, in accordance with the research goals. Namely, mathematical-statistical argumentation of the research results in the descriptive statistics is mostly based on the final and countable universal set, while in the inferential statistics samples are used for assessment of parameters of the universal set. Contrary to that, biometrical analysis in accordance with the research goal is mostly based on experimental samples, on basis of which are modeled or projected new and under certain treatment sustainable sets. Modeled universal biometrical set is sustainable only during the period the applied treatment is active (e.g. hybrid effect of heterosis). Also, universal set of a single fruit variety, grafted on a vegetative scion, represents a set of genetically identical organisms (vegetative clones – totipotency). However, in the given environment some production characteristics of those biologically uniform systems vary over 50%, without regard to the number of repetitions in the samples. Therefore, variation in the universal set (donor of biometrical observational units) can only tell how to chose individuals into the experimental sample, but it does not tell us what will their variation will be in terms of response to the applied treatment in the sample, i.e. modeled biometrical universal set. Hence, the variations in biometrical samples represent basis of the logical-mathematical argumentation of the central tendency of the treatments and on that basis also the reliable projecting of the modeled universal set. By having insight into available research papers with the published results of the researches of growth processes and development of the biological systems, the issue of allowed variations in the argumentation of the central tendencies points to the following two methodological issues: 1.) Defining the basic relations confirming or denying the research goal, but also the relations which are logical and in accordance with the research goal, but where the statistical argumentation is absurd as the consequence of variation in the samples, which finally leads to the absurd conclusions. 2.) Analysis of variations in the experimental samples where the variations are outside of the interval of allowed variations in order to argument the central tendency. In this paper the problem issue is defining the research goal or defining the benchmark of the treatment effect which has to be reliably realized in the experimental samples in order for those to have biological or economical justification of the accomplished goal, and relation in terms of samples where the variations are outside of interval allowed to argument the central tendencies, without regard to the number of repetitions in the samples. |

Jazbec A, Pecina M, Sonicki Z, Šimić D, Vedriš M, eds. (2014) Book of Abstracts BIOSTAT 2014 – 21st International Scientific Symposium on Biometrics, Dubrovnik 11-14 June 2014. Zagreb: Croatian Biometric Society. ISSN 1849-434X

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| Title: | Structural parameters analysis of forest cultures in Croatia |
| Authors: | Sanja Perić, Martina Tijardović |
| Affiliation: | Croatian Forest Research Institute |
| Abstract: | Croatia is a country which possesses significant biological and ecological diversity due to its geografical position. Those differences, together with related social, historical and management circumstances provide different silvicultural options and significance of afforestation activities. Specific issues together with afforestation potential of the area present a basis for any planning related to land use management and afforestation planning and therefore possess high significance for any future activities. Curently, there is a low share of newly established forest cultures in relation to total forest area (< 3%). Planned amount of areas for afforestation according to Management plan for the whole country is rather low comparing to the amount of available areas. In addition, there is no special and comperehensive management plan for afforestation activities in Croatia. The lack of interest, proper data provision and related research created vast space in management decisions related to afforestation activities in Croatia for the near future. Structural parameters of monocultures and mixed forest cultures will be analysed with different statistical methods which will provide the basis for more successful decision making. The potential for newly established forests and the significance of their pronounced functions for this part of the Country will be given in the presentation. For instance, this region has pronounced protection and production function which have strong influence on selection of species and silvicultural methods. Also, this overwiev creates a need for harmonisation of afforestation potential for individual tree species with the nursery production plans which are currently insuficient. |

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|---|---|
| Title: | ANALYSIS OF DEFOLIATION USING LOGISTIC REGRESSION MODEL WITH ORDINAL RESPONSE |
| Authors: | Anamarija Jazbec, Damir Ugarković, Mislav Vedriš |
| Affiliation: | Faculty of Forestry University of Zagreb, Croatia, Svetošimunska 25, Zagreb |
| Abstract: | We analyzed defoliation of beech-fir forests on two permanent plots (locations) "Brloško" (BRO) N=81 and "Bitoraj" (BIT) N=194. The emphasised vulnerability of fir and beech-fir forest on the edge of their areal stimulated us to conduct the research in these forests. Site BRO is Dinaric beech-fir forest on calcocambisol upon limestone, and BIT is fir forest with hard fern located on a dystric cambisol upon silicate bedrock. Visual assessment of defoliation was done in 2007 and estimates were classified in three levels as following: 1 (≤ 25%) healthy (BRO: 0.259; BIT: 0.134), 2 (25-60%) damaged (BRO: 0.148; BIT: 0.247), 3 (> 60%) severely damaged (BRO: 0.593; BIT: 0.619). The main goal was to estimate probability and odds ratio of transition from one level of defoliation to another and compare it between two observed locations. In order to assess odds ratio of transition from one level of defoliation to another we first wanted to use a cumulative logit model, but unfortunately Proportional Odds Assumption (chi2=7.84; df=1; p=0.0051) was not satisfied. We estimated model in a way that we do separate binary logit analyses for each phase comparison of dependent variable. The first phase is modelling the second level of defoliation to the first. The second phase is modelling the third level of defoliation to the second. For that we use dummy indicator variable. For each phase comparison we construct a data set that excludes all trees that did not make it to that phase. Finally we estimate a single model (binary logistic) on combined data set. In the first model we tested the difference between the phases, locations and interaction of phase and location. The results show that there is a statistically significant difference between phases (2/1; 3/2)(chi2=15.6327; df=1; p<0.001), between locations (chi2=8.8634; df=1; p=0.0029) and the interaction between the phase and location are also statistically significant (chi2=8.3396; df=1; p=0.0039) what indicates that the defoliation in 2007 behave differently at the analysed locations. For sake of better analysis of the observed defoliation at analysed locations and the relationship between the diameter at breast height (DBH), as a measure of physiological maturity, and defoliation, we modelled each phase separately, and the independent variables were location and DBH, and also their interaction if it significantly contributed to the model. In the model without interaction for the first phase (2/1) odds ratio for the transition to the second level of defoliation for BRO is 6.004 (95% CI 1.838-19.607), and DBH (cm) OR = 1.022 OR (95% CI 0.995-1.050). The interaction between location and DBH in 2007 is a statistically significant and left in the mode. The final model for the analysis of the first phase (2/1): Logit (p2/1)=0.575 - 3.137 location - 0.017 DBH + 0.119 locationxDBHThe results of the second phase, for modelling the third level of defoliation regard to the second (3/2) in the model without interaction OR for BIT = 0.427 (95% CI 0.147-1.244), and for DBH was OR = 0.99 (95% CI 0.970-1.010). When we put the interaction in, interaction significantly improves the model (-2logL = 19.9898, df = 1, p <0.001), and the location and DBH are becoming statistically significant. So the final model for the second phase (third level to the second level) is:Logit (p3/2)=-0.807+ 3.774 location + 0.035 DBH - 0.095 locationxDBH |

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Dubrovnik, Croatia, **11 - 14 June 2014**


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# BIOSTAT 2015

## 22nd International Scientific Symposium on Biometrics

## Dubrovnik, Croatia, 28 - 30 June 2015

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Researchers and practitioners in the field of biometrics, development and application of statistical and mathematical methods for data analysis in life sciences are encouraged to take part in this symposium.

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