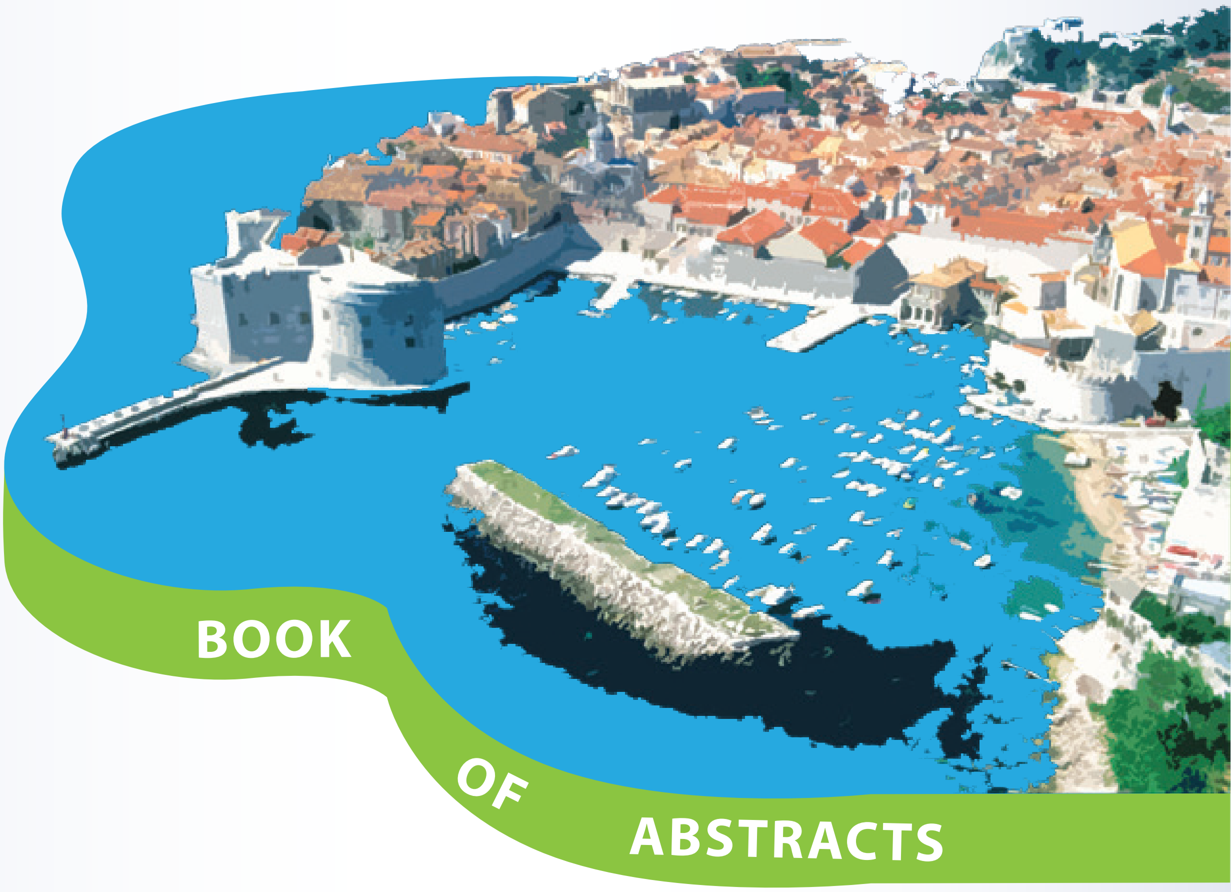
BIOSTAT 2015

22nd International Scientific Symposium on Biometrics



BOOK OF ABSTRACTS

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

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BOOK OF ABSTRACTS

BIOSTAT 2015

22^{nd} International Scientific Symposium on Biometrics

Dubrovnik, Croatia, **28 June - 1 July 2015**

EDITORS:

Anamarija Jazbec
Marija Pecina
Zdenko Sonicki
Diana Šimić
Mislav Vedriš

Zagreb, 2015.

IMPRESSUM

BIOSTAT 2015

22nd International Scientific Symposium on Biometrics

Dubrovnik, Croatia, 28 June - 1 July 2015

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Croatian Biometric Society

UNDER THE AUSPICES of the
University of Zagreb

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20th SCHOOL OF BIOMETRICS

Lynne Billard
University of Georgia, USA

KEYNOTE LECTURES

Viswanathan Ramakrishnan
Medical University
of South Carolina, USA

Rado Pišot
University of Primorska, Slovenia

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Croatian Biometric Society
c/o University of Zagreb, School of Medicine,
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University of Zagreb,
Don Frana Bulića 4,
HR - 20000 Dubrovnik, Croatia
www.caas.unizg.hr

FOR THE PUBLISHER:
Professor Anamarija Jazbec, Ph.D., President
University of Zagreb, Faculty of Forestry
Svetošimunska 25, HR-10000 Zagreb, Croatia
hbmd@hbmd.hr

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BIOSTAT 2015

22nd International Scientific Symposium on Biometrics
Dubrovnik, Croatia, 28 June - 1 July 2015

ABSTRACTS

BIOSTAT 2015

22nd International Scientific Symposium on Biometrics

Dubrovnik, Croatia, 28 June - 1 July 2015

Welcome to the Book of Abstracts of BIOSTAT 2015 – The 22nd International Scientific Symposium on Biometrics organized by the Croatian Biometric Society in Dubrovnik, Croatia, June 28 – July 1, 2015.

BIOSTAT 2015 comprises 20th School of Biometrics, keynote lectures and contributed papers. This brochure contains 25 abstracts written by 42 authors from six countries – Bosnia and Herzegovina, Croatia, France, Slovenia, Turkey 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.

After organizing 18 Schools and 20 BIOSTATs within ITI – International Conference on Information Technology Interfaces – this is the second year in which BIOSTAT and the School are held as independent events.

We hope that this year our friendship, socializing and interchange of knowledge contribute to the progress of Biometric science.

Invited lecturer of the 20th School of Biometrics is University Professor **Lynne Billard** (University of Georgia, USA) with the

Topic of the 20th School of Biometrics is:

Topic: **Multiple Sets of Multivariate Time Series**

This year we have two keynote lectures:

Professor Viswanathan Ramakrishnan, PhD (Medical University of South Carolina, USA)
Topic: **Is the adaptive paradigm shifting the perception of clinical trials?**

Professor Rado Pišot, PhD, (University of Primorska, Slovenia)
Topic: **Bed rest as a model for studying mechanisms of functional decline**

We thank Ministry of Science, Education and Sports of the Republic of Croatia for financial support. We hope to share with you pleasant moments, lively discussions, successful networking and forge new partnerships and friendships.

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, 2015

SYMPOSIUM PROGRAM At Glance

	Sunday, June 28	Monday, June 29	Tuesday, June 30	Wednesday, July 1
9 - 10:30		**School of Biometric** **Lynne Billard** Multiple Sets of Multivariate Time Series *Chair: Anamarija Jazbec*	Contributed session *Chair: Diana Šimić*	Contributed session *Chair: Ksenija Bosnar*
10:30 - 11		COFFEE BREAK	COFFEE BREAK	COFFEE BREAK
11 - 12		**School of Biometric** **Lynne Billard** University of Georgia, Athens, USA Multiple Sets of Multivariate Time Series Continuation *Chair: Anamarija Jazbec*	**Keynote Lecture** **Viswanathan Ramakrishnan** Medical University of South Carolina, Charleston, USA Is the adaptive paradigm shifting the perception of clinical trials? *Chair: Zdenko Sonicki*	**Keynote Lecture** **Rado Pišot** University of Primorska, Koper, Slovenia Bed rest as a model for studying mechanisms of functional decline *Chair: Franjo Prot*
12 - 13			Contributed session *Chair: John Vena*	Contributed session *Chair: Želimir Kurtanjek*
13 - 14		LUNCH BREAK	LUNCH BREAK	LUNCH BREAK
14 - 15:30		Contributed session *Chair: Annie Morin*	Contributed session *Chair: Janez Stare*	Closing
15:30 - 16		COFFEE BREAK	COFFEE BREAK	COFFEE BREAK
16 - 17			ISPC Meeting	
17 - 18				
18 – 19	Registration & Welcome Cocktail		Dinner	
19 – 20				

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

BIOSTAT 2015

22nd International Scientific Symposium on Biometrics
Dubrovnik, Croatia, **28 June - 1 July 2015**

SYMPOSIUM PROGRAM In Detail

Sunday June, 28	18:00	**Registration** **&** **Welcome Cocktail**	
	19:00		
Monday, June, 29	9:00 – 10:30	*Chair: Anamarija Jazbec* **Lynne Billard**	**School of Biometrics:** **Multiple Sets of Multivariate Time Series** *Part 1*
	10:30 – 11:00	COFFEE BREAK	
	11:00 – 12:45	*Chair: Anamarija Jazbec* **Lynne Billard**	**School of Biometrics:** **Multiple Sets of Multivariate Time Series** *Part 2*
	13:00 – 14:00	LUNCH BREAK	
	14:00 - 15:30	*Chair: Annie Morin*	Contributed session
		AUTHOR	TITLE
		Mirta Benšić, Kristian Sabo	Estimating object dimension from its image
		Maja Zagorščak, Mirta Bujanović, Kristina Gruden, Pavle Goldstein	Iterative Motif Scanning in HMM Framework
		Melike Bahcecitapar, Özge Karadağ, Serpil Aktaş	Specification of variance-covariance structure in bivariate mixed model for unequally time-spaced longitudinal data
		Özge Karadağ , Serpil Aktaş	Generalized Estimating Equations for Genetic Association Studies of Longitudinal Family Data
	15:30 – 16:00	COFFEE BREAK	
Tuesday, June, 30	9:00 - 10:30	*Chair: Diana Šimić*	Contributed session
		AUTHOR	TITLE
		Lewis Frey	Big Data Analytics in Clinical Research
		Želimir Kurtanjek, Mihaela Stoia	Chemometric and kinetic statistical modeling of lead poisoning
		Janez Stare	Bad luck of cancer – or misinterpreted statistics?
		Paul Thompson	Reproducible methods in biostatistics
	10:30 – 11:00	COFFEE BREAK	
	11:00 – 12:00	*Chair: Zdenko Sonicki* **Viswanathan Ramakrishnan**	**Keynote Lecture:** **Is the adaptive paradigm shifting the perception of clinical trials?**
	12:00 – 13:00	*Chair: John Vena*	Contributed session
		AUTHOR	TITLE
		Yuko Palesch, Wenle Zha	Some Caution for Interim Analysis
		Caitlyn Ellerbe, Jordan Elm, Viswanathan Ramakrishnan, Bruce Turnbull, Valerie Durkalski	The use of continuous repeated measures data for dose selection in a two-stage adaptive dose selection design
	13:00 – 14:00	LUNCH BREAK	

	14:00 - 15:30	*Chair: Janez Stare*	Contributed session
		AUTHOR	TITLE
		Bojan Basrak, Miljenko Huzak, Anamarija Jazbec	The Cohort Mortality Tables for Croatian Population
		Annie Morin	Bibliometric analysis using data analysis methods: an application using Medline abstracts.
		Martina Mavrinac, Gordana Brumini, Mladen Petrovečki	Development of Attitude Towards Plagiarism Questionnaire
		Želimir Kurtanjek	Statistical analysis of random forest models
	15:30 – 16:00	COFFEE BREAK	
	16:00 – 17:00	**ISPC Meeting**	
	17:00 – 18:00		
	18:00 – 24:00	**Dinner**	
Wednesday, July, 1	9:00 - 10:30	*Chair: Ksenija Bosnar*	
		AUTHOR	
		Franjo Prot, Rado Pišot, Petr Blahuš	Kinesiometrics or Kinesimetrics or Kinesmetrics or What's in a name?
		Uroš Marušič, Rado Pišot	Contemporary approaches for monitoring functional and cognitive status in elderly people
		Saša Pišot	Behind the numbers – qualitative issues when designing experimental measurements
		Franjo Prot, Sara Prot	On General Image Transformation in Kinesiometrics Context
	10:30 – 11:00	COFFEE BREAK	
	11:00 – 12:00	*Chair: Franjo Prot* **Rado Pišot**	**Keynote Lecture:** **Bed rest as a model for studying mechanisms of functional decline**
	12:00 – 13:00	*Chair: Želimir Kurtanjek*	Contributed session
		AUTHOR	TITLE
		Olena Orobinska, Jean-Hugues Chauchat	How to use online linguistic tools for ontology learning from a domain corpus? Illustration on radiation safety.
		Maja Moro	Trends in production of industrial round wood in croatia and surrounding countries
		Borut Bosančić, Marija Pecina, Nikola Mičić	Effect size and its statistical significance in published papers as metadata in horticultural sciences for application of meta-analysis
		Mislav Vedriš, Anamarija Jazbec	Discrete choice analysis of forest inventory plot types in Croatian uneven-aged forests
	13:00 – 14:00	LUNCH BREAK	
	14:00 – 15:00	**Closing Ceremony**	
		COFFEE BREAK	

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20th SCHOOL OF BIOMETRICS

20th SCHOOL OF BIOMETRICS

Lynne Billard
University of Georgia,
Department of Statistics
Athens, GA 30602, USA

http://www.stat.uga.edu/people/faculty/lynne-billard

Topic:

Multiple Sets of Multivariate Time Series

Abstract:

The focus will be on multiple (S) sets of multivariate (p) time series. In particular, it is frequently the case that there will be dependencies across the S sets of series, as well as across the p variables within each series. A key feature will be that the distinctiveness of these two sets of variables needs to be retained while simultaneously dependencies within and between the S sets need to be measured, along with the usual dependencies over time for time series. Therefore, vector time series (here of order S·p) are inappropriate. For example, it is reasonable to assume that adjacent pixels in an fMRI data set (from measurements of p different stimuli, say) are correlated, or meteorological data (measuring p different weather conditions such as temperature, moisture, pressure, …) for different cities can be correlated across nearby cities, or financial data for S different economic sectors, or network traffic, or communications; the list is long.

Initially, we will look at two approaches (canonical correlation analysis and principal component analysis) for clustering subsets of the S series. Then, we will look at how the data overall can be set up as a matrix time series model, and consider some properties of this new class of model.

Much of this research is done jointly with Yaser Samadi.

KEYNOTE LECTURES

KEYNOTE LECTURE

Viswanathan Ramakrishnan
Medical University of South Carolina
Charleston, SC, 29425, USA

http://academicdepartments.musc.edu/faculty-directory/FacultyDetails.aspx?facultyId=5910

Topic:

Is the adaptive paradigm shifting the perception of clinical trials?

Abstract:

A fundamental difference between clinical trials and other experiments (such as field, basic science, or animal experiments) is, in human clinical trials the accrual of the participants often has to occur sequentially, in multiple centers. A natural question that arises in such trials is, could the experience and the information accumulated over time be used to modify the future course and the design of the trial? Traditional designs that include interim analyses and stopping rules prespecify the course of the trial, prior to the first participant is registered in the trial and do not allow adaptations. The current paradigm of adaptation has wide acceptance in the field and several methods for adaptation have been proposed for all phases of the clinical trials. In this presentation, I will introduce basic as well as complex adaptive designs. I will discuss my philosophy regarding the application of these designs. I will also briefly present a few of the designs that my colleagues and I have proposed.

KEYNOTE LECTURE

Rado Pišot
University of Primorska,
Science and Research Centre
Institute for Kinesiology Research
Koper, Slovenia

http://www.zrs.upr.si/institut-za-kinezioloske-raziskave

Topic:

Bed rest as a model for studying mechanisms of functional decline

Rado Pišot, Boštjan Šimunič

Abstract:

The lifestyle of humans included physical activity on a regular basis throughout their evolutionary history except for the past two or three generations (Malina, Little, 2008). Currently global physical inactivity is implicated in the recent worldwide epidemic of obesity and indicated as a major risk factor for morbidity and second leading risk factor for global death in adults as well as an independent risk factor for metabolic morbidity in children and adolescents (American College of Sports Medicine, 2001; Caballero, 2007; Strong et al., 2005; World Health Organization, 2005, World Health Organisation, 2014).The force of gravity has a very important role in forming the structure and function of the human organism and its demands necessary adaptations of the human organism, which are mostly determined and conditioned by physical activity. Scientists approach to this problem in different manners – many of them research how prolonged physical inactivity affects the human body. Among such studies we can classify prolonged living in space (Harm et al., 2001; LeBlanc et al., 2000; Stein et al., 1999), simulated weightlessness (Pavy-Le Traon et al., 1998, Adams et al., 2003; Blottner et al., 2006; Mekjavić et al., 2005; Kortebein et al, 2007; Pišot et al., 2008, 2009, 2012, Paddon-Jones, 2009), and the immobilisation of healthy (Rittweger et al., 2006, Ferrando et al., 1996) or injured (Hyeteok et al., 2003; Pathare et al., 2005) parts of the human body. Bed rest was standardized as a ground based model for studying the effect of microgravity in space physiology but can be also a perfect model to mimic physical inactivity and affect functional decline. In Slovenia, simulated weightlessness studies have been introduced at the University of Primorska, Science and Research Centre, Institute of Kinesiology Research a few years ago. Until today, we have performed five extensive studies in cooperation with numerous partners. Healthy volunteers are included in those studies and they are studied before, during, and after submitting to bed rest. Thirty-seven males (approx. average age: 24±3 years) and 16 older adults (59.7±3.5 years) have been submitted to horizontal (BR 2006, 2007, 2012) and 7 degrees head down tilt bed rest (BR 2008); ten of them each year from 2006 to 2008. There were two types of interventions carried out: during BR 2012 were included cognitive training intervention; during BR 2007, 2008 and recovery 2012 were included nutrition countermeasures with individually balanced energy intake. The changes and mechanisms of effects of bed rest and subsequent recovery of specific subsystems of human organism were studied and will be presented.

CONTRIBUTED SESSIONS

Title:	**Estimating object dimension from its image**
Authors:	Mirta Benšić, Kristian Sabo
Affiliation:	University of Osijek, Department of Mathematics
Abstract:	There are many real problems where we face an image of an object captured with an additive error, which means that the targeted object image has an unclear border. Many procedures are available for border reconstruction in the field of image processing but sometimes we are interested in a specific dimension such as the length of the line or the circle radius. These problems can occur, for example, in the recognition of objects observed with fluorescent microscope or various devices for medical diagnostics. Here we discuss several models that can be used for estimation and hypothesis testing in such cases. The models we use for statistical inferences are based on the assumption that the data come from the uniform distribution on some region spoiled with additive error. We consider Gaussian and Laplace distributions as possible error distributions. For the one-dimensional models maximum likelihood approach is applied. We discuss consistency and asymptotic efficiency of the estimator as well as the existence of the estimator for the length of the uniform support. Also, we illustrate in simulations the behavior of estimators in the presence of outliers. For the two-dimensional problems we suggest the algorithm that cuts the image in strips and, in the end, uses the one-dimensional model for estimation. Finally, we show how to transform the specific monochromatic image into data which can be used for our purpose and discuss possible problems with this procedure.

Title:

Iterative Motif Scanning in HMM Framework

Authors:

Maja Zagorščak, Mirta Bujanović, Kristina Gruden and Pavle Goldstein

Affiliation:

Department of Mathematics, Faculty of Science, University of Zagreb, Croatia;
Department of Biotechnology and Systems Biology,
National Institute of Biology, Slovenia

Abstract:

Conserved substring patterns, called sequence motifs, are highly related to protein structure and function. Given a collection of protein sequences (e.g. a proteome), we want to find the closest match to a given motif in each sequence. This is achieved by iteratively building a probabilistic model of the motif, also called profile. A crude profile is initially built for a given motif, and used to obtain the initial list of positive hits. Positive hits are then used to build a new profile, and the data set is scanned again, which produces a new list of positives, hence a new model. The iterative process stops when there are no changes in the list of positives, or when a prescribed number of iterations is reached.

This method provides two novelties. First, to scan for motifs, we use a standard Viterbi/PSSM decoding (VD), but in combination with a version of posterior decoding (PD). This discards spurious assignments, increases specificity in each iteration, so the end-model has greater sensitivity. Second, the method that we implemented is automatic. After the initial parameters have been selected, no user input is required. This is achieved by combining results of VD and PD assignments, analysing the distribution of Viterbi/PSSM scores, and considering only the hits with scores in the tail of the distribution. Finally, the method does not have a limit on the number or percentage of positives and requires only a moderate-size input data set.

Title:

Specification Of Variance-Covariance Structure In Bivariate Mixed Model For Unequally Time-Spaced Longitudinal Data

Authors:

Melike Bahcecitapar, Ozge Karadag, Serpil Aktas

Affiliation:

Hacettepe University, Department of Statistics

Abstract:

In medical studies, the longitudinal data is mostly analyzed to investigate the change in repeated measurements taken from each subject over time. It is possible to take measurements for more than one response variables and covariates at different time points. Multivariate mixed model can be used for the analysis of these kind of data sets, because it provides the joint analysis of multiple response variables over time and enables researchers to examine both the correlations of response variables and autocorrelation between measurements from each response variable over time. However, variance-covariace structure, i.e. autocorrelation structure over time between measurements from same response variable should be truly specified. It has been shown that misspecification of covariance structure for longitudinal data affects the parameter estimation. If measurements are not equally spaced, covariance patterns such as the first-order ante dependence, heterogenenous first-order auturegressive , unstructured and spatial power can be considered for unequal measurement spacing and changes in the autocorrelation structure between measurements from same response variable. In this study we illustrate and compare different parameter estimation methods provided by SAS including the covariance patterns on a real-life data set to evaluate the effect of variance-covariance structures under unequally spaced time intervals in the joint analysis of two response variables. Results show that misspecification of the covariance matrix has a negative impact on the parameter estimates.

Title:

Generalized Estimating Equations for Genetic Association Studies of Longitudinal Family Data

Authors:

Özge Karadağ , Serpil Aktaş

Affiliation:

Department of Statistics, Hacettepe University, Ankara, Turkey
ozgekaradag@hacettepe.edu.tr, spxl@hacettepe.edu.tr

Abstract:

In genetic epidemiology studies, many diseases are multifactorial that can be both environmental and genetic inherited pattern. The relationship between genetic variability and individual phenotypes is usually investigated by genetic association studies. In genetic association studies, longitudinal measures are very important scale in detecting disease variants. They enable to observe both factors in the progress of disease. Generalized Linear Modeling (GLM) techniques offer a flexible approach for testing and quantifying genetic associations considering different types of phenotype distributions. Due to population stratification, the assumption on independent observations, which is required for maximum likelihood estimation, is often violated. Advanced models such as mixed and multilevel models are used for revealing the possible similarities among the subjects which may be represented as latent correlations. These kind of models also allows modeling the serial correlation, which arise in repeated experimental designs. Generalized Estimating Equations (GEE) method which is an extension to GLM is often employed to analyze longitudinal and other correlated response data. In this study, it is aimed to accommodate GEE method for genetic association studies in the presence of both familial and serial correlation. For this purpose, a real genotyped data set with the pedigree information and a continuous trait measured over time is used to model the association between the disease and the genotype by analyzing several SNPs (Single Nucleotide Polymorphism), which have been associated with the disease. Estimates from GEE method are compared to random effects model.

Title:	**Big Data Analytics in Clinical Research**
Authors:	Lewis Frey
Affiliation:	Associate Professor, Department of Public Health Sciences, Medical University of South Carolina Charleston, SC
Abstract:	An unsolved problem in health informatics is how to apply the past experiences of patients, stored in large-scale medical records systems, to predict the outcomes of patients and to individualize care. One approach to prediction, heretofore impractical, is rapidly finding a patient cohort “similar enough” to an index case that the health experiences and outcomes of this cohort are informative for prediction. This task is formidable because of large variability of the vast numbers of patient attributes with the added complexity of sequences of patient encounters evolving over time. Epidemiological considerations such as confounding by indication for treatment also come into play. The Dr. Frey will discuss improvements and issues with the use of big data methodologies for predictive analytics in clinical research. Big data will be characterized by volume, variety, veracity and velocity. He will draw upon his experience with the development of the Clinical Personalized Pragmantic Predictions of Outcomes (Clinical3PO) developed for the Veterans Affairs in the USA. Extant findings support that empiric prediction of outcomes from similar patients is possible. For example, McCormick and colleagues (McCormick, Rudin et al. 2011) use Bayesian prediction rules from patient data. Neuvirth and colleagues (Neuvirth, Ozery-Flato et al. 2011) describe the application of clinical data prior to an index event to empirically predict response to treatment in diabetes. The goal of Clincal3PO is to develop approaches that apply “big data” methodologies, including Hadoop and Accumulo, to store “medical log” files. The content of these “logs” will be processed in combination with strategies for conceptual markup of events and matching of event streams, to rapidly retrieve and identify patients that are sufficiently similar to an index case to be able to make clinical personalized pragmatic predictions of outcomes. The objectives are to (1) create a modular test bed that uses a “big data” systems architecture to support research in rapid individualized prediction of outcomes from large clinical repositories and (2) to explore various approaches to making “pragmatic” near-term predictions of outcomes from clinical data. Using the Department of Veterans Affairs’ (VA) Informatics and Computing Infrastructure (VINCI) database, Dr. Frey is exploring two synergistic strategies for rapidly finding a cohort of patients that are similar enough to an index patient to predict near-term treatment response and/or adverse effects in an elastic cloud environment: (1) temporal, based on similarity in the sequence of clinical events (including epidemiology abstractions) experienced by the patient, and (2) clinical or biological, based on reported history, clinical features, genomics and laboratory testing. This also includes epidemiology similarity based on certain critical events in a patient’s history (for example, past exposure to a drug or chemical, or the current presence of a set of symptoms or physiological derangements).The focus is on predicting treatment outcomes in patients with type 2 diabetes, a growing epidemic. The VINCI database has 2.5 million patients with at least one ICD-9 code representing a diagnosis of type 2 diabetes. Dr. Frey extends the notion of patient

	cohorts to including modeling of the response to treatment over time and understanding what variations in the trajectory of response are important. The ability to compare outcomes across different patients' cohorts will support the development of novel quality measures and cost control strategies, addressing the critical issue of determining "value" in healthcare.Alignment of the sequence of events experienced by patients may be an important factor in creating cohorts for prediction. Extending the sequence of events requires better, faster and more flexible technologies for assessment of similarity, and it is only possible with access to very large databases of patients, where one can compare an index case to millions of other patients to find the similar cohort. SummaryImplementing big data solutions holds many opportunities. Dr. Frey is developing strategies for producing cohorts of nearest neighbors for prediction of near-term outcomes designed to improve and personalize patient care. Hadoop and other big data systems provide an ecosystem that is affordable, scalable and highly available, while allowing clinical research and clinical practice to coexist in the same system.

Title:	**Chemometric and kinetic statistical modeling of lead poisoning**
Authors:	Zelimir Kurtanjek (1), Mihaela Stoia (2)
Affiliation:	(1) University of Zagreb, Faculty of Food Technology and Biotechnology, Croatia, (2) Blaga University of Sibiu, Faculty of Medicine, Romania
Abstract:	In this work are presented long term data at significant risk for occupational lead poisoning, and evaluation of principal factors by applying ANOVA, chemometric analysis and prediction models. Background exposure of each subject at the same workplace, gender (males), and the absence of clinical signs of poisoning ("healthy" workers) were eligible criteria for study design. The database obtained from current medical surveillance of lead exposed workers consisted of (1) biological monitoring data, respectively blood lead level - BLL - and urine deltaaminolevulinic acid level - DALA - as common biomarkers, and (2) individual data regarding age, exposure duration, and workplace. Post ANOVA (Tucker HSD) reveals significant differences among working conditions corresponding to the plant production sections. Since the data are long term time series (exposure) high degree of time related correlations are present. Effects of correlations are accounted by principal component analysis and based on biplots of samples (individual workers) and experimental data interpretative models are proposed. Also, linear discriminant analysis is applied to discern variable importance factors responsible biochemical data and sickness reports. To develop predictive models applied are decision tree predictions for classification and regression of biological data showing dominant role of workplace for BLL, and respectively dominant role of exposure duration for DALA in predicting lead poisoning. Especially exposure duration - working life - accounts for cumulative dose and subsequently adverse health effects of lead even after retirement, therefore biological database should be kept as a permanent reference record. In conclusion, chemometric may be a valuable tool in occupational risk assessment to point out dose-effect and dose-response relationship in chemical exposed workers. Since lead is a cumulative toxicant, further research is needed to elucidate the relationship between cumulative dose (bone lead level) and other health effects.

Title:	**Bad luck of cancer – or misinterpreted statistics?**
Authors:	Janez Stare
Affiliation:	Faculty of Medicine, University of Ljubljana
Abstract:	A recent paper in Science (January 2015) claimed that the majority, 64% to be precise, of cancers is due to bad luck, so non-preventable. The message was spread quickly through media, including serious ones like BBC (and also radio Slovenia, if I may add). And while the paper has been criticized by many, the authors seem to stick to the original message. In this talk I'll give my view of the paper and try to defend a counter message that their analysis gives them absolutely no grounds to make such a claim. The arguments that I'll present have, to my knowledge, not appeared in published reactions to the paper. I'll also show another way of using their data to estimate the proportion of random cancers. Whether this estimate is close to 64% I'll reveal at the talk.

Title:	**Reproducible methods in biostatistics**
Authors:	Paul Thompson
Affiliation:	Sanford Research & Sanford School of Medicine, University of South Dakota
Abstract:	Reproducible research methods are an increasingly important component of research. Reproducible methods have been under development for about 30 years. Beginning with intense computational areas (geophysics, signal processing), the need was found for researchers to document, re-run, and completely redo the process of research, to both communicate their results to others, and also simply to ensure that they themselves could rerun processes to reliably obtain results. In biostatistics, bioinformatics, and computational statistics, the same issues have arisen recently. In particular, in the areas of medical research with bioinformatics, recent cases have shown that data management, systematic processes for analysis, and structural approaches to analysis are key to reproducible methods. Two cases will be briefly described. There are a number of key methods which should be a component of all computational approaches which will be discussed. These involve data curation, data management, data analysis, and integration of analysis with documentation.

Title:	**Some Caution for Interim Analysis**
Authors:	Yuko Palesch and Wenle Zhao
Affiliation:	Medical University of South Carolina
Abstract:	Interim analysis has become a staple in large multi-center definitive Phase III trials, especially when subject recruitment occurs over several years. Beyond the potential cost savings, the clinical and ethical benefits of interim analysis are clear: early stopping for overwhelming efficacy would facilitate getting the effective treatment to the target patient population earlier; or stopping early for futility would prevent exposing additional subjects to ineffective (and sometimes unsafe) treatments. Obvious disadvantages to stopping a study at an interim analysis are: potential bias in the treatment effect estimate and reduced statistical power for analysis of secondary and safety outcomes. But are there other downsides? While a large expected sample size motivates conducting interim analyses, caution is required in their interpretation for many trials because of associated trial implementation issues -- specifically, the large number of sites and long period of time needed to meet recruitment goals. The former amplifies site variability in the standard of care and the protocol learning curve; and the latter introduces temporal variability in the standard of care (e.g., due to rapid advances in technology of therapeutic devices). Both sources of variability are likely to affect subject outcomes, and ultimately, could mislead inferences from interim analyses. Examples with data from two recently terminated trials are provided to illustrate some of these issues, including one where interim analysis nearly resulted in an incorrect decision about the treatment effectiveness. These trials speak to the importance of monitoring temporal trends, as well as the choice of interim analysis timing and boundary. Finally, one potential strategy to find the right timing of the first interim analysis will be presented.

Title:	**The use of continuous repeated measures data for dose selection in a two-stage adaptive dose selection design**
Authors:	Caitlyn Ellerbe, Jordan Elm, Viswanathan Ramakrishnan, Bruce Turnbull, Valerie Durkalski
Affiliation:	Department of Public Health Sciences, Medical University of South Carolina; Department of Statistical Science, Cornell University
Abstract:	In response to the frequency of randomized controlled trials failing during late stages of clinical development, adaptive designs offer investigators the ability to modify trial parameters to promote safety and trial efficiency. However, in phase II/III trials with repeated measures, adaptive designs are limited in the ability to use partial information without inflating the type I error. A two-stage design is proposed for a continuous endpoint measured at several visits after enrollment. In the first stage several doses of interest are compared to a placebo control, and the optimal dose is selected using all available data. In the second stage, the efficacy of the selected dose relative to the control arm is tested using data from new subjects as well as the data used for the dose selection in the first stage. It is a well-known problem that the selection procedure used to adapt a trial results in positively biased treatment estimates in the selected treatment arm. The proposed design allows for simultaneous estimation and testing of the null hypothesis using bias corrected estimates in the case of one or more repeated measures. A generalized estimation approach is discussed that allows for additional design modifications including flexible dose response modeling. In addition, sample size considerations for each stage are addressed.

Title:	**The Cohort Mortality Tables for Croatian Population**
Authors:	Bojan Basrak, Miljenko Huzak, Anamarija Jazbec
Affiliation:	University of Zagreb
Abstract:	In 2014 Croatian Actuarial Society and Croatian Insurance Bureau initiated the project of making the first Croatian annuity tables. The essential part of this project is estimation and projection of the general Croatian population mortality for generations born from 1951 to 2010 based on available census data. We used the Poisson log-bilinear model for projection, and combination of simple linear regression and Poisson model for estimation the mortality. Since some annual census data were not available we needed to interpolate the data for estimating annual central exposition to risk. The same quantity we needed for estimation the unisex force of mortality in cases when we had only death rates by both sexes.

Title:	**Bibliometric analysis using data analysis methods: an application on Medline abstracts**
Authors:	Annie Morin
Affiliation:	AASMA, Rennes France
Abstract:	One way to track the evolution of scientific research in a given field or to detect the emerging areas is to apply textual analysis methods to the abstracts that we could have loaded from databases such as Medline for medical topic. A few years ago, we conducted a bibliometric study on malaria for the period 2002-2006. We used a data analysis method called factorial correspondence analysis which is based on singular value decomposition We found four major subtopics in malaria research, each of the subtopic was described by a group of words that we called metakeys. In the last years, the number of publications on malaria exploded. We loaded abstracts using the same query which is the keyword malaria for the period 2006 to 2015 and we start again a bibliometric study. The main subtopics are more or less the same but the metakeys have changed for some of them. We will present the results of both studies, focusing on their similarities and differences. We will also provide some thoughts and perspectives on textual data analysis methods for this kind of data.

Title:	**Development of Attitude Towards Plagiarism Questionnaire**
Authors:	Martina Mavrinac1, Gordana Brumini1, Mladen Petrovečki1,2
Affiliation:	1Department of Medical Informatics, Rijeka University School of Medicine, Rijeka, Croatia 2Department of Clinical Laboratory Diagnostic, Dubrava Clinical Hospital, Zagreb, Croatia
Abstract:	Aim. To construct and test the factorial structure and psychometric characteristics of a questionnaire measuring attitude towards plagiarism. Methods. For the first versions of the questionnaire 67 statements were developed based on the relevant literature, after expert revisions the number of statements decreases to 36. For the validation process a research was conducted from March to June 2009. Participants were 227 undergraduates and graduate students (128 women and 99 men) from three Croatian universities; with a median age 21 years (range 18 to 48). Principal component analysis (PCA) was used to find out the factor structure of the questionnaire and to measure construct validity. The number of factors to retain was determined by the Scree-test and interpretability criteria. Results. A three-factor structure was disclosed addressing different aspects of attitudes towards plagiarism: factor I - approving attitude towards plagiarism (12 items); factor II - disapproving attitude towards plagiarism (7 items); and factor III - subjective norms towards plagiarism (10 items). The final version of the questionnaire consisted of 29 items. Cronbach's alpha was calculated to confirm the reliability of the scale: factor I, alpha = 0.83; factor II, alpha = 0.79; and factor III, alpha = 0.85. Correlations among factors were: –0.37 between I and II, –0.41 between I and III and +0.31 between II and III. Conclusion. Attitudes Towards Plagiarism (ATP) questionnaire has been developed with good psychometric requirements. The Croatian version of the ATPQ has been retested in 2013, confirming the obtained factor structure. The English version was used in different researches measuring attitudes towards plagiarism in USA, SAR, Thailand, Pakistan, Malaysia, Latvia, Philippines, Indonesia, etc. It will be still used in future research as a standardized tool for measuring attitudes towards plagiarism. Key words: attitude; factor analysis, statistical; plagiarism; validation study; questionnaire

Title:	**Statistical analysis of random forest models**
Authors:	Zelimir Kurtanjek
Affiliation:	University of Zagreb, Faculty of food technology and biotechnology (retired)
Abstract:	Applied are random forest models on a large data set of LC-MS data from cancer cell lines. The data set constitutes of 10 000 raw m/z data spectrograms, from two parallel experiments, for 800 samples divided into control, benign and positive classes. The objective is to discern the key m/z signatures responsible for the classification. The data set is effectively decomposed by SVD into principal components with about 100 components accounting for 99.9 % of the total variance. Application of linear discriminant analysis, with the first component accounting for 72 % classification of the complete data rendering distinct clusters in the two dimensional LDA plane. Based on the LDA components ranked are importance of the individual m/z data. Effective random forest models are derived based on the SVD eigenvectors. Random forest models are thoroughly validated by several 10-30% folding sets. Decomposition of the random forest eigenvector variable importance ranked lists (Gini and variance order) enabled evaluation of importance individual m/z signatures.

Title:

Kinesiometrics or Kinesimetrics or Kinesmetrics or What's in a name?

Authors:

Franjo Prot (1), Rado Pišot (2) and Petr Blahuš (3)

Affiliation:

(1)Faculty of kinesiology, University of Zagreb,
(2)Faculty of applied kinesiology, University of Primorska,
(3) Department of Physical education and sport, Charles Universty Prag

Abstract:

Standing upon a broad shoulders of previous experiences in measurement of human movement the term kinesimetrics in Franch language as kinesimetrie “kinesimetrie s.f. (ki-ne-zu-me-tri) – from greek: kinesis, movement; metron, mesur). Mecan. Art ou mainere de mesurere du movement” (adj. kinesimetrique) in mechanical sense have been introduced by Piere Larouse (1870) Grand Dictionnaire Universel de XIX siecle. Tome 9th page 1211 and repeated in Complement de Dictionarie de l’Academie Francaise(1881), page 659. It was Momirović (1969), who introduced the term kinesiometrics “kineziometrija” i.e. “kinesiometry” in few papers published as outcome of Zagreb methodological circle and incorporate the term in his lectures as recorded in lecture notes entitled “Short course in kinesiometry”(“Kratki kurs iz kineziometrije”) conducted at postgraduate study of Kinesiology during 1971/72; what became sub discipline of kinesiology (Mraković, Momirović, Hošek-Momirović, Metikoš, Hofman and Prot; 1987). Finally, the term “kineziometrija” had been included and presented in Sport Leksikon (1984) and Anić and Goldstein (1999) dictionary. Based on full assimilation of developments from psychometrics and ideas of Guttman (1954) and Harris (1963) methods for determination of internal metric properties of composite measurement instruments had been in focus continuously, what relaxed and generalized classical test theory model. Three latest among 46 macro programs for internal psychometric analysis of composite tests are performing kinesiometric/psychometric analysis: on standardized input data – RTT12G; on sigmoid (0,1) transformation of standardized input data – RTT12GS, on sigmoid (-1,1) transformation of standardized input data – RTT12GSS. The code names of these macro programs indicate continuous developments from the earlier versions. Finally, kinesmetrics as a term for a discipline intended to develop and apply mcasurement theory, statistics, and mathematical analysis in the area of kinesiology (Zhu, 2003). The term "kinesmetrics" was coined by Weimo Zhu (Silverman, 2003) in 1998 when later on he created a new doctoral program at the University of Illinois at Urbana-Champaign, USA in1999. The major areas of kinesmetrics research and applications include development of research design, statistical and mathcmatical modeling, data analysis, computers technologv, and measurement theory development. Although the term was introduced more than a decade ago, it is still unfamiliar to a certain number of professional kinsesiologist outside North America. The obvious conclusion could be that despite the differences in used terms the unified tretment of subject is obvious.

Title:	**Contemporary approaches for monitoring functional and cognitive status in elderly people**
Authors:	Uroš Marušič, Rado Pišot
Affiliation:	University of Primorska, Science and Research Centre, Institute for Kinesiology Research, Slovenia
Abstract:	Functional and cognitive decline and/or impairment are among the most feared and costly aspects of aging (Deary et al., 2009; Morrison & Newell, 2012). The aging process is commonly defined as an accumulation of diverse adverse changes that increase the risk of death, and changes that are attributed to development, genetic defects, the environment, disease, and the in-born aging process (Harman, 1998). To be able to develop an effective countermeasure within the aging period, new approaches are needed. Extensive research has shown that healthy elderly people have a more complex gait pattern compared to their younger counterparts. This is reflected in reduced comfortable gait speed, shorter stride and step length, increased double support phase and increased step-to-step variability (Menz, Lord, & Fitzpatrick, 2003; Winter, Patla, Frank, & Walt, 1990). The currently available research suggests that the effects of divided attention on motor performance and gait control could be assessed by a “dual-task” methodology. By using modern technology (e.g. Optogait system) and adding an additional task while walking (e.g. walking and counting backwards) we are able to access the inside of human brain and thereby study mechanisms of human gait control and cognitive functioning at the same time. In this presentation, the data of PANGeA project (bed rest, mass measurement and rehabilitation hip study) will be presented with a focus on dual-task methodology approach.

Title:

Behind the numbers – qualitative issues when designing experimental measurements

Authors:

Saša Pišot

Affiliation:

University of Primorska, Science and Research centre

Abstract:

This article describes background procedures as “silent protocols” including the possible impacts related to experimental measurement quality, the relevance of study results when measuring a given population. The example discussed herein was based upon a longitudinal project entitled: “Analysing fundamental motor pattern, skeletal and muscle adaptation on specific sedentary lifestyle factors amongst 4four and seven year old children,” financed by the Slovenian Research Agency (J5-2397). This project consisted of testing 107 (52 boys) four year old children, of which88 (40 boys) completed three test batteries for three consecutive years (from 2009 to 2012). All testing procedures conformed to the Declaration of Helsinki, approved by the Slovenian National Medical Ethics Committee. This included providing parents with written, informed consent prior to children participating in the study. Data collection was performed during the regular measurement days, which included these “silent” protocols, thus enabling the researchers to manage and stimulate full participation and cooperation of the children in all measurements. The “silent” protocols were defined as actions taking place before, during and after the typical measurement day, and divided into either:- Organisational tasks- included information, communication, logistics, and accommodation (e.g. an introduction of the project, design of the measurements; food and beverage consumption, any additional equipment or accessories)- Psycho-social engagement tasks- for building confidence and acceptance (e.g. meetings with parents and kindergarten teachers, correspondence and feedback information, social games to enhance children’s confidence building, and personal support action). Assuming that real time of all measurements for five stations was estimated at 90-min duration for each child, the children spend from 8.30 to 13.00 with the researchers. Therefore, the “silent” protocol included an additional 3-h of carefully designed activities. The standard project measurement battery consisted of: an anthropometry test, morphological characteristics, a test of maximal strength, coordination and agility, and finally one test of muscle activation. All analyses were completed in the most common fundamental motor patterns (FMP, walking, running, crawling, climbing and jumping). Standardised items for latent variables were then developed, with the aid of modern instruments, and a complete kinematic evaluation of FMPs were also completed. This analysis included: summarising any peculiarities of the measured FMPs, adaptations and interdependencies found between different FMPs, the impact of morphological characteristics on FMP adaptation, and a comparison between the analysed FMP and lifestyle characteristics of the children and their families. In closing, only 19 (of 109) children did not complete testing within the three years of measurements. Of those, 12 children had reported illness or moving to another town as the main reasons for not completing the study. In conclusion, the researchers found that analysing the “silent” protocol assisted with project management to optimise study time management, and choose the best study researchers all of which are crucial for a successful project outcome when testing children.

Title:	**On General Image Transformation in Kinesiometrics Context**
Authors:	Franjo Prot (1) and Sara Prot (2)
Affiliation:	(1)Faculty of kinesiology, University of Zagreb; (2) Department of Psychology, Iowa State University
Abstract:	Transformation of row variables into other metric as the preliminary procedure in data analysis is sometimes convenient and sometimes necessary. It is recalled that one Momirović, Zakrajšek and Štalec (1973) published paper from Zagreb methodological (data analysis and statistics) circle on the application of generalized image transformations in analysis of relations between groups of variables had anticipated some new developments in methodological treatment of multivariate relations among sets of variables for decades after. For Z1 a standardized data matrix, obtained by the description of a random sample E of n objects on a sample V1 of m1 normally distributed quantitative or quantified variables in time point t1, and for Z2 and other standardized data matrix, also, obtained by the description of E on a sample V2 of normally distributed quantitative or quantified variables in time point t2, such that V1 V2 = 0. The generalized image transformation of variables from V1 and V2 , where R11 = Z1t Z1 n-1 and R22 = Z2t Z2 n-1 are inter correlation matrices of variables in the sets V1 and V2, respectively, and by R12 = R21t = Z1t Z2 n-1 is cross correlation matrix between variables from V1 and V2 where R11 and R22 are both nonsingular, can be defined as follows: Let be B12 = R11-1 R12 and B21 = R22-1 R21 are matrices of the standardized partial regression coefficients obtained by the solution of regression problem in a symmetric way. The vector variables from H2 = Z1 B12 will be now the image of the variables from V2 in the space spanned by the vectors of variables from V1, and the vector variables from H1 = Z2 B21 will be the image of the variables from V1 in the space spanned by the vectors of variables from V2. Denote now by Q22 = H2t H2 n-1 = B12t R11 B12 the covariance matrix of image variables from G2, and denote by Q11 = H1t H1 n-1 = B21t R22 B21 the covariance matrix of image variables from G1. The matrix defined by Q12 = H1t H2 n-1 = B21t R12 B12 is now the cross covariance matrix of variables from H1 and H2. Let are D12 = diag Q11 and D22 = diag Q22 matrices with variances of variables from H1 and H2, obviously equal to coefficients of determination of variables from V1 and V2 on the basis of their mutual relationships. Standardized generalized image variables are now G1 = H1 D1-1 and G2 = H2 D2-1 with inter correlation matrices M11 = G1t G1 n-1 = D1-1 Q11 D1-1 and M22 = G2t G2 n-1 = D2-1 Q22 D2-1 and cross correlation matrix M12 = G1t G2 n-1 = D1-1 Q12 D2-1.Based on the Konstantin Momirović legacy of algorithms and macro programs (Prot, F., K. Bosnar, A. Hošek, V. Lužar-Stiffler, V. Hljuz Dobrić, Z. Bekić and M. Gredelj; 2008) the aim of the contribution is to present same complementary solutions named nuclear analysis where nucleus of two sets of quantitative variables is defined as the cross covariance matrix of the variables mutually transformed to generalized image form. Spectral analysis of any cross covariance matrix, and in this case nuclear matrix, is actually canonical covariance analysis of two sets of variables transformed to general image form, what can be helpful to understand the data.

Title:	**How to use online linguistic tools for ontology learning from a domain corpus? Illustration on radiation safety.**
Authors:	Olena OROBINSKA & Jean-Hugues CHAUCHAT
Affiliation:	ERIC Lab, Université de Lyon, France
Abstract:	In computer science and information science, an ontology is a formal naming and definition of the types, properties, and interrelationships of the entities that really or fundamentally exist for a particular domain of discourse. We propose a semi-automatic method to complete a domain ontology, illustrated by an example on the field of Radiological Safety. Our hybrid method combines different (statistical, linguistic, lexical) techniques which can detect the lexical variations (different lexical entries) of the initial concepts list built by domain experts. Online linguistic tools (tagger and synonym dictionaries) are intensively used. From our point of view, verbs play a key role to describe actions and other properties of the subjects; in other words, verbs explicitly reveal the properties of names. So, we focused on verbs as the primary means of semantic search for words that are synonyms (for this domain) but do not have lexical similarity (e.g., not the same root). The first stage of our algorithm is the tagging of the corpus. The thesaurus gives us the names that are synonymous with the initial concepts; among all available synonyms, we only keep the nouns that are in the corpus. Meanwhile, we look for verbs that are associated in the corpus to initial concepts and their synonyms; among these verbs, we only keep those present in the corpus. Finally, we look in the corpus for all pairs "name - verb" where one of the original concepts (or a synonym) is subject of a sentence, and where one of the selected verb is its predicate: the list of such names is checked by the domain expert. So the expert works only at the beginning, to form the first short list of initial concepts, and in the end to validate the proposed new names.

Title:	**Trends in Production of Industrial Round Wood in Croatia and Surrounding Countries**
Authors:	Maja Moro
Affiliation:	University in Zagreb, Faculty of Forestry, Department of Processes Engineering
Abstract:	On the basis of established values for period 1993-2013, in this paper discuss a possibility to predict trends in production of industrial round wood in Croatia and surrounding countries. The data of production values of industrial round wood through analyzed period are gathered from Croatian Bureau of Statistics and FAO base. In order to predict a future trends of industrial round wood production for Croatia and surrounding countries, dynamic economic analysis of time series data was performed. Prediction is limited to year 2020, because of turbulences in this market and the length of analyzed time series.

Title:	**Effect size and its statistical significance in published papers as metadata in horticultural sciences for application of meta-analysis**
Authors:	Borut Bosančić [1,2], Marija Pecina [2], Nikola Mićić [1,3]
Affiliation:	1. Faculty of Agriculture, Univestity of Banja Luka; 2. Faculty of Agriculture, University of Zagreb; 3. Genetic Resources Institute, University of Banja Luka
Abstract:	In order to conduct meta-analysis abundance of quality metadata are required. Meta-analysis in horticultural sciences is novel approach and the standard methodology for finding metadata is to conduct the data search from related research papers through available databases. In the course of planned meta-analysis available databases were searched for metadata on hail protection of apple orchards specifically regarding impact of hail nets on fruit characteristics.It is observed that in horticultural literature sometimes the case that effect sizes are reported without clearly specifying estimates of variations, sample sizes and even without reporting p-values of applied statistical tests. This is especially often in the cases when several groups are compared with post-hoc test hence indicating the grouping pattern with letters rather than actual biometrical test results. Such practice is understandable from the perspective of simplification of data presentation and comprehension of research results. However from the perspective of possible summarizing and reviewing the results from the multiple researches especially for application in meta-analysis a full set of average effect sizes, with related variability estimates and tested values with its exact significance are recommended to be included in publications.

Title:

Discrete choice analysis of forest inventory plot types in Croatian uneven-aged forests

Authors:

Mislav Vedriš, Anamarija Jazbec

Affiliation:

University of Zagreb, Faculty of Forestry

Abstract:

Reliable forest inventory is a basis for sustainable forest management. Forest inventory basically consists of terrestrial measurement being done on sample plots. Choice of sample is an essential component of forest inventory that has to ensure sound results by means of precision and accuracy. Balance between available resources (money, time) and results is always demanding task that has to be taken into account.

As part of investigation on sample plot type that could optimize efficiency by ensuring best possible results at minimum cost, a questionnaire has been carried out among 60 forest inventory experts in Croatia. Seven previously field-tested circular plot types were proposed for expert evaluation: 250 m2, 500 m2, 750 m2, concentric plot 78,5/452,4 m2 , concentric plot 254,5/615,8 m2 , concentric plot 153,9/530,9/1256,6 m2 and factor 3 Bitterlich plot. Experts were asked to chose appropriate plot type(s) and confirm their choice by addressing aspects of chosen type: simplicity, reliability, familiarity, expert recommendation and cost. Answers were analysed by discrete choice analysis considering groups of experts by institution and age. Reliability, cost and efficiency of listed methods obtained by field check were later compared to experts' attitudes from questionnaire. Most of experts prefer familiar and more used methods, especially experts from state forest company. Experts from other institutions and private companies in addition to well known would also accept improved and more complex types as concentric plots. On the other hand, most experts think of reliability as the most important aspect, followed by cost and simplicity. Reliability is even more important for experts from private companies and scientific institutions. For these experts simplicity is the least important aspect, unlike state experts who favor simplicity as much as reliability. Younger experts, unlike the older ones, have an inclination to favor recommendation of colleagues in their choice. Although experts would chose methods that are familiar with, it is interesting that familiarity is generally assessed as being the least important aspect. Case study results on efficiency support the choice of 500 m2 plots, favoring also concentric type plots that were mostly neglected by the experts. Improvement of the forest inventory is continuous and ever lasting task aiming at better efficiency. Better suited plot types could significantly contribute to that aim. However, since implementation of plot type relies on people doing field measurements, their experience, knowledge and attitudes should be taken into account when changes in inventory system occur.