BIOSTAT 2023

26th International Scientific Symposium on Biometrics

ZADAR, CROATIA, 14 - 17 JUNE 2023

BOOK OF ABSTRACTS

EDITED BY:
Anamarija Jazbec
Azra Tafro
Diana Šimić
Marija Pecina
Mislav Vedriš
Slavica Sović
Vladimir Brajković
Zdenko Sonicki

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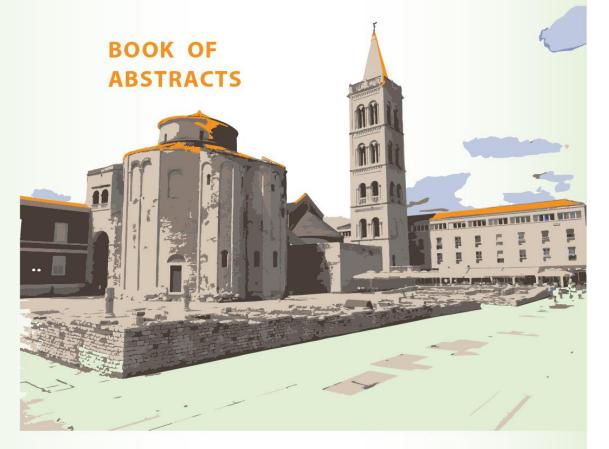- ZAGREB -

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Zagreb, 2023.

IMPRESSUM

ORGANISER

Croatian Biometric Society

UNDER THE AUSPICES of

University of Zagreb

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Gregor Gorjanc
University of Edinburgh
The Roslin Institute
Scotland, UK

VENUE:
Hotel Kolovare
Ul. Bože Peričića 14.
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PREFACE

Welcome to the Book of Abstracts of BIOSTAT 2023 – The 26th International Scientific Symposium on Biometrics organized by the Croatian Biometric Society, held in Zadar, Croatia, June 14-17, 2023.

BIOSTAT Symposium is held under the auspices of the University of Zagreb.

The symposium is an intrinsically interdisciplinary meeting accepting papers from a wide array of research disciplines at the intersection of data sciences and life sciences as evidenced by this Book of Abstract. BIOSTAT 2023 comprises 24th School of Biometrics, keynote lectures, and contributed papers. This brochure contains 20 (2 students) abstracts written by 57 authors from 8 countries – Austria, Bosnia and Hercegovina, Croatia, Czech Republic, Netherlands, Slovakia, Slovenia and United Kingdom.

The Symposium takes place in Zadar, a city whose past goes back 3,000 years, when it was first mentioned as a settlement in written documents and historical artefacts. It became a fully urbanized centre during ancient Roman times and remained as such continuously for another two millennia. Zadar is both an atmospheric time machine and an open air museum. Here on display, you will find some of the most beautiful monuments of architecture and cultural heritage of the eastern Adriatic coast. Its city walls are the ancient guardians of this still vibrant historic museum in the open, end they were rightly added to UNESCO's World Heritage List.

We are continuing this year with our traditional 24th School of Biometrics. Our guest lecturer is professor **Tomáš Mrkvička** from the Department of Applied Mathematics and Informatics at the University of South Bohemia Faculty of Economics (Czech Republic) with the topic of "Global envelopes in R".

This year the keynote speaker is professor **Gregor Gorjanc** from the Roslin Institute at the University of Edinburgh, with a lecture on "Novel biometric tools for managing and improving populations in the era of mega-scale genomics".

Following our tradition from previous years, we award the best presentations for Students and for Scientists. Furthermore, we encouraged BS and MS students to participate in the Symposium with or without abstracts (presentations) with a popular registration fee of 0 €.

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

Editors:
Anamarija Jazbec, Azra Tafro, Diana Šimić, Marija Pecina, Mislav Vedriš, Slavica Sović, Vladimir Brajković and Zdenko Sonicki
Zadar, June, 2023

PROGRAM

SYMPOSIUM PROGRAM at a Glance

Wednesday, June,	19:00 – 20:00	Registration & Welcome Cocktail	
Thursday, June, 15	9:00 – 9:30	Opening ceremony	
	9:30 – 11:00	*Chair: Anamarija Jazbec*	School of Biometrics – *Part I* **Tomáš Mrkvička:** Global Envelopes in R
	11:00 – 11:30	COFFEE	
	11:30 – 13:00	*Chair: Anamarija Jazbec*	School of Biometrics – *Part II* **Tomáš Mrkvička:** Global Envelopes in R
	13:00 – 14:00	LUNCH	
	14:00 – 15:00	*Chair: Janez Stare*	Contributed session
	15:00 – 15:30	COFFEE	
	15:30 – 16:30	*Chair: Mislav Vedriš*	Contributed session
	18:00	Sightseeing	
Friday, June, 16	9:30 – 10:30	*Chair: Marija Pecina*	Keynote Lecture: **Gregor Gorjanc:** Novel biometric tools for managing and improving populations in the era of mega-scale genomics
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	11:00 – 12:00	*Chair: Vladimir Brajković*	Contributed session
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	16:00	Excursion	
Saturday, June, 17	9:30 – 10:15	*Chair: Azra Tafro*	STUDENTS SESSION
	10:15 – 11:15	*Chair: Zdenko Sonicki*	Contributed session
	11:15 – 12:00	COFFEE	
	12:00 – 12:30	Closing ceremony	
	12:30 – 13:30	LUNCH	

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SYMPOSIUM PROGRAM

Day	Time		
Wednesday, June,	19:00 – 20:00	Registration & Welcome Cocktail	
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	13:00 – 14:00	LUNCH	
Thursday, June, 15	14:00 – 15:00	*Chair: Janez Stare*	Contributed session
		AUTHOR	TITLE
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		Ana Martinčić Špoljarić	Convergence of Telomere Loss Process With and Without Abrupt Shortening
		Azra Tafro	Gaussian mixture model for PET image reconstruction with reduced sample size
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		Nikola Zorić, Dinka Matošević	Exploring Spatio-temporal Distribution of Forest Pests and Diseases in Croatia for Effective Management
		Martina Đodan, Sanja Perić	Improvement of stability and growth of p. oak stands - does provenances matter?
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		AUTHOR	TITLE

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Saturday, June, 17	9:30 – 10:15	*Chair: Azra Tafro*	STUDENTS SESSION
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	12:00 – 12:30	Closing ceremony	
	12:30 – 13:30	LUNCH	

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

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24th SCHOOL OF BIOMETRICS

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Tomáš Mrkvička

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Prof. Tomáš Mrkvička studied Theory of Probability and Mathematical Statistics at Charles University, Prague. He has worked at the University of South Bohemia in České Budějovice, Czech Republic since 2002. From the beginning, his interest has been in spatial statistics and functional data analysis. He is especially interested in developing new statistical methodologies in those fields. Nowadays, his main research interest is in testing statistical hypotheses, especially with functional test statistics, and he has written several influential papers on this topic.

As such, he is a co-author of three R-packages.
GET – the global envelope testing,
NTSS - Nonparametric Tests in Spatial Statistics and
binspp - Bayesian Inference for Neyman-Scott Point Processes.
On the other hand, he is also interested in cooperation with scientists from other fields, where he helps analyze data and suggest new approaches.

Topic:

Global envelopes in R

1 Course objectives

Traditionally, one-dimensional or multivariate test statistics have been used to test different hypotheses. Today the handling of the data is more rich, and we can have data that can provide more insight on the studied phenomena if a functional test statistic is used. But this can be quite challenging: one has to take care of the multiple testing problem and changes in the distribution across the domain; often the test statistic is a specific one so its distribution is not known; and often the user requires a graphical interpretation of the testing results so that the interpretation of results is more understandable. Therefore, we have developed a non-parametric method that is based on Monte Carlo simulations or permutations, which handles all the above challenges. The methodology is implemented in the freely available R (R Core Team, 2021) package GET (Myllymäki and Mrkvička, 2020; Myllymäki et al., 2017). The official release can be found in Comprehensive R Archive Network (CRAN) and its development version via a github repository:

- Official release: https://cran.r-project.org/package=GET
- Development version: https://github.com/myllym/GET

We introduced the methodology first for a general Monte Carlo test with any functional test statistic in the case where the functions are simulated under the null model (Myllymäki et al., 2017). We have further considered and developed the methodology for general multiple Monte Carlo testing (Mrkvička et al., 2017), functional ANOVA (Mrkviˇcka et al., 2020) and general linear models (Mrkvička et al., 2021; Mrkvička et al., 2021), functional outlier detection and clustering (Dai et al., 2020b,a). The methods have already shown their usefulness in many areas, e.g., spatial statistics (Myllymäki et al., 2017; Mrkvička et al., 2017; Mrkvička et al., 2016; Myllymäki et al., 2020), functional data analysis (Narisetty and Nair, 2016; Mrkvička et al., 2020; Mrkvička et al., 2021; Mrkvička et al., 2021; Racine et al., 2021) and image analysis (Mrkvička et al., 2021) with applications to agriculture, architecture and art, astronomy and astrophysics, ecology and evolution, economics, eye movement research, fisheries, forestry, geography, material science, and medicine, health and neurosciences (see Myllymäki and Mrkvička, 2020, and references therein).

2 Learning outcomes

- The participants will have basic understanding of a Monte Carlo and permutation test based on a single, multivariate and functional test statistic. They know the basic principles of running a global envelope test in R, and have tested it in example situations.
- The participants are aware that the global envelope is a general tool that can be used also for other purposes than testing such as central regions of functional data, functional clustering and confidence and prediction bands.

3 Prerequisites

We expect the participants have some basic knowledge/understanding of statistics and the R software. The course is not intended to discuss very basics of the R code itself. Also the participants should have the newest version of R (https://cran.r-project.org/), and preferably also Rstudio (https://www.rstudio.com/), installed on their computers, if they want to test things themselves. They could additionally also install the GET library in advance by starting R and typing install.packages('GET') there.

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KEYNOTE LECTURE

KEYNOTE SPEAKER

Gregor Gorjanc

University of Edinburgh
The Roslin Institute, Scotland, UK
Email: Gregor.Gorjanc@roslin.ed.ac.uk
Web site: https://www.ed.ac.uk/profile/dr-gregor-gorjanc

Topic:

Novel biometric tools for managing and improving populations in the era of mega-scale genomics

Abstract:

The field of genetics has recently experienced tremendous growth and this pace will accelerate. When Gregor Mendel discovered the key principles of genetics, he had no knowledge of the inheritance mechanism. Similarly, Ronald Fisher almost singlehandedly defined the field of quantitative genetics without the knowledge of genome. These, and other, key genetics principles were recently unleashed with the affordable generation of genomic data. Animal and plant breeding are at the forefront of applying genomic data to accelerate genetic improvement. This improvement is much needed to address increasing demand for food in the face of climate change. In this contribution, I will highlight our work in using or developing novel biometric tools for improving agricultural populations. First, I will summarise the concept of genomic prediction and selection, where we regress observed phenotype values on genome-wide markers to estimate allele substitution effects, which are then used to predict genetic value for any genotyped individual. I will show how such genomic predictions can significantly improve a hybrid plant breeding programme. Combined with environmental data, such genomic predictions are now starting to unravel the challenging genotype- by-environment interactions. These methods hold promise for personalised medicine. Second, I will summarise our animal breeding work in adopting genomic selection, optimising model fitting with millions of genotyped individuals, and analysing trends in genetic mean and variance in animal breeding programmes, particularly dairy cattle. Our results show that genomic selection increased the rate of genetic change, both in mean and variance. To better understand global genetic variation in cattle, we are studying whole-genome genealogies, efficiently encoded with tree sequences. I will show first results of inferring whole-genome genealogies from the 1000 bull genomes project. Third, insects have been used for food and feed production for millennia, but have only recently been recognised as a major future source of feed and food. I will show our results on studying genetic variation in honey bees by inferring wholegenome genealogies across 30 sub-species. I will also summarise our collaboration with black soldier fly breeders to boost future insect protein production. Much of our work involves simulating quantitative genetic data and breeding programmes, for research and education. To this end we have create a free online course on "Breeding programme modelling with AlphaSimR" – register at https://edin.ac/3wfGSEj.

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CONTRIBUTED SESSIONS

Title:	**Asymmetric 2-group k-adic similarity coefficient**
Authors:	**Perišić Ana[1], Vanbelle Sophie[2]**
Affiliation:	[1]University of Split, Polytechnic of Šibenik [2]CAPHRI, Maastricht University
Abstract:	Binary classifiers are used in various research fields to assess the presence of a trait. Applying different binary classification rules by different raters could result in different classifications, observed as binary data groups. Although measuring similarity of two binary variables is an active research field, measuring similarity of two groups of binary variables still offers limited methodological solutions. In particular, two binary states might not be equally important, and the interest can be put on the presence of a trait, rather than on the absence. In this work, we propose an asymmetric approach suitable when the goal is evaluating similarity between groups of binary variables when only the presence of a trait is of interest. The approach takes into account both between and within group similarity. Proposed coefficients are based on the k-adic formulation of the Jaccard index. We present some desirable properties of the coefficients and possible applications.

Title:	**Convergence of Telomere Loss Process With and Without Abrupt Shortening**
Authors:	**Ana Martinčić Špoljarić**
Affiliation:	Rimac Technology d.o.o.
Abstract:	Studying the telomere shortening mechanism is important for understanding cellular aging in biology. Presented model is trying to capture telomere-controlled cell senescence by considering two modes of telomere shortening – gradual and abrupt shortening, without the effect of telomerase enzyme. In order to investigate how the stochastic behaviour of telomeres affects the cell with time, time – discrete processes of telomere length are approximated by the time – continuous processes. Dependent on sources of randomness included in the model, we arrive at limit processes with continuous trajectories and jump-diffusion regime-switching processes. Their limit distributions and asymptotic properties are analysed, with the emphasis on the expected time of senescence.

Title:	**Gaussian mixture model for PET image reconstruction with reduced sample size**
Authors:	**Azra Tafro**
Affiliation:	University of Zagreb Faculty of Forestry and Wood Technology
Abstract:	In positron emission tomography (PET) image reconstruction, one of the main goals is to achieve accurate reconstruction from a very small set of measurements, in order to minimize patients' exposure to radiation. While most reconstruction methods are based on a discrete set of values on a pre-defined grid, in this research we propose a parametric Gaussian mixture model that significantly reduces the required sample size. The issue that arises with this approach is that the raw measurements are pairs of gamma rays emitted from a radioactive substance in opposite directions, which the scanner records as lines whose point of origin is unknown. Therefore, the task is to estimate the parameters of a two- or three-dimensional Gaussian mixture distribution using lower-dimensional data. In our ongoing research, we propose several estimators for single distribution parameters that utilize favorable properties of the normal distribution. To estimate the entire mixture model, an algorithm is developed that adapts the traditional maximum-likelihood method to novel estimators. Simulations on artificial data show that accurate reconstruction can be achieved from lower dose exposure. Furthermore, this approach yields a high-resolution model that can be readily used in further analysis. This is part of joint work with Damir Seršić and Tomislav Matulić at the University of Zagreb Faculty of Electrical Engineering and Computing.

Title:	**Testing the accuracy of terrestrial laser scanning technology for individual tree DBH estimation in a urban pine stand**
Authors:	**Andro Kokeza[1]*, Fran Domazetović[2], Luka Jurjević[3], Ivan Marić[2], Ante Šiljeg[2], Ivan Balenović[1]**
Affiliation:	[1]Croatian Forest Research Institute, Jastrebarsko [2]Department of Geography, University of Zadar, Zadar [3]Geo Unit d.o.o., Zadar
Abstract:	Terrestrial laser scanning technology has been of interest in researches about the possibilities of its practical application in forest surveys. A number of studies have already been conducted in the last decade for the static terrestrial laser scanning (TLS) while in the recent years hand-held personal laser scanning (PLS) has increased the interest of laser scanning making its way into forest practices. The main goal of this research is to test the accuracy that terrestrial laser scanners have for diamater at breast height (DBH) estimation of individual trees. The research was conducted in one circular sample plot with radius of 15 m located in a urban black pine (*Pinus nigra* L.) forest stand in Zadar. For this purpose, a detailed comparison of the estimation accuracy of the DBH of individual trees, between the data obtained on the basis of classic field measurements (caliper, diameter tapes), TLS and PLS, was carried out on 37 pine trees. TLS was carried out using multi-scan approach while PLS_{HH} was carried in four different scanning schemes of different complexity (from least to most complex). DBH measured with diamater tapes was used as a reference data (ground-truth data) and the following results are presented by mean absolute error (MAE). DBH measured by calliper produced MAE of 0.51 cm. The dataset obtained by TLS was modeled i.e. fitted by circle, column and ellipse for the DBH estimation in the LiDAR360 software. Fit by circle DBH estimation gave the best result among the three fitting methods (0.89 cm). With that knowledge, PLS_{HH} datasets DBH estimation were carried out with fit by circle method. The most complex scanning scheme gave the best results (1.91 cm) while the least complex scanning scheme gave the worst results (2.79 cm). The obtained results confirmed the great potential of terrestrial laser scanning technology in the operational forest surveys, and further research should include forest stands of different managment and age classes.

Keywords: forest measurements, hand-held personal laser scanner, static terrestrial laser scanner |

Title:	**Exploring Spatio-temporal Distribution of Forest Pests and Diseases in Croatia for Effective Management**
Authors:	**Nikola Zorić, Dinka Matošević**
Affiliation:	Croatian Forest Research Institute Division for Forest Protection and Wildlife Management Cvjetno naselje 41, Jastrebarsko, Croatia
Abstract:	Forest pests and diseases play a major role in shaping Croatia's ecology and economy, as they affect forest health, timber production, and biodiversity. In this presentation, our goal is to examine the spatio-temporal distribution patterns of forest-related issues during the last five years and to identify factors that could influence their spread. We rely on local-level disturbance data from state and private owned forests to study forest pests and diseases in Croatia. Our presentation seeks to enhance understanding of the environmental and anthropogenic factors that could contribute to the distribution patterns of forest pests and diseases, such as climate variables, forest composition, and human intervention. The insights gained from this research could help inform forest management and policymaking in Croatia, emphasizing the need for targeted, region-specific interventions. Furthermore, we will touch upon potential future research directions, such as exploring the impacts of climate change on the distribution of forest pests and diseases and evaluating the effectiveness of proposed management strategies. This presentation underlines the significance of spatio-temporal analysis in tackling complex ecological challenges in Croatia

Title:	**Improvement of stability and growth of p. oak stands - does provenances matter?**
Authors:	**Martina Đodan, Sanja Perić**
Affiliation:	Croatian Forest Research Institute
Abstract:	Climate changes rapidly induce shifts in site conditions which are favourable for certain tree species and their provenances. Furthermore, other threats (e.g. oak lace bug, frost, storm events) as well as social and economic circumstances (e.g. increase of wood prices and wood demand) act as drivers to push forest management into more intensive, but more adaptive and efficient one. If the most important economic tree species in Croatia are taken into consideration, such as Pedunculate oak (*Quercus robur* L.), shifts in site conditions and consequently selection of more adaptive provenances for regeneration and restoration purposes is of the utmost importance. Due to biology of p. oak, regeneration of forest stands is quite demanding while more than ¾ of produced total forests seedlings in Croatia is serving for this purpose. The high cost and resources needed to be invested in such production cannot be neglected on the national level. The first step in nursery production is procurement of forest seeds, which is limited in recent years while related problems culminated in the year 2022. Which provenances are the most appropriate from the standpoint of growth and production is crucial problem, growing each year and reaching its peak recently. Long term provenance tests, quite expensive and rare on European level, provide necessary background for silvicultural decision making in terms of provenances' growth, production, vitality and consequently nursery production plans. The aim of the research was to answer the question is there significant differences in tree height and diameter at breast height (DBH) between provenances and localities. If so, we aimed to single out the best provenances which could be supported and the worse ones to be excluded from management. Research included 16 provenances on two localities situated in two localities - Gajno (trial plots in central Croatia) and Slavir (trial plot sin Eastern Croatia). Provenances originate from natural distribution of p. oak in Croatia, from the most eastern edge (provenance Mitrovica, Serbia, just at border with Croatia) up to the most western distribution edge (provenance Motovun). Trial is set identically on both localities, in four repetitions, with the same 16 p. oak provenances in the spring of 1988. Trees on Slavir locality were measured in the winter/spring of 2023, while trees in Gajno were measured in the spring of 2021 and 2023. All trees in the trial were measured (tree height with Haglöf/Vertex IV and DBH with calliper) according to their unique number. Data were analysed using Statistica soft. ANOVA for both localities for 2023 data, and RMANOVA for Gajno locality for 2021/2023. data sets. Analisys showed significant differences among studied provenances both between localities and among provenances pointng to the conclusion that selection of provenance must be based on scientific results since it has prominent role in growth and development of p. oak trees. These findings are strongly advised to be used for artificial regeneration of p. oak stands in Croatia and for planning of nursery production on the national scale.

Title:	**Calibration and validation of the model Biome-BGCMuSo for simulation of SOC change in oak forests in Croatia**
Authors:	**Doroteja Bitunjac[1], Maša Zorana Ostrogović Sever[1], Katarína Merganičová[2,3], Hrvoje Marjanović[1]**
Affiliation:	[1]Croatian Forest Research Institute, Jastrebarsko, Croatia [2]Institute of Landscape Ecology, Slovak Academy of Sciences, Nitra, Slovakia [3]Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague, Prague, Czech Republic
Abstract:	Soil organic carbon (SOC) is the largest terrestrial carbon (C) pool and one of five mandatory C pools in national greenhouse gas (GHG) inventory reports (NIR). In Croatia, oak forests are naturally regenerated under continuous crown cover and with this management practice, it is assumed they preserve stable SOC stocks. Currently, Croatia reports no change in atmospheric C under the SOC pool in its NIR, but due to the ongoing climate change impacts, it is reasonable to expect certain alterations in SOC stocks. In order to reduce the uncertainty of SOC stock changes estimates, repeated national soil inventory is required. When repeated inventories are missing, the alternative is using a cost-effective method of SOC modelling. The aim of our research is to calibrate and validate the terrestrial ecosystem model Biome-BGCMuSo for the simulation of SOC stock changes in oak forests as an additional tool for use in national GHG inventory reporting. Parameter sensitivity analysis was performed by testing individual model parameters and a group of parameters. The model was calibrated using the generalised likelihood uncertainty estimation (GLUE) optimization method using different data sources (eddy-covariance site and chronosequence experiment) and different data types and frequencies (long-term C stocks and high-frequency C fluxes) for various ecosystem variables (aboveground live wood C (AGC), forest floor C, SOC, Net Ecosystem Exchange (NEE), Gross Primary Productivity (GPP) and Ecosystem Respiration (RECO)). In the final step in model calibration, we used decision tree algorithms. For model validation, we used annual data on C stocks in the AGC, forest floor C and mineral soil in the top 30 cm from seven stands of pedunculate oak chronosequence in the Jastrebarsko forest. All analyses were performed in R software. The calibration using only daily NEE fluxes resulted in a better overall agreement of model output with observed data for this variable but at the cost of the reduction in its intra-seasonal variability. The calibration using C stocks, AGC and SOC, improved the agreement of modelled and observed values for these variables but caused greater discrepancies between measured and modelled daily NEE fluxes. Both measured and modelled SOC stocks showed no age trend with higher between-stand spatial variability observed in measured data. The model validation showed a good agreement for C stocks in AGC and SOC for some chronosequence stands and a high disagreement between measured and modelled C stocks in the forest floor for several forest stands.

Title:	**Genomic connectedness between flocks – case study on Istrian sheep breed**
Authors:	**A. Kasap[1], J. Ramljak[1], M. Špehar[2], G. Gorjanc[3]**
Affiliation:	[1]University of Zagreb, Faculty of Agriculture, Department of Animal Science and Technology, Svetošimunska 25, 10000 Zagreb, Croatia [2]Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia [3]The University of Edinburgh, Royal (Dick) School of Veterinary Studies, The Roslin Institute, Easter Bush, Midlothian, EH25 9RG, Scotland, UK
Abstract:	The genetic connectedness between flocks is crucial for unbiased ranking of estimated breeding values obtained under the framework of across-flocks BLUP genetic evaluation system. Connectedness between flock is weak in many sheep populations worldwide, thus significantly limiting the accuracy of genetic evaluation and often leading to sub-optimal usage of the available genetic variation. Until recently, due to very complex and exhaustive calculations, estimation of connectedness was limited to researchers with advanced experience in both quantitative genetics and programing. Fortunately, now there is an R package, GCA, which utilizes both pedigree and genomic data to measure the connectedness between individuals across management units. This "tool" can be used with much less efforts to manage risks associated with biased comparison of estimated breeding values of animals belonging to different flocks. The issue of disconnectedness has been neglected in many animal breeding programs, usually wrongfully relying on the unconditional power of BLUP. This has been especially pronounced in the era of genomic selection which is supposed to alleviate this issue by detecting relationships between animals that cannot be determined through the pedigree. Therefore, the main aim of this study was to estimate the level of connectedness between flocks of Istrian sheep with both pedigree and genomic data (SNP array with 54K markers) to determine if usage of genomic data can unravel the true connectedness between flocks under the BLUP framework. Two PEV-derived statistics were analyzed: the prediction error variance of difference ($PEVD$) and coefficient of determination (CD). The estimated $PEVD_{ped}$, $PEVD_{gen}$ CD_{ped} and CD_{gen} were 0.78, 0.071, 0.61, and 0.69, respectively. The determined change $\Delta PEVD_{ped \rightarrow gen}$ = -10%, and $\Delta CD_{ped \rightarrow gen}$ = +13%, consistently showed the contribution of genomic information in unraveling connectedness between flocks under the BLUP framework, which will translate in more accurate estimates of breeding values for genomic selection versus traditional pedigree-based selection.

Title:	**multiOmics data analysis, integration, and visualisation - a case study in potato stress response**
Authors:	**Maja Zagorščak, Andrej Blejec, Špela Baebler, Carissa Bleker, Jan Zrimec, Anže Županič, and Kristina Gruden**
Affiliation:	Department of Biotechnology and Systems Biology, National Institute of Biology (NIB), Ljubljana, Slovenia
Abstract:	Potato, a dominant staple food across the globe, requires minimal amounts of fertilisers and crop management, thus making it a perfect candidate for economic, environmental, and social sustainability. On the other hand, keeping up with major factors negatively affecting agricultural yield, such as abiotic (i.e. heat, drought, salinity) and biotic (i.e. Colorado potato beetle, potato virus Y, *Phytophtora infestans*) stressors, is becoming more and more difficult in the face of intensifying climatic changes. The Horizon 2020 EU project Accelerated Development of multiple-stress tolerAnt PoTato (ADAPT) is focused on understanding potato responses to a combination of abiotic stresses and thus identify targets for breeding of new potato varieties. High-throughput phenotyping and multi-omics analysis of potato under single- and combined abiotic stresses was conducted on the well-known cultivar *Désirée*. The main questions addressed were: i) what are the markers (phenotypical, physiological, molecular) for individual vs. combined stress treatment, ii) which response mechanisms are triggered in each stress/multi-stress exposure, and iii) what are the common stress mechanisms (shared between all stresses). Data preprocessing, overall inspection of the multi-omic data, interpolation and imputation were conducted using R programming language. For statistical analysis of individual omics data layers, common 'omics analysis libraries were utilised. To assess the difference and similarity in the response, correlation based network inference within each omics level was conducted. Integration across different omics datasets was conducted using Canonical Correlation Analysis, N-Integration Discriminant Analysis with DIABLO, and Leave-One-Out graphs. The resulting output was supplemented with a prior knowledge network built upon hormone synthesis, regulation and signalling pathways and pathways involved in plant responses to stress. Integrated results will facilitate domain knowledge experts to answer the addressed questions in a holistic way. The protocol for species-agnostic multiOmics data integration is publicly available from institutional GitHub (https://github.com/NIB-SI/multiOmics-integration). Acknowledgement: We would like to thank the ADAPT consortium for generating Phenomics, Metabolomics, Proteomics, and Hormonomics data (https://adapt.univie.ac.at/).

Title:	**Multivariate analysis combined with melissopalynology improves insight into honey origin, environment and potential environmental disturbance**
Authors:	**Borut Bosancic[1,2]**
Affiliation:	[1]University of Banja Luka Faculty of Agriculture [2]University of Banja Luka Genetic Resources Institute
Abstract:	Melissopalynology is a method for identifying pollen grains in honey samples. It is in essence an expert method which requires knowledge of pollen grain shapes in order to correctly identify the plant of origin. Real floral honey originating from the bees and beehives contains pollen grains which are upon identification used to indicate the category of honey i.e., mostly to distinguish the monofloral honeys. However, this data can also be used for further analysis and in order to provide much more information on the honey. Upon melissopalynological visual analysis of honey from different environments data were analysed through methods of multivariate analysis in order to confirm hypothesis that it can indicate also the ecological origin of the honey and the potential disturbances in the environment. The PCA was used in order to provide straight visual classification of individual products in relation to its characteristics vis-à-vis pollen content and pollen origin. The results indicated strong grouping of honeys with regard to its origin. Each type of honey was characterised by specific composition of plants from which the pollen grains originated. It was not just the composition but also the sheer diversity of plants that pollen originated form that indicated potential disturbance and possible pollution. Therefore, the combination of melissopalynology and multivariate analysis provides precise information of not only the honey quality and origin, but also potentially vital information on the environment. Importance of such approach in current situation where global decrease of bees and bee diversity is taking place reflects also in its potential to provide answers to yet unknown crucial facts in relation the decline of bees and its diversity.

Title:	**Causal model of biosphere based on EU LTER Northern Adriatic Sea project**
Authors:	Želimir Kurtanjek
Affiliation:	University of Zagreb Faculty of Food Technology and Biotechnology Croatia
Abstract:	The focus of this work is to apply structural causal modeling ("Structural Causal Model", SCM) to gain a scientific-level contribution to the determination of functional causal dependencies in complex ecological systems. The experimental data are the outcome of the long-term and extensive investigation as a part of the EU project "LTER Northern Adriatic Sea" and are freely available within the EU Open Science policy. The data set is Big Data with 110 000 samples of 43 spatial-temporal, physical-chemical and biological descriptors. For causal discovery is applied Hilbert-Schmidt conditional independence test (HSCI). The test results are interrelated and graphically presented as a Directed Acyclic Graph (DAG) Bayes network. The causal model is derived from the obtained DAG by application of Pearl's d-separation criteria to obtain unconfounded direct and indirect causal paths between individual non-biotic and biotic descriptors. Functional causal dependencies are evaluated from the causally adjusted sets to block confounding and contra-causal back door interference. Marginal probability distributions are inferred by Bayes Neural Networks (BNN) with a single interior neuron layer the outputs are presented as partial dependency plots (PDP). The most important causal effect is due to temperature (−0,07 µg chlorophyll/°C). The model predicts reversed positive causality between chlorophyll concentration and dissolved oxygen (0.2 mg DO_2/µg chlorophyll).

Title:	**A cautionary note on the *c*-index in survival analysis**
Authors:	**Janez Stare, Tina Košuta, Damjan Manevski, Robin Henderson**
Affiliation:	University of Ljubljana, University of Newcastle
Abstract:	The concordance index is used extensively in survival analysis (for the last 10 years Google Scholar gives over 11000 hits, and Medline close to 1000). It is usually understood as a measure of quality of prediction, so something like a measure of explained variation. In this talk we show, using simulations and a well known real data set, that its behaviour can be quite contrary to what we expect, and get, from such measures. And we conclude that its usage should be less if not abandoned.

Title:	**The Disparate Goals of Statistics and Machine Learning: Survival Analysis and Prediction on Liver Transplantation Data**
Authors:	**Ivan Stresec[1], Miran Bezjak[2], Stipislav Jadrijević[2], Branislav Kocman[2], Tajana Filipec Kanižaj[2], Danko Mikulić[2], Bojana Dalbelo Bašić[1]**
Affiliation:	[1]University of Zagreb, Faculty of Electrical Engineering and Computing [2]University Hospital Merkur
Abstract:	Survival analysis is a widely known branch of statistics that analyzes the duration of time until some event occurs. Regression modelling of survival data is somewhat atypical and predicated on the common occurrence of censored data. Like other biomedical data, survival data are often scarce due to the nature of their acquisition. In the last couple of decades, survival prediction, a machine learning (ML) approach to survival data, is becoming increasingly prominent. Like other supervised ML models, survival prediction models are designed to extract generalizable patterns from the data to make predictions on new, unseen data. The performance of an ML survival model is most commonly measured by the concordance index (c-index), a metric that tells us how well a model orders samples based on their survival time. The difference in statistical and machine learning models is not quantifiable, making the comparison between the two nontrivial. Nevertheless, it is not uncommon to see nonsensical c-index comparisons of ill-developed Cox models and ML models. This nonperception of the disparity between traditional statistical models and machine learning might indicate a lack of understanding on the practitioners' side. Our current research is concerned with both analysis and prediction of survival times of liver transplantation patients. While analyzing survival times in terms of donor and recipient variables can be used to infer knowledge about a sample to verify and challenge old and new hypotheses, survival prediction is more appropriate for systems designed to aid in donor-recipient matching decisions. We discuss our analysis of the survival outcomes of patients who underwent liver transplantation for hepatocellular carcinoma (HCC). Conversely, we also mention our performance-based comparison between statistical prognostic scores and commonly used survival ML models in the context of donor-recipient matching. As a final point of interest, we briefly touch upon interpretation. The interpretation of ML models is inherently more complicated and less transparent than the interpretation of statistical models. The comparison between the models' interpretations, much like the comparison between the models themselves, is not straightforward.

Title:	**Thyroid function and metabolic syndrome: a two-sample bidirectional Mendelian randomization study**
Authors:	**Nikolina Pleić, Ivana Gunjača, Mirjana Babić Leko, Tatijana Zemunik**
Affiliation:	Department of Medical Biology, University of Split, School of Medicine, Croatia
Abstract:	Thyroid function has been associated with metabolic syndrome (MetS) in a number of observational studies. In spite of that, the direction of effects and the exact causal mechanism of this relationship is still unknown. Mendelian randomization (MR) – the random combination of parents' genes that occurs at conception and the formation of offspring gametes, provides a unique method for identifying the causal nature of environmental risk factors. Using this kind of randomization, MR methodology can, to some extent, construct a natural analogue of a randomized controlled trial. MR analysis is based on the realization that a genetic variant associated with exposure can be used as an instrumental variable to estimate the exposure's causal effect on an outcome of interest. Here we performed a two-sample bidirectional MR study using summary statistics from the most comprehensive genome-wide association studies (GWAS) of thyroid-stimulating hormone (TSH, n=119,715), free thyroxine (fT4, n=49,269), MetS (n=291,107), as well as components of MetS: waist circumference (n=462,166), fasting blood glucose (n=281,416), hypertension (n=463,010), triglycerides (TG, n=441,016) and high-density lipoprotein cholesterol (HDL-C, n=403,943). We chose the multiplicative random-effects inverse variance weighted (IVW) method as the main analysis. Sensitivity analysis included weighted median and mode analysis, as well as MR-Egger and Causal Analysis Using Summary Effect estimates (CAUSE). Our results suggest that higher fT4 levels lower the risk of developing MetS (OR=0.96, p=0.037). In addition, genetically predicted fT4 was positively associated with HDL-C (β=0.02, p=0.008), while genetically predicted TSH was positively associated with TG (β=0.01, p=0.044). These effects were consistent across different MR analyses and confirmed with the Bayesian CAUSE analysis. In the reverse direction MR analysis, genetically predicted HDL-C was negatively associated with TSH (β=-0.03, p=0.046) in the main IVW analysis. Our study suggests that variations in normal-range thyroid function are causally associated with the diagnosis of MetS and with lipid profile, while in the reverse direction, HDL-C has a plausibly causal effect on reference-range TSH levels.

Title:	**Using artificial intelligence to optimize decision making and improve outcomes in surgery – our experience**
Authors:	**Meštrović T[1], Premužić Meštrović I[2], Crkvenac Gregorek A[3], Pavić P[1], Đaković Bacalja I[4], Sonicki Z[1]**
Affiliation:	University of Zagreb School of Medicine[1] Clinical Hospital Center Merkur, Zagreb[2] University Hospital Center Zagreb – "Rebro"[3] Vascular Surgery Department, Clinic Hospital Hietzing, Vienna[4]
Abstract:	Artificial Intelligence (AI) has shown great promises as an adjuvant technology in the field of vascular surgery in recent years. One of its especially useful applications is using predictive analytics to improve outcome prediction and identification of patients at risk for complications, as well as to facilitate the development of personalized treatment plans and generate tailored recommendations. AI systems can also provide real-time decision support to surgeons during procedures and in critical moments, enhancing patient safety. However, there are still several unresolved problems for optimal usage of AI in surgery. The first and the foremost is the problem of acquiring adequate data, since smaller or inappropriate datasets, frequently encountered in surgical domains, are prone to bias and other errors. Therefore, AI models trained on one dataset may be difficult to adapt to different populations. Deep learning models are also considered as "black boxes", as they lack human interpretability. The need for human supervision is important for critical decisions and further emphasized by the facts that AI systems are not infallible. Also, surgeons might become overly reliant on AI systems, potentially downgrading their own clinical decision-making skills. Hereby we report our experience, together with successes and obstacles, in applying machine learning (AI) techniques for analysis of surgical datasets in the domain of ruptured aortic aneurysms (rAAA), vascular surgical site infections (VSSI) and factors affecting chronic wound healing (CWH). Preliminary results showed great potential for prediction of operative mortality in rAAA patients, elucidating risk-factors for resistant bacterial infections, and factors that improve CWH, but we also acknowledge the presence of bias related to small datasets, and fluctuation of variable values along the time coordinates, namely, that some of the models we obtained relied on the analyzed time period, as well as the fact that the models should also be validated multicentrically. In conclusion, the abovementioned advantages of using AI in surgery hold tremendous potential to transform surgical practices, but the field is still rapidly evolving, and quite a few challenges remain, such as limited adaptability, ethical considerations, overreliance on AI and financial implications, that must be addressed to ensure effective integration of AI in surgical settings. By addressing these drawbacks, AI has the potential to improve surgical procedures and patient outcomes, and ultimately shape the future of surgical practice.

Title:	**SRCE Advanced Computing service and bioinformatics**
Authors:	**Marko Kvakić, Emir Imamagić**
Affiliation:	University of Zagreb University Computing Centre (SRCE), Advanced Computing Department
Abstract:	In 2023 University of Zagreb University Computing Centre (SRCE) successfully completed the e-infrastructure project Croatian Scientific and Educational Cloud (HR-ZOO); a project which brings significant changes to the scientific computing landscape in Croatia. In parallel and under the H2020 project EuroCC, a consortium of partners led by SRCE established a National Competence Centre (NCC) for HPC. As a result of project HR-ZOO two new advanced resources are established, named by Croatian great scientists: Supek and Vrančić, which are geared towards HPC and HTC computing needs respectively. These two provide a tenfold increase in computing capability which, with NCC's support and services for HPC, create an improved environment tailored to the needs of the Croatian scientific community. The main goals of these new resources are 1) to support ever-increasing scientific workloads and 2) to provide scalable and customizable environments for various computational needs. The main features of these resources will be demonstrated, as well as the manner in which they will ultimately support science and bioinformatics in the coming period. Bionformatics applications have had a considerable stand in the history of advanced computing at the SRCE, with projects that analyze vast amounts of genetic data in the context of ecological and agronomical study. Within this frame, existing services and experiences will be presented, as well as current efforts to further augment the support for the bioinfo community.

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STUDENT SESSION

Title:	**Survey analysis: "Citizens about green infrastructure in Zagreb"**
Authors:	Iva Šikić
Affiliation:	**University of Zagreb, Faculty of Forestry and Wood Technology- Graduate study of Urban Forestry, Nature Conservation and Enviromental Protection**
Abstract:	In times of climate change and environmental awareness green infrastructure and green spaces are becoming a crucial part of the city fabric. Green infrastructure provides varied services, such as ecological, social services, and esthetic value. To fulfill its purpose, green infrastructure has to be well-planned and maintained professionally. A crucial aspect of planning and care is the opinion of the users of the space - the citizens. As part of the course "Statistical methods and modeling in forestry" (graduate studies of Urban Forestry, Nature Conservation, and Environmental Protection, Faculty of Forestry and Wood Technology) questionnaire was designed. For survey purposes, 183 citizens participated. The survey consists of 30 questions divided into three sets of question types: basic information about participants (age, gender, city quarter, etc.), educational group of questions, and floating scale type. After the database was created, datasets were summarized with descriptive statistics. Pearson correlation was applied to measure the linear correlation between variables. A chi-square test has used to determine if there was a statistically significant difference between the expected and observed frequencies, a chi-square test was used. Lastly, an analysis of variance was applied. A research survey method is a good tool for obtaining different user opinions. The results of statistical data analysis can and should be applied in the management plans for green infrastructure and green spaces. This holistic approach ensures that green infrastructure fulfills all services, and at the same time is adapted to the needs of the users - citizens.

Title:	**Adrian vs Predators: An Analysis of Professor's Inbox**
Authors:	**Adrian Goršeta**
Affiliation:	University of Zagreb, School of Medicine, student
Abstract:	In the world of scientific publishing and the growing popularity of open access journals, researchers now have numerous avenues to disseminate their research and contribute to scientific progress. Unfortunately, this trend has also led to an increase in predatory publishing practices, posing a serious problem for the academic community. Poor-quality research and misinformation can spread, causing significant harm. Therefore, it is crucial for researchers to carefully evaluate the credibility of the journals and conferences they submit their work to. Our goal was to conduct an analysis of unwanted emails received by respected university professors from the fields of biostatistics, medical informatics, health care, and clinical research. Our aim was to identify whether the offers presented in the emails were predatory and to provide a practical guide to help others recognize such emails. We collected a total of 541 emails between June 2022 and January 2023 and categorized them into two groups: journals and conferences. Of these, 82 were excluded due to non-relevance. The remaining 459 emails comprised 220 conferences (94 unique entries) and 239 journals (158 unique entries). To identify predatory journals, we conducted a comprehensive literature review and developed a set of criteria for evaluation. These criteria included general information (e.g., date of sent email, email domain, date of journal submission, email domain, grammatical or spelling errors, font, size and color of letters), journal information (e.g., publisher, official journal webpage, is publisher listed on Bell's list or KSCIEN's list, aim and scope of the journal), article-related information (e.g., previous articles, reviews), submission charges, and editorial board information. Similarly, we evaluated conferences based on several factors, including the accuracy of professor name spellings, email domain, website characteristics, price, participation/speaker details, and editorial board information. We emphasize that the presence or absence of a single criterion does not determine a conference or journal's legitimacy. Rather, the evaluation must consider all relevant factors. By providing this practical guide, we aim to help researchers make informed decisions and avoid predatory publishing practices. *special thanks to Lovela Machala Poplašen