

# BIOMETRIC BULLETIN

International Biometric Society Internationale Biometrische Gesellschaft Société Internationale de Biométrie

*“Biometry, the active pursuit of biological knowledge by quantitative methods.” - R.A. Fisher, 1948*

## President's Corner



By the time this contribution will be published, most members from the northern hemisphere will be back at work after a summer holiday, while our members from

the southern hemisphere still have their summer break ahead of them. I hope that you have enjoyed, or soon will enjoy, a well-deserved relaxing period, away from work, together with your beloved ones.

We are now less than ten months away from IBC2022. As you know, the meeting is scheduled to take place in Riga (Latvia) from Monday July 11 to Friday July 15, 2022, with pre-conference short courses on Sunday July 10. We are still hopeful that, four years after our last in-person meeting in Barcelona, we will again be able to meet in person. As indicated before, we are sensitive to the fact that traveling may still not be possible for all our members so we are exploring options for a hybrid program in which some selected components of the in-person meeting will be offered online as well. Nevertheless, preparations for the Riga meeting have now reached full speed with bi-weekly meetings of the program chair, local organizers, officers and representatives from our conference management company. Also, several officers intend to have a second site visit in September to fine-tune some organizational and logistic aspects with the local organizers.

Program wise, the meeting is shaping up very well. The International Program Committee chaired by Kerrie Mengersen (Australia)

has selected 21 invited sessions on a wide range of topics, including machine learning, software development, disease mapping, surrogate marker evaluation, the analysis of wearable device data, and dynamic risk prediction, amongst many others. Also, our Education Committee, chaired by Annette Kopp-Schneider identified (Germany) identified 3 full-day short courses and 4 half-day short courses, as well as a Statistics in Practice session on effective visual communication for quantitative scientists. Detailed information on all invited sessions and short courses can be found at the IBC2022 website (<https://www.ibt2022.org/home>). I realize that proposers of sessions or courses that have not been selected will be disappointed. However, we received many excellent proposals and the competition was tough. Thank you to all who contributed in any way to any of the proposals.

In parallel, José Pinheiro (U.S.A), who will serve as IBS president at the time the Riga meeting will take place, has identified the keynote speaker for the Presidential Invited Address during the opening session. It is a pleasure to announce that David Madigan, who currently is Provost and Senior Vice President for Academic Affairs at Northeastern University (U.S.A.), has accepted to give a presentation entitled “Real Real World Evidence” on methodology for performing observational research that can be evaluated, calibrated, and applied at scale to generate a more reliable and complete evidence base than previously possible. As with previous IBC meetings, other special sessions such as the Biometrics and JABES showcase sessions and the IBS / ISI Young Ambassador Showcase session will soon be added to the program. Also, jointly with the Club

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## Region Key

### Regions

RArg - Argentinean Region  
AR - Australasian Region  
ROeS - Austro-Swiss Region  
RBe - Belgian Region  
GBot - Botzwanian Region  
RBras - Brazilian Region  
BIR - British and Irish Region  
RCAC - Central American-Caribbean Region  
GCI - Chilean Region  
CHINA - Chinese Region  
EMR - Eastern Mediterranean Region  
ENAR - Eastern North American Region  
ECU - Ecuadorian Region  
GEth - Ethiopian Region  
RF - French Region  
DR - German Region  
GGha - Ghanian Region  
IR - Indian Region  
RItl - Italian Region  
JR - Japanese Region  
GKe - Kenyan Region  
Rko - Korean Region  
GMal - Malawi Region  
GNi - Nigerian Region  
NR - Nordic-Baltic Region  
PKSTAN - Pakistani Region  
GPol - Polish Region  
GRo - Romanian Region  
SING - Singaporean Region  
GSaf - South African Region  
REsp - Spanish Region  
ANed - The Netherlands Region  
GUgan - Ugandan Region  
WNAR - Western North American Region  
GZim - Zimbabwean Region

### Networks

CEN - Central European Network  
CN - Channel Network  
EAR - East Asian Network  
SUSAN - Sub-Saharan Network

# President's Corner

*Continued from p. 1*

of Past IBS Presidents, we are planning a special session on the history of IBS to celebrate the 75th anniversary of our Society.

At the time of writing this contribution, it is still unclear how many submissions for contributed presentations (oral or poster) will have been received by the time the call closes on September 30. Submissions from a broad range of perspectives and applications are encouraged. Accepted oral contributions will be arranged in themed sessions of six presentations with some time for discussion. I'm hopeful that many of you will submit your work and will contribute to the success of our meeting. Details about the submission and selection processes can be found at the IBC2022 website (<https://www.ibc2022.org/home>).

I also want to draw your attention to a number of awards. The Young Statisticians award is open to MSc or PhD candidates or graduates who obtained their degree in 2019 or later. Five papers (one each from Africa, Asia & Australasia, Europe, North America, and South America) will be selected for presentation in the Young Statistician Showcase session. The winners will each receive a stipend of 3000 USD to cover their expenses in attending IBC2022 in Riga. The Travel Award is open to individuals who reside in a Lower-and-middle income country according to the World Bank and to those individuals who have submitted an abstract which has been selected for oral or poster presentation at IBC2022. If selected, funding may be utilized for travel, accommodations, and registration to the conference. The Best Student Oral Presentation Award aims at encouraging students to participate in the oral program at the conference and to improve the quality of scientific communication. The Best Poster Presentation Award is a competition open to all IBS members (including student members) and aims to encourage the use of poster presentations and the participation of all delegates in the poster sessions. Award winners are recognized at the Closing Conference Awards Ceremony of the conference, in the Biometric Bulletin, and on the website and social media platforms. More information on all these awards can be found at the IBC2022 website (<https://www.ibc2022.org/home>).

Apart from the above IBS awards, IBS and the Caucus for Women (CWS) in Statistics jointly sponsor the Florence Nightingale Award which was initially created and presented at the virtual IBC2020 meeting in honour of the 200th birth year of Florence Nightingale (1820-1910) who was a very inspirational woman with a passion to serve and care, but who also was an acclaimed statistician. Our Executive Board recently agreed to extend the award to future IBC meetings and to establish, jointly with CWS, a regular biennial Florence Nightingale Award to be conferred at each of the IBC conferences, following the example of IBC2020. IBS and/or CWS members who can demonstrate a record of services and care for the cause of women and other honourable causes that raise the standing of disadvantaged groups in our profession are strongly encouraged to apply. The awardee will be presented a cash prize at the concluding ceremony of IBC. Details about the application and selection process will soon be made available through our website.

I would like to conclude by drawing your attention to various regional meetings that will be organized in the near future. Last year, many regional meetings could not take place due to the COVID-19 pandemic and the lack of time to move to online meetings. I'm happy to note that, between now and the end of 2021 many of our

regions will hold regional meetings. Examples include the Austro-Swiss region, the Italian region, the Brazilian region, and the Sub-Saharan network. The fact that these meetings will be held virtually may very well attract members from other regions who otherwise would not be able to attend. More information can be found on the IBS website (<https://www.biometricsociety.org/home>). In any case I hope that the increased regional activity is an indication that many regions are recovering from the pandemic and are slowly starting up their regional activities again. Also, the pandemic has forced us to reflect on alternative ways to meet and interact and eventually may turn out to have created new opportunities that otherwise never would have been considered feasible or valuable.

**Geert Verbeke**  
**IBS President**

## From the Editor

I repeatedly realized that suggestions from esteemed colleagues should always be respected. Reacting to the earlier 'Basic-Themes' published by the editor in Vols 36 and 37 of BB during 2019-20 and also to the valuable inputs received and shared through the 'Response to the Editor' columns, some of our colleagues have urged that the interesting developments made in recent years with regards to p-values should also be open to academic debate through the forum of BB that is widely circulated in more than 35 regions of the globe. I was coolly brooding over it and wanted to raise the issue in previous issues of the Bulletin but with my own personal hesitations failed to do so. My loud thinking has been more towards 'how much justice the philosophy and science of Statistics' can still do to the fast-developing modern sciences?

It is believed that 'Genetics' the most sophisticated science of creation and reproduction can never be decoded in true sense to be practiced for its exact replication by humans. In other words, the 'Uncertainties' prevailing around us and throughout the dynamic Universe, affecting each moment of time, can never be measured precisely even by the science of Statistics. But the optimism being the foundation of core sciences shall never allow us to surrender to such a pessimistic thought. The Science of Approximation can do wonders even without waiting and achieving perfection in spying God's natural secrets. One school of thought strongly believes that nothing happens by chance, rather it should be attributed or credited to our ignorance at this point of time. A day should come to bid goodbye to luck or chance factor. Looking backwards to the rapid developments in Statistical-thinking and especially its focus on Biometry or Biometrics or Biostatistics, satisfying the logical requirements in understanding the fundamental principles as well providing the rational explanation of the facts is an evidence in favor of this optimism. Measuring uncertainties in terms of probabilities to help decision making is now well established for long. Whereas, the process of statistical estimation and hypotheses testing has an inbuilt role of 'confidence intervals' and 'p-values', the conventional CIs with 95% confidence and the cut-off p-values of less than 0.05 (rather conceptually fixed level of significance) has been in debate in recent years. The dichotomous approach of accepting or rejecting the null hypothesis on the basis that often is not the best available evidence in favor and thereby deciding the fate of the research hypothesis has been in question. Researchers had always been eager to know

is there a scope for furtherance of the experimentation beyond the repeated rejections of their research hypothesis? At what stage of continued exploration should finally be given-up?

We may observe and appreciate that in this issue of BB the news on regional activities from a few correspondents' have also included the contents of academic interest. Incidentally, our regional correspondent, Dr Daniel Nevo while looking for contributions from the EMR region for the bulletin, came forward with an interesting proposal. He suggested that a short statement that was issued recently by the ASA's president Task-Force about statistical significance and replicability should be of definite importance to most of the statisticians and members of the IBS. Working on his advice, I approached Prof. Yoav Benjamini, who is both the current president of the EMR region and one of the authors of the statement, requesting to provide an informative write-up on that to help me invite further exchange of thoughts on that very interesting aspect of statistics. I am grateful to both of them for the favour and eagerly looking forward for the inputs from esteemed members please.

**Ajit Sahai**  
Biometric Bulletin, Editor

## Response to the Editor

### On p-Values Statistical Significance and Replicability

(Yoav Benjamini) [ybenja@tauex.tau.ac.il](mailto:ybenja@tauex.tau.ac.il); <https://www.tau.ac.il/~y-benja/>

Most scientific research has been using significance testing (based on P-value) as a decision tool to separate the highlighted experimental results from those prone to be generated by pure chance. Therefore, when replicability problems emerged in different fields of science, it was natural that most questionable practices related to the use of statistics centered about the use of p-values, which, in turn, led to an attack on the p-value in particular and statistical inference, et large. The Board of the American Statistical Association (ASA) responded by issuing guidelines on the use of p-values (Wasserstein & Lazar, *The American Statistician* 2016). The guidelines were very cautious about the use and value of the p-value, while discussing other well-known statistical tools as alternatives. A follow-up ASA initiated conference titled "Statistics in the 21st century: the world beyond  $p < 0.05$ ", ended with *The American Statistician* devoting it to a special issue. The editorial stated "It is time to stop using the term 'statistically significant' entirely. Nor should variants like 'significantly different', ' $p < 0.05$ ' and 'nonsignificant' survive". With two of its authors being the same as of the 2016 guidelines, and with Wasserstein serving as the executive director of ASA, the editorial that contained no disclaimer was interpreted as a formal negative position of the largest learned statistical society on the use of p-values and tests of significance. In some circles, including biostatistical and medical circles, this interpretation was transformed into actions, in others into confusion.

In response to this situation, the 2019 ASA President, Karen Kafadar convened a Task Force to address issues surrounding the use of p-values and statistical significance, as well as their

connection to replicability. It was chaired by Xuming He and Linda J. Young and included Kafadar (ex officio) and 12 other statisticians (see below). **The ASA President's Task Force Statement given below is reprinted with permission of Institute of Mathematical Statistics**, and will be published (together with [Karen's Editorial](#)) in the September 2021 issue of the *Annals of Applied Statistics*.

On a personal note, I had the privilege of taking part in all three above mentioned ASA initiatives. From my perspective, only the last statement represents an effort to reach a consensus among its participants. Every paragraph, sentence, word and even comma were debated, some at length, in order to reach an agreed-by-all short statement targeted at consumers of statistics in science, government, and business. We managed to achieve such a consensus within the Task Force, and I hope that this consensus will be adopted in the wider statistical community as well. This will allow different schools of thoughts and seemingly conflicting methodologies their continued development under a single umbrella of statistical principles.

### THE ASA PRESIDENT'S TASK FORCE STATEMENT ON STATISTICAL SIGNIFICANCE AND REPLICABILITY

Over the past decade, the sciences have experienced elevated concerns about replicability of study results. An important aspect of replicability is the use of statistical methods for framing conclusions. In 2019 the President of the American Statistical Association (ASA) established a task force (listed below at the end) to address concerns that a 2019 editorial in *The American Statistician* (an ASA journal) might be mistakenly interpreted as official ASA policy. (The 2019 editorial recommended eliminating the use of " $p < 0.05$ " and "statistically significant" in statistical analysis.) This document is the statement of the task force, and the ASA invited us to publicize it. Its purpose is twofold: to clarify that the use of P -values and significance testing, properly applied and interpreted, are important tools that should not be abandoned, and to briefly set out some principles of sound statistical inference that may be useful to the scientific community.

P -values are valid statistical measures that provide convenient conventions for communicating the uncertainty inherent in quantitative results. Indeed, P -values and significance tests are among the most studied and best understood statistical procedures in the statistics literature. They are important tools that have advanced science through their proper application.

Much of the controversy surrounding statistical significance can be dispelled through a better appreciation of uncertainty, variability, multiplicity, and replicability. The following general principles underlie the appropriate use of P -values and the reporting of statistical significance and apply more broadly to good statistical practice.

**Capturing the uncertainty associated with statistical summaries is critical.** Different measures of uncertainty can complement one another; no single measure serves all purposes. The sources of variation that the summaries address should be described in scientific articles and reports. Where possible, those sources of variation that have not been addressed should also be identified.

**Dealing with replicability and uncertainty lies at the heart of statistical science.**

Study results are replicable if they can be verified in further studies with new data. Setting aside the possibility of fraud, important sources of replicability problems include poor study design and conduct, insufficient data, lack of attention to model choice without a full appreciation of the implications of that choice, inadequate description of the analytical and computational procedures, and selection of results to report. Selective reporting, even the highlighting of a few persuasive results among those reported, may lead to a distorted view of the evidence. In some settings this problem may be mitigated by adjusting for multiplicity. Controlling and accounting for uncertainty begins with the design of the study and measurement process and continues through each phase of the analysis to the reporting of results. Even in well-designed, carefully executed studies, inherent uncertainty remains, and the statistical analysis should account properly for this uncertainty.

**The theoretical basis of statistical science offers several general strategies for dealing with uncertainty.** P-values, confidence intervals and prediction intervals are typically associated with the frequentist approach. Bayes factors, posterior probability distributions and credible intervals are commonly used in the Bayesian approach. These are some among many statistical methods useful for reflecting uncertainty.

**Thresholds are helpful when actions are required.** Comparing P-values to a significance level can be useful, though P-values themselves provide valuable information. P-values and statistical significance should be understood as assessments of observations or effects relative to sampling variation, and not necessarily as measures of practical significance. If thresholds are deemed necessary as a part of decision-making, they should be explicitly defined based on study goals, considering the consequences of incorrect decisions. Conventions vary by discipline and purpose of analyses.

**In summary, P-values and significance tests, when properly applied and interpreted, increase the rigor of the conclusions drawn from data.** Analyzing data and summarizing results are often more complex than is sometimes popularly conveyed. Although all scientific methods have limitations, the proper application of statistical methods is essential for interpreting the results of data analyses and enhancing the replicability of scientific results.

*“The most reckless and treacherous of all theorists is he who professes to let facts and figures speak for themselves, who keeps in the background the part he has played, perhaps unconsciously, in selecting and grouping them.” (Alfred Marshall, 1885)*

## SUPPLEMENTARY MATERIAL

**Supplement to “The ASA president’s task force statement on statistical significance and replicability”** (DOI: 10.1214/21-AOAS1501SUPP;.pdf). Brief biographies of Task Force members.

**# The Task Force:** YOAV BENJAMINI<sup>1</sup>, RICHARD D. DE VEAUX<sup>2</sup>, BRADLEY EFRON<sup>3</sup>, SCOTT EVANS<sup>4</sup>, MARK GLICKMAN<sup>5,\*</sup>, BARRY I. GRAUBARD<sup>6</sup>, XUMING HE<sup>7</sup>, XIAO-LI MENG<sup>8,†</sup>, NANCY REID<sup>8</sup>, STEPHEN M. STIGLER<sup>9</sup>, STEPHEN B. VARDEMAN<sup>10</sup>, CHRISTOPHER K. WIKLE<sup>11</sup>, TOMMY WRIGHT<sup>12</sup>, LINDA J. YOUNG<sup>13</sup> AND KAREN KAFADAR<sup>14</sup>

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## Update from the Club of Presidents



The IBS Club of Presidents comprises all living past Presidents of the Society and is chaired by the Immediate Past President, for now, that’s me! Traditionally, the Club of Presidents meets at IBC meetings to talk about current issues of relevance to the Society. Sometimes, the Officers will also call on them to offer advice on particular issues. Like everyone else these days, even the Club of Presidents has resorted to conducting some of their meetings via Zoom. Here is a screenshot taken from a meeting held in early August 2021. From left to right, starting with the top row, we have Louise Ryan (President 2018-2019), Tom Louis (2006-2007), Lynne Billard (1994-1995), Byron Morgan (1996-1997), Clarice G. B. Demétrio (2012-2013), Elizabeth Thompson (2016-2017), John Hinde (2014-2015), Kaye Basford (2010-2011). Our oldest living president, Calyampudi Radhakrishna Rao (1974-1975), who recently celebrated his 100th birthday, was unable to join the meeting. Thanks to Tom Louis for his thoughtfulness in taking this screenshot and passing it along to me.

**Respectfully submitted,  
Louise Ryan**



**SAVE THE DATE!**  
10 - 15 JULY 2022

# 31ST INTERNATIONAL BIOMETRIC CONFERENCE

Hosted by the Nordic-Baltic Region of the IBS. It is a pleasure to work with Andrejs Ivanovs and Krista Fischer, co-chairs of the Local Organizing Committee currently putting together the social program which includes the Welcome and Young Statisticians Receptions, excursions, and a gala dinner.

Submit your abstract for presentation during IBC2022 by 31 October 2021. Help shape a diverse program built by IBS Members, statisticians, mathematicians, biological scientists, students, and others devoted to interdisciplinary efforts in advancing the collection and interpretation of information in the biosciences. Visit [ibc2022.org](http://ibc2022.org) for more information.

## TOPICS

- DIGITAL TECHNOLOGIES AND BIOMETRY
- CHALLENGES IN GENOMICS
- STATISTICAL MODELLING IN ECOLOGY
- ADAPTIVE DESIGNS
- PREDICTIVE MODELLING
- NEW TECHNIQUES IN AGRICULTURE RESEARCH
- MODELLING GROUPED ENVIRONMENTAL DATA
- SPATIAL AND SPATIO-TEMPORAL DATA ANALYSIS
- CLINICAL TRIALS
- ANALYSIS OF OBSERVATIONAL COHORT DATA
- INFERENCE IN NATURAL RESOURCE SURVEYS
- ADVANCEMENTS IN SURVIVAL ANALYSIS
- BIOINFORMATICS
- EPIDEMIOLOGY
- BIG DATA METHODOLOGIES



## PARTNER OPPORTUNITIES

Over 900 attendees participated in IBC 2018 (our most recent in-person event), including 237 students. Our virtual IBC 2020 (transformed due to the pandemic) reached nearly the same number of delegates and brought increased exposure to statisticians and biometricians from around the world.

Companies and institutions have unique opportunities to support diversity, and support the planet as part of this year's IBC. For more information visit [ibc2022.org](http://ibc2022.org).



# International Biometric Conference

**10-15 July 2022 - Radisson Blu Latvija Conference & Spa Hotel, Riga, Latvia**

## **Call for Contributed Sessions - Deadline Approaching**

Submit your abstract for presentation at the International Biometric Conference (IBC2022) and share your research with a global community of supportive peers.

Topics across a wide range of both methodological topics and application areas relevant to the IBS mission to promote the development and application of statistical and mathematical theory and methods in the biosciences, including agriculture, biomedical science and public health, ecology, environmental sciences, forestry and allied disciplines will be accepted!

Looking for inspiration for your abstract submission? Check out the [Methodological Topics & Application Areas](#) that have been covered at previous conferences to spark an idea for your own submission!

**For additional information and instructions please click here:** <https://bit.ly/2SaIDSf>

**If you're ready to submit your abstract today, please click here:** <https://ibc2022.abstractcentral.com/>

During the submission of your abstract you will have the opportunity to participate in one of the many awards we offer. For additional information about the available awards please click here, <https://www.ibc2022.org/events/cs22/awards>, and review prior to submitting your abstract.

## **Invited Session Program Confirmed**

21 Invited Sessions have been selected to present during the IBC2022. The sessions include a wide range of topics, including ecology, clinical trials, general modelling approaches, health, epidemiology, and environmental health. To view the selected Invited Sessions, their motivation and proposed speakers topics visit the IBC2022 Scientific Program tab or click here: <https://www.ibc2022.org/events/is22>

## **Short Course Program Confirmed**

Four half day and three full day Short Course proposals have been selected for presentation just before the International Biometric Conference begins on 11 July 2022. All Short Courses will take place on Sunday, 10 July 2022. These courses are taught by experienced professionals who are experts in their fields, so you do not want to miss out! To view the selected course, abstracts and speakers visit the IBC2022 website here: <https://www.ibc2022.org/events/short-course22>

## **Future Conferences...**

**XXXII International Biometric Conference (IBC2024)**

Early December 2024  
Buenos Aires, Argentina

**XXXIII International Biometric Conference (IBC2026)**

Northern Hemisphere Summer, 2026  
Seoul, Korea

# Editorial Update

## Biometrics

### December 2021 Issue Highlights

The December issue features articles across a broad spectrum of applications and methodology. The Biometric Methodology section sets out with a paper on “Causal mediation of semicompeting risks,” by Yen-Tsung Huang, and with discussion contributions by Kwun Chuen Gary Chan, Fei Gao, and Fan Xia; by Mats J. Stensrud, Jessica G. Young, and Torben Martinussen; and by Isabel Fulcher, Ilya Shpitser, Vanessa Didelez, Kali Zhou, and Daniel O. Scharfstein. The regular papers in the Biometric Methodology Section include: “Brain connectivity alteration detection via matrix-variate differential network model,” by Jiadong Ji, Yong He, Lei Liu, and Lei Xie; “Receiver operating characteristic curves and confidence bands for support vector machines,” by Daniel J. Lockett, Eric B. Laber, Samer S. El-Kamary, Cheng Fan, Ravi Jhaveri, Charles M. Perou, Fatma M. Shebl, and Michael R. Kosorok; “Histopathological imaging-based cancer heterogeneity analysis via penalized fusion with model averaging,” by Baihua He, Tingyan Zhong, Jian Huang, Yanyan Liu, Qingzhao Zhang, and Shuangge Ma; “Modeling excess hazard with time-to-cure as a parameter,” by Olayidé Boussari, Laurent Bordes, Gaëlle Romain, Marc Colonna, Nadine Bossard, Laurent Remontet, and Valérie Jooste; “Penalized Fieller’s confidence interval for the ratio of bivariate normal means,” by Peng Wang, Siqi Xu, Yixin Wang, Baolin Wu, Wing Kam Fung, Guimin Gao, Zhijiang Liang, and Nianjun Liu; “Semiparametric partial common principal component analysis for covariance matrices,” by Bingkai Wang, Xi Luo, Yi Zhao, and Brian Caffo; “Efficient nonparametric inference on the effects of stochastic interventions under two-phase sampling, with applications to vaccine efficacy trials,” by Nima S. Hejazi, Mark J. van der Laan, Holly E. Janes, Peter B. Gilbert, and David C. Benkeser; “Evaluating multiple surrogate markers with censored data,” by Layla Parast, Tianxi Cai, and Lu Tian; “A stacked approach for chained equations multiple imputation incorporating the substantive model,” by Lauren J. Beesley and Jeremy M. G. Taylor; and “Using the ‘hidden’ genome to improve classification of cancer types,” by Saptarshi Chakraborty, Colin B. Begg, and Ronglai Shen.

The Biometric Practice section is dedicated to a discussion paper, entitled: “Improving precision and power in randomized trials for COVID-19 treatments using covariate adjustment, for binary, ordinal, and time-to-event outcomes,” David Benkeser, Ivan Diaz, Alex Luedtke, Jodi Segal, Daniel Scharfstein, and Michael Rosenblum; and discussed by Michael A. Proschan; by Min Zhang and Baqun Zhang; and by Lisa M. LaVange.

As a reminder, lists of papers to appear can be found at the Biometrics website. Papers to appear in future issues may also be found under the “Early View” link at the Wiley-Blackwell website, which may be accessed by IBS members by visiting <http://www.biometricsociety.org/>, selecting “Biometrics” from the drop-down menu at the “Publications” link at the top of the page, and accessing the “Click here” link.

### Editorial Board News

As we did last year, two entirely virtual Biometrics Editorial Board Meetings took place in July 2021, on 16 July and on 30 July

to be precise. Different times of day were chosen so that every Associate Editor from around the globe could participate in at least one of them at a reasonable moment.

The idea is to hold on to the two online meetings also in the future, even when the pandemic situation will have cleared. Evidently, when physical International Biometric Conferences will take place - hopefully in Riga in 2022 – there will additionally be an on-site Board Meeting.

### Biometrics News

The journal’s impact factor was 1.524 in 2017, 1.755 in 2018, and 1.711 in 2019. For 2021, the figure has risen to 2.571. Impact factors for the immediately preceding years are typically released around June of the current year. The journal ranks 26/125 in the category “Statistics & Probability;” 43/93 in “Biology;” and 22/58 in “Mathematical & Computational Biology.” All of these ranks are an improvement over those of the year before.

The journal’s backlog has gone up a bit, from about 12 months a year ago, to about 15 months now. Of course, thanks to EarlyView, papers are available much more rapidly but still, it is an editorial point of attention to try and keep the backlog at reasonable levels.

### 2022 - 2024 Co-Editor for Biometrics identified

The search committee to identify a successor for Co-Editor Mark Brewer, whose term will end 31 December 2021, has proposed Katja Ickstadt (German Region), as Mark’s successor. The Editorial Advisory Committee and the IBS Board have approved the appointment. Katja will serve from 1 January 2022 to 31 December 2024. The search committee consisted of Geert Molenberghs, Biometrics Executive Editor, Chair (Belgian Region); Bill Rosenberger, Biometrics CE (ENAR); Alan Welsh, Biometrics CE (Australasian Region); Mark Brewer, Biometrics CE (British & Irish Region); Hans-Peter Piepho, EAC Chair (German Region); Tomasz Burzykowski (Polish Region); Ronald Geskus (Netherlands Region); Rebecca Hubbard (ENAR); Liliana Lopez Kleine (Central America and Caribbean Region); Peter Njuho, EAC member (South African Region).

### Associate Editor Panel Turnover

The panel of Associate Editors is composed of colleagues who each serve two-year terms. This means that every 1 July a number of them end their terms. The Co-Editors have invited new Associate Editors to replace colleagues retiring. New Associate Editors are chosen to replace expertise lost by retiring Associate Editors, as well as to fill in gaps in expertise in certain areas, especially in emerging fields. The panel now consists of about 100 members, and has been operational since 1 July 2021.

We are grateful for the service, rendered by our retiring Associate Editors: Adam Branscum, Marco Carone, Vanessa Didelez, Jianhua Hu, Katja Ickstadt, Jaeyong Lee, Stephane Robin, Bill Rosenberger, Russell (Taki) Shinohara, Peter Thall, Lan Wang, You-Gan Wang, Yang Yang, Yi-Hui Zhou. Bill Rosenberger and Katja Ickstadt retired as Associate Editors in view of their past and present transitioning to the role of Co-editor, respectively.

Incoming Associate Editors are: Mouna Akacha, Ariel Alonso Abad, Dipankar Bandyopadhyay, Jay Bartroff, Jonathan Bradley, Werner Brannath, James Bell, David Benkeser, Steve Coad, Bailey Fosdick,



# STRENGTHENING ANALYTICAL THINKING FOR OBSERVATIONAL STUDIES (STRATOS): INTRODUCING THE INITIAL DATA ANALYSIS TOPIC GROUP (TG3)

Saskia le Cessie<sup>1</sup>, Carsten Oliver Schmidt<sup>2</sup>, Lara Lusa<sup>3</sup>, Mark Baillie<sup>4</sup>, Marianne Huebner<sup>5</sup> on behalf of TG3

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The aim of the Topic Group on Initial Data Analysis (TG3) of the STRATOS initiative is to improve awareness of initial data analysis (IDA) as an important part of the research process and to provide guidance on conducting IDA in a systematic and reproducible manner. Researchers need to have a clear understanding about the underlying features and quality of their data to ensure its suitability for the intended statistical models in a statistical analysis plan. Initial Data Analysis primarily consists of all steps performed on the data of a study before the start of those statistical analyses that address research questions and are typically described in the statistical analysis plan. Ideally, IDA should already be performed during ongoing data collections. The Biometric Bulletin introduced TG3 with an overview of the framework for IDA and problems of inadequate handling of IDA in research studies [1]. We will provide here an update of our recent activities here.

Members of this topic group are Mark Baillie (Switzerland), Marianne Huebner (USA), Saskia le Cessie (Netherlands), Lara Lusa (Slovenia), Carsten O. Schmidt (Germany).

In 2018, our topic group published a conceptual framework paper where we discussed the role of IDA in the research process and identified steps in a systematic and reproducible IDA process [2]. We distinguished six steps: setting up the meta-data, data cleaning, data screening, initial reporting of the cleaning and screening findings, if needed, adapting the statistical analysis plan in a transparent way, and reporting results in research papers.

To explore current practices in performing and reporting IDA in research papers, we conducted a literature review on IDA reporting in observational studies [3]. We observed that the reporting of IDA was limited and not systematically described with IDA statements spread throughout the papers. Of the 25 reviewed papers, 40% included a statement about data cleaning, 44% provided information on item missingness and 60% on unit missingness. Based on the findings of the review, we provided a set of recommendations to improve reporting of IDA. This includes describing IDA methodology, reporting missingness, and discussing the impact of IDA findings.

The review motivated to develop a step-by-step guide on systematically conducting and reporting of IDA in several examples with publicly accessible data and code. The project “Regression without regrets” is a joint project between TG3 and STRATOS topic group TG2 (Selection of variables and functional forms in multivariable analysis). The focus is to provide explanation and elaboration on conducting IDA in a reproducible manner in the context of regression analyses in a low dimensional setting (3 to 50 explanatory variables). First results have been presented in 2020 at the ISCB and MEMTAB conferences and a video poster is available [4].

Longitudinal studies add to the complexity of conducting IDA. In a joint project between TG3 and Katherine Lee from STRATOS TG1 (Missing data) we develop workflows and propose data visualizations to empower researchers to efficiently work with longitudinal data. All code and data sets for the case studies will be made publicly available. A main conclusion from the current projects is that an IDA plan is needed in advance and should accompany a statistical analysis plan. Recently the results were presented at the European Congress of Mathematics (2021).

TG3 members furthermore collaborated on the development of a framework to describe and assess data quality in observational studies along with R routines to conduct such assessments [5]. The framework distinguishes four dimensions of data quality: compliance with structural and technical requirements on the data (integrity); the availability of data values (completeness); inadmissible, impossible, or uncertain data values or combinations of data values (consistency); unexpected distributions and associations (accuracy). Each dimension forms part of a comprehensive data quality assessment workflow that distinguishes more than 30 indicators. A dedicated web page comprehensively introduces the framework and related tools to visualize distinct aspects of data quality (<https://dfg-qa.ship-med.uni-greifswald.de/>). Conceptually, the framework has considerable overlap with IDA steps [3] particularly concerning the meta-data, data cleaning, data screening, and initial reporting steps.

An overview of current and past activities of our Topic Group and links to materials can be found at our website <https://www.stratosida.org/>. More information on the activities of all topic groups is given on the central website of the STRATOS initiative <http://www.stratos-initiative.org/>.

## References:

- [1] Schmidt CO, Vach W, le Cessie S, Huebner M. STRATOS: Introducing the Initial Data Analysis Topic Group (TG3). *Biometric Bulletin* 2018; 35 (2): 10-11.
- [2] Huebner M, le Cessie S, Schmidt C, Vach W. A contemporary

conceptual framework for initial data analysis. *Obs. Studies* 2018; 4: 171-192.

[3] Huebner M, Vach W, le Cessie S, Schmidt CO, Lusa, LL. Hidden analyses: a systematic review of current reporting practice of initial data analyses. *BMC Med Res Meth* 2020; 20 (1): 1-10.

[4] Heinze G, Huebner M, Baillie M. Video Poster Presentation at Presentation at the International Symposium of Methods for Evaluating Tests and Biomarkers (MEMTAB) 2020. Link: [https://mediaspace.msu.edu/media/t/1\\_1n07g3j0](https://mediaspace.msu.edu/media/t/1_1n07g3j0)

[5] Schmidt CO, Struckmann S, Enzenbach C, Reineke A, Stausberg J, Damerow S, Huebner M, Schmidt B, Sauerbrei W, Richter A. Facilitating harmonized data quality assessments. A data quality framework for observational health research data collections with software implementations in R. *BMC Med Res Meth* 2021; 21(1): 1-15.

## Software Corner

### R packages for selecting important interactions via regularization

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Have you ever presented null results to disappointed researchers, and then been asked the question “but what about interactions; are any of those significant?” I have heard this question from clinicians and researchers from many fields of science. While usually asked in earnest, **this question is a dangerous one**; the sheer number of interactions can greatly inflate the number of false discoveries in the interactions, resulting in difficult-to-interpret models with many unnecessary interactions. Still, there are times when these expeditions are necessary and fruitful. Thankfully, useful tools are now available to help with the process. This article discusses two regularization-based approaches: Group-Lasso INTERaction-NET (glinternet) and the Sparsity-Ranked Lasso (SRL). The glinternet method implements a hierarchy-preserving selection and estimation procedure, while the SRL is a hierarchy-preferring regularization method which operates under ranked sparsity principles (in short, ranked sparsity methods ensure interactions are treated more skeptically than main effects a priori).

### Useful package #1: ranked sparsity methods via `sparseR`.

While currently in a beta-phase, the `sparseR` package has been designed to make dealing with interactions and polynomials much more analyst-friendly. Building on the `recipes` package, `sparseR` has many built-in tools to facilitate the prepping of a model matrix with interactions and polynomials; these features are presented in the package website located at <https://petersonr.github.io/sparseR/>. The simplest way to implement the SRL in `sparseR`

is via a single call to the `sparseR()` function, here demonstrated with Fisher’s iris data set:

```
(srl <- sparseR(Sepal.Width ~ ., data = iris, k = 1, seed = 1))
Model summary @ min CV:
```

```
-----
lasso-penalized linear regression with n=150, p=18
(At lambda=0.0015):
  Nonzero coefficients: 10
  Cross-validation error (deviance): 0.07
  R-squared: 0.62
  Signal-to-noise ratio: 1.64
  Scale estimate (sigma): 0.267
```

SR information:

|                     | Vartype | Total | Selected | Saturation | Penalty |
|---------------------|---------|-------|----------|------------|---------|
| Main effect         | 6       | 4     | 0.667    | 2.45       |         |
| Order 1 interaction | 12      | 6     | 0.500    | 3.46       |         |

Model summary @ CVIse:

```
-----
lasso-penalized linear regression with n=150, p=18
(At lambda=0.0070):
  Nonzero coefficients: 7
  Cross-validation error (deviance): 0.08
  R-squared: 0.57
  Signal-to-noise ratio: 1.33
  Scale estimate (sigma): 0.285
```

SR information:

|                     | Vartype | Total | Selected | Saturation | Penalty |
|---------------------|---------|-------|----------|------------|---------|
| Main effect         | 6       | 3     | 0.500    | 2.45       |         |
| Order 1 interaction | 12      | 4     | 0.333    | 3.46       |         |

`summary(srl, at = “cvIse”)`

```
lasso-penalized linear regression with n=150, p=18
At lambda=0.0070:
```

```
-----
Nonzero coefficients          : 7
Expected nonzero coefficients : 1.38
Average mfd (7 features)     : 0.198
```

|                                  | Estimate  | z       | mfd      | Selected |
|----------------------------------|-----------|---------|----------|----------|
| Species_setosa                   | 0.810513  | 17.9513 | < 1e-04  | *        |
| Sepal.Length                     | 0.191210  | 9.3371  | < 1e-04  | *        |
| `Petal.Length:Petal.Width`       | 0.119640  | 5.0379  | < 1e-04  | *        |
| `Petal.Width:Species_versicolor` | 0.275341  | 3.1640  | 0.055680 | *        |
| `Sepal.Length:Petal.Length`      | -0.052711 | -3.2466 | 0.078121 | *        |
| `Sepal.Length:Species_setosa`    | 0.062782  | 2.5978  | 0.251076 | *        |
| Species_versicolor               | -0.001653 | -0.8052 | 1.000000 | *        |

We see (via print and summary functions) that two models are displayed by default corresponding to two “smart” choices for the

penalization parameter  $\lambda$ . The first model printed refers to the model where  $\lambda$  is set to minimize the cross-validated error, while the second one refers to a model where  $\lambda$  is set to a value such that the model is as sparse as possible while still being within 1 SD of the minimum cross-validated error. Visualizations are also available via **sparseR** that can help visualize both the solution path and the resulting model (interactions can be very challenging to interpret without a good figure!)

```
plot(srl)
effect_plot(srl, "Petal.Width", by = "Species", at = "cvmin")
effect_plot(srl, "Petal.Width", by = "Species", at = "cv1se")
```

Note that while ranked sparsity principles were motivated by the estimation of the lasso (in a paper currently under review), they can also be implemented with MCP, SCAD, or elastic net and for binary, normal, and survival data. Finally, **sparseR** includes some functionality to perform forward-stepwise selection using a sparsity-ranked modification of BIC, as well as post-selection inferential techniques using sample splitting and bootstrapping.

## Useful package #2: hierarchy-preserving regularization via **glinternet**

Some argue that when it comes to interactions, hierarchy is very important (i.e., an interaction shouldn't be included in a model without its constituent main effects). While ranked sparsity methods do prefer hierarchical models, they can often still produce non-hierarchical ones. The **glinternet** package and the function of the same name uses regularization for model selection under hierarchy constraint, such that all candidate models are hierarchical. **glinternet** can handle both continuous and categorical predictors, but requires pre-specification of a numeric model matrix. It can be performed as follows:

```
X <- iris %>%
  select(-Sepal.Width) %>%
  mutate(Species = as.numeric(Species) - 1)
set.seed(321)
cv_fit <- glinternet.cv(X, Y = iris$Sepal.Width, numLevels =
c(1,1,1,3))
```

The `cv_fit` object contains necessary information from the cross-validation procedure and the fits themselves stored in a series of lists. A more in-depth tutorial to extract coefficients (and facilitate a model interpretation) using the **glinternet** package can be found at <https://strakaps.github.io/post/glinternet/>. Importantly, both the **glinternet** and **sparseR** methods have associated predict methods which can yield predictions on new (or the training) data, shown below. For comparison, we also fit a "main effects only" model with **sparseR** by setting  $k = 0$ .

```
me <- sparseR(Sepal.Width ~ ., data = iris, k = 0, seed = 333)
p_me <- predict(me)
p_srl <- predict(srl)
p_gln <- as.vector(predict(cv_fit, X))
```

With a little help from the **yardstick** package's `metrics()` function, we can compare the accuracy of each model's predictions using root-mean-squared error (RMSE), R-squared (RSQ), and mean absolute error (MAE); see table below. Evidently, **glinternet**

and **SRL** are similar in terms of their predictive performance. However, both outperform the main effects model considerably, suggesting interactions among other variables do have signal worth capturing when predicting `Sepal.Width`.

| Metric | <b>glinternet</b> | <b>SRL</b> | <b>Main effects only</b> |
|--------|-------------------|------------|--------------------------|
| RMSE   | 0.24              | 0.24       | 0.26                     |
| RSQ    | 0.69              | 0.70       | 0.63                     |
| MAE    | 0.19              | 0.18       | 0.20                     |

## Other packages worth mentioning: **ncvreg**, **hierNet**, **visreg**, **sjPlot**

The **SRL** and other sparsity-ranked regularization methods implemented in **sparseR** would not be possible without the **ncvreg** package, which performs the heavy-lifting in terms of model fitting, optimization, and cross-validation. The **hierNet** package is another hierarchy-enforcing procedure that may yield better models than **glinternet**, however the latter is more computationally efficient especially for situations with a medium-to-large number of covariates. Finally, when interactions or polynomials are included in models, figures are truly worth a thousand words, and packages such as **visreg** and **sjPlot** have great functionality for plotting the effects of interactions.

All code used in this article can be found [here](#).

## References

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# Region News

## Argentinian Region (RARG)

[www.biometricsociety.org/about/regions-networks/argentinean](http://www.biometricsociety.org/about/regions-networks/argentinean)

The Argentinean Region (RARG) will carry out the Ibero-American Statistical Analysis Board (ISAB), as a Project within the framework of the Network and Inter-Regional Activities Funding Program. The ISAB aims to promote articulation between biometricians through the offer of statistical analysis workshops, and to generate a wide network of junior and senior expert researchers in Biometrics and related disciplines.

Three “Collaborative Approach for Data Analysis – CADA”, will be held with the participation of graduate students who will present data from ongoing research that demand the development, implementation and validation of statistical methods.

In each workshop, referred to one area (Ecology and Environment, Omics Data Applications or Epidemiology and Health Sciences), three presenting researchers and at least three tutor specialists in Biometrics from the IBS participating regions (Argentina, Brazilian, Ecuadorian, Central American and Caribbean and / or Spanish) will participate.

During webinars the research problem and the database will be presented and statistical analysis strategies will be proposed in a participatory manner. The data analysis strategies will be designed and implemented in the panel and the effective communication of statistical results will be discussed.

The proposal of the Ibero-American Statistical Analysis Board is aimed at developing and mainstreaming the interdisciplinary work of biometricians with biosciences researchers, and could motivate young participants to join as members of one of the IBS regions.

The virtual meetings will be open to any researcher who wants to participate as an observer, creating an outreach channel for our International Biometric Society.

The webinars, scheduled between September and December 2021, will be advertised on the IBS webpage.

**Silvia Sühring**

## Australasian Region (AR)

[www.biometricsociety.org.au/about.html](http://www.biometricsociety.org.au/about.html)

### IBS-AR Student Scholarships

To help attract enthusiastic and talented students to career paths in biometrics, the Australasian Region offers scholarships for suitably qualified students who intend to undertake a fourth or honours year of study, or a coursework Masters, in statistics, mathematical statistics, biostatistics, bioinformatics or biometrics. We are delighted to announce the winners of this year’s highly contested award: Vicky He (Honours student at the University of Otago) and Kieren Brodnik (Honours student at the University of Wollongong). Congratulations!

### Biography – Vicky He



*Vicky He, IBS\_AR Student Scholarship recipient*

I am always passionate about science, so my high school subjects were all science-related. For my undergraduate study, I first chose psychology as my major. But then I thought statistics would help me with my research in psychology, and I decided to add statistics to my major as well.

Throughout my undergraduate degree, I learned a lot of fascinating psychology studies, and I also learned the importance of statistics in research. In addition to that, the statistics department at the University of Otago is absolutely fantastic, the people there always make me feel loved, and the department has nice coffee machines :-)

Anyway, after three year of undergraduate studies, the statistics department successfully converted me, and I am now studying towards an Honours degree in statistics. However, I still like psychology and neuroscience, so my Honours project is about analysing neuroimaging data, with a focus on Diffusion Tensor Imaging, under primary supervision of Dr. Matthew Schofield. There are many interesting (and hard) problems around the standard analysis pipeline, and we wished to improve the standard methods.

If I can survive my Honours year, I would love to carry out future studies in statistics! I hope I can do a PhD next year so that I can learn more about exciting research in statistics. I also look forward to new challenges in the future.

### Biography – Kieren Brodnik



*Kieren Brodnik, IBS\_AR Student Scholarship recipient*

My name is Kieren Brodnik and I am currently undergoing my Honours degree in Mathematics at the University of Wollongong with the Centre of Bioinformatics and Biometrics (CBB) under the supervision of Professor Brian Cullis. I completed my HSC in 2017 at Smiths Hill High School in Wollongong and continued on with my studies to undertake a Bachelor’s degree in Mathematics (Advanced) with a double major in Mathematics and Statistics.

I completed a Summer internship program with CBB after my second year of university and loved working with the team in areas of applied statistics such as single site analysis on field data. This experience was an extremely rewarding one and gave me a strong interest in the field of biostatistics which led to myself undertaking an Honours degree with CBB. I am excited to continue working in this area of statistics as I believe it is making a strong difference to the world and is allowing me to develop as a statistician in the real world.

Outside of academia I am an extremely active person. I currently play first grade football in the Illawarra Premier League which takes a large amount of commitment. As well as this, I also climb regularly both indoors and outdoors. I also love to play music with my friends which is something I have grown to love over the years. I have found that it is super important to maintain a strong balance of keeping active and focusing on studies in order to get the most out of my work and still live a balanced lifestyle.

I am honoured to have been awarded an IBS-AR scholarship as I have been working extremely hard in my degree and really appreciate being recognised for such a prestigious award. I'm excited to continue working with CBB in applied statistics for the future to come both in my current Honours degree and any projects which may arise after the Honours degree is complete.

### **Australian and New Zealand Virtual Statistical Conference 2021**

More than two years ago, planning started for the ANZSC2020, a joint conference of the New Zealand Statistical Association (NZSA) and the Statistical Society of Australia (SSA). After everything was prepared for an exciting week at the Gold Coast, the pandemic happened, and the conference had to be postponed for one year. Slowly adjusting to the reality that any travelling will be difficult for a while, the ANZSC2021 was moving online.

On 5-9 July 2021, the conference finally happened with around 400 participants meeting virtually, attending more than 160 contributed talks, mini tutorials, and panel discussions. Highlights were, among others, the keynote lectures by Frauke Kreuter (Uni Mannheim, Uni Maryland), Kerrie Mengersen (QUT), Renate Meyer (UoA), Robert Gould (UCLA), Noel Cressie (Uni Wollongong), and Li-Chun Zhang (Uni Southampton).

Opening each conference day with a video from the Gold Coast, every attendant was probably regretting a bit not being able to join the conference in-person as previously planned, but the virtual platform based on Slack and Zoom presented an excellent alternative to connect and interact with fellow statisticians, especially during round table discussions, the Women in STEM event, the Trivia Night, and Would I lie to you ... statistically? A team of elves, organised by technical committee co-chair David Warton, was always present and guiding participants around the virtual platform, running training sessions, and helping with any technical problem.

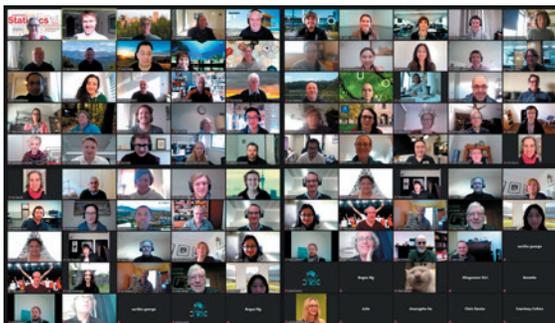
Many thanks to everyone, who turned the event into a smoothly running meeting and a great success!

Daniel Gerhard

Organising Committee Co-chairs: Mark Griffin (SSA), Daniel Gerhard (NZSA)

Programme Committee Co-chairs: Berwin Turlach (SSA), Beatrix Jones (NZSA)

Technical Committee Co-chairs: David Warton (SSA), David Cowen  
<https://anzsc2021.com.au/>



*ANZSC2020 conference photo*

**Rina Hannaford**

### **Central American-Caribbean Region (RCAC)**

[www.biometricsociety.org/about/regions-networks/central-american-caribbean](http://www.biometricsociety.org/about/regions-networks/central-american-caribbean)

### **IBS RCAC Members Meeting 2021**

Contributed by:

Members of the IBS Central American-Caribbean Region met via the WebEx platform on March 18, 2021. Some sixteen members were able to attend this meeting which was convened by Luis Fernando Grajales, President of the IBS RCAC. After the introduction and presentation of attendees at the meeting the following items were discussed:

- Description of the new website by IBC and the location of the virtual presentations of IBS2020
- Description of the invitation and deadlines for short courses and invited sessions for IBS2022
- Invitation to attend IBS2022 in Latvia
- Description of the travel award request from low and middle countries members
- Description of the journals by the society: Biometrics and JABES
- Reminder of the Biometrics Bulletin with the news from the different regions and opportunities listed
- Notification for members to renew their fees and to invite students and others to join IBS and RCAC
- Announcement about the International Symposium of Statistics to be held virtually in 2021 and the date is pending to be defined.
- Submission of proposal for Inter-Regional Activity with the Spanish and Argentinian regions for the summer 2023
- Fostering the distribution of the podcast generated by the Department of Statistics at the Universidad Nacional De Colombia (Colombian National University) to the members of the RCAC

The discussion increased the awareness of members about research and collaboration opportunities available from the IBS. As a result of this meeting, it is hoped that there will be more active participation of our members in the activities of the IBS regionally and globally.

Contributed by: Adriana Pérez MS PhD, Professor Department of Biostatistics and Data Science, Michael & Susan Dell Center for Healthy Living, Austin, TX 78701, e-mail : [adriana.perez@uth.tmc.edu](mailto:adriana.perez@uth.tmc.edu)

### **Options for the analysis of Edinburgh Postnatal Depression Scale Data**

Contributed by: Novie Younger-Coleman Ph.D., Senior Lecturer/ Statistician, CAIHR-UWI, Mona, Jamaica, e-mail: [novie.younger@uwimona.edu.jm](mailto:novie.younger@uwimona.edu.jm)

Listed below are options for analysis of data aimed at quantifying the similarity between two different nationalities of pregnant women, who are from the same ethnic group, with respect to their expression of antenatal depression symptoms. Pregnancy trimester three data gathered from these women using a depression screening tool (questionnaire) would be subjected to the analysis methods. Each woman's response to a questionnaire item on the Edinburgh Postnatal Depression Scale (EPDS) reported frequency of experiencing given depression symptoms and indicated the severity of their expressions of individual symptoms.

A total symptom score would be calculated for each woman by summing the scores or codes for each questionnaire item response that a woman provides. A higher total score would indicate that the woman has a more severe depression symptomatology. A woman with a score above a stipulated threshold – determined from previous work that assessed the validity and reliability of the tool – is regarded as being at risk for antenatal depression.

Steps in the plan for exploitation of the data and the rationale for each method used, are the following:

1. For each questionnaire item, data analysis will estimate a kappa statistic that quantifies the degree to which women classified as having a depression symptom based on their response to a single item on the screening tool, are also classified as having above-threshold scores based on the total sum of their response items scores.

**Rationale:** This kappa statistic would be assumed to quantify the degree to which each questionnaire item, when used in subgroups of women, is likely to detect, also, a woman who is at risk for antenatal depression (based on her having an above-threshold score). The reliability of each item at detecting women at risk for antenatal depression is assumed to be captured by the kappa statistics. The values of the kappa statistics can also be the basis for assessing which depression symptoms as represented by EPDS items may need to be the basis of targeted interventions aimed at providing mental health support in these ethnic subgroups.

2. With the kappa statistics in step 1 regarded as coming from two independent samples of data, one sample from each ethnic subgroup, an analysis will compare these samples of data using a nonparametric method.

**Rationale:** The results of this statistical nonparametric test would indicate whether the distribution of the reliability of the items at detecting women at risk for antenatal depression, is the same in both groups. Differences in the distributions could be an indication that the approaches to tackling the depression symptoms are not the same in both groups.

3. Obtain for each of the groups of women, separate Cronbach's alpha estimates for the items and confidence intervals for these estimates.

**Rationale:** These Cronbach alpha estimates would be an indication of whether the same underlying construct is measured by the same sets of items in both groups of women.

4. Compare the Cronbach's alpha estimates using the approach posited by Cumming and Finch 2005'.

**Rationale:** Comparison of Cronbach alpha interval estimates would determine whether the strength of the internal consistency of the items is the same in both groups of women.

5. Use the data-driven principal components analysis method to obtain for the women another group-specific composite score for the screening tool.

**Rationale:** These scores would provide another basis for assessing the expression of the symptoms in these groups of women.

6. Assess and compare the groups with respect to

a) the nature of the correlation between the PCA component scores and the summed scores obtained from the tool.

b) whether, based on component coefficients that exceed |0.3| There are differences in the definitions of the principal components that have eigen values greater than 1.

**Rationale:** The investigations specified in a) and b) will enable determination of the reliability of the EPDS screening tool as well as whether this reliability differs with the ethnic subgroups.

7. Use the data-driven cluster analysis to determine sets of individuals who are in the same clusters (and have similar symptoms) and define clusters according to the occurrence of symptoms among persons within the clusters.

a. Use logistic regression to assess how the occurrence of above-threshold summed score for the screening tool predicts belonging to a cluster.

8. Use of latent class analysis to determine the probability with which the following occur together in the same latent class: categorisation in the above-threshold categories; the clusters from cluster analysis; categories defined using the principal components scores; and the identified risk factors for above-threshold scores in these women.

**Rationale:** The investigations specified in items 7 and 8 assess the construct validity of the EPDS screening tool in these subgroups of women.

I Cumming, G., & Finch, S. (2005). Inference by eye: confidence intervals and how to read pictures of data. *American psychologist*, 60(2), 170.

## Eastern North American Region (ENAR)

<https://www.enar.org/>

### WebENARs

Be sure to check the ENAR Webinar website for updates regarding the upcoming WebENAR series and links to past WebENARs and their recordings: <http://www.enar.org/education/index.cfm>.

### 2021 JSM, 8-12 August

The 2021 JSM was held virtually from 8-12 August due to the COVID-19 pandemic. The theme of the 2021 meeting was "Statistics, Data, and the Stories They Tell." This year's program included 9 invit-

ed paper sessions and 2 invited panel sessions primarily sponsored by ENAR. These covered topics about data analytic practice, sensitivity analysis with non-ignorable missing data, statistical methodologies in microbiome sequencing, genomics in neuroscience, functional data in biomedical research, statistical challenges of the COVID-19 crisis, clinical trial design and analysis of COVID-19 treatment/prevention, network meta-analysis, communicating statistics to the public, and mentoring. An additional 4 topic-contributed paper and 1 contributed speed paper sessions primarily sponsored by ENAR included presentations on causal inference, integrative inference with data from multiple sources, statistical considerations in nursing education and research, high dimensional data, and biostatistics education and more. Several slides and video recordings from JSM sessions are available at <https://www2.amstat.org/meetings/jsm/2021/index.cfm>. ENAR received many proposals for invited and topic-contributed sessions, and ENAR thanks everyone who put forth an idea. ENAR is thankful to Mark Meyer at Georgetown University for serving on the Program Committee for the 2021 JSM.

### **2022 ENAR Spring Meeting, 27-30 March, Houston, TX, USA**

The 2022 ENAR Spring Meeting is currently scheduled to take place in person in Houston, Texas, at the Marriott Marquis Houston. Contributed oral and poster presentation submissions are due 15 October. ENAR would like to thank Program Chair Harrison Quick ([hsq23@drexel.edu](mailto:hsq23@drexel.edu)), Associate Chair Stacy Cobb ([scobb0522@gmail.com](mailto:scobb0522@gmail.com)), and the Local Arrangements Chair Peng Wei ([pwei2@mdanderson.org](mailto:pwei2@mdanderson.org)) for their hard work in planning the ENAR 2022 Spring Meeting. More details may be found at: <https://enar.org/meetings/spring2022/>.

### **2022 JSM, 6-11 August, Washington, DC, USA**

The 2022 Joint Statistical Meetings are currently scheduled to take place in person in Washington, DC, USA, from 6-11 August 2022. The theme for the 2022 meeting is “Statistics: a Foundation for Innovation.” Invited Session Proposal submissions are accepted until 8 September, with decisions expected by 9 October.

### **2023 ENAR Spring Meeting, 19-22 March, Nashville, TN, USA**

The 2023 ENAR Spring Meeting will be held in Nashville, Tennessee, USA, from 19-22 March 2023 at the JW Marriott Nashville.

### **French Region (RF)**

<https://sfb.pages.math.cnrs.fr/asso/>

Some news from the French Region of the IBS “Société Française de Biométrie (SFB)”.

Due to the COVID crisis, the 8th Channel Network Conference, co-organised by the Belgian, British and Irish, Dutch and French regions of the IBS, could not be organized in-person in Paris as planned initially. It finally took place virtually, April 7 to 9, and gathered 100 participants.

Despite the situation, all participants enjoyed a very exciting scientific program (see <https://cnc21.sciencesconf.org/resource/page/id/4> for details), including three short courses on “Practical deep learning in R” by Sigrid Keydana (Rstudio, München), “Co-data learning in high-di-

mensional regression problems” by Mirreliijn van Nee, Magnus Münch and Mark van de Wiel (Amsterdam University medical Center) and “Nonparametric Bayesian methods for classification” by Boris Hejblum and Anaïs Rouanet (University of Bordeaux) and two keynote talks, one by Pr. Jeanine Houwing-Duistermaat (University of Leeds, School of Mathematics, Statistics Institute ) about “Statistical sciences and interdisciplinary research” and the other one by Pr. Mathias Drton (University of München) about “Causal discovery from observational data”. Three invited sessions were also proposed on “Data integration”, “Statistical modeling in movement ecology” and “Infectious diseases”.

The organisers and the scientific committee of the Channel Network Conference are pleased to announce the following conference awards:

#### Best student oral presentation

- Fast marginal likelihood estimation of penalties for group-adaptive elastic net by [Van Nee Mirreliijn](#) Epidemiology and Biostatistics, Amsterdam University Medical Centers (joint work with Tim Van De Brug and Mark Van De Wiel)
- Honorable mention: A Bayesian model for heterogeneous treatment effects on the additive risk scale in meta-analysis by Doranne Thomassen, Leiden University Medical Center (joint work with Ewout Steyerberg and Saskia Le Cessie)

#### Best poster

- Robustness of Supervised Clustering Methods to Different Types of Inactive Variables by Rebecca Marion, Université Catholique de Louvain (joint work with Johannes Lederer, Bernadette Govaerts and Rainer Von Sachs)
- Honorable mention: Abundance and distribution of the blue shark in the Bay of Biscay by Lea Pautrel, Rindra Ranaivomanana, Emma Rouault, Institut Agro - Agrocampus Ouest (joint work with Mathieu Genu, Matthieu Authier, Marie-Pierre Etienne)

The next CNC will take place in the Netherlands in 2023.

More information can be found on our website <https://sfb.pages.math.cnrs.fr/asso/>

### **Japanese Region (JR)**

<http://www.biometrics.gr.jp/>

### **The 2021 Annual Membership Meeting of the Biometric Society of Japan**

The Annual Meeting of the Biometric Society of Japan (BSJ) was held on 13-14 May, 2021, via online. Three hundred twenty-five people attended the meeting. Two invited sessions on an introduction to machine learning and the winner of the 2020 BSJ Award for Outstanding Scientific Contribution were organized. In one invited session, Dr. Ryuji Hamamoto (National Cancer Center Japan), Dr. Kota Matsui (Nagoya University), and Dr. Satoshi Hara (Osaka University) introduced medical applications of deep learning, basics of deep neural network models, and explanation of judgement rationales for machine learning models, respectively. In the other invited session, Prof. Yutaka Matsuyama (The University

of Tokyo) delivered the commemorative lecture entitled “Causal inference and estimands” with his related valuable works on development of biostatistical methodologies in clinical and epidemiological research. In general sessions, there were sixteen oral and two poster presentations, where the Best Presentation Award for Young Researcher was conferred on Yuka Sano (Kyoto University) and Dr. Kenichi Hayashi (Keio University). This award is conferred for a student member and a regular member who is less than 40 years old. The tutorial seminar entitled “Causal discovery” was also organized jointly with the Japanese Society of Applied Statistics. Two hundred seventy-five attended the seminar.

The BSJ is pleased to announce that the society conferred the BSJ Award for Outstanding Scientific Contribution on Prof. Satoshi Hattori (Osaka University) for his excellent contributions to development of biostatistical methodologies in medical research, such as robust inference on cancer registry data, and meta-analysis of diagnostic and prognostic studies. The BSJ Honorary Award was conferred on Dr. Nobuhiro Minaka (National Agriculture and Food Research Organization) for his long-term great contributions to the society. The Young Biostatisticians Award was conferred on Dr. Yasuhiro Hagiwara (The University of Tokyo) for his recent publication in Biometrics. This award is annually conferred by the BSJ for researchers, who are less than 40 years old and publishes their research of high standard in recent issues of Biometrics, Journal of Agricultural, Biological and Environmental Statistics, or Japanese Journal of Biometrics, which is the official journal of the BSJ.

### The 2021 Japanese Joint Statistical Meeting

The Virtual Japanese Joint Statistical Meeting will be held on 5-9 September 2021, being hosted by Japanese Federation of Statistical Science Association, which consists of six sponsoring organizations, including the BSJ. Since many from other organizations will attend this meeting, it is a good opportunity for BSJ members to communicate with researchers from various fields other than biometrics. The BSJ is organizing two invited sessions, the Biometric Symposium and the Young Biostatisticians Award session. In the Biometric Symposium entitled “Practices and challenges of counterfactual approaches to causality for real-world evidence”, the BSJ is inviting outstanding researchers to discuss this topic. In the Young Biostatisticians Award session, the winner of the award conferred by the society will make a presentation on g-estimation of structural nested restricted mean time lost models to estimate effects of time-varying treatments on a failure time outcome.

**Takashi Daimon**

**Meetings: 5-9 September, The 2021 Japanese Joint Statistical Meeting, via online**

### The Netherlands (BMS-ANed)

<https://www.vvsor.nl/biometrics/>

Last Spring, 21 May 2021, the BMS-ANed organised a meeting jointly with Pariya Behrouzi, the winner of the Hans van Houwelingen award 2020:

### “GRAPHICAL MODELS AND THEIR APPLICATIONS IN GENOMICS”

The event was again online due to the Corona restrictions. But it was very successful: as a positive side effect, we noticed that the number of participants was really high (100-150), compared to a live event, where usually around 50 participants are attending. The title of the program reflected very well the focus of the meeting and the afternoon was well received.

After the opening by **Mark van de Wiel** (president of BMS-ANed), **Pariya Behrouzi**, statistician at the Mathematical-Statistical Method Group at the Wageningen University and winner of the Hans van Houwelingen award, started off with the topic of the winning paper, ‘Detecting epistatic selection with partially observed genotype data by using copula graphical models’, published in JRSS C in 2019. In this talk, Pariya addressed several problems related to modeling complex systems. Fields such as genetics and genomics often involve large-scale models in which thousands of components are linked in complex ways. What is perhaps most distinctive about the graphical model approach is its suitability in formulating probabilistic models of complex phenomena, while maintaining control over the computational cost associated with these models. In the real world, not all datasets are continuous. The ordinal data or mixed ordinal-and-continuous data routinely arise in many fields. She introduced a copula graphical model for reconstructing a conditional independence network for such data. As a motivating example, she focused on detecting loci – locations on a genome – in *A.thaliana* that do not segregate independently of other loci, thus leading to various plant disorders.

**Marco Scutari** (SUPSI, Switzerland), followed with “Mapping complex data with Bayesian networks”. Bayesian networks are an important model in machine learning due to their flexibility and intuitive graphical representation. They have been adapted to handle several types of data with structures that are more complex than the complete, discrete data they were originally defined on. In this talk Marco discussed how to learn and apply them to incomplete data, time series, and collections of related data sets.

**Marloes Maathuis** (ETH, Switzerland), followed by “False Discovery Rate Control for Gaussian Graphical Models”. She proposed a method to control the finite sample false discovery rate (FDR) when learning the structure of a Gaussian graphical model. The method builds on the recently proposed knockoff idea of Barber and Candès for linear models. Their approach is extended to the graphical model setting by using a local (node-based) and a global (graph-based) step: construct knockoffs and feature statistics for each node locally, and then solve a global optimization problem to determine the threshold for each node. Then estimate the neighborhood of each node, by comparing its feature statistics to its threshold, resulting in a graph estimate. Finite sample FDR control of this procedure is established. According to Marloes, the proposed method is very flexible, in the sense that one has a lot of freedom in the choice of the feature statistics, the optimization problem and the way in which the final graph estimate is obtained. For any given data set, it is not clear a priori what choices of these hyperparameters are optimal. Therefore she uses a sample-splitting-recycling procedure that first uses half of the sample to select the hyperparameters, and then learns the graph using all samples, in such a way that the finite sample FDR control still holds. Finally, she showed the results of comparisons with the state-of-the-art methods, using simulations and a real data set.

**Sach Mukherjee** (DZNE, Germany and University of Cambridge, UK), followed with “Graphical models for heterogeneous data”.

Contemporary large-scale biomedical data are often heterogeneous, in the sense of spanning multiple, possibly latent, groups (such as disease subtypes, population strata etc.), which may be statistically non-identical. Sach discussed the estimation of graphical models in this setting, with an emphasis on high-dimensional data. He also discussed connections to clustering and regression modeling, showing how a combination of suitably defined mixtures, data reduction and regularised estimation can allow effective analysis in very high dimensions, even when mean signals (i.e. cluster-like mean shifts between latent groups) are weak.

Abstracts and slides can be found at <https://www.vvsor.nl/biometrics/events/graphical-models-and-their-applications-in-genomics/>.

## Western North American Region (WNAR)

<http://wnar.org/>

### 2021 WNAR/IMS/KISS/JR Meeting

The 2021 Annual Meeting of WNAR/IMS/KISS/JR was held virtually due to COVID-19.

Two short courses were offered: “Master Protocols: Tackling Complex Disease (and COVID-19!) with Bayesian Adaptive Platform Trials” presented by Ben Saville, Anna McGlothlin, and Christina Saunders and “RMST-based Survival Analysis Methods for Non-Promotional Hazards” presented by Lu Tian (Stanford University),

There were 29 invited sessions (24 WNAR, 3 IMS, 2 JR), two invited panels, eight student paper sessions, and five contributed sessions. We also had 20 posters during our Poster Session. Professor Rachel Fewster from University of Auckland gave the Presidential Invited Address “How to Count the Things You Didn’t See: The Magic and Mystery of Estimating Population Size.”

WNAR thanks Yingqi Zhao (Fred Hutchinson Cancer Research Center) for her efforts as the Program Chair and the Executive Operations Committee for their many efforts to facilitate the virtual conference: Audrey Hendricks (Chair; University of Colorado Anschutz Medical Campus), Jennifer McNichol (University of New Brunswick), Lingling An (University of Arizona), and Subodh Selukar (University of Washington).

### 2021 WNAR/IMS/KISS/JR Student Paper Competition

Twenty-seven students participated in the virtual student paper competition.

The winners in the written category were:

- Zitong Zhang, University of California Davis: “Learning Network Formation Patterns with Stochastic Block Models”
- Kun Yue, University of Washington: “REHE: Fast Variance Components Estimation for Linear Mixed Models”
- Yige Li, Harvard University: “Effectiveness of Localized Lockdowns in the COVID-19 Pandemic”

The winner of the oral category was:

- Yiqun Chen, University of Washington: “Quantifying Uncertainty in Spikes Estimated from Calcium Imaging Data”

The students received their award at a virtual meeting. Certificates will be mailed.

We give a special thanks to the chair of the student paper competition, Laura Saba from University of Colorado Anschutz Medical Campus) and the other Student Competition judges: Jarret Barber (Arizona State University), Cindy Feng (Dalhousie University), Camille Moore (National Jewish Health), Holly Steeves (University of Victoria), Mourad Tighiouart (Cedars-Sinai Medical Center), and Julie Zhou (University of Victoria).

### 2022 WNAR/IMS meeting

The 2022 WNAR/IMS meeting will be in Davis, California from 12-15 June 2022 on the University of California Davis campus. Davis is in the Sacramento Valley, which is in the northern portion of the Central Valley in Northern California. Davis has a vibrant downtown, which is very accessible by walking and biking. Kyoungmi Kim (University of California Davis) is the Local Organizer. Registration information and other details about the meeting will be available on the WNAR web page [www.wnar.org](http://www.wnar.org) in the coming months.

### 2022 WNAR Student Paper Competition

WNAR sponsors students who enter the student paper competition. All WNAR-region entrants receive their registration fees and banquet dinner ticket for free. Monetary prizes will be awarded to the best papers in written and oral competitions. Information on the 2022 WNAR Student Paper Competition, registration information, and program details for the meeting will be posted as they become available: <http://www.wnar.org>.

Megan Othus

## Announcements & Upcoming Events

### Network and Inter-Regional Activities Funding Program

#### Upcoming deadline for proposals for the first half of 2022

#### DUE: 31 October 2021

You may start sending in your applications for Network and Region joint activities that are scheduled to start in the first half of 2022 (January 1 - June 30). We understand that we still might not be able to meet in person during this period due to the continuing COVID-19 pandemic so we will be accepting applications for joint virtual conferences as well. The guiding principle is that the activity must encourage inter-regional interaction. Additionally, there should be some contribution from the participating regions and some general benefit to the Society at large.

As a reminder, the Executive Board allocates \$20,000 in total per year to this funding program. Each activity award is subject to a maximum of \$5,000. Applications can be submitted twice a year: by March 31 for activities that are scheduled to start in the second

half of the same year (July 1 - December 31) and by September 30 (extended deadline 31 October 2021) for activities scheduled to start in the first half of the following year (January 1 - June 30).

**All submissions should be sent to [Regions@biometricsociety.org](mailto:Regions@biometricsociety.org) by 31 October 2021.**

Additional details about the submission can be found on the IBS Website [here](#).

## Journal Club

Journal Club is an online webinar initiative developed by the IBS Education Committee in order to offer a platform for IBS Members and Networks to discuss recent papers published in the IBS Journals, *Biometrics* and *JABES*.

IBS members are able to register for each Journal Club session free of charge, and also view previous Journal Club sessions. To see previously-recorded sessions, visit the Video Sessions page.

### 21 October 2021 AT 15:00 GMT

**Title:** Improving precision and power in randomized trials for COVID-19 treatments using covariate adjustment, for binary, ordinal, and time-to-event outcomes, [Biometrics](#)

**Authors:** David Benkeser, Iván Díaz, Alex Luedtke, Jodi Segal, Daniel Scharfstein, Michael Rosenblum

**Speaker:** David Benkeser

[RSVP for the October session!](#)

You must be logged into your IBS member-only portal to register. To login click “Sign In” at the top right corner of this page. Once logged in, scroll down to “Upcoming Webinars” and click to RSVP for the session(s) you wish to attend.

If you need help with your username/password contact us at [ibs@biometricsociety.org](mailto:ibs@biometricsociety.org).

**Do you have a favorite paper that you just discovered? Or possibly a paper that you have bookmarked and revisit often? Let us know about it.** Please email the IBO with your suggestions and we will present them to our Journal Club Organizer and Chair, Joshua Tebbs, for review.

Kristina Wolford, [ibs@biometricsociety.org](mailto:ibs@biometricsociety.org).

## IBS, IBS Regional and Non-IBS Events and Meetings

[View the meetings calendar here!](#)

Is something missing? Would you like to add your meeting or event to our calendar? If so, please send an email to [IBS@biometricsociety.org](mailto:IBS@biometricsociety.org) with the following information:

1. Event Title
2. Event Description & Location
3. Event Category (IBS Regional Event, IBS Event, Non-IBS Event)
4. Event Link
5. Start/End Date

Follow IBS on Social Media!

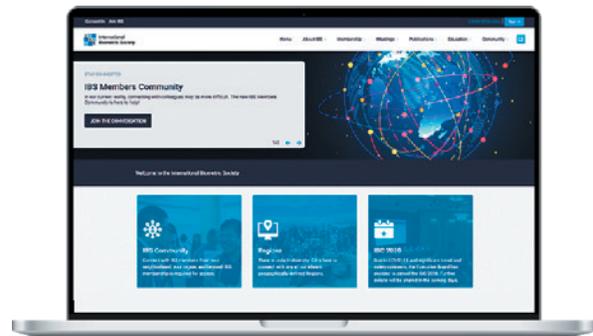
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## Get Connected!



Participate in the IBS Members Community:

1. [Sign in](#) to [biometricsociety.org](https://biometricsociety.org) with your existing credentials. [Contact us](#) if you need assistance.
2. Visit your **profile** to update your personal information and edit privacy settings.
3. Click **Community** in the main navigation and select **All Communities**. Members will see a brand new **IBS Members** community to join.
4. After you join the community, be sure to click on the group **Settings** and customize **Email Notifications** so you can only receive the information you want (real-time updates, a daily digest, or no emails). You may set your preferred **email** address here as well.
5. The final step, **post an update or topic!** This channel is for IBS members, the goal is to empower 6,000 colleagues worldwide to share their unique perspectives, reach out, and connect. It will take some time to cultivate these discussions organically so we appreciate your patience and also your input.

We welcome all comments and feedback about the new website. [Let us know](#) what you think!