



# 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



The summer season is entering its final stretch in the northern hemisphere, with many folks taking well deserved vacation time to re-energize for the remainder of the year. It has been a busy last

quarter at the IBS, with activities picking up on various fronts, especially in the preparations for next year's IBC. The submission deadlines for invited sessions and short courses are already behind us, with an encouraging large number of proposals having been submitted in both categories. The International Program Committee (IPC), chaired by Dimitris Rizopoulos (Dutch Region), is busy reviewing the invited session proposals, while the short course proposals are being selected by the Education Committee, led by its chair, Annette Kopp-Schneider (German Region). The submission process for contributed presentations and posters will open in mid-December this year. The IBC Planning Committee has continued to meet every three weeks, following the progress with local venues and planned activities in Atlanta.

I am delighted to share the positive developments regarding the change of publishers for IBS' flagship publication, *Biometrics*. After a request for proposals (RFP) seeking a new publisher for *Biometrics* was issued last year, an RFP review committee was formed, led by Geert Molenberghs (Belgian Region), *Biometrics* Executive Editor. The com-

mittee made the recommendation to select the proposal from Oxford University Press (OUP), receiving the enthusiastic endorsement from the Editorial Advisory Committee (EAC), the Executive Board (EB), and the IBS Officers. Geert Molenberghs and Peter Doherty (IBS Executive Director) have worked diligently with OUP representatives on the finalization of the new contract for publishing *Biometrics*, which has already been signed by IBS and OUP, going into effect in January 2024. Geert and Peter are also working closely with OUP and Wiley representatives to ensure a smooth transition between publishers. We are well-positioned to have a flawless handover of publishing operations between Wiley and OUP. I would like to express my heartfelt gratitude to Geert, Peter, Hans-Peter Piepho (EAC chair, German Region), the entire RFP review committee, Chantal Brodie and Ann Hanhart (*Biometrics* Editorial Managers), and all others from IBS and the IBO who have helped in the challenging and critical effort of identifying a new publisher for *Biometrics* and ensuring a smooth transition between publishers.

The International Business Office (IBO) has successfully concluded the process of making the 87 hours of recorded presentations from IBC2022 available for on-demand viewing. The available recorded material includes a variety of invited sessions, short courses, special sessions, etc. I encourage all to read the announcement of the deployment of the recorded content, which includes a list of the available recordings and instructions on how to access them. Many

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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  
GCMr - Cameroon Region  
GCI - Chilean Region  
GCMr - Cameroon 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*

thanks to Peter Doherty and Alexander Iula (IBO) for making this great learning resource available to the IBS membership, as well as non-IBS members (for a small fee).

The newest region to join the IBS, the Cameroon Region, is off to an exciting start, well-reflective of the dynamism and enthusiasm of its founding members. The region has officially joined the Sub-Sahara African Network (SUSAN) and is in the process of organizing its first regional scientific meeting, to be held at the University of Buea, Cameroon, on October 13 and 14 of this year. Stay tuned for more details about the conference, including its exciting scientific program, to be posted later on the IBS website.

The annual face-to-face meeting of the Executive Board (EB) took place in early September, during the 5th Conference of the Central European Network (CEN), in Basel, Switzerland. We have welcomed seven new EB members, which is the largest turnover on the Board in many years. I would like to thank the CEN2023 organizing committee (in particular the conference chair, Frank Bretz, from the Austrian-Swiss Region) for encouraging us to have the EB meeting during the conference

and for securing the room space at the conference venue. Many of the Board members decided to stay longer in Basel to enjoy the exciting scientific and social program of CEN2023.

As a final note, I would like to acknowledge IBS' participation in the 2023 ISI World Statistical Conference (WSC), held last month in Ottawa, Canada. Peter Doherty represented the Society at the International Prize of Statistics ceremony, in which C. R. Rao's family members accepted the prestigious award on his behalf. Two IBS Young Ambassadors had their papers selected by the ISI-IBS Selection Committee to be presented at the 2023WSC: Suryo Adi Rakhmawan (Australasian Region) and Marcelo Bourguignon Pereira (Brazilian Region). Congratulations to both students and thanks to the Selection Committee for the essential work they do to keep this fruitful collaboration between IBS and ISI thriving.

Happy end of summer/winter to all.

**José Pinheiro**

International Biometric Society President  
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## IBS Confirms Dates and Location of IBC2024

The Society is pleased to announce that the confirmed dates and location for our next International Biometric Conference will be 8-13 December 2024, in Atlanta, Georgia, USA.

After careful consideration and in response to the evolving local landscape, we have made the decision to relocate our biennial conference from Buenos Aires, Argentina to the city of Atlanta. In addition, the conference date was originally scheduled for the first week of December and will now be held one week later. Society leadership is currently notifying all partners of these changes.

The decision to move the conference location was not made lightly, and all involved share the ultimate goal of a successful IBC program for the Society, its members, and attendees, in keeping with the rich tradition of past IBCs. Every effort was made, and every option was fully explored to remain in Buenos Aires. We acknowledge and share the disappointment many will feel in not going to Argentina. We look forward to returning there in the future. We would like to personally thank the members of the Local Organizing Committee and especially Co-Chairs María Gabriela Cendoya and Sylvia Suring of the Argentinean Region, for their incredible engagement and support during our site visit and the early planning phases. We are confident that their involvement will contribute to making IBC2024 a great experience. We also wish to thank the IBS staff for their flexibility and responsiveness in finding and securing a world-class alternate venue.

Our dedicated team is working diligently to ensure a successful International Biometric Conference in 2024. Atlanta, known for

its rich history, diverse culture, and dynamic environment, offers a wonderful setting for our biennial conference. Atlanta served as the backdrop during America's Civil War, the era of Reconstruction, and the Civil Rights Movement, making it a fascinating, historic city to explore and learn. It offers world-class facilities, excellent international transportation connections, and a wide range of attractions, so we are assured of a memorable experience. Atlanta is easily accessible with non-stop travel available from 75 international destinations. Attractions and entertainment districts include the Georgia Aquarium, the Atlanta Botanical Garden, and Centennial Olympic Park, as well as plenty of inviting local dining options for attendees to enjoy.

We hope you will join us for 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.

Further updates will be coming soon regarding the conference schedule, accommodation, and travel information, as we work to make this change as seamless as possible. If you have submitted an abstract for either the Short Course or Invited Sessions, we will be reaching out to you in the coming days. The Society's goals of accessibility, diversity, and engagement during IBC will continue to be a priority as planning for the Atlanta conference continues. We can't wait to welcome you to Atlanta. If you have any questions or need assistance, please don't hesitate to reach out to our team.



# From the Editor

Commemorating the fortieth year of successful journey of the *Biometric Bulletin* we dedicated the opening paragraph of the latest Editor's column remembering the founding efforts made by the IBS leadership towards its launching in May 1984. We also expressed our sincere gratitude to earlier editors of the *Bulletin* who had helped significantly during its innovative period of decades. It's our duty to once again salute the entire fraternity of IBS, especially to those who were directly responsible in shaping the *Bulletin* in whatever ways to its present status. I feel happy in sharing the fact that during the current years more than thirty percent of the IBS regions have been reporting regularly each quarter to the *Biometric Bulletin* (BB). Interestingly, some of the regional correspondents representing established larger membership continents do participate and contribute to each issue of BB without fail. We must congratulate their respective regional leaderships. It is not only reporting rather reflects the continuous academic activities planned and organised throughout the globe round the year.

In continuity with highlights in the President's corner, I also recall the words mentioned in this very editor's column in the last issue of BB in honour and the recognition bestowed on Prof. C. R. Rao, who basically belonged to IBS(IR) and had served as IBS President decades ago. We were confident of celebrating his 103rd Birthday in September 2023, in a grand manner across the countries around the globe. But we have just missed it, unfortunately. We published a dedicated column in BB celebrating his Birth Centenary exactly three years back, and I encourage you to read it to learn more about this great soul.

I repeatedly mention and personally feel that the BB is incomplete without the Editorial updates from *Biometrics* and *JABES*. The contents of these updates are of high merits and very informative on the latest ongoing research and the specific topics of interest. Furthermore, these core journals of IBS have a long waiting list of articles of excellence standing in order for publications. I am reminded of reviving our earlier initiative in coordination with the Chair-EAC, Prof. Hans-Peter, for the periodic reappearances of the editorial-updates from our own regional efforts namely *Biometrical Journal* under the oversight together with German, Austrian-Swiss and Italian regions and *Biostatistics and Epidemiology* from Chinese region.

A good article titled "Future-verse-Worry-Free Parallelization in R" by Henrik Bengtsson is appearing under the 'Software Corner'. I am grateful to the entire STRATOS configuration leadership for their regular contributions to BB. This time Group 9 (TG9) of STRATOS has contributed an elaborate article of interest on High-dimensional data (HDD).

We would once again like to request the members for newer ideas to further improve the contents of the *Bulletin* in its fortieth year.

**Ajit Sahai**  
Biometric Bulletin, Editor

## Update from the IBO

Hello to all Society members!

Today, I would like to share a few updates from your International Business office and offer a warm public welcome to some of our newest team members! Isabel Jasper, our newest administrator, joined the team approximately six months ago. Since that time, Isabel has been reaching out to many of our IBS regions to assist them in managing administrative processes related to membership. She is also the key contact on staff for any membership questions that you may have and is currently working with one of our regions to launch a brand-new administrative tool that will ensure the seamless and secure transfer of contact information from Regions to the IBO, resulting in faster service and synchronized data across all IBS administrative offices. Unless you are an administrator for your region, you likely will not hear very much about this tool in regular communications. But rest assured, the time saved and improved accuracy of member data will result in more time being devoted in the future to the service of members like you!

Heidi Lapka, another new team member, is serving the Society in a variety of ways as a special projects director. She is currently assisting the Awards Fund Committee in managing our current travel awards fund grants, managing the Journal Club web series, working with the editor of the *Biometric Bulletin* in bringing you our latest edition and uncovering some older editions of the *Bulletin*, hoping soon to post them publicly via the website, and creating a brand-new open discus-



Peter and IBS Young Ambassadors/members meet at the recent ISI conference in Ottawa, ON Canada.

sion board through which we can share information useful to members and non-members alike. Welcome, Heidi and Isabelle!

As always, please reach out to the Society's office with any questions by sending an e-mail to [ibs@biometricsociety.org](mailto:ibs@biometricsociety.org). Thanks for your attention.

Best wishes,  
**Peter Doherty, CAE**  
Executive Director

### December 2023 Issue Highlights

The December issue features articles across a broad spectrum of applications and methodology. The *Biometric Methodology* section sets out with a Discussion paper on “Optimal test procedures for multiple hypotheses controlling the familywise expected loss,” by Willi Maurer, Frank Bretz, and Xiaolei Xun, and with discussion contributions by Yoav Benjamini, Ruth Heller, Abba Krieger, and Saharon Rosset; Sudipto Banerjee; Lisa M. LaVange, Ethan M. Alt, and Joseph G. Ibrahim; and Werner Brannath.

#### Regular papers include:

- “Additive subdistribution hazards regression for competing risks data in case-cohort studies,” by Adane F. Wogu, Haolin Li, Shanshan Zhao, Hazel B. Nichols, and Jianwen Cai;
- “Stabilized direct learning for efficient estimation of individualized treatment rules,” by Kushal S. Shah, Haoda Fu, and Michael R. Kosorok;
- “Optimal sampling for positive only electronic health record data,” by Seong-ho Lee, Yanyuan Ma, Ying Wei, and Jinbo Chen;
- “Combining observational and experimental datasets using shrinkage estimators,” by Evan T. R. Rosenman, Guillaume Basse, Art B. Owen, and Mike Baiocchi;
- “Entropy balancing for causal generalization with target sample summary information,” by Rui Chen, Guanhua Chen, and Menggang Yu;
- “A seasonality-adjusted sequential test for vaccine safety surveillance,” by Rex Shen, Keran Moll, Ying Lu, and Lu Tian;
- “Bayesian nonparametric adjustment of confounding,” by Chanmin Kim, Mauricio Tec, and Corwin Zigler;
- “DROID: Dose-ranging approach to optimizing dose in oncology drug development,” by Beibei Guo and Ying Yuan;
- “Analyzing data in complicated 3D domains: smoothing, semiparametric regression and functional principal component analysis,” by Eleonora Arnone, Luca Negri, Ferruccio Panzica, and Laura M. Sangalli;
- “Improved inference for doubly robust estimators of heterogeneous treatment effects,” by Heejun Shin and Joseph Antonelli;
- “Latent deformation models for multivariate functional data and time warping separability,” by Cody Carroll and Hans-Georg Mueller;
- “Efficient and flexible estimation of natural direct and indirect effects under intermediate confounding and monotonicity constraints,” by Kara E. Rudolph, Nicholas Williams, and Ivan Diaz;
- “FDR controlled multiple testing for union null hypotheses: A knock-off-based approach,” by Ran Dai and Cheng Zheng;
- “Nonparametric failure time: time-to-event machine learning with heteroskedastic Bayesian additive regression trees and low information omnibus Dirichlet process mixtures,” by R.A. Sparapani, B.R. Logan, M.J. Maiers, P.W. Laud, and R.E. McCulloch;
- “Estimation of time-specific intervention effects on continuously distributed time-to-event outcomes by targeted maximum likelihood estimation,” by Helene C.W. Rytgaard, Frank Eriksson, and Mark J. van der Laan;
- “A Bayesian zero-inflated Dirichlet-multinomial regression model for multivariate compositional count data,” by Matthew D. Koslovsky;
- “Interim monitoring of sequential multiple assignment randomized trials using partial information,” by Cole Manschot, Eric Lafer, and Marie Davidian;
- “Longitudinal incremental propensity score interventions for limited resource settings,” by Aaron Sarvet, Kerollos N. Wanis, Jessica Young, Roberto Hernandez-Alejandro, and Mats J. Stensrud;
- “Detecting the spatial clustering of exposure-response relationships with estimation error: a novel spatial scan statistic,” by Wei Wang, Sheng Li, Tao Zhang, Fei Yin, and Yue Ma;
- “Identifying and estimating effects of sustained interventions under parallel trends assumptions,” by Audrey Renson, Michael G. Hudgens, Alexander P. Keil, Paul N. Zivich, and Allison E. Aiello;
- “Estimating optimal individualized treatment rules with multistate processes,” by Giorgos Bakoyannis;
- “Sparse estimation in semi-parametric finite mixture of varying coefficient regression models,” by Abbas Khalili, Farhad Shokoochi, Masoud Asgharian, and Shili Lin;
- “On interquantile smoothness of censored quantile regression with induced smoothing (CQRIS),” by Zexi Cai and Tony Sit;
- “An accelerated failure time regression model for illness-death data: A frailty approach,” by Lea Kats and Malka Gorfine;
- “Instability of inverse probability weighting methods and a remedy for non-ignorable missing data,” by Pengfei Li, Jing Qin, and Yukun Liu;
- “Prior and posterior checking of implicit causal assumptions,” by Antonio R. Linero;
- “Conditional inference in cis-Mendelian randomization using weak genetic factors,” by Ashish Patel, Dipender Gill, Paul Newcombe, and Stephen Burgess;
- “Ensuring valid inference for Cox hazard ratios after variable selection,” by Kelly Van Lancker, Oliver Dukes, and Stijn Vansteelandt;
- “A semiparametric Cox-Aalen transformation model with censored data,” by Xi Ning, Yinghao Pan, Yanqing Sun, and Peter B. Gilbert; and
- “Transportability of causal inference under random dynamic treatment regimes for kidney-pancreas transplantation,” by Grace R. Lyden, David M. Vock, Erika S. Helgeson, Erik B. Finger, Arthur J. Matas, and Jon J. Snyder.

#### The Biometric Practice section includes papers on:

- “Spatially adaptive calibrations of AirBox PM2.5 data,” by Hsin-Cheng Huang;
- “Bayesian design of multi-regional clinical trials with time-to-event endpoints,” by Nathan W. Bean, Joseph G. Ibrahim, and Matthew A. Psioda;
- “Estimating population size: the importance of model and estimator choice,” by Matthew R. Schofield, Richard J. Barker, William A. Link, and Heloise Pavanato;
- “Latent trajectory models for spatio-temporal dynamics in Alaskan ecosystems,” by Xinyi Lu, Mevin B. Hooten, Ann M. Raiho, David K. Swanson, Carl A. Roland, and Sarah E. Stehning;
- “A nonparametric test of group distributional differences for hierarchically-clustered functional data,” Alexander S. Long, Brian J. Reich, Ana-Maria Staicu, and John Meitzen;
- “Finding influential subjects in a network using a causal framework,” by Youjin Lee, Ashley Buchanan, Elizabeth Ogburn, Samuel R. Friedman, M. Elizabeth Halloran, Natallia V. Katenka, Jing Wu, and Georgios Nikolopoulos;
- “Modelling Covid-19 contact-tracing using the ratio regression capture-recapture approach,” by D. Böhning, R. Lerdsuwansri, and P. Sangnawakij;

- “A synthetic data integration framework to leverage external summary-level information from heterogeneous populations,” by Tian Gu, Jeremy M.G. Taylor, and Bhramar Mukherjee;
- “Conditional cross-design synthesis estimators for generalizability in Medicaid,” by Irina Degtiar, Tim Layton, Jacob Wallace, and Sherri Rose;
- “Imputation-based Q-learning for optimizing dynamic treatment regimes with right-censored survival outcome,” by Lingyun Lyu, Yu Cheng, and Abdus S. Wahed;
- “A case study of glucose levels during sleep using multilevel fast function on scalar regression inference,” by Renat Sergazinov, Andrew Leroux, Erjia Cui, Ciprian Crainiceanu, R. Nisha Aurora, Naresh M. Punjabi, and Irina Gaynanova;
- “Correcting for bias due to mismeasured exposure history in longitudinal studies with continuous outcomes,” by Jiachen Cai, Ning Zhang, Xin Zhou, Donna Spiegelman, and Molin Wang;
- “Dirichlet process mixture models for the analysis of repeated attempt designs,” by M.J. Daniels, M. Lee, and W. Feng;
- “Dynamic enrichment of Bayesian small sample, sequential, multiple assignment randomized trial (snSMART) design using natural history data: A case study from Duchenne muscular dystrophy,” by Sidi Wang, Kelley M. Kidwell, and Satrajit Roychoudhury; and
- “Analyzing clustered continuous response variables with ordinal regression models,” by Yuqi Tian, Bryan E. Shepherd, Chun Li, Donglin Zeng, and Jonathan J. Schildcrout.

## Biometrics News

The journal's impact factor was 1.329 in 2016, 1.524 in 2017, 1.755 in 2018, 1.711 in 2019, then rose to 2.571 in 2020, and returned to 1.701 for 2021. The impact factor for 2022, released in July 2023, is 1.900. The journal ranks 39/125 in the category “Statistics & Probability,” 59/94 in “Biology,” and 36/55 in “Mathematical & Computational Biology.” All three rankings have improved relative to last year.

The journal's backlog has lengthened further, from about 14-16 months last year to 17-19 months at present. Fortunately, EarlyView ensures that an article is available for reading and citation as soon as it is typeset. Nevertheless, as part of the transition to Oxford University Press, the June, September, and December 2023 issues contain nearly three times the usual number of papers, so that 2024 will start with a much shorter backlog.

For the remainder of 2023, 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 on 7 July and 21 August 2023, at different times of day, to accommodate our global Associate Editors community. Given that this is a non-IBC year, there is no face-to-face Editorial Board Meeting in 2023. Next year, we will supplement both virtual meetings with a face-to-face one during the International Biometric Conference, in December 2024.

Oxford University Press to Publish *Biometrics* from 2024 Onwards.

The IBS received two competitive bids in response to its Request for Proposals to publish *Biometrics*. An ad hoc committee, consisting of Geert Molenberghs (Belgian Region, Chair and Executive Editor); Chantal Brodie and Ann Hanhart (Editorial Managers); Peter Doherty (IBS Executive Director); José Pinheiro (ENAR, IBS President); Iris Pigeot (German Region, IBS Vice-President); Geert Verbeke (Belgian Region, IBS Outgoing Vice-President); Henry Mwambi (SUSAN, IBS Secretary); Vicente Nunez-Anton (Spanish Region, IBS Treasurer); Hans-Peter Piepho (German Region, Editorial Advisory Committee Chair); and Nandita Mitra (ENAR, Budget and Finance Committee Chair) found that Oxford University Press presented the most favorable bid. This assessment was ratified by the Editorial Advisory Committee, the Budget and Finance Committee, and the Executive Board. The rest of 2023 is devoted to a seamless transition between publishers. For authors, editors, associate editors, and referees, little or nothing will change, while procedures will be optimized where possible. Articles will be assigned to a volume and an issue as soon as they have been accepted and typeset. This will improve searchability and simplify citation.



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## 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. Both the outgoing and the incoming panel consist of nearly 110 Associate Editors.

We are grateful for the service, rendered by our retiring Associate Editors: James Bell, Werner Brannath, Anabel Forte Deltell, Ying Guo, Katerina Kechris, Markus Pauly, Maroussa Zagoraiou.

We welcome our incoming Associate Editors: Björn Bornkamp, Fei Gao, Guanyu Hu, Frank Konietzschke, Ben Stevenson, and Diane Uschner.

Last but not least, a warm word of thanks to our continuing AEs, those starting a new term 2023-2024, and those serving ongoing terms 2022-2024!

Find us on twitter at [@Biometrics\\_jbs](https://twitter.com/Biometrics_jbs).

**Geert Molenbergh**  
Biometrics Executive Editor

# *The Journal of Agricultural, Biological, and Environmental Statistics (JABES)*

We are running the following special issue with related information and open calls published at  
<https://www.springer.com/journal/13253/updates>.

Special Issue on The Hawkes Process: Theory, Methodology, Algorithms, Extension, and Applications in Environmental Sciences.

Point process models are common in research as a natural tool to describe the patterns of discrete events that occur in a continuous space, time, or a space-time domain. In recent decades, the Hawkes point-process model, which was proposed by Alan G. Hawkes in the 1970s, has become one of the most useful point processes in event-type data analysis, such as earthquakes, crimes, forest fires, terrorist attacks, society networks, genomes, etc., due to its powers in detecting the clustering effect and the positive interactions among individual events/particles. Equipped with the Hawkes process and general statistical inference tools, we can determine the potential causal relationship among discrete events, especially for nowadays, with the rapid development of observation and data-storage technologies, big data has unavoidably become a hot issue in point-process data analysis. As the Hawkes process provides us with a quick tool and general framework to quantify and forecast the clustering or the trigger-

ing effect among events, it is important for us to develop more advanced theory, methodology and algorithms related to this process and its extensions, so that we can solve the challenging problems that are encountered in its applications.

Guest Editors: Jorge Mateu, Jiancang Zhuang, Feng Chen, Rick Schoenberg

**Deadline for submission: 15 October 2023.**

The open call for the 2023 competition of the Section on Statistics and the Environment (ENVR) of the ASA is now open and, as in past editions, JABES will invite the winners and those receiving a mention to publish their winning papers with us.

We will soon make the public announcement of the best JABES paper, and an honorable mention, among all papers published in 2022. These two papers will be presented in the next IBC2024 in Atlanta.

June issue features a discussion paper based on the topic “Saving Storage in Climate Ensembles:

A Model-Based Stochastic Approach” by Huang Huang, Stefano Castruccio, Allison H. Baker, and Marc G. Genton, with five discussants and a rejoinder.

Indeed, June 2023 issue of JABES (Vol 28 (2)) features the following papers:

- “A Causal Mediation Model for Longitudinal Mediators and Survival Outcomes with an Application to Animal Behavior” by S Zeng, E. C. Lange, E.A. Archie, F.A. Campos, S C. Alberts and F. Li
- “A Case-Crossover Study of the Impact of the Modifying Industrial Operations Protocol on the Frequency of Industrial Forestry-Caused Wildland Fires” in Ontario, Canada by K Granville, D. G. Woolford, C. B. Dean and C. B. McFayden
- “Detecting Changes in Dynamic Social Networks Using Multiply-Labeled Movement Data” by Z. L. Boulil, J. W. Durban, H Fearnbach, T. W. Joyce, S. G. M. Leander and H. R. Scharf
- “Spatiotemporal Exposure Prediction with Penalized Regression” by N. A. Ryder & J. P. Keller Scalable Semiparametric Spatio-temporal Regression for Large Data Analysis by T. F. Ma, F. Wang, J. Zhu, A. R. Ives and K. E. Lewinska
- “An Approach for Specifying Trimming and Winsorization Cutoffs” by K. Cheng and D. S. Young
- “Saving Storage in Climate Ensembles: A Model-Based Stochastic Approach” by H. Huang, S. Castruccio, A. H. Baker and M. G. Genton
- “Discussion on “Saving Storage in Climate Ensembles: A Model-Based Stochastic Approach” by A. Poppick
- “Discussion on “Saving Storage in Climate Ensembles: A Model-Based Stochastic Approach” by W. S. Burr
- Discussion on “Saving Storage in Climate Ensembles: A Model-Based Stochastic Approach” by A. Datta
- Discussion on “Saving Storage in Climate Ensembles: A Model-Based Stochastic Approach” by J. Bessac, R.

Underwood and S. Di

- Discussion on “Saving Storage in Climate Ensembles: A Model-Based Stochastic Approach” by S. Banerjee
- Rejoinder on “Saving Storage in Climate Ensembles: A Model-Based Stochastic Approach” by H. Huang, S. Castruccio, A. H. Baker & M. G. Genton
- BOOK REVIEW: “Review of Handbook of Graphs & Networks in People Analytics: With Examples in R & Python” by Keith McNulty by S. Ren

JABES should be home for Data Science broadly defined as the science of learning from data, incorporating advances in computation and data analytics, with statistical theory and inference for problems coming from the branches that sustain the journal. I would like to encourage interdisciplinary submissions that involve collaboration between statisticians and other data scientists to find solutions to these challenges, through innovative methodological developments and applications, bringing together data science and statistics. The innovative methodology should be directly motivated by real world data problems in agricultural, biological and environmental settings.

For more information on upcoming issues, the editorial board, and the aim and scope of the journal, please visit our website <http://link.springer.com/journal/13253>. We also accept submissions of books to review in the upcoming issues of JABES; to submit a book for review, please see the above website (click on “Editorial Board”) or contact Eleni Matechou ([e.matechou@kent.ac.uk](mailto:e.matechou@kent.ac.uk)).

Please follow us on Twitter: [@JabesEditor](https://twitter.com/JabesEditor).

**Jorge Mateu**  
Editor-in-Chief

## Software Corner

### Futureverse—Worry-Free Parallelization in R

Henrik Bengtsson (Department of Epidemiology and Biostatistics, University of California San Francisco (UCSF), United States)

#### Introduction

Slow code is never fun. How often haven't we said, “I'll just run a quick analysis in R,” just to find ourselves waiting for hours or even days for it to complete? There can be many reasons for our code not running as fast as we want. Inefficient programming is one reason for slow code performance, but we can often improve it with minor changes, with some experience. For example, R users quickly discover that iterating element by element is slow, but vectorized function calls are much faster. If you want to learn how to write more efficient R code, I recommend Gillespie & Lovelace (2016), and Wickham (2019).

However, it is not always possible for us to speed up the code we run. A common reason is that it is not our code that is slow. Instead, it may be an R package maintained by someone else that is slow, and it may not be worth our time, or it might be beyond our skill levels, to improve on that code. Another reason could be that the underlying algorithm is computationally expensive, and its implementation is already optimized. Even after considering options and rewriting code, we may still have slow-running code. This is when we could turn to parallelization to shorten the processing time.

This article gives a brief overview of The Futureverse (Bengtsson, 2021), which is a framework making simple to parallelize R code. The learning curve is low and most users are up and running within minutes. As we will see below, sometimes it is just a matter of renaming a function call to make it run in parallel. The Futureverse

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makes it straightforward to write robust and statistically sound R code that can run in parallel on a variety of compute resources available to the end-user.

## Background

Where does the Futureverse position itself in the R ecosystem and where can it be used? To answer those questions, it is helpful to know what solutions for parallel processing already exist in R. For starters, all R installations come with the **parallel** package, which provides some rudimentary, built-in functions for running R code in parallel. You might have heard of the `mclapply()` function. We can use it to turn a sequential `lapply()` call:

```
y <- lapply(X, slow_fcn)
```

into a parallel version:

```
library(parallel)
```

```
y <- mclapply(X, slow_fcn)
```

that calls `slow_fcn()` on each `X` elements in parallel. The `mclapply()` function works only on Linux and macOS, because it relies on a concept called *forked processing*, which R does not support on MS Windows. If used on MS Windows, it falls back to running sequentially just like `lapply()`. Importantly, `mclapply()` is not stable in all environments, or in combination with certain R packages, resulting in abrupt crashing of R. The R documentation - `help("mclapply")` - warns about this, and the RStudio GUI engineers [recommend against using it](#) when running R in the RStudio software.

Another famous function of the **parallel** package is `parLapply()`. We can use it somewhat similarly to `mclapply()`, with the advantage that it works on all operating systems. The downside is that it requires more low-level orchestration, e.g., we need to set up a cluster of background workers using `makeCluster()`, manually load required packages on the workers using `clusterEvalQ()`, and export all variables needed by the workers using `clusterExport()`. Only then can we call `parLapply()`. When we are done, we must remember to shut down the workers using `stopCluster()`. This makes it tedious and error prone to use, and it clutters up our R code with a lot of verbatim code, which blurs the algorithm of interest.

There are also solutions outside of base-R and the **parallel** package. Almost everyone trying to run R in parallel ends up discovering the popular **foreach** package (Kane et al., 2013), which is available on the Comprehensive R Archive Network (CRAN). This package has a beautiful design that simplifies how we write parallel code in R. When it was first released in 2009, it introduced the idea of separating the code to be parallelized from the code that controls how and where parallelization is performed. For example,

```
library(foreach)
library(parallel)
```

```
## Create a cluster of 4 parallel R workers running in the background
cl <- makeCluster(4)
```

```
## Configure foreach to process elements in parallel on these workers
doParallel::registerDoParallel(cl)
```

```
## For each element in 'X' call slow_fcn().
## Multiple elements are processed concurrently.
y <- foreach(x = X) %dopar% {
  slow_fcn(x)
}
```

```
## Stop workers, when done
stopCluster(cl)
```

This separation allows the developer to focus on the parts that should run in parallel (i.e., the `foreach()` call) without having to worry too much about how and where the code is run. Instead, it is the end-user that have the control over how to parallelize, e.g., `registerDoParallel()`. In this example, we used four workers on the local machine, but we could equally well have set up four workers on four external computers—all without having to rewrite the `foreach()` statement. This design philosophy of **foreach** is powerful. Unfortunately, there are some pitfalls that prevent us from writing code that is guaranteed to work with all parallel backend. For example, `foreach()` takes backend-specific arguments breaking the developer-user separation. That said, the separation of responsibilities between the developer and the end-user is one of the main reasons **foreach** being popular.

## What is the Futureverse?

The Futureverse was created in order to remove most of the friction and hurdles that we are experiencing with the traditional parallel-programming techniques in R. It is based on a programming construct referred to as futures (Hibbard, 1976; Hewitt & Baker, 1977; Friedman & Wise, 1978), which is particularly well suited for functional programming languages such as R. The Futureverse is designed to make it as simple as possible to parallelize existing code letting the developer focus on the algorithm without being distracted by technicalities related to parallelization. For instance, it automatically identifies and exports objects that the parallel workers need. It will also protect against common mistakes that may occur when running code in parallel. As an example, Futureverse detects and warns us when we use random numbers that are not statistically sound because they were generated in parallel. You can easily install all Futureverse packages from CRAN, such as **future** with the command `install.packages("future")`.

The Futureverse follows the lead of **foreach** by strictly separating what to parallelize from how to parallelize it. The developer can also stay with their favorite coding style, e.g. base-R, Tidyverse, or **foreach**. For instance, if you prefer base-R apply functions such as `lapply()`, `mapply()`, and `by()`, you can use the plug-and-play replaceable `future_lapply()`, `future_mapply()`, and `future_by()` functions available in the **future.apply** package. For example,

```
library(future.apply)
plan(multisession) ## parallelize on the local machine
```

```
y <- future_lapply(X, slow_fcn)
```

works just like `lapply()`, except that it runs in parallel via the multisession backend. The multisession backend uses background R workers running on the same machine similar to the cluster workers created by `parallel::makeCluster()`.

If you prefer the Tidyverse style, the pipe operator (`|>`), and functions like `map()` of the **purrr** package, there are parallel versions in the **furrr** package. For example,

```
library(furrr)
plan(multisession)

y <- X |> future_map(slow_fcn)
```

Alternatively, if you like the **foreach** style of iterating over elements, you can use the `doFuture` package and its `%dofuture%` operator. For example,

```
library(doFuture)
plan(multisession)

y <- foreach(x = X) %dofuture% {
  slow_fcn(x)
}
```

The above examples produce identical results to the corresponding `lapply()` call. Note how `plan()` controls which parallel backend is used - the end-user can easily switch to an alternative backend with a single change of settings. For example, a user with SSH access to additional local and remote machines can harness them by using:

```
plan(cluster, workers = c("mydesktop", "anotherdesktop", "server.myuni.edu"))
```

There are other parallel backends available in the Futureverse, e.g. **future.batchtools** can be used to parallelize via job schedulers on high-performance compute (HPC) clusters, and **future.callr** provides an alternative to multisession. One of the advantages of the future ecosystem is that all types of backends, including those that will be developed in the future, will automatically work without having to modify any code.

There are a few things to be aware of when running algorithms in parallel. For example, variables and functions that exist on the current machine have to be available on the parallel workers – workers that may run on a remote machine across the world. With traditional techniques such as `parLapply()` of the **parallel** package, it is the developer's responsibility to identify such objects and make sure they are exported to each parallel worker upfront. This is not necessary when using futures. The future framework identifies and exports required objects automatically, removing this often tedious and error-prone task and helps keep the code tidy.

Another important thing to keep in mind when running code in parallel is random number generation. Some techniques we use in statistical analysis require high-quality RNG, e.g. permutation tests and bootstrapping. Without it, there is a risk that the results become biased. R uses the Mersenne-Twister RNG (Matsumoto & Nishimura; 1998) by default, which has good random properties when running sequentially. However, when running parallelly there is a risk that such random numbers generated by one parallel worker are not independent of those generated in another parallel worker. To address this problem, special RNGs have been designed that works well also in parallel processing, e.g. the L'Ecuyer-CMRG method (L'Ecuyer, 1999). The Futureverse has built-in support for L'Ecuyer-CMRG RNG. When used, any random numbers generated, and therefore also the results, are numerically reproducible, regardless of which parallel backend and the number of parallel workers being used. If the developer forgets to use it, the future framework will detect the mistake and produce a warning detailing that the results may not be valid and how to solve it.

Another advantage with futures is that output, messages, warnings and errors work the same as when running sequentially. For more details, and additional arguments for using futures to parallelize R code, see Bengtsson (2021).

### Who is using Futureverse?

The uptake of the future ecosystem by the R community has grown steadily since it was first released in 2015. The **future** package is now among the top-1% most downloaded packages on CRAN. Nearly 300 packages on CRAN and Bioconductor rely on it directly, and many more rely on it indirectly – often without the end-user even being aware.

Prominent examples where the future framework is used for parallel and asynchronous processing are **Seurat** (Large-Scale Single-Cell Genomics), **shiny** (Scalable, Asynchronous UX), **plumber** (An API Generator for R), **mlr3** (Next-Generation Machine Learning), **targets** (Pipeline Toolkit for Reproducible Computation at Scale), and **EpiNow2** (Estimate Real-Time Case Counts and Time-Varying Epidemiological Parameters).

### Summary

The goal of the Futureverse is that you should not have to spend much time and mental efforts on getting your existing R code to run in parallel. In contrast to the more traditional approaches, you only have to do minor rewrites to make code run in parallel and you can stay with your favorite coding style. The future framework aims at making parallelization something that “just works,” allowing you to keep a focus on the analysis. As a developer, you rarely know who your end-users are and less so what their compute resources are. One user might want to parallelize on a laptop, whereas another one wants to scale out a cloud service. When using the Futureverse, you give the end-user full control on how and where to parallelize. Strict requirements and validation of the future backends guarantee that your code will work anywhere.

If you wish to learn more about the Futureverse, please visit <https://www.futureverse.org>, which provides documentation, examples, tutorials, presentations, and blog posts on how to use futures for running R in parallel.

### Acknowledgments

The work on Futureverse was sponsored by the R Consortium Infrastructure Steering Committee (ISC) and the Chan Zuckerberg Initiative (CZI) Essential Open Source-Software (EOSS) program.

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

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# STrengthening Analytical Thinking for Observational Studies (STRATOS):

## Overview of methodological issues when analyzing high-dimensional biomedical data

De Bin R., McShane L., Rahnenführer J. on behalf of STRATOS TG9 (2023)

Here we describe accomplishments and current activities of the STRATOS Topic Group 9 (TG9): High-dimensional data (HDD). In the last year, three new members have joined STRATOS TG9. Current members of the group are: Co-chairs Riccardo De Bin (Norway), Lisa McShane (USA) and Jörg Rahnenführer (Germany); Federico Ambrogi (Italy), Axel Benner (Germany), Harald Binder (Germany), Anne-Laure Boulesteix (Germany), Kevin Dobbin (USA), Roman Hornung (Germany), Lara Lusa (Slovenia), Stefan Michiels (France), Eugenia Migliavacca (Switzerland), Willi Sauerbrei (Germany), and Martin Treppner (Germany).

Proliferation of HDD in biomedical research has brought unprecedented opportunities to advance knowledge. In order to exploit the potential of new analysis methods to reveal useful insights from

HDD, it is imperative that researchers have access to guidance on the methods available and their proper application.

In May 2023, TG9 published an extensive overview of statistical approaches for high-dimensional biomedical data in BMC Medicine. Biomedical research now frequently involves high-dimensional data generated from observational studies, controlled laboratory experiments, and clinical trials, including omics data and data from electronic health records. In the overview paper, a solid statistical foundation is provided for researchers, including statisticians and non-statisticians, who have limited familiarity with methods for HDD or simply want to better evaluate and understand the results of HDD analyses. The paper introduces basic concepts and useful strategies for design and analysis of studies involving HDD, with primary focus on omics data. For commonly used analytical methods, minimally technical descriptions are provided. The strengths and limitations of competing approaches are discussed, and some gaps in the availability of appropriate analytical methods are identified. In addition, an extensive list comprising 234 key references is provided.

The section “IDA: Initial data analysis and preprocessing” discusses the importance of initially checking the data for technical artifacts such as batch effects or inconsistent values, which can be especially challenging for HDD. Methods for preprocessing and normalization that have been specifically developed for HDD are explained. Understanding data sources and data generation methods is critical for appropriate initial data analysis and subsequent interpretation of analysis results in collaboration with scientists familiar with the often complex technical and biological aspects of the data and processes used to generate them.

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The section “EDA: Exploratory data analysis” of the overview deals with methods for identifying interesting data characteristics and gaining insight into the data structure. New graphical displays to visualize data in lower dimensions have been developed for HDD, such as t-SNE and UMAP. These can capture different aspects of the data structure than a standard principal components analysis. Such methods can provide additional biological insight and help to generate scientific hypotheses.

The section “TEST: Identification of informative variables and multiple testing” reviews methods for identifying variables informative for an outcome or phenotype, for performing multiple testing, and for identifying informative groups of variables. For identifying informative variables, methods appropriate for HDD like limma and DESeq2 have been developed. Approaches such as these exploit the extremely large number of variables by sharing information across test statistics applied to single variables. Methods for low-dimensional data often rely on distributional assumptions that are not reasonable for HDD and will produce misleading results. Some classical methods to address multiplicity such as those that control family-wise error rate are often infeasible in the context of extremely large numbers of variables or tests, and alternate approaches based on criteria such as control of false discovery rate are now widely used in HDD settings. On the other hand, the large number of available variables in HDD may even be an advantage for identification of groups of variables associated with an outcome or phenotype of interest, as these groupings may reveal additional biological insights, such as associations with functional gene groups.

A popular goal in biomedical research is the construction of prediction models, but use of extremely large numbers of predictors to build these models presents multiple challenges and risks, if done inappropriately. The construction of prediction models, the assessment of their performance, and their validation are discussed in detail in the section “PRED: Prediction”. New methods and software have been developed for HDD-based prediction modelling, in both statistics and machine learning fields. Unfortunately, such models are often subject to the false belief that highly accurate predictions can always be made as long as there is a sufficiently large amount of data. In the biomedical literature, one can find numerous models that have not been correctly constructed and evaluated, and their predictive quality is thus often dramatically overestimated. In the review, all steps in the model construction and evaluation process are discussed, particularly from an HDD perspective.

Beyond TG9’s major goal of providing up-to-date guidance on available methods for HDD analysis, current activities include development of HDD-focused guidance for sample size calculation, influence and choice of tuning parameters, and use of plasmode data for simulations. These points are briefly explained below.

A research protocol or plan should specify the study design, including planned sample size, which will depend on the primary endpoint, analysis goal, and other key assumptions. In HDD settings, traditional sample size calculations break down, for example due to a large number of hypotheses being tested, due to complex modeling or analysis strategies employed, or due to requirements for extensive or complex assumptions that are difficult to specify or are unverifiable. Several approaches for sample size calculation tailored to HDD settings have been proposed in the literature, but utility and uptake of these methods in practice has not been systematically evaluated. Often the rationale behind the sample size is not provided for studies using HDD. TG9 has initiated an extensive

literature search to identify common practices and discuss pitfalls and challenges for sample size calculations for studies involving HDD. Statistical and Machine Learning models for classification or prediction that utilize HDD often require specification or selection of hyper parameters to optimize model performance. Adjusting hyper parameters to achieve more favorable performance is called hyper parameter tuning and is an essential task for fitting many models to data. Especially for HDD, this tuning process can result in overoptimistic prediction performance estimates. TG9 is developing an overview of approaches for hyper parameter tuning along with guidance about appropriate procedures to follow to avoid overly optimistic assessments of the quality of resulting models.

Simulation studies are especially challenging for HDD, yet they are essential tools needed to perform evaluation and comparison of different methods. The typical approach for simulation studies is to use synthetic data, for which the entire true data generating process is known, which is called “parametric” simulation. Parametric simulations of HDD are usually based on overly simplistic assumptions about the high-dimensional multivariate data distribution; therefore, they produce data lacking in realistic complexity. One alternative is to perform so-called “plasmode simulations” that preserve a realistic data structure by re-sampling covariate data from real-life datasets instead of using pseudo-random numbers. This idea seems particularly promising for HDD, but its usefulness has not yet been properly evaluated in the literature. TG9 plans to pursue research on simulation strategies for HDD and to eventually provide guidance on suitable methods.

TG9 continues to monitor the landscape of new approaches for processing and analysis of HDD and to evaluate existing methods. These efforts will inform ongoing development and updating of guidance materials for both statisticians and non-statisticians.

I. Rahnenführer J., De Bin R., Benner A., Ambroggi F., Lusa L., Boulesteix A.L., Migliavacca E., Binder H., Michiels S., Sauerbrei W., McShane L., for topic group “High-dimensional data” (TG9) of the STRATOS initiative (2023): Statistical analysis of high-dimensional biomedical data: a gentle introduction to analytical goals, common approaches and challenges. BMC Medicine. DOI: <https://doi.org/10.1186/s12916-023-02858-y>

On 7 September, STRATOS has a satellite symposium ‘Ten years of the STRengthening Analytical Thinking for Observational Studies (STRATOS) initiative – progress and looking to the future’ at the CEN2023 Conference (Central European Network of IBS; <https://cen2023.github.io/home/>).

Everybody can join the STRATOS symposium for free. In advance, a Zoom link will be made available on the STRATOS website <https://www.stratos-initiative.org/en/news>

*Jörg Rahnenführer will speak about the overview paper.*



# Region News

## Argentinian Region (RArg)

### Argentine Region Academic Activities

The Argentine Group of Biostatistics (GAB), the Argentine Region of the International Biometric Society (IBS), in collaboration with the Faculty of Natural Sciences of the National University of Salta, is organizing the XXVII Scientific Meeting of the Argentine Group of Bioeststatistics & Biostatistics Teaching Conference, scheduled to take place from 9-12 Oct. 2023, in the captivating city of Salta.

These events welcome researchers, teachers, and students who share a keen interest in the practical applications of Statistics in the field of Biosciences, covering diverse areas such as Biology, Agronomy, Medicine, and the Environment. Research work in these fields will be showcased, emphasizing the innovative use of statistical analysis tools, to foster knowledge exchange among fellow researchers, receive constructive feedback, and facilitate professional networking. This is the first time we are proposing the organization of a specific event focused on the teaching of Biostatistics, during which experts will provide talks and workshops. The program offers a diverse array of activities, featuring prominent national and international experts. Participants can expect enlightening conferences, interactive workshops, comprehensive short courses, engaging panel discussions, and stimulating oral and poster presentations. This dynamic platform aims to provide experiential learning, enhance the impact of statistics in both professional and academic domains, and inspire productive collaborations leading to groundbreaking projects.

Furthermore, as a highlight of the congress, we will be hosting the Young Biometricians Contest, offering students at both undergraduate and postgraduate levels the opportunity to tackle real-life biological challenges through statistical data analysis. Participants will be required to propose and present their analytical solutions for the same dataset, and the preselected finalists will defend their proposals during the event to determine the ultimate winner.

We believe that these events will offer a chance to engage at the forefront of Biostatistics research, contributing to the advancement of knowledge in this field.

**Silvia Sühning**

Biometric Bulletin Correspondent

## Australasian Region (AR)

### Joint IBS-AR/SEEM Regional Conference 2023

The 2023 International Biometric Society Australasian Region conference will be held from 27 November to 1 December 2023. Titled "Biometrics in the Bay of Islands," it will be held at the Copthorne Hotel and Resort Bay of Islands, Waitangi, New Zealand. As was intended for 2021, the 2023 conference aims to be a joint event with the Statistical Ecology and Environmental Monitoring (SEEM) conference.

Invited speakers:

- Lisa Warbrick- Te Pu Oranga Whenua, NZ
- Poppy Miller- Plant and Food Research Ltd., NZ
- Joanne Potts- The Analytical Edge, AU
- Adrian Baddele- Curtin University, AU
- Hans-Pieter Piepho- University of Hohenheim, DE
- David Warton- University of New South Wales, AU

See the [website](#) for more information and to [register](#).

### Ihaka Lecture Series

In March 2017 the Department of Statistics at the University of Auckland launched an annual lecture series named after Associate Professor Ross Ihaka in honour of his contributions to the field.

The 2023 Ihaka Lecture Series brings together three speakers whose work focuses on making data visualisations that communicate well, provide user interaction, and look spectacular.

- Antony Unwin, First Professor of Computer-Oriented Statistics and Data Analysis, Augsburg University, Germany. *Interactive Graphics and Data Analysis*, 28 September.
- Danielle Navarro, Pharmacometrician, Certara. *Unpredictable paintings: Making generative artwork in R using data visualisation tools*, 12 October.
- Chris McDowall, Surveillance and Intelligence Specialist, Te Whatu Ora. *What's Behind the Map: The Process of Data Visualisation*, 19 October.

**Garth Tarr**

Biometric Bulletin Correspondent

## Brazilian Region (RBras)

### Brazilian Journal of Biometrics

The *Brazilian Journal of Biometrics* publishes articles indexed with DOI digitally. The periodicity of a new edition is every three months, totaling four new issues per year. The articles can be accessed through the website: <https://biometria.ufla.br/index.php/BBJ/index>.

The BJB committee granted an honorable mention in "The 2022 Best Paper Warded" to:

- Kirch, J. L., Ferneda, B. G., Garcia, F. H. S., Piedade, S. M. S., & Lara, I. A. R. (2022). "Alternatives to the classical frequentist confidence interval for describing zero-inflated leaf disease severity." *Brazilian Journal of Biometrics*, 40(2).
- Salvador, M. L., Ribeiro Jr., E. E., Taconeli, C. A., & Lara, I. A. R. (2022). "Analysis of multinomial data with overdispersion diagnostics and application." *Brazilian Journal of Biometrics*, 40(3).

"The 2022 Best Paper Warded" was awarded by the BJB committee to:

- Carrilho, J., & Lopes, M. B. (2022). "Classification and biomarker selection in lower-grade glioma using robust sparse logistic regression applied to RNA-seq data." *Brazilian Journal of Biometrics*, 40(4), 371–381.

Congratulations to the winning authors! We encourage you to read the winning papers.

### Summary & Highlights of the 67th RBras & 20th SEAGRO

The 67th Annual Meetings of the Brazilian Region of the International Biometric Society (RBras) and 20th Symposium on Applied Statistics to Agricultural Experimentation (SEAGRO) were held from 24-28 July 2023, in Londrina, Paraná, Brazil. The theme of these events was “(Bio)statistics and Biometry in the era of the digital revolution,” one of the most important and current themes in statistics, computer sciences and other areas of knowledge.

The 67th RBras and the 20th SEAGRO had nine plenary conferences, four mini-conferences for young researchers, eight thematic sessions, four mini-courses, four tutorials, one round table, one special session, and oral and poster communications. The events had 262 participants, 155 professionals, 98 graduate students and 49 undergraduate students.

More information about 67th RBras and 20th SEAGRO can be found on the website <https://67rbras20seagro.com.br> and on the Instagram page @rbras\_seagro2023.

68th RBras will be in May or June 2024 in Piracicaba-SP and it is being organized by the Department of Exact Sciences, “Luiz de Queiroz” College of Agriculture, University of São Paulo.

### Highlights of the Young Researchers from the RBras

The group of young researchers from RBras is undergoing a restructuring process and currently consists of 19 members. The new coordinator of the group is Prof. Dr. Guilherme Aparecido Santos Aguilar (Unesp - Presidente Prudente). One of the group's activities is the organization of OmegaTalk, a series of seminars in partnership with the Federal University of Paraná (UFPR).

### Recovery of former RBras members

The Brazilian region of the International Biometric Society (RBras) will promote the process of reinstating former members with overdue membership fees from 1 September 2023 to 2-November 2023. During this period, interested individuals can pay the 2023 membership fee and have their outstanding debts (unpaid fees from previous years) forgiven, thus enjoying the benefits of membership. Simply visit the RBras website (<https://rbras.org.br/filiacao>) and follow the easy steps to reactivate your membership.

### Event support fund

The Brazilian region of the International Biometric Society (RBras) has issued an ongoing call for proposals to support scientific events in the fields of Biometrics and Statistics. The regulations can be found on the RBras website (<https://rbras.org.br>)



67th RBras and 20th SEAGRO participants

**Cristian Villegas and Marcelo Andrade da Silva**  
Biometric Bulletin Correspondents

## British and Irish Region (BIR)

### Upcoming meetings of the British and Irish Region

- Intro to modern Generalised Additive Models in R, 31 August – 1 September 2023, University of Edinburgh. Short course
- Researcher's toolkit – Publishing, progression, people, 17 November 2023, University of Galway. Special session at the YISA.
- AGM + Ethical issues in statistics, November 2023
- Continuous time modulated Markov processes; Applications in ecology and beyond, December 2023, University of Edinburgh

**Kirsty Hassall**

Biometric Bulletin Correspondent

## Cameroon Region (GCmr)

The IBS Cameroon region will be hosting their Inaugural meeting 13 of October 2023, followed by their first research seminar meeting on the 14 October 2023 in Buea, Cameroon. Both sessions will be in-person, with the possibility for online attendance and presentations.

**Che Henry Ngwa**

Biometric Bulletin Correspondent

## Central American-Caribbean Region (RCAC)

The 2023 XXXII International Symposium of Statistics (ISS) was held in Ibagué, Colombia, from 31 July to 4 August 2023, and was based on the theme Biostatistics and Functional Data. A total of 174 national and international participants attended the symposium (see photo 1). The attendees included 54 professors from different universities, 81 students, 25 professionals from outside the field of statistics and 14 invited speakers.



Participants who attended the International Symposium of Statistics that was held in Ibagué, Colombia, from 31 July to 4 August 2023.

The talks from the invited speakers were the following (with names of speakers shown in the brackets below):

1. “Weighted Interval Survival Analysis to estimate the age of initiation of tobacco products with longitudinal cohorts in youth and young adults” (Dr. Adriana Pérez)



2. "A Knockoff procedure for non-Gaussian data" (Dr. Jose Ulises Marquez)
3. "Artificial Intelligence, an alliance in the production and the cost benefit in poultry farming" (Dr. Henry Vaquiro)
4. "Understanding complex models with ghost variables" (Dr. Pedro Delicado)
5. "Additive Density-on-Scalar Regression in Bayes Hilbert Spaces with application to gender economics" (Dr. Sonjan Greven)
6. "Mean and variance beta regression and beta binomial regression models" (Dr. Edilberto Cepeda)
7. "Preprocessing in matrix data, robust imputation" (Dr. Camilo Rengifo)
8. "Geostatistics with functional data" (Dr. Ramon Giraldo)
9. "Selection bias in observational studies: very problematic and poorly understood" (Dr. Juliana Cuervo)
10. "Sequential data of single cell RNA Aseq: progress and challenges" (Dr. Liliana López)
11. "Binary two-dimensional image classification: tensor regression model vs total variation model" (Dr. Ruben Guevara)
12. "Causal inference and artificial intelligence" (Dr. Fatma Shebl)
13. "Population, precision, and validity" (Dr. Carlos J. Rincon)
14. "The combination of several sources: The new frontier in the production of official statistics" (Dr. Piedad Urdinola)



Participants who attended the talk entitled "Casual inference and artificial intelligence," given by Dr. Fatma Shebl who is seated on the front row (first from the right).

Six continuing education courses were offered. They were as follows:

- "Functional data analysis: An introduction"
- "Causal inference and real-world data"
- "Introduction to network meta-analysis"
- "Functional data analysis in demography"
- "Replicability: an introduction to the knock-off method for selection variables"
- "Planning biostatistical analysis in health sciences with complex samples."



Participants in the short course entitled "Planning and biostatistical analysis in health sciences with complex samples." Dr Adriana Pérez, course presenter, is third from left (stooping) in front row.

In addition, 69 talks were contributed by other speakers & there were 56 poster presentations. During the ISS, the annual meeting of the IBS-RCAC region was held in hybrid format on Thursday, 3 Aug 2023. We thank the sponsors & organisers of the ISS for facil-

itating the meeting of the IBS-RCAC. At the IBS-RCAC meeting, there was a report of the financial status of the RCAC *Biometric Bulletin*, Volume 40 Issue 3 *IBS RCAC contributions\_Final.docx* region & number of members who had paid for the 2023 yr. As Dr. Luis Alberto Lopez has already retired, and Dr. Luis Fernando Grajales is planning to retire in a few years, there was a proposal to request for volunteers to serve as representatives for the IBS RCAC. Drs. Liliana López, Adriana Pérez, Vrijesh Tripathi and Martha Patricia Bohorquez volunteered to serve, and more candidates can send their interest to serve to Luis Fernando Grajales before 16 August 2023. Dr. Raul Macchiavelli will work on providing members with a Microsoft Teams link for the voting in September 2023. Virtual continuing education courses to be organised are: (i) How to write manuscripts; (ii) Updates on programming in Python, Julia, and R, and (iii) How to write research proposal. Finally, the members discussed the possibility of hosting the 9th IBS-RCAC Biostatistics Meeting in 2025. It was unclear to the members if the IBS has a lifetime membership fee.



Virtual and in-person attendees at the annual meeting of the IBS-RCAC region held during the ISS.

We thank the sponsors of the ISS: Universidad del Tolima, Universidad Nacional de Colombia-Sede Bogotá, Pontificia Universidad Javeriana, Instituto Colombiano de Credito Educativo y Estudios Tecnicos en el Exterior (ICETEX), The International Biometric Society and Dr. Leonardo Duván Restrepo (Dean of the School of Science from the Universidad del Tolima).

We also thank the organisers who made this symposium a reality: Drs. Gisou Diaz, Rubén Guevara, José A. Jimenez, Sergio A. Calderon, Ramon Giraldo, and Martin A. Rondón.

**Novie Younger-Coleman Ph.D**  
Biometric Bulletin Correspondent

## Eastern Mediterranean Region (EMR)

After a long break, the 12th International Conference of the International Biometric Society's Eastern Mediterranean Region (EMR 2023) was held face-to-face at İzmir Ege Palas Hotel. More than 150 participants from 24 different countries showed interest in this meeting, which included conferences by esteemed speakers, excellent scientific sessions, oral and poster presentations, and roundtable sessions. On the other hand, in the first day of the conference, three pre-conference courses (all hands-on and included quite up-to-date topics such as explainable machine-learning,

RNA-sequencing data analysis and data science on cloud) and an honorary symposium (dedicated to marking the retirement of Refik Burgut and Ergun Karaagaoglu) were organized. An additional 60 participants showed interest in the hybrid short courses online.

EMR-IBS congratulations all the oral and poster presentation awards winners: Berk Piskin (Dokuz Eylül University), Aylin Alın (Dokuz Eylül University), Rim Khazhin (Eye Checkup), Ahmet Mert Saygu (Eye Checkup), Ahmet Ömer Özgür (Eye Checkup), Naama M. Kopelman (Holon Institute of Technology), Yonatan Woodbridge (Holon Institute of Technology), Sharon Amit (Sheba Medical Center), Amit Huppert (Tel-Aviv University), Esra Kutsal Mergen (Hacettepe University), Sevilay Karahan (Hacettepe University), Duygu Korkmaz Yalçın (Çukurova University), İlker Ünal (Çukurova University), Elifsu Polatlı (Izmir Biomedicine and Genome Center), Burak Kahveci (Izmir International Biomedicine and Genome Institute), and Sinan Güven (Dokuz Eylül University).

At the Business Meeting held on the last day of the EMR 2023 meeting, new representatives of the EMR-IBS region were elected. Congratulations to our newly elected members, who are listed below:

#### President

- Gökmen Zararsız (Erciyes University, Türkiye)

#### Vice President

- Philip Tzvi Reiss (University of Haifa, Israel)

#### Secretary

- Denitsa Grigorova (Sofia University)

#### Publicity Officer

- Necla Koçhan (İzmir Biomedicine and Genome Center, Türkiye)

#### National Representatives

- Denitsa Grigorova (Sofia University, Bulgaria)
- Konstantinos Fokianos (University of Cyprus, Cyprus)
- Giorgos Bakoyannis (Athens University of Economics and Business, Greece)
- Philip Tzvi Reiss (University of Haifa, Israel)
- Osman Dağ (Hacettepe University, Türkiye)



Arne Bathke, Ralph Brinks, Filomena Maggino, Bhramar Mukherjee, and Amit Huppert discussing "The role of statistical experts during the COVID-19 Pandemic" in the Round Table moderated by Geert Molenberghs and David Steinberg.



EMR2023 attendees visiting Ephesus.

**Necla Koçhan**

Biometric Bulletin Correspondent

## Eastern North American Region (ENAR)

### 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>.

### 2023 JSM, 5-10 August, Washington, DC, USA

The 2023 Joint Statistical Meetings (JSM) was held from 5-10 August. The theme of the meeting was "One Community: Informing Decisions and Driving Discovery." The meeting has been a resounding success! As always, ENAR, one of the founding societies of JSM, has been instrumental in organizing an outstanding program, and has sponsored many exciting sessions. These include invited paper sessions on new advances in causal inference with complex health datasets, integrating information from different data sources, estimating heterogeneous treatment effects to inform decisions, differential privacy for data science, precision medicine, innovative methods for time-to-event outcomes, planning observational studies with unobserved confounding in mind, and statistical methods for cell-type-specific analysis using bulk and single cell data, and invited panel sessions on frontiers of statistics, training, retaining, and integrating staff biostatisticians to enhance academic research, and Biostatistics or Data Science: choosing the right path. ENAR owes an enormous debt of gratitude to Liangyuan Hu at Rutgers University ([lh707@sp.h.rutgers.edu](mailto:lh707@sp.h.rutgers.edu)) for representing us at the 2023 JSM. For more



Yoav Benjamini giving a plenary lecture about "Replicability issues in medical research: Science and politics" on the second day of EMR-IBS 2023.



details about the 2023 JSM meetings, please visit: <https://www2.amstat.org/meetings/jsm/2023/index.cfm>.

### **2024 ENAR Spring Meeting, 10-13 March, Baltimore, MD USA**

The 2024 ENAR Spring Meeting is scheduled to take place in Baltimore, TN, USA, at the Baltimore Marriott Waterfront. Distinguished student paper award submissions are due 6 October and contributed oral and poster presentation submissions are due 17 October. ENAR is very thankful to Program Chair Program Chair Sameera R. Wijayawardana at Eli Lilly ([sameera.r.wijayawardana@gmail.com](mailto:sameera.r.wijayawardana@gmail.com)) or Program Co-chair Christina Mehta at Emory University ([christina.mehta@emory.edu](mailto:christina.mehta@emory.edu)) and local arrangement chair John McGready at the Johns Hopkins University ([jmcgreal@jhu.edu](mailto:jmcgreal@jhu.edu)) for their hard work in planning the ENAR 2024 Spring Meeting. More details may be found at: <https://enar.org/meetings/spring2023/>.

### **2024 JSM, 3-8 August, Portland, OR USA**

The 2024 Joint Statistical Meetings will be held in Portland, Oregon, USA from 3-8 August 2024. The theme for the 2022 meeting is “Statistics and Data Science: Informing Policy and Countering Misinformation.” Invited Session Proposal submissions are accepted until 7 September 2023. For more details about the conference, please visit <https://www2.amstat.org/meetings/jsm/2024/>. ENAR is grateful to Benjamin Risk at Emory University for representing ENAR at JSM 2024.

**Saptarshi Chakraborty**  
Biometric Bulletin Correspondent

## **French Region (RF)**

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

In partnership with the French Region of the IBS, as well as the IBS region of Belgium and Great Britain/Ireland, the Dutch region held the Channel Network Conference (CNC), 23-25 August 2023 at Wageningen University & Research (WUR), Netherlands. More information on the conference website: <https://cnc23.sciencesconf.org>

### **Coming events of the French Region of the IBS include:**

The annual Biostatistics Days, a joint conference with the research group “Statistics and Health”, and the group “Biopharmacy and Health” of the French Society of Statistics (SFdS), 16-17 November 2023, in Toulouse, France. Participation is free of charge but requires *registration by 5 November 2023* using the online form. <https://indico.math.cnrs.fr/event/9989/registrations/923/>. Contributed communications from young researchers are welcome: abstracts are to be *submitted by 1 October 2023*, using the online form] <https://indico.math.cnrs.fr/event/9989/abstracts/>

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

**Anne Thiébaud**  
Biometric Bulletin Correspondent

## **German Region (DR)**

Two online lecture series “Modern statistical methods for the life sciences” is presented by young talents is an online lecture series read by and addressed to the younger statisticians. On 17 January, Tina Lang spoke on “Dress up your research – Practical help for pretty presentations.” On 18 April, Julian Rodemann presented on “Learning under weak supervision: Some insights from decision theory.” The online lecture series by experienced statisticians was continued by Harald Binder: “Deep learning, modeling, and small data sets” on 24 March 2023, Anja Sander and Stefan Englert: “Translating trial objectives into clear clinical questions of interest: How to succeed? A practical introduction to the estand framework” on 24 May, and Friedrich Pahlke: “R for beginners and infrequent users: Know R, RStudio and Quarto better and master them with the help of ChatGPT” on 5 July.

It will be continued by honorary member Edgar Brunner on 27 September: “Multiple Endpoints and Prioritized Outcomes: Effects and Nonparametric Analysis Methods” and on 6 November by Vanessa Didelez: “Statistical Methods for Causal Inference in Epidemiology.”

### **Adaptive Designs and Multiple Testing Procedures**

At this year’s workshop 19-21 April 2023 in Basel (Switzerland), invited speakers were Chris Jennison and Tobias Mielke on the topics “Optimizing sequential and adaptive designs: the power of dynamic programming” and “Adaptive platform trials: complex and innovative– but how useful?” More than 100 participants made the trip. The workshop was organized by a team led by Lisa Hampson. Presentations may be viewed online at <https://admt2023.github.io/presentations.html>.

The next workshop will take place in Ibiza (Spain) on *25-26 April 2024*.

### **Non-Clinical Statistics**

This working group gathered for its fall workshop at Boehringer Ingelheim Pharma GmbH & Co. KG in Ingelheim 24-25 November 2022 in presence in hybrid format. Invited speakers were H.-J. Delzeit, J. Rahnenführer and U. Tölch. The nine other speakers gave interesting and instructive presentations. Intensive and constructive discussions followed, in which about 35 participants took part. The topics encompassed modern statistical methods in toxicology, dose-response, robust analysis of cancerogeneity studies and in general, nonparametrics, design of experiments, meta analysis with R shiny and R markdown, special requirements in CMC statistics, equivalence of dissolution profiles, and some more.

Abstracts are available at <http://www.biometrische-gesellschaft.de/herbstworkshop-2022.html>.

The next workshop is planned for *16-17 November 2023* in presence at Bayer AG Berlin, and in the hybrid format. Find further details at: <https://www.biometrischegesellschaft.de/en/herbst-workshop-2023.html>

### **Agricultural research**

The working group met 29-30 June 2023, in Monheim at Bayes AG Crop Science, as the focus was on plant protection, a topic in the political focus at the time. Slides are available at <https://www.biometrische-gesellschaft.de/en/arbeitsgruppen/landwirtschaftliches-versuchswesen/tagungsberichte-ab-1996/sommertagung-monheim-2023.html>

## Statistical Computing

The annual workshop at Reissensburg castle 30 July – 2 August 2023, featured invited lectures: “Towards reliable empirical evidence in methodological computational research: Recent developments and remaining challenges” by Anne-Laure Boulesteix, “Efficient privacy-preserving machine learning for precision medicine” by Nico Pfeifer, and “From trial simulation to in-silico trials” by Tim Friede. There were 16 more talks. All abstracts are available: <https://sys-bio.uni-ulm.de/ocs/public/pdf/statcomp2023/program.pdf>

## Computational Models in Biology and Medicine

Working groups “Mathematical Models in Medicine and Biology” and “Statistical Methods in Bio informatics” met in Stuttgart on 15-16 June. The 20 talks were grouped in sessions on “FAIR model and data principles,” “Dynamical modeling in health and disease,” “Statistical analysis and machine learning” and “Open topics.” The abstracts of these and of the 31 posters are available at [https://www.biometrische-gesellschaft.de/fileadmin/AG\\_Daten/MethodenBioinformatik/PDFs/workshop\\_abstracts\\_2023\\_final.pdf](https://www.biometrische-gesellschaft.de/fileadmin/AG_Daten/MethodenBioinformatik/PDFs/workshop_abstracts_2023_final.pdf)

## Causal Machine Learning

Four working groups of IBS, GMDs, DGEpi, and DGSMP will meet in Mainz on **9-10 November 2023** for this workshop. Please find the call for papers at <https://www.unimedizin-mainz.de/smde/autumn-workshop-2023.html>

## Bayesian methods

The Bayesian working group met for its workshop on “Design of experiments under uncertainty” in Ingelheim, at Boehringer Ingelheim Pharma GmbH & Co. KG on 8-9 December 2022, in presence and in hybrid format. Claire Rothery (York) gave a tutorial “Introduction to the value of information (with examples).” The full program with abstracts and slides is available at <http://www.biometrische-gesellschaft.de/arbeitsgruppen/bayes-methode/workshops/2022-ingelheim.html>

**Reinhard Vonthein**

Biometric Bulletin Correspondent

## Japanese Region (JR)

### The 2023 Annual Membership Meeting of the Biometric Society of Japan

The Annual Meeting of the Biometric Society of Japan (BSJ) was held on 20-21 April 2023, in hybrid combining online and on-site at the Hokkaido University Conference Hall, Sapporo, Japan. A total of 351 people, including 113 for on-site participation and 238 for online participation, attended the meeting. Two invited sessions on omics data analysis and on the 2022 BSJ Award for Outstanding Scientific Contribution were organized. In the former session, Dr. Atsushi Fukushima (Kyoto Prefectural University) gave an excellent lecture on basic knowledge of omics data, and information analysis and sharing of plant metabolomics data by mass spectrometry; Dr. Akio Onogi (Ryukoku University) provided a great lecture on plant phenotype prediction using statistics and machine learning; Dr. Yasunori Ichihashi (Institute of Physical and Chemical Research (RIKEN)) gave a wonderful lecture with the title “From multi-omics analysis to agricultural digital twin development;” and Dr. Naoyoshi Nagata (Tokyo Medical University) provided an outstanding lecture entitled “Individual differences in the intestinal environment and the risk of new coronavirus infectious diseases unraveled from omics information analysis.”

In the latter session, Prof. Satoshi Morita (Kyoto University) delivered the commemorative lecture entitled “Contemplation, commitment, and contribution” with his related valuable works on development of bio-statistical methodologies in medical research. In general sessions, there were twenty-nine oral presentations, where the Best Presentation Award for Young Researcher was conferred on Shouko Suzuki (Yokohama City University), Nodoka Seya (Tokyo Medical University), and Shintaro Yuzuki (Doshisha University) as winners in the student membership category, and Dr. Sho Komukai (Osaka University) and Dr. Tomohiro Ohigashi (Tsukuba University) as winners in the regular membership category. The tutorial seminar entitled “The basics and applications of causal inference” was also organized jointly with Japanese Society of Applied Statistics. Three hundred eighty-one people, including 114 for on-site participation and 267 for online participation, attended the seminar.

The BSJ is pleased to announce that the society conferred the BSJ Honorary Award was conferred on Prof. Hideki Origasa (The Institute of Statistical Mathematics, and Shiga University) for their long-term great contributions to the society. The Young Bio-statisticians Award was conferred on Yumi Takagi (Kyoto University) for her recent publication in Japanese Journal of Biometrics. This award is annually conferred by the BSJ for researchers, who are less than 40 years old and publish 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 2023 Japanese Joint Statistical Meeting

The Japanese Joint Statistical Meeting will be held on 3-7 September 2023, in hybrid combining online and on-site at Kyoto University, Kyoto, Japan. This meeting is 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 an invited session and the Young Bio-statisticians Award session. In the former symposium entitled “New Developments in Biometrics and Ecology,” the BSJ is inviting outstanding researchers to discuss this topic. In the latter session, the winner of the award conferred by the society will make a presentation on a statistical graph for evaluation of the primary endpoint in a clinical trial using the alternative hypothesis, Bayes factor, and confidence interval.

**Takashi Daimon**

Biometric Bulletin Correspondent

## The Netherlands Region (BMS-ANed)

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

On the occasion of announcing the winner of the Hans van Houwelingen Biometry Award 2022, the BMS-ANed organized on 15 June, a half-day symposium in the beautiful city of Utrecht attended by approximately 60 participants. Invited speakers were the members of the international award committee who shared their own research with the audience:

- Manuela Zucknick, University of Oslo: "Machine learning with small data: examples from pharmacogenomic screens for personalized medicine."
- Emmanuel Lesaffre, Catholic University of Leuven: "Borrowing information from historical data: A pharmaceutical perspective."
- Tim Friede, University Medical Center Göttingen: "Combining randomized controlled trials and real-world data."

The meeting started with the annual BMS-ANed General Assembly, where we discussed several topics: the meetings and online seminars that we organized last year; discussion and approval of finances, changes in the board. We welcomed our two new members: Kim Luijken (Utrecht University) and Floor van Oudenhoven (Danone Nutricia Research).

After a short break and opening by the chair Kim Luijken, the jury announced the winners. The 2022 Hans van Houwelingen Biometry Award winner is Anirudh Tomer (Erasmus MC) for his paper with Dimitris Rizopoulos, Ewout Steyerberg, Daan Nieboer and Monique Roobol: "Shared decision making of burdensome surveillance tests using personalized schedules and their burden and benefit," published in 2022 in *Statistics in Medicine*. Anirudh may organize a BMS-ANed meeting with speakers of his choice. There were also two honorary mentions given to: Mirko Signorelli (Leiden University) for his paper with Roula Tsonaka and Pietro Spitali ("Poisson–Tweedie mixed-effects model: A flexible approach for the analysis of longitudinal RNA-seq data," published in 2021 in *Statistical Modeling*) and to Chengyuan Lu (Leiden University Medical Center) for his paper with Hein Putter and Jelle Goeman ("Maximum likelihood estimation in the additive hazards model," published in 2022 in *Biometrics*). Congratulations to all!

After the award ceremony, we proceeded with the scientific part of the day with talks from the jury members. Presentation slides are available online. Of course the scientific program was followed by discussion, drinks and snacks.

Further, we organized the fifth online seminar in the Biostatistics Seminar Series which was given on Thursday 22 June 2023 by Bart Mertens from the Leiden University Medical Center in the Netherlands. Bart's talk was about: "Integrated Nested Laplace Approximation (INLA) – A breakthrough computational innovation for biostatistics, random effect and Bayesian modeling."

Bart started with a brief introduction on the theoretical background of INLA, he shared with us illustrations of models fitted using INLA, and closed with a short presentation of his work on estimation of complex joint models using INLA. The online seminars aim at a broad bio-statistical audience, in particular PhD students. Similar to the previous online sessions this seminar was attended by many PhD Students, but also more senior statisticians. The next online seminar in the Biostatistics Seminar Series will be announced soon.

We are now making preparations for our next BMS-ANed meeting, which will be a PhD Day on Wednesday 29 November. More information will follow in the next issue!

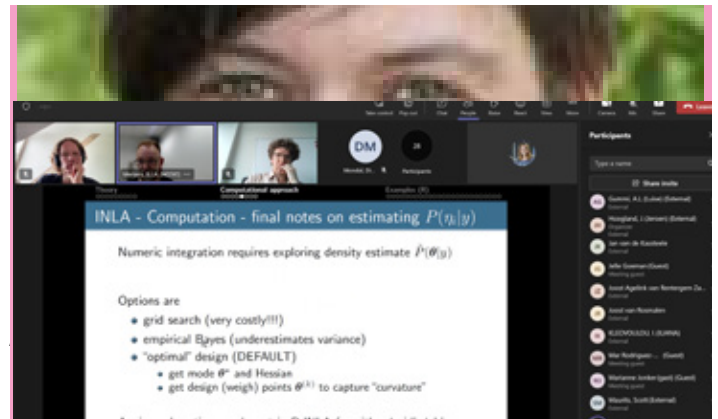
Finally, we are looking forward to the 2023 Channel Network Conference in Wageningen, the Netherlands from 23-25 August. The conference is organized at the Wageningen University and research as an in-person event. Links to the conference website and further information are available [here](#).



(From left to right) Mirko Signorelli (HvH honorary mention), Anirudh Tomer (HvH award winner), Hans van Houwelingen and Chengyuan Lu (HvH honorary mention)



(From left to right) Jury members of the HvH award Emmanuel Lesaffre and Tim Friede



Screenshot from Bart Merten's online seminar.

**Roula Tsonaka**  
Biometric Bulletin Correspondent



## Spanish Region (REsp)

### XIXth Spanish Biometric Conference

Responding to the request of the Spanish Society of Biostatistics (SEB), the XIX Spanish Biometric Conference (CEB) took place this year in Vigo, Spain. On this occasion, the conference was held together with the VIII Ibero-American Biometric Meeting (EIB), and six regions of the International Biometric Society (IBS) were involved in the organization:

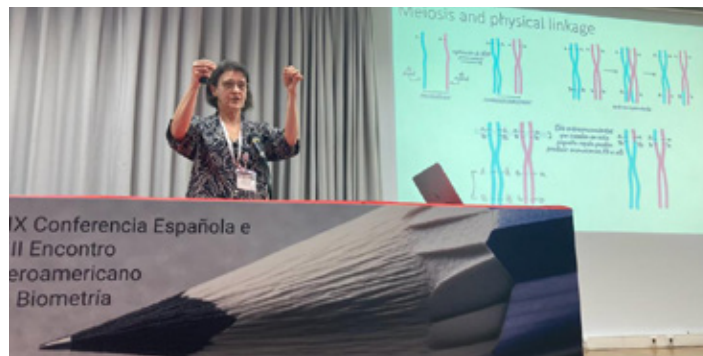
Argentina, Brazil, Spain, Central America and the Caribbean, Chile and Ecuador. The CEB-EIB 2023 was organized by the Department of Statistics and Operations Research and the research group SiDOR (Statistical Inference, Decision and Operations Research) of the Universidade de Vigo, with the invaluable help of colleagues from all the regions involved.

Special mentions are deserved by the Organizing Committee, led by María Xosé Rodríguez-Álvarez, and the Scientific Committee, led by Javier Roca Padiñas, given the excellent organization and high scientific quality of the conference. In particular, the plenary lectures, given by María Gabriela Cendoya, Andreas Mayr and Anabel Forte Deltell, were of the utmost interest, as was the pre-conference course, given by María Amalia Jácome and Ricardo Cao. It is also worth highlighting the Ibero-American Special Session, which brought together representatives from the regions involved in organizing CEB-EIB 2023.

The response to CEB-EIB 2023 was exceptionally positive. The conference garnered participation from 187 researchers, with a noteworthy highlight being the presence of Ibero-American colleagues, who constituted approximately 15% of the attendees. The scientific programme encompassed a comprehensive total of 153 contributions, comprising 100 oral presentations and the remaining presented as posters. As in previous editions, the involvement of young researchers remained pivotal, with 68 of the 153 contributions originating from this vibrant group. A dedicated session exclusively for the Young Statistician Showcase further underscored this commitment, affording the opportunity for 5 young researchers, who had been chosen by the Scientific Committee, to present their work.

This edition was marked by a tribute session to Carmen Cadarso Suárez, who unexpectedly passed away on 3 June 2022. Carmen was a Galician bio-statistician, professor in the Department of Statistics, Mathematical Analysis and Optimization at the Universidade de Santiago de Compostela, coordinator and promoter of the National Biostatistics Network BIOSTATNET and director of the research group Biostatistics and Biomedical Data Science (GRID-BDS), among many other achievements. This special session served as a tribute to her remarkable contributions, and it featured the participation of Wenceslao González Manteiga, Thomas Kneib and Jenifer Espasandín Domínguez.

Last but not least, the CEB-EIB 2023 had a vibrant social program that fostered interaction among all participants. The social program started on the first day of the conference, 27 June, with a welcoming cocktail event held at the “Pazo Quiñones de León.” The following day featured a guided tour of Vigo and its surroundings, granting attendees a chance to immerse themselves in the rich historical and cultural essence of the city. The culmination of these social engagements took place on 29 June with the fellowship dinner, providing a delightful finale to the event.



Plenary Lecture given by Maria Gabriela Cendoya



Plenary Lecture given by Andreas Mayr



Local Committee and Anabel Forte

**Ester Boixadera**  
Biometric Bulletin Correspondent

## Western North American Region (WNAR)

The Annual WNAR meeting took place in Anchorage, Alaska, 18-21 June 2023. There were a total of 356 participants with 44 invited sessions, 5 student paper competition oral sessions, 3 contributed paper sessions, 2 Speed Talk Sessions, 7 IMS Sessions. The Presidential Address presentation was delivered by Dr. Kimberly Sellers from Georgetown University and US Census Bureau with title :Dispersed Methods for Handling Dispersed Count Data.”

At this annual meeting we celebrated the 75th Anniversary of WNAR. Past WNAR leaders gathered at the WNAR 2023 Banquet.





Past, Current, and Future Presidents of WNAR at the WNAR 2023 Meeting celebrating the 75th Anniversary of WNAR

An important activity of the annual meeting is student competition paper. The winners in the written category were: Soumik Purkayastha, University of Michigan, with runner up Norihiro Suzuki, Tokyo Medical University. The winners in the oral category were: Michael Christensen, Duke University, with runners up Elizabeth Wynn, University of Colorado Anschutz Medical Campus, Seth Temple, University of Washington, and Soumik Purkayastha, University of Michigan.



Student Competition Award Ceremony, Participants, Awardees, and Judges

Two short courses were offered: "IT tools and best practices for statistical Professionals," with instructor Angelique Zeringue, PhD, Senior Consultant and Data Science Competency Lead, Daugherty Business Solutions; and "Real-World Evidence in Drug Development and Regulatory Decision-Making: Current Status, Challenges, and Opportunities," with instructor Jie Chen, Ph.D., Chief Scientific Officer, Elixir Clinical Research.

WNAR thanks Audrey Hendricks (UC Denver), Wen (Rick) Zhou (Colorado State University) for their efforts as Program Chairs, Hua Zhou (UCLA) IMS Program chair, and the Organization Committee: Mengli Xiao, Jignshen Wang, Zhixin Lun, Jing Ma, Bo Huang.

### 2023 IBS/WNAR Outstanding Impact Award and Lectureship

On behalf of WNAR and the WNAR Award Committee, we would like to congratulate Steve Horvath as the recipient of the 2023 WNAR Outstanding Impact Award and Lectureship. Congratulations, Dr. Horvath!

The WNAR of IBS Outstanding impact and Lectureship Award was established in 2021 to recognize an outstanding individual or team, regardless of race, gender, sexual orientation, nationality or citizenship, who has made a significant impact on our society through service and/or research in the development and application of statistical, mathematical, and data science theory and methods in the biomedical or environmental sciences. A significant impact can comprise either a single contribution of extraordinary merit or an outstanding aggregate of contributions that significantly impacts to biosciences and environmental sciences.

Dr. Steve Horvath is a Principal Investigator at the Altos Labs San Diego Institute of Science. Prior to joining Altos, he was a Professor of Human Genetics and Biostatistics at UCLA. Dr. Horvath's nomination package clearly demonstrated his highly impactful research contributions to the fields of bio informatics and aging biology, especially for his development of the widely used weighted correlation network analysis (WGCNA) method for studying biological networks and for his revolutionary development of the highly accurate and widely used epigenetic clocks, also known as Horvath's clocks, for age estimation based on DNA methylation data. WNAR is very proud of its outstanding members, represented by Dr. Horvath.

Congratulations as well to our other nominees, all of whom were outstanding and highly impressive in their contributions.

As a recipient of the award, Dr. Horvath gave a talk in the WNAR Outstanding Impact Award Lecture at the JSM on Tuesday, 8 August 2023, entitled "Epigenetic Clocks and Weighted Correlation Network Analysis."

2024 IBS/WNAR Outstanding Impact Award Nominations due 1 November 2023 WNAR members, please plan to submit nomination materials for the 2024 award by 1 November 2023. We look forward to recognizing our outstanding members with this honor. More information about the award process can be found on the WNAR award website: <https://wnar.org/IBS/WNAR-Outstanding-Impact-Award>

### 2024 WNAR/IMS Meeting

The 2024 WNAR/IMS meeting will be in Fort Collins, Colorado, from 9-12 June 2024. This will be a joint event with the Graybill Conference at Colorado State University. The local organizing chair is Rick Zhou at Colorado State University.

Registration information and other details about the meeting will be available on the WNAR web page [www.wnar.org](http://www.wnar.org)

### 2024 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 2024 WNAR Student Paper Competition, registration information, and program details for the meeting will be posted as they become available.

**Jessica Minnier**  
Biometric Bulletin Correspondent

# Announcements & Upcoming Events

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

**27 Nov 2023**

### **IBS-AR/SEEM Regional Conference**

Waitangi, New Zealand

**5 December 2023**

### **Modelling continuous-time capture-recapture data**

Edinburgh, United Kingdom

**10 - 13 March 2024**

### **2024 ENAR Spring Meeting**

Baltimore, MD

**8-13 December 2024**

### **32nd International Biometric Conference (IBC2024)**

Atlanta, Georgia USA

[View the full meetings calendar here!](#)

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

[View the full 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)



## Brazilian Journal of Biometrics

The *Brazilian Journal of Biometrics* (BJB) serves as a valuable resource for researchers and practitioners who utilize statistical methods to address key challenges and advance knowledge in these fields.

BJB serves as a platform for the dissemination of original research papers that explore, promote, and extend statistical, mathematical, and data science methods in applied biological sciences.

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