October - December 2024 Vol. 41 No. 4 • 2024

BIOMETRIC BULLETIN

International Biometric Society Internationale Biometrische Gesellschaft Société International de Biométrie

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

President's Corner

I am just on my flight back from Atlanta, recollecting a lot of wonderful moments of this year´s IBC. It was a really well-organized conference, at a fantastic venue and with short distances between the different session rooms. I enjoyed very much talking to so many people, meeting old friends and making new ones, as well as making a lot of plans for future IBCs and for the Society as a whole. For instance, we will reach out to further potential regions of the IBS, work out a sustainability plan, and give women in our Society even more visibility by including a recurrent women´s corner column in the Biometric Bulletin and by planning an invited women´s session at our next IBC in Seoul. We would also like to increase the visibility of our networks by encouraging them to submit invited session proposals for the next IBC and by encouraging other regions to also establish networks. Finally, we will increase the visibility of our Society as a whole by working out a strategy for our social media activities and by picking up topics of major public health relevance to be featured during our conferences. For Seoul, for example, we plan to organize a roundtable discussion on climate change, inviting some of the key quantitative scientists in the field.

But let´s come back to this year´s IBC. To those of you who were not able to join us for this conference, let me tell you that you missed many inspiring talks followed by lively discussions. In particular, you missed a very thought provoking Presidential Keynote Address, given by Sander Greenland, but, perhaps even more importantly, you also missed the numerous opportunities for meeting friends and colleagues from all over the world. And there was much more: the reception at the 10th floor of the Marriott Marquis, the party of the young statisticians, with transportation to the venue provided by these fantastic yellow school buses, our wonderful Gala dinner at the Georgia Aquarium and, last but not least, Atlanta itself and its surroundings, with a lot of world class attractions. More than 500 attendees from 48 countries, of whom more than 100 came from low to middle income countries and more than 150 were students, participated in 88 sessions offered in the scientific program, with 365 speakers delivering a total of more than 100 hours of education. Check the website and this bulletin to find out more information on IBC2024, including Sander´s slides and numerous photos taken throughout the event.

We also were very excited to welcome three new regions to our Society: Cameroon, which joined us last year, Namibia and Croatia, which joined the IBS just recently. As already mentioned above, we will reach out to further potential regions in 2025, aiming to grow our scientific network.

Keeping with tradition, one session was dedicated to the IBS award winners: The Rob Kempton Award for Outstanding Contributions to the Development of Biometry in the Developing World was awarded to Girma Taye Aweke, of the Ethiopian Region, for his exceptional leadership and groundbreaking contributions to biometrics in Africa, inspiring future generations. Three of our members were recognized as new

Continued on p. 3

IN THIS ISSUE

BIOMETRIC BULLETIN

ISSN 8750-0434

Biometric Bulletin will be published four times a year in
March, June, September, and December.

International Biometric Society
1120 20th Street, NW, Suite 750 • Washington, DC 20036-3441 USA
Telephone: +1 (202) 712-9049 • Fax: +1 (202) 216-9646
Email: ibs@biometricsociety.org Website: http://www.biometricsociety.org

The *Biometric Bulletin* is available to members of the Society as part of their annual dues. The views and contributions to this publication should not be ascribed to the International Biometric Society. Reproduction for commercial purposes is allowed if the source is acknowledged.

Editor

Ajit Sahai, Ex. Founder-Professor & Chair, Department of Medical Biometrics;
JIPMER, Pondicherry; India editor.bb2019@gmail.com

Associate Editor

Garth Tarr, University of Sydney, Australia - garth.tarr@sydney.edu.au

International Biometric Society Executive Board

President - Iris Pigeot (German Region)
Outgoing President - José C. Pinheiro (Eastern North America)
President-Elect - Maria Gabriela Cendoya (Argentina Region)
Treasurer - Sarah Ratcliffe (Eastern North American Region)
Outgoing Treasurer - Vicente Núñez-Antón (Spanish Region)
Secretary - Tarylee Reddy (South African Region)

Directors

Thomas Ochieng Achia (GKe); Andrea Berghold (ROeS); Scarlett Bellamy (ENAR); Maria Gabriela Cendoya (RArg); Kate Crespi (WNAR); Clelia Di Serio (RItl); Tim Friede (DR); Simone Gray (ENAR); Amy Herring (ENAR); Ruth Keogh (BIR); Taesung Park (RKo); Chris Triggs (AR); and Ricardus Vonk (DR Region)

Biometrics Editorial Team

Executive Editor: Geert Molenberghs, Interuniversity Institute for Biostatistics & statistical Bioinformatics, Hasselt University & KU Leuven, Belgium;
EMAIL: geert.molenberghs@uhasselt.be

Co-Editor: Cécile Proust-Lima, INSERM, University of Bordeaux, France;
EMAIL: cecile.proust-lima@u-bordeaux.fr

Co-Editor: Erica Moodie, McGill University, Canada;
EMAIL: erica.moodie@mcgill.ca

Co-Editor: Matthew Schofield, University of Otago, New Zealand;
EMAIL: Matthew.schofield@otago.ac.nz

Book Review Editor: Andrew Spieker, Vanderbilt University Medical Center, USA;
EMAIL: andrew.spieker@vumc.edu

Editorial Managers: Chantal Brodie and Ann Hanhart;
EMAIL: biometrics@biometricsociety.org

Journal of Agricultural, Biological and Environmental Statistics (JABES) Editor

Jorge Mateu; EMAIL: mateu@uji.es

Biometric Bulletin Regional Correspondents

Silvia Suhring (RARG); Charley Budgeon (AR); Sonja Zehetmayer (ROeS); Herbert Thijs (RBe); Njoku Ama (GBot); Cristian Marcelo Villegas Lobos (RBras); Marcelo Andrade da Silva (RBras); Kirsty Hassall (BIR); Che Henry (GCmr); Novie Younger (RCAC); Katja Ickstadt (CEN); Dr. Xing Zhao (CHINA); Necla Kochan (EMR); Saptarshi Chakraborty (ENAR); Gema Alexandra Zambrano (ECU); Thomas Achia (Geth); Anne Thiébaut (RF); Reinhard Vonthein (DR); Agnes Ankomah (GGha); Harichandra Kumar KT (IR); Marco Bonetti (RItl); Professor Takashi Daimon (JR); Thomas Achia (GKe); Sangbum Choi (Rko); Jupiter Simbeye (Gmal); Olayemi Oluwasoga (GNi); Esa Läärä (NR); Alia Sajjad (PKSTAN); Elzbieta Kubera (GPol); Jialiang Li (SING); Iain McDonald (GSAF); Ester Boixadera (REsp); Henry G. Mwambi (SUSAN); Hein Putter (The Channel Network)' Roula Tsonaka (ANed); Jessica Minnier (WNAR); and Thomas Chikwanya (Gzim)

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
GCl - Chilean Region
GCmr - Cameroon Region
CHINA - Chinese Region
CROA - Croatian 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
NAM - Namibian 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
EAN – East Asian Network
SUSAN - Sub-Saharan Network

Get Connected!

Follow IBS on Social Media!
Facebook • LinkedIn

President's Corner

Continued from p. 1

Honorary Life Members: Louise Ryan (Australasian Region) for fostering lasting connections between the Regions and the Society, and for promoting the advancement of women and future generations, Maria Grazia Valsecchi (Italian Region) for exceptional contributions to research in the field of medical statistics and her tireless dedication to advancing biostatistical research, and Geert Verbeke (Belgian Region) for scientific, educational, editorial, and administrative leadership to the biostatistics profession and to the International Biometric Society.

This 32nd biennial conference of our International Biometric Society was an exceptional experience that was only made possible by the tireless efforts of so many people. A big Thank You to our IBC2024 Organizing President, José Pinheiro (ENAR); to Dimitris Rizopoulos (Netherland Region) and all members of the International Program Committee (IPC), who have overseen all invited session and contributed paper submissions, which was a tremendous task; to Lance Waller (ENAR), as well as María Gabriela Cendoya and Silvia Sühring (both Argentinean Region) for (co-)chairing the Local Organizing Committee (LOC), ensuring everything ran smoothly onsite at the meeting; to the Education Committee chaired by Annette Kopp-Schneider and Rafael De Andrade Moral, who together worked hard to select the best short courses; and to Sarah Ratcliffe (ENAR) and Vicente Nuñez Anton (Spanish Region), our current and former treasurer, for keeping an attentive eye at our finances. All of them received great support from Jenna Beak (MCI), who took care of our social events and local arrangements with the hotel, Courtney Fowler (IBO), who worked out a detailed marketing strategy providing up-to-date information to our Society members and beyond, and Peter Doherty, Alexander Iula, and Ryan Dee (IBO) who took care of all the many issues related to organizing such an amazing conference. Last, but certainly not least, our heartfelt thanks to the twelve student volunteers who were a great help during the conference.

During the Closing Ceremony, we were all taken on a fantastic virtual trip to Seoul, South Korea, where our next IBC in 2026 will take place. The co-chairs of the Seoul Local Organizing Committee, Sohee Park and Ho Kim, gave an enthusiastic presentation of our next meeting venue, the brand new COEX Magok. Seoul is such a great place to visit that you should not miss the opportunity to combine a unique travel experience with an inspiring scientific conference.

Last, but not least, you are probably extremely curious to get to know where IBC2028 will take place. There were two extremely good bids and the final decision was a hard one to be made. In the end, the Conference Advisory Committee recommended to accept the joint bid of the Austro-Swiss Region, the German Region and the French Region to organize IBC2028 as a joint effort in Basel, Switzerland, and the Executive Board followed this recommendation. However, since the competitive proposal was quite strong, we hope and encourage the runner-up region to submit their bid again for the 2030 IBC!

Please also note that now it is time to say Goodbye and a big Thank You to José Pinheiro (ENAR) for his many years of dedication, and for his wisdom, creativity, vision, and extraordinary leadership as IBS President and to Vicente Nuñez Anton (Spanish Region) for his very thorough supervision of all financial matters, his careful consideration of conflicting requests, and his wise decisions on what to finance as IBS Treasurer. At the same time, we give our warm welcome to María Gabriela Cendoya (Argentinian Region) as our Incoming IBS President.

Since you won't get these greetings until early 2025, I hope that you all had a wonderful and relaxing holiday season, and a great start and a fantastic and prosperous New Year,

Iris Pigeot
International Biometric Society President
pigeot@leibniz-bips.de

From the Editor

The beauty of IBS management is that the preparation process for the next IBC starts before the hangover effect of the previous conference evaporates. Even though for many of us it has not been possible to physically participate in the grand academic feast at Atlanta, the President's corner as well the update from the IBO in this issue makes us feel to be part of the IBC2024. We would like to congratulate various awards winners and the volunteers of IBC that has a long list with a wide spectrum of senior dignitaries to young academicians. The initiative for starting a women's corner column in future issues of the Bulletin that has been announced by the President would certainly enhance the strength of IBS. During my tenure of six years as editor Biometric Bulletin I had the opportunity to work with four Presidents namely Louise Ryan (Australasian Region); Geert Verbeke (Belgian Region); José Pinheiro (ENAR); and the present on chair, Iris Pigeot-Kubler (German Region); and if I also count on the incoming IBS president, María Gabriela Cendoya (Argentinian Region); a total of three of five (60%) belong to superior gender. That also reflects a good representation of various regions confirming the democratic setup of IBS functioning.

Before I say goodbye to my role as BB Editor, I must appreciate the close cooperation and bondage maintained by IBO staff throughout the past six years in publishing six volumes and 24 issues successfully that too always per the pre-pronounced time schedule. I am deeply indebted to each one of the present IBO staff as well those who served earlier under the continued leadership of the Executive Director, Peter Doherty. Our heartiest congratulations and warm welcome to Prof Garth Tarr for his taking over as the executive editor of the Biometric Bulletin w.e.f. 1st January 2025. We have an added advantage of his continuity with us as Associate editor during the past six years, that helped a lot in making a smooth and pleasant transition. I am sure under his editorship Biometric Bulletin would progress further in a variety of ways touching newer dimensions.

It was just a coincidence that the IBS 75th anniversary as well the fortieth anniversary of Biometric Bulletin have taken place during my tenure. Honestly speaking, working as editor BB was a good learning experience and by virtue of that I had the opportunity to closely observe the entire functioning of IBS and IBO as well overseeing the regional activities and establishing rapport with regional correspondents. Regular editorial updates by Biometrics and JABES, and the high level contributions of academic interest provided through Software corner and STRATOS platform are well appreciated. Continuance of these four regular contributions is an asset to the Bulletin. Finally, I must confess that with my close involvement of six years I developed an attachment to IBS that would certainly last for years to come and for all that feeling and effect credit goes to the supportive working environment provided by IBS even to the volunteers.

Ajit Sahai
Biometric Bulletin, Editor

Update from the IBO

Hello and greetings to all of our International Biometric Society members! As we close out our reporting related to 2024, I also come to you with a message of hope and solidarity for 2025. Regardless of the challenges that you may have faced personally this past year or the trials that lay ahead, remember that there are always positives that come with change (and also interesting data sets). It's how we meet these challenges and work together as a global community that will make a lasting difference. As we embrace the opportunities of a new year, rest assured that your International Business Office remains a wholly independent resource for you, and the Society continues as a non-profit entity devoted to the service of all members, wherever they are located.

As with any other year, some of our volunteers find themselves at the end of their terms. And I would personally like to thank all of the following members who have completed significant volunteer roles this year:

- **José C. Pinheiro** (Eastern North American Region), for your leadership as Organizing President for the 2024 International Biometric Conference in Atlanta, Georgia USA. Thanks for everything, José!

- **Dimitris Rizopoulos** (Netherlands Region), for your many hours coordinating with the IBO, IBS leadership and committee volunteers as Chair of the IBC 2024 International Program Committee!

- **Lance Waller, Silvia Sühring and María Gabriela Cendoya** for helping to bring a local flavor to IBC 2024 as Co-Chairs of the Local Organizing Committee.

- **Geert Verbeke** (Belgian Region), for your completion of your term as Immediate Past President and for your pivotal leadership on the Nominating Committee. Thank you, Geert!

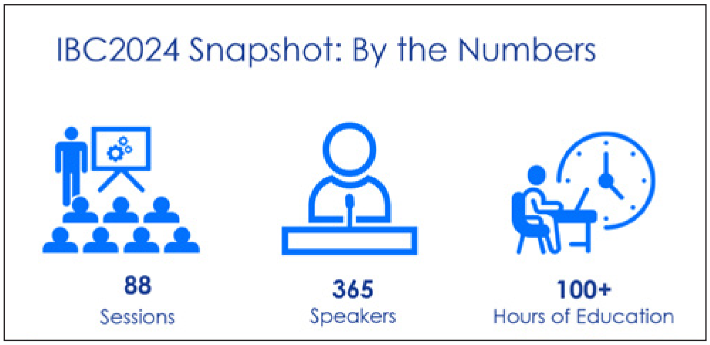
- **Ricardus Vonk** (German Region), for completing your recent term on the Executive Board and for your continued support in furthering the development of a new program that will improve communications between the IBO and the Regions. We could not have made our recent progress without your help, Richard!

- **Annette Kopp-Schneider and Rafael De Andrade Moral,** the former and current Chairs of our Education Committee, also deserve special thanks for their role in selecting interesting short courses as part of our IBC 2024 planning efforts.

- **Amy Herring** (Eastern North American Region), for completing your recent Board term and for your leadership as we are striving to improve Board and committee operations. Thanks so much, Amy!

- **Simone Gray** (Eastern North American Region), for your willingness to serve on the Executive Board during 2024. Many thanks!

- **Vicente Núñez-Antón** (Spanish Region), for countless hours of support as Outgoing Treasurer, not to mention your past leadership to help improve the Board's understanding of our finances. Best of luck to you in your next adventure, Vicente!



- *Biometrics* Co-Editors **Bill Rosenberger** (Eastern North American Region), through 2023, and **Katja Ickstadt** (German Region), through 2024.

- *Biometric Bulletin* Executive Editor **Ajit Sahai** (Indian Region), through 2024. Thank you all for your efforts!

It is of course quite likely that not everyone I mentioned here represents the entire list of those who should be recognized, and so I apologize for any omissions, which we will surely rectify in a future issue! I'd also like to be among the first to welcome our new Board members whose terms are beginning in January, including:

- **Christopher Triggs*** (Australasian Region)
- **Leslie McClure** (Eastern North American Region)
- **Mike Daniels** (Eastern North American Region))
- **Ruth Keogh*** (British-Irish Region)
- **Guadalupe Gómez Melis** (Spanish Region)
- **Luiz Alexandre Peternelli** (Brazilian Region)

*Re-elected to a second term

These six Directors will serve a four-year term ending 31 December 2028. The President-Elect Gabriela Cendoya shall serve a one-year term ending 31 December 2025, and shall then automatically succeed to the office of President, serving for two years. Best wishes to Gabriela as she begins the next chapter in her leadership journey!

I would now like to recognize those award winners who have not yet been mentioned in this issue of the *Biometric Bulletin*. Congratulations to our IBC 2024 Young Statistician Showcase winners!

Africa

- **Getahun Mulugeta Awoke,** for *Developing Prognostic Models to Predict Renal Graft Survival: Comparison of Statistical and Machine Learning Models*

Australasia / Asia

- **Abhiram Dinesh Kumar Bindhu Mol,** for *A Statistical Evaluation of ZINBMM and ZICMPMM Using Simulated Data*

Europe

- **Alessio Albanese**, for *Multi-Omics Network Reconstruction: Collaborative Graphical Lasso*

North America

- **Yijun Li,** for *BSNMani: Bayesian Scalar-on-network Regression with Manifold Learning*

During our IBC in Atlanta, we were visited by two of our colleagues from the International Statistical Society having won the prestigious "Ambassador to the IBC" award! Congratulations to these young professionals:

- **Renata Rojas Guerra** (Brazil)

- **Janet Van Niekerk** (Saudi Arabia)

We are thrilled that, as part of this award, these individuals will also be joining the International Biometric Society. So, we look forward to welcoming them to other IBS and Region events in the future.

Congratulations to these *JABES* Best Papers for 2022 and 2023!

2022 Best Paper

- **Probabilistic Forecasts of Arctic Sea Ice Thickness** Peter A. Gao, Hannah M. Director, Cecilia M. Bitz, & Adrian E. Raftery [JABES, 27, 2 (2022) pages 280-302]

- **A Bayesian Approach for Data-Driven Dynamic Equation Discovery** Joshua S. North, Christopher K. Wikle, & Erin M. Schliep [JABES, 27, 4 (2022) pages 728-747]

Dates are tentative. Jointly supported by the IBS Austro-Swiss (ROeS), German (DR), and French (FR) Regions

2023 Best Paper

- **Asynchronous Changepoint Estimation for Spatially Correlated Functional Time Series** Mengchen Wang, Trevor Harris, Bo Li [JABES, 28, 1 (2023) pages 157-176]

Honorable Mention

- **Modeling Community Dynamics Through Environmental Effects, Species Interactions and Movement** Becky Tang, James S. Clark, Peter P. Marra, Alan E. Gelfand [JABES, 28, 1 (2023) pages 178-195]

We expect a virtual session honoring these papers to be offered via Zoom very soon. Watch your email for more details. Our *Biometrics* journal also celebrated their Best Papers awards for 2022 and 2023 during the IBC..

2022 Best Paper

- **"A spatial Bayesian latent factor model for image-on-image regression."** Cui Guo, Jian Kang, and Timothy D. Johnson

2023 Best Paper

- **"Multiwave validation sampling for error-prone electronic health records."** Bryan E. Shepherd, Kyunghee Han, Tong Chen, Aihua Bian, Shannon Pugh, Stephany N. Duda, Thomas Lumley, William J. Heerman, and Pamela A. Shaw

Thanks also to these Biometrics Peer Referees:

- **Niccolo Anceschi**
- **Zach Branson**
- **Tian Gu**
- **Chris Jennison**
- **Kevin Lin**
- **Shaun Seaman**

Congratulations to our IBC 2024 Best Poster Winner and runners-up:

- 3rd place: Iris Reinhard (Heidelberg University, Germany)
- 2nd place: Giovanni Piccirilli (University of Sao Paulo, Brazil)
- **1st place: Moka Komaki** (Yokohama City University, Japan)

As well as our Best Oral Paper winner and runners-up:

- 3rd place: Marta Cipriani (Leiden University, Netherlands)

- 2nd place: Stefan Embacher (Medical University, Graz)
- **1st place: Mohammad Samsul Alam** (Duke University, USA)

Many others deserve recognition, such as our current IBS Officers, LOC and IPC committee members, our Travel Awardees and IBC 2024 student volunteers, not to mention our IBC sponsors. We even presented an award to the most prolific mobile app user at the IBC!

Believe it or not, there is one award that has not yet been chosen, due to travel restrictions related to IBC 2024. And that will soon be remedied! We hope you will join us in early February for the first of two virtual sessions with four of our finalists for the **Florence Nightingale Award.** All finalists will present their talks over the course of two online sessions. The Florence Nightingale (1820-1910) Award honors the most outstanding eligible candidate who has demonstrated exceptional scholarship. The top ranked presentation will receive a cash prize of $1,000.00 USD. All members and IBC attendees will be invited to attend both Florence Nightingale sessions free of charge.

There are also plans for another virtual IBC session related to our mentoring program, so please continue to watch IBS communications for details. Happy New Year, and best wishes!

Sincerely,

Peter Doherty
Executive Director

In Memoriam Anna Barkowiak

With great sadness, we share the news of the passing of Professor Anna Bartkowiak, PhD, DSc, a longtime member of the International Biometric Society. She passed away on December 18, 2024 in Wroclaw, Poland.

Professor Bartkowiak was an expert in computational statistics, multivariate statistics, graphical methods, and neural networks. She was a long-time employee of the Institute of Computer Science at the University of Wrocław (since 1960). She served as Vice Dean of the Faculty of Mathematics and Computer Science and Head of the Department of Numerical Methods at the Institute of Computer Science.

She authored over 200 publications in international journals and conference proceedings, and pioneered statistical software in Poland.

Revered and a dedicated pedagogue, she will be greatly missed.

Give to the IBS Travel Awards Fund by 1 March, 2025

Hello, IBS and Region Members and Leaders!

The **International Biometric Society Travel Awards Fund** helps support the allocation of travel grants to a selected group of members from lower and middle-income countries (LMICs), with the goal of allowing them to travel to IBS Region and Network events during the current year.

We would greatly appreciate your donation by 1 March, 2025.

Donations are now being accepted at **https://members.biometricsociety.org/about/donate**.

Give Today!

You may be interested to know that the Society has instituted a matching funds policy. For every dollar (USD) an individual, company, IBS Region or IBS Network donates, IBS will match it up to $20,000.00. This gives us the opportunity to fund more travel, bringing professionals from eligible countries together at local Region and Network events to collaborate, share knowledge, learn new perspectives and build lifelong friendships!

Donations are vital to the continued success of this program, as the IBS is typically able to fund less than half of the applicants who apply. Donations also foster our membership growth in LMICs and serve our global audience. Please donate today. Note that all funds donated are passed along to eligible members, and each donation received from an individual or region will be acknowledged with a note of appreciation and a receipt. Please contact us directly at ibs@biometricsociety.org with any questions related to tax deductions or related matters. And look for more information on the application process in the next issue of the Biometric Bulletin.

Poster from the Society's 10th international conference, held 6-10 August 1979 at the Delphin Hotel Guaruja, Brazil. President John Nelder was one of the signers. Thanks to our colleague Guntram Deichsel for offering us this photo!

Editorial Updates

Biometrics

September 2024 Issue Highlights

The September 2024 issue features articles across a broad spectrum of applications and methodology. The Biometric Methodology section sets out with a Discussion paper on "LEAP: The following papers are being published in Biometrics Methodology:

- The latent exchangeability prior for borrowing information from historical data," by Ethan M. Alt, Xiuya Chang, Xun Jiang, Qing Liu, May Mo, Hong Amy Xia, and Joseph G. Ibrahim.
- The paper is discussed by: Darren Scott and Alex Lewin; Shannon D. Thomas and Alexander M. Kaizer; and Harlan Campbell and Paul Gustafson.
- Regular Methodology papers include: "Causal inference using multivariate generalized linear mixed-effects models," by Yizhen Xu, Jisoo Kim, Laura K. Hummers, Ami A. Shah, and Scott Zeger;
- "Leveraging independence in high-dimensional mixed linear regression," by Kai Deng, Ning Wang, Qing Mai, and Xin Zhang;
- "Designing cancer screening trials for reduction in late-stage cancer incidence," by Kehao Zhu, Ying-Qi Zhao, and Yingye Zheng;
- "Semi-parametric benchmark dose analysis with monotone additive models." By Alex Stringer, Tugba AkkayaHocagil, Richard Cook, Louise Ryan, Sandra W. Jacobson, and Joseph L. Jacobson;
- "Adjusting for incomplete baseline covariates in randomized controlled trials: A cross-world imputation framework," by Yilin Song, James P. Hughes, and Ting Ye;
- "A Bayesian latent-subgroup platform design for dose optimization," by Rongji Mu, Xiaojiang Zhan, Rui (Sammi) Tang, and Ying Yuan; "Sensitivity analysis for publication bias in meta-analysis of sparse data based on exact likelihood," by Taojun Hu, Yi Zhou, and Satoshi Hattori;
- "Visibility graph-based covariance functions for scalable spatial analysis in non-convex partially Euclidean domains," by Brian Gilbert and Abhirup Datta;
- "High-dimensional multivariate analysis of variance via geometric median and bootstrapping," by Guanghui Cheng, Ruitao Lin, and Liuhua Peng;
- "Summary statistics knockoffs inference with family-wise error rate control," by Catherine Xinrui Yu, Jiaqi Gu, Zhaomeng Chen, and Zihuai He;
- "Towards automated animal density estimation with acoustic spatial capture-recapture," by Yuheng Wang, Juan Ye, Xiaohui Li, and David L. Borchers;
- "Factor-augmented transformation models for interval-censored failure time data," by Shuwei Li, Hongxi Li, Liuquan Sun, and Xinyuan Song; "Testing for similarity of multivariate mixed outcomes using generalized joint regression models with application to efficacy-toxicity responses," by Niklas Hagemann, Giampiero Marra, Frank Bretz, and Kathrin Möllenhoff;
- "The multivariate Bernoulli detector: Change point estimation in discrete survival analysis," by Willem van den Boom, Maria De Iorio, Fang Qian, and Alessandra Guglielmi;
- "Semiparametric inference of effective reproduction number dynamics from wastewater pathogen surveillance data," by Isaac H. Goldstein, Daniel M. Parker, Sunny Jiang, and Volodymyr M. Minin;
- "Improving prediction of linear regression models by integrating external information from heterogeneous populations: James-Stein Estimators," by Peisong Han, Haoyue Li, Sung Kyun Park, Bhramar Mukherjee, and Jeremy M.G. Taylor;
- "Nonparametric second-order estimation for spatiotemporal point patterns," by Decai Liang, Jialing Liu, Ye Shen, and Yongtao Guan;
- "Joint structure learning and causal effect estimation for categorical graphical models," by Federico Castelletti, Guido Consonni, and Marco L. Della Vedova;
- "An interpretable Bayesian clustering approach with feature selection for analyzing spatially resolved transcriptomics data," by Huimin Li, Bencong Zhu, Xi Jiang, Lei Guo, Yang Xie, Lin Xu, and Qiwei Li;
- "Controlling false discovery rate for mediator selection in high- dimensional data," by Ran Dai, Ruiyang Li, Seonjoo Lee, and Ying Liu;

- "A Gaussian-process approximation to a spatial SIR process using moment closures and emulators," by Parker Trostle, Joseph Guinness, and Brian J. Reich;
- "Multiply robust estimation of marginal structural models in observational studies subject to covariate-driven observations," by Janie Coulombe and Shu Yang;
- "PathGPS: Discover shared genetic architecture using GWAS summary data," by Zijun Gao, Trevor Hastie, and Qingyuan Zhao;
- "Nonparametric receiver operating characteristic curve analysis with an imperfect gold standard," by Jiarui Sun, Chao Tang, Wuxiang Xie, and Xiao-Hua Zhou;
- "Absolute risk from double nested case-control designs: cause-specific proportional hazards models with and without augmented estimating equations," by Minjung Lee and Mitchell H. Gail; and
- "Bayesian inference for multivariate probit model with latent envelope," by Kwangmin Lee and Yeonhee Park.

The Biometric Practice section includes work on:

- "Planning cost-effective operational forest inventories," by Santeri Karppinen, Liviu Ene, Lovisa EngbergSundstrom, and Juha Karvanen;
- "A Bayesian nonparametric approach for causal mediation with a post-treatment confounder," by Woojung Bae, Michael J. Daniels, and Michael G. Perri;
- "Nonparametric worst-case bounds for publication bias on the summary receiver operating characteristic curve," by Yi Zhou, Ao Huang, and Satoshi Hattori;
- "A generalized outcome-adaptive sequential multiple assignment randomized trial design," by Xue Yang, Yu Cheng, Peter F. Thall, and Abdus S. Wahed;
- "Propensity weighting plus adjustment in proportional hazards model is not doubly robust," by Erin E. Gabriel, Michael C. Sachs, Ingeborg Waernbaum, Els Goetghebeur, Paul F. Blanche, Stijn Vansteelandt, Arvid Sjölander, and Thomas Scheike; and
- "Optimal refinement of strata to balance covariates," by Katherine Brumberg, Dylan S. Small, and Paul R. Rosenbaum. Best Paper Awards for 2022 and 2023 at the International Biometric Conference in Atlanta In keeping with tradition, the International Biometric Conference will host a Biometrics Showcase Session, featuring the co-editor selected Best Papers Published in Biometrics by an IBS Member for 2022 and 2023:
- Guo, C., Kang, J., and Johnson, T.D. (2022). A spatial Bayesian latent factor model for image-on-image regression. Biometrics, 78, 72—84.
- Shepherd, B.E., Han, K., Chen, T., Bian, A., Pugh, S., Duda, S.N., Lumley, T., Heerman, W.J., and Shaw, P.A. (2023). Multiwave validation sampling for error-prone electronic health records. Biometrics, 79, 2649-2663.

Celebrating Excellent Referees for Biometrics

The Co-editors, active during the calendar years 2022 and 2023, selected six colleagues who refereed papers submitted to Biometrics and did an outstanding job. It is a difficult choice, as so many referees provide high-quality reports. It goes without saying that the journal's scientific health crucially depends upon referees' willingness and work. We are delighted to celebrate: Chris Jennison, Zach Branson, Tian Gu, Shaun Seaman, Kevin Lin, and Niccolo' Anceschi.

Geert Molenbergh
Biometrics Executive Editor

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

We have recently opened a new special issue named "The Next Wave of Statistical Learning for Spatial Functional Data Analysis" which closed on 30 January 2025. Spatial Functional Data Analysis (SFDA) is a branch of statistics that focuses on analyzing data where there are both spatial dependencies and functional (or infinite-dimensional) structures. In this type of analysis, each observation is not a scalar or vector, but a function (or curve) observed over a spatial domain.

This kind of data is commonly encountered in scientific fields such as environmental science, climatology, and neuroimaging, where measurements are continuously recorded over time or space, resulting in complex data structures. Initially, SFDA primarily utilized traditional functional data analysis techniques extended to spatial settings. However, as the applications of SFDA became more complex, the need for advanced techniques led to the development of a second-generation framework. This newer framework is designed to handle the increasing complexity of spatial dependencies, non-linear dynamics, high-dimensionality, and multi- resolution data. Potential topics that could be covered under The Next Wave of Statistical Learning for Spatial Functional Data Analysis include:

- Statistical models for spatial functional data: This encompasses models such as mixed effects models, Gaussian processes, and generalized additive models specially designed for spatial contexts.
- Functional data analysis techniques: This involves exploring methods like functional principal component analysis (FPCA) and functional regression techniques within a spatial framework.
- Spatial correlation structures: This focuses on modeling and evaluating spatial correlations present in functional data.
- Machine learning approaches: Application of machine learning techniques, including random forests, support vector machines, and neural networks, for analyzing spatial functional data.

- Bayesian hierarchical models: Utilizing Bayesian frameworks with Gaussian processes to effectively model uncertainty and complex dependencies inherent in spatial functional data.
- Spatio-temporal data: Extending models to incorporate spatio-temporal settings, addressing non- separable space-time covariances.
- Multivariate and multi-resolution analysis: Employing multivariate approaches to manage multiple functional variables and utilizing multi-resolution model including network for functional data.
- Functional-Driven Spatial Point Processes: Combining point process modeling with spatial functional data to analyze and predict events occurring in space where the intensity or characteristics of the events are influenced by continuous data that vary over space and time.

Guest Editors are: (a) **Elvira Romano**, Department of Mathematics and Physics, University of Campania "Luigi Vanvitelli" Caserta, Italy; (b) **Fabrizio Maturo**, Department of Economics, Statistics and Business, Faculty of Technological and Innovation Sciences, Universitas Mercatorum Rome, Italy; (c) **Antonio Irpino**, Department of Mathematics and Physics, University of Campania "Luigi Vanvitelli," Caserta, Italy

December 2024 issue (Volume 29, Number 4) featured the following papers:

- Two Tests of Significance for Preferred Direction in Tree Radial Growth Under a Linear-Circular Regression Model with Correlated Random Errors, Pierre Dutilleul, Tomoaki Imoto, Kunio Shimizu
- A Spatial Mixture Model for Spaceborne Lidar Observations Over Mixed Forest and Non-forest Land Types, Paul B. May, Andrew O. Finley, Ralph O. Dubayah
- Models to Support Forest Inventory and Small Area Estimation Using Sparsely Sampled LiDAR: A Case Study Involving G-LiHT LiDAR in Tanana, Alaska, Andrew O. Finley, Hans-Erik Andersen, Sudipto Banerjee
- 3D Point Cloud Semantic Segmentation Through Functional Data Analysis, Manuel Oviedo de la Fuente, Carlos Cabo, Celestino Ordóñez
- Design and Analysis of a Microplate Assay in the Presence of Multiple Restrictions on the Randomization, Alexandre Bohyn, Eric D. Schoen, Peter Goos
- Model-Based Geostatistics Under Spatially Varying Preferential Sampling, André Victor Ribeiro Amaral, Elias Teixeira Krainski, Paula Moraga
- Geographically Weighted Regression-Based Model Calibration Estimation of Finite Population Total Under Geo-referenced Complex Surveys, Bappa Saha, Ankur Biswas, Nobin Chandra Paul
- Estimating Species Abundance from Presence–Absence Maps by Kernel Estimation, Ya-Mei Chang, Ying-Chi Huang
- Order Restricted Randomized Block Designs, mOmer Ozturk. Richard Jarrett, Olena Kravchuk
- Two Gaussian Regularization Methods for Time-Varying Networks, Jie Jian, Peijun Sang, Mu Zhu
- Deep Neural Network Identification of Limnonectes Species and New Class Detection Using Image Data, Li Xu, Yili Hong, Laura J. Freeman

Some current Journal Statistics as per September 2024:

- 44 Articles Published Online for Q1-Q2 2024
- 160 Submissions for Q1-Q2 2024 (An increase from 159 Submissions in Q1-Q2 2023)
- Average of 24 Days from Submission to First Decision for Q1-Q2 2024
- 82,370 Article Downloads for Q1-Q2 2024 (An increase from 75,898 in Q1-Q2 2023 and 41,706 in Q1-Q2 2022)
- 2023 Impact Factor: 1.4 (112 Citations from 78 Articles); 2022 Impact Factor: 1.4 (109 Citations from 80 Articles)
- As per November 25, 2024, JABES has received 295 papers during 2024.

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. We 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 Vanda Inancio de Carvahlo (vanda.inacio@ed.ac.uk), University of Edinburgh, UK. Please follow us on Twitter: @JabesEditor.

Jorge Mateu
Editor-in-Chief

Software Corner

ClassifyR: Advancing precision medicine through robust multi-view classification frameworks

Dario Strbenac, Jasmine Gu, Harry Robertson, Jean Yang and Ellis Patrick.

Precision medicine and the need for advanced classification tools

Precision medicine is a personalised approach to healthcare that tailors prevention, diagnosis, and treatment to an individual's unique characteristics such as genetics, environment, lifestyle, and molecular data. By integrating diverse data types, the ultimate goal of precision medicine is to deliver the right decision or treatment to the right patient at the right time. While this has driven the development of complex classification strategies, realising this vision relies on robust evaluation of model performance at both cohort and patient levels.

What is ClassifyR?

This article presents ClassifyR, a comprehensive machine learning framework tailored for multi-omics classification problems in a precision medicine context. ClassifyR was first introduced in 2015 as a tool for assessing classification performance in omics research, particularly evaluating feature selection approaches in transcriptomics (Strbenac et al., 2015). It provides systematic comparison of predictive models, emphasising accuracy, stability and interpretability. While machine learning evaluation frameworks such as caret and mlr in R and scikit-learn in Python provide general-purpose machine learning frameworks, they lack specific capabilities for preprocessing, feature selection, feature interrogation, multi-omic integration and cross-platform performance evaluation. Standardising these procedures into a unified framework can facilitate more systematic and robust evaluations. Thus, ClassifyR distinguishes itself in multiple ways:

- Bioconductor ecosystem integration: ClassifyR is interoperable with established omics data structures in the Bioconductor Project, ensuring seamless access to single-cell, multi-omics, and spatial technologies.
- Full cross-validation workflow: The package performs comprehensive cross-validation by including feature selection and hyperparameter tuning within the cross-validation procedure, which is essential for handling large-scale omics datasets.
- Cross-dataset and cross-modality validation: Models can be both constructed and evaluated across cohorts and omics platforms, addressing issues of reproducibility and transferability.
- Precision medicine focus: ClassifyR includes frameworks for assessing model appropriateness at an individual patient level which is crucial for evaluating which model or modality is appropriate for which patient.

By addressing these critical gaps, ClassifyR enables researchers to explore complex disease mechanisms, optimise diagnostic workflows, and guide treatment strategies in precision medicine.

Illustrations of ClassifyR analytical innovations

Since its inception, the package has undergone continuous development to address modern challenges in precision medicine. Sample-specific performance and the development of decision pathways for precision medicine: Traditional classification evaluation focuses on cohort-level performance, which can limit insight into the relevance of a classification method for individualised decisions. ClassifyR introduces sample-based prediction accuracy (Patrick et al., 2017) and sample-based prediction consistency (Tran et al., 2024) to quantify the reliability of predictions for individual samples. These approaches highlight samples that appear easy or hard to classify, enabling targeted investigation to improve model performance. The flexibility of this method allows its application to both classification tasks and time-to-event (survival) analysis. For instance, a heatmap of individual classifiability can identify heterogeneity within a cohort (Figure 1), guiding the development of subgroup-specific models.

Figure 1

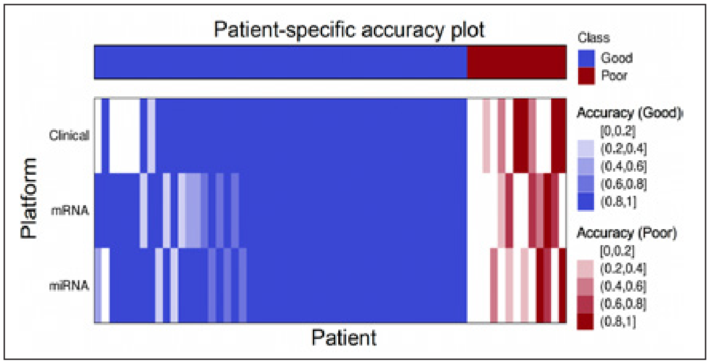


Figure 1: ClassifyR is used to perform 100 repeats of 10-fold cross-validation on a stage III melanoma cohort of 62 patients to predict prognosis (Good and Poor) with three platforms; Clinical data, mRNA microarray (mRNA) and microRNA microarray (miRNA). The sample-specific prediction accuracy is plotted for each patient and each platform using samplesMetricMap(). There are some patients that are correctly predicted by all platforms, while there are others that are predicted accurately by a single platform.

Inspired by clinical diagnostics, ClassifyR incorporates frameworks for constructing and optimising multi-platform precision pathways using sample-specific performance. These pathways simulate clinical decision-making by balancing diagnostic accuracy and cost-effectiveness (Tran et al., 2024, Figure 2).

Figure 2

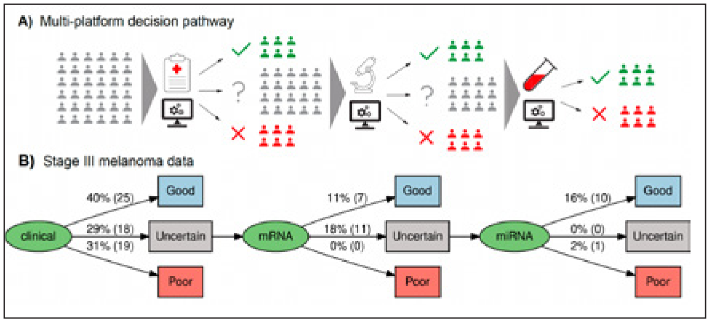


Figure 2 A): A multi-platform decision pathway illustrating how predictions are made for a patient. Patients that can not be confidently predicted for a particular platform are passed onto the next stage of the pathway. B) ClassifyR is used to construct a multi-platform precision pathway to predict prognosis of stage III melanoma patients using three platforms: clinical, mRNA and miRNA. As clinical data is accessible, it was chosen to initiate the pathway.

Integration of multi-view data: ClassifyR leverages multi-view learning principles to integrate diverse omics data types, including transcriptomics, proteomics, single-cell, and spatial features. Designed to work seamlessly with Bioconductor data objects, ClassifyR can operate with structures such as MultiAssayExperiment to store measurements from multiple omics in a single data object. This enables users to compare classification performance across multiple omics types with just a single line of code. ClassifyR also incorporates multiple ways of summarising information from single-cell and spatial omics technologies to create multiple views of a patient. By leveraging feature engineering strategies from tools like scFeatures (Cao et al., 2022), ClassifyR not only identifies optimal representations of complex datasets but also combines feature-sets to identify optimal models from multi-view data (Figure 3).

Figure 3

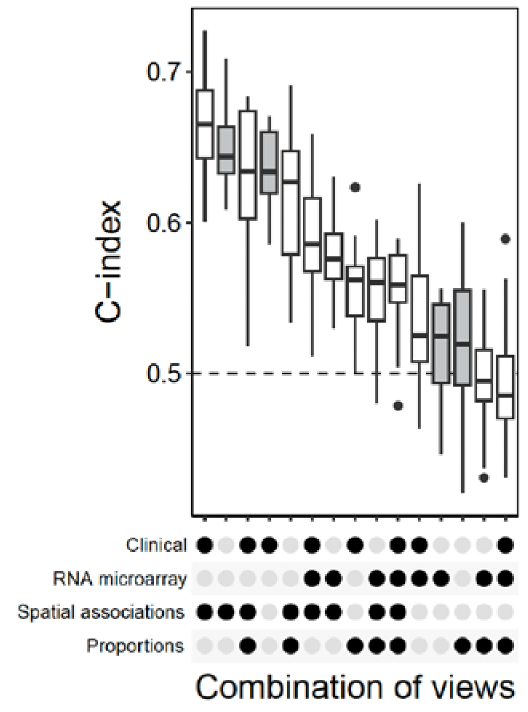


Figure 3: ClassifyR is used to evaluate time-to-event survival prediction in METABRIC, a cohort of breast cancer patients that, amongst many others, contains measurements from gene expression microarrays and a spatial omics technology called imaging mass cytometry (IMC). Two different views from the IMC data have been quantified using scFeatures to get the proportion of each cell type and using spicyR to get spatial associations between pairs of cell types. A single call to the crossValidate() function can facilitate the comparison of all the different views of the data, as well as all of their combinations. performancePlot() is used to compare the C-indexes from 100 repeats of 10-fold cross-validation of each view and combination of views.

Evaluation of model transferability: Omics data often exhibit platform- and cohort-specific variability, posing challenges for model generalisation and clinical application. ClassifyR includes approaches like Cross-Platform Omics Prediction (CPOP) and Transferable Omics Prediction (TOP) to develop ratio-based features that are robust across datasets (Wang et al., 2022; Robertson et al., 2024). This enables at-scale validation of models on independent cohorts (Figure 4).

Figure 4

Figure 4: ClassifyR is used to evaluate the transferability of models to predict organ rejection using gene expression data in four kidney transplant cohorts. Using crissCrossValidate() ClassifyR trains a classifier for each dataset and evaluates it in every other dataset. Additionally, we have used ClassifyR to construct a Transferable Omics Prediction (TOP) model that is trained on all datasets except the testing dataset.

Summary

ClassifyR is a versatile R package designed to address the unique challenges of classification performance under a precision medicine paradigm. Leveraging the Bioconductor ecosystem, ClassifyR empowers researchers and clinicians to integrate and analyse multi-omics, single-cell, and spatial omics data; evaluate model performance systematically across cohorts and platforms; and develop patient-level insights. Detailed examples with code are available on https://sydneybiox.github.io/ClassifyRPlaybook/

Acknowledgement

We would like to thank Andy Tran for contributing to the generation of Figure 2.

References

Strbenac, Dario, et al. 2015. "ClassifyR: An R Package for Performance Assessment of Classification with Applications to Transcriptomics." Bioinformatics 31 (11): 1851–53.

Cao, Yue, et al. 2022. "scFeatures: Multi-View Representations of Single-Cell and Spatial Data for Disease Outcome Prediction." Bioinformatics 38 (20): 4745–53.

Patrick, Ellis, et al. 2017. "A Multi-Step Classifier Addressing Cohort Heterogeneity Improves Performance of Prognostic Biomarkers in Three Cancer Types." Oncotarget 8 (2): 2807–15.

Tran, Andy, et al. 2024. "Construction and Optimization of Multi-Platform Precision Pathways for Precision Medicine." Scientific Reports 14 (1): 4248.

Wang, Kevin Y. X., et al. 2022. "Cross-Platform Omics Prediction Procedure: A Statistical Machine

Learning Framework for Wider Implementation of Precision Medicine." NPJ Digital Medicine 5 (1): 85.

Robertson, Harry, et al. 2024. "Decoding the Hallmarks of Allograft Dysfunction with a Comprehensive Pan-Organ Transcriptomic Atlas." Nature Medicine.

Canete, Nicolas P., el al., 2022. spicyR: spatial analysis of in situ cytometry data in R, Bioinformatics 38 (11): 3099–3105.

STRengthening Analytical Thinking for Observational Studies (STRATOS): Estimands – Summary from the "STRATOS Accelerated Guidance for Real World Data Analysis" Workshop

Nicholas Bakewell 1 , Jonathan Bartlett 2 , Kelly Van Lancker 3 , Els Goetghebeur 3 , Pamela Shaw 4 , Doranne Thomassen 5 , Emmanuelle Boutmy 6 , Suzanne M Cadarette 1 , Saskia le Cessie 3,5,7 , Nan van Geloven 5

1 Leslie Dan Faculty of Pharmacy and Dalla Lana School of Public Health, University of Toronto, Canada.
2 Department of Medical Statistics, London School of Hygiene and Tropical Medicine, UK.
3 Department of Applied Mathematics, Computer Science and Statistics, Ghent University, Belgium.
4 Biostatistics Division, Kaiser Permanente Washington Health Research Institute, USA.
5 Department of Biomedical Data Sciences, Leiden University Medical Center, the Netherlands.
6 Merck KGaA, Germany.
7 Department of Clinical Epidemiology, Leiden University Medical Center, the Netherlands.

Introduction

In September 2024, the STRengthening Analytical Thinking for Observational Studies (STRATOS) initiative brought together 55 researchers for a one-week workshop at the Lorentz Center in Leiden, the Netherlands. Presentations and working sessions were organised around key themes of observational research methods where STRATOS aims to bring guidance to applied researchers. We summarise the Workshop's discussions on the key theme 'Estimands.'

Estimands as a bridge between statistics and its application

Successful application of statistics in empirical sciences requires appropriate study design, data collection procedures and statistical method(s), which should all be steered by the research question. A clearly specified research question grounded in subject-matter knowledge is of the utmost importance. The estimand translates the research question into a precise unequivocal quantity (or quantities) of interest that we aim to estimate from data [1] .

Clearly defined estimands serve as a communication tool among and between statisticians and non-statisticians, and reduce the risk of misinterpretation of results by providing clarity to the reported effect(s) and the population(s) for which they hold [2] .

Model-free estimands

Traditionally, estimands have been (implicitly) defined as parameters in parametric statistical models. However, as Breiman [3] highlighted over two decades ago, statistical modelling relies on a priori assumptions about the true data generating model that may not be satisfied, potentially leading to questionable or irrelevant conclusions.

Consequently, there is a growing interest in moving away from model-based estimands and defining model-free estimands in causal inference [4, 5] . While statistical modelling will remain needed for estimating estimands and delivering insight into complex data structures, it has been argued that the estimand itself should not be defined with reference to particular statistical assumptions, since these may often not be correct and cannot be assessed at the study design stage [6] .

Are estimands a new phenomenon? Defining estimands and assessing the plausibility of identification assumptions (i.e., conditions needed to estimate estimands) are not new to statistical practice. For example, randomized controlled trials (RCTs) have been using frameworks like Population, Intervention, Comparison, Outcome, (Time) (PICO(T)) for a long time. However, PICO(T) may lack the precision for an unequivocal estimand definition.

There are comprehensive textbooks on causal inference that describe how the estimand(s) may be defined using mathematical notation (e.g., potential outcomes or counterfactuals) and how to assess the plausibility of identification assumptions in practice [7-9] . However, textbooks and the statistically oriented causal inference literature may not be accessible to all applied researchers.

Several frameworks that may be used to define estimands with the applied researcher in mind have been developed. These frameworks may be useful for providing (1) guidance without requiring in-depth knowledge of the vast literature on causal inference that may be difficult to navigate for the novice; and (2) clarity and standardization in the reporting of empirical research, which may mitigate potential biases and misinterpretations.

Defining estimands: Insights from four frameworks

Among frameworks that may be used to define estimands, four were discussed at the Workshop (Box). In earlier work, the STRATOS Causal Inference Topic Group developed eight steps for the empirical evaluation of research questions [1] . They outline a principled approach encouraging researchers to think carefully about what they are estimating and to be transparent in reporting, including underlying assumptions.

The Causal Roadmap (CR) provides a seven-step process for causal inference from defining the estimand to identifying and estimating it [10]. A key objective of the CR is to ensure a well-specified estimand, which can be rewritten in terms of the observed data given appropriate identification assumptions, reflecting both the research question and challenges in the data.

Target Trial Emulation (TTE) provides a structured process for designing an observational study when comparing treatments by specifying the ideal "target trial" [11] . The "target trial" refers to a hypothetical RCT one would ideally design to answer the study question if there were no ethical or financial constraints.

Lastly, the addendum to the ICH E9 harmonised guideline on statistical principles for clinical trials (i.e., ICH E9(R1) addendum) presents five key attributes of the estimand in an RCT [12] . In particular, the ICH E9(R1) addendum emphasizes intercurrent events which are post-randomization events (e.g., treatment switching) that affect the outcome and/or the collection of the outcome.

There is a clear overlap between these frameworks, but they vary in scope and focus, and therefore, may result in estimands being defined differently or may not be appropriate to address all types of research questions. For example, TTE and the ICH E9(R1) addendum focus on clinical studies comparing treatments, while the other two frameworks enable the definition of estimands for a wider range of causal questions.

It is of interest to further assess how these frameworks may complement, supplement, or conflict with each other. The STRATOS initiative aims to address this gap by synthesizing the extensive literature on these four frameworks (and potentially others) and by providing practical recommendations to applied researchers for effectively defining and using estimands.

Avoiding nonsensical estimands

The general recommended order in the estimand frameworks is to first define the estimand(s) and then delineate the assumptions needed to identify them; subsequently, specify how to estimate the estimand(s) from the data; and then start the actual data analysis. Identification assumptions include common assumptions such as consistency, no unmeasured confounding (i.e., (conditional) exchangeability) and positivity [13]. While identification assumptions may seem plausible by design or given a conceptual (structural) model, they are usually not empirically verifiable. Therefore, there must be a feedback loop with subject-matter experts assessing whether relevant identification assumptions are plausible for the setting at hand. This may ultimately avoid targeting nonsensical estimands; and reporting estimates with limited to no applicability in the real world [5].

Estimands are not just for causal effects

Having a well-defined inferential goal is not unique to the context of quantifying causal effects of treatments or exposures. The need for avoiding ambiguity and misinterpretation of results equally holds for studies with a descriptive, predictive or diagnostic aim. Therefore, estimands can also prove to be an extremely valuable tool in these types of studies.

For instance, recent work points out how age adjustment in descriptive studies may change the descriptive estimand from "What is the burden of disease in different racial/ethnic groups?" to "What would be the burden of disease in different racial/ethnic groups if they had the same age distribution as a chosen reference population?" [14]. Which one of these two is appropriate depends on the descriptive research question, and this research question needs to be unequivocal before we can decide on the appropriate analysis.

Similarly, misalignment between the intended use of prediction models and how the models handle treatments received by individuals in the development/training data has formed the basis of the prediction estimand framework [15-18]. For example, imagine a prediction model built on historical data where patients were treated according to a certain policy. If the treatment policy has evolved, the model might not be applicable in a contemporary setting.

In addition, the prediction estimand framework helps to clarify whether predictions are suitable for informing treatment decisions.

Lastly, in diagnostic studies, a well-defined estimand may ensure alignment between the target population (i.e., individuals for whom the diagnostic test is intended to be used in routine clinical practice) and the study population (i.e., individuals that are included in the study, and received both the diagnostic test under evaluation and the reference ("gold") standard test).

Conclusion

In conclusion, the size of the literature on estimands can be overwhelming even for the experienced statistician. We hope the summary of the Workshop's discussions on 'Estimands' and planned work from these discussions will chart a practical way forward through the literature and guide those conducting observational studies on the estimand frameworks. Interested readers are encouraged to visit the STRATOS initiative website for updates on this work (https://stratos-initiative.org).

Components of four frameworks to define estimands

STRATOS Causal Inference Topic Group

- Define the treatment that corresponds to the research question(s)
- Define the outcome that corresponds to the research question(s)
- Define the population(s) of interest
- Formalize the research question in terms of potential outcomes
- Specify the estimand as a contrast between potential outcome distributions
- State underlying assumptions validating the causal effect estimation
- Estimate the estimand
- Evaluate the validity of assumptions & perform sensitivity analyses

Causal Roadmap

- Causal question, causal model, and causal estimand
- Describe the observed data
- Assess identifiability: Can the proposed study provide an answer to our causal question?
- Define the statistical estimand
- Choose a statistical model and estimator that respects available knowledge and uncertainty based on statistical properties
- Specify a procedure for sensitivity analysis
- Compare alternative complete analytic study designs

Target Trial Emulation

- Eligibility criteria
- Treatment strategies
- Assignment procedures
- Follow-up period
- Causal contrasts of interest
- Analysis plan

ICH E9(R1) Addendum

- Population
- Treatment
- Variable [outcome]
- (Population-level) summary measure
- Intercurrent events

References

1. Goetghebeur, E., et al., Formulating causal questions and principled statistical answers. Statistics in Medicine, 2020. 39(30): p. 4922-4948.

2. Kahan, B.C., et al., Eliminating ambiguous treatment effects using estimands. American Journal of Epidemiology, 2023. 192(6): p. 987-994.

3. Breiman, L., Statistical modeling: The two cultures (with comments and a rejoinder by the author). Statistical science, 2001. 16(3): p. 199-231.

4. Vansteelandt, S. and O. Dukes, Assumption-lean Inference for Generalised Linear Model Parameters. Journal of the Royal

Statistical Society Series B: Statistical Methodology, 2022. 84(3): p. 657-685.

5. Vansteelandt, S. and K. VanLancker, Chasing Shadows: How Implausible Assumptions Skew Our Understanding of Causal Estimands. Statistics in Biopharmaceutical Research, 2024(just-accepted): p. 1-11.

6. Vansteelandt, S., Statistical modelling in the age of data science. Observational Studies, 2021. 7(1): p. 217-228.

7. Hernan, M.A. and J.M. Robins, Causal Inference: What If. 2023: Taylor & Francis.

8. Pearl, J., Causality: Models, reasoning, and inference. Causality: Models, reasoning, and inference. 2000, New York, NY, US: Cambridge University Press. xvi, 384-xvi, 384.

9. Imbens, G.W. and D.B. Rubin, Causal inference for statistics, social, and biomedical sciences: An introduction. Causal inference for statistics, social, and biomedical sciences: An introduction. 2015, New York, NY, US: Cambridge University Press. xix, 625-xix, 625.

10. Dang, L.E., et al., A causal roadmap for generating high-quality real-world evidence. J ClinTransl Sci, 2023. 7(1): p. e212.

11. Hernán, M.A. and J.M. Robins, Using Big Data to Emulate a Target Trial When a Randomized Trial Is Not Available. Am J Epidemiol, 2016. 183(8): p. 758-64.

12. International Council For Harmonisation Of Technical Requirements For Pharmaceuticals For Human Use. Addendum on estimands and sensitivity analysis in clinical trials to the guideline on statistical principles for clinical trials E9(R1). 2019; Available from: https://database.ich.org/sites/default/files/E9-R1_Step4_Guideline_2019_1203.pdf.

13. Rosenbaum, P.R. and D.B. Rubin, The central role of the propensity score in observational studies for causal effects. Biometrika, 1983. 70(1): p. 41-55.

14. Zalla, L.C. and C.R. Lesko, RE: "Eliminating ambiguous treatment effects using estimands". Am J Epidemiol, 2023. 192(6): p. 1029-1030.

15. Prosepe, I., et al., The disconnect between development and intended use of clinical prediction models for Covid-19: a systematic review and real-world data illustration. Frontiers in Epidemiology, 2022. 2: p. 899589.

16. Sperrin, M., et al., Using marginal structural models to adjust for treatment drop-in when developing clinical prediction models. Statistics in medicine, 2018. 37(28): p. 4142-4154.

17. van Geloven, N., et al., Prediction meets causal inference: the role of treatment in clinical prediction models. Eur J Epidemiol, 2020. 35(7): p. 619-630.

18. Luijken, K., et al., Risk-Based Decision Making: Estimands for Sequential Prediction Under Interventions. Biom J, 2024. 66(8): p. e70011.

Region News

Austro-Swiss Region (ROeS)

ROeS 2025 Conference

The preparations for our 34th ROeS conference have already started and the conference will take place from 14-18 September 2025, at the Medical University of Graz, Austria. Our conference theme is "Empowering Statistical Methods: Connecting Theory and Application." More information, e.g., the key dates, are available on our homepage: www.roes2025.at. We are looking forward to welcoming you to Graz.

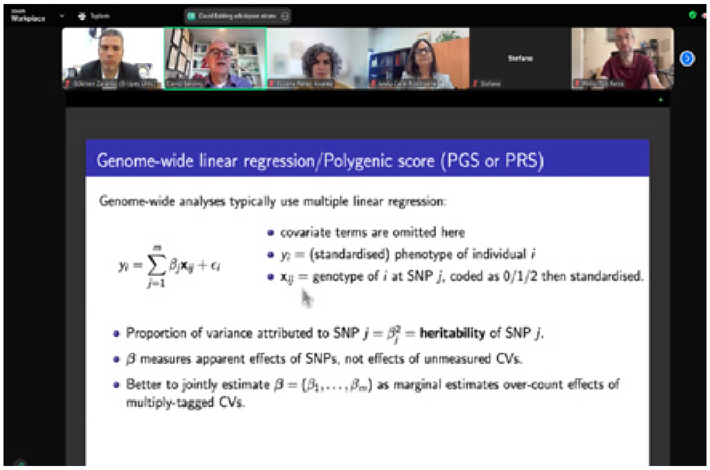
The ROeS 2025 Conference will take place in the beautiful city of Graz © Graz Tourismus - Harry Schiffer

Sonja Zehetmayer
Biometric Bulletin Correspondent

Eastern Mediterranean Region (EMR)

Joint Webinars Between Eastern-Mediterranean, Italian and Spanish Regions of the IBS

The 3rd webinar in the joint series between the Eastern-Mediterranean, Italian, and Spanish regions of the IBS was both successful and highly fruitful. Prof. David Balding's insightful presentation on "Genome-wide genetic models for association, heritability analyses, and prediction" sparked engaging discussions and provided attendees with a deeper understanding of advanced genetic modeling approaches.



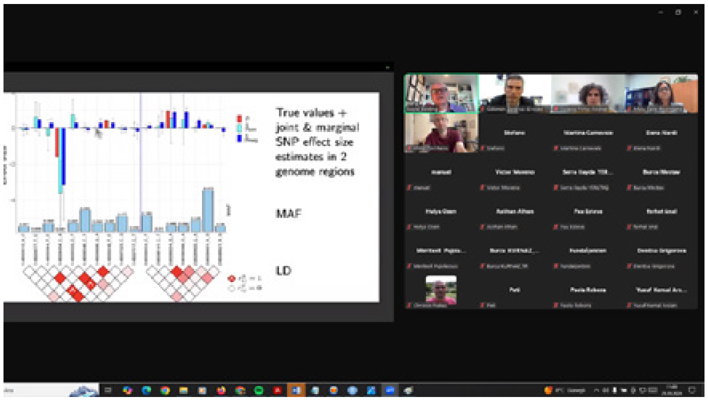
Genome-wide linear regression/Polygenic score (PGS or PRS)

Genome-wide analyses typically use multiple linear regression:

$$y_i = \sum_{j=1}^{m} \beta_j \mathbf{x}_{ij} + \epsilon_i$$

- covariate terms are omitted here
- y_i = (standardised) phenotype of individual i
- $\mathbf{x}_{ij}$ = genotype of i at SNP j, coded as 0/1/2 then standardised.

- Proportion of variance attributed to SNP $j = \beta_j^2$ = **heritability** of SNP j.
- β measures apparent effects of SNPs, not effects of unmeasured CVs.
- Better to jointly estimate $\beta = (\beta_1, \ldots, \beta_m)$ as marginal estimates over-count effects of multiply-tagged CVs.



David Balding *giving a webinar about "Genome-wide genetic models for association, heritability analyses and prediction."*

Necla Kochan
Biometric Bulletin Correspondent

French Region (RF)

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

The annual joint conference of the "Statistics and Health" axis of the CNRS Math-Bio-Health thematic network, the group "Biopharmacy and Health" of the French Society of Statistics (SFdS) and the French Region of the IBS (SFB), was held 21-22 November 2024 in a snowy Paris Santé Campus. Julie Bertrand (Inserm IAME, Paris), the invited speaker for the SFB, gave a presentation on "Nonlinear joint models for drug development." Other invited speakers were Agathe Guilloux (Inserm-Inria HEKA, Paris) on "Advances and pitfalls of AI for prognostic medicine." as well as Sandrine Guilleminot and Estelle Lambert who presented "Statistical challenges at Servier." Coming events of the French Region of the IBS include:

- The Young Researcher Day 22 January 2025 in Bordeaux, France, during which the Biennial Daniel Schwartz dissertation prize will be awarded to Marinna Gaudin and Kateline Le Bourdonnec.
- The Annual General Meeting 28 January 2025 online.

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

Anne Thiebaut
Biometric Bulletin Correspondent

German Region (DR)

Non-Clinical Statistics Conference

The Non-Clinical Statistics Conference 2024, organized by the IBS Belgian Region, i.e. the Quetelet Society, and the IBS German Region working group Nonclinical Statistics, took place in Wiesbaden, Germany, from September 25-27. Nearly 120 colleagues from different major pharmaceutical companies, CROs, academia, and regulatory bodies attended this extraordinary conference – an impressing number of participants, underlining the conference's top quality.

It was a great pleasure to listen to excellent talks held by outstanding invited speakers – "Borrowing from external data in early clinical trials using Bayesian methods" by Annette Kopp-Schneider (DKFZ Heidelberg), "Current uses of AI in the medicinal product lifecycle" by Liam Childs (Paul-Ehrlich-Institut), "Synergizing statisticians and scientists: the essential 'salt' in CMC process development" by Silke Werz (Roche), "Open Source: from Statistical Computing to Generative AI" by Tobias Verbeke (OpenAnalytics), and "Beyond the Bench: Bridging Biostatistics and Biomedical Research for Reproducibility and Translation" by Ulrich Dirnagl (Charité Berlin) – and to attend a panel discussion on "Patient-Centric Drug Product Quality Specifications", which was chaired by Stan Altan (Johnson & Johnson) and included four excellent panelists: Hans Coppenolle (Johnson & Johnson), Katharina Reckermann (Roche), Sandra Suarez Sharp (Simulations Plus, formerly FDA), and Trine Kvist (Novo Nordisk). In addition, approximately 50 talks covering a wide range of topics, including early discovery, toxicology, translation into the early clinic, CMC (chemistry, manufacturing, and controls), artificial intelligence and many more, turned this conference into a great success.

Foto (IBS-DR): Organizers of the Non-Clinical Statistics Conference.

To find out more details about the program, please visit the conference website at: https://ncs-conference.org.

Bernd-Wolfgang Igl

Drug Development in Rare Diseases

The Pharmaceutical Research Working Group convened in Munich on November 29th, 2024. The event, hosted by Staburo, saw the participation of 150 attendees.

It commenced with opening remarks from Bavarian Minister of Health, Care and Prevention Judith Gerlach and Anne-Laure Boulesteix, President of the German Region of the International Biometric Society (IBS-DR) and professor at Munich University.

The agenda featured several insightful talks, including:

- "Virtual Control Arms in Early Clinical Development" by Michael Kunz (Bayer AG)
- "Creating Value with Bayesian Borrowing and Synthetic Patients at Boehringer Ingelheim" by Oliver Sailer (Boehringer Ingelheim Pharma GmbH & Co. KG)
- "Combining RCT and RWD in Rare Diseases" by Tim Friede (University Medical Center Göttingen)
- "Rare Disease" by Franz König (University of Vienna)
- "Evidence Synthesis: An RShiny Tool for Matching-Adjusted Indirect Comparisons - Overview on the Tool, Possibilities, Limitations, and the Role of the Statistician" by Tobias Bluhmki and Katrin Kupas (Bristol Myers Squibb)

These presentations were followed by a panel discussion with Tobias Mielke (Janssen-Cilag GmbH), Tim Friede, Franz König, Tobias Bluhmki and Katrin Kupas moderated by Hans-Juergen Lomp (Freelance Statistical Advisor).

Frank Langer

Hierarchical models in preclinical research

Working groups Non-Clinical Statistics and Bayes-Methods met December 5-6 in Göttingen for a joint workshop on "Hierarchical models in preclinical research" in the hybrid format. Nearly 60 participants, half of them in presence, enjoyed the excellent tutorial "Applied modelling in drug development via brms" by Sebastian Weber and Lukas Widmer (both Novartis AG, Basel). The four parts: „Historical controls", „Dose finding (nonlinear Emax models, model averaging)", „Mixed models with repeated measurements" and „Longitudinal data" stretched over both days. After short theoretical introductions, R code and exercises were shared and results discussed.

The six contributed talks were similarly varied. On the first day, Lea Vaas (Bayer AG, Berlin) spoke on "Virtual control groups in toxicity studies", Jonathan Rathjens (Chrestos GmbH, Essen) on „Prediction intervals based on historical controls for the micronucleus test", and Reinhard Vonthein (Lübeck University) on „A study in which I could not help, not even with Bayesian hierarchical models". The lively discussion was carried on in the evening at a restaurant. The second day started with „Assessing the relative effect in hierarchical binomial models for meta-analysis" by Renato Pennaro (Göttingen University Medical Center), a stratified approach to meta-analysis of studies, that respects randomization while using rare events in an efficient way. Christian Röver (Göttingen University Medical Center) gave the big picture "Prior distributions from meta-analytic predictions". Matthias Kloft (Marburg University) introduced an application-tailored location-scale model with a link function from compositional analysis in his talk „The interval truth model: A cultural consensus model for continuous bounded interval responses".

Special thanks are due to Christian Röver and his co-workers at Göttingen University for the perfect organization. Abstracts, presentation files, and teaching material are accessible via the websites of the working groups. https://www.biometrische-gesellschaft.de/arbeitsgruppen/bayes-methodik/workshops/2024-goettingen.html

Foto (IBS-DR): Participants of workshops „Hierarchical models in preclinical research".

Bernd-Wolfgang Igl, Reinhard Vonthein

Upcoming Meetings

February 24-27 2025 in Regensburg
English language two-day tutorial "Bayesian Adaptive Trials" and two-day workshop of transregional working group "Adaptive Designs and Multiple Testing Procedures"
https://admtp.github.io/ADMTP2025/

March 19-21, 2024 in Bonn
10th conference "Survival Analysis for Junior Researchers"
https://safjr2025.uni-bonn.de/

March 24-28 2025 in Berlin
DAGStat Conference, i.e. triennial joint meeting of several learnt societies of statisticians, including the German Region of IBS.
https://dagstat2025.de/

June 2-5 2025 in Strobl am Wolfgangsee (Austria)
Sommer school "Longitudinal and Incomplete Data" with Geert Molenberghs and Anna Ivanova (both Universities Hasselt & Leuven). Registration is possible until Februar 1, 2025.
https://www.biometrische-gesellschaft.de/fileadmin/1_Daten_Haupt-Website/Docs_Termine/2025_Sommerschule_Strobl.pdf

June 26-27 2025 in Karlsruhe
Summer conference of the working group Landwirtschaftliches Versuchswesen at LTZ Augustenberg with the main topic: "From theory to reality: approaches for experimental systems with limited randomisation and repetition possibilities'
https://www.biometrische-gesellschaft.de/arbeitsgruppen/landwirtschaftliches-versuchswesen.html

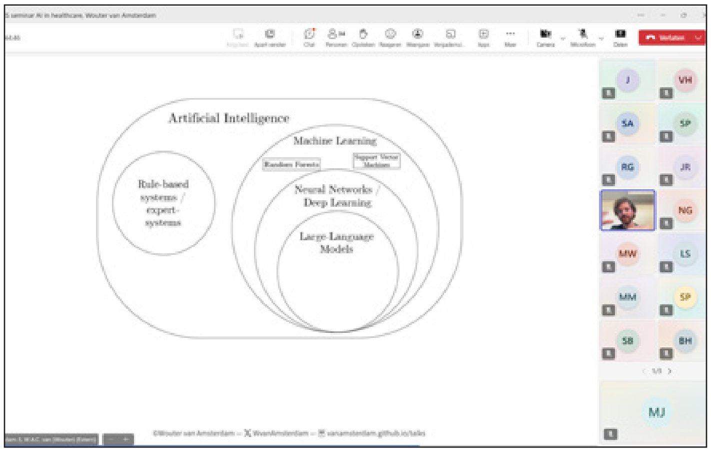
Reinhard Vonthein
Biometric Bulletin Correspondent

The Netherlands Region (ANed)

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

Wouter van Amsterdam: Speaker of online seminar

As part of our ongoing series of online seminars in Biostatistics we are honoured that Wouter van Amsterdam from the University Medical Center in Utrecht presented on Thursday, 26 September 16h-17h on: "AI in healthcare." Presentation slides are available online. The seminars aim at a broad biostatistical audience, in particular PhD students. Similar to the previous online sessions this seminar was attended by many PhD students, but also more senior statisticians. For our next BMS-ANed activity, we are delighted to host Dimitris Mavridis from the University of Ioannina, who will give the tenth online seminar in the Biostatistics Seminar Series on Thursday, 30 January16h-17h on: "A gentle introduction to network meta-analysis. Current state and future challenges." The abstract and link to follow Dimitris' talk will soon appear online. An update will follow on the next issue!



Kit Roes: Speaker of course "Data and Safety Monitoring Boards (DSMBs)

We announced that nominations for the Hans van Houwelingen Biometry Award 2025 are now welcome. Every two years, the BMS-ANed rewards the best paper published in a refereed journal in the Biostatistics and Biometrics field. The eligibility criterion is that the first author has a Dutch affiliation (as indicated in the manuscript) or Dutch nationality. This time the award will cover papers published in 2023 and 2024. The winning paper will be chosen by an international jury installed by the board of BMS-ANed.

Nominations, including a PDF of the article, should be sent before 17 January 2025, to the BMS-ANed board: bmsaned@gmail.com. Only one 'first author' paper can be submitted per person. The conditions and previous winners of the Hans van Houwelingen Award can be found online.

On 27 November 2024 the BMS-ANed board organized in Utrecht (Vredenburg 19) a full-day course for methodologists interested in serving on Data and Safety Monitoring Boards (DSMBs). The course was given by Prof. Kit Roes (Radboud UMC), Prof. Saskia le Cessie (LUMC), and Dr. Rob Kessels (Utrecht UMC). The course combined expert-led lectures with interactive small group sessions, where participants worked through practical scenarios that reflect the challenges faced by DSMBs. Both junior and senior methodologists attended the course, actively engaging in stimulating discussions and sharing their experiences.

Finally, we are now making preparations for our next BMS-ANed meeting on Friday 20 June. More information will follow on the next issue!

Roula Tsonaka
Biometric Bulletin Correspondent

Polish Region (GPol)

The 53rd International Biometric Colloquium was held in Poznań from 8-11 September 2024. The conference was organized by the Polish Biometric Society in collaboration with the Department of Mathematical and Statistical Methods at the Poznań University of Life Sciences, the Department of Mathematics and Computer Science at the University of Life Sciences in Lublin, and the Department of Genetics, Plant Breeding, and Bioresource Engineering at the University of Warmia and Mazury in Olsztyn. The event took place on the campus of the University of Life Sciences in Poznań, hosted in the picturesque Runge College building.

Tour participants at the center point of Poznań.

The conference featured eight oral sessions, primarily conducted in English, during which 36 research presentations about new advances and research results in the fields of mathematical statistics and biometry were delivered. Participants represented a wide range of countries, including the Czech Republic, France, Germany, Poland, Portugal, the Republic of Serbia, Switzerland, and Turkey. Attendees had the opportunity to enjoy cultural and social activities, such as a performance by the Laptop Orchestra and an excursion to the Ciphers Museum and Poznań's historic Old Town. A meeting of the Scientific Committee of the Polish Biometric Society also took place during the event, focusing on the organization's future plans and upcoming conference.

The event provided an excellent platform for scientists from across Europe to exchange ideas, share research findings, and foster professional collaborations.

The participants of the 53. International Biometrical Colloquium on the University of Life Sciences in Poznań campus.

Elzbieta Kubera
Biometric Bulletin Correspondent

Western North American Region (WNAR)

2025 WNAR/IMS meeting

The 2025 WNAR/IMS meeting will be held in Whistler, BC, Canada, from 15-18 June 2025. Whistler is 75 miles (120 km) north of Vancouver, B.C. The town includes Olympic Village and is a compact, chalet-style pedestrian village at the base of the Whistler and Blackcomb mountains. Whistler is a year-round destination that provides a true Canadian west coast mountain experience and offers a wide selection of restaurants, bars, spas, boutiques, and activities. Whistler's summer experiences offer a range of adventure from the legendary Bike Park and championship golf courses to glacier-fed lakes and alpine hikes. There will be short courses, a plenary lecture, invited and contributed sessions, young investigator events, and a Student Paper Award with oral sessions. Lihong Qi (UC Davis) is the WNAR program chair, and Catherine Lee (UCSF), Yuchen Han (CU Anschutz), and Zhixin Lun (CU Anshutz) are serving on the program committee along with WNAR President David Rocke (UC Davis). The Local Organizing Committee Chair is Michelle Miranda (University of Victoria). Registration information and other details about the meeting will be available on the WNAR web page www.wnar.org/wnar2025.

2025 WNAR/IMS Session Proposals

Invited session proposals were due 15 January 2025. Contributed session proposals will have a later deadline. Please see www.wnar.org/wnar2025 for details and submission forms. Email wnarprogramchair@gmail.com with questions.

2025 WNAR Diversity Workshop

WNAR Diversity Workshop is a satellite workshop held in conjunction with WNAR for underrepresented students, and it emphasizes the importance of mentorship and belonging in the health and science fields. It is organized by the WNAR Justice, Equity, Diversity, and Inclusion (JEDI) Committee and the WNAR Leadership Committee. Details will be posted on the WNAR 2025 meeting website as they become available.

2025 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 2025 WNAR Student Paper Competition, registration information, and program details for the meeting will be posted as they become available.

WNAR Indigenous Student Travel Award

WNAR offers a travel supplement for an Indigenous student from within the WNAR region attend our annual conference. Eligible students include Indigenous peoples of North America and the Pacific Islands. To apply, please send a letter outlining your connection to Indigenous peoples and why you are looking forward to attending the WNAR annual conference, to: wnar@wnar.org. Please encourage your students to apply.

Deadline for applications is 1 May 2025.

Jessica Minnier
Biometric Bulletin Correspondent

Laureates of the Second Rousseeuw Prize for Statistics

Caption: (from l to r: Daniel Yekutieli, Yaov Benjamini, Ruth Heller, and Peter Rousseeuw (sponsor). copyright "© KU Leuven – Johan Van Droogenbroeck