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# 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

A lot has changed in the world since my last President's Corner column, with the most consequential change certainly being the advent of the war in Ukraine. My thoughts and wishes of peace are with the Ukrainian people and all others who are suffering the consequences of this tragic humanitarian crisis. There is dim hope of a diplomatic breakthrough leading to an end to the war in the near term, but it may be all we can wish for, at this point.

A considerable amount of the IBS Officers' time over the past couple months has been dedicated to IBC2022, the critical decision on how to move forward with holding an in-person meeting in Riga, Latvia, on July 10-15. Initial concerns on that front were mostly related to the evolution of the COVID-19 pandemic and associated local guidelines and restrictions in Latvia. Following the Omicron wave of earlier this year, the outlook of the pandemic has improved considerably, and restrictions have been lifted in most places, including Latvia. The war in Ukraine has become a more pressing concern to us, including its potential impact on IBC2022. The IBS leadership, in collaboration with members of the Local Organizing Committee (LOC), venue representatives and other local partners in Riga has been closely monitoring the situation in Latvia: the consensus position is that the chances of the conflict in Ukraine expanding to a NATO country (such as Latvia and other Baltic countries) remain quite small. With the date of the conference fast approaching, we reached a decision point on holding an in-person conference in Riga. Because of the proximity to the date of the meeting, converting it to a virtual or hybrid format would be too costly, if at all feasible. The only two realistic options were to proceed with the in-person conference as planned or to cancel it altogether. After considering all information available to us at this point and evaluating the implications of each alternative (including, but not limited to, the financial losses that would be incurred by the Society), the Officers reached the decision to proceed with the plans for an in-person IBC2022 in Riga, which has been ratified through a vote of the Executive Board (EB). We will of course continue to closely monitor the situation in Latvia and surrounding countries, regarding the evolution of the war in Ukraine and the COVID-19 pandemic, re-evaluating the plans for the conference as needed, with the safety of the conference attendees being of paramount importance to us. I am really looking forward to seeing many of you in Riga, enjoying once again a vibrant, in-person scientific conference of the highest caliber, with all the networking opportunities the IBC has to offer.

While the focus has been on this year's conference, plans for IBC2024 in Buenos Aires, Argentina, are well underway. Dimitris Rizopoulos (Netherlands region) has been nominated chair of the International Program Committee (IPC) and has already made great progress in selecting members for the IPC, which should be completely formed and approved by the EB by the

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## Region Key

### Regions

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

### Networks

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

# President's Corner

*Continued from p. 1*

time of IBC2022. The LOC for the conference has already been selected, being formed by members of the Argentinean region and chaired by its current president, Silvia Sühring.

It has also been a busy period on the IBS 75th Anniversary celebration front. The group established to plan activities to mark the occasion throughout the year, formed by members of the Committee on Communications and the IBO (and led by Stephanie Roll, chair of the Committee on Communications) has been hard at work, meeting on a biweekly basis and has already rolled out several of the ideas that came out during their discussions. I encourage you to check out the 75th Anniversary Corner column in this bulletin for further details and to actively engage in the activities the planning group has made available to the entire IBS membership.

In closing, I would like to acknowledge the passing in March of two past IBS Presidents: Pierre Dagnelie (Belgian region, 1984-1985 term) and Niels Keiding (Nordic-Baltic region, 1992-1993 term). Both were giants in the statistical profession and made highly impactful contributions to the IBS during their long and productive careers. The IBS has been shaped by leaders such as Pierre and Niels and it is upon all of us to carry on their legacy moving forward. I encourage you all to read the touching in memoriam remarks on Pierre and Niels that have been posted in the IBS Members Community.

**José Pinheiro**
**International Biometric Society President**
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# From the Editor

Through this issue of the Bulletin, I wish to draw the attention of the regional office bearers, hopefully already busy planning and organizing the best feasible academic events during this special year of IBS. Although, per a critical review of the regional reports, not much planning of the special events are visualized so far, I am sure it must be in making. Furthermore, in continuity with our earlier requests and the commitment to celebrate the long successful journey of IBS, we once again promise that the special slots would be made available to accommodate the regional information updates in upcoming September and December 2022 issues of the Bulletin. Rather, we shall eagerly be looking forward to receiving them in the coming months. Also, as already hinted a special issue of the Bulletin should be published if updates par-excellence are received simultaneously almost from all the thirty-five regions of IBS. Additionally, quite exciting is to go through the section in this issue '75th Anniversary Call for Stories – Share Them Now!' under the quite informative and not to be missed 'Anniversary Corner – The Celebration Starts at the IBC'. I would further list; Oh' how nostalgic or nostalgia-inspiring it is to go through 'The Process of Writing the IBS History' under the column 'History of the International Biometric Society' being published. We all must have the advantage of reading those 2 or 3 pages.

The most recent decisions and assurances with regards to IBC2022 are clearly spelt out in 'President-Corner' and also the latest preparation details with specific information to participants are well outlined under 'International Biometric Conference' caption. Hopefully, as usual the members shall enjoy reading 'Software corner' and STRATOS columns. Per the recent decisions we shall continue to encourage the periodic coverage of successful regional efforts of excellence, as in the previous issue we brought out 'Editorial updates' from 'Biometrical Journal' also in addition to line-listing of the featured articles of interest from 'Biometrics' and 'JABES'. Once again this time we do not have any response to the editor.

I wish to share that a special issue in Frontiers Digital Health has just been launched on "Challenges and Advances in Long-term Forecasting in the Health Sciences". Please refer to the link to their call: https://www.frontiersin.org/research-topics/36584/challenges-and-advances-in-long-term-forecasting-in-the-health-sciences

Suggestions are invited from the members to enhance and enrich the contents of the Bulletin during this special year of IBS. Say, I am thinking of publishing a series of photographs, of course-if available, of our past Presidents and other key officials along with a couple of lines dedicated to them, and so on. Your valuable inputs are welcomed please.

**Ajit Sahai**
Biometric Bulletin, Editor

# 31ST INTERNATIONAL BIOMETRIC CONFERENCE

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

## TOPICS

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

## KEYNOTE SPEAKER

David Madigan, Ph.D.

## REGISTER NOW AT IBC2020.ORG

# International Biometric Conference

Thank you in advance to the Nordic-Baltic Region of the International Biometric Society, the International Program Committee, and all volunteers for what is expected to be a very successful conference! Our organizers, the IBC Organizing President and the current leadership and staff addressed a wide array of challenges, some of which should be expected, and many that were not. Who knew that a second conference might be adversely affected by the pandemic, not to mention the invasion of Ukraine? Through it all, the planning group maintained a steady hand and communicated our progress to members. In the end, and given feedback from many members and with the approval of the Executive Board, the decision was made to move forward with the meeting. We hope that all who are fortunate to join us in Riga will experience a conference that meets your expectations.

For those of you unable to travel to Riga, our intention is to share many of the presentations from the conference in a recorded format. We expect most of this content to be available before the end of July. More information on this option will be offered in a separate communication. A full IBC 2022 report will be provided in our 3rd quarter edition of the Biometric Bulletin.

## IBC 2022 Schedule for Contributed Oral/ Poster Presentations

Click here for a list of all Oral and Poster presentations expected to be held during IBC 2022.

## LMIC Travel Award Winners Announced

As many of you know, travel awards are provided through the generous contributions of the IBS Regions, International Biometric Society (IBS) and individual members. The awards serve to assist IBS members from lower and middle-income countries (LMIC) as they make travel arrangements for the International Biometric Conference (IBC). The International Business Office (IBO) received nearly 80 applications for the IBC travel awards funds grant this year. Of those applications, 18 travel grants were awarded to a mix of IBS Regular and Student LMIC members.

**Congratulations to the following:**
Abukari Alhassan - Ghanian (GGha)
Atinuke Adebanji - Ghanian (GGha)
Cecilia Bruno - Argentinean (RArg)
Paulo Henrique Sales GuimarÃ£es - Brazilian (RBras)
Monica Balzarini - Argentinean (RArg)
Ebun Dosumu - Nigerian (GNi)
Zakir Hossain - At-Large Member
Jupiter Simbeye - Malawi (GMAL)
Gajendra Vishwakarma - Indian (IR)
Yankam Brenda - Nigerian (GNi)
Collins Okoyo - Kenyan (GKe)
Chisimkwuo John - Nigerian (GNi)
Nicholas Siame Adam - Malawi (GMAL)
Carlyle McCready - South African (GSAf)
Charles Natuhamya - Ugandan (UGANDA)
Zvifadzo Matsena Zingoni - At-Large Member
Carol Ogira - Kenyan (GKe)
Mustafa Mumtaz - Pakistan (PKSTAN)

## IBS Major Award Winners Announced

The Representative Council of the IBS is charged with reviewing and voting on the selection of the Society's major awards from many submissions during every even-numbered year, and we wish to thank Chair Agnes Kiragga and all members who participated in this process during the current term. These major awards are bestowed upon worthy recipients and are typically presented during the IBS Awards Ceremony at the International Biometric Conference. This year will be no exception. We are pleased to honor some of our most deserving members during our next IBC, scheduled for July 10-15 in Riga, Latvia.

The **Rob Kempton Award for Outstanding Contributions to the Development of Biometry in the Developing World** will be bestowed upon Mary Lou Thompson, of the Western North American Region. Mary Lou is known for her passion and contributions towards the further development of biometry and biostatistics in South Africa.

**Elizabeth Thompson (WNAR), Jean-Louis Foulley (French), and Lynne Billard (ENAR)** will all be named Honorary Life Members during one of two IBC 2022 awards ceremonies in Riga. Congratulations to our three newest and highly distinguished Honorary Life Members of IBS.

And finally, the **Award for Outstanding Contribution to the Development of the IBS** will be presented to **Jürgen Kübler of the German Region,** to honor his significant contributions to the development of the Society and the Region, not to mention cross-region collaboration within the IBS.

Look for more IBC awards announcements and details regarding these major award winners' accomplishments, which will be shared following the completion of the IBC. We encourage all to join us for the IBS Awards Ceremony in Riga on 12 July. Congratulations to these winners!

## Tours offer an Excellent Local Mid-Week Experience at the IBC

It is a tradition that the IBC offers attendees a midweek break, during which they can explore the host city, the surrounding countryside, and the people of Riga. IBC attendees may register now for a variety of optional tours and excursions that are sure to add many happy memories to your conference experience. Visit https://www.ibc2022.org/info2022/tours-excursions for more information. Thanks to our conference organizers and the Nordic-Baltic Region for their suggestions!

## Download the IBC 2022 Mobile Application

For this year's IBC, we and our supporters have an opportunity to serve our audience while also serving the planet. We see the importance of recycling programs, clean air and water, and the need to preserve our natural resources. The Society is taking steps to limit paper programs, increase the use of recyclable materials throughout the conference, and expand its recorded session and mobile application offerings. For 2022, we have decided to offer our full conference program only through the IBC mobile application this year. A shorter program-at-a-glance will be offered to those unable to download or access information and schedules through our mobile app or the IBC website. Visit https://www.ibc2022.org/home for more information and to begin the app download process.

## Accommodations Still Available

As of this printing, rooms were still available at the Radisson Blu Latvija Conference & Spa Hotel, considered the host hotel for IBC 2022 and the location for all scientific sessions. Please use code "IBSIBC" when reserving your room.

If you are having difficulty with booking your room on the hotel website, the hotel recommends trying the following browsers:

Google Chrome - New Incognito window (Ctrl+Shift+N)

Microsoft Edge - New Incognito window (Ctrl+Shift+N)

Mozilla Firefox - New Private window (Ctrl+Shift+N)

A list of alternate hotels may also be found here: https://www.ibc2022.org/info2022/hotel-info

## Future Conferences:

**XXXII International Biometric Conference (IBC2024)**

Early December 2024 - Buenos Aires, Argentina

**XXXIII International Biometric Conference (IBC2026)**

Northern Hemisphere Summer, 2026 - Seoul, Korea

## Anniversary Corner – The Celebration Starts at the IBC

If you'd like to be among the first to celebrate the Society's 75th anniversary, the best way to do that is to join us in Riga, Latvia for the 75th Anniversary Gala Dinner. The dinner will take place at the Society House Riga on Thursday, 14 July 2022, starting at 18:45 local time. The evening will start with a cocktail reception, followed by a meal with local flavor worthy of this IBS milestone. A local dance troupe will provide entertainment for the evening, and the venue will be bathed in classic "IBS blue". Best of all, the venue for our gala is located within walking distance of our host hotel! Tickets were still available at the time we published this edition of the Biometric Bulletin. Let's raise a glass to the anniversary! For the latest information on the Gala Dinner, visit https://www.ibc2022.org/info2022/ibc2022-gala.

There's more anniversary programming planned for the IBC in Riga. **A special 75th anniversary session,** featuring past presidents of the Society, is planned for 12 July. Registration to the IBC is required for entry. More information is available at https://www.ibc2022.org/home.

Can't make the IBC, but still want to participate? Take part in the **"Call for Stories"** campaign by submitting an interview, photo or e-mail to the Society. Look for more details in the companion article in this issue of the Biometric Bulletin.

Also, mark your calendars for the official start of the celebration on **5 September 2022**.

And in September, we will launch our brand-new **Distinguished Lecture Series**. This series will be offered virtually via Zoom. Joining us for our first Distinguished Lecture will be featured speaker E**ric J. Tchetgen, Professor of Statistics and Data Science from the University of Pennsylvania**. As you know, the IBS is something of a unique society because of its international footprint, so the new series offers a powerful outreach opportunity. We hope that, among other things, this virtual series might offer inspiration to the next generation about how they can succeed in their careers. Eric's story is a powerful one, and we are honored that he has agreed to share his story with us this September. More information and instructions on how to register will be shared through the IBS Members Community and at www.biometricsociety.org.

Finally, as a reminder, we are still collecting **"fun facts"** about the IBS and its history. Have something to contribute? Send them to llane@bostrom.com . We'd love to hear and to share what you know! For instance, can you name the three newest Regions of the Society? Here they are… 2017: Tanzanian, 2016: Malawi, 2015: Ecuadorian.

Be sure to check our next update in the *Biometric Bulletin* for more anniversary news!

Respectfully,

Peter Doherty, CAE, Executive Director

## 75th Anniversary Call for Stories – Share Them Now!

The IBS celebrates its 75th anniversary in 2022. **We would like to capture the experiences, history, and dreams of our members through a series of interviews, representing every region of the world.**

As part of this project, we'd love to share your personal story with Society members! We have compiled a list of questions to help support your interviews. We are happy to share this list upon request. Interviews may be conducted in audio or video format, or even via e-mail! You may also submit a self-recorded video or audio file if you'd prefer. And we can even provide you with an anniversary background for web-based interviews if you'd like!

Interviews are now being accepted through June 30, 2022 (for content intended for use at the IBC in Riga) and July 31, 2022 (for content intended for use later this year). We suggest that interviews be no more than 15 minutes in length.

With your approval, interviews will be shared across IBS marketing platforms to help spread the word about the incredible impact that the Society's diverse membership has made, and how they have helped to shape IBS's mission and vision.

Want to learn more? Visit https://www.biometricsociety.org/celebrate-75 and click on the link in the "Call for Stories" section. And please contact Libby Lane (llane@bostrom.com) with questions about the process. We can't wait to feature you at the IBC starting next month!

# History of the International Biometric Society

## The Process of Writing the IBS History

The International Biometric Society (Society) was founded at Woods Hole on September 6, 1947. Records of events leading up to that momentous day, as well as extensive records of events since then, have resided in the Society Archives which for years had dwelt in the various Society Business Offices. The "Business Office" started as a part-time secretary set up in a living room working with/for Chester Bliss, the first Society Secretary. Over the years this evolved into a more formal set-up when in 1969 Larry Nelson became the business manager responsible for the "business" side of Biometrics and the routine tasks of the Society Secretary and Treasurer roles; when Nelson stepped down in 1978, his assistant Elsie Thull took over and the physical office itself moved to rented quarters housed inside the American Statistical Association's (ASA) building. Then, in December 1994 with the duties now too extensive for a single person to manage, the Society moved to a professional management firm to operate its business responsibilities. This evolution is described more fully in the history monograph (see Billard, 2022).

Charlie McGrath was the incoming Executive of this new International Business Office (IBO), and so he was with Elsie on the hand-over day to be apprised of what's what about the office and related issues. Anyone who had visited Elsie in earlier days knew the office was overflowing with files (the Archives in fact). Rather than throwing them out, Charlie phoned me for advice and instructions (I was Society President at the time). Time was of the essence; so it was decided that the files would be boxed up and sent to me and that their future would be determined later. [I did ask that a letter be placed in the current files saying where the archives were being held for safe-keeping.] Thus it was that these Archives found a temporary home in my office. It was quite a surprise to see just how voluminous the files were; of course the Society was almost fifty years old and its officers (Presidents, Secretaries and Treasurers, and regions) for the most part were very assiduous about keeping good records. Even ballots and votes from early days had been kept!

It was many years before I eventually found the time to see what those boxes contained. The first folder pulled out consisted of the Minutes of the meeting on Saturday morning September 6, 1947 at Woods Hole at which the Society was founded. This was fascinating, at least to me, and seemed to speak loudly of pure gold-dust. Another startling find came later when a folder containing letters written to Bliss and Fisher's son with details of Sir Ronald Fisher's death and funeral service appeared. Clearly, these boxes were a treasure trove about the Society. It was also apparent that these materials had to be shared with Society members rather than being hidden away in obscurity; the question was how this could, or should, be done. More time passed, until in August 2010, I phoned then President Kaye Basford. Subsequently, after their September 2010 Executive Committee meeting, Kaye reported back and asked me to write a History of the Society based on the archival files. This became a two-part process; the first focused on Fisher's role in establishing the Society (see Billard, 2014), with the second dealing with the first fifty years of the Society as a whole with no undue focus on any one person though the dominant role played by Chester Bliss cannot be denied (see the monograph Billard, 2022).

Thus, it came to be that I started to read, to digest, to summarize all these pages buried in this gold-mine. Given how extensive the files were, it was essential to set up some sort of realistic procedures to follow. It seemed to me that any one page (of a letter, report, or what-have-you) was extremely valuable, so much so that I did not allow myself the privilege to write on any of these pages (the easy way out). Consequently, after reading a document, a determination was made as to whether or not any part of it was worthwhile to be added to the archival story. If so, a xerox copy was thus made, a note of which folder from which a file drawer was indicated on each copy, and then important pieces highlighted. Setting up a running latex file proved fortuitous, allowing cryptic notes to be added as the reading progressed, and as various heading and/or subheadings suggested themselves. Reading, and copying where deemed important, through all the files essentially took three years. Then, digesting these treasures and starting the serious writing had to begin; this was an approximately two-year process. It would be nice to think that all the components of any one issue/event/story were together in one folder. Unfortunately, nothing could be further from the truth. Remember email and later electronic avenues did not exist, so that most communications were by letter and therefore slow by today's standards; there were also discussions at scientific meetings (especially International Biometric Conferences, IBCs). Rather, the many and various components were typically spread across several folders (and several filing cabinets) across changing guards of officers. For me, this took many readings and re-readings of the notes to pull all relevant parts into their rightful places. It was akin to assembling a gigantic multi-dimensional jigsaw puzzle from millions of pieces but without a guiding picture, i.e., without knowing what that picture/puzzle was.

Once written, checking had to be prominent, had to be careful, and it had to be very faithful to the records. As it happened, the "first" draft consisted of four aspects of our "history" (History H1-2-3-4). The first completed history covered Regions and Groups and Networks (which became three chapters in the monograph). When it came time to cross check this regional sub-history, the expected 2-3 days believed adequate to do this, quickly became 3+ weeks (full-time)! That I had underestimated how long this would take is an understatement. Indeed, cross-checking, and then more cross-checking, became a huge time component of the entire enterprise. By now, I had gained a new respect and understanding of those academics in the arts/humanities who typically wrote one book every five years or so. The so-called eighty-twenty rule reigned supreme.

Another aspect of this History was the task of obtaining photos of players. A few were already housed in the Archives, but not all. Rightly or wrongly, I wanted to showcase a portion of the past as Galleries of the Society officers. I also wanted to include photos of regional officers, especially the regional presidents; but that goal had to be abandoned, as even finding all the presidents of any one region proved impossible. Settling on just the first such regional president was hard enough, though in the end all but one was included. Here, modern technologies such as internet sources were invaluable; but also journal articles from years past were very helpful. A real bonus here for me was reading the many and varied articles by and about so-and-so; some of our earlier leaders were quite the renaissance folks and it was fascinating to learn about them, their science and their non-scientific pursuits. Nevertheless, it took time and it was quite difficult to find some of the needed photos. Towards the end, it became necessary to contact known collaborators and/or departments where those missing-in-action leaders had worked. This proved fruitful. As an aside, quite unexpectedly, when seeking permissions to use the different photos, the relevant persons often replied with a better quality photo than the one I had (my photo had been included in the permission request email, along with reasons as to why their person was important to our story); it almost felt like these folk were joining in with their own excitement of the whole enterprise.

Perhaps the most startling of all these photo searches concerned the first Italian Regional President Claudio Barigozzi. Close to four years had been spent searching high and low for a photo of Barigozzi, to no avail; the IBO even joined the search. Therefore, eventually, I reluctantly gave up that goal. Meantime, in seeking permission to use a certain photo of former Society President Luigi Luca Cavalli-Sforza (1966-67, from the Italian Region), occasion had it that I contacted Anthony W F Edwards (British Region) for permission to use a photo of Cavalli-Sforza that had appeared in one of Edwards's papers; he acceded of course but also gave me a copy of one of his articles about Cavalli-Sforza. By now it was an established custom to read any such proffered article; imagine my ecstatic surprise to see a photo of Barigozzi embedded in another photo in Anthony's article. This elicited more contact with Anthony whereby I learnt that the photo was owned by Cavalli-Sforza's son Francesco. In a matter of days, Francesco not only gave permission for me to crop out Barigozzi, he sent me a different photo of his father (which was the one actually used in the Gallery of Presidents in the monograph). This bonus photo (see below) shows Barigozzi, Fisher and Cavalli-Sforza; what a gem! There have been many enjoyable and unexpected moments as this road was traveled. It is my hope that you too find the journey enjoyable as you read of our Society forefathers, and fore-mothers (we cannot forget Gertrude Cox!), and their roles in fostering the Society to the important place it occupies today.

*Figure 1: Barigozzi's wife, Barigozzi, Fisher, Cavalli-Sforza's wife, Cavalli-Sforza*

**References**

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Billard, L. (2022). The History of the International Biometric Society. 2022. Chapman and Hall, in press (availability expected for/at Riga IBC July 2022).

**Lynne Billard**
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# Editorial Updates

## Biometrics

### September 2022 Issue Highlights

The September issue contains a broad area of Biometric Methodology papers. It opens with a Discussion paper entitled "Estimating vaccine efficacy over time after a randomized study is unblinded," by Anastasios A. Tsiatis and Marie Davidian, and with discussion contributions by M. Elizabeth Halloran; Holly Janes, Fei Gao, and Alex Luedtke; and Dean Follmann. Further papers include: "Multivariate survival analysis in big data: a divide-and-combine approach," by Wei Wang, Shou-En Lu, Jerry Q. Cheng, Minge Xie, and John B. Kostis; "A consistent version of distance covariance for right-censored survival data and its application in hypothesis testing," by Dominic Edelmann, Thomas Welchowski, Axel Benner; "Semiparametric analysis of clustered interval-censored survival data using Soft Bayesian Additive Regression Trees (SBART)," by Piyali Basak, Antonio Ricardo Linero, Debajyoti Sinha, and Stuart R. Lipsitz; "Feature screening with large scale and high dimensional survival data," by Grace Yi, Wenqing He, and Raymond J. Carroll; "Regression with interval-censored covariates: application to cross-sectional incidence estimation," by Doug Morrison, Oliver Laeyendecker, and Ron

Brookmeyer; "Modeling semi-competing risks data as a longitudinal bivariate process," by Daniel Nevo, Deborah Blacker, Eric B. Larson, and Sebastien Haneuse; "Semiparametric estimation of structural nested mean models with irregularly spaced longitudinal observations," by Shu Yang; "A semi-parametric model for between-subject attributes: applications to beta-diversity of microbiome data," by J. Liu, X. Zhang, T. Chen, T. Wu, T. Lin, L. Jiang, S. Lang, L. Liu, L. Natarajan, J.X. Tu, T. Kosciolek, J. Morton, T. Nguyen, B. Schnabl, R. Knight, C. Feng, Y. Zhong, and X.M. Tu; "Spatial correlation structures for detections of individuals in spatial capture-recapture models," by Ben Courtney Stevenson, Rachel M. Fewster, and Koustubh Sharma; "A transformation-free linear regression for compositional outcomes and predictors," by Jacob Fiksel, Scott L. Zeger, and Abhirup Datta; "A Bayesian nonparametric approach for inferring drug combination effects on mental health in people with HIV," by Wei Jin, Yang Ni, Leah H. Rubin, Amanda B. Spence, and Yanxun Xu; "Simulation-based estimators of analytically intractable causal effects," by Antonio R. Linero; and "Testing for association in multi-view network data," by Lucy L. Gao, Daniela Witten, and Jacob Bien.

Also the Biometric Practice section of the journal opens with a Discussion paper, entitled "Distributional independent component analysis for diverse neuroimaging modalities," authored by Ben Wu, Subhadip Pal, Jian Kang, and Ying Guo, and with discussion contributions by Heather Shappell and Sean L. Simpson; Amanda Mejia; Kan Keeratimahat and Thomas E. Nichols; and Beatrijs Moerkerke and Ruth Seurinck. Further, there are articles on "Inferring UK COVID-19 fatal infection trajectories from daily mortality data: were infections already in decline before the UK lockdowns?," by Simon N. Wood; "Efficient detection and classification of epigenomic changes under multiple conditions," by Pedro L. Baldoni, Naim U. Rashid, and Joseph G. Ibrahim; and "Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data," by Lingjing Jiang, Niina Haiminen, Anna-Paola Carrieri, Shi Huang, Yoshiki Vazquez-Baeza, Laxmi Parida, Ho-Cheol Kim, Austin D. Swafford, Rob Knight, and Loki Natarajan.

### 2023– 2025 Co-Editor Search Ongoing

The search committee to identify a successor for Co-Editor Alan Welsh, whose term will end 31 December 2022, is in the process of identifying a successor. The search committee consists of Geert Molenberghs, Biometrics Executive Editor, Chair (Belgian Region); Bill Rosenberger, Biometrics CE (ENAR); Alan Welsh, Biometrics CE (Australasian Region); Katja Ickstadt, Biometrics CE (German Region); Hans-Peter Piepho, EAC Chair (German Region); Andrea Lavalle (Argentinian Region); Liliana Lopez Kleine (Central American & Caribbean Region); Renato Asunção (Brazilian Region).

### Associate Editor Panel Turnover

The panel of Associate Editors is composed of colleagues who each serve two-year terms. This means that every 1 July a number of them end their terms. The Co-Editors are in the process of inviting new Associate Editors to replace colleagues retiring and, in view of the large number of submissions received, also to expand the size of the panel. 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. It aims to have about 100 members, starting 1 July 2022.

### Biometrics Editorial Board Meetings

In pre-pandemic times, in odd-numbered years, it was customary to have an Editorial Board meeting, traditionally coinciding with the North-American based Joint Statistical Meetings, late July or early August. In even-numbered years, there would be two such meetings, including one during the International Biometric Conference in addition to the JSM based meeting. In 2020, two virtual Editorial Board meetings were organized, one in the middle of July and one near the end of the month, at times of day that would allow our truly global panel of Associate Editors to attend at least one of these at a reasonable hour. While this solution was forced upon us by the pandemic, it turned out to be a huge success, in terms of attendance and participation. So, even though we thought in July 2020 that this would be a one-off circumstance, we did the very same thing in 2021.

This year, even numbered and thus with the IBC2022 in Riga, Latvia, coming up, there will be two virtual Editorial Board Meetings (July 7, 2022 and August 3, 2022), but now supplemented with a live meeting during IBC2022. This will give those attending our biennial meeting a chance to interact, while the online meetings will ensure that all can attend a meeting at a date and time convenient to them.

**Geert Molenberghs**
**Biometrics Executive Editor**

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

We have one running Special Issue on Causal Inference with C. Zigler (Cory.Zigler@austin.utexas.edu) and Shu Yang (syang24@ncsu.edu) as guest editors. We are closing this issue, expecting to be ready for the second semester of 2022. If you have a suggestion for a special issue, we would be pleased to hear from you. We are also keen to publish papers that summarize the state of methodological development in subject areas for which technological advances are generating a demand for new statistical approaches. If you feel that you could offer such a paper, or can suggest a topic together with possible authors, please let me know.

We have approached the winners of the 2022 competition of The Section on Statistics and the Environment (ENVR) of the ASA. Their papers are eligible for review in the Journal of Agricultural, Biological, and Environmental Statistics, and we are currently working with some of them.

Authors from selected papers from JABES 2021 will be actively taking part in the upcoming Joint Statistical Meeting in Washington, DC, JSM 2022, in a session entitled "Modern and innovative spatial methods in Ecology and the Environment". The Chair will be Brian Reich and the authors are: David L. Miller (Variance Propagation for Density Surface Models), Giri Gopalan (A Higher-Order Singular Value Decomposition Tensor Emulator for Spatiotemporal Simulators), Théo Michelot (Varying-Coefficient Stochastic Differential Equations with Applications in Ecology), Robert Richardson (Spatial Generalized Linear Models with Non-Gaussian Translation Processes).

The June, 2022 issue of JABES features the following papers:

Bayesian Analysis of Nonnegative Data Using Dependency-Extended Two-Part Models by M Rodrigues-Motta and J Forkman

An Extreme Value Bayesian Lasso for the Conditional Left and Right Tails by M de Carvalho, S Pereira, P Pereira and P de Zea-Bermudez

Estimation of Multivariate Dependence Structures via Constrained Maximum Likelihood by NA Adegoke, A Punnett and MJ. Anderson

Sample Design and Estimation When Using a Web-Scraped List Frame and Capture-Recapture Methods by LJ Young and M Jacobsen

Probabilistic Forecasts of Arctic Sea Ice Thickness by PA Gao, HM Director, CM Bitz and AE Raftery

Population Size Estimation Using Zero-Truncated Poisson Regression with Measurement Error by W-H Hwang, J Stoklosa and C-Y Wang

A Two-Species Occupancy Model with a Continuous-Time Detection Process Reveals Spatial and Temporal Interactions by KF Kellner, AW Parsons, R Kays, JJ Millspaugh and CT Rota

Hidden Markov and Semi-Markov Models When and Why are These Models Useful for Classifying States in Time Series Data? by S Ruiz-Suarez, V Leos-Barajas and JM Morales

Improving Wildlife Population Inference Using Aerial Imagery and Entity Resolution by X Lu, MB Hooten, A Kaplan, JN Womble and MR Bower

Greater Than the Sum of its Parts: Computationally Flexible Bayesian Hierarchical Modeling by DS Johnson, BM Brost and MB Hooten

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).

Please follow us on Twitter: @JabesEditor.
Jorge Mateu
Editor-in-Chief
April 2022

# Software Corner

## Ridge learning of static and dynamic Gaussian graphical models using the rags2ridges and ragt2ridges packages

**C.F.W. Peeters**
**Wessel N. van Wieringen**

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### Brief background

Networks are ubiquitous in modern science. They are a visual means to grasp and communicate a complex of interrelations, providing a systems view on a set of entities. A network is a graph comprising nodes and edges. The nodes depict (the random variables representative of characteristics of) the entities, while the edges indicate relatedness between the node pair that it connects. Networks thus provide an encompassing perspective on the whole in terms of its constituents. This may yield insights not offered by traditional reductionistic (read: univariate) approaches. However, networks are not handed to us by nature but need to be reconstructed from data. Here we briefly illustrate how two R packages, **rags2ridges** and **ragt2ridges**, facilitate network reconstruction.

To reconstruct a network from data we need a link between the data and the network. This link is provided by graphical models. Such models comprise a probabilistic description of the whole and a network that captures certain probabilistic properties of this description. For a static network our probabilistic description is a multivariate Gaussian distribution, while for dynamic networks we assume a vector autoregressive process. For both models, the probabilistic property is some form of conditional (in)dependence. In particular, the (absence or) presence of an edge in the network represents such conditional (in)dependence, respectively. In the case of a static network, the conditional independencies correspond to zeroes in the inverse of the distribution's covariance matrix. Similar parametric criteria for conditional independencies exist in the dynamic network case.

Both packages have been developed to reconstruct networks from high-dimensional data. Such data are typically undersampled in relation to the number of model parameters. This is a common issue in the age of high-throughput techniques. In the biomedical context this issue is often encountered in omics studies, where a patient is characterized by techniques that measure the abundance of many molecule types simultaneously. Such undersampling hampers the estimation of the model parameters. This issue can be overcome by regularization: augmenting the loss function, e.g. the likelihood, with a penalty to ensure a well-defined parameter estimator. Both packages implement methodology that takes a so-called ridge approach to penalization. This is in part motivated by mathematical convenience, but more importantly it aligns with the dense reality of biology.

Below we give a quick taste of the **rags2ridges** and **ragt2ridges** packages to give the reader an impression of what these packages can bring to network reconstruction. We focus on the following situations:

1. Extracting a single network from steady-state data **(rags2ridges);**
2. Simultaneously extracting multiple networks from multiple related data sets and/or data consisting of distinct (disease) subclasses **(rags2ridges)**;
3. Extracting networks from time-course data **(ragt2ridges**).

For each of these situations, the packages provide means to reconstruct and exploit the networks in order to enhance their practical value.

## rags2ridges

We first illustrate the extraction, visualization, and analysis of a single network by means of the **rags2ridges** package. We then shortly turn to the joint extraction, visualization, and analysis of multiple networks.

For our illustration, we employ data stemming from a study into Alzheimer's Disease (AD) that aims to identify disease-specific changes in the underlying biochemical process. Hereto, peripheral fluids of patients have been sampled and interrogated metabolically. The data comprise metabolomic profiles of 127 patients, comprising individuals with (AD class 2) and without (AD class 1) a known genetic predisposition for AD. Each profile contains the abundance of 230 metabolites. These metabolites each belong to one of four compound families: amines, organic acids, lipids, or oxidative stress compounds. More details on the data can be found in de Leeuw et al. (2017). The package and data are loaded into memory by the first few lines of the R-code block below.

```
# needed package
library(“rags2ridges”)

# load, extract and scale data for AD Class 2
data(“ADdata”)
ADclass2    <-    scale(t(ADmetabolites[,sampleInfo$ApoEClass==”Class 2”]))

# precision matrix estimation with given penalty value**
P <- ridgeP(covML(ADclass2), lambda = .15)

# extract Network**
P0 <- sparsify(P, threshold=”localFDR”, FDRcut=.999)

# visualize Network with node-coloring**
PcorP   <- pruneMatrix(P0$sparseParCor)
Colors <- rownames(PcorP)
Colors[grep(“Amine”,      rownames(PcorP))] <- “lightblue”
Colors[grep(“Org.Acid”,  rownames(PcorP))] <- “orange”
Colors[grep(“Lip”,         rownames(PcorP))] <- “yellow”
Colors[grep(“Ox.Stress”, rownames(PcorP))] <- “purple”

# plot network
Ugraph(PcorP, type=”fancy”, lay=”layout_with_fr”,
      Vcolor=Colors, Vsize=7, Vcex=.3)

# find and visualize the communities for the extracted network
Commy <- Communities(PcorP, Vcolor=Colors, Vsize=7, Vcex=. 3)
```

As an illustration we concentrate on the reconstruction of the metabolic network for AD class 2, which comprises 87 individuals. Hereto we fit a Gaussian graphical model. Effectively, this amounts to the estimation of the inverse of the covariance matrix of a multivariate normal. As the variable dimension (230) exceeds the sample size (87), we use ridge-regularization as carried out by the ridgeP-function in the R-code. One then obtains an estimate of the regularized inverse covariance matrix for a given value of the penalty parameter. The value of the penalty parameter can also be chosen in a data-driven manner. For instance, by k-fold cross-validation as provided through the optPenalty-function. The resulting inverse covariance estimate does not harbor any off-diagonal zero entries, i.e. it does not represent a sparse network. For the purpose of network reconstruction, the inverse covariance matrix estimate is ‘sparsified', i.e. its support is determined by the identification of elements that are indistinguishable from zero. The sparsify-function implements several pragmatic but also more sophisticated, probabilistically motivated procedures to this end (such as a local false discovery rate). The sparsified matrix then represents the reconstructed network and can be plotted for visual inspection by the Ugraph-function. Here, we have added attributes to the nodes: they are colored according to compound family (left-hand side of Figure 1). This highlights the role of the compound families in the network topology. The amines and organic acids (light blue and orange nodes) form a core structure, while the oxidative stress and lipid compounds (purple and yellow nodes) can be found more at its periphery.

The rags2ridges-package offers, to enhance the practical value of the results, several options for downstream analysis of the reconstructed network. A natural starting point is the GGMnetworkStats-function that calculates various node statistics like centrality measures. These provide a quantification of the nodes' importance in the network. An alternative analysis, implemented in the GGMpathStats-function, quantifies the contribution of all paths that connect a node pair. This sheds light on the strongest routes by which a signal propagates in the network from one node to the other. A different perspective is provided by community analysis of the network through the Communities-function. This identifies functional modules (or subnetworks) within the full network. The result is portrayed in the right-hand side panel of Figure 1, which overlays the network with the found communities.

All the above functionality has also been implemented in the rags2ridges-package for the multi-group case, with the aim to identify differential network features among groups or subclasses. This implementation carries identical function names suffixed with .fused. The downstream functions implement the same analyses as above, but now executed group-wise. The ridgeP.fused-function, however, performs the joint estimation of multiple, class-specific inverse covariance matrices using a fused ridge penalty. This fusion enables the estimation to borrow information across groups. This may yield estimates that have been shrunken towards each other, should the data support that.

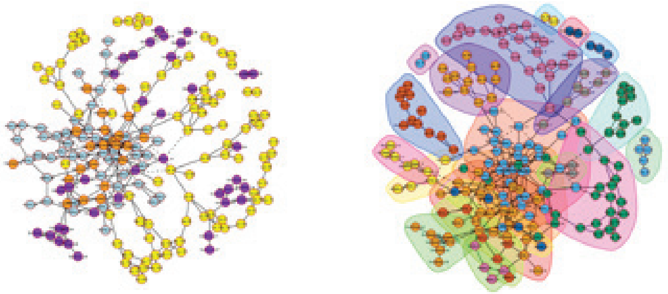


*Figure 1: Left: conditional independence graph with node colors corresponding to metabolite compound family. Right: the conditional independence graph overlayed with communities.*

## ragt2ridges

The **ragt2ridges** package is **rags2ridges**' sister package but focuses on dynamic networks. Like its sister, **ragt2ridges** implements methodology to reconstruct dynamic networks but also provides handles for their downstream exploitation.

A brief illustration of the **ragt2ridges** package uses an in vitro oncogenomics study with a longitudinal experimental design conducted to unravel the dynamic interactions among genes during cervical carcinogenesis. The human papilloma virus (HPV), a carcinogenic entity, is inserted into normal cells, yielding an immortalized cell line that faithfully mimics cervical cancer development morphologically and genetically. As the infected cell line goes through distinct phenotypic phases, cells are profiled transcriptomically at eight time points distributed over the transformation process. The observed changes in transcript levels shed light on the underlying process of carcinogenesis. A full description of the experiment can be found in Babion et al. (2020). The data are loaded into memory by the first few lines in the block of R code below and stored in the Y object of the array class.

```
# load package and data
library(ragt2ridges)
library(Biobase)
data(hpvP53)

# reformat and zero center data
Y <- centerVAR1data(longitudinal2array(t(exprs(hpvP53rna))))

# fit the model
VAR1hat <- ridgeVAR1(Y=Y, lambdaA=100, lambdaP=1)

# support determination
zerosA <- sparsifyVAR1(A=VAR1hat$A,
SigmaE=symm(solve(VAR1hat$P)),
                threshold="top", top=50)$zeros
VAR1hat$A[zerosA] <- 0
VAR1hat$P <- sparsify(VAR1hat$P, threshold="top",
top=10)$sparseParCor

# plot time-series chain graph
graphVAR1(VAR1hat$A, VAR1hat$P,
nNames=featureNames(hpvP53rna))

# motif detection
motifStatsVAR1(VAR1hat$A)
```

The experimental data are analyzed by means of a vector autoregressive (VAR) model, describing the temporal and contemporaneous relations among the genes. The VAR model is a regression-type model. It explains the current vector of observations by linear combinations of the elements of such vectors from preceding time points plus a noise vector. The estimation of the VAR model is however hampered by the high-dimensionality of the cervical cell line data. This is overcome by ridge penalized maximum likelihood estimation of the VAR model as performed by the ridgeVAR1 function in Listing 2. For simplicity, the penalty parameters are set in the R-code but need – of course – be chosen in a more informed fashion by, e.g. a cross-validation scheme as provided through the optPenaltyVAR1-function. The implemented ridge estimation procedure allows for the incorporation of both quantitative and qualitative information regarding the unknown parameters, in particular the absence of temporal and contemporaneous relations. Moreover, attention has been paid to ensure a computational and memory-efficient implementation.

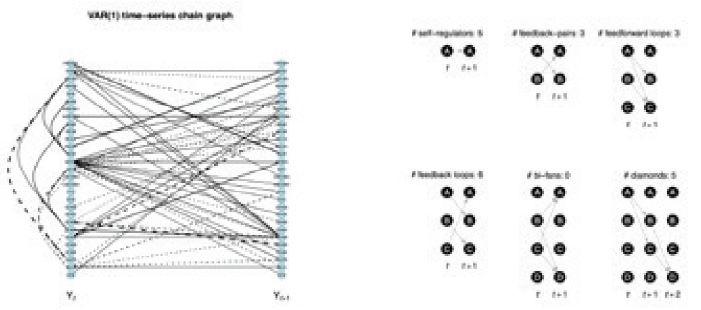


*Figure 2: Left: time-series chain graph with temporal (straight) and contemporaneous (bended) edges. Right panel: visual representation of the motif tally.*

The **ragt2ridges** package offers various strategies for the downstream utilization of the estimated VAR model. For starters, the spasifyVAR1-function provides a selection procedure for the identification of interesting temporal and contemporaneous edges of the time series chain graph. In the R-code above, simply the strongest edges are selected but a more sophisticated, probabilistically motivated option is also implemented. With the support of the time-series chain graph reconstructed, the graphVAR1-function offers various ways to visualize it (see the left panel of Figure 2 for an example). Descriptive node statistics of this network are calculated by the nodeStatsVAR1- and mutualInfoVAR1-functions. Alternatively, the motifStatsVAR1-function tallies network motifs, i.e. subnetworks that are associated with particular dynamic behavior. The right-hand side panel of Figure 2 shows the output of this function. The impulseResponseVAR1-function offers a different view through the quantification of the downstream effect of a node's perturbation.

The illustration and R-code above implicitly center on the use of a VAR(1) model, i.e. a VAR model with lag one. Such a model only uses the directly preceding observation vector to explain the current one. The **ragt2ridges-**package also include functionality to learn a VAR(2) model, a VAR model with lag two. Or, a VARX(1) model, a VAR model with lag one and time-varying covariates.

## Conclusion

We hope to have given a little taste of what our two packages are capable of and how they may assist you in your network analysis. Should you previously not have reconstructed networks from data, we hope that our software exposé lowers the threshold to do so and convinces you that network analysis is worth a try. Finally, should you attend the International Biometric Conference 2022 in Riga, we will teach a pre-conference course that explores the possibilities of these packages more in-depth.

**References**

Babion, I., Miok, V., Jaspers, A., Huseinovic, A., Steenbergen, R. D., van Wieringen, W. N., and Wilting, S. M. (2020). Identification of deregulated pathways, key regulators, and novel miRNA-mRNA interactions in HPV-mediated transformation. *Cancers*, 12(3), 700.

de Leeuw, F. A., Peeters, C. F. W., Kester, M. I., Harms, et al. (2017). Blood-based metabolic signatures in Alzheimer's disease. *Alzheimer's & Dementia: Diagnosis, Assessment & Disease Monitoring*, 8, 196–207.

All code used in this article can be found here.

# STRengthening Analytical Thinking for Observational Studies (STRATOS): Progress in the Topic Group on Evaluating Diagnostic Tests and Prediction Models (TG6)

Ewout W Steyerberg[1], Ben Van Calster[1,2], on behalf of STRATOS TG6

1 Department of Biomedical Data Sciences, Leiden University Medical Center, Leiden, the Netherlands

2 KU Leuven, Department of Development and Regeneration, Leuven, Belgium

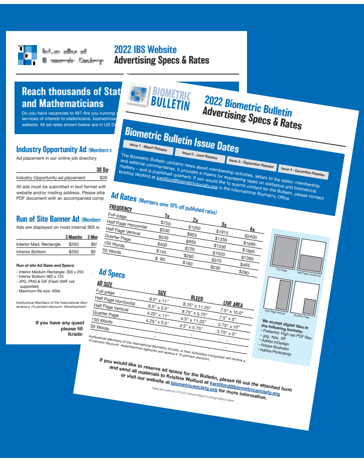
In this note, we provide an update of the exciting activities of TG6 of the STRATOS initiative, which is concerned with Evaluating Diagnostic Tests and Prediction Models. TG6 has links with all other topic groups in the STRATOS initiative, and specifically with TG2 (Selection of Variables and Functional Forms in Multivariable Analysis) and TG8 (Survival Analysis).

Members of TG6 met in 2018 at the STRATOS workshop in Leiden (the Netherlands, https://www.lorentzcenter.nl/the-future-of-statistical-modeling-in-medical-data.html), and another great Banff meeting in 2019 (http://www.birs.ca/events/2019/5-day-workshops/19w5198).

Both workshops had two, closely interrelated, overarching objectives to (i) further boost and consolidate the research activities of the STRATOS Topic Groups, and to (ii) identify and initiate new interdisciplinary collaborations between experts in different areas of statistical methodology, regrouped in different TGs. The members of TG6 agreed on preparing an overview of sensible approaches to the evaluation of performance in survival models in collaboration with TG8.

In medical research, many data analyses are conducted by analysts with varying levels of statistical education, experience and interests. In the paper introducing the STRATOS initiative[1], statistical knowledge is categorized into three levels: (1) Low statistical knowledge (2) Experienced statistician (3) Expert in a specific area. We submitted 2 papers that are in category 1, providing guidance for applied researchers on acceptable methods that are easily implemented and highlighting weaknesses of common approaches.

The first paper was led by David McLernon (Aberdeen) on the evaluation of performance in standard survival models[2]. We all recognize that risk prediction models need thorough validation to assess their performance. Validation of models for survival outcomes poses challenges due to the censoring of observations and the varying time horizon at which predictions can be made. In this review paper, we give a description of measures to evaluate predictions and the potential improvement in decision making from survival models based on Cox proportional hazards regression. As a motivating case study, we consider the prediction of the combined outcome of recurrence and death (the 'event') in breast cancer patients following surgery. We develop a Cox regression model with three predictors as in the Nottingham Prognostic Index in 2982 women (1275 events within 5 years of follow-up) and externally validate this model in 686 women (285



events within 5 years). The improvement in performance was assessed following the addition of circulating progesterone as a prognostic biomarker. Model predictions were evaluated across the full range of observed follow up times or for the event occurring by a fixed time horizon of interest. We discuss recommended statistical measures that evaluate model performance in terms of discrimination, calibration, or overall performance. Furthermore, we evaluate the potential clinical utility of the model to support clinical decision making. SAS and R code is provided to illustrate apparent, internal, and external validation, both for the simple 3-predictor model and when adding progesterone.

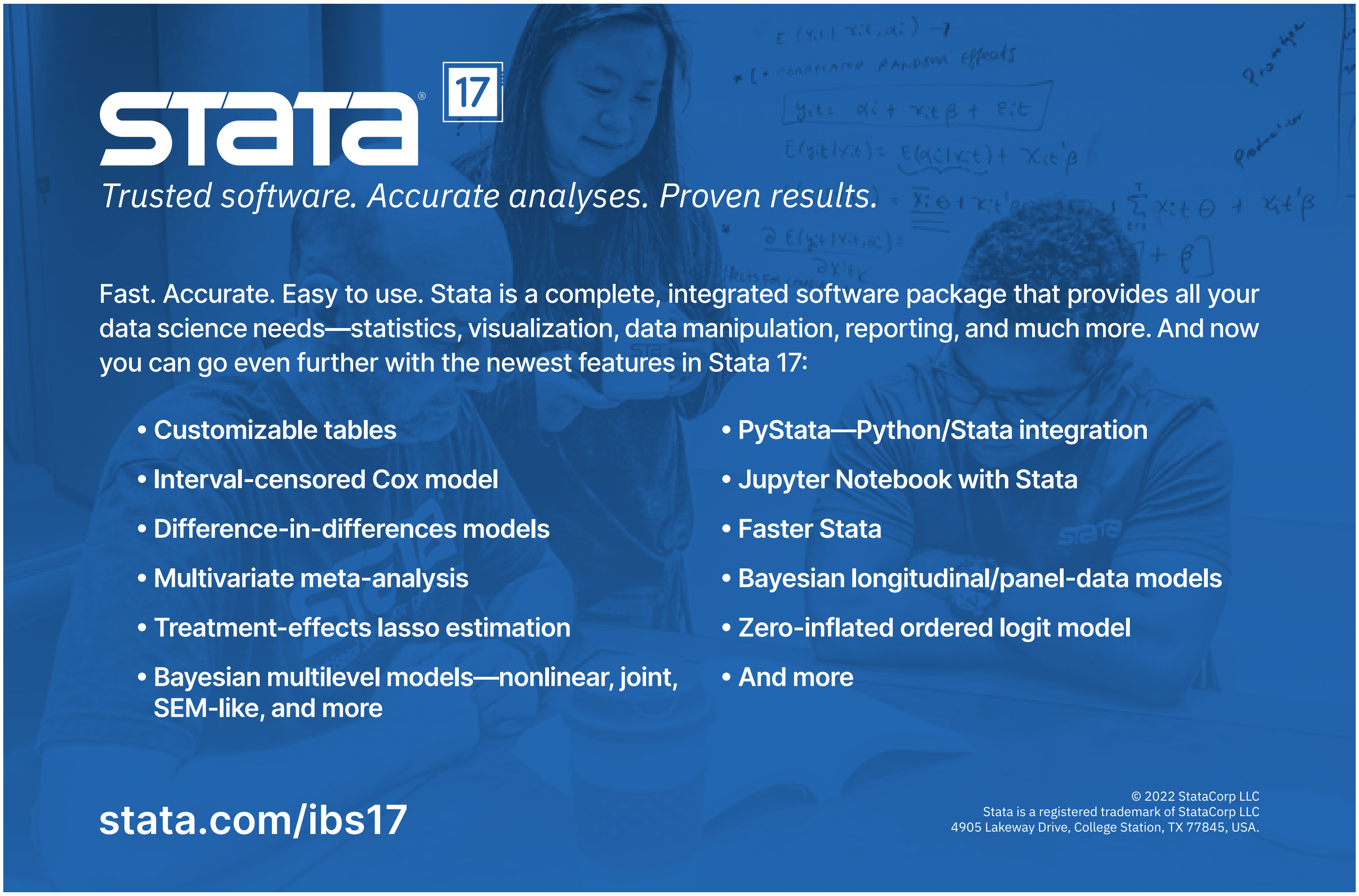
The second paper was led by Nan van Geloven (Leiden) and will be published in the British Medical Journal[3]. In this paper, we consider competing risks and the evaluation of predictive performance. We recognize that for time-to-event outcomes such as breast cancer recurrence, death from other causes is a competing risk. Model performance measures must account for such competing events. We present a comprehensive yet accessible overview of performance measures for this competing event setting, including the calculation and interpretation of statistical measures for calibration, discrimination, overall prediction error, and clinical utility by decision curve analysis. All methods for model development and validation are illustrated for patients with breast cancer, with publicly available data and R code. Both papers have had a lengthy trajectory of exchanging different perspectives by e-mail and videoconferencing. A particular challenge was the issue on how to deal with censored observations in a validation context. Also, we had to remain within acceptable word count limits, which was solved by providing extensive supplementary material, including details on the data and R, and SAS code.

Future work will focus on the evaluation of performance in dynamic survival models (with Hein Putter) and models which use age as the time axis for prediction (with Terry Therneau).

1. Willi Sauerbrei, Michal Abrahamowicz, Douglas G. Altman, Saskia le Cessie, James Carpenter, on behalf of the STRATOS initiative. STRengthening Analytical Thinking for Observational Studies: the STRATOS initiative. Stat Med 2014 Dec 30;33:5413-32

2. David McLernon, Daniele Giardiello, Ben Van Calster, Laure Wynants, Nan van Geloven, Maarten van Smeden, Terry Therneau, Ewout Steyerberg; on behalf of STRATOS TG6 and TG8. Assessing performance in prediction models with survival outcomes: practical guidance (submitted)

3. Nan van Geloven, Daniele Giardiello, Edouard Bonneville, Lucy Teece, Chava Ramspek, Maarten van Smeden, Kym Snell, Ben van Calster, Maja Pohar-Perme, Richard Riley, Hein Putter, Ewout Steyerberg on behalf of STRATOS TG6 and TG8. Validation of prediction models in presence of competing risks: a guide through modern methods (in press, BMJ 2022)



# Region News

## Australasian Region (AR)

### IBS-AR Student Scholarships

To help attract enthusiastic and talented students to career paths in biometrics, the Australasian Region offers scholarships for suitably qualified students who intend to undertake a fourth or honors year of study, or a coursework Masters, in statistics, mathematical statistics, biostatistics, bioinformatics or biometrics. We are delighted to announce the winners of this year's highly contested award: *Sophie Giraudo* (Honors student at the University of Western Australia, Perth, Australia) and *Victor Tsang* (Honors student at the University of NSW, Sydney, Australia). Congratulations!

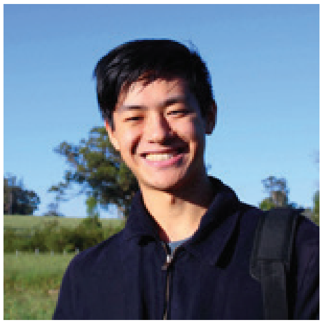
### Biography - Sophie Giraudo

*Sophie Giraudo*

Sophie Giraudo is currently studying Honors in Mathematics and Statistics at The University of Western Australia. Her Honors project is using clustering techniques to detect the presence of lymph node metastasis in endometrial cancer patients. Sophie was the 2021 President of the UWA Data Science Club and is still part of the committee as an Ordinary Sub-Committee Member. Outside of university, Sophie is the Secretary of Combined Districts Concert Band and plays clarinet, saxophone, and percussion, and is also the Marketing and Communications Co-coordinator for West Coasters Netball Club where she also plays and coaches netball. In her free time, she also plays cricket, sews, paints, and does cross stitch and embroidery.

Professionally, Sophie has completed data science internships at Visagio, the UWA System Health Lab, and Woodside. Her work in these roles included mine plan scheduling using linear optimisation, reliability analysis, and using artificial intelligence to detect duplicate documents in file storage systems. After Honors Sophie plans to pursue a PhD and a career in academia, and is particularly interested in the application of statistics to health and the biosciences. She is passionate about sharing her knowledge through teaching, and advocating for women in STEM.

### Biography - Victor Tsang



*Victor Tsang*

Hi, I'm Victor! I'm studying Data Science at the University of New South Wales and I'm in my honors year. My honors project is around estimating extinction times using fossil data, with a particular focus on applying stochastic approximation techniques to come up with faster and better estimates. I'm under the excellent supervision and guidance of Dr. David Warton, and every week I'm reading and learning something new!

I've always had a mixed-bag of interests, and have always taken up any and all opportunities to try new and challenging things to see where I end up. Truth be told, I decided to major in Quantitative Data Science because I wasn't very good at first year math and thought I should get better — a goal that is still a work in progress :'). During the degree, I did a few internships (mostly in the finance/product space) and wanted to learn something outside of those fields, get a taste of research, and continue developing my stats skills. That's how I ended up adding on an optional honors year in ecological stats!

Outside of uni and work, I play volleyball, tinker with computers, and try to spend as much time with friends and family as I can. My life at home mostly revolves around our family dog Benji (his Instagram handle is @benjiibeans), who is a lovely and terrifically smart Cocker Spaniel-Poodle.

As for life after honors, it's looking pretty researchy and statsy - I love the rigor and widespread applicability of statistics, but it also adds an element of decision-paralysis for people like me. I do think a Master's/PhD will be on my radar sometime in the future, although my top priority right now is to survive honors!

### Francis Hui Awarded Christopher Heyde Medal

*Francis Hui*

IBS-AR member Dr Francis Hui was recently awarded the Christopher Heyde Medal by the Australian Academy of Science. The Christopher Heyde Medal recognises outstanding research in the mathematical sciences by researchers up to 10 years post PhD and honors the contributions to mathematics by the late Professor Christopher Charles Heyde AM, DSc, Hon DSc(Syd), FAA, FASSA. Professor Heyde was the Foundation Dean of the School of Mathematical Sciences at the Australian National University, and Professor Emeritus of Statistics at Columbia University, New York.

Francis joins a stellar list of highly distinguished recipients, including IBS-AR member Prof David Warton who was the recipient in 2014.

Congratulations to Francis, Sophie and Victor!

## Brazilian Region (RBras)

### RBras and the Brazilian Journal of Biometrics

Aiming at full internationalization, the official journal of RBras, Revista Brasileira de Biometria has just changed its name to Brazilian Journal of Biometrics (BJB), with a new ISSN: 2764-5290. The journal publishes articles quarterly, is open access and does not charge publication fees. The aim of the journal is to publish original research papers, discussion articles or case studies that explore, promote and extend statistical methods in applied biological sciences. The Editors would like to invite all of you to consider submitting an article to our journal. The BJB is listed in google scholar, Scopus and other national and international databases and only accepted articles written in English. Complete details about the journal and submission procedure can be found here: https://biometria.ufla.br/index.php/BBJ.

### RBras 2022 Annual Conference

The next annual meeting of RBras will be held in Florianópolis, Santa Catarina, Brazil, from November 16-18, 2022. The Conference has a diverse program built by the committee members from the Federal University of Santa Catarina (UFSC), with six invited sessions, including the IBS President, nine invited paper sessions, four short courses, and contributed paper and poster sessions. All the IBS community is welcome to attend this conference in the same beautiful city where the IBS 2010 was organized in a very successful way. We hope to see many of you in Florianópolis.

### RBras and the Ômega Talks

Since September 2021, every last Wednesday of each month the RBras has a space in the Omega Talks, where the speakers are invited by the RBras. The Omega Talks are organized by some of the RBras members from the Federal University of Paraná. All the videos can be found in the RBras YouTube channel: https://www.youtube.com/c/RBras-IBS/videos.

## Eastern Mediterranean Region (EMR)

### 34th Panhellenic Statistics Conference

The 34th Panhellenic Statistics Conference took place in Athens, Greece on May, 19-22, 2022, and was a hybrid event. The conference focused on statistical methods for experimental design in the life sciences, however, the topic was not exclusive since there were sessions in all aspects of statistical methodology and data/application driven developments. Researchers from Greece, the rest of Europe and North America attended the conference, while several sessions were held in English. The 2022 Inaugural Theo Cacoullos Memorial Lecture was given by Professor Narayanaswamy Balakrishnan (McMaster University). The three keynote speakers were Professor Petros Dellaportas (Athens University of Economics and Business and University College London), Professor Georgios-Ioannis Nychas (Agricultural University of Athens) and Professor Petros A. Tarantilis (Agricultural University of Athens)

### ISA annual meeting

The Israel Statistical Association annual meeting (ISA) will take place in Tel Aviv University on June 16, 2022. The conference will feature a keynote talk by Peter Bühlmann from ETH Zurich. The conference will also feature a poster session, annual thesis awards, and parallel invited sessions on a variety of contemporary topics, among which: statistics in medicine, machine learning for the public good, model-free statistical inference and more.

## Eastern North American Region (ENAR)

### WebENARs

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

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

The 2022 Spring Meeting of the IBS Eastern North American Region was held in a hybrid in-person/virtual format during 27-30 March. ENAR extends congratulations to John Van Ryzin award winner Heejun Shin (University of Florida, Department of Statistics), and all recipients of the Distinguished Student Paper Award: Sunyi Chi (University of Texas MD Anderson Cancer Center, Department of Biostatistics), Anass El Yaagoubi Bourakna (King Abdullah University of Science and Technology), Chenqi Fu (Pennsylvania State University, Department of Public Health Sciences), Mengtong Hu (University of Michigan, Department of Biostatistics), Jeremiah Jones (University of Rochester, Department of Biostatistics and Computational Biology), Brian King (Rice University, Department of Statistics), Yang Li (University of Michigan, Department of Statistics), Huiming Lin (Rice University, Department of Statistics), Zikai Lin (University of Michigan, Department of Biostatistics), Mochuan Liu (University of North Carolina at Chapel Hill, Department of Biostatistics), Maria Masotti (University of Minnesota School of Public Health, Division of Biostatistics), Ksheera Sagar K N (Purdue University, Department of Statistics), Emily Wang (Rice University, Department of Statistics), Mengli Xiao (University of Minnesota, Division of Biostatistics), Wenyi Xie (University of North Carolina at Chapel Hill, Department of Biostatistics), Haoran Xue (University of Minnesota School of Public Health, Division of Biostatistics), Siyun Yang (Duke University, Department of Biostatistics and Bioinformatics), and Laura Zhou (University of North Carolina at Chapel Hill, Department of Biostatistics).

*Recipients of the 2022 ENAR Distinguished Student Paper Award. ENAR Spring Meeting, Marriott Marquis Houston, Houston, TX, USA.*

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

The 2022 Joint Statistical Meetings will be held from 6-11 August. The theme of the 2022 meeting is "Statistics: a Foundation for Innovation". As always, ENAR, one of the founding societies of JSM, has been instrumental in organizing an outstanding program, including sponsoring many exciting sessions. These include invited sessions on analysis of spatially-resolved cell imaging data, statistical methods applied to racial equity research, novel methods for causal inference, statistical methods for microbiome research, recent developments in mobile/wearable device data analysis, novel methodology development in high-dimensional longitudinal data analysis, Spatio-temporal statistical learning in healthcare and environmental Science, cross-disciplinary research on health data science, statistical advances for heterogeneous transcriptomics data, modern statistical methods for large biomedical data, statistical challenges in large-scale imaging studies, analysis of incomplete data, new areas in complex high-dimensional data analysis, new advances in multi-group and multi-view data, novel statistical methods for single-cell genomic data, analysis of multivariate functional data, prediction and inference in statistical machine learning, innovations in clinical trial designs, confronting global climate change, statisticians in the reproducibility and research reform movement, crossing boundaries between non-academic and academic domains, challenges and opportunities for funding statistical innovation, and discussion on twenty years after Leo Briemann's Two Cultures. This year's program also features several ENAR sponsored topic-contributed and contributed paper, poster, and speed sessions. These include new methods for structured variable selection, dimension reduction and feature interpretability in neuroimaging, functional and high-dimensional data analysis, statistical methods for assessing genomic heterogeneity, recent developments in nonparametric and semi-parametric methodologies and their applications, statistics in social sciences and survey research, causal inference in neuroimaging and radiology, and analysis of time-to-event data. ENAR owes an enormous debt of gratitude to Laura Hatfield at Harvard University for serving on the Program Committee for the 2022 JSM. For more details about the upcoming JSM meetings, please visit: https://ww2.amstat.org/meetings/jsm/2022/index.cfm.

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

The 2023 ENAR Spring Meeting is scheduled to take place in Nashville, TN, USA, at the JW Marriott Nashville. Please suggest ideas and potential speakers and/or develop a formal proposal. Proposals on topics that have broad potential scientific impacts are particularly encouraged. Invited sessions are 105 minutes long, and different formats are encouraged, such as sessions with four speakers, three speakers plus a discussant, or a panel discussion. Formal invited paper session, short course, and tutorial course suggestions will be selected by the Program Committee, which includes the Program Chair, Associate Chair, and ASA representatives ASA sections and ENAR at-large members. To informally suggest ideas, topics, or names of potential speakers, please contact Program Chair Elizabeth Handorf (Elizabeth.Handorf@fccc.edu) or Associate Program Chair Sameera Wijayawardana (sameera.r.wijayawardana@gmail.com). Questions about short course and tutorial sessions should be directed to the Educational Advisory Committee (EAC) Chair Leslie McClure (lam439@drexel.edu). The local arrangements chair is Andrew Spieker (andrew.spieker@vumc.org). The deadline for submitting invited session proposals is 17 June 2022.

### Future Meetings

The 2023 Joint Statistical Meetings will be held in Toronto, Ontario, Canada from August 5 – 10, 2023. ENAR is fortunate to have Liangyuan Hu from Rutgers University to be our representative to the Program Committee. If you have ideas for the meeting, please contact Liangyuan at lh707@sph.rutgers.edueeting to be held in Marriott Baltimore Waterfront in Baltimore, MD, USA, from March 10 – 13, 2024!

**Saptarshi Chakraborty**

## German Region (DR)

### DAGStat Conference

The DAGStat Conference 2022 was the sixth conference of the Deutsche Arbeitsgemeinschaft Statistik and took place in Hamburg, from March 28 to April 1, 2022. The conference was hosted by the Universitätsklinikum Hamburg-Eppendorf in close cooperation with the Universität Hamburg and the Helmut-Schmidt-Universität. The conference was also the 68th Biometric Colloquium of the German Region of the International Biometric Society (IBS-DR), the 'Spring Meeting' of the German Statistical Society, and the 45th annual conference of the Gesellschaft für Klassifikation (GfKl) – Data Science Society. The conference was conducted in presence limited to vaccinated and recovered persons. The conference program included all fourteen associations of the DAGStat. Matching the motto 'Mind the gap - Interplay between theory and practice', the plenary talks addressed current topics such as statistics in medicine, economics, engineering and social sciences as well as methodological statistics. This broad view of statistics encouraged enriching scientific discussions at the conference and social meetings for statisticians of various application areas. As the DAGStat conferences are international conferences, the conference languages were English and German.

The scientific program commenced on Monday with five tutorials, a teacher's event that drew social studies teachers rather than mathematics teachers and a lecture for the general public. The 31 talklets, i.e. short online video presentations at https://www.dagstat2022.uni-hamburg.de/scientificprogram/taklets.html, and 33 posters were exhibited throughout, with wine being offered at the posters on Thursday after 7. Each day had a live-streamed plenary talk by prominent American statisticians. The 67 sessions had 33 invited speakers. The full program is still online including the book of abstracts.

**The young statistician's session had the following talks:**

Sabrina Schmitt: Time-to-event analysis with competing risks considering cluster structures - Comparison of methods based on a simulation study.

Julian Rodemann: Prior-mean-RObust Bayesian Optimization (PROBO).

Michael Lau: Evaluation of tree-based statistical learning methods for constructing genetic risk scores.

Kristin Blesch: Conditional Feature Importance for Mixed Data.

Maximilian Kertel: Learning the Joint Distribution with Missing Data under the Gaussian Copula Model.

Jana Kleinemeier: Scalable Estimation for Structured Additive Distributional

Regression Through Variational Inference.

### Young talents awards

This year's honors for best papers were awarded at the DAGStat conference.

### In the "post-doc" category:

Moritz Fabian Danzer: Adaptive group sequential designs for single-arm phase II studies with multiple time-to-event outcomes.

Nadja Klein: Bayesian variable selection for non-Gaussian responses: a marginally calibrated copula approach.

### In the "pre-doc" category:

Saide Atmaca: Evaluation of Misspecified Linear Regression Models for Subgroup Analysis.

Eric Samuel Knop: Robust confidence intervals for mixed-effects meta-regression with interaction.

Sabrina Schmitt: Time-to-event analysis with competing risks considering cluster structures - Comparison of methods based on a simulation study.

### Election results

Anne-Laure Boulesteix (LMU Munich) was elected vice-president, and will serve as president of the German region 2023 to 2024. The new treasurer for 2022-2026 is Joachim Gerß (WWU Münster).

## Japanese Region

### The 2022 Annual Meeting of the Biometric Society of Japan

The 2022 Annual Meeting of the Biometric Society of Japan (BSJ) will be held on 13-14 May 2022 in hybrid combining online and onsite at the Katsushika Campus of Tokyo University of Science, Tokyo, Japan, due to the coronavirus pandemic. Two invited sessions on deep learning and the 2021 BSJ Award for Outstanding Scientific Contribution will be organized. The tutorial seminar entitled "Recent Advances in Sparse Estimation" will also be organized jointly with the Japanese Society of Applied Statistics.

### The 2022 Japanese Joint Statistical Meeting

The BSJ is one of the six sponsoring organizations of the meeting and the 2022 Japanese Joint Statistical Meeting will be held on 4-8 September at Seikei University, Tokyo, Japan. The BSJ is organizing an invited session entitled "Recent Advances and Further Developments in Biometrics." The society is also organizing an invited session in which the winner of the Young Biostatistician Award conferred by the society will present his research.

**Takashi Daimon**

### Meetings:

13-14 May
The 2022 Annual Meeting of the Biometric Society of Japan
Katsushika Campus of Tokyo University of Science, Tokyo, Japan

4-8 September
The 2022 Japanese Joint Statistical Meeting
Seikei University, Tokyo, Japan

## The Netherlands (BMS-ANed)

In the previous Bulletin we announced a new seminar series: approximately four times a year a 45-minute session, aiming at a broad biostatistical audience, in particular PhD students, will be held.

By now we have had our first seminar with **Stéphanie van der Pas** (Amsterdam UMC), on Thursday Feb 24. This seminar had the challenging title **"Causal conclusions from a cut-off"**, a concept that is very useful in situations where a randomized controlled trial is not possible or not yet available. To give an example: if persons get a different treatment, depending on whether their age (or blood pressure or …) is either above or below a certain threshold, the persons just around the threshold in general are very similar, apart from this treatment. For instance, if the cut-off to get treatment A or B is 45 years, people with an age of 44 are on almost all aspects very similar to people of 45 years, but they got treatment A, whereas people of 45 got treatment B. This allows a comparison of the treatment effects without conducting an experiment. But of course, you are not only interested in people of 44-45 years of age: in case you want to learn more, specifically about people of other ages, using regression discontinuity designs becomes relevant.

This (online) seminar was a huge success, with almost 60 participants and a lot of discussion afterwards.

With regard to the near future (already past, when you read this): we will have our first in-person meeting in two years on May 13, 2022, in Rotterdam. We will start with the general assembly, followed by a very interesting scientific program on Modern mixed models:

- Paul Eilers, Erasmus MC: Smoothing, splines and mixed models
- Elrozy Andrinopolou, Erasmus MC: Investigating the impact on dynamic predictions and effect sizes when miss-specifying the association between longitudinal outcomes
- Matteo Amestoy, Amsterdam UMC: Linear mixed models for high-dimensional data: extending the functionalities of the LMER package
- Martin Boer, Wageningen University: Multidimensional smoothing using sparse mixed models in R package LMMsolver

Of course, the scientific program will be followed by discussion, drinks, and snacks, now that we can finally meet again. We are very much looking forward to this afternoon!

On behalf of BMS-ANed,

**Joanna IntHout**

## Spanish Region (SEB)

### VI Student Conference of the Spanish Region

We are pleased to inform you that the **6th Student Conference of the Spanish Region** of the International Biometric Society (REsp) will be held on **14-16 September 2022 in Valencia**. After the 5th edition finally had to be held in online format due to the situation caused by COVID-19, this 6th edition will be held physically at the University de Valencia (Faculty of Mathematical Sciences, Burjassot campus).

The Organizing Committee, exclusively composed of students from the Spanish Region, is very grateful to the REsp, and to the University of Valencia for all the received support. We hope that this conference will be as fruitful and successful as the previous ones have been. We are very excited and looking forward to the event. We will upload the information on this website (http://www.biometricsociety.net/vi-jornadas-cientificas-de-estudiantes-de-la-seb/).

**The Organizing Committee**

The Spanish Region of the IBS (SEB) continued with the bimestrial organization of SEB-talks (cycle of virtual conferences) oriented to researchers, biostatisticians, and the general public to highlight the main advances in the area of Statistics developed by researchers mainly from this region but also from abroad. Last seminar was:

- **Bioestadística en Bayesiano, ¿para qué?**, by Anabel Forte (Universidad de Valencia).

The Organizing Committee and the Spanish Biometric Society want to thank all the attendees and speakers of these virtual conferences and encourage other researchers to attend these as well as to contribute with oral talks. The talks are recorded and posted on the Spanish Biometric Society's YouTube channel (https://www.youtube.com/channel/UC2PMj-JhzeKFhW4jok_0rEA).

We look forward to seeing you there!

## Western North American Region (WNAR)

The 2022 WNAR/IMS meeting will be held virtually June 12 to June 15, 2022. The Program Chair is Damla Senturk from UCLA, and the Virtual Conference Operations Chair is Subodh Selukar from University of Washington. Please submit your abstracts and join us for invited and contributed sessions and panels, student paper presentations, as well as professional development opportunities. The WNAR website, www.wnar.org, will have the most up-to-date status of the meeting.

**Jessica Minnier**
**(WNAR Secretary)**

# Announcements & Upcoming Events

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

### Machine Learning Boot Camp: Analyzing Biomedical and Health Data

Starts: Jun 16, 2022 10:00 (ET)
Ends: Jun 17, 2022 17:00 (ET)

The Machine Learning Boot Camp is a two-day intensive boot camp of seminars combined with hands-on R labs and data applications to provide an overview of statistical concepts, techniques, and data analysis methods with applications in biomedical research.

### Electronic Medical Records Boot Camp: Biostatistical methods for analyzing EMR data

Starts: Jun 29, 2022 10:00 (ET)
Ends: Jun 30, 2022 17:00 (ET)

The Electronic Medical Records Boot Camp is a two-day intensive boot camp of seminars and hands-on analytical sessions to provide an overview of electronic health data opportunities, statistical challenges, and latest techniques.

### 3rd Corsican Summer School

Starts: Jul 4, 2022 09:00 (FR)
Ends: Jul 8, 2022 17:00 (FR)

As part of the HEAR+STAT series of courses, this intensive course covers the field of net survival and excess mortality, investigating both theoretical and application aspects using R software. The Summer School is aimed at biostatisticians, statisticians, epidemiologists; researchers and students; those working in a registry of cancer, of chronic disease or in any other field relevant to these methodologies and applications.

View the meetings calendar here!

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

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

# Get Connected!

Participate in the IBS Members Community:

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

We welcome all comments and feedback about the new website. Let us know what you think!

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