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THE ISBA BULLETIN

OFFICIAL BULLETIN OF THE INTERNATIONAL SOCIETY FOR BAYESIAN ANALYSIS

MESSAGE FROM THE PRESIDENT

Antonio Lijoi
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Welcome to the first ISBA Bulletin of 2026! It is a real honor for me to serve as ISBA President this year, especially as it promises to be a very special one for our community, with the World Meeting as the main highlight. I am also very happy to contribute to the Bulletin again—it feels a bit like a déjà vu, as I served as editor of the *"News from the World"* column during my postdoc years. I have great memories of the time, when Fabrizio Ruggeri was the Bulletin Editor, and I remain very grateful to him for involving me in that experience.

As always at the start of the year, the Executive Council has seen a few changes. First of all, we owe our deepest thanks to Aad van der Vaart, who has completed three years of truly outstanding service. We are delighted to welcome Judith Rousseau as our new President-Elect, and Leo Duan as Treasurer, taking over from Yanxun Xu, to whom we are very grateful for her amazing job in this role. Michele Guindani deserves special thanks for his leadership as President, and I am very pleased that he will continue to contribute as Past President. Finally, I would like to warmly acknowledge the continuous efforts of our Executive Secretary, Xinyi Xu: her work is absolutely essential to the smooth running of the Society.

As anticipated, the ISBA World Meeting in Nagoya (June 28 – July 3) will be the highlight of the year. We are grateful to the Scientific Committee as it has put together an outstanding program, under the tireless leadership of Sameer Deshpande, and to the Named Lectures Committee, chaired by Sergios Agapiou, for selecting wonderful speakers for the de Finetti and Bayarri lectures. A special thank you goes to the Local Organizing Committee, chaired by Kazuhiko Kakamu, for their tremendous work in making this event possible. Many of us still have great memories of the 2012 ISBA World Meeting in Kyoto, and we are all very much looking forward to Nagoya!

IN THIS ISSUE

The program will feature plenary talks, invited sessions, contributed talks, and poster sessions. I would especially like to highlight the Savage Award session, where the eight finalists will present their PhD work: this is always one of the most inspiring moments of the meeting. Poster sessions are another key part of the conference, as they foster discussion, exchange of ideas, and often the start of new collaborations. You can find the tentative schedule here. Let me also remind you that the early-bird registration deadline is April 30, so do not miss the opportunity to benefit from reduced fees.

Supporting early-career researchers remains a key priority for ISBA. The call for Junior Researcher Travel Awards is currently open, with a deadline of April 8. In addition to the regular travel awards, there will be the Pilar Iglesias Award for candidates from developing countries and the ISBA Lifetime Members Travel Award. We very much hope to see many PhD students and early-career researchers in Nagoya!

As usual, the World Meeting will be complemented by satellite events. Among these I would mention the j-ISBA flagship meeting BAYSM 2026, which will take place at Chiba University on June 26–27, just before the main conference. You can find more information on this and other exciting Bayesian events in 2026 in the "News from the World" section of this Bulletin.

Speaking of meetings, I would also like to remind you of the ISBA survey on the future of our meetings, prepared by the dedicated committee on this topic. The survey was announced in the December 2025 issue of the Bulletin, and the deadline has been extended to March 31. Your feedback is extremely important: it will help guide future decisions on how to make our meetings more sustainable and inclusive, while preserving their scientific strength and financial viability. This will also be a topic of discussion within the leadership and, more broadly, at the World Meeting.

Turning to awards, nominations for both the Savage and Mitchell Awards are now open, with a deadline of May 31, 2026. Please see the article by Botond Szabó and Natalia Bochkina in this issue for further details. We look forward to receiving many nominations highlighting outstanding PhD work and influential contributions to Bayesian statistics. The awards will be presented at the 2027 JSM in Chicago.

ISBA is also proud to support, together with other professional societies, the documentary *Game of Genius: The Untold Story of David H. Blackwell*. Initiated by filmmaker (and David Blackwell's granddaughter) Leeza Blackwell, the documentary offers a powerful reflection on Blackwell's legacy, including aspects that have often been overlooked. It is a fitting tribute to one of the most influential probabilists and statisticians of the 20th century, whom we also honor through the Blackwell-Rosenbluth Award by the j-ISBA section.

Our Society continues to grow and evolve. Last year saw the creation of two new Sections (Bayesian AI and Bayesian Social Sciences), both of which will be represented at the World Meeting with their own invited sessions. A proposal for a new Section on Bayesian Structural Learning is currently under consideration, and support for its creation can be expressed by following Nadja Klein's instructions in this Bulletin. The vitality of our Society is also reflected in the success of *Bayesian Analysis*: the increase in submissions and the shorter turnaround times reported by the Editor-in-Chief, Igor Prünster, in this issue are truly impressive. This is the result of a collective effort of the Editor, the co-Editors and members of the Editorial Board, to whom we are deeply indebted.

We will soon begin the process of identifying candidates who will run for vacant offices, most notably the next President-Elect and new members of the Board of Directors. You are invited to suggest names for the Nominating Committee: we very much look forward to your input, which can be sent to president@bayesian.org.

I would also like to take a moment to thank all those who contribute to ISBA in so many different ways. The strength of our Society relies on the time, energy, and dedication of its members, often behind the scenes. In particular, I would like to thank the Board members who have recently stepped down - Tamara Broderick, Subhashis Ghosal, Claire Gormley, and Matteo Ruggiero - as well as Past Program Chair Sergios Agapiou, for their dedicated service. At the same time, we warmly welcome our new Board members Alejandra Avalos-Pacheco, David Dahl, Beatrice Franzolini, and Stephanie van der Pas, as well as our new Program Vice-Chair David Frazier. We are also grateful to Catherine Forbes (Finance Committee) and Federico Camerlenghi and Marcos Prates (Prize Committee) for agreeing to serve in such important Committees.

Let me conclude with a reminder to renew your membership, if you have not yet done so. You are also invited to encourage your students, postdocs, and colleagues to join ISBA. The support of our members is essential for sustaining all our activities, including the World Meeting and our efforts to support junior researchers. You can renew your membership and join Sections here.

FROM THE EDITOR

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Hello Bayesians,

Welcome to the first ISBA Bulletin of 2026! A huge welcome to our incoming officers and a sincere thank you to all our contributors.
This issue covers all the essential community updates, featuring reports from the Program Council, the BA Editor, the Awards Committee, and j-ISBA. We are also pleased to share a proposal for a new ISBA Section on Bayesian Structure Learning, alongside a “News from the World” section packed with global events.
To cap it all off, we feature a special contribution celebrating the 80th anniversary of Jeffreys’ prior, as well as a Software Highlight showcasing the flexibility of the NIMBLE probabilistic programming language.

ISBA community, enjoy the read!

FROM THE PROGRAM COUNCIL

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New Member. David Frazier has joined the Program Council as our new Vice-Chair. We are thrilled to welcome him to this role and look forward to the energy he brings to the team. We also want to express our deepest gratitude to Sergios Agapiou for his dedication and exceptional service over the past three years. Sergios has been instrumental in organizing multiple World Meetings all the way through 2030. Thank you, Sergios, for your incredible impact, and a very warm welcome to David!

(Co)-sponsorship & Endorsement Requests. If you are planning a meeting and would like to request financial sponsorship (or co-sponsorship) or non-financial endorsement from ISBA, please submit your request to the Program Council at `program-council@bayesian.org`. Detailed information on how to submit requests for sponsorship or endorsement is available here.

Upcoming ISBA-Sponsored/Endorsed Events. In 2026, ISBA will sponsor or endorse many exciting events. You can find all the details in the “News from the World” section of this bulletin.

UPDATES FROM BA

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As spring approaches, I am pleased to share a few updates from *Bayesian Analysis*.

Editorial Updates

We closed 2025 with well over 300 submissions, an almost 30% increase compared to 2024. I am also very pleased to report that our streak of sending decisions within four months from submission remains intact: we have just issued a decision on the last paper submitted in November 2025, leaving only one more month to complete a full-year streak. This achievement is entirely due to the dedication of our Editorial Board members and referees, and I am very grateful for their efforts. I believe that the community has now fully embraced this shared commitment to timeliness, and that it will benefit the journal in the long run by combining the *Bayesian Analysis* tradition of constructive and thorough feedback with consistent and predictable turnaround times.

I would also like to warmly thank Maria Kalli (King's College London), who is stepping down as Managing Editor, for her outstanding work and dedication. At the same time, I am delighted to welcome Francesco Sanna Passino (Imperial College London) as the new Managing Editor for the 2026–2028 term.

Enhancements to Reference Formatting

With Francesco's help, we are close to finalizing a redesigned reference format for *Bayesian Analysis* papers. We are very pleased with the result and hope you will be as well. Beginning in April, papers will start appearing on Advance Access with the new formatting. I would also like to thank the VTeX production team for their patience and responsiveness as we worked through the many implementation details.

As part of this work, we also tackled the challenge of citing conference proceedings consistently. Many journals struggle with this, and there is no fully automated solution that reliably enforces uniformity across sources. For that reason, we have chosen to rely more explicitly on authors' help, and we have updated the Author Guidelines accordingly. I am grateful in advance for the community's collaboration on this, and I encourage everyone to consult the updated guidelines before submitting their next paper to *Bayesian Analysis*. In the coming months, we also plan to refresh the BA style file itself.

Upcoming Discussion Paper

I am pleased to announce the next discussion paper to appear in *Bayesian Analysis*:

"Robust Probabilistic Inference via a Constrained Transport Metric"

by Abhisek Chakraborty, Anirban Bhattacharya, and Debdeep Pati.
The paper will feature invited discussions from Marco Avella Medina, Jonathan Huggins, Tony Linero, and Yuexi Wang.

We now welcome contributed discussions. Contributions should be no more than two pages long and prepared using the BA LaTeX style (available via the *Bayesian Analysis* author resources on Project Euclid). Please submit your discussion via EJMS by May 10, 2026, and remember to select "Contributed Discussion" as the manuscript type. All accepted discussions will be shared with the authors, who will have the opportunity to respond in a rejoinder. We look forward to receiving thoughtful and engaging contributions from the community.

Lindley Prize

I would also like to provide a brief update concerning the Lindley Prize. The Lindley Prize Committee has now completed its work on the 2025 prize, based on the set of eligible papers published in the December 2025 issue of *Bayesian Analysis*. I am very grateful to the Committee for their careful and thoughtful efforts: David Frazier, Ryan Giordano, Jonathan Huggins, Nadja Klein, Li Ma, Minerva Mukhopadhyay, Ilsang Ohn, and Yixin Wang. The winner will be announced at the ISBA World Meeting in Nagoya, and I hope to see many of you at the awards ceremony.

BA Sessions at ISBA 2026 and JSM 2026

The *Bayesian Analysis* sessions at the 2026 meetings are scheduled as follows:

- ISBA World Meeting (Nagoya) on Friday, July 3, 2026, from 9:00am to 10:30am
- JSM (Boston) on August 4, 2026, from 10:30am to 12:20pm.

The lineups for these sessions were announced in the December 2025 issue of the ISBA Bulletin.

As always, I encourage you to browse the many excellent papers recently accepted and now available in the Advance Publication section of the journal.

FROM THE PRIZE COMMITTEE

Natalia Bochkina and Botond Szabo (co-chairs)

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The Prize Committee of ISBA is pleased to open the call for submissions for the 2026 Mitchell Prize and Savage Award. The deadline for submissions is May 31, 2026. The Mitchell Prize is given in recognition of an outstanding paper that describes how Bayesian analysis has solved an important applied problem. The prize includes a check for $1000 and a plaque; the winner(s) will be announced at the Joint Statistical Meetings in Chicago, Illinois, US, between August 7–12, 2027. For details on the Mitchell Prize, including names of past winners, eligibility details, and submission information, please visit this website.

The Savage Award, named in honor of Leonard J. "Jimmie" Savage, is bestowed each year to two outstanding doctoral dissertations in Bayesian econometrics and statistics, one each in Theory & Methods and Applied Methodology. Up to two awards of $750 will be awarded. Finalists will be notified by January 2027 and invited to present their dissertation research at a special contributed session at the Joint Statistical Meetings in Chicago. The winners will also be announced at the same meeting. For details on the Savage Award, including names of past winners, eligibility details, and submission information, please visit this website. Nominations for the Mitchell Prize and Savage Award may be made by any ISBA or SBSS member. To join ISBA please go to this link. Questions regarding any of the Prizes or Awards may be sent to the ISBA Prize Committee at prizecommittee@bayesian.org.

JUNIOR ISBA

Francesca Panero
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New j-ISBA Board Members. With the start of 2026, the newly elected officers have joined the j-ISBA Board. Please join me in welcoming our new Chair-Elect, Francesco Gaffi; new Secretary, Emma Landry; and new Program Chair, Nicolas Bianco. You can find their brief biographies on the j-ISBA website at this link. A big "thank you" goes to our outgoing Board Members Matteo Giordano, Filippo Ascolani, and Jordan Bryan for their hard work and outstanding service to j-ISBA in 2024 and 2025! j-ISBA will hold elections again this year for the positions of Chair-Elect and Treasurer; announcements will follow in the coming months.

Upcoming Events (and collaborations to celebrate!)

- BAYSM 2026 will take place in Chiba, Japan, on June 26–27, 2026. We are honored to have Professors Kerrie Mengersen and Kengo Kamatani as keynote speakers. In addition, our Blackwell-Rosenbluth award winners Beniamino Hadj-Amar, Geoff Pleiss, Nianqiao Jiu, Beatrice Franzolini, Jun Yang, and Francesco Denti will give a talk in two dedicated sessions. We have received a large number of interesting abstracts, and we will soon send out acceptance notifications and open registration!
- In an effort to broaden its geographic reach, j-ISBA has started a collaboration with the Young African Statisticians Association. The first joint event was a webinar in February, "A Journey Through Bayes: How Bayesian Statistics Improves Our Understanding of Cancer," delivered by Dr. Adolphus Wagala (Dana-Farber Cancer Institute). He gave an excellent talk on Bayesian statistics and its applications in cancer research. The webinar was attended by over 50 participants. The next webinar is planned for June - stay tuned for details. P.S.: Are you following our LinkedIn page?
- Another edition of the Blackwell-Rosenbluth Award awaits us! The award recognizes outstanding junior Bayesian researchers based on their overall contributions to the field and to the community. While the call will open in April 2026, you may already start thinking about nominations. PhD students or early-career researchers who obtained their PhD after January 1, 2021, will be eligible. We will also consider nominations with a PhD date before 2021 in cases of particular circumstances (e.g. maternity leave, health issues...).
- j-ISBA is sponsoring the session "Recent Advances from Junior Bayesians" at the 2026 ISBA World Meeting, Nagoya, Japan, June 28–July 3.
  Speakers: Déborah Sulem, Jack Jewson, Noirrit Kieran Chandra
  Chair: Matteo Giordano

If you can, please remember to join the j-ISBA section by adding USD 5 when you renew your ISBA membership (which is only USD 5 for students).

PROPOSAL FOR A NEW ISBA SECTION

Nadja Klein
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We are excited to share that we are proposing a new ISBA Section on **Bayesian Structural Learning (BSL)**! We are currently collecting signatures from those who would like to support the creation of this section. If you are interested in learning more or would like to add your support, please reach out at this email address with your full name, affiliation, email address, and specifying whether you are an ISBA member. The initial officers will be David Dunson, Nadja Klein, Rodney Sparapani, and Deborah Sulem.

Bayesian Structural Learning (BSL) refers to methods that uncover the hidden structure of complex stochastic systems while explicitly quantifying uncertainty. This is essential in modern data science: it allows us to reason about competing structural explanations, assess their implications, and make robust decisions under uncertainty.

BSL brings together:

- The core statistical activity of modeling and understanding structural aspects of high-dimensional and complex data
- Bayesian principles that enable coherent uncertainty quantification, principled model comparison, and transparent integration of prior knowledge.

We believe these ideas are currently spread across multiple ISBA Sections, but not explicitly represented by any of them — motivating the need for a dedicated BSL Section. The proposed section aims to provide an inclusive home for researchers working on methods for high-dimensional or structurally complex data, including flexible regression via latent variable and hierarchical models, dependence modeling (e.g., graphical models, copulas, networks), causal inference, spatio-temporal analysis, factor models, and clustering.

Thank you very much for your support!

NEWS FROM THE WORLD

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Q&A: what do you ~~believe~~ think?

How has Generative AI impacted your research and research group?

Sam Power (University of Bristol, UK)

My experience with Generative AI in the context of research is still evolving, but has already been quite interesting. Socially, I have found there to be an interesting mix of responses, whereby (i) many people are intrigued by the possibilities, and don't want to risk missing out on an interesting tool, but equally (ii) many *people struggle to identify which of their tasks are well-suited to the present capabilities of these tools (and I have had both responses myself!). One might hear stories of other researchers solving their own problems 'with the help of GenAI tools', without obtaining much clarity as to what the AI-assisted research process looks like in concrete terms. In this regard, I think it's highly valuable to share more stories of exactly how researchers in our field can use these tools productively.*

A major use-case among colleagues seems to be in integrating LLM tools into writing code. I have not been using this so much so far for, e.g., algorithm development - my recent projects have been focused on more theoretical questions - but I have already had some success in using LLMs to write informal applets for familiar methods; think of rudimentary visualisations of, e.g., the Random Walk Metropolis sampler, a Particle Filter, the Optimal Scaling phenomenon in MCMC, and similar. These methods are routine enough that one can get a basic applet up-and-running in seconds, add in some buttons, sliders, graphs, ... quickly after, and then have a rather interactive representation to play around with. I have also found this approach useful in cooking up animations for seminar presentations.

Anecdotally, I know of many colleagues who have found these tools to be particularly useful for literature review, and entering into unfamiliar research areas. I can see the potential here, but my own tastes still lean towards first-hand reading and making connections with (human) experts where possible, each having their own charms.

While stories of AI systems, e.g., autonomously solving Erdos problems are exciting from the outside, I do not yet have the optimism to ask an LLM to do the same for a tough statistical problem (indeed, a common point of discussion is that Statistics does not really have a conventional culture of 'open problems' anyways). Nevertheless, there does seem to be a case that LLMs can be useful for advancing a given project. For intermediate tasks like turning a rough idea into something more formal, turning some new definitions into some basic supporting theory, finding extensions to and applications of some basic results, etc. , synthetic feedback from LLMs stands out in being quick to obtain and concrete in its recommendations. A ubiquitous challenge in research is to critically assess which ideas are worth persisting with and developing into something more serious, and in this regard, these tools already seem to have some value.

To conclude, a vignette from my own research: for my own reasons, in my more mathematical work, I am somewhat guilty of "constant-chasing", to the effect of working hard to sharpen inequalities and bounds where possible. This fervour is (understandably!) not shared by all collaborators, and I would rarely insist that every constant in a paper be optimised - one needs to finish a project at some stage, after all! With this being said, this sort of task is sufficiently 'routine' that several current LLM tools can provide useful guidance on specific calculations, and it is common that one can make some appreciable improvements based on a few rounds of LLM feedback. Moreover, on the occasions that this strategy does pay off, I tend to learn (or at least remember) something useful from the experience of re-writing any 'borrowed' proofs in my own words. It stands to reason that other similar 'routine' tasks will also interface favourably with LLM tools, either already or in the near future.

Some side details (not essential to include, but maybe useful context): The answer above is entirely written by me. When using GenAI tools, I mostly use Gemini, and occasionally ChatGPT, both in their unpaid versions. I have written some non-publication research notes (A, B) which involve low-level mathematical contributions from LLMs.

Upcoming Meetings, Conferences, and Workshops

ISBA sponsored or endorsed events

- 2026 Best of Statistical Science Workshop (BOSS 2026), 24-25 April 2026, Department of Statistics at Texas A&M, USA. BOSS 2026 brings together leading experts, faculty, and students for two days of engaging discussions, presentations, and networking opportunities. Whether you're a student, researcher, or industry professional, this event is a great opportunity to connect and explore the latest advancements in statistical science.

- The Bayesian Young Statisticians Meeting (BAYSM) 2026, 26-27 July 2026, Chiba University, Japan. The keynote speakers will be Prof. Kerrie Mengersen and Prof. Kengo Kamatani.
- 4^{th} Bayesian Nonparametrics (BNP) Networking Workshop, 6-10 July 2026, Seoul, South Korea. This meeting is organised by the Bayesian Nonparametrics (BNP) Section and aims to enhance networking within the BNP community, particularly for junior researchers.
- The 9th Eastern Asia Chapter Conference (EAC-ISBA 2026), 23-25 July 2026, Yunnan University in Kunming, China. The conference will include keynote presentations, parallel invited sessions, contributed sessions, and poster sessions. Further details and updates are available on the conference website.
- 16th European Seminar on Bayesian Econometrics (ESOBE), 27-28 August 2026, LUISS University, Rome, Italy. This conference features keynote speakers Concepción Ausín (Universidad Carlos III de Madrid), Radu Craiu (University of Toronto), and Petros Dellaportas (University College London). The submission deadline for contributed talks and posters is 27 April 2026. Submissions from all fields of Bayesian econometrics (macro, micro, and financial) are welcome, as well as papers on Bayesian theory, computing, and machine learning. PhD students who are members of the EFaB section of ISBA may apply for a travel support grant. Students and researchers who received their PhD after August 2021 may apply to present their work in the dedicated oral "Young Researchers Session".
- Rethinking the Role of Bayesianism in the Age of Modern AI Workshop, 26-30 October 2026, Edinburgh, UK. This workshop will bring together researchers exploring the frontiers of Bayesian machine learning and deep learning in a collaborative atmosphere. The scientific programme will consist of invited talks, open discussions, interactive breakout sessions, poster sessions for junior participants, and lightning talks.
- International Conference on Statistics, Data Science, and Computing for the Environment and Climate Change (LACSC-TIES-EnviBayes-EnvrASA) 2026, 7-11 December 2026, Mexico City, Mexico. This international conference is jointly organised by the Latin American Regional Section of the International Association for Statistical Computing (IASC-LARS ISI), the Mexican Association of Statistics Asociación Mexicana de Estadística (AME), the International Environmetrics Society (TIES) Section on Environmental Sciences of the International Society for Bayesian Analysis (EnviBayes ISBA) and the Section on Statistics and the Environment of the American Statistical Association (ENVR ASA). The theme of this conference is "Climate Change in 2026". Deadline for abstract submissions: 31 May 2026.

Other events

- 12th International Workshop on Spatio-Temporal Modelling (METMA XII), 8-10 June 2026, Zaragoza, Spain. METMA XII will be held in Zaragoza, Spain, from 8 to 10 June 2026. The conference aims to promote the development and application of spatial, temporal, and spatio-temporal statistical methods in the context of health and environmental research, with a particular emphasis on Bayesian methods. The scientific program will include four keynote speakers (A. Gelfand, S. Banerjee, G. Jona-Lasinio and R. Huser) and invited speakers; contributions in the form of oral presentations and posters are welcome. The deadline for abstract submission is 15 April 2026. Further details can be found on the official conference website.
- 7^{th} meeting of the Institute of Mathematical Statistics Asia Pacific Rim Meeting (IMS-APRM), 13-16 June 2026, The Chinese University of Hong Kong, Hong Kong. This event serves as a global forum for scientific communication and collaboration among researchers from Asia and the Pacific Rim. It aims to foster connections and partnerships between researchers in this

region and colleagues from around the world. Deadline for submitting contributed talks: 31 March 2026.

- Statistical Methods for Dynamical Stochastic Models (DYNSTOCH 2026), 15-17 June 2026, Gothenburg, Sweden. This conference is hosted by the Department of Mathematical Sciences at Chalmers University of Technology and the University of Gothenburg, and brings together researchers who are working on various topics in inference and simulation for stochastic processes. Abstract submission deadline: 15 April 2026.
- 10^{th} Bayesian, Fiducial, and Frequentist Statistics (BFF) conference, 10-11 July 2026, Salzburg, Austria. The scientific program will include keynote lectures by Richard Samworth and Peter Grünwald. Poster submission deadline: 30 May 2026.
- Institute of Mathematical Statistics Annual Meeting 2026, 6-9 July 2026, Salzburg, Austria. The scientific program will feature the 2026 Wald Lecture (Tilmann Gneiting), the 2026 Blackwell Lecture, three 2026 Medallion Lectures (Ian McKeague, Bodhisattva Sen, Jelle Goeman), the IMS Lawrence D. Brown Ph.D. Student Awards, and more than 60 invited and contributed sessions. Deadline for submitting contributed talks: 1 April 2026.
- European Meeting of Statisticians 2026, 24-28 August 2026, Lugano, Switzerland. This conference is sponsored by the European Regional Committee of the Bernoulli Society, and is the main conference in statistics and probability in Europe. This meeting features 7 plenary speakers, 21 invited sessions and many contributed sessions. Submission deadline for contributed talks/posters: 31 March 2026.

THE JEFFREYS PRIOR AT 80: A FOUNDATION FOR OBJECTIVE BAYESIAN INFERENCE

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Bayesian parametric inference requires the specification of a prior distribution. In many applications, however, choosing a meaningful prior can be difficult due to the lack of reliable expert knowledge or the limited interpretability of model parameters. This has motivated the search for prior distributions that can be interpreted as "non-informative" (or, less controversially, "weakly informative") and that are preferably obtained from a formal mathematical rule. This idea dates back to the work of Thomas Bayes and Pierre-Simon Laplace, who employed uniform priors, later justified by Laplace through the "principle of insufficient reason".

The Jeffreys Prior

A pioneering example of a prior based on a formal mathematical rule is the Jeffreys prior [11], published eighty years ago, which crystallised the invariance argument initially proposed in [10]. For a parameter vector θ, this prior is defined as $\pi(\theta) \propto \sqrt{\det I(\theta)}$, where $I(\theta)$ denotes the Fisher information matrix. The main motivation behind the Jeffreys prior is to obtain a prior that is invariant under reparameterisations, which can also be interpreted through concepts from information geometry, then providing a principled rule for prior specification. This proposal is often regarded as marking the beginning of what is now known as "Objective Bayes", a research area devoted to constructing prior distributions from formal principles [12].

Alternative Approaches

Since then, a number of alternative constructions have been proposed [5]. Notably, the reference prior [2] is defined by maximising the asymptotic expected information gain from the data and has been developed for a wide variety of models of practical interest. In multi-parameter models, the construction depends on the parameter of interest, so that different reference priors may arise depending on the inferential focus. Other approaches construct priors by assigning distributions to interpretable quantities of interest, such as measures of the effect or impact of parameters [18, 17], and penalised complexity priors [19]. A different line of work develops priors that produce posterior distributions with desirable frequentist properties, such as probability matching priors [6]. Further proposals have been based on alternative optimality criteria, including constructions derived from scoring rules [13]. More recently, priors based on information measures other than the Fisher information have been proposed. For example, the Wasserstein prior [14] is invariant under reparameterisations in a similar spirit to the Jeffreys prior, but is derived from the Wasserstein information matrix.

Current Challenges

The literature on objective prior construction has grown substantially over the past decades, to the extent that comprehensive book-length treatments of the subject are now available [3]. Despite this progress, several important challenges remain open. These include

- deriving conditions for posterior propriety when the objective prior is improper is often challenging in complex models and, arguably, frequently neglected for this reason,

- the development of objective priors for increasingly complex models (*e.g.*, mixed models, high-dimensional models, models with discrete parameters, or models with intractable likelihoods; see [8, 15]) or Bayesian Non-parametrics,
- the use of objective priors in situations where model uncertainty is resolved through Bayes factors. In principle, this precludes priors that are improper on model-specific parameters, but many different solutions have been proposed in the literature. One approach is to use part of the data as a training sample to convert improper priors into proper ones, leading to the intrinsic Bayes factors of [1]. Instead of a training sample, [16] proposed using a fraction of the likelihood, resulting in fractional Bayes factors,
- the formulation of rules based on utility functions other than the likelihood, which may lead to extensions within the framework of Generalized Bayesian inference [4], now sometimes referred to as "post-Bayes" methods,
- exploring the meaning and implementation of objective Bayesian inference in other post-Bayes settings where Bayesian inference is constructed from a likelihood and a predictive, rather than from a likelihood and a prior, such as in the recursive predictives of [9] and the martingale posteriors of [7].

Overall, Objective Bayes remains an active area of research that has attracted sustained interest over many decades. Although its popularity has fluctuated over time, its importance for statistical theory and practice can not be denied and it continues to be supported by a vibrant research community, with a strong presence within the International Society for Bayesian Analysis. We fully expect that considerable progress on dealing with the challenges mentioned above (and undoubtedly many others) will have been made by the time the 100th anniversary of [11] comes around.

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SOFTWARE HIGHLIGHT:
PROGRAMMING WITH MODELS USING NIMBLE

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NIMBLE (r-nimble.org) is a system, first released in 2014, for building and sharing analysis methods for statistical models, especially for hierarchical models and computationally-intensive methods. NIMBLE is built in R but compiles models and algorithms using C++ for speed [1].

NIMBLE includes three components:

1. A system for writing models in the JAGS/BUGS-compatible NIMBLE model language.
2. A language embedded in R for programming algorithms for models, including general support for automatic differentiation (AD; via the `CppAD` library) and with both models and algorithms compiled through C++ code and loaded into R.
3. An extensive library of built-in algorithms, including:
    - MCMC, which can be used directly or after customizing sampler choice,
    - Hamiltonian Monte Carlo (via the `nimbleHMC` package),
    - sequential Monte Carlo (via the `nimbleSMC` package),
    - Laplace and adaptive Gauss-Hermite quadrature (AGHQ) approximation and an INLA-like nested approximation (via the `nimbleQuad` package),
    - and support for specialized components including Dirichlet process-based nonparametric distributions, conditional auto-regressive models, and reversible jump for variable selection.

NIMBLE has some key features in comparison with other probabilistic programming systems, and with method- or model-specific software packages, that can make it a good choice for various problems. First, by providing easy-to-use implementations of a variety of modern methods, one can easily try out different methods on a model, without having to switch systems or recode the model. For MCMC, the system provides particular flexibility: users can mix-and-match various built-in samplers (e.g., conjugate/Gibbs, slice, Metropolis-Hastings, Barker, Pólya-gamma, HMC) within a single MCMC as well as adding their own samplers. Second, NIMBLE's algorithms are written in an R-like syntax, so it is generally straightforward for users to inspect, modify, extend, add, and combine algorithms. In addition to standard mathematical and statistical operations, one can use AD to get derivatives (including Hessians and third-order derivatives) with respect to both functions and model log-probabilities for use in algorithms. Finally, the model language is a slight variation (including various enhancements) on that used in BUGS and JAGS that also allows one to easily define new functions and distributions, including a macro functionality for shorthand code for more complicated motifs.

While NIMBLE is often used with Bayesian hierarchical models, it is not only for Bayesian models and not only an MCMC engine. For example, one can use Laplace (and more general AGHQ) approximation for approximate maximum likelihood estimation and one can build other non-Bayesian algorithms (e.g., our implementation of Monte Carlo EM uses NIMBLE's MCMC engine for the E-step and NIMBLE's optimization and AD capabilities for the M-step). NIMBLE's newest algorithm is an INLA-like deterministic nested posterior approximation whose methodology borrows heavily from both INLA [5] and the extended latent Gaussian models approach implemented in the `aghq` package in R [6] to produce deterministic univariate marginals for parameters and joint posterior samples for latent variables (and optionally for parameters) [7]. NIMBLE has seen its most widespread adoption in the field of ecology (where the ability to very flexibly specify a model for complicated data, including discrete parameters, is often critical), but it is a general purpose system and has been used for problems in a wide variety of disciplines.

One additional area of use is for teaching. Students can easily define a probabilistic model and fit the model using various methods, including exploring different MCMC samplers. It is straightforward to look at the R-based internal implementations, including modifying an implementation to create an alternative algorithm that can then be as easily used as NIMBLE's built-in algorithms.

NIMBLE does have some limitations, which we are working to improve in a heavily-revamped NIMBLE 2.0. First NIMBLE is primarily for serial (non-parallel) execution, though some parallelization of MCMC chains and threaded linear algebra is possible. Second, NIMBLE does not scale well to large problems in some cases, particularly with large numbers of nodes in the graphical structure of the model (e.g., hundreds of thousands of nodes), although some tricks can help improve performance (e.g., combining nodes into larger non-scalar nodes as seen in the example). Third, because NIMBLE compiles the model and algorithm code to C++ and then machine code, there is some initialization overhead, particularly for larger models. In return, though, users have full control over defining essentially arbitrary models and algorithms.

NIMBLE 2.0 will be based on a new `nCompiler` package that thoroughly redesigns the NIMBLE compilation system, in particular providing a general-purpose tool to define functions and classes in R that will be compiled to C++, leveraging the capabilities of `Rcpp` and `Eigen`, plus parallelization via the `TBB` library. `nCompiler` will interface with a new (internal) NIMBLE model structure that represents nodes in the model graph more compactly. It should greatly improve NIMBLE's scalability and make for a better programming experience in the NIMBLE system, including using NIMBLE to build one's own package (e.g., using NIMBLE's MCMC engine or AD system within a package that implements an algorithm).

Example: one model, many methods

We fit a multi-species occupancy model (MSOM) using multiple methods: NIMBLE's general MCMC system, HMC, Laplace approximation and nested deterministic posterior approximation. Occupancy models are used in ecology to analyze the presence of animal species in relation to covariates across multiple locations (sites) under imperfect detection, disentangling presence from detection based on replication in time. The models involve two binary regression components, one for detection given presence (occupancy) and a second for occupancy, with each related to covariates. MSOMs add an additional layer of analyzing multiple species, generally tied together using species-level random effects.

We fit an MSOM to 15 carnivore species in northern California, using camera trap data collected by the California Department of Fish and Wildlife (CDFW) [2], using seven occupancy covariates and five detection covariates. Here is the model code, which is specified using NIMBLE's model language and comes from a specific analysis done in collaboration with CDFW, but the model code is easily altered for model variations.

```
code <- nimbleCode({   # Model code is specified in R.
  # (hyper)parameter priors
  for(k in 1:k_occ) {
    mu_occ[k] ~ dnorm(0, sd = 100) # Various parameterizations possible; `sd` here.
    sd_occ[k] ~ dunif(0, 100)      # Avoid inverse-gamma priors per Gelman (2006).
  }
  for(k in 1:k_detect) {
    mu detect[k] ~ dnorm(0, sd = 100)
```

```
    sd detect[k] ~ dunif(0, 100)
  }
  for (i in 1:n_species) {
    # Random effects distributions for regression coefficients.
    for(k in 1:k_occ)
      beta_occ[k, i] ~ dnorm(mu_occ[k], sd = sd_occ[k])
    for(k in 1:k_detect)
      beta_detect[k, i] ~ dnorm(mu_detect[k], sd = sd_detect[k])

    # Probability of occupancy with covariates varying by site.
    logit(prob_occ[1:n_sites,i]) <- X_occ[1:n_sites,1:k_occ] %*% beta_occ[1:k_occ,i]

    # Probability of detection, covariates varying by site-time or site-time-species.
    logit(prob_detect[1:n_sites, 1:max_num_sites, i]) <- beta_detect[1,i] +
      beta_detect[2,i] * X_detect1[1:n_sites,1:max_num_sites] +
      beta_detect[3,i] * X_detect2[1:n_sites,1:max_num_sites] +
      beta_detect[4,i] * X_detect3[1:n_sites,1:max_num_sites] +
      beta_detect[5,i] * X_detect4[1:n_sites,1:max_num_sites,i]

    ## User-defined vectorized distribution for obs. matrix, one term per species.
    y[1:n_sites, 1:max_num_sites, i] ~ dOcc_multisite(
      probOcc = prob_occ[1:n_sites,i],
      probDetect = prob_detect[1:n_sites, 1:max_num_sites, i],
      reps = reps[1:n_sites],  # Number of time points per site.
      n_sites = n_sites)
  }})
```

This is a marginalized version of the model. One could also use MCMC, but not HMC (nor Laplace-based methods), to fit a latent-variable version of the model with indicator variables representing presence of a species at a site. In previous work we found generally better MCMC performance using the marginalized model (i.e., summing over the discrete latent variable values). The marginalized distribution for the observations is not a built-in distribution, so we need to write a user-defined distribution. Here we extend the occupancy distribution defined in the `nimbleEcology` package (`nimbleEcology::dOcc_v`) to create a vectorized distribution over sites (`dOcc_multisite`), writing the joint density for the observation matrix (site by replicate), shown in detail later. This reduces the size of the model graph to improve compilation efficiency by reducing overhead in NIMBLE (which creates objects for every node in the graph).

We first define a model object in R (with a corresponding compiled version of the model):

```
model <- nimbleModel(code, data = list(y = y),
                     constants = list(n_sites = n_sites, n_species = n_species,
                       max_num_sites = max_num_sites, reps = reps, k_occ = k_occ,
                       k_detect = k_detect, X_occ = X_occ,
                       X_detect1 = X_detect1, X_detect2 = X_detect2,
                       X_detect3 = X_detect3, X_detect4 = X_detect4),
                     inits = inits, buildDerivs = TRUE)  # Inits not shown here.
cmodel <- compileNimble(model)   # Compiled (C++) version of the model.
```

Now we fit the model using the various methods chosen. We retain only key illustrative output. First we use HMC:

```
library(nimbleHMC)
monitors <- c('mu_occ','sd_occ','mu_detect','sd_detect','beta_occ','beta_detect')
conf <- configureHMC(model, control = list(warmupMode = 'iterations',
                     warmup = 1000), monitors = monitors)
hmc <- buildMCMC(conf)
chmc <- compileNimble(hmc, project = model)
samples_hmc <- runMCMC(chmc, niter = 6000, nburnin = 1000)
```

Next we exploit NIMBLE's flexible MCMC system to define a customized MCMC sampler configuration to improve MCMC efficiency (defined as effective sample size per minute), specifically using slice sampling for the random effect standard deviations, conjugate (Gibbs) samplers for the random effect means, and Barker sampling [3] for blocks of the random effects, as developed in previous work. The Barker sampler is a gradient-based adaptive Metropolis-Hastings algorithm that provides more robustness to tuning than Metropolis-adjusted Langevin sampling and is less computationally intensive than HMC.

```
# Set up initial MCMC sampler config just on the means (NIMBLE detects conjugacy).
conf <- configureMCMC(model, nodes = c('mu_occ','mu_detect'), monitors = monitors)
sd_nodes <- model$expandNodeNames(c('sd_occ','sd_detect'))
for(node in sd_nodes)
  conf$addSampler(node, type = 'slice')  # Slice sampling for variance components.
for (i in 1:n_species){
  # Specialized block (Barker) sampling for random effects (regression coefficients),
  # with a block for each species within each logistic regression component.
  blockNodes <- model$expandNodeNames(paste0('beta_occ[,',i,']'))
  conf$addSampler(blockNodes, type = 'barker')
  blockNodes <- model$expandNodeNames(paste0('beta_detect[,',i,']'))
  conf$addSampler(blockNodes, type = 'barker')  }

mcmc <- buildMCMC(conf)
cmcmc <- compileNimble(mcmc, project = model)
samples_custom <- runMCMC(cmcmc, 25000, nburnin = 2000)
```

Next we use (approximate) maximum likelihood estimation via Laplace approximation.

```
library(nimbleQuad)
laplace <- buildLaplace(model, control = list(ADuseNormality=FALSE))
## `ADuseNormality=FALSE` changes configuration to use AD for all derivatives
## rather than analytically-determined for Gaussian distributions, which allows
## use of more efficient AD-based gradient of Laplace approximation in optimization.
claplace <- compileNimble(laplace, project = model)
fit_laplace <- runLaplace(cmLaplace)
```

Finally, we apply NIMBLE's nested posterior approximation.

```
library(nimbleQuad)
fit_approx <- buildNestedApprox(model, control=list(ADuseNormality=FALSE))
```

`buildNestedApprox` reports the automated determination of parameters versus latent nodes, and conditional independence between species allows use of 15 smaller Laplace approximations rather than one large approximation (improving efficiency), also the case for Laplace approximation above.

```
Building nested posterior approximation for the following node sets:
  - parameter nodes: mu_detect (5 elements), mu_occ (7 elements), sd_detect ...
  - latent nodes: beta_detect (75 elements), beta_occ (105 elements)
  with CCD grid for the parameters and Laplace approximation for the latent nodes.
  [Warning] There is a large number of parameter nodes. Computation may be slow.
Building 15 individual Laplace approximations (one dot for each): ...............
```

```
capprox <- compileNimble(approx, project = model)
results <- runNestedApprox(capprox)
samples_nested <- results$sampleLatents(500)
```

Here are the estimates, with uncertainty, for one of the detection coefficients (for all 15 species) and for the 12 random effect means.

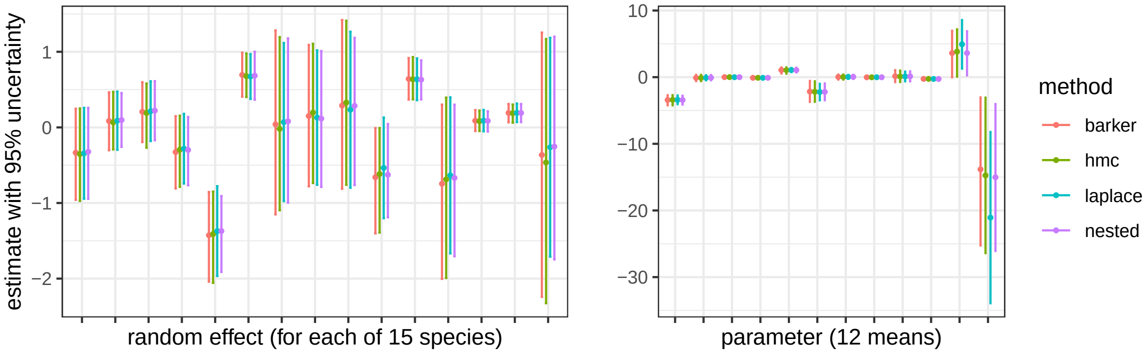

Figure 1: Estimates for one detection coefficient (left) and random effect means (right).

Here are some high-level comments comparing fitting using the four approaches:

- HMC took 290 minutes to generate 6000 samples, while our customized sampler took 55 minutes to generate 25000 samples. The effective sample sizes per minute varied by parameter but were generally 2-50 times larger with the customized sampler than HMC. We are not claiming that a customized approach will generally outperform HMC (and indeed effort is involved to determine the customization), but we have found various cases where other MCMC configurations do markedly better than HMC.
- Laplace-based maximum likelihood estimation took 9 minutes. The standard errors for the estimates were generally a bit smaller than the MCMC-based posterior standard deviations. One potential use for Laplace is for initial model selection and determining starting values, with MCMC reserved for one or a small number of "final" models.
- Nested posterior approximation approach is slow with this model because it has 24 hyperparameters. While an initial approximation to the joint hyperparameter posterior (using the integration-free method developed for INLA [4]) is feasible (taking 17 minutes), improvement via AGHQ marginalization for the univariate marginals is not computationally feasible, while sampling for the latent values is slow (83 minutes) because the method evaluates the Laplace approximation at 1073 hyperparameter grid points (using the CCD grid pioneered by INLA). The approximate posterior credible intervals are reasonably consistent with the MCMC-based estimates but in some cases are too narrow.

Extending the NIMBLE model language

As discussed, a key feature of NIMBLE is the ability to extend the model language with custom distributions and functions. As an example, here is the `dOcc_multisite` distribution that we wrote for the MSOM example that marginalizes over latent variables for presence of a species at a site and does so jointly for all sites at once.

```
dOcc_multisite <- nimbleFunction(run =
  function(x = double(2), probOcc = double(1), probDetect = double(2),
    reps = double(1), n_sites = integer(0), log = logical(0, default = TRUE)) {
    returnType(double(0))    # Return type annotation for compilation to C++.
    logProb <- 0
    for(j in 1:n_sites) {
      nrep  <- ADbreak(reps[j])    # Avoid differentiation w.r.t. `reps[j]`.
      logProb_x_given_occupied <- 0
      prob_x_given_unoccupied <- 1
      for(i in 1:nrep) {
        x_ji <- ADbreak(x[j,i]) # Avoid differentiation w.r.t. x[j,i].
        if(!is.na(x_ji)) {
          logProb_x_given_occupied <- logProb_x_given_occupied +
            dbinom(x[j,i], prob = probDetect[j,i], size = 1, log = TRUE)
          if(x_ji == 1) prob_x_given_unoccupied <- 0
        }
      }
      logProb <- logProb + log( exp(logProb_x_given_occupied) * probOcc[j] +
                    prob_x_given_unoccupied * (1 - probOcc[j]) )
    }
    if(log) return(logProb) else return(exp(logProb))
  }, buildDerivs = list(run = list(ignore=c('i','j','x_ji','nrep')))) # Ignore in AD.
```

The distribution is written as "nimbleFunction", which is a function written in the NIMBLE algorithm language, an enhanced subset of R syntax from which NIMBLE can generate C++ code. Some type annotation is required to assist NIMBLE's compilation to statically-typed C++ code. This particular nimbleFunction supports AD, which is needed for use with derivative-based algorithms such as those used in the example. One can define the nimbleFunction in a user session and the NIMBLE compilation system will find it when compiling the model.

Writing new methods

For new general or application-specific methods, a key aspect of NIMBLE is the ability to write your own algorithms, either in whole, as a part of a NIMBLE-provided algorithm, or by combining pieces from existing algorithms in NIMBLE, all while leveraging NIMBLE's model infrastructure. Examples include user-defined functions in model specifications, user-defined MCMC samplers for use within the NIMBLE MCMC engine, and more general algorithms, all implemented using one or more nimbleFunctions. These nimbleFunctions are similar to the user-defined distribution above, but with some additional structure.

As illustration, we write a simplified version of the Barker sampler, shown in the HTML version of the bulletin. Of course this sampler exists in the NIMBLE MCMC sampler library, but any NIMBLE user could write this sampler if it were not already provided. A user-defined MCMC sampler can be used in combination with the standard samplers provided by NIMBLE without any additional steps, with NIMBLE's MCMC engine applying all the samplers in an MCMC configuration to carry out a complete MCMC algorithm.

In general, nimbleFunctions have "setup" code, written in R, that allows an algorithm to be applied (specialized) to any model. For example, for an MCMC sampler, the setup code uses NIMBLE's model processing functionality to determine relationships amongst nodes in the model graph to determine what nodes are involved in the specific calculations of the sampler (e.g., child nodes when setting up a Metropolis sampler for a specific parameter). Then the "run" code implements the algorithm in a model-agnostic way using "generic" variables defined in the setup code, via one or more functions (methods) written in the NIMBLE algorithm language. For the Barker sampler, we have a main `run` function and auxiliary functions that carry out specific calculations: calculating the log-density (`calcLogProb`), the gradient (`gradient`), parameter transformation (to the real line)(`inverseTransformStoreCalculate`), and adapting the proposal covariance (`adaptPropCov`).

All the algorithms in NIMBLE's algorithm library are defined using nimbleFunctions and found in the `nimble` package source code's `R` directory.

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