

THE ISBA BULLETIN



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The official bulletin of the International Society for Bayesian Analysis

A MESSAGE FROM THE PRESIDENT

- Marina Vannucci -
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Howdy! It is a great honor to serve as ISBA President for 2018!

I would like to start by thanking Kerrie Mengersen for her dedicated service to our Society as the 2017 ISBA President, and also for currently leading our SafeISBA Task team. Many thanks also to Steve McEachern, who retires as Past-President, to the four retiring Board members, Sudipto Banerjee, Carlos Carvalho, Vanja Dukic, and Alessandra Guglielmi, and all retiring section and chapter officers. A very warm welcome goes to Rachel Prado, who joins the Executive team as President-Elect, to Alicia Carriquiry, Michele Guindani, Lurdes Inoue and Surya Tokdar, who join the ISBA Board, and to all the newly appointed section and chapter officers. I thank you all for your service. ISBA is extremely grateful to all those who contribute valuable time and effort!

ISBA has grown tremendously over the past several years, becoming one of the largest professional societies. In spite of such growth, we still retain a strong identity and a genuine sense of community. Of course, such growth has also presented challenges at times, including the recent events where ISBA has been at the center of a debate on sexual harassment. As incoming President, I was proud to see the Executive members and our community come together with a strong and unanimous reaction to those unfortunate events. More is in the works. The safeISBA Task Team (<https://bayesian.org/membership/safe-isba/>) has been hard at work drafting a Code of Conduct and a set of policies and procedures, which we plan to have in

place before the 2018 ISBA World Meeting. The current members of the SafeISBA Task Team are: Kerrie Mengersen (chair), myself, Clara Grazian, Amy Herring, Daniele Durante, Christian Robert and David Rossell. At the World Meeting, all members will have the opportunity to engage with the Task Team and the ISBA officers to enable the exchange of scientific information and networking opportunities in an environment that is as safe and welcoming as possible. ISBA will also participate in a panel (continued p. 2)

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at the JSM that will address issues of harassment in our profession. All those activities will hopefully generate greater engagement on the issue, enable broader input and discussion, and provide an opportunity for ISBA to participate in a profession-wide endeavor to create more awareness about safety and harassment in the future.

Of course, we are all excited about the ISBA world meeting, that will take place in Edinburgh, UK, on June 24-29 (<https://bayesian.org/isba2018/>). The local organizing committee is doing a great job putting together the program and preparing a wonderful meeting for all participants. Veronika Rockova has just been named the Bayarri lecturer, and you can find details of other keynote, foundational, and named lecturers in the Program Council section of this *Bulletin*. The conference program will be completed with sessions on a wide range of topics, such as advances in computational methods, nonparametric methods, theory and foundations, graphical models and networks, and many others, including contributions from all the ISBA sections and highlights from Bayesian Analysis. Moreover, as per our tradition, at the world meeting we will recognize the recipients of the ISBA prizes and awards, including the Lindley Prize, the Mitchell Prize, the DeGroot Prize and the Savage Awards for outstanding doctoral dissertations, and we will honor the newly named ISBA fellows. Do not forget: early registration to the conference is available until March 31st, so hurry up!

There are several other exciting ISBA co-sponsored or endorsed meetings happening during summer 2018 in convenient proximity to the World Meeting. These will provide more focused gatherings and are mostly led by members of our Society's Sections. See the program council section or visit the ISBA website for more information!

Looking ahead, the 2020 World meeting will be held in Kunming, Yunnan, China, on June 29-July 3rd, and we are now ready to send out a call for proposals to host the 2022 World Meeting. I strongly encourage anyone interested in hosting the meeting to submit a pre-proposal. Organizing our main scientific gathering is an excellent opportunity to contribute to the life of our society! The deadline for submissions is May 31st, 2018. Selected pre-proposals will be invited to submit a full proposal later in 2018. Further information can be found on page 5.

Finally, the ISBA Editorial search committee is working on finding our next Bayesian Analysis Editor in Chief, Editor of ISBA Bulletin and Web Editor. Editor in Chief candidates are being considered now (deadline March 23); the application deadline for the other two positions is April 15-see page 3 for details. The search committee will follow-up with each nominee. Please consider stepping in for these crucial service roles!

-Marina

FROM THE EDITOR

- Beatrix Jones -

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Those of you in some parts of the world will have participated in a "Research Assessment Exercise." Here in New Zealand, part of this exercise involves enumerating and explaining our various activities and how they contribute to the research environment. So I have just written a stirring paragraph about how being Editor of the *ISBA Bulletin* is such a contribution because it involves publicising ISBA's research meetings and the highlights of our research journal, *Bayesian Analysis*; includes articles about our research and researchers in features like the software highlight and interviews; and in general facilitates the work of our Society, which promotes research both about Bayesian analysis and using Bayesian analysis. As well as looking good in exercises such as this, being editor of the *Bulletin* has taught me a lot about what ISBA does and how it does it. Would you like to be the next editor of the *ISBA Bulletin*? Expressions of interest are being sought. Or if a newsletter sounds a bit 20th century to you, a new web editor is also being sought. As you will be aware, the position of web editor is absolutely fundamental to how ISBA interacts with its members. See the advertisements for both roles that immediately follow this column, and get in touch by April 15.

In this issue, we welcome Clara Grazian as an associate editor. Clara will be bringing us the latest from j-ISBA each quarter, and starts off by catching us up with what has been happening with this very active section over the past year. I also want to draw your attention to the Software Highlight, which features a Matlab interface for nonparametric Bayesian analysis of fMRI data, developed by Jeong Hwan Kook and Marina Vannucci; correspondence on the “Witches of Bayes” story from our last *Bulletin*; and a report on the 2017 O-Bayes meeting. Finally, check the call for proposals for the 2022 World Meeting, the Program Council column for the latest on the upcoming World Meeting as well as other ISBA endorsed events, and News of the World for the call for nominations to the nominating committee, and other announcements.

Best,
Beatrix

CALL FOR EDITORS

ISBA Bulletin Editor

Description: The International Society for Bayesian Analysis (ISBA) publishes a quarterly bulletin to its members with content including, but not limited to, a message from the president, updates on the journal Bayesian Analysis, information on upcoming meetings and various scientific highlights. The Editor of the ISBA Bulletin is responsible for coordinating the team of associate editors to solicit relevant articles for the publication and editing the content for correctness. The editor then compiles the articles into the final *Bulletin*.

Qualifications: Strong reliability, easily contacted, LaTeX (what is currently used) or equivalent. Ideas about what ISBA members would be interested in reading.

To Apply: Send a short CV (or link to one) and 1 paragraph statement to the ISBA Editorial Search Committee via beatrix.jones@auckland.ac.nz. The statement should briefly detail relevant qualifications for the position and any ideas for improvement of the Bulletin. Expressions of interest for Associate Editor roles are also welcome.

Deadline for applications is April 15, 2018.

ISBA Web Editor

Description: The Web Editor for the International Society for Bayesian Analysis (ISBA) will maintain the ISBA website and oversee all content contained and posted to the society’s website.

Qualifications: Understanding of ISBA’s operations; experience using WordPress (or other content management system), HTML, CSS, php and Javascript is encouraged but not required.

To Apply: Send a 2 page CV and 1 paragraph statement to calder@stat.osu.edu. The statement should detail prior involvement with ISBA and web development experience.

Deadline for applications is April 15, 2018.

FROM THE PROGRAM COUNCIL

program-council@bayesian.org

ISBA 2018 World Meeting

24-29 June, Edinburgh, UK. We're please to announce the speakers for keynote/foundational/named sessions, the selection of ISBA section-contributed and member-contributed talks, two satellite meetings and an open call for travel support.

- Keynote lectures: Nicolas Chopin (ENSAE, France), Montse Fuentes (Virginia Commonwealth University), Michael Jordan (UC Berkely) and Steve MacEachern (Ohio State University).
- Foundational lectures: Alan Gelfand (Duke University), Ed George (University of Pennsylvania), Tony O'Hagan (University of Sheffield) and Judith Rousseau (University of Oxford).
- Named lectures. De Finnetti lecture given by Phil Dawid (Cambridge University). The Bayarri lecture will be given by Veronika Rockova.
- Proposals by ISBA sections and member-contributed sections have been selected. Individual abstracts for posters and oral contributions are currently being assessed, with outcomes expected to be announced by April 1st.
- Satellite meetings: we're please to announce two satellite meetings BAYES2018 and Baysm 2018 taking place before and after ISBA 2018 respectively. See below for more information.
- Travel support applications for junior researchers: the opens from March 15 to April 15. Please see <https://bayesian.org/isba2018/local-info-travel/> for more information.

Other Upcoming ISBA-endorsed meetings and events

- Bayescomp 2018. Meeting of the ISBA Computational Section. March 26-28, Barcelona, Spain. <http://www.maths.nottingham.ac.uk/personal/tk/bayescomp>
- RCEA 12th Rimini Bayesian Worskhop. June 14-15, Rimini (Italy) <http://rcea.org/wp-content/uploads/2018/02/RCEA-12th-Annual-Bayesian-Workshop-CFP.pdf>
- Bayesian Biostatistics meeting 2018 (BAYES 2018). 20-22 June. Cambridge, UK. <http://www.mrc-bsu.cam.ac.uk/event/bayes-2018-bayesian-biostatistics-workshop-satellite-isba-2018>
- Baysm 2018. Official meeting of the j-ISBA Section. July 2-4, University of Warwick, UK. <https://warwick.ac.uk/fac/sci/statistics/staff/academic-research/wade/2018baysmconference>
- BNP 2019. Meeting of the ISBA non-parametrics section. June 24-28, 2019, Oxford, UK.

Meeting Planning

- See the call for proposals for the 2022 ISBA World Meeting in this *Bulletin*, or find the full information at: <https://bayesian.org/events/world-meeting-planning/>!
- If you're planning a meeting and would like to request financial sponsorship or an endorsement from ISBA please see <https://bayesian.org/events/request-sponsorshipendorsement>. Requests should be emailed to the ISBA Program Council at program-council@bayesian.org.

CALL FOR ISBA 2022 PROPOSALS

ISBA announces a call for pre-proposals for the ISBA World Meeting 2022. We strongly encourage any interested members to contribute to the main scientific gathering of our society by submitting a pre-proposal. The deadline for submissions is May 31st 2018. Selected pre-proposals will be invited to submit a full proposal later in 2018.

Pre-proposals should provide as much detail as possible regarding dates, conference venue, estimated meeting expenses broken down by fixed costs and per-participant costs, suggested registration fee and expected participant costs (hotels, shuttles). Meetings should be planned to be revenue neutral. The pre-proposal should also indicate a local organizing committee and chair. This local organizing committee has primary responsibility for organizational tasks and seeking local funding. A scientific committee will be appointed by the ISBA Program Council and will have primary responsibility over the scientific program and seeking non-local funding.

World Meetings are typically held in June or July at a time of year that helps maximize attendance, although timing may vary depending on the local circumstances of the chosen venue. The venue should be a location accessible to a large proportion of ISBA membership. Submissions and questions should be sent to the ISBA Program Council at program-council@bayesian.org. Further guidelines on hosting the ISBA World meeting can be found at <https://bayesian.org/events/world-meeting-planning/>.

UPDATES FROM BA

From the BA Editor
- Bruno Sansó -
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The March issue of the journal is available online at <https://projecteuclid.org/current/euclid.ba>. This issue includes eleven papers on a wide variety of interesting topics in Bayesian methods. One of the papers is the discussion paper: “Computationally Efficient Multivariate Spatio-Temporal Models for High-Dimensional Count-Valued Data” by Jonathan R. Bradley, Scott H. Holan, and Christopher K. Wikle. The invited discussants are Catherine Calder and Candace Berrett; Stefano Castruccio; and Dani Gamerman. William Weimin Yoo; and Andrew Hoegh, Kenneth Flagg, and Christian Stratton; and Kevin He, and Jian Kang contributed to the discussion. The core of the paper is based on the development of a multivariate log-gamma distributions that can be used to leverage conjugacy with a Poisson likelihood to obtain an effective method to fit flexible spatio-temporal models for data corresponding to counts.

The discussion paper for the June issue will be the paper “Bayesian cluster analysis: Point estimation and credible balls” by Sara Wade and Zoubin Ghahramani. The invited discussants for this paper are: Nial Friel, Stefano Monni and Peter Müller. The paper is already available in advanced publication at <https://projecteuclid.org/euclid.ba/1507687687>.

ISBA 2018 is coming soon, and, as has become traditional, BA will have an invited session that focuses on some the main topics of interest for the readership of the journal and highlight the work of researchers that contribute to Bayesian Analysis. The session will have the title: Lassos and horseshoes for the sparse Bayesian cowboy. It will feature the speakers: Nic Polson, on “Lasso Meets Horseshoe;” Botond Szabo on “Uncertainty quantification and model selection for sparse Bayesian methods;” James Scott on “Bayes-optimal post-selection inference under sparsity;” and Ryan Martin on “Empirical priors for wranglin’ with structured high-dimensional problems.” In case you wonder where to find the right attire to attend the session, visit <http://www.orientaltrading.com/cowboy-hat-a2-13605891.fltr?categoryId=551197>. See you in Edinburgh!

THE WITCHES OF BAYES

In our last *Bulletin* we solicited your responses to “The Witches of Bayes,” a fairy tale written by staff at the Italian National Institute of Statistics (ISTAT), Italy’s body for official statistics. Readers of Italian can find the original version here: <https://www.istat.it/it/archivio/204260> (“The Witches of Bayes” starts on page 42, with an appendix on page 62). Non-readers of Italian can refer to the last issue of the Bulletin for a synopsis. We received two commentaries on the story, from Luca La Rocca, and from Giulio D’Agostini, who originally brought the story to our attention.

- Luca La Rocca-

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First, as a native Italian speaker, I should like to make some minor remarks on the synopsis:

- the randomly selected witch places her hat (not her hut) outside the entrance of the cave, and the villagers from Bayes leave the food on a plate beside it (not inside it);
- the witches have either black or purple hats (not pink—who would be scared by a witch dressed in pink?!) and of course, since 6/7 of the purple hatted witches like sweet food, the remaining 1/7 (not 1/6) like savory food.

Next, if the goal is to minimize the number of dreadful days, the strategy presented in the story is not optimal, leading to 12/49 dreadful days when a purple hat is presented, against 7/49 dreadful days if sweet food is always given in this situation. However, in my opinion, what is really missing is more direction for teachers on how this is meant to be used in the classroom: as our *Bulletin* editor Beatrix put it, simply following up the story with the question “is Nora’s strategy the very best that can be done?” could lead on to a very interesting lesson. Discussion of optimality can also be non-trivial. When I spoke to the story’s authors, they acknowledged that the story should clarify this aspect, but they also pointed out that minimizing dreadful days would leave 1/7 of the witches with purple hats forever hungry, and starving witches for an infinite time promises no good.

The authors also acknowledged that the story is about conditioning, and not about Bayes theorem. I should perhaps conclude that the title is inappropriate, but with such a catchy title I dare not do so. In the end, I still love the story. The proposed strategy is better than the previous one (leading to 1/2 dreadful days whatever the color of the hat) and it teaches the importance of conditioning on the available information. There is arguably room for improvement, but one should be wary of excessive complexity for a target audience of children, and the atmosphere of the story should be preserved.

- Giulio D’Agostini -

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My first reaction to the fairy tale “The Witches of Bayes” was to think it a kind of anti-Bayesian bad joke. However the appendix made it clear that the authors were not anti-Bayesian, but had done a poor job communicating not only about what Bayesian reasoning means, but also about other more ‘classical’ issues. I contacted the authors, who seemed strangely unbothered by the non-optimality of Nora’s solution and the absence of Bayes’ rule from their Bayesian village. Probably I would have abandoned the story, if it had been just any book. But it wasn’t. Behind it there was a clear endorsement by ISTAT. Not only was the book on the ISTAT web site, but it was recommended by an ‘editorial note’, sent directly to Italian schools (see e.g. a copy of the original mail I picked up on the internet in <https://www.roma1.infn.it/~dagos/Nota-editoriale-ISTAT.pdf>). And I found out that, as it happens nowadays, the editorial note had been uncritically reposted by bloggers and zealous teachers.

Encouraged by the feedback of the editors of the ISBA Bulletin, I decided to write something. A kind of ‘antidote,’ a paper in Italian that could possibly reach teachers and students. I have been encouraged to proceed in this direction by the mathematician Mario Barra, one of the closest pupils of Bruno de Finetti in Rome. Having written dialogues in the recent past, I chose the form of the

dialogue, because the argument would help clarify the issues and to anticipate the doubts of the readers. The other two dialoguers were teachers of ‘scuola media’ (school-girls/boy in the age 11-14). So, due to the gap among us on probabilistic and statistical issues, the interaction has been stimulating and productive, and the ensuing dialogue is a kind of long lecture on probabilistic issues, with even some calculations. The paper is presently on the arXiv (<https://arxiv.org/abs/1802.10432>) and it will be published on the “Progetto Alice”, a journal addressed to high school math teachers, directed by Mario Barra.

In the dialogue we analyze the fairy tale, which, contrary to the indication of the appendix, does not contain any Bayesian reasoning. Moreover the proposed tortuous decision strategy is simply mistaken and there are other issues which might confuse children and grown ups. It was not easy to transform the story in order to make it consistent with the indication of the appendix. At most we solved several inferential and predictive problems related to the story: infer the composition of black and purple hats in the cave (under a simplifying hypothesis based on the pieces of information provided by the story); evaluate the probability of a black or purple hat the next morning, based on the series of colors observed the previous days. The solutions are worked out in detail and the problems are illustrated by using little Bayesian networks, which have had a key role in aiding understanding. For this reason the dialogue is a quite long paper (in the fiction it takes a long Sunday afternoon, broken by tea and other pretexts to allow four pauses to the reader). Since several other topics were sketchily touched, a second part is planned, with more details and with the solutions of the assigned problems.

j-ISBA

- Clara Grazian -

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2017 has been a great year for j-ISBA. We designed an official j-ISBA logo and created a brand new website which can be found at <https://j-isba.github.io/>. To keep in touch with our community beyond the Facebook page, also a new blog is now live at <https://jisbablog.wordpress.com/> and will serve as a platform where to present all j-ISBA activities, propose events which may be of interest for junior researchers and create networks among young Bayesians. We are a junior and dynamic Section, and we are always looking for new members and board officers bringing in new enthusiasm and ideas. For these reasons, j-ISBA and ISBA approved a change of our bylaws reducing the previous two plus two terms of the j-ISBA Chair-Elect and Chair offices to one plus one. Besides this, we are also active in working with our ISBA society on the Safe-ISBA documents.

There have been also several sessions and seminars organized by j-ISBA last year. Two j-ISBA sponsored seminars were held at Bocconi University (Milan, Italy) last year, hosting junior Bayesian speakers. James Johndrow, currently a Stein fellow in the Statistics Department at Stanford, will be the next one in July 2018. We hope this stimulating tradition can motivate similar ideas in other Bayesian departments. We also organized two sessions: one at JSM2017 in Baltimore, Maryland, and another at ERCIM WG (CMStatistics) 2017 in London. The first one focused on Junior research in Bayesian modeling for high-dimensional data with talks by Rajarshi Guhaniyogi, Willem van den Boom, Roberta de Vito, Jeff Miller, Frank Marrs, and James Johndrow as chair. The topic of the second session was instead Nonparametric Bayesian analysis of copula models and featured talks by Luca Rossini, Alan Riva Palacio Cohen, Shaoyang Ning and Gianluca Mastrantonio, with Giovanna Jona Lasinio serving as chair. These sessions raised interest, with a good audience and very interesting discussion at the end of each talk.

And this is not the end! We are organizing great events for 2018. j-ISBA is currently helping in the organization of the 4th Bayesian Young Statistician Meeting (BAYSM2018) to be held July 2-3, 2018 at the University of Warwick (<http://warwick.ac.uk/baysm>) and will sponsor two poster awards. Moreover, for the ISBA2018 World Meeting in Edinburgh we organized a stimulating session on Bayesian Modeling of Complex Data and hope to see many of you there. We will be also at JSM2018

in Vancouver, Canada, with a j-ISBA sponsored session on Junior Research in Bayesian nonparametric modeling of complex or unknown populations.

Last but not the least, we would like to thank Silvia Montagna, Lucia Paci and Valerie Poynor for their tireless work for j-ISBA. We would also like to welcome Federico Camerlenghi, Ilaria Bianchini and Weixuan Zhu as new j-ISBA board members. So, who are this year's j-ISBA board members? Let's present them below:

Daniele Durante (Chair): Daniele Durante is currently an Assistant Professor at the Department of Decision Sciences of the Bocconi University, Milan. Previously he was a Post-Doctoral Research Fellow at the department of Statistical Sciences of the University of Padova, where he also obtained his PhD in Statistical Sciences on April 2016, under the supervision of Professors Bruno Scarpa and David B. Dunson. His research is characterized by an interdisciplinary approach at the intersection of Bayesian methodology, complex data (e.g. networks, functions, arrays), modern applications, and statistical learning.

Federico Camerlenghi (Chair Elect): Federico is an Assistant Professor at the Department of Economics, Management and Statistics of the University of Milan-Bicocca. He received his Ph.D. in Mathematics and Statistics from the University of Pavia in December 2015 under the supervision of Prof. A. Lijoi and Prof. I. Pruenster, with a thesis entitled "Hierarchical and Nested Random Probability Measures with Statistical Applications". His research interests encompass both computational and methodological aspects of Bayesian nonparametric statistics, including applications to species sampling problems, disclosure risk assessment and survival analysis.

Clara Grazian (Treasurer): Clara is a Postdoctoral Scientist who has joined the Nuffield Department of Medicine of the University of Oxford in January 2017, after completing a double PhD in Applied Mathematics and Statistics in Universite' Paris-Dauphine and Sapienza University of Rome, where she studied methods to perform Bayesian inference for complicated models, such as dependence and mixture models. She is currently involved in studying the mechanisms of development of drug resistance in Mycobacterium Tuberculosis, by using genome-wide association studies. In her work, she tries to use both frequentist and Bayesian methodologies to work with large datasets.

Weixuan Zhu (Program Chair): Weixuan got his PhD in Statistics from Universidad Carlos III de Madrid. His thesis was entitled "Flexible Bayesian Nonparametric Priors and Bayesian Computational Methods." Then he went to the University of Sheffield as a postdoc research associate, working on the applications of ABC methods in Ecology population modelling. In 2017, he joined Xiamen University as an Assistant Professor. His research interests include Bayesian nonparametric models, Approximate Bayesian Computation, and MCMC algorithms.

Ilaria Bianchini (Secretary): Ilaria is about to conclude a PhD in "Mathematical models and methods for engineering" at Politecnico di Milano, where she graduated in Mathematical Engineering, with a specialisation in applied statistics. Her research has been focused on Bayesian nonparametric models, clustering and biomedical applications. She was member of the local organising committee of BAYSM, the Bayesian young statistician meeting, held in Florence in June 2016. Currently, she is working as a research data scientist in a start-up, dealing with statistical models for natural language processing.

We are currently working on many new stimulating ideas, both scientific and social, to support our junior Bayesian members this year and in the upcoming ones! Stay tuned and join our Section!

CONFERENCE REPORT: O-BAYES17

INTERNATIONAL WORKSHOP ON OBJECTIVE BAYES METHODOLOGY

Austin, TX, December 10–13, 2017 Guido Consonni

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This was the 12th meeting of one of the longest running and preeminent meetings in Bayesian statistics, following earlier meetings held in West Lafayette, IN, USA, 1996; Valencia, Spain, 1998; Ixtapa, Mexico, 2000; Granada, Spain, 2002; Aussois, France, 2003; Branson, MO, USA, 2005; Roma, Italy, 2007; Philadelphia, PA, USA, 2009; Shanghai, China, 2011; Durham, NC, USA 2013; and Valencia, Spain, 2015.

The scientific committee did an excellent job in setting up a very interesting program, and the local organizing committee made sure everything went smoothly.

The first day was devoted to tutorials on Objective Priors, Bayesian Asymptotics, Model Choice, Multiple Testing, Causal Inference and the project “O’Bayes wiki (Wikiprevia)”. In the next three days we listened to uniformly high-level talks on a variety of topics, followed by invited discussions and questions from the floor. Many talks were outright brilliant, innovative and far-reaching. Posters were also generally of very good quality, held on two separate evenings together with a reception. The conference website <https://sites.google.com/site/obayes2017/home/> contains all the details about the schedule; it also hosts slides for most of the presentations.

The next O’Bayes conference will take place in Warwick, UK, on June 29-July 02, 2019 in temporal and geographical connection with BNP, which will be in Oxford, UK, June 24-28.



NEWS FROM THE WORLD

Announcements

ISBA Nominating Committee

Suggestions are sought for members to serve on the ISBA Nominating Committee, which will be charged with selecting candidates for President-Elect, Executive Secretary, and the ISBA Board in our elections this autumn. Please send your suggestions to Marina Vannucci (marina@rice.edu) by 31 March.

Registration and travel support for the ISBA 2018 World Meeting

ISBA 2018 World Meeting is coming up soon in Edinburgh, UK on June 24-27, 2018! This meeting is the continuation of the traditional Valencia/ISBA Meetings regularly held since 1979. They represent a unique event where the Bayesian community gathers together to discuss recent advances and the future of our profession, at the same time looking back to our roots and traditions, following the footsteps of those who laid the foundations of where we are now.

Registration is now open, and early registration will be available until March 31. Detailed information including transportation and accommodation can be found at <https://bayesian.org/isba2018/>.

Travel Support is available for junior researchers (students currently enrolled in an MSc/PhD program or have graduated no more than 3 years ago) who are already registered and whose poster/oral presentation has been approved. Applications should include as a single PDF (named LAST-NAME.FIRSTNAME.ISBAtravel.pdf) file that contains

1. a one-page letter with basic CV info (place/date of academic qualifications) and summarize the research the applicant will present;
2. proof of current enrollment (letter from school or MSc/PhD certificate featuring the graduation date).

Applications should be emailed as an attachment to isba_program2018@griffith.edu.au with

the subject header Travel Support Application. Submission of applications starts on March 15 2018 and ends on April 15 2018. Awardees will be notified as soon as possible afterwards.

Meetings and conferences

Bayesians who are traveling to Edinburgh for the ISBA 2018 World Meeting may want to extend their European stay by attending the following conferences and workshops in the surrounding weeks:

Bayesian Biostatistics Workshop, Homerton College, Cambridge, UK. June 20-22, 2018.

This workshop will bring together scientists interested in the latest applications and methodological developments of Bayesian Biostatistics in trial designs, addressing the need for more efficient and flexible approaches to answer key clinical questions; and in the analysis of complex observational data, to enhance causal understanding of disease processes in support of personalized clinical care and public health policies.

It will comprise of one day training course on Bayesian approaches to incorporate historical data into clinical trials, and two days of keynote talks and contributed oral and poster presentations. If interested, please submit your abstract of contributed presentations to bayes-biostats2018@mrc-bsu.cam.ac.uk by March 31.

More information about the workshop can be found at the conference webpage: <http://www.bayes-pharma.org>. The registration deadline is April 15.

Approximate Bayesian Computation (ABC) in Edinburgh, Edinburgh, UK. June 24, 2018.

This workshop is the latest item of a series of “ABC in...” workshops on approximate Bayesian computation (ABC) and likelihood-free inference, which started with ABC in Paris in 2009! It is a satellite workshop immediately before the main ISBA world meeting.

The site of the workshop is <https://sites>.

google.com/view/abc-in-edinburgh/. Registration is done via the ISBA world meeting webpage. This workshop is part of the “short courses”, and there is an extra 50 Euros charge for attendance. Contributed talks and posters can be submitted prior to May 1.

International Conference in Monte Carlo and Quasi-Monte Carlo (MCqMC) Methods in Scientific Computing, Rennes, France. July 1-6, 2018.

The MCqMC Conference is a biennial meeting on Monte Carlo and quasi-Monte Carlo methods. It usually attracts 150 to 200 mathematicians, computer scientists, statisticians and researchers in related fields.

Early registration is starting soon until May 12. For more information, please visit the conference website <http://mcqmc2018.inria.fr>.

4rd Bayesian Young Statisticians Meeting (BAYSM), Warwick, UK. July 2-3, 2018.

BAYSM is dedicated to Ph.D. Students, M.S. Students, Post-Docs, Young and Junior Researchers working in the field of Bayesian statistics, providing an opportunity to connect with the Bayesian community at large. Senior discussants will be present at each session, providing participants with advice and comments on their work. Recognized figures of the Bayesian community will also participate as keynote and plenary speakers, making an altogether exciting program. It will include social events, providing the opportunity to get to know other junior Bayesians.

Registration is now open and will be available with an early bird discount until May 7 at <https://warwick.ac.uk/fac/sci/statistics/staff/academic-research/wade/2018baysmconference/registration1>. Young researchers, PhD students and MSc students interested in giving a talk or presenting a poster at BAYSM 2018 are cordially invited to upload an extended abstract describing their research work. All authors whose contribution has been accepted for an oral talk or a poster presentation are also invited to extend their papers to be considered for publication in a book of the series Springer Proceedings in Mathematics & Statistics. If you'd like to be considered for travel support, please indicate so in your submission form and attach a short CV. The submission deadline is March 26, 2018.

International Symposium on Business and Industrial Statistics (ISBIS), Athens, Greece. July 4-6, 2018.

This symposium would be of special interest to members of the ISBA Sections on Industrial Statistics, on Economics, Finance and Business, and on Biostatistics and Pharmaceutical Statistics. ISBIS promotes applications, research, and best current practices in business and industrial statistics, facilitates technology transfer, and fosters communications among members and practitioners worldwide.

Contributed Papers/Posters can be submitted by March 28. Early registration is open until April 15. More details about the ISBIS symposium are at <http://www.stat.duke.edu/~banks/barcelona>.

LMS Invited Lecture Series and CRISM Summer School in Computational Statistics, University of Warwick, UK. July 9-13, 2018.

The lecture series and summer school are aimed at both those interested in learning more about the area and established researchers in areas of computational statistics. The initial lectures will focus on foundational aspects of simulation, followed by a series of lectures on four more specialist topics going from the fundamentals of the specialist topic to state-of-the-art

Information about the short courses and the registration be found on the conference website at <https://warwick.ac.uk/fac/sci/statistics/crism/workshops/lms2018>.

Bayesian machine learning in the social sciences, Barcelona Graduate School of Economics (Spain), July 2-6 2018

<http://www.barcelonagse.eu/study/summer-school/data-science> The course will develop the following main components of modern statistical methodology:

1. High-dimensional regression and estimation of treatment effects in presence of very large number of instruments. We cover both modern optimization-based penalized likelihood approaches, such as the lasso, but also probabilistic inference approaches such as Bayesian variable selection and model averaging.
2. Probabilistic models for high-dimensional data, such as latent variable models (fac-

tor models, independent component analysis, latent topic models), hierarchical models and graphical models.

3. Advanced computational methods for statistical learning with models as in (1) and (2), such as Markov chain Monte Carlo and variational Bayes. We also develop one successful approach to learning content from text data, known as topic modelling, which is an instance of the high-dimensional Bayesian models we discuss in (1), (2) that computationally relies on the methods covered in (3).

Alongside the presentation of these statistical tools, we will discuss economic applications that use them, for example treatment effect estimation

and central bank communication. The course includes also lab sessions that provide a hands-on experience with the material.

València International Bayesian Analysis Summer School, València (Spain), July 16-20 2018.

VIBASS2 is the second edition of the summer school on Bayesian Statistics to be held from 16th until 20th July 2018 in València Spain (<http://vabar.es/events/vibass2/>). The summer school offers an opportunity to be introduced into the Bayesian reasoning without previous knowledge in the subject. Participants in VIBASS2 are encouraged to present a poster with their research or projects. Early bird registration available until May 15.

SOFTWARE HIGHLIGHT

NPBAYES-FMRI: NONPARAMETRIC BAYESIAN GENERAL LINEAR MODELS FOR SINGLE- AND MULTI-SUBJECT FMRI DATA

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Functional magnetic resonance imaging (fMRI) is a noninvasive neuroimaging technique which measures the blood oxygenation level dependent (BOLD) contrast, i.e. the difference in magnetization between oxygenated and deoxygenated blood arising from changes in regional cerebral blood flow. In a typical task-related fMRI experiment, a subject is presented a set of stimuli while the whole brain is scanned at multiple time points. Each scan is arranged as a 3D array of volume elements (or “voxels”), and the experiment produces time series of BOLD responses acquired at each voxel.

Common modeling approaches for the analysis of task-related fMRI data rely on the general linear model formulation that was first proposed by [8] and subsequently investigated by many other authors, particularly for single-subject data, see for example [7, 23, 21, 13, 18, 11, 25], among many others. For multi-subject studies, two-stage “group analysis” approaches are often adopted as computationally attractive methods where summary estimates of model parameters are obtained at the individual level and then used in a second stage model at the group/population level, see for example [1, 20, 19, 12]. Also, newer data-driven methods for analyzing fMRI, for example those that use model-free methods such as independent component analysis (ICA) and tensor-product ICA (T-PICA), have been developed to detect the presence of subgroups of participants within a population as in [3], but these approaches still involve multiple estimation steps, and therefore do not properly take into account variability and heterogeneity in the data.

NPBayes-fMRI [10] is a user-friendly MATLAB [14] GUI that practitioners can use for both model fitting and visualization of the results. For inference, the software extends a unified, single-stage Bayesian approach for the analysis of task-related brain activity proposed by [24]. This

model formulation considers a spatio-temporal linear regression model that specifically accounts for between-subject heterogeneity in neuronal activity via a spatially informed multi-subject non-parametric variable selection prior.

1 Bayesian spatio-temporal models for fMRI data

For subject $i = 1, \dots, N$, let $Y_{iv} = (Y_{iv1}, \dots, Y_{ivT})^T$ be the vector of the BOLD response data at voxel ν , with $\nu = 1, \dots, V$. We model the data as

$$Y_{iv} = X_{iv}\beta_{iv} + \varepsilon_{iv}, \quad \varepsilon_{iv} \sim N_T(0, \Sigma_{iv}), \quad (1)$$

where X_{iv} is a known $T \times p$ covariate matrix and $\beta_{iv} = (\beta_{iv1}, \dots, \beta_{ivp})^T$ is a $p \times 1$ vector of regression coefficients. Without loss of generality, we center the data and thus do not include the intercept term in the model. Let X_{ivj} be the j th column of X_{iv} . Then X_{ivj} is modeled as the convolution of the j -th stimulus pattern with a hemodynamic response function (HRF) [2], that is

$$X_{ivj}(t) = \int_0^t x_j(s)h_{\lambda_{ivj}}(t-s)ds, \quad (2)$$

where $x_j(s)$ represents the stimulus pattern. One common choice is a Poisson HRF, that is $h_{\lambda_{ivj}} = \exp(-\lambda_{ivj})\lambda_{ivj}^t/t!$. The parameter λ_{ivj} can be interpreted as the delay of the response with respect to the stimulus onset and it is often modeled as an unknown voxel-dependent parameter.

The error term in equation (1) is modeled as auto-correlated, specifically long memory and Discrete wavelet transforms (DWT) are employed as a way to decorrelate the data. This is a common approach in the fMRI literature [4, 15, 19, 25]. After applying the DWT to equation (1) the model in the wavelet domain can be written as

$$Y_{iv}^* = \sum_{j=1}^p X_{ivj}^* \circ \beta_{ivj} + \varepsilon_{iv}^*, \quad \varepsilon_{iv}^* \sim N_T(0, \Sigma_{iv}^*), \quad (3)$$

with \circ the element-by-element (Hadamard) product, and where W is a $T \times T$ matrix corresponding to the wavelet transform, $Y_{iv}^* = WY_{iv}$, $X_{iv}^* = WX_{iv}$, and $\varepsilon_{iv}^* = W\varepsilon_{iv}$, and with the covariance matrix Σ_{iv}^* approximately diagonal with elements $\psi_{iv}\sigma_{imn}^2$ indicating the variance of the n th

wavelet coefficient at the m th scale. We follow the variance progression method of [22] for the wavelet coefficients,

$$\psi_{i\nu}\sigma_{imn}^2 = \psi_{i\nu}(2^{\alpha_{i\nu}})^{-m}, \quad (4)$$

with $\psi_{i\nu}$ the innovation variance and $\alpha_{i\nu} \in (0, 1)$ the long memory parameter. This structure encompasses the general fractal process, which includes long memory.

Detecting voxels that activate in response to a stimulus is equivalent to identifying the non-zero regression coefficient $\beta_{i\nu j}$ in model (3). In formulas, let $\gamma_{i\nu j}$ be a binary indicator of whether a given voxel is activated or not, that is, $\gamma_{i\nu j} = 0$ if $\beta_{i\nu j} = 0$ and $\gamma_{i\nu j} = 1$ otherwise. A spiked nonparametric prior is imposed on the coefficients

$$\beta_{i\nu j} | \gamma_{i\nu j}, G_i \sim \gamma_{i\nu j} G_{ij} + (1 - \gamma_{i\nu j}) \delta_0, \quad (5)$$

where δ_0 is a point mass at zero and G denotes a known distribution. With multiple subjects, a hierarchical Dirichlet Process (HDP) prior can be specified as the nonparametric slab, inducing clustering among voxels within a subject on one level and between subjects on the second level. This construction enables the model to borrow information from subjects exhibiting similar activation patterns in estimating parameters of interest and also capture spatial correlation among distant voxels. For single-subject analysis, the HDP reduces to a Dirichlet process (DP) prior.

In addition to the prior construction above, spatial correlation among neighboring voxels within a subject is modeled via a Markov Random Field (MRF) prior imposed on $\gamma_{i\nu j}$,

$$P(\gamma_{i\nu j} | d, e, \gamma_{ikj}) \sim \exp(\gamma_{i\nu j} (d + e \sum_{k \in N_{i\nu}} \gamma_{ikj})),$$

with $N_{i\nu}$ the set of neighboring voxels of voxel ν for subject i , and $p(\gamma_{i\nu}) = \prod_{j=1}^P p(\gamma_{i\nu j})$. The sparsity parameter $d \in (-\infty, \infty)$ represents the expected prior number of activated voxels, while the smoothness parameter $e > 0$ controls the probability of identifying a voxel as active based on the activation of the neighboring voxels. The prior model is completed by considering a uniform prior distribution on the delay parameter, $\lambda_{i\nu j} \sim U(u_1, u_2)$, an Inverse Gamma (IG) prior on the innovation variance parameter, $\psi_{i\nu} \sim IG(a_0, b_0)$, and a Beta distribution on the long memory parameter, $\alpha_{i\nu} \sim \text{Beta}(a_1, b_1)$.

For posterior inference, [24] use Variational Bayes (VB) algorithms which, unlike MCMC

methods, does not rely on numerical integration. VB methods have been employed successfully in Bayesian models for single-subject fMRI data [17, 6, 9]. These methods find an optimal approximation to the posterior that minimizes the Kullback-Leibler (KL) divergence. Typically, VB approaches provide good estimates of means, although they tend to underestimate posterior variances and also to poorly estimate the correlation structure of the data. This can still be an acceptable trade-off for our inferential purposes, as we are only interested in the identification of broad areas of activations. When analytically tractable updates for some of the parameters are not available, the VB algorithm can be combined with importance sampling. Table 1 reports a schematic representation of the algorithm used in [24].

The primary interest of the inference is in the estimation of the selection parameters, γ , and the regression coefficients, β . These can be used to obtain activation maps, by subject and by stimulus. Using the output from the VB algorithm, posterior probabilities of inclusion (PPIs) for stimulus j , $p(\gamma_{i\nu j} = 1)$, for $j = 1, \dots, P$, are approximated as weighted averages of the variational distribution values $q(\gamma_{i\nu j} = 1)$ estimated across the iterations of the outer loop of the algorithm (see Table 1). Activation maps can then be obtained by thresholding the PPIs using a threshold value to ensure a pre-defined Bayesian false discovery rate (FDR) [16]. This produces a spatial mapping of the activated brain regions, for each subject. Corresponding posterior β -maps can be calculated by estimating the β coefficients via weighted averages of the variational distribution values, on active voxels. An additional feature of the modeling approach of [24] is that the use of the nonparametric HDP prior construction (5) can be exploited to obtain a clustering of the subjects for possible discovery of differential activations. For an individual stimulus, and given a pre-specified threshold (or FDR) value on the PPIs, a dissimilarity matrix can be calculated based on the squared Euclidean distances between each pair of subjects and transformed into a tree via hierarchical clustering, then a dendrogram can be obtained using the linkage method with Ward's minimum variance. An optimal number of clusters can finally be selected by visual inspection of the dendrogram and group-level β -maps can be calculated by averaging the posterior maps of the non-zero β coefficients in each cluster. Finally, when analyzing experimental data with multiple stimuli, contrast maps can be produced to compare the effects of different

Algorithm 1 VB Algorithm (with Poisson HRF)

for $l = 1 : L$ iterations **do**
 Update α_{iv}^l and λ_{iv}^l $i = 1, \dots, N, v = 1, \dots, V, j = 1, \dots, P$, via importance sampling.
for $m = 1 : M$ iterations **do**
 Using the VB method,
 Update ψ_{iv}^m as the mean of its variational distribution $q(\psi_{iv})$.
 Update γ_{ivj}^m from its variational distribution $q(\gamma_{ivj})$.
 This update takes the neighboring structure of voxels into account via the MRF prior.
 Update β_{ivj}^m when $\gamma_{ivj}^m = 1$. Otherwise, set $\beta_{ivj}^m = 0$.
 Store the last update at $m = M$ as final update.
end for
end for
 Compute the importance sampling weights w_{ivl} and normalize them to \hat{w}_{ivl} .
 Estimate the model parameters as weighted averages.

treatments, by subject, by estimating probability maps of the type $p(\beta_j - \beta_{j'} > \kappa)$, with j and j' a pair of stimuli and κ a pre-defined hypothesized value.

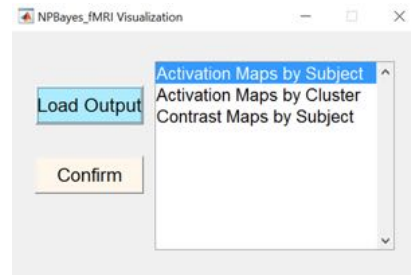


Figure 2: Main interface for Visualization.

2 Software design and implementation

In this section, we discuss the interface of NPBayes-fMRI. More details regarding parameter setting and input arguments can be found on [10]. NPBayes-fMRI comprises of two main interfaces, one for model fitting and one for the visualization of the results. They are organized as shown on Figures 1 and 2.

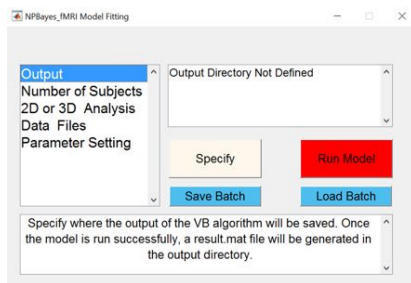


Figure 1: Main interface for Model Fitting

Model Fitting – Inference Stage. For model fitting, a set of parameters must be defined using the *NPBayes-fMRI: Model Fitting* shown in Figure 1, by first selecting the object in the listbox and then clicking the Specify button:

- **Output:** The user specifies where to save the final output of the VB algorithm. Once the model is run successfully, a `result.mat` file will be generated in the output directory.
- **Number of Subjects:** The user inputs the number of subjects used for the analysis. When this variable is set to 1, a DP will be used for the slab distribution in equation (5), while a HDP is used otherwise.
- **2D or 3D Analysis:** This option allows to specify the type of analysis, that is, whether it is performed on a single 2D slice or on a 3D whole-brain parcellation. Based on this, the user will be prompted to either define or load additional files. These arguments will be used later for visualization of the results.
- **Data Files:** The user needs to load a .mat file that consists of two matrices: `xtdat`, a $T \times P$ binary design matrix, with T the number of time points and P the number of stimuli, and `y_dat`, a $T \times (N \times V)$ ma-

trix of BOLD signals, with N the number of subjects and V the number of voxels (for 2D analyses) or ROIs (for 3D analyses). For both 2D and 3D analyses, the percent signal change normalization and the DWT are applied as part of the model fitting stage. For DWT, Daubechies minimum phase wavelets with 4 vanishing moments are used.

- **Parameter Setting:** The user can choose to run the model with a default parameter setting or to manually set the parameters.

Visualization – Visualization Stage. This interface is used to visualize the results using the *result.mat* file obtained from running the algorithm with the *NPBayes-fMRI: Model Fitting* interface. It comprises of three components, described below. For simplicity, we consider 3D data.

- **Activation Maps by Subject:** This function allows the user to view the activation maps, the posterior β -maps and the HRF maps for a single subject. Clicking on Map Type allows the user to select either Probability Map, which allows to view PPI activation maps, or Activation Map, to view the posterior β -maps, or HRF Map, to view posterior maps for the HRF parameters. Matlab's built-in colormaps can be selected via the Color Map pop-up menu. Range lets the user define the axes limits. Two sliders appear on the right-hand side of the interface. The bigger slider can be used to adjust the PPI threshold and the FDR value. These values can also be set manually by the user. The smaller slider, circled in red in Figure 3, appears only when a Brain Template Image has been uploaded for 3D Analysis. This slider allows the user to control the transparency of the activation map that will be overlaid on top of the Reference Image. The X , Y and Z sliders are used to define the coordinates of the 3D NIFTI brain image in sagittal, coronal and axial orientation. If the user desires to view multiple slices of the brain in one particular orientation for a given stimulus, the Multi-Slice option can be used instead. The Viewing Options tab can be used to view either all stimuli at once or a single stimulus at a time, as shown in Figure 3.

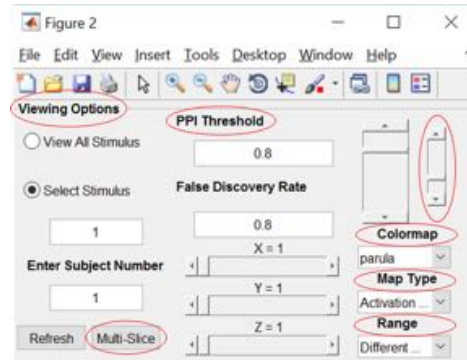


Figure 3: NPBayes-fMRI: Visualization. Interface for viewing activation maps by subject. The Viewing Options tab allows the user to view all stimuli at once or one at a time. By clicking on the Map Type, Range and Colormap pop-up menus, the user can define the type of maps to visualize, set the axes ranges and the desired colormap setting.

- **Activation Maps by Cluster:** This function is used to view cluster-level activation maps, for a given stimulus and PPI (or FDR) threshold. Clusters are defined based on a dendrogram obtained by applying hierarchical clustering with Ward's linkage method to a dissimilarity matrix defined based on the posterior mean estimates of the non-zero β coefficients. By clicking on Load Cluster Defined From Dendrogram as shown in Figure 4 the user can insert the number of clusters by which the subjects will be grouped.

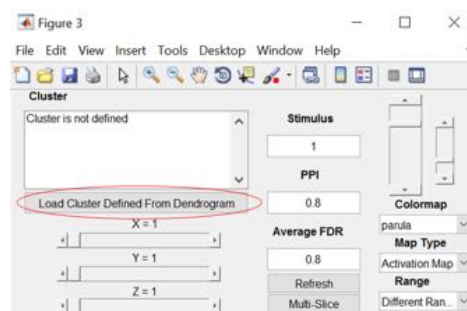


Figure 4: NPBayes-fMRI: Visualization. Interface for viewing activation maps by cluster, for a given stimulus. The user selects the stimulus and the PPI (or FDR) threshold. The corresponding dendrogram will be displayed, and the user can then specify the number of clusters and click on the Load Cluster Defined from Dendrogram tab. When confirmed, the cluster indices will be displayed in the Cluster tab.

- **Contrast Maps by Subject:** For multiple stimuli, this function lets the user define a

contrast by subject by defining a Contrast Vector and Hypothesis Value using the Define Contrast option. The length of the Contrast Vector must not be greater than the number of stimuli and the entries must sum to 0. Once a contrast has been defined, the user can use the slider to adjust the Threshold Probability and view different subjects by entering the subject numbers. The interface is shown Figure 5.

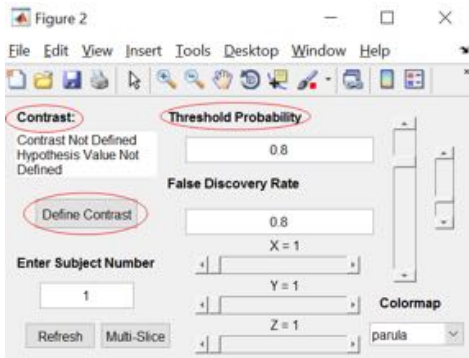


Figure 5: NPBayer-fMRI: Visualization. Interface for viewing contrast maps by subject (for multiple stimuli). The user must use the Define Contrast tab to insert the contrast vector and hypothesized value. The slider bar can be used to adjust the PPI (or FDR) value.

3 Inference and Visualization on 3D data

NPBayer-fMRI includes data of 30 subjects performing an experiment with three different stimuli. The dataset is part of a pilot study on variability in the cognitive and neural processes involved in reading, conducted at Rice University [5]. A 3D parcellation of the data was performed using the MarsBaR toolbox in SPM 12. The Automatic Anatomical Labeling (AAL) brain atlas was used to obtain the parcellation, resulting in 90 ROIs, excluding the regions associated with the cerebellum. Instructions on how to upload the data into the toolbox are given in Table 2. A neighboring matrix is also available, based on thresholded Euclidean distances between pairs of ROIs, calculated using the coordinates defined in the Montreal Neurological Institute (MNI) space. The threshold was chosen so that ROIs would have five neighbors on average. This matrix can be used to define the neighboring structures among ROIs for the specification of the MRF prior.

Figure 6 shows the posterior β -maps for one

of the subjects, for stimulus 2, obtained at a PPI threshold of 0.9. A multi-slice sagittal view is shown in the middle panel. The smaller slider can be scrolled down if one wishes to see more of the brain structure through the overlaid activation map. The bottom subplot displays the activation map at coordinates $X = 92, Y = 115, Z = 111$. If View all Stimulus is selected under Viewing Options, then a 3×3 plot of activation maps will be displayed. Different locations of the brain can be examined by using the three sliders to control the X, Y, Z coordinates.

For stimulus 2 and a PPI threshold of .9, Figure 7 shows the dendrogram (middle), obtained by clustering the posterior β estimates of all 30 subjects, and the cluster-level β -maps (bottom) when 3 clusters are selected. The subject numbers corresponding to each cluster are displayed on the interface that controls the dendrogram and activation maps (top).

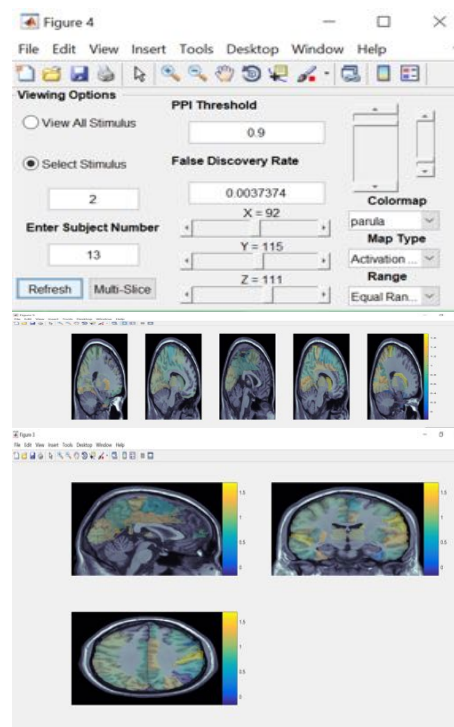


Figure 6: 3D Analysis: Example of activation β -maps, with Range set to Equal Range, for stimulus 2 and PPI threshold of .9. The middle subplot displays a multi-slice sagittal view, the bottom subplot displays the activation map at coordinates $X = 92, Y = 115, Z = 111$.

Algorithm 2 Instructions for running the example dataset

Once you run *NPBayes-fMRI*, select **Model Fitting** and follow these instructions:

1. Define the output directory by clicking on "OUTPUT"
2. Insert 30 for Number of Subjects
3. For 2D or 3D Analysis, select "3-Dimensional" and insert the following:
 - Matrix of ROI names: Select *ROI_names.mat* from the Example_ROIs subfolder
 - Neighbor Matrix: Select *nei_vec.mat* from the Example folder
 - ROI NIFTI Directory: Select the Example_ROIs folder
 - Brain Template Image: Select 'Load Nifti Brain Template Image' and load the *ch2.nii* file found in the Example folder
4. For "Data Files", select:
 - multi_data.mat* file found on the Example folder
5. For Parameter Setting select the default setting by clicking "yes"
6. Initiate model fitting by pressing "Run Model"

To visualize the results, select Visualization and load the *result.mat* file located in the output directory using Load Output.

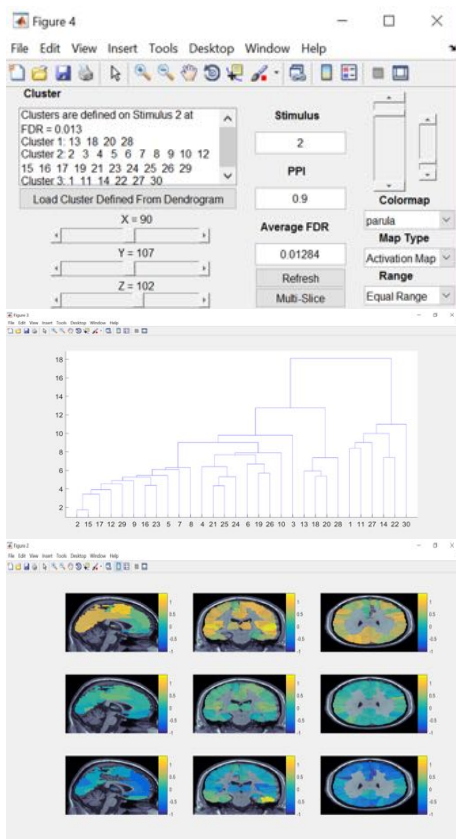


Figure 7: **3D Analysis:** Example of dendrogram (middle), for stimulus 2 and a PPI threshold of .9, and cluster-level β -maps (bottom), obtained with three clusters. The subject cluster memberships are displayed in the *Cluster* tab of the interface (top).

4 More information

The NPBayes-fMRI software is available for download at: https://github.com/rimehi/NPBayes_fMRI and <http://www.stat.rice.edu/~marina/software.html>

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