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MESSAGE FROM THE PRESIDENT

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More than one year has passed since the start of the Covid-19 pandemic, which brought much suffering throughout the world and completely changed our lives. Switching to work and teach remotely required some effort and adaptation but offered also new opportunities. Still, I believe most of us are starting to feel fatigue and for many, especially junior and female researchers, the mix of stress, insecurity and pressure can become overwhelming. See, e.g., this Nature piece on burnout in academia. We all have to become aware of those problems: they will not disappear instantaneously as the pandemic will come to an end. We have to come together as a community to help each other and foremost support students and junior colleagues. ISBA will play its part.

Junior Support

The focus on junior researchers has been a unique feature of ISBA ever since. With the steadily increasing competition for grants, positions and resources, often across areas, it is fundamental for ISBA to provide adequate recognition to its best young scholars. Even more so during these difficult times. Several initiatives in this direction are currently in the making: (a) **Savage Awards**: Resuming a good practice of the past, a total of four finalists for each of the two categories (Theory & Methods and Applied Methodology) will be publicly announced each year, hence officially commending 4+4 brilliant PhD graduates (not just winners and runner-ups). Leveraging

on the greater flexibility of the virtual format of ISBA 2021, for the first time there will be two Savage Award Sessions, one per category. (b) **Multiple awards** will be assigned for presentations by early career researchers **at ISBA 2021**. Stay tuned for details! (c) **j-ISBA** is currently designing a **new set of highly innovative awards** to be launched soon! (d) An ad-hoc committee of junior researchers will be created to survey how other societies and disciplines support their early career researchers and to make proposals to ISBA for new initiatives in this direction. Further ideas and suggestions would be very welcome!

2021 ISBA Awards & Honors

Calls for all ISBA awards have been published. Please consider nominating most deserving Bayesians and remember that the deadline for the De Groot, Mitchell and Savage awards is May 31, 2021, whereas it is August 31, 2021 for ISBA Fellows and the Zellner Medal.

> IN THIS ISSUE FROM THE EDITOR REMEMBERING DONALD FRASER ZELLNER MEDAL 2020 SOFTWARE HIGHLIGHT FROM THE PROGRAM COUNCIL UPDATES FROM BA JUNIOR ISBA

2021 ISBA World Meeting

As you all know, the ISBA 2020 World Meeting, to be held in Kunming (China), was first postponed to 2021 and then turned into a virtual meeting scheduled for June 28 to July 2, 2021. Although we will all miss the personal interactions, the scientific program is simply impressive: it will feature the **Named**, **Foundational and Keynote Lectures** as well as the **Invited Sessions** originally planned for the ISBA 2020 meeting combined with **330+ Contributed Presentations**, which will consist of **pre-recorded videos combined with live recaps + Q&A and optional posters**. Careful planning is underway to maximize the attendance across time zones. A big thanks is due to the ad–hoc organizing committee led by Ming-Hui Chen and Christian Robert with great help from j-ISBA representatives Roberta De Vito, Xenia Miscouridou, Sally Paganin and Daeyoung Lim, to the Scientific Committee chaired by Li Ma and to Feng Liang, who is pivotal to any ISBA endeavour.

An important aspect to highlight is that ISBA 2021 will be **completely free to everyone**! Spread the word and remember to register by May 1. This decision has been taken jointly by the Executive Committee and Program Council when turning the meeting into a virtual event: we wanted to be as inclusive as possible in these challenging times for the ISBA community and beyond. The US National Science Foundation (NSF) has been extremely supportive with our project, which we are all grateful for.

ISBA 2022 & Awards Ceremony

The 2022 ISBA World Meeting in Montréal (June 26 to July 1, 2022) will mark **ISBA's 30th anniversary** and hopefully represent our return to normalcy! The Scientific Committee is already working on the program and calls for contributions will be issued soon. The Executive Committee decided to have a joint ceremony in Montréal for all ISBA 2019-2021 awards. This will make it the **biggest awards ceremony in ISBA's history**! We count on your participation to make it also the largest Bayesian conference ever.

Thanks to Past and New Officers

First I would like to thank Sylvia Frühwirth Schnatter, who has wonderfully led ISBA with great balance and dedication during this arduous year. It is great that she is still part of the Executive Committee as Past President for 2021. I also want to thank Raquel Prado (Past President) and Li Ma (Past Program Chair), who completed their terms at the end of 2020, for their incredible work and commitment to our society. Special thanks are due also to Maria De Yoreo for serving as Editor of the ISBA Bulletin and to the four retiring ISBA Board members Alicia Carriquiry, Michele Guindani, Lurdes Inoue, and Surya Tokdar. A warm welcome to Sudipto Banerjee (President-Elect), Matthias Katzfuß (Program Council Vice-Chair) and Gregor Kastner (new Editor of the ISBA Bulletin) as well as to the new Board members, Veronica Berrocal, Cathy W.S. Chen, David Dahl and Mario Peruggia, and to all new officers of Sections, Chapters and standing committees. Last but not least, ISBA is fortunate to be able to continue to count on Feng Liang (Executive Secretary), Marian Farah (Treasurer) and Michele Guindani (BA Editor).

ISBA Membership

Finally I would like to remind you to **renew your ISBA membership** or, even better, to **become a lifetime member**! A large membership base is essential to expand the support for our junior members and keep our journal completely open and free.

Stay safe! igor

FROM THE EDITOR

Gregor Kastner

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Welcome to the first ISBA Bulletin edition of 2021! Apart from our traditional columns, this edition also features a wonderful obituary for Donald Fraser, kindly provided by Christian Genest. Having not been around when most of Professor Fraser's highly influential work was published, I finally got the chance to catch up. As a noteworthy treat, we showcase JASP, a very intuitive and easy-to-use piece of software for elementary Bayesian analyses. For those among us who have the pleasure to teach statistics to not-so-tech-savvy audiences: here is a great chance to use Bayesian methods even for the faintest of heart. Furthermore, in a special feature we announce the 2020 Zellner medalists!

This year, Igor Prünster took over as new ISBA President, following now Past President Sylvia Frühwirth-Schnatter. Following Athanasios Kottas, Botond Szabo serves as chair of the program council, presenting updates about ISBA sponsored/endorsed events. For j-ISBA, Sally Paganin took on the task of wrapping up some news from the younger Bayesians; most prominently the 2021 edition of BAYSM. In his traditional column, Francesco Denti gives an overview of past and upcoming events, and Michele Guindani reports the latest from Bayesian Analysis.

Thanks to all contributors of this issue, and thanks to you, dear fellow Bayesians, for taking the time to read these lines. Enjoy those to come!

REMEMBERING DONALD FRASER

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IN MEMORIAM: DONALD A.S. FRASER (1925–2020)



On December 21, 2020, Canada and the world lost one of their most eminent and influential statisticians, Donald Alexander Stuart Fraser, OC, FRSC, who passed away at the age of 95. By his side was his wife, Nancy Reid, herself a distinguished statistician.

Don's exceptional path as a scientist, which spanned over 70 years, was characterized by creative thinking, deep intuition, and a singular passion for statistics. As the author of over 280 articles, two research monographs and three widely used textbooks which were the first exposure to the subject for generations of students in the 1950s, 60s and 70s, he had a profound and lasting influence on the advancement of the field in Canada and internationally.

Based at the University of Toronto throughout his career, which began in 1949, Don was for decades the foremost intellectual leader of the discipline in Canada. He schooled many generations of statisticians and data scientists, supervising 55 PhD students. He played a key role in the establishment of his university's Department of Statistical Sciences, serving as its first chairman from 1977 to 1983. His stature attracted talent and helped the University of Toronto to become the center of excellence in statistics which it remains to this day. He was also involved in the creation of a national statistical association and brought prestige to *The Canadian Journal of Statistics* (CJS) by serving as editor-in-chief from 1977 to 1980. He continued to exercise leadership beyond his retirement in 1986, spending eight years as a Professor at York University, where he helped to build up statistics.

Elected to the Royal Society of Canada at the age of 42, Don was the first recipient of the Gold Medal of the Statistical Society of Canada (SSC) in 1985. He later received honorary degrees from the University of Waterloo (1992) and the University of Toronto (2002), and was appointed Officer of the Order of Canada in 2011 in recognition of his contributions to science and society. His accolades include fellowships in the Institute of Mathematical Statistics (1954), the Royal Statistical Society (1956), the American Statistical Association (1962), the American Association for the Advancement of Science (1971), and the American Mathematical Society (2015), as well as an elected membership in the International Statistical Institute (1962). Moreover, he was the 1990 recipient of the R.A. Fisher Award and Lectureship, became an honorary member of the SSC in 1991, and received the Gold Medal of the Islamic Statistical Society in 2000.

Don was born in Toronto on April 29, 1925, to Maxwell John Fraser and Ailie Jean Stuart. Raised in Stratford, Ontario, he attended St. Andrew's College in Aurora from 1939 to 1942, and the University of Toronto from 1942 to 1947, completing a BA in mathematics, physics and chemistry in 1946 and an MA in 1947. He distinguished himself very early as a Putnam fellow and member of the first-place team in the Putnam international mathematics competition in 1946. This singular achievement qualified him for a graduate scholarship at Princeton University, where he completed his PhD within two years. It is there that under the mentorship of John Tukey and Samuel Wilks, he specialized in statistics, which was then a newly developing field.

Upon graduating from Princeton in 1949, Don returned to the Department of Mathematics at the University of Toronto as an assistant professor of statistics. He quickly acquired a reputation both in teaching and research, and became a full professor at the age of 33. He was responsible, virtually single-handedly, for developing statistics at his institution. He succeeded in building a strong and broadly based research group there; many of his students became successful academics in Canada and abroad. While his own research was focused on theory, he recognized early the importance of statistical computing and the need to develop infrastructure and to hire in that field.

From his exchanges in the early 1950s with Sir Ronald Fisher to the very end of his career, Don's work was marked with audacity and extraordinary originality. He quickly became one of the early leaders in pedagogy by writing two widely used textbooks: *Nonparametric Methods in Statistics* (1957) and *Statistics: An Introduction* (1958). As his reputation in both research and teaching grew, these books became classic references. In 1976 he wrote a third book, *Probability and Statistics: Theory and Applications*, that was also well received.

From the beginning of his career, Don made many highly original and important contributions to statistical theory. One of the most widely cited is a landmark paper called "Structural probability

and a generalization" (*Biometrika*, 1966). Authored solo, as were most of his writings between 1951 and 1970, this paper provided the outline for a new approach to inference called structural inference which used in an essential and innovative way the mathematical structure of a wide class of stochastic models. With colleagues and students, Don later developed and extended this theory in a large number of research papers and in the research monographs *The Structure of Inference* (1968) and *Inference and Linear Models* (1979). In recognition of the importance of Don's contribution, his 1966 paper was reprinted in *Breakthroughs in Statistics: Foundations and Basic Theory* (Springer, 1992).

Don's work on structural inference emphasized the central role of the likelihood function in statistical inference. This point of view, which is broadly accepted today, ran counter to widely held views at the time. In the 1980s and 1990s, much research was devoted to approximations in the area of likelihood asymptotics. Don's research, conducted in large part with Nancy, was at the forefront of these developments, from his groundbreaking introduction of the tangent exponential model in *Biometrika* (1990) to his paper with Davison, Reid, and Sartori on directional inference, which appeared in 2014 in the *Journal of the American Statistical Association*. His contributions to the asymptotic theory of inference, combined with his earlier work on structural inference, helped to shed new light on the interface between the Bayesian and Fisherian schools of thought in unexpected ways. His 2010 paper in the *Journal of the Royal Statistical Society, Series B*, coauthored by Reid, Marras, and Yi, directly addressed this debate.

Throughout his career, Don maintained an exceptionally active program in research, publishing important work in all the leading statistical journals. With characteristic originality, he saw links between likelihood inference and areas which most people would have viewed as tangential to his interests. For example, his 2007 paper with Bédard and Wong, published in *Statistical Science*, was noteworthy for proposing an innovative approach to Markov chain Monte Carlo sampling, whose computational aspects he developed to considerable success.

Don's influence in research has been profound, but perhaps more striking still is the influence he had on several generations of scientists. Among many others, David Brillinger, Arthur Dempster, and Stephen Fienberg repeatedly acknowledged the importance of Don's mentorship in starting their careers. Don's long list of PhD graduates includes three SSC Gold Medalists, Irwin Guttman (1955), Ivan Fellegi (1961), and David Andrews (1968), but also Keith Hastings (1962) of Metropolis–Hastings fame, Ross Prentice (1970), former director of the Public Health Sciences Division at the University of Washington, Kai-Wang Ng (1975), professor at the University of Hong Kong, former CJS Editor and 2010 CRM-SSC Prize winner Grace Yi (2000), as well as several other research statisticians working in Toronto and elsewhere in Canada. Don also had a special connection with Nancy Reid, a kindred spirit with whom he published over 50 papers and had two daughters.

Don's personal life was as extraordinary as his professional accomplishments. He was a man of insatiable curiosity, always in search of the unique and the unconventional, highly energetic and constantly seeking to test his limits, both mental and physical. He spoke enthusiastically of the canoe trip he made in his twenties to James Bay and he remained, late in his life, an avid swimmer, a waterskier in the summer, and a snowmobiler in the winter. His lifelong interest in architecture also occupied his mind; at Lake Temagami, where he spent nearly all his summers, he oversaw the construction of several cabins, docks, etc. His passion for building is also immortalized in the "Fraser House" at 4 Old George Place, in Toronto's neighborhood of Rosedale, which he commissioned the famous architect Ronald J. Thom to design for him in 1964.

Don leaves in mourning his wife Nancy, their daughters Ailie and Donelle, five other daughters from previous marriages, Julie, Danae, Maia, Andrea, and Ailana (the latter three are professors of mathematics in Canadian universities), as well as several grandchildren and great grandchildren. He will continue to live on through the many scholarly contributions that made him a titan of statistics, but also through the positive influence he had on so many people, including over 350 academic descendants, and the lasting impression he gave of a kind, joyful, humorous, enthusiastic, energetic, hard-working, clever human being.

In his 2009 book entitled SUM: Forty Tales from the Afterlives, David Eagleman wrote: "There are three

deaths: The first is when the body ceases to function. The second is when the body is consigned to the grave. The third is that moment, sometime in the future, when your name is spoken for the last time." Speaking of the third death, Don Fraser will outlive most of us.

Additional information on Don's career and his views on statistics and science can be found in his discussion with Tom DiCiccio and Mary Thompson published in the May 2004 issue of *Statistical Science* (vol. 19, no. 2, pp. 370–386). An interview of Don is also available from the Videotape Archives of the American Statistical Association.

ZELLNER MEDAL 2020

Gregor Kastner

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The Zellner Medal is awarded every even year to recognize ISBA members who have rendered exceptional and distinguished service to ISBA over an extended period of time, and whose contributions have had an impact on the society beyond the time of his or her incumbency. The call for the 2022 edition has just been issued and nominations can be submitted here.

Under normal circumstances the Zellner medal is announced at the ISBA World Meeting. However, all award ceremonies are now postponed to 2022. Thus, it is my pleasure to announce the winners of the 2020 Zellner Medal in this issue of the ISBA Bulletin! Many thanks go to Christian Robert, who chaired the 2020 prize committee, and to Merlise Clyde and Sonia Petrone serving as committee members.

Alicia Carriquiry

Honored for her leading roles in the formation and development of ISBA and the journal Bayesian Analysis; for sustained and exceptional service to the society through outstanding impact in many administrative roles and conference organization; for being an ambassador for ISBA, especially in the extensive developments of Chapters and conferences in South America; for being an excellent role model and advocate for young statisticians; and for outstanding contributions to science and the advocacy of Bayesian methods in science.





Marina Vannucci

Honored for her effort in pushing the modernization, efficiency and standing of the flagship journal of ISBA, Bayesian Analysis, for fostering the collaboration between ISBA and other statistical societies, and for her contribution to establishing long-standing ethical guidelines for all ISBA members.

Congratulations to the awardees!

SOFTWARE HIGHLIGHT

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BAYESIAN INFERENCE WITH JASP

JASP is an open-source, cross-platform statistical software program with an intuitive 'drag-and-drop' graphical user interface. Developed at the University of Amsterdam, JASP aims to liberate students, teachers, and researchers from the statistical stranglehold of *p*-values and eliminate the financial strain imposed by commercial programs such as SPSS and Minitab [13, 31, 30].

In the past, most Bayesians have been content to implement their statistical procedures as R packages; after all, R is the *lingua franca* of statistics. However, this R-package-only approach has failed to put much of a dent in the popularity of the *p*-value, especially in empirical fields such as psychology, medicine, economics, and biology. These empirical fields largely continue to ignore Bayesian inference – both in their statistics courses and in their published articles. Despite recurring Bayesian protestations, the *p*-value remains dominant as the final arbiter of scientific success, be it in medical clinical trials, particle physics, or clinical psychology. Pessimistic Bayesians may well conclude that *something has gone terribly wrong*.

With JASP we aim to change the status quo and make Bayesian inference a common alternative (or supplement) to *p*-values and frequentist confidence intervals. JASP has several features intended to facilitate the transition from frequentist to Bayesian statistics:

- 1. JASP is open-source, cross-platform, and can be freely installed from jasp-stats.org. Both for academic institutions and for students, the fact that JASP is *gratis* is an important consideration.
- 2. JASP offers Bayesian *and* frequentist statistics. Students and researchers who use JASP for frequentist analyses are only a few mouse clicks away from a Bayesian analysis.
- 3. JASP has an attractive GUI where output is requested and adjusted on the fly, just by dragging and dropping variables and ticking boxes. This allows teachers to focus on statistical concepts instead of on computer code. Students may feel safer knowing it is impossible to make a programming mistake.
- 4. JASP implements both Bayesian estimation and Bayesian hypothesis testing. In most empirical disciplines, hypothesis testing is an essential step in the scientific process, one that transcends the distinction between Bayesian and frequentist statistics [11].
- 5. For many statistical procedures, a single mouse click can produce a new Bayesian analysis. Whether it be a sensitivity check, a sequential analysis, a one-sided test, or the choice of a custom prior distribution: a few actions suffice to create a relatively comprehensive set of Bayesian analyses. With JASP, executing a Bayesian analysis takes little extra effort.
- 6. JASP 0.14.1 includes a first version of a *Learn Bayes* module, which was specifically developed to introduce students to the basics of Bayesian inference.

Bayesian Methods Available in JASP 0.14.1

In recognition of Bayesian pioneer Sir Harold Jeffreys, JASP stands for *Jeffreys's Amazing Statistics Program*. In line with Jeffreys's vision, JASP aims to provide a Bayesian echo of popular frequentist

Procedure	Estimation	Testing	R Packages
T-Tests	✓	~	BayesFactor[17]
ANOVA	~	~	BayesFactor[17]
Mixed Models	~		rstanarm[5], stanova[25]
Regression	~	~	BAS[3]
Frequencies	~	~	abtest[6], BayesFactor[17], conting[18]
Bain	~	~	bain[9]
Equivalence T-Tests	~	~	BayesFactor[17]
JAGS	~		rjags[21], coda[22]
Meta-Analysis	~	~	metaBMA[10], RoBMA[1]
Reliability	~		Bayesrel[19]
Summary Statistics	~	~	BayesFactor[17]
Learn Bayes	~	~	stats[23]

Table 1: Overview of Bayesian inference procedures implemented in JASP 0.14.1.

procedures such as the *t*-test and the correlation test. JASP also respects Jeffreys's distinction between estimation and testing [15, 14, 24]. In *estimation*, the researcher wishes to learn about the size of a treatment effect under the assumption that it exists; typically a continuous prior distribution is updated to a continuous posterior distribution, which may then be summarized by a point estimate and a credible interval. In *testing*, the researcher wishes to learn whether or not a specific parameter value ought to be retained. This is typically done by pitting the predictive adequacy of the null hypothesis $\mathcal{H}_0 : \delta = 0$ with priors on the nuisance parameters against the alternative hypothesis $\mathcal{H}_1 :$ $\delta \in \mathbb{R}$ with an additional prior on the test-relevant parameter δ . The resulting ratio of marginal likelihoods is known as the Bayes factor which Jeffreys proposed as an alternative to the *p*-value. Jeffreys argued that testing comes logically prior to estimation, and that a more complex model should only be adopted when the data undercut the simpler one: "The onus of proof is always on the advocate of the more complicated hypothesis." [11, p. 343]. Bayes factors are often difficult to compute; with JASP, practitioners can obtain Bayes factors easily.

Table 1 provides an overview of the Bayesian functionality on offer in the current version of JASP, 0.14.1. The first five procedures form the common core, whereas the other procedures are included as add-on modules that can be activated upon request. As the final column of the table suggests, R and R packages constitute the statistical nucleus of JASP. The JASP program may therefore be considered as a GUI for a specific set of R packages. JASP could not exist without the statistical foundation provided by R.

As we demonstrate below, only a few mouse clicks and keystrokes are needed in JASP to generate a comprehensive set of Bayesian analyses for common analysis problems.

Example I: The Bayesian *t***-Test**

Here we use data from a replication experiment [29] to demonstrate the Bayesian independent samples *t*-test. We first start JASP and then navigate to the JASP Data Library in order to open the *Kitchen Rolls* data set (i.e., click the blue hamburger icon on the top left \triangleright Open \triangleright Data Library \triangleright 2. T-Tests \triangleright Kitchen Rolls). In the replication experiment, students were asked questions about their openness-to-experience while rotating kitchen rolls. One group of students turned the rolls clockwise, and the other group turned them counterclockwise. The dependent variable mean_NEO is the mean openness-to-experience score, and Rotation indicates the direction of movement (clockwise or counterclockwise). The hypothesis of interest stipulates that students who turn the rolls clockwise



Figure 1: Screenshot of a Bayesian independent samples *t*-test in JASP. The left input panel serves to select variables and specify analysis options; the right output panel shows the associated output (with annotations). The ribbon on top shows a range of alternative analysis methods. The blue '+' sign in the top right corner opens a modules menu that allows more functionality to be activated on demand.

report a higher openeness-to-experience than students who turn the rolls counterclockwise.

An analysis using *Descriptives* shows that mean openness in the clockwise condition equals 0.64 (N = 48; SD = 0.50) whereas it equals 0.71 (N = 54; SD = 0.47) in the counterclockwise condition (t(100) = -0.75; p = .45). The results are therefore in the direction opposite to what was found in the original experiment [26]. With the *t*-value and sample sizes in hand we could conduct a complete Bayesian analysis by activating the *Summary Statistics* module. This JASP module was developed to facilitate a Bayesian reanalysis of published frequentist results in the absence of access to the raw data. However, with only the summary statistics a sequential analysis is not possible, which is why we continue by selecting *T*-*Tests* from the ribbon and then, under the subheading **Bayesian**, the option *Independent Samples T*-*Tests*. The resulting interface is shown in the left panel of Figure 1.

Dragging mean_NEO into the *Dependent Variables* box and Rotation into the *Grouping Variable* box immediately produces a table with results of a default Bayesian analysis. Ticking the *Prior and posterior* checkbox produces the distributions shown in the right panel of Figure 1. The dotted line is the default prior under \mathcal{H}_1 – a Cauchy distribution with an interquartile range of $1/\sqrt{2}$. The solid line is the resulting posterior distribution, with a median of -0.132 and a 95% central credible interval extending from -0.503 to 0.233. These results may be of interest whenever the focus is on estimation.

When the focus is on testing, the average predictive performance of \mathcal{H}_1 is contrasted with that of \mathcal{H}_0 (i.e., effect size $\delta = 0$) to yield the Bayes factor. The information on top of the prior and posterior distributions indicates that the Bayes factor is 3.71 in favor of \mathcal{H}_0 over \mathcal{H}_1 . The probability wheel to the right provides a visual impression of this strength of evidence. Finally, the Bayes factor is also visualized as the ratio between the two grey dots on the prior and posterior densities at $\delta = 0$ [4].

The test above was undirectional, as the Bayes factor was based on a symmetric Cauchy prior around $\delta = 0$ under \mathcal{H}_1 . However, the hypothesis under scrutiny clearly entails a direction: student who turn



Figure 2: Example JASP output for the independent samples *t*-test. Top left: a directional test with a default Cauchy prior truncated to positive values; top right: a sensitivity analysis that explores the impact of the Cauchy prior width; bottom left: a directional test with an informed prior (i.e., \mathcal{H}_+ : $\delta \propto N(\mu = 0.30, \sigma = 0.15)1_{[0,\infty)}$; bottom right: sequential analysis for the default Cauchy directional test.

the rolls clockwise are assumed to display *more* openness to experience, not *less*. In order to respect the directional nature of the alternative we can tick the option *Group* 1 > Group 2. The resulting prior and posterior distributions from JASP are shown in the top left panel of Figure 2. The directional form of the alternative (denoted by \mathcal{H}_+) excludes negative effect sizes in the prior, and consequently also in the posterior [11, pp. 277-278 and p. 283]. Because the effect size in the sample is opposite to that predicted by \mathcal{H}_+ , the restriction increases the evidence in favor of \mathcal{H}_0 : the Bayes factor for \mathcal{H}_0 versus \mathcal{H}_+ is 7.749.

The sensitivity of this Bayes factor outcome to different specifications of the Cauchy prior width can be visualized by ticking the checkbox *Bayes factor robustness check*. The resulting Bayes factors BF_{0+} are shown in the top right panel of Figure 2. A width of zero reduces \mathcal{H}_+ to \mathcal{H}_0 and yields $BF_{0+} = 1$ by definition. Increasing the width allows \mathcal{H}_+ to make predictions that differ from those of \mathcal{H}_0 ; the more this is allowed, the stronger the evidence for \mathcal{H}_0 becomes. For reasonable values of the prior width, the evidence in favor of \mathcal{H}_0 falls in Jeffreys's 'moderate' category [12, p. 105].

For the *t*-test, the default prior distribution under \mathcal{H}_1 is a Cauchy with a mode at $\delta = 0$ (recommended by Jeffreys for testing) and interquartile range $1/\sqrt{2}$. JASP allows users to change both the mode and the interquartile range. Users may also assign δ a normal distribution or a *t*-distribution, with no restriction on the location and scale parameters [7]. One alternative analysis may assign δ a positive-only normal distribution with mean 0.30 and standard deviation 0.15. This "Vohs prior" was suggested as a reasonable specification for small to medium effect sizes in psychology [28]. The results from the Vohs prior are shown in the bottom left panel of Figure 2. The Bayes factor is 5.40, support for \mathcal{H}_0 that falls in between that of the undirectional and directional default Cauchy tests.

Returning to the default directional Cauchy test, ticking the checkbox *Sequential analysis* produces the bottom right panel of Figure 2. The sequential analysis assumes that the order with which the data arrived is given by the rows of the data file, and then computes the corresponding evidential flow – the fluctuations in support that would be experienced by a Bayesian who updates their knowledge after every new observation.

Finally, JASP also offers a Bayesian version of the Mann-Whitney test, useful in scenarios where one desires conclusions that are invariant to monotonic transformations of the measurement scale [27]. The directional Mann-Whitney test yields $BF_{0+} = 7.8$, again indicating moderate evidence in favor of \mathcal{H}_0 .

Example II: The Learn Bayes Module

Supported by the Association for Psychological Science Fund for Teaching and Public Understanding of Psychological Science, the *Learn Bayes* module aims to make it easier for students to explore the basic principles of Bayesian estimation and testing. The current, first version of *Learn Bayes* focuses exclusively on binomially distributed data. To activate the *Learn Bayes* module, first click the blue '+' icon on the top right and then tick the *Learn Bayes* checkbox.

Our first illustration of the Learn Bayes module focuses on updating knowledge in an estimation setting. Assume we wish to learn about the chance θ that any student attending a class on Bayesian inference self-reports to use Windows rather than Mac. A fictitious data set (available here) contains a single column, operating system, the rows of which indicate the results for 60 individual students, 40 of whom use Windows. After opening this data set in JASP we select the Binomial Estimation analysis from the *Learn Bayes* module. In the resulting GUI we drag the variable operating system into the Selected box and then define the level Windows as Successes and the level Mac as Failures. In the *Model* section we specify a model with a beta prior distribution on θ . We keep the α and β parameters at their default values (i.e., $\alpha = \beta = 1$). Under the *Inference* section we tick the *Posterior* distribution checkbox and select Mode as the *Point estimate* and Custom as CI. We specify an interval that ranges from 0.4 to 0.6. The resulting figure is shown in the left panel of Figure 3. The solid line corresponds to the posterior distribution of θ , with a dot marking the posterior mode at $\theta = .667$, and a highlighted posterior probability mass of 15% in between 0.4 and 0.6. The *Binomial Estimation* analysis can also be used to visualize the sequential updating of the posterior distribution. This analysis assumes that the row order of the data file is the order in which the students indicated their operating system. Opening the Sequential Analysis section and ticking the Stacked option checkbox yields the right panel of Figure 3. This panel shows the evolution of the posterior distribution for θ as the data come in, starting with the uninformative beta(1, 1) prior distribution at the top and ending at the bottom with the peaked beta(41, 21) posterior distribution.

Our second illustration of the *Learn Bayes* module focuses on quantifying evidence in a testing setting. Consider the decimal expansion of π and assume that we wish to grade the evidence that the data provide for or against the hypothesis that the even and odd digits occur equally often (cf. [8]). Specifically, we wish to compare the predictive performance of \mathcal{H}_0 : $\theta = 1/2$ against that of \mathcal{H}_1 in which θ is assigned a beta distribution. For demonstration purposes, we use the dome-shaped beta(2,2) prior distribution.

We open a data set that contains the first 100 digits of π (see this link). The data set contains two columns: digit with the decimal digits and oddEven with the matching classification into odd and even. Out of the first 100 digits of π , 51 are even and 49 are odd. We then select the *Binomial Testing* analysis from the *Learn Bayes* module.



Figure 3: Example JASP output for the binomial estimation of the latent proportion θ of Windows users based on a fictional data set with 40 Windows users and 20 Mac users. Left: posterior distribution with the mode marked by a dot and shaded probability mass of 15% in the interval from $\theta = 0.4$ to $\theta = 0.6$; right: sequential posterior updating from top to bottom.



Figure 4: Example JASP output for the binomial test of the proportion of even digits in the decimal expansion of π , based on the first 100 digits from which 51 are even. Left: prior predictive distributions; right: sequential Bayes factor analysis.

We drag the oddEven column into the *Selected* box and define the level even as *Successes* and the level odd as *Failures*. In the *Hypothesis* section we define two competing hypotheses: $\mathcal{H}_0: \theta = 1/2$ and $\mathcal{H}_1: \theta \sim \text{beta}(2,2)$. After defining the models we can inspect their predictions by selecting *Prior predictive distribution* under the *Inference* section. The left panel of Figure 4 displays the resulting comparison of the predictions from the rival hypothesis for the first 100 digits of π . The actual number of even digits is 51, which means that the \mathcal{H}_0 has outpredicted \mathcal{H}_1 ; the extent to which this is the case is the Bayes factor, that is, the ratio of the two prior predictive distributions evaluated at the observed number of even digits.

As in the *t*-test example, we may wish to monitor the evidential flow, that is, the fluctuations in the Bayes factor as the data accumulate. This can be achieved by selecting the *Bayes factor* option underneath the *Test results* checkbox in the *Sequential Analysis* section. After identifying the specific comparison model we obtain the right panel of Figure 4. The plot shows that the evidence in favor of \mathcal{H}_0 tends to increase as additional digits are entered into the analysis. After the 100^{th} digit the result stands at BF₀₁ = 5.31 – moderate evidence in favor of \mathcal{H}_0 versus this specific form of \mathcal{H}_1 .

In addition to the options highlighted above, the *Learn Bayes* module also offers visualisation and numerical summaries for prior distribution, sequential interval updating, and posterior predictive distributions.

Future Directions

In the near future we seek to improve JASP in several ways. For instance, we have set up a translation system. Currently JASP is available in English, German, and Dutch, but we aim to add more languages soon. We also hope to expand our data editing functionality beyond what JASP currently offers. At the moment, JASP allows users to edit the data by double-clicking the data view pane, which then opens the users' preferred spreadsheet editor (e.g., Excel or Calc). JASP also allows new columns to be computed and filters to be set up – either by using R code or by dragging-anddropping operators and variables.

Another major target is to present an option "copy R code". Although analyses in JASP are already fully reproducible (the .jasp file retains both the input options as well as the analysis output), providing the corresponding R code would allow researchers to fully reproduce the JASP output in R and further build on the analysis within R.

With respect to Bayesian analyses, we intend to add a Stan [2] module to complement our current JAGS [20] module. We are also interested in adding an interface for blavaan [16], Bayesian network analyses, Bayesian time series analysis, and more. It is now easier than ever to add new functionality to JASP, and the JASP YouTube channel offers a video that provides an introduction with concrete examples.

We hope that JASP can help popularize Bayesian inference, especially in empirical fields such as psychology and medicine. Bayesian inference has much to offer, but in order for researchers to look beyond the *p*-value it is imperative that the feedback loop between teaching and research be disrupted. With JASP we aim to increasing the chances that Bayesian methods will be taught at universities and applied in empirical research.

More Information

The website jasp-stats.org acts as a hub for all JASP-related content: teaching materials, books, manuals, videos, blog posts, workshop announcements, and more. You can also follow JASP on Facebook or on Twitter at @JASPStats. JASP will always remain open-source. We welcome feature requests and bug reports via our GitHub page.

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FROM THE PROGRAM COUNCIL

Botond Szabo

Welcome New Member

Matthias Katzfuss has joined the Program Council as the new Vice-Chair. At the same time, we are very grateful to our departing member Li Ma for his dedication and exceptional service in the past three years. Li still continues serving as the chair of the Scientific Committee of the ISBA 2021 World Meeting, working in close collaboration with the Program Council. Thank you, Li, and welcome, Matthias!

The Program Council is working on the organizations of the ISBA 2021 and ISBA 2022 World Meetings, along with the respective Scientific Committees, and in consultation with the ISBA Executive Committee.

ISBA 2021

The virtual ISBA 2021 World Meeting will take place online on June 28 to July 2, 2021. Registration is already open at the conference website and is free to everyone until the 1st of May, 2021.

ISBA 2022

The ISBA 2022 World Meeting is scheduled to be held in Montréal, Canada from June 26 to July 1, 2022. The Scientific Committee has selected the foundational (Subhashis Ghosal, Steffen Lauritzen,

Kerrie Mengersen, Nancy Reid) and keynote lecturers (Francesca Dominici, Pierre Jacob, Antonio Lijoi, David Stephens), and is working on the rest of the program. Information about the meeting will be added to the website. We encourage members to start thinking about potential contributions to the program; a call for invited sessions will be made around the end of April.

(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 either sponsorship or endorsement can be found here.

Upcoming ISBA-Sponsored/Endorsed Events

- ABC in Svalbard, April 12-13, 2021, Svalbard, Norway.
- NSF-CBMS Conference on "Bayesian Forecasting and Dynamic Models", University of California, Santa Cruz, CA, USA. (Postponed to Summer 2021).
- European Seminar on Bayesian Econometrics (ESOBE) 2021, September 2-3, 2021, Madrid, Spain.
- 11th BAYES-PHARMA Applied Bayesian Biostatistics Workshop (BAYES2020), Rockville, MD, USA. (Postponed until September 2021).
- The 5th EAC-ISBA Conference: A Satellite Meeting of the 2021 ISBA World Meeting in Celebrating James O Berger's 70th Birthday. (Postponed to Fall 2021).
- BAYSM 2021, September 1-3, 2021, virtual format.

UPDATES FROM BA

Michele Guindani

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We welcome **public contributions** to the Discussion of the manuscript the manuscript *Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC* by A. Vehtari, A. Gelman, D. Simpson, B. Carpenter and P.C. Bürkne, which will be featured as a **Discussion Paper in the June 2021** issue of the journal. You can find the manuscript in the Advance publication section of the journal website. The contributions should be no more than two pages in length, using the BA latex style and should be submitted to the journal using the Electronic Journal Management System (EJMS) submission page, before **May 10th, 2021**. An announcement for the public Webinar presentation will follow. As a reminder, all BA Discussion Webinars can be viewed on the ISBA YouTube channel.

A Bayesian Analysis session will be featured at the **ISBA 2021 World Meeting** which will be held virtually. The Bayesian Analysis session is titled *Highlights from Bayesian Analysis: Inference in Graphical Models and Networks.* The session will include three presentations, respectively by Jami J. Mulgrave on *Bayesian Inference in Nonparanormal Graphical Models,* Yuguo Chen on *Mixed Membership Stochastic Blockmodels for Heterogeneous Networks,* and Jian Kang on *Bayesian Network Marker Selection via the Thresholded Graph Laplacian Gaussian Prior.* Abel Rodriguez will prepare a Discussion. The session is scheduled for Friday, July 2nd, 5pm-6:30pm (US Eastern Daylight Saving Time). A great way to conclude the World meeting!

j-ISBA

Sally Paganin

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Dear ISBA community, I would like to introduce Xenia Miscouridou as the new Chair-Elect and myself as the new Treasurer of j-ISBA section. We are both excited to be more involved in the ISBA activities, and we thank the community for the participation in the voting process. We would like to extend our thanks to Brenda Betancourt and Trevor Campbell for their hard work in the past years, with special kudos to Brenda for having maintained the j-ISBA section of the ISBA Bulletin so far!

The j-ISBA section is happy to announce that the official j-ISBA conference Bayesian Young Statisticians Meeting (BAYSM) 2021 will be held Online in September 1-3, 2021. This will be a great opportunity for young researchers from all over the world to connect and share their work. Preparations are underway, and information about the meeting will be added to the conference website.

With the start of this new year, the j-ISBA section is working on new initiatives to strengthen our community, so stay tuned! We encourage everyone to join our section (only \$5 with your ISBA membership) and keep in touch with us and the community via our Facebook page or Twitter account @j_ISBA!

NEWS FROM THE WORLD

Francesco Denti

Reports from Important Events and Conferences

• BNP Webinar Series by Alessandra Guglielmi

In September 2020, the BNP board started the BNP webinar series, whose main goal was to encourage interactions within the Bayesian Nonparametric community during COVID-19 times. This consists of a series of monthly webinars (held on the first Wednesday of the month) which are designed to disseminate research results and ideas. The invited speakers are distinguished scholars working in different areas of Bayesian Nonparametrics.

Although the series was partially motivated by the COVID-19 pandemic and related restrictions, our aim is to continue this initiative and transform it into a series of regular meetings to encourage disseminating and discussing BNP ideas.

The series is hosted on Zoom by one member of the BNP section board. If the speaker agrees, we also record the webinar and post the video later on the BNP website. The webinar is advertised one week before on the ISBA mailing list. Participation has been a great success, with an average of 60-70 people per seminar.

Recently we have given the possibility to our speakers to share the presentation with younger co-authors. We also plan to put in place a formal system where members of the community can propose potential speakers. Moreover, we will organize two-hour virtual symposia on specific topics. We will announce these new initiatives in due course. See here for more information.

Upcoming Meetings, Conferences, and Workshops

• Mixtures Hidden Markov Models Clustering 2021 (MHC2021), June 2-4, 2021 at the Institut de Mathématique d'Orsay, Paris, France.

The MHC2021 international conference aims to bring together some particularly renowned and active researchers in the latent variable models community to share their most recent contributions and introduce a community of young researchers to this topic in constant change. The conference intends to create a momentum in which interesting perspectives will be discussed, such as theoretical open problems, new modeling requirements driven by applications, and today's role of latent variable models in understanding massive and high dimensional data structures.

Both physical participation, as well as participation by video conferencing, will be possible. Registration is free but mandatory. The number of physical participants will be limited to 100 or less if necessary for sanitary reasons. More information at this link.

• useR! 2021 conference, July 5-9, 2021, online.

useR! conferences are non-profit conferences organized by community volunteers for the community, supported by the R Foundation. Attendees include R developers and data scientists, business intelligence specialists, analysts, statisticians from academia and industry, and students. The useR! 2021 conference will be the first R conference globally designed, both in audience and leadership. Abstract submission is open until March 22, 2021. Registration opens on April 15, 2021. More info at this link.

And don't forget:

- The **ISBA 2021 World Meeting** will be **fully online** during the week of June 28 to July 2, 2021. Registrations are open and free for everyone before May 1, 2021, thanks to the generous support of the National Science Foundation (USA). Short courses will be offered between June 23 and June 28, 2021. All the info can be found at this link.
- The **Joint Statistical Meetings 2021 (JSM)** is the largest gathering of statisticians and data scientists in North America. The 2021 Joint Statistical Meetings will be held at the Washington State Convention Center, 705 Pike St., Seattle, WA 98101. The conference is scheduled for August 7-12, 2021. The early registration will open on May 3, 2021. More info at this link.
- The Bayesian nonparametric section of ISBA (**BNP-ISBA**) has organized a **series of monthly webinars**. The aim is to disseminate research progress made by distinguished scholars working in our vast area. Webinars will take place on the first Wednesday of each month, starting in September of 2020. Check out the next webinar at this link.
- The 11th European Seminar on Bayesian Econometrics will occur on September 2-3, 2021, at Universidad Carlos III de Madrid, Spain. Depending on the pandemic situation, the conference will take place in a hybrid or fully online format. In addition to invited presentations, the workshop will have contributed sessions, a special session by junior researchers, and poster presentations. Submissions for all sessions should be sent to esobe2021@gmail.com by March 31, 2021 (first deadline). Successful submissions will be notified by May 3, 2021. See this link for more information.
- Unfortunately, the **BAYES2020: Bayesian Biostatistics** conference is canceled and delayed until September 2021. Keep an eye on the conference website for updates regarding BAYES2021 accessible at this link.
- The **2020 Orange County Biostatistics Symposium**, scheduled initially on October 16-17, 2020, has been postponed. Based on the current situation and per health advisories, the organizing committee has decided to defer the Symposium to 2021. The exact date of the 2021 Symposium is to be decided by considering the COVID-19 pandemic and health authority guidelines. More information can be found at this link.

• Two-day virtual Course Sequence for 2021: Using R for Bayesian Spatial and Spatio-Temporal Health Modeling, June 1-2, 2021. This workshop sequence is designed for those who want to cover mapping methods and the use of various software and variants in application to small area health data. The course will include theoretical input and practical elements. Participants will be involved in hands-on use of R, BRugs(OpenBUGS), Nimble, CARBayes, and INLA in disease mapping applications. More information at this link.

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