

THE ISBA BULLETIN

Vol. 13 No. 3

September 2006

The official bulletin of the International Society for Bayesian Analysis

A MESSAGE FROM THE PRESIDENT

by Alan Gelfand
ISBA President

alan@stat.duke.edu

As I enter the final quarter of my year as president, I write to mention two issues that we have been dealing with since the Valencia gathering. First, we are trying to accomplish some consolidation with regard to the various prizes that ISBA oversees (DeGroot, Lindley, Savage, and Mitchell). These prizes are now well-established. To paraphrase Jay Kadane, who is chair of our Constitution and Bylaws Committee, the idea is to bring these prizes within the ISBA bylaws, to streamline structure, to allow flexibility, and ensure original intent. We are currently working on a mechanism for ISBA oversight in this regard. A second matter we wrestle with is our financial affairs. Here, we are trying to deal with setting appropriate dues levels, building travel funds to support young researchers, maintaining Bayes's grave site, providing financial contributions to ISBA-sponsored in-

ternational meetings, and making somewhat optimal investment decisions for the resources we do have.

I am happy to report that Brad Carlin has agreed to take over the role of Editor-in-chief of Bayesian Analysis from Rob Kass. We owe Rob a huge debt of gratitude for his effort in getting the journal off to a very promising start. In this regard, we are moving forward with a decision to produce and sell a bounded, printed version of Bayesian Analysis. We propose to work with the R.T. Edwards publishing house and, if successful, a percentage of the proceeds will be returned to the Society.

Finally, we have announced the location and dates for the next ISBA world meeting. It will be from 14-17 July, 2008 on Hamilton Island in Queensland. Kerrie Mengersen from QUT is the local organizer for this event and we appreciate her efforts in bringing an opportunity to enjoy a meeting at this spectacular venue. More details will be forthcoming in the next few months and I hope you will begin planning to attend.

- Alan E. Gelfand, ISDS, Duke University

A MESSAGE FROM THE EDITOR

by J. Andrés Christen

jac@soe.ucsc.edu, jac@cimat.mx

This issue of the ISBA Bulletin is specially varied with several interesting columns to read, an Interview section and a Software Review. Of special interest for ISBA members are the ISBA Elections section. I decided to wait until all candidates' statements were complete and that is why this issue is a bit delay; apologies. I hope you enjoy reading this issue of the ISBA Bulletin.

Contents

- INTERVIEW
 • Page 2
- SOFTWARE REVIEW
 • Page 4
- ISBA ELECTIONS
 • Page 9
- NEWS FROM THE WORLD
 • Page 12

SUGGESTIONS

PLEASE, FEEL COMPLETELY FREE TO SEND US SUGGESTIONS THAT MIGHT IMPROVE THE QUALITY OF THE BULLETIN

jac@cimat.mx

INTERVIEW WITH GEORGE CASELLA

by Elias Moreno

emoreno@goliat.ugr.es

George Casella is Distinguished Professor and Chair, Department of Statistics, University of Florida. He has been in Florida since 2000, and before that he spent 19 years at Cornell, starting there as Assistant Professor and finishing as the Liberty Hyde Bailey Professor of Biological Statistics. He is married to Anne Kendall, who holds a Ph.D. in Nutrition and also teaches at the University of Florida. They have two children, Benjamin, 14, and Sarah, 12, who take up much of their time.

In addition to many research articles, Casella has written four books (Statistical Inference with Roger Berger, Variance Components with S. R. Searle and C. E. McCulloch, Theory of Point Estimation, Second Edition, with E. L. Lehmann, and Monte Carlo Statistical Methods with Christian Robert). He has served as the Theory and Methods Editor of JASA (1996 - 1999) and the Executive Editor of Statistical Science (2001-2004). This interview was done while George Casella was visiting the University of Granada, Spain, in June 2006. You can find out more information about George Casella at: <http://www.stat.ufl.edu/~casella/>

1. Your undergraduate training was in mathematics, and then you went to graduate school in statistics at Purdue, writing a thesis on minimaxity. How long were you interested in minimaxity, decision theory, etc.?

I worked for a long time on decision theory, first on point estimation then on interval estimation and confidence sets.

2. Can you describe the evolution of your research interests?

When I was in graduate school many people were working on Stein estimation. First I studied minimaxity of point estimation and other properties of estimators. After Purdue I went to Rutgers University where I worked with Bill Strawderman on more decision theory problems. At Rutgers, and continuing at Cornell, I became very interested in the problem of improving on the usual multivariate normal confidence interval. With Gene Hwang I wrote a number of papers on this topic, one of which (Hwang and Casella 1982) was the first paper to prove that a confidence set centered at a Stein estimator would uniformly dominate the usual one

3. After your work on confidence sets, you seem to have become interested in matters of evidence and Bayes/Frequentist reconciliation. In 1987 you published a paper in JASA on reconciliation of inference. Do you feel that nowadays there is a need to reconcile both theories?

People were more disparate then - there was more disagreement and I never thought that the disagreement was healthy. We should all do good statistics and not try to decree which way, Bayes or frequentist, is better. When we fight among ourselves, statistics loses.

Around 1985 I saw a technical report by Jim Berger and Tom Sellke about the irreconcilability of Bayes/Frequentist evidence. I was in North Carolina at the time, working with Roger Berger on what was to become our book on statistical inference, and we discussed about how we thought that we could reconcile evidence in the one-sided testing problem. All this work led to the 1987 JASA paper.

4. Statisticians measure the uncertainty in an assertion. I think that some of the frequentist tools for measuring uncertainty (say p-values, or confidence intervals) are not a measure of evidence, and from here comes the disagreement. What do you think of this?

I have thought a lot about measures of evidence, and how frequentist statistics do not give measures of evidence - things like confidence levels and α levels are pre-data evaluations, and don't tell you how the data bears on your conclusions. I worked on a number of papers in the late 80's and early 90's that attempted to fix this problem, and to allow for frequentist post data inference, but, unfortunately, there was never a satisfactory solution. I always think about a conversation that I had with David Cox when he visited Cornell in the 90s. We talked about what is the best way to do statistics, Bayesian or frequentist, and he said, as I recall, that we should all use whatever we have to solve the problem at hand. I think that is a very healthy way to approach statistics, and I think that statisticians today are more in agreement, and are willing to use procedures that are a combination.

To me, Bayes and frequency have two complementary roles. Using Bayes, or hierarchical models, we can derive estimators and intervals for very complex problems. Using frequency theory, we can evaluate the performance of our estimators in order to get some guarantee of repeatable performance. This is combining the best of both disciplines.

5. *How long were you interested in post-data inference?*

Until the early 90s. In 1991 I organized a conference at Cornell on Conditional Inference. It was very small, about 15 people, but we had some very good people there like Susie Bayarri, Jim Berger, Larry Brown, Ed George, Bill Strawderman, Christian Robert, Larry Wasserman, Robert Wolpert, and others. We talked a lot about conditional inference, but we also talked a lot about Gibbs sampling, as that subject was starting to develop.

6. *So from your interest in decision theory and inference, you then moved to computation. What was the reason for changing?*

There really was no change. What we, as statisticians, try to do is to make good methods for solving problems. My original research always evaluated the performance of estimators. What happened with the Gibbs revolution was that now we could solve many more problems with new types of procedures. My interest has never been in the actual computations, but rather in evaluating the performance of the resulting estimators. That is, in doing statistical inference for procedures computed with algorithms rather than formulas. Two papers that illustrate this approach are my 1996 JASA paper with Jim Hobert on Gibbs with improper priors, and my 1996 Biometrika paper with Christian Robert on Rao-Blackwellization of sampling schemes. I work on these types of problems throughout the 90s, and finally wrote the Monte Carlo book with Christian Robert.

7. *You have also been interested in empirical Bayes methods. How has that played a role in your work?*

Empirical Bayes and I go back a long way. Empirical Bayes was tied to Stein estimation in the work of Efron and Morris in the 70s, as a way of constructing good shrinkage targets and actually doing data analysis with Stein estimators. I first used empirical Bayes in a 1983 JASA paper to construct improved confidence sets, and still use it today. But now, it seems that the tool of the hierarchical model itself is the important thing, and now I like to use empirical Bayes as a means of estimating hyperparameters.

8. *Can you explain that last sentence. For example, why should we use empirical Bayes instead of fully hierarchical Bayes?*

At some point the hierarchy must stop, and we are left with either finding a prior for a hyperparameter, or estimating it. Since there is usually

no intuition for hyperparameters, typically a flat improper prior is used. This can cause problems, by making variable generation difficult or, worse, by causing impropriety in the posterior distribution. Using empirical Bayes, we can estimate these parameters with marginal likelihood, and provide what I feel is a better solution.

9. *What kind of problems are you working on today?*

As always, my research is driven by applications. Most people do not know that, starting from graduate school, I have spent most of my career in colleges of agriculture, and still work closely with many applied scientists. The revolution in genetics and genomics has spawned interest in classification and model selection procedures - clustering, variable selection, etc.

With this motivation, and the work that we have been doing together on objective Bayes methods, we have been able to develop new methods for clustering and model selection. Our 2006 JASA paper reflects this work.

10. *You have written four books. Before I ask you which of your books is your favorite, can you tell me what is your favorite book outside of those you have written?*

There are many books that I like very much, but one that has always been a favorite is Kendall and Stuart.

11. *Can you explain why?*

Perhaps because they developed the theory of statistics within itself, rather than an application of mathematics, which was the way many of us were originally taught. It was interesting to see the theory of statistics developed that way.

12. *So now I must ask you - of your own books, which is your favorite?*

I guess that would be Statistical Inference with Roger Berger. We worked hard to develop and present statistical theory in a logical order, and trying to explain all of the important details and necessary techniques. We had a lot of fun writing that book. And, from my perspective, I think that Kendall and Stuart had a big influence on the way we developed the topics.

13. *Well, of your books, the one with Lehmann is one of my favorite. Can you tell us something about writing with Lehmann. For example, how did the collaboration start?*

As I recall, John Kimmel, the Editor at Springer-Verlag, asked me if I would be interested in working on the second edition of Theory of Point Estimation with Erich Lehmann. As you understand, this is an offer that no sane person would ever turn down. Erich and I worked together for about three years on the revision.

14. *What was it like, working with Lehmann?*

It was an incredible experience. At that point in my career I had written two textbooks, but I soon realized that I knew nothing about writing textbooks. Erich is the master, and such a gentleman that, when he pointed out to me how we could do something better, he felt bad about correcting me. He taught me what a textbook should be - It should tell the complete story, with no loose ends. All details, proofs and examples should be fully worked out. I think that my later books really benefited from everything that I learned from Erich.

15. *Lets talk about another topic. As Editor of JASA, you were in the mirador, the observation tower, for statistics. How do you see the health of statistics today?*

The health is good. Now, more than ever we are driven by applications, and we work to solve real problems. Moreover, with the oncoming "data flood" (one of my favorite expressions) practitioners need us more than ever and they are finally starting to realize it! My only concern is that I think, at this point, the cycle has swung a bit too far toward applications, and some of us are forget-

ting that we must pay attention to the theory - to actually figure out what are the properties of the procedures we are proposing, and not just through simulations. But I also think that we are starting to realize this, and we are paying more attention to the methodology.

16. *We have known each other for a long time, and in recent years you have spent more time in Spain. You have worked very hard to learn Spanish, to the extent that you have given research talks and a course in Monte Carlo all in Spanish. Why have you worked so hard at this?*

First, I really enjoy trying to learn a language - during the 90s when I was working a lot with Christian Robert and visiting France, I got reasonably good at French. But more importantly, I think that it is valuable to speak more than one language so that we can communicate our science to an even wider audience. I still remember that when I gave introductory talks about Monte Carlo methods in Spain four years ago, I had more than 70 people in the audience. I think that if I had spoken in English, there would only been half as many. If I got one or two extra students interested in statistics, I think that all of my efforts to learn Spanish were worthwhile.

17. *Lastly, you have recently travelled through much of Spain -Valencia, Santander, Granada, Murcia, Málaga. What are some of your favorite memories?*

That is the easiest question that you have asked me! El vino de Ribera de Duero, el lechazo de Aranda de Duero y el jamón de la Alpujarra!

Thanks George! ▲

BAYESIAN SOFTWARE FOR EPIDEMIOLOGY: THE ANALYSIS OF DATA FROM DIAGNOSTIC TESTS AND SAMPLE SIZE DETERMINATION

by Lawrence Joseph* and Patrick Bélisle†

*Lawrence.Joseph@mcgill.ca,

†PBelisle@epimgh.mcgill.ca

Introduction

It is undeniable that the many, perhaps even a majority, of methodological advances published in the

statistical literature find few users in real practice, and hence have little impact on substantive applications. This is true of both Bayesian and non-Bayesian methods, even though the former is enjoying increasing use in applied fields such as epidemiology, with many of the major epidemiology journals encouraging the analysis of studies from this viewpoint (see, for example, Dunson 2001 or Goodman 2001).

A main reason for this state of affairs is that many scientists, including most epidemiologists, lack sufficiently rigorous statistical training, meaning that these new methods are difficult or impossible for them to apply in practice. This is true even

if they have an analysis problem that ideally would benefit from a recently published approach.

One solution to this problem is for statisticians to write more articles explaining their methods to applied audiences, and to accompany these articles with easy-to-use software that implements their novel approaches. Bayesian methods can be complex numerically, typically requiring specialized software. While programs such as WinBUGS have gone a long way towards making Bayesian analysis more accessible, not everyone has time to become a WinBUGS programmer, so software requiring less skill in programming can be useful.

In this article, we describe some very user-friendly software for two of the most frequently occurring epidemiology problems, the determination of sample size for common study designs, and the analysis of diagnostic testing data, especially in the absence of a perfect gold standard test. Each software package we describe is easy enough for non-experts to use, after reading the manuals or help files, and an article that describes the methods.

Diagnostic Tests in the Absence of a Gold Standard

It is common in medical diagnosis and population screening studies to have results from one or more diagnostic tests, none of which can be considered a perfect (gold standard) test. In fact, this is almost always the case, since virtually no test is perfect, and even theoretically perfect tests are subject to human errors. This gives rise to a misclassification problem, as truly diseased subjects may be diagnosed as non-diseased, and vice versa. In the absence of a gold standard test, it is not straightforward to estimate the rate of disease in the population or to investigate the properties of new diagnostic tests, because the number of subjects testing positive on any test is not necessarily the true number of disease positive subjects in the sample. Consider the data in the table below:

		Test 2		
		+	-	
Test 1	+	40	60	100
	-	5	95	100
		45	155	200

If test 1 is to be believed, the prevalence (i.e., pro-

portion of truly positive cases in the population) is estimated to be 50% (i.e., $\frac{40+60}{200} = 0.5$), but if test 2 is more reliable, the estimate should be closer to 22.5% (i.e., $\frac{40+5}{200} = 0.225$).

What if it is known, however, that test 1 tends to have a high sensitivity but low specificity (i.e., tends to find the real cases, at the expense of misclassifying some true negatives as positive), while test 2 is the opposite (i.e., high specificity but lower sensitivity)? It seems logical to use the combined information from the two tests together, without considering either to be error free. Accordingly, a Bayesian approach that uses prior information about the test properties to derive posterior densities about the prevalence was described in Joseph, Gyorkos and Coupal (1995).

BayesDiagnosticTests

The *BayesDiagnosticTests* program is a very user-friendly implementation of the methods discussed in Joseph et al (1995). A Windows based stand-alone application, it is built on a combination of other free software packages (WinBUGS, R, and Perl), which must be installed and which the *BayesDiagnosticTests* program calls as needed. Opening the program, a series of consecutive windows prompts the user for information required as input. This includes the data set, the prior information for each unknown parameter, and, if desired, more experienced users may change some of the Gibbs sampler run-time properties, including the possible to run up to five simultaneous chains with five different sets of starting values. Many of these inputs can be saved for future use, and prior distribution inputs can either be in the form of parameters of beta distributions, or as means and standard deviations, which are then automatically converted into the closest fitting beta parameters. Upon completion, several files of output are saved to a user-specified location, containing posterior summaries of all unknown parameters.

BayesContinuousDiagnosticTest

While the *BayesDiagnosticTests* program can handle up to three dichotomous tests, like those in the table above, it does not allow for continuous test data. An analogous program, *BayesContinuousDiagnosticTest*, extends the above analyses to the case of continuous diagnostic tests, as described in Scott et al (2006). The program operates in a very similar fashion to *BayesDiagnosticTests*, except that data from one continuous test, either alone or together with up to two dichotomous diagnostic tests are input. Outputs are both saved to a file, and accessible immediately from a pop-up box that opens

when the program completes its run. Outputs include posterior summaries of all unknown parameters, as well as ROC curves, sensitivity and specificity curves across all possible cutoff values for the continuous tests, and the probability of being truly positive for each value of the continuous test. Once again, this program assumes that none of the tests used are a gold standard.

Predictive Values

Finally, *PredictiveValues* is a simpler program designed to output the probability of being positive for any combination of up to three possibly imperfect diagnostic test results. Unlike the more complex programs described above, this is a stand-alone application that does not require any other software to be installed, and is intended for clinicians offices, to aid in the interpretation of diagnostic test results for their patients. The inputs are the test results and the test properties (prior distributions for the sensitivities and specificities) for each test, and the output is the probability of a patient being positive, given their test results.

Bayesian Sample Size Determination

Experimental design can be viewed as a naturally Bayesian problem, since the design must be based on prior knowledge about the relationships between and values of the key parameters to be estimated in the study. While classical methods usually only consider point estimates of these quantities, Bayesian methods can make full use of a prior distribution which reflects the uncertainty in the parameter values which is almost always present at the design stage of an experiment (otherwise the experiment would not be needed!). Recently there has been much activity in Bayesian sample size determination, see the reviews by Adcock (1997) and Wang and Gelfand (2002).

We have created several software packages that implement a Bayesian approach to sample size determination, which makes full use of the available prior information, while not requiring precise point estimates for truly unknown parameters. Prior distributions lead to predictive (marginal) distributions for the data that include the dependence of the final inferences on both the unknown parameter values and sampling variation. One can then define various sample size criteria in terms of the average coverage probability or the average length of intervals of posterior credible sets over all possible data sets, weighted by the pre-

dictive distribution. Criteria we consider include the Average Coverage Criterion (ACC), the Average Length Criterion (ALC), the Worst Outcome Criterion (WOC) and the Modified Worst Outcome Criterion (MWOC). We also consider variations on these criteria that use prior information for the predictive distribution of the data, but switch to uniform priors for calculating posterior interval coverages and widths. These so-called “mixed Bayes/likelihood” methods are intended for those who want to use prior information for predicting the data sets most likely to arise, but plan to use diffuse prior distributions for analysis. See Joseph et al (1997) or M’Lan et al (2006) for definitions and a full discussion of these criteria.

Calculating sample sizes from several criteria clearly expose the compromises and risks related to choice of particular sample sizes. S-PLUS or R programs are available for both normal (*Normal means*) and binomial sampling (*Binomial proportions*) situations. These cover the most common sample size situations arising in clinical trials and other studies.

Sample size determination for diagnostic test studies

It is of great interest to combine the above two areas of study, in particular, to investigate sample size requirements for diagnostic testing studies in the absence of a perfect (gold standard) test. When a gold standard is available, the sample size problem for prevalence estimation or estimating the sensitivities and specificities of new diagnostic tests reduces to binomial parameter estimation. However, when no gold standard is present, the situation is considerably more complex, because the problem becomes non-identifiable, so that in certain cases even an infinite sample size is not sufficient for accurate estimation of the unknown parameters. This crucial fact is often not appreciated when carrying out diagnostic test studies, leading to reports of test properties that are often misleadingly optimistic. See Dendukuri et al (2004) for more details about this problem.

Our Windows software package, *PropMisclass-SampleSize*, provides researchers with sample size estimates from all of the criteria discussed above (except the mixed Bayes/likelihood criteria, which are not appropriate for non-identifiable problems), in the context of planning diagnostic test studies in the absence of a perfect test. Through a series of pop-up windows, researchers specify the parameter of interest (prevalence, sensitivity or specificity), the number of tests they will use (up to

three), the prior information about the prevalence and the properties of each test, the desired accuracy of their final inferences (in terms of credible interval widths and coverages), and the criterion they wish to use. The program then returns the required sample size for their study. It also provides asymptotic interval lengths and coverages as the sample size approaches infinity, so that researchers can appreciate when the imperfections in their diagnostic tests preclude accurate estimation, regardless of the number of subjects included in their study.

Conclusion

The production of software packages to accompany new statistical methods is intended to hasten the “technology transfer” from statisticians to applied researchers. By making our software easy to use, we hope to enable epidemiologists and others to use our methods with little trouble, hopefully enhancing study design and analysis of diagnostic test and other studies.

Of course, even our “user-friendly” software requires some basic knowledge of Bayesian analysis, which is why we have links titled “related papers” on our web site, so that readers can learn more about how the methods work. We also offer software support for users via email.

All software packages and related research articles discussed in this review are freely available from <http://www.medicine.mcgill.ca/epidemiology/Joseph/>

Dynamic Bayesian networks

In order to model systems that evolve with time, as for example those studied in reliability analysis, it is necessary to take the temporal dimension into account. Even if it is possible to do it with a static Bayesian network, by unrolling it on the desired number of time steps (i.e. by duplicating the network for each time step), this solution is possible only for a limited and previously known number of time steps. Dynamic Bayesian networks provide a much more compact representation for stochastic dynamic systems. This compactness is based on the following assumptions: (A1) the process is Markovian, i.e. the variables of time step t depend only on the variables of the preceding time step $t - 1$; (A2) the system is time invariant, i.e. the probability tables do not evolve with respect to time. This last assumption can be partially relaxed in BayesiaLab by using the time variable to modify the probability distributions according to the value of the current time step by the means of the equations. This rep-

resentation allows representing stochastic dynamic systems only with two time slices. The first slice describes the initial network at time step t_0 and the second one describes the temporal transitions $t + 1$.

Conclusion

An evaluation version of BayesiaLab and a dynamic presentation are available on

<http://www.bayesia.com>.

This website also contains some application examples that describe the use of BayesiaLab in various domains: Modeling and simulation of complex systems, Risk analysis, Mining customer data bases, Intrusion detection, Text Mining, MicroArrays analysis and Health Trajectory analysis. ▲

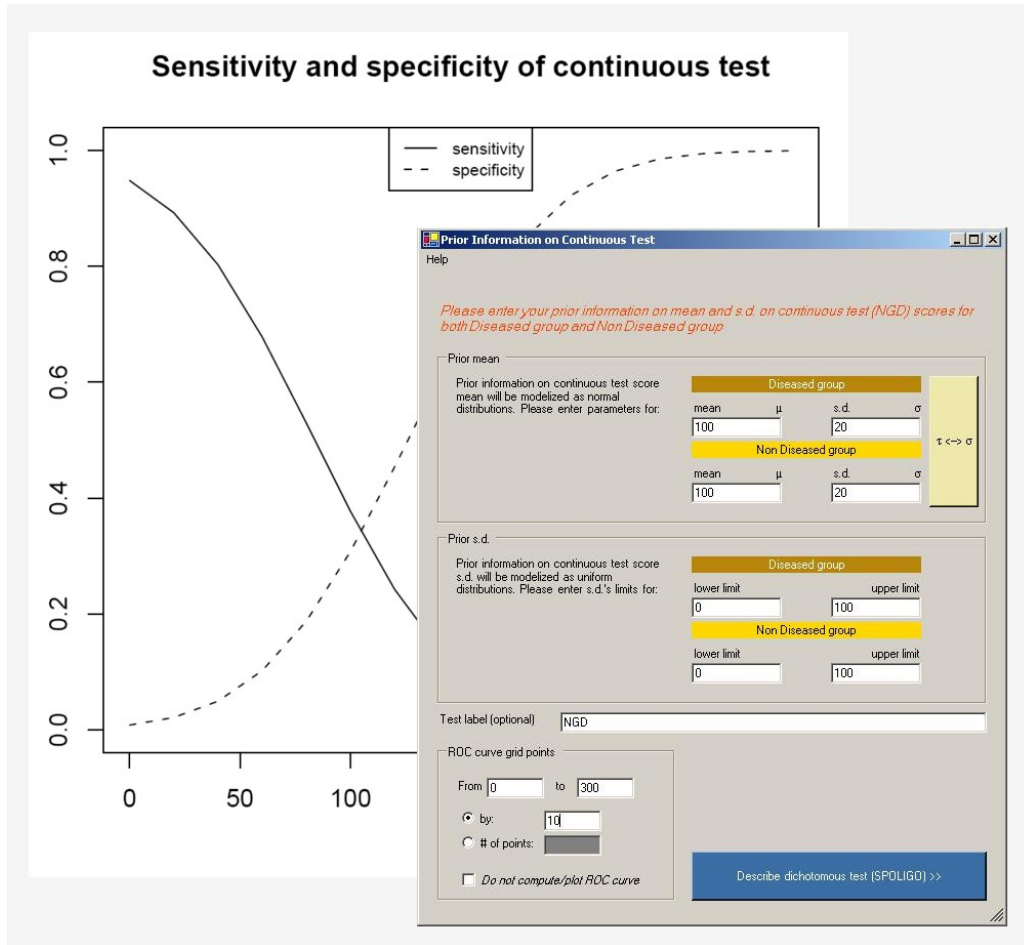
References

- Adcock A. Sample size determination: A review. *The Statistician* 1997;46:261-283.
- Dendukuri N, Rahme E, Bélisle P, Joseph L. Bayesian sample size determination for prevalence and diagnostic studies in the absence of a gold standard test. *Biometrics* 2004;60:388-397.
- Dunson D. Practical advantages of Bayesian analysis of epidemiologic data. *American Journal of Epidemiology* 2001;153(12):1222-1226.
- Goodman S. Of P-Values and Bayes: A Modest Proposal. *Epidemiology*. 2001;12(3):295-297.
- Joseph L, du Berger R, and Bélisle P. Bayesian and mixed Bayesian/likelihood criteria for sample size determination. *Statistics in Medicine* 1997;16(7):769-781
- Joseph L, Gyorkos T, Coupal L. Bayesian estimation of disease prevalence and the parameters of diagnostic tests in the absence of a gold standard. *American Journal of Epidemiology* 1995;141(3):263-272.
- M’Lan E, Joseph L, Wolfson D. Bayesian sample size determination for case-control studies. *Journal of the American Statistical Association* 2006;101(474):760-772.
- Scott A, Joseph L, Bélisle P, Behr M, Schwartzman K. Bayesian estimation of tuberculosis clustering rates from DNA sequence data (submitted).

- Wang F, and Gelfand, Alan E. A simulation-based approach to Bayesian sample size determination for performance under a given

model and for separating models. *Statistical Science* 2002;17(2):193-208.

Figure 1: Screenshots from the program *BayesContinuousDiagnosticTest*



ISBA/SBSS ARCHIVE FOR ABSTRACTS

All authors of statistics papers and speakers giving conference presentations with substantial Bayesian content should consider submitting an abstract of the paper or talk to the ISBA/SBSS Bayesian Abstract Archive. Links to e-prints are encouraged. To submit an abstract, or to search existing abstracts by author, title, or keywords, follow the instructions at the abstract's web site,

<http://www.isds.duke.edu/isba-sbss/>

THIS YEAR ELECTIONS

For President 2008 (President Elect 2007, Past President 2009):

- Don Berry (MD Anderson, USA).
- Christian Robert (Paris, FR).

For Executive Secretary, 2007-2009:

- Fernando Quintana, (PUC, Chile).
- Robert Wolpert, (Duke, USA).

For the board, 2007-2009:

- Bertrand Clarke (U. British Columbia, CA) .
- Mike Daniels (U. of Florida, USA).
- David Heckerman (Microsoft, USA).
- Susan Holmes (Stanford, USA).
- Bani Mallick (Texas A&M).
- Xiao-Li Meng (Harvard, USA).
- Gareth Roberts (Lancaster, UK).
- Alexandra Schmidt (Rio de Janeiro, Brasil).

Biographical information for each of the candidates appears below. The candidates for president have also included statements about what they intend to accomplish. This information is also currently accessible on the ISBA web-site. The 2006 elections of future ISBA officers will take place electronically at the ISBA web-site (<http://www.bayesian.org/election/voter.html>) from 15 October through 15 November. Instructions for voting will be emailed to all current ISBA members prior to the election.

President Elect Nominees

Don Berry

Affiliation and current status: University of Texas, M.D. Anderson Cancer Center.

Statement

I am honored to have been nominated as a candidate for President of ISBA, and to be opposed by Chris Robert, someone I greatly respect. Like other ISBA candidates, I'm interested in promoting all things Bayesian. My previous record in this regard has been mixed. I've tried to have an effect on introductory statistics courses in universities, including writing an elementary Bayesian textbook. The book still lives, but its impact has not been nearly what I'd hoped. Much of my professional life has been spent promoting the Bayesian approach in medical research. After many years of disappointment, we are finally seeing real progress. I've been at the University of Texas's M.D. Anderson Cancer Center for the last 7 years, during which we have designed over 200 Bayesian clinical trials, which is probably more than the rest of the world combined. Bayesian approvals of medical devices in the U.S. by the FDA's Center for Devices and Radiological Health are becoming commonplace. And in the last year or so there has been enormous progress in the pharmaceutical industry, with more than half of the 40 biggest drug companies setting up Bayesian adaptive trials. A Japanese pharmaceutical newsletter had a cover story with the apt title (translated), "The Coming Bayesian Tsunami in Clinical Development." My term will be dedicated to bringing biostatistics and biostatisticians closer to ISBA by moving a focus of ISBA closer to them. In biostatistics, using Bayesian design is arguably more important than using Bayesian analyses. So maybe we could add "design" to our name: ISBAD. (My campaign slogan could be, "ISBAD is good!") Well, perhaps a name change is not important, but a moderate shift in emphasis would be good for ISBA—and for medical research as well.

Christian Robert

Affiliation and current status: Paris, FR.

Statement

While I am very honoured to be asked to be a candidate for the ISBA Presidency, I must admit I also feel rather unsecure about my adequacy for this position, especially taking into account the perfect adequacy of Don! Anyway, while I think that ISBA is doing a terrific job in terms of international representation and of world-class meetings, I think it should gain in increasing its visibility as the Bayesian Statistics reference society. In particular, it seems to me that there are many fields of

application of Bayesian Statistics where researchers have convinced themselves of the worth of the Bayesian approach without connecting with mainstream statisticians, both to our loss [as a society and as researchers] and to theirs. Finding ways to reach towards those new communities appears to me as a major task for the coming years. This may be achieved by means of cosponsoring meetings and workshops, running broader summer schools, but also maybe via an even broader spectrum for our journal...

Nominees for Executive Secretary, 2007-2009

Fernando Quintana

I am Profesor Adjunto (Associate Professor) at the Department of Statistics, Pontificia Universidad Catlica de Chile. My main areas of interest are Nonparametric Bayesian Models and their Applications, Bayesian Clustering, and Models for Longitudinal Binary Data. I have published in several journals, including JASA, JRSS B, JCGS, CJS and JSPI. I am currently an elected Board Member of ISBA. Also, I co-organized the ISBA 2004 World Meeting in Viña del Mar, Chile. See more at <http://www.mat.puc.cl/~quintana>.

Robert Wolpert

Robert Wolpert (PhD Princeton Univ Mathematics). I am a Professor of Statistics and Decision Sciences at Duke University, with courtesy appointments in Mathematical Sciences at Queensland University of Technology in Brisbane, in Epidemiology & Public Health at Imperial College in London, and in Environmental Science here at Duke. I began my career as a probability theorist, but was overjoyed to discover in Bayesian Statistics an opportunity to apply probability theory to a much broader and more interesting class of problems, and to find in ISBA and its precursors a thriving community of statisticians and scientists sharing ideas and encouragement in ways that were quite surprising and exciting to someone brought up in the more austere world of pure mathematics.

My research interests vary widely over time, but recurring themes are Bayesian nonparametric methods (building on the stochastic processes of my earlier life) and foundational matters, like the Likelihood Principle, that may offer us some guidance as we face sticky new problems. I've served on the ISBA board of directors and some of its committees, and would welcome a chance to work again in planning and reporting on ISBA activities.

Nominees for Board of Directors 2005-2007

Bertrand Clarke

Bertrand Clarke (PhD 89, U. of Illinois) is Associate Professor of Statistics at Univ. of British Columbia. His early interest was prior selection (mostly information-theoretic), and asymptotics, especially involving conditioning on statistics rather than on the full data set. More recently, his interest has turned to model uncertainty from a predictive standpoint. His main area of application has been network models for biochemical processes. He has published in a large number of journals in several fields (Statistics, Engineering, Biology) including Ann. Stat., JASA, CJS, IT Transactions, JSPI and is currently an AE for 2 journals (JASA and JSPI).

Interest in the future direction of Bayesian statistics, and statistics more generally, is of great interest to him. The breakneck pace of development in recent years has led to an exciting proliferation of ideas and techniques. There must be a way to maintain this vibrancy while retaining the unity of the field. Also, the manifold professional matters that arise as the field matures may require more open discussion than before.

Mike Daniels

Mike Daniels (ScD Harvard, 1995) is currently the Division Chief of Biostatistics and Associate Professor in the Department of Epidemiology and Biostatistics at the University of Florida. He also holds a joint appointment with the Department of Statistics. His research interests include Bayesian methods for (incomplete) longitudinal data, priors for covariance matrices (and modelling dependence in general), and environmental applications. He has published papers in Biometrika, JASA, JRSS-C, JCGS, Biometrics, and Biostatistics. He is an associate editor for Biometrics and JASA. He is currently finishing a book on Bayesian methods for dropout in longitudinal studies to be published by Chapman & Hall next summer. Further information about his research can be found at his web page (<http://www.stat.ufl.edu/~mdaniels>).

David Heckerman

I have been a Senior Research at Microsoft Research since 1992 and, for most of that time, have been manager of the Machine Learning and Applied Statistics Group. Using Bayesian methodology, I have created applications including the first content-based spam filter, data-mining tools

for SQL Server and Commerce Server, handwriting recognition for the Tablet PC, text mining software for Sharepoint Portal Server, troubleshooters for Windows, and the Answer Wizard for Office. My main technical interest is graphical models. I have published in the *Annals of Statistics*, the *Journal of Machine Learning Research*, *Machine Learning*, and *Artificial Intelligence*. I am a member of the Program Committee for the Bayesian Statistics/Valencia Conference and am a founding editor for Bayesian analysis. <http://research.microsoft.com/~heckerman/>.

Susan Holmes

Affiliation and current status: Professor of Statistics, Statistics Department, Sequoia Hall, Stanford, CA 94305, USA. on leave from INRA, Montpellier, France. email address: <http://www-stat.stanford.edu/~susan/>; susan@stat.stanford.edu. Areas of interest: Computational Biology and Phylogenetic Analysis, Stein's method, Applied Probability, Bayesian computation and MCMC, multivariate analysis, gene expression studies, applications to immunology and physics. Fellow of IMS, journals and books: *JASA*, *Statistical Science*, *Annals of Applied Probability*, *Erkenntnis*, *PNAS*, *IMS Lecture Notes on Stein's Method*.

I am interested in creating more interdisciplinary conversations with physicists and biologists in particular. I have co-taught a course on the Statistics and Physics and would like more interaction with other disciplines. An important part of our vocation as volunteers is to keep our journals and publications at low costs or open access.

Bani Mallick

Bani Mallick (Ph.D., University of Connecticut) is a Professor in the Department of Statistics at the Texas A&M University. Bani's research interests include Bayesian classification and regression, Generalized linear models, Spatial modeling, Nonparametric Bayesian modeling, MCMC based computational methods, applications of Bayesian methods to Bioinformatics, atmospheric sciences, Petroleum Engineering. He is the director of newly developed Bayesian Bioinformatics Lab at Texas A&M University. He has published papers in journals which include *JRSSB*, *Jasa*, *Biometrics*, *Biometrika* *JCGS*, *IEEE*. Bani wrote a book on Bayesian classification and regression and edited a book on Bayesian GLM. He is currently the President of Southeast Texas chapter of ASA and associate editor of several statistical journals.

Xiao-Li Meng

Professor and Chair, Department of Statistics, Harvard University. Research Interests: Statistical modeling and computation, incomplete and missing data, Bayesian analysis and inference foundations, applications in social sciences, astronomy and engineering. Journals and books: *Annals of Statistics*, *Biometrika*, *JASA*, *JRSSB*, *Statistical Sciences*, *Statistics Sinica*. Gelman, A and Meng, X.L. (eds) (2004). *Applied Bayesian Modeling and Causal Inference from Incomplete-data Perspectives*. U.K.: Wiley & Sons. Previous Services to ISBA: Editor, *Bayesian Analysis*.

A main reason that within one year I had accepted nominations for Vice President for ASA (negative outcome), to serve on IMS council (positive outcome), and now to serve on ISBA Board (unknown outcome), is to contribute my share in further strengthening the collaboration among major professional societies for statisticians and probabilists. I believe strong collective leadership from major societies is the key in speeding up the pace for advancing our profession. The three areas where I would like to see stronger joint efforts are (1) assessing the "deserved market value" of statisticians and related professions, and thereby to ensure that we stay competitive in attracting the best minds into our profession; (2) increasing the general awareness that a faster publication process helps to improve our "relevance" in the general scientific community; and (3) advocating that better teaching is also about improving our image in the general public, because it helps to convey more effectively that statistics and probability are much more than taking averages or flipping coins.

Gareth Roberts

I obtained my PhD from Warwick University in 1989, and subsequently held lecturer positions in Nottingham University and then Cambridge University, before becoming Professor of Statistics at Lancaster in 1998. In May 2007, I shall be moving to Warwick to take up the Chair in the Centre for Research in Statistical Methodology.

I am interested in the theory, methodology and applications of MCMC methods. Currently, I am particularly interested in Bayesian (and non-Bayesian) inference for stochastic processes, particularly diffusions, population models, and models for non-parametric Bayesian analysis. I also work on inference for infectious diseases, with particularly applications to Avian Influenza and Foot and Mouth disease.

I publish research work in a broad range of journals across probability and statistics, especially An-

nals of Applied Probability, JRSS B, Biometrika, Bernoulli, Annals of Statistics, Statistics and Computing.

Alexandra M. Schmidt

Alexandra M. Schmidt (PhD 2001, Sheffield, UK) is an Assistant Professor at the Federal University of Rio de Janeiro (UFRJ), Brazil, since August 2002. She helped create the Statistics Ph.D. Program at UFRJ, known for its strong Bayesian flavour. She has published in the Journal of the Royal Statistical Society Series B and C, Environmetrics, Test, Brazilian Journal of Probability and Statistics, among

others. Currently, she is also a Research Fellow at CNPq, one of the main research agencies in Brazil. Her main area of research is on the modeling of spatial and spatio-temporal processes. For more details, please, visit www.dme.ufrj.br/~alex. She served on ISBA's nomination committee (2003-2004) and currently is an Associate Editor of the ISBA Bulletin. She is also a board member of the Brazilian Statistical Association. As a board member of ISBA, she believes she would be strengthening the international profile of our Society. She is very interested on the spread of the Bayesian thinking to other areas of research such as Environmental and Ecological Statistics. ▲

ISBA Bulletin, 13(3), September 2006

NEWS OF THE WORLD

NEWS FROM THE WORLD

by Alexandra M. Schmidt

alex@im.ufrj.br

I would like to encourage those of you who are organizing any event around the World, to get in touch with me to announce it here.

Last month, our President, Alan E. Gelfand, announced the next world meeting of the International Society for Bayesian Analysis (ISBA). It will be held 9-12 July, 2008 on Hamilton Island, Queensland, Australia. Hamilton Island is one of 74 islands in the Coral Sea between Queensland and the Great Barrier Reef. Apart from offering a spectacular location, it is well set up for handling an international gathering. The local hosts for the meeting will be the Australasian Society for Bayesian Analysis (ASBA) and the Chair of the Organising Committee is Kerrie Mengersen of QUT Australia. A website will soon be available with more details. This promises to be a special and unique conference.

We also would like to announce the

Call for 2006 L.J. Savage Awards

The International Society for Bayesian Analysis, the American Statistical Association Section on Bayesian Statistical Science (SBSS), the Trustees of the L. J. Savage Memorial Fund, and NBER/NSF Seminars on Bayesian Inference in Econometrics are pleased to announce two Savage Awards for outstanding Bayesian dissertations in Theory and Methods and Applied Methodology. A dissertation may be nominated by the author, by the advisor or other reader, by the department chair or professor, or by any ISBA/SBSS member. A dissertation may be nominated for only a single award year. Nomination is made by submission of the dissertation and a letter that describes the main theoretical, methodological, and/or applied contribu-

tions of the thesis and specifies that the thesis is being nominated for either the Theory and Methods award or the Applied Methodology award.

For details on how to submit a thesis for the 2006 Savage Award please visit: <http://www.isds.duke.edu/research/isba-sbss/SavageAward>. The deadline for submission is September 30, 2006. More information about the Savage Award and past winners may be found at <http://www.bayesian.org> under ISBA Awards.

Events

Spring Bayes, Queensland University of Technology, Gardens Point Campus, Brisbane, Australia, September, 27th-29th, 2006.

You are warmly invited to Spring Bayes - a meeting of people involved or interested in Bayesian research and applications. Previous meetings in 2004 and 2005 were known as Bayesian Topics in the Tropics. The programme will include keynote talks, contributed talks and a poster session. The keynote speakers are Prof. Gavin Gibson of Heriot-Watt University, Scotland and Dr. Scott Sisson of the University of New South Wales. Prospective participants are invited to submit an abstract and preferred method of presentation (oral or poster) to Programme Chair, Ross McVinish (r.mcvinish@qut.edu.au) by 31st August 2006. Registration is now available, with early-bird registration closing on 31st August, 2006 and standard registration closing on 18th September. If you would like to receive more information about this event, please visit the website below or contact organising co-chairs Clair Alston or Ian Wood (c.alston@qut.edu.au, i.wood@qut.edu.au). For more information on registration, hotel bookings or the meeting location, please contact Chris-

tine Gustafson (c.gustafson@qut.edu.au), phone: 07 3864 4422, fax: 07 3864 5160. This meeting is being organized by the local chapter ASBA (Australasian Society for Bayesian Analysis). The web site for the meeting is at: <http://www.maths.qut.edu.au/asba/docs/sb/>.

International Symposium to the Centenary of Birth of Bruno de Finetti, Rome, November, 15th-17th, 2006.

An International Symposium will be held on November 15-17 in Rome, as one of several events dedicated to the Centenary of Birth of Bruno de Finetti. Please visit the web-site <http://www.mat.uniroma1.it/ricerca/convegn/definetti/>. The format is of a very small number of general talks given by invited speakers, with no parallel sessions, no contributed papers, free participation of all attendees (provided a pre-registration on the web page is made). A few other events have already taken place in Italy in the last few months. Other events are going to take place: in Trieste (in the frame of a yearly meeting of Italian Society of Maths Applied to Economics and Social Sciences) in Bologna (dedicated to questions in Philosophy of Science) in Trento (dedicated to de Finetti's activity related to the Teaching of Mathematics) besides the one in Rome (dedicated to more technical aspects of de Finetti's contributions to Probability Theory and Economics). For further details, please visit www.brunodefinetti.it.

REASON PARK Sixth INTERNATIONAL SCHOOL on "REASONing under PARTial Knowledge", Foligno (Perugia), Italy, November 22nd-25th, 2006.

This year (because of the centenary of Bruno de Finetti's birth) the School REASON PARK will focus on "Bruno de Finetti's Probabilistic Logic" and on its connections to Fuzzy Theory and Default Reasoning. The scope of the School is to provide

Ph.D. students and, in general, young researchers with a basic training in some different topics which play an important role in "Reasoning under Partial Knowledge" and their application in various fields, including Computer Science, Economics, Engineering, Medicine, Biology. More details can be found on the web site: <http://www.dipmat.unipg.it/reasonpark>.

The 4th Meeting of the Eastern Mediterranean Region of the International Biometric Society (EMR-IBS), Hilton Hotel, Eilat, Israel, January, 23rd-25th, 2007.

The fourth meeting of the Eastern Mediterranean Region of the International Biometric Society (EMR-IBS) will be held at the Hilton Hotel, Eilat, Israel, on January 23-25, 2007. A pre-conference reception will be held on the evening before the conference. The lead organizers of the conference are Orly Manor, Hebrew University School of Public Health, and David Zucker, Hebrew University Department of Statistics. The conference will include three full days of sessions. The first of these three days will be a special one-day symposium in honor of Marvin Zelen on the occasion of his 80th birthday. This special symposium is under the joint auspices of EMR-IBS and the Harvard School of Public Health, and is being organized jointly by Marvin's former doctoral student Ori Davidov, now at Haifa University, and Stephen Lagakos of the Harvard Department of Biostatistics. A slate of distinguished invited speakers has been lined up for the conference, and we look forward to a very stimulating meeting. The conference website is <http://www.congress.co.il/emr-ibs2007>. The website provides further details about the conference and a mechanism for submitting abstracts. Abstracts in all areas of biometrics are welcomed. ▲



INTERNATIONAL SOCIETY FOR BAYESIAN ANALYSIS

Executive Committee

President: Alan Gelfand
Past President: Sylvia Richardson
President Elect: Peter Green
Treasurer: Bruno Sansó
Executive Secretary: Deborah Ashby

Program Council

Chair: Kerrie Mengersen
Vice Chair: Peter Müller
Past Chair: José Miguel Bernardo

Web page:
<http://www.bayesian.org>

Board Members 2006–2008:

Marilena Barbieri, Wes Johnson, Steve MacEachern, Jim Zidek,

Board Members 2006–2007:

Carmen Fernandez, Valen Johnson, Peter Müller, Fernando Quintana.

Board Members 2006:

Brad Carlin, Merlise Clyde, David Higdon, David Madigan.

EDITORIAL BOARD

Editor

J. Andrés Christen <jac@soe.ucsc.edu, jac@cimat.mx>

Associate Editors

Annotated Bibliography
Marina Vannucci <mvannucci@stat.tamu.edu>
Applications
Catherine Calder
<calder@stat.ohio-state.edu>
Interviews
Brunero Liseo <brunero.liseo@uniroma1.it>
News from the World

Alexandra M. Schmidt <alex@im.ufrj.br>
Software Review
Ramses Mena <ramses@sigma.iimas.unam.mx>
Student's Corner
Vacant
Bayesian History
Vacant