A MESSAGE FROM THE PRESIDENT

by Christian Robert
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Dear friends and Isba members, as pointed out by Raphael Gottardo below, this is a welcome time for most of us to clean up our desks from the clutter that accumulated over the semester and to get ready for our summer round of conferences and visits, including hopefully some vacation time as well. While my last conference took place in June in the grand amphitheater of La Sorbonne, in downtown Paris, and thus only required a Metro ticket (plus some arguing with the security guard at the entrance who did not want to let me in wearing shorts as he could not believe I was a plenary speaker ...), my next meeting in Hamilton Island, Australia, for ISBA 2008 will take me to the other extreme (at least travel-wise, since I do hope to wear shorts there too!). As mentioned in my previous message, I came to realise that such a long distance-trip was a deterrent for many of you, despite the high quality of the program, the attractiveness of the dream-like location (if you forget about the sharks), and the huge side benefits of sharing a good time with fellow Bayesians. This would have impacted on the audience of the meeting on a "regular" year but the current continued increase of travel costs makes it even more acute and hints at growing difficulties in attending meetings in faraway places. *Continue in page* .

A MESSAGE FROM THE EDITOR

by Raphael Gottardo
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Summer is here, at least for some of us, and it feels good to enjoy the nice, warm, weather. Summer also means traveling, vacation, finishing the few papers we put off all year long, etc. In short, we end up being more busy than during the regular year! As a consequence, it was quite difficult for some of the associate editors to get people to send them their sections on time for this summer issue. Even though a few of the regular sections are missing, you will find many interesting articles including a nice interview from Alan Gelfand, a summary of the CRISM workshop that took place in Warwick, UK, in April, as well as the usual software review, the student section and the news from the world. I would also like to remind YOU that we want YOU to contribute to the bulletin, so if you have any interesting material you'd like to include in the bulletin, feel free to contact me or any of the associate editors. ▲

WORDS FROM THE PRESIDENT, *Continued from page 1.* While the appeal of holding small focussed workshops in spots you can reach by public transportation rather than planes is clear (and the Highly Structure Stochastic System network sponsored by the European Science Fundation in the mid-1990's comes to my mind as a hugely successful local process that worked as an incubator for the young European MCMC groups), our field would greatly lose, both scientifically and humanely, if it could not meet as a whole at regular occurrences. In order to accomodate the conflicting imperatives of reducing our travel amount and of keeping the thread with all branches of the Bayesian community, I think we should start investigating the possibility of holding mirror meetings at several loca-

tions worldwide and simultaneously. Thanks to videoconferencing, the same talk could be broadcast in all of those locations at the same time with interactions from all groups. True, sharing a beer with a colleague at another location would be a bit of a difficulty but time zones would not be such a problem since, keeping with the Valencia tradition, ISBA meetings have developed a time zone of their own. (Do you know of many other meetings where the poster sessions start at 10:30 pm?!) This may sound over-pessimistic, but I think we should give it a try, if only to hold the first meeting where the sun never sets!!! In the meanwhile, I wish to all of you a profitable and enjoyable season before the semester starts again and hope to meet many of you on Hamilton Island. ▲

INTERVIEW

ALAN GELFAND

by Donatello Telesca

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Alan Gelfand is chair of the Statistical Science Department, J.B. Duke Professor of Statistical Science and Professor of Environmental Science and Policy at Duke University. His research interests include spatial statistics, modeling and model determination, Bayesian computation and Bayes and empirical Bayes inference.

Dr. Gelfand has served ISBA from its very beginnings, covering different roles in the Society and was President in 2006. A recent search on the Web of Science, reports that his seminal paper, *Sampling–based approaches to calculating marginal densities* with Adrian Smith (JASA 1990), has been cited an impressive 1,773 times.

I had the pleasure of meeting Alan in different recent occasions and he agreed to answer some of my questions.

1. *How did you get interested in Statistics and, in particular, Bayesian Statistics?*

I followed a fairly typical course for my time, starting as an undergraduate major in Mathematics. In my senior year I took an introduction to mathematical statistics course from the book

by Hogg and Craig (embarrassingly, using the first edition, spanning all of 240 pages). The material was so elegant, I was smitten, and thus, I applied to graduate programs in Statistics, going off to California, to Stanford (as far from New York City as I could go!) But, as I have told many people, in some ways I had a "wasted youth", not discovering until the late 1980's, that I was born to be a Bayesian!

2. *Who were the people that had the most influence on your career?*

Early on, it was my adviser from Stanford, Herbert Solomon, a wonderful, generous man who was particularly good at recognizing how people could best contribute to projects. He was one of the earliest "team builders" in our field. In a more remote way, I was influenced by Charles Stein from Stanford. I believe I hold the record for most courses ever taken by a single student from Charles! His beautiful, deep thoughts in decision theory led me down that research path which, in turn, led me to empirical Bayes and, eventually, to research within the fully Bayesian paradigm. Finally, Adrian Smith would be the most influential. Following conversations with him in the mid-to-late '80's, I arranged a sabbatical to work with him at Nottingham University. I arrived seeking to use his numerical integration

software for certain empirical Bayes problems and left with the Gibbs sampler!

3. *You have an impressive list of publications in a variety of fields. Which do you feel is your most important contribution?*

I guess it would have to be the use of Gibbs sampling for addressing the problem of posterior integration. Working with Adrian, it was a remarkable feeling to come upon the Gibbs sampler, from the paper of Geman and Geman, and recognize that it was better suited for handling Bayesian computation than it was for its original purpose, sampling Markov random fields.

4. *What are you currently working on?*

For the last 12 years I have found myself primarily immersed in the world of space and space-time data modeling and analysis. It has been a pleasure to watch this field move from the periphery of statistical work to a much more mainstream position.

5. *What do you think are the advantages of the Bayesian approach to problems of spatial inference?*

Arguably, the primary advantages are those that we attach to working in general in the Bayesian framework - fully model-based inference with accurate assessment of uncertainty. But, it is also noteworthy that customary asymptotics that are employed in time series, so-called expanding domain asymptotics, may be inappropriate for spatial data where infill asymptotics are perhaps more relevant. But the latter asymptotics typically reveal that information is bounded in terms of inference. In this regard, the Bayesian framework provides exact inference, avoiding possibly inappropriate asymptotics. However, the caveat is that the data never overwhelms the prior; we must be more attentive to prior sensitivity than in other areas.

6. *As a former ISBA President, what do you think is the role and future challenges of this organization?*

As ISBA President, I wrote several mails to the constituency expressing my thoughts regarding the future of the Society. I think we have made wonderful strides in the past decade, now with a good sized membership (which could, of course, be bigger!), involvement in a broad range of international meetings, and a journal that has become well-established, publishing work of very good quality. If we accept the premise of a Bayesian 21st century, then I think our primary objective must be outreach to, education for, collaboration with, scientists in other disciplines.

7. *What is the part of your job that you enjoy the most? And least?*

It has emerged, more clearly than ever, that my greatest strength is as a stochastic modeler. In this sense, what is most exciting for me is to be part of a team of researchers assembled to "brainstorm" a complex problem. The role of the modeler in this setting is particularly exciting. She/he becomes a central player in synthesizing inputs from the team members, in shaping progress on the problem. Least exciting? Well, now that I am Department Chair, there are a few obligations that are not so much fun but, overall, I do not find anything onerous in the job.

8. *Is there something that keeps you sane, when you are not sampling from conditional posteriors?*

A wonderful question! Many of us know that, living in a "fast-lane" research world, it is easy to work all of the time, to become one-dimensional. I definitely fall victim to this but find some relief with my avid interest in music and in automobiles.

9. *Do you want to talk about the recent changes there at Duke? What will those changes imply in terms of the future of Statistics in the Research Triangle?*

The new Department of Statistical Science is in a very exciting mode these days. We are now a full-function unit within Arts and Sciences at Duke, including an undergraduate major and minor. Our graduate program is the largest it has ever been, roughly 35 students, Ph.D. only, 100% committed to research. And we will be growing, with authorization to hire six new tenure-track faculty during the next few years.

10. *As the Department Head, what is your vision for the newly born Department of Statistical Science? But, more importantly, (I am sure the new generation of job seekers will find this interesting) what will you be looking for when trying to hire junior Faculty?*

Duke University is a naturally collaborative insti-

tution; research teams develop all over the campus with strong encouragement from the University. And, what program on campus is more naturally interdisciplinary than Statistics? So, my vision for the Department is to continue to grow existing bridges and to build new ones. I want us to be players in as many of the exciting initiatives that are being undertaken here as we can. I want to bring in new tenure-track faculty, research faculty, visiting faculty, post-docs, and visitors to help us accomplish this. And, I encourage readers of this interview to think of us, perhaps join us, in this capacity.

11. *You have advised a number of very successful statisticians. What do you try and emphasize in the academic formation or your students?*

I have always viewed my role as an adviser as one of training students for a research career. This means helping them to build the skills they need across multiple dimensions - theory, modeling, computation, and data analysis. Also, in this regard, they need to learn how to "play the game". Research is an endeavor with lots of highs and lots of lows - in terms of solving problems, getting papers published, securing external funding, etc. What you must do is keep working hard and you must not overreact to the lows.

12. *One last cheesy question. What do you think is something that Frequentist can learn from Bayesian and, the other way around, what do you think we should learn from our Frequentist colleagues.*

Definitely cheesy and I do not have a profound answer! It seems evident that hierarchical modeling with fitting through MCMC methods is primarily what the Bayesian community offers and is what seems to resonate very well in working with scientists in other fields. By the same token, simpler models, fitted using classical methods and standard software, enable useful insights regarding unknowns in more complex models as well as sanity checks with regard to inference from more complex models.

Thanks to Alan, for taking time off his even busier schedule to answer our questions.

ANNOTATED BIBLIOGRAPHY

CRiSM WORKSHOP "BAYESIAN ANALYSIS OF HIGH DIMENSIONAL DATA"

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The CRiSM workshop "Bayesian Analysis of High Dimensional data" (University of Warwick, UK, April 16th-18th) has succesfully highlighted recent methodological and applied advances in the analysis of complex data. Keynote and themed talks focussed on selected topics in biostatistics, computational systems biology and mathematical statistics. Despite the notoriously wet and gloomy British weather, participants from sunny California, Texas, Florida, Italy, France, Germany, Turkey, The Netherlands, Canada and Norway uniformly converged to Coventry for this workshop.

This exquisitely Bayesian event partially overlapped with a Composite Likelihood workshop. Participants in both events were encouraged to share their perspectives over joint coffee breaks, evening meals and pub sessions. One keynote speaker, Nils Hjort, heroically gave intriguing talks in both workshops. Also the themes of several other talks demonstrated a considerable overlap between the research interests of both communities, reiterating the relevance of an adogmatic view of statistical inference.

In the following sections we provide an annotated bibliography of all invited talks of the Bayesian workshop. (The annotations are shortened versions of the author's abstracts; the full program can be viewed at the conference website, http://www.warwick.ac.uk/go/bhdworkshop.) Where possible we have provided a link to a related paper or manuscript. If you are viewing an electronic version of the bulletin, you will see that these references are 'clickable' links, as are the authors names; check their pages for updates and additional background on this exciting work!

Methodological talks

- Nils Hjort (University of Oslo, Norway), "Finding influential regressors in $p >> n$ models": I work with methodology for generalised linear models where the number p of covariates is larger than the number n of individuals. Methods more general than e.g. those of ridging emerge when priors are used that correspond to mixtures of lower-dimensional structures. These lead to strategies for finding say the k most promising covariates, for k not exceeding a user-defined threshold number k_0. The methods are applied to survival data in combination with gene-expression data.

- Feng Liang (University of Illinois at Urbana-Champaign, USA), "Bayesian Learning with Overcomplete Sets": In contrast to the orthonormal basis traditionally used in function estimation, overcomplete (or redundant) representations have been advocated due to their flexibility and adapatation. Bayesian methods provide several advantages in learning an overcomplete representation: regularization is specified through priors; inferences on hyperparameters are easily obtained via Markov Chain Monte Carlo; probabilistic outcomes provide a full spectrum to summarize the prediction or estimation. Our recent progress on Bayesian inference with overcomplete wavelet dictionary and reproducing kernel Hilbert space is presented along with examples.

- **Longhai Li** (University of Saskatchewan, Canada), "Avoiding Bias for Feature Selection": For many classification and regression problems, although a large number of features are available for possible use, for computational or other reasons only a small subset of these features are selected for use in a model. This procedure may introduce an optimistic bias in which the response variable appears to be more predictable than it actually is because the high correlation of the selected features with the response may be partly or wholly due to chance. We show how this bias can be avoided when using a Bayesian model for the joint distribution of features and response. Related paper with J. Zhang and R. Neal: "A Method for Avoiding Bias from Feature Selection with Application to Naive Bayes Classification Models" Bayesian Analysis 3: 171-196.

- Adrian Dobra (University of Washington, USA), "The Mode Oriented Stochastic Search for Log-linear Models with Conjugate Priors": We describe a novel stochastic search algorithm for rapidly identifying regions of high posterior probability in the space of decomposable, graphical and hierarchical log-linear models. Our approach is based on the conjugate priors for log-linear parameters introduced in Massam, Liu and Dobra, 2008. We discuss the computation of Bayes factors through Laplace approximations and the Bayesian Iterate Proportional Fitting algorithm for sampling model parameters. We also present a clustering algorithm for discrete data. We compare our model determination approach with similar results based on multivariate normal priors for log-linear models. Related manuscript, with Helene Massam "The mode oriented stochastic search (MOSS) algorithm for log-linear models with conjugate priors."

- Michele Guindani (University of New Mexico, USA), "The Optimal Discovery Procedure and Bayesian Decision Rules": We discuss an interpretation of the optimal discovery procedure (ODP, Storey 2006) as an approximate Bayes rule in a nonparametric Bayesian model for multiple comparisons. An improved approximation defines a nonparametric Bayesian version of the ODP statistic (BDP). The definition includes multiple shrinkage in clusters. In a simulation study and a data analysis example we show a (small) improvement in frequentist summaries. The BDP allows easy modifications for dependence of the comparisons and other extensions of the ODP.

- Rob Kass (Carnegie Mellon University, USA), "Challenges in Analyzing Neural Spike Train Data": One of the most important techniques in learning about the functioning of the brain has involved examining neuronal activity in laboratory animals under varying experimental conditions. Neural information is represented and communicated through series of action potentials, or spike trains, and the central scientific is-

sue in many studies concerns the physiological significance that should be attached to a particular neuron firing pattern in a particular part of the brain. Scientific questions involving spike trains may be posed in terms of point process intensity functions, and may be answered using Bayesian methods. In my talk I outline some of the problems that have been addressed, the progress that's been made, and the challenges to be faced as dimensionality increases. Recent paper with Behseta, Moorman and Olson "Testing equality of several functions: analysis of single-unit firing rate curves across multiple experimental conditions." See presentation slides for an extensive reference list.

Statistical Modelling

- **Volker Schmid** (Imperial College, London, UK), "A Bayesian Hierarchical Model for the Analysis of a Longitudinal Dynamic Contrast-Enhanced MRI Cancer Study": This paper focuses on kinetic modeling in DCE-MRI. Instead of summarizing each scanning session as a single kinetic parameter we propose to analyze all voxel time courses from all scans and across all subjects simultaneously in a single model. The kinetic parameters from the usual nonlinear regression model are decomposed into unique components associated with factors from the longitudinal study; e.g., treatment, patient and voxel effects. A Bayesian hierarchical model provides the framework in order to construct a data model, a parameter model, as well as prior distributions. The posterior distribution of the kinetic parameters is estimated using Markov chain Monte Carlo (MCMC) methods. The proposed method is validated with a breast cancer study demonstrating the clinical potential of this method to longitudinal oncology studies.

- Malay Ghosh (University of Florida, USA), "Gene Expression-Based Glioma Classification Using Hierarchical Bayesian Vector Machines": This talk considers several Bayesian classification methods for the analysis of the glioma cancer with microarray data based on reproducing kernel Hilbert space under the multiclass setup.

We consider the multinomial logit likelihood as well as the likelihood related to the muliclass Support Vector Machine (SVM) model. It is shown that our proposed Bayesian classification models with multiple shrinkage parameters can produce more accurate classification scheme for the glioma cancer compared to the several existing classical methods. We have also proposed a Bayesian variable selection scheme for selecting the differentially expressed genes integrated with our model. This integrated approach improves classifier design by yielding simultaneous gene selection.

- Jeffrey Morris (MD Anderson Cancer Center, USA), "Bayesian Inference for High Dimensional Functional and Image Data using Functional Mixed Models": High dimensional functional data are increasingly encountered in scientific research. For example, MALDI-MS yields proteomics data, array CGH or SNP chip arrays, 2D gel electrophoresis and LC-MS images and fMRI three-dimensional brain images observed over a sequence of time points on a fine grid. In this talk I discuss how to identify regions of the functions/images that are related to factors of interest using Bayesian wavelet-based functional mixed models. I demonstrate how to identify regions of the functions that are significantly associated with factors of interest, in a way that takes both statistical and practical significance into account and controls the Bayesian false discovery rate to a pre-specified level. Related paper with PJ Brown, RC Herrick, KA Baggery and KR Coombes "Bayesian Analysis of Mass Spectrometry Proteomic Data Using Wavelet Based Functional Mixed Models" Biometrics 64:479-489.

- Yee Whye Teh (Gatsby Computational Neuroscience Unit, UK), "Bayesian Language Models": Models of sentences from natural languages like English are an important component of many natural language processing technologies, including speech recognition, machine translation, and text retrieval. Due to the complexity and size of natural languages, such language models are necessarily very complex and high dimensional. I will first discuss some recent advances using hierarchical and nonparametric modelling ap-

proaches giving state-of-the-art predictive results, then address the problems of adapting language models to specific domains, and the syntactic and semantic representations of words.

- Bruno Sansó (University of California at Santa Cruz, USA), "A Climatology for North Atlantic Sea Surface Temperatures": We consider the problem of fitting a statistical model to historical records of sea surface temperatures collected sparsely in space and time. The purpose of the model is to produce an atlas of sea surface temperatures. This consists of climatological mean fields, estimates of historical trends and a spatio-temporal reconstruction of the anomalies, i.e., the transient deviations from the climatological mean. Our model improves upon the current tools used by oceanographers in that we account for all estimation uncertainties, include parameters associated with spatial anisotropy and non-stationarity, transient and long-term trends, and location-dependent seasonal curves. The model is based on discrete process convolutions and Markov random fields. Particular attention is given to the problem of handling a massive data set. This is achieved by considering compact support kernels that allow an efficient parallelization of the Markov chain Monte Carlo method used in the estimation of the model parameters. Related technical report with RT Lemos: "A spatial temporal model for mean, anomaly and trend fields of North Atlantic sea surface temperature."

- Doug Nychka (National Center for Atmospheric Research, USA), "Reconstructing past climate using hierarchical models".

- John Haslett (Trinity College Dublin, Ireland), "Modelling the Paleoclimate": This paper discusses some of the successes of Bayesian spacetime inference and several of the challenges; a first attempt was reported in Haslett et al (2006), Bayesian Palaeoclimate Reconstruction - with discussion, JRSS(A). Our focus here is on Europe for the period since the onset of rapid deglaciation towards the end of the last glacial stage, a little less than $15,000$ calendar years ago. The presentation will convey the general scientific context and will con-

centrate on the methodological challenges for Bayesian space-time modelling.

Computational Systems Biology and Machine Learning

- Darren Wilkinson (University of Newcastle, UK), "High-throughput data for systems biology modelling": Much of computational systems biology is concerned with building dynamic mechanistic models of cellular processes. Post-genomic technologies are able to generate high-throughput data such as time course microarray data that are potentially useful for helping to build and refine such models. This talk will describe some of the challenges associated with Bayesian modelling of high-dimensional time course data from a dynamic mechanistic perspective.

- **Vilda Purutcuoglu** (Middle East Technical University, Ankara, Turkey), "Variational approximation in inference of the kinetic parameters of the MAPK/ERK pathway": The MAPK/ERK pathway is one of the major signal transaction system which regulates the growth control of all eukaryotes. In our previous study, we model this pathway by using a quasi reaction list. In this study our aim is to investigate the application of exact, rather than Metropolis-within-Gibbs, sampling by using variational approximation. For this purpose we define an approximate distribution by adding variational parameters in transition kernels and initial state probabilities of the tractable substructure of the true observation matrix used in the estimation. The underlying substructure is generated in such a way that the necessary links between states are decoupled, thereby, Gibbs sampling can be applied. The loss of information from removing the links is, then, regained by linking the updates of variational parameters. These free parameters are calculated by minimizing the Kullback-Leibler divergence between the true and approximate distribution of states.

- Carl Rasmussen (University of Cambridge, UK), "Data Analysis using Gaussian Processes": Gaussian processes (GPs) are well known non-parametric Bayesian models,

but surprisingly they are not used extensively in practice. In this mainly methodological talk I'll show three very different types of GP models used commonly in the machine learning community: 1) inferring complex structures in regression via hierarchical learning of covariance functions, 2) non-linear dimensionality reduction using the GP Latent Variable Models (GP-LVM) and 3) GP classification using the Expectation Propagation algorithm. These examples highlight that the fundamental ability of GPs to express and manipulate (Bayesian) distributions over functions make them a powerful, practical foundation for numerous types of applications.

SOFTWARE HIGHLIGHT

inla: APPROXIMATE BAYESIAN INFERENCE FOR LATENT GAUSSIAN MODELS

by Sara Martino and Håvard Rue

Integrated Nested Laplace Approximation (INLA) is a tool for estimating latent Gaussian models using accurate deterministic approximations instead of MCMC simulations. In particular INLA provides with accurate approximations of posterior marginals both for the latent Gaussian field and for the hyperparameters of the model. The quality of such approximations is extremely high, such that even long MCMC runs could not detect any error in them. A detailed description of the method can be found in [1] (which will be read before the RSS on October the 15th 2008), where also a thorough comparison with MCMC results is shown.

The main advantage of the INLA approach is computational: a full Bayesian analysis can be performed in minutes even for quite complex models. All algorithms involved in the INLA approach are efficiently implemented in the (ANSI) C and FORTRAN library `GMRFLib` [3].

The `inla` program, built upon the `GMRFLib` library, is a tool which allows the user to easily specify and solve a large group of structured additive regression models. Structured additive regression provides a unifying framework for a wide class of regression models including generalised additive mixed models, geoadditive models, time series models, and model with random coefficients. In practice using `inla` it is possible to solve a subset of the models which can be handled with the BayesX software [4].

Both the `GMRFLib` library and the `inla` program are available free of charge from

http://www.math.ntnu.no/~hrue/GMRFLib

A detailed manual for the `inla` program which includes a large sample of worked out examples is also available from the web site above.

An (experimental) R interface to the `inla` program is at the moment under development. This is meant to make the INLA approach available for a larger class of users. The latest version of the R interface is available from the web page above.

Changes which make future versions of the R interface not compatible with the present one might be performed. In its current version, the R interface to the `inla` program operates only under various versions of the Linux operating system. A Windows version is planned for the (near) future.

Model Specification

The `inla` program allows to specify structured additive regression models where the response belongs to the univariate exponential family. At the moment supported response distributions are: Gaussian, Poisson, Student-t, and Binomial distribution. Moreover it is possible to implement also various Stochastic Volatility models.

As for the model components, structured additive regression can be build from arbitrary combinations of the following model terms:

- *Nonlinear effects* of continuous covariates can be estimated based on random walk prior models

- *Spatial effects* can be specified via Gaussian Markov random fields

- *Time effects and Seasonal effects*

- Cluster-specific i.i.d. Gaussian *random intercepts and slopes*

- *Interaction surfaces* between two continuous covariates can be specified through Gaussian Markov random fields specified on a grid.

An easy example using the R interface

Generalised linear (mixed) models form a large class of latent Gaussian models. We consider the Epil example of the OpenBUGS [2] manual Vol I. The data come from a clinical trial of 59 epileptics patients. Each patient i is randomised to a new drug ($\text{Trt}_i = 1$) or a placebo ($\text{Trt}_i = 0$), in addition to the standard chemotherapy. The observations for each patient $y_{i1}, \ldots, y_{i4}$, are the number of seizures during the two weeks before each of the four clinic visits. The covariates are age (Age), the baseline seizure counts (Base) and an indicator variable for the 4th clinic visit (V4). The model is

$$
\begin{aligned}
y_{ij} &\sim \text{Poisson}\{\exp(\eta_{ij})\} \\
\eta_{ij} &= \beta_0 + \beta_1 \log(\text{Base}_j/4) + \beta_2 \text{Trt}_j \\
&\quad + \beta_3 \text{Trt}_j \times \log(\text{Base}_j/4) + \beta_4 \text{Age}_j \\
&\quad + \beta_5 \text{V4}_j + \epsilon_i + \nu_{ij}; \\
&\qquad i = 1, \ldots, 59, \quad j = 1, \ldots, 4,
\end{aligned}
$$

using centred covariates. We use the same priors as in the OpenBUGS manual: $\epsilon_i \overset{\text{iid}}{\sim} \mathcal{N}(0, 1/\tau_\epsilon)$, $\nu_{ij} \overset{\text{iid}}{\sim} \mathcal{N}(0, 1/\tau_\nu)$, $\tau_\epsilon, \tau_\nu \sim \Gamma(0.001, 0.001)$, and all the β.'s are assigned $\mathcal{N}(0, 100^2)$ priors. In this example the latent Gaussian field is of dimension $n = 301$ and consists of $\{\eta_{ij}\}, \{\epsilon_i\}, \beta_0 \ldots, \beta_5$. The hyperparameters are $\theta = (\tau_\epsilon, \tau_\nu)^T$. The R code to implement the model is:

```
Epil <- read.table(file="Epil.dat",
header=T)
attach(Epil)
  # make standardised variables
M.Trt <- Trt-mean(Trt)
```

```
M.lBase4 <- log(Base/4)-mean(log(Base/4))
M.V4 <- V4-mean(V4)
M.lAge <- log(Age)-mean(log(Age))
M.BT <- Trt*M.lBase4-mean(Trt*M.lBase4)
  # model formula
formula <- y   M.lBase4 + M.Trt + M.BT
+ M.lAge + M.V4 + f.inla(Ind,model="iid")
+f.inla(rand,model="iid")
  # run inla
model=glmm.inla(formula,family="poisson")
```

The computational time necessary to solve the model is 2.4 seconds on a laptop with an Intel(R) Pentium(R) processor 1.86GHz.

Figure 1 shows the posterior marginal for parameter β_0, overlayed is an histogram obtained from a very long OpenBUGS run.

References

[1] Rue, H., Martino, S. and Chopin N. (2007) Approximate Bayesian inference for Latent Gaussian Models Using Integrated Nested Laplace Approximations. http://www.math.ntnu.no/~hrue/reports *Statistics Report No 1, Dept. of Mathematical Science, NTNU, Trondheim*

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[4] Brezger, A., Kneib, T. and Lang, S. (2003) BayesX: Software for Bayesian inference. *Dept. if Statistics, University on Munich, version 1.1* http://www.stat.uni-muenchen.de/~lang/bayesx

STUDENTS' CORNER

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We kick off this quarter's Students' Corner with an article discussing the how and why of

graduate student fellowships by Kary Myers. Following this we have two recent dissertation abstracts, one hailing from Duke, and the other from George Washington. As always, if you (or your student) have recently graduated and
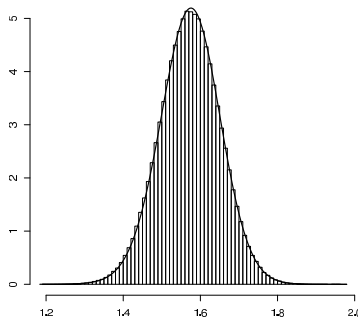
Figure 1: Posterior marginals for the regression parameter β_0. The histogram comes from a very long OpenBUGS.

would like your dissertation abstract published, please contact me.

STRATEGIES FOR PURSUING GRADUATE SCHOOL FELLOWSHIPS

by Kary Myers
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Statistical Sciences, Los Alamos National Laboratory

You probably know there's a lot of money out there for graduate school, particularly in technical programs like statistics (your liberal arts friends might have a different story). Many statistics departments provide tuition and a stipend to their doctoral candidates, usually in the form of a teaching or research assistantship. You might know less about the availability—or value—of fellowship support for graduate school. I hope to convince you that fellowships are worth finding and pursuing, and I'll give you some leads for finding them and strategies for pursuing them.

Note that I'm coming at this from a U.S.-centric viewpoint: I developed my "expertise" through my success pursuing graduate fellowships from U.S. sponsors as a U.S. citizen applying to U.S. universities. You'll find many of my suggestions universal, though, and I'm sure you'll get ideas that are relevant to your own situation. Here's how I got that expertise: When I was making plans for graduate school, I applied for six national fellowships—three from government agencies, two from industry, and one from a national consortium between government, industry, and higher education. I was offered two (I accepted one), was a finalist for a third, and got an honorable mention for a fourth. So let's see if I can convince you this is worth doing.

Why should you bother applying for fellowships?

When you're scrambling to finish your undergraduate degree and apply to graduate programs, it's hard to get excited about completing more applications and writing more essays. Since departmental support comes with acceptance to many graduate programs, what's the incentive?

I'll argue that a fellowship can bring many benefits, both to you and to your department and institution. The big fellowships pay your tuition plus a stipend. Some also guarantee one or more paid summer internships (pay that's in addition to your stipend). But these are things you could get even without a fellowship. Other advantages of having a fellowship:

It brings prestige to you. You've got a named fellowship on your CV! That becomes a tremendous advantage later on as you're applying for jobs or pursuing other funding.

It brings prestige to your department and university. Your institution looks great when it can say, "We have an NSF fellow in our program." That can attract more NSF fellows and students of that caliber, which in turn makes your program stronger.

It creates networking opportunities. By having a fellowship (or just going through the fellowship selection process) you'll meet or become known to people at the funding institutions. You'll also meet other fellowship recipients. The more people you know, the better time you'll have later when you're looking for collaborators and jobs. It makes conferences more fun too.

It makes your time your own. Bringing your own money to graduate school often means that you

don't have to be a TA or RA to cover your tuition and stipend. Without these obligations, you have much more time to focus on your classes and your own research.

It can lead to more money. Having a fellowship means that a selection committee identified you as a top-quality student and scientist. That makes other people with money (like conference organizers giving travel scholarships or employers offering internships) feel confident giving it to you because they know you're a good gamble.

*It often **is** more money.* You might find that your pay through the fellowship is better than your department's stipend (especially when you add in associated summer internship pay).

How do I find out about fellowships?

As always, Google is your friend. You can get leads from faculty and your career center. Several institutions host searchable databases of fellowships, like these at Cornell and North Carolina State:

cuinfo.cornell.edu/Student
/GRFNtemp.php
www.ncsu.edu/grad/financial-support
/fellowships.html

What's great about being a statistician is that you're not restricted to fellowships that specify "statistics" as a field they support. I was offered a fellowship from the National Physical Science Consortium, which supports "physical sciences, biochemistry, computer science, and related fields of science and engineering." If you want to pursue statistics in the context of say finance or biomedical imaging or education policy, search for fellowships in those areas. You'll stand out because you're coming from a different angle than most other applicants.

Fellowships in the U.S. often target women and minorities, either exclusively or as part of their full application pool. This is a rare advantage in a technical field like ours. Being a woman certainly gave me a larger range of fellowships to pursue: Three of the six fellowships for which I applied were only available to women and minorities.

What makes you stand out as an applicant?

Once you find some fellowships that seem appropriate, how do you make those funding agencies notice you? Just as with graduate school applications, it helps to look different from other applicants. Many strong students will be applying for these fellowships, so what makes you special? My strategy was to craft a "story" about my reasons for pursuing graduate school—how my

background fostered and supported my goals, why graduate school was the natural next step in achieving those goals. Some ideas for components of such a story:

Undergraduate research experience. Working on research projects as an undergraduate is a great prelude to graduate school. Maybe you want to continue developing the work you started or to explore a new direction. Maybe your projects are what turned you on to statistics. Explain what you did and how it inspired your decision to go to graduate school.

Interdisciplinary experience or interests. Interdisciplinary work always sounds exciting. And statistics is the consummate interdisciplinary field. Showing that you have expertise in another field and know how to collaborate with people in another field will make you a distinctive candidate.

Strong letters of recommendation. Give your letter writers suggestions on what to include in their letters; that way they can directly support your story. For instance, remind them to mention your work in computational biology or your initiative in collaborating with faculty from the business school.

An often-overlooked strategy is having your letter writers address anomalies in your academic history; that way you won't spend limited essay space explaining why two years elapsed between your sophomore and junior years or why you took organic chemistry three times before passing. Your letter writers can pitch things in a good light (if appropriate) or explain why you're on the right track now.

Well-articulated goals for graduate school and beyond. If you can explain why graduate school is a critical component of your career plans, you'll look like a compelling candidate for funding.

Relevant coursework. Coursework that prepares you for your planned direction in graduate school—not just required courses for your major but thoughtfully chosen courses that introduced you to or furthered your interest in your field—will strengthen your story.

What about grades?

Certainly good grades are important, but grades alone won't necessarily make you stand out from other applicants. Lots of students have top-notch grade point averages, but that doesn't automatically make them well-suited to graduate school or good candidates for fellowship funding. Furthermore, you can be a good candidate even if your transcript isn't stellar, particularly

if you can show a strong trend of improvement. Case in point: In my first three semesters of college, my grade point averages were 3.something, 1.something, and 0.00, at which point I was academically suspended. When I returned some years later, I finished with all A grades (ok, one B), and my disappointing cumulative GPA didn't hold me back from getting fellowship support. In fact, I think it helped me. I'm not saying you should tank a few classes so your transcript won't be so uniformly excellent. Rather I'm saying that 1) having an excellent GPA is not necessarily enough to land a fellowship, and 2) having a subpar transcript is not necessarily a barrier. Graduate school is notoriously difficult in ways high school and college just aren't, so if you can show a history of prevailing over tough times and setbacks, you become a much better gamble for funding agencies.

What if you don't get a fellowship after all?

At the risk of sounding too glass-half-full, I'll argue that the process of applying for fellowships is worthwhile regardless of the outcome. Just articulating your story in a coherent way will give you an advantage as you start graduate school. It's a way to get your head around the big picture—why you're pursuing an advanced degree, what long-term possibilities are available and exciting to you. In addition, all the people who write letters for you will know you're serious about pursuing funding, so they might think of you for future opportunities. The people on the selection committees will know your name, too, which can only be good for your career. And don't forget that many departments will provide TA or RA support regardless. In short, go for it. There's really no downside.

Dissertation Abstracts

LEVY RANDOM MEASURES - POSTERIOR CONSISTENCY AND APPLICATIONS

by Natesh Pillai
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Non-parametric function estimation using Lévy random measures is a very active area of current research. In this thesis further contributions, both theoretical and methodological, are made towards non-parametric function estimation using Lévy random measures.

In chapter 2, it is observed that Lévy random measures lead to a unified perspective of non-parametric function estimation using Bayesian methods and those using kernel methods such as Tikhonov regularization used in the machine learning literature. A coherent Bayesian kernel model based on an integral operator defined as the convolution of a kernel with a signed measure is studied. A few results on Fredholm integral operators are derived and a general class of measures whose image is dense in the reproducing kernel Hilbert space (RKHS) induced by the kernel is identified. These results lead to a function theoretic foundation for using non-parametric prior specifications in Bayesian modeling, such as Gaussian process and Dirichlet process prior distributions.

In chapter 3, easily verifiable conditions are derived for posterior consistency to hold in commonly used regression models with prior distributions on infinite dimensional spaces constructed from Lévy random fields. On route to proving conistency, convergence properties of finite dimensional approximations of Lévy random fields are studied. The key technical issues involved are outlined, and the results are illustrated by proving the posterior consisteny in concrete examples.

In chapter 4, the posterior consistency for non-parametric Poisson regression models is proved. The key step is to construct test functions that separate points, and have exponentially decaying type I and II errors.

In chapter 5, a novel application of Lévy random measures is discussed. It is shown that Lévy random measures can be used for constructing prior distributions for spectral measures. Together with Bochner's theorem, this leads to a construction of non-parametric prior distributions on the cone of positive definite functions.

A PROBLEM IN PARTICLE PHYSICS AND ITS BAYESIAN ANALYSIS

by Joshua Landon
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PhD Supervisor: Nozer Singpurwalla

An up and coming field in contemporary nuclear and particle physics is "Lattice Quantum Chromodynamics", henceforth Lattice QCD. Indeed the 2004 Nobel Prize in Physics went to the developers of equations that describe QCD. In this dissertation, following a layperson's introduction to the structure of matter, we outline the statistical aspects of a problem in Lattice QCD faced by particle physicists, and point out the difficulties encountered by them in trying to address the problem. The difficulties stem from the fact that one is required to estimate a large – conceptually infinite – number of parameters based on a finite number of non-linear equations, each of which is a sum of exponential functions.

We then present a plausible approach for solving the problem. Our approach is Bayesian and is driven by a computationally intensive Markov Chain Monté Carlo based solution. However, in order to invoke our approach we first look at the underlying anatomy of the problem and synthesize its essentials. These essentials reveal a pattern that can be harnessed via some assumptions, and this in turn enables us to outline a pathway towards a solution. We demonstrate the viability of our approach via simulated data, followed by its validation against real data provided to us by our physicist colleagues. Our approach yields results that in the past were not obtainable via alternate approaches.

The contribution of this dissertation is two-fold. The first is a use of computationally intensive statistical technology to produce results in physics that could not be obtained using physics based techniques. Since the statistical architecture of the problem considered here can arise in other contexts as well, the second contribution of this dissertation is to indicate a plausible approach for addressing a generic class of problems wherein the number of parameters to be estimated exceeds the number of constraints, each constraint being a non-linear equation that is the sum of exponential functions.

NEWS FROM THE WORLD

Announcements

I would like to encourage those who have any announcements or would like to draw attention to an up-coming conference, to get in touch with me and I would be happy to place them here.

Call for 2008 Mitchell and Savage Prizes

Nominations for the Mitchell and Savage Prizes will soon be accepted. So if you know of a great paper and/or PhD thesis please start thinking about these two prizes! Please visit the following page for more details on ISBA prizes http://www.bayesian.org/awards/MitchellPrize.html. An official announcement should appear soon on the ISBA website at http://www.bayesian.org/news.html.

Events

Summer School on Bayesian Modeling and Computation, Vancouver, Canada, 14-18 July, 2008.

The summer school, sponsored by the PIMS Collaborative Research Group, will be a mix of theoretical and practical courses, taught by world experts in the field. It will be organized in modules (2x1.5h of lectures) over 5 days. Modules will include model selection, stochastic computation, MCMC, non parametric Bayes, introduction to WinBUGS and machine learning. The maximum number participants that will be accepted to the summer school is 40. As we except the number of applicants to exceed this number, students will be offered a place based on academic record. Registration fees will be covered by PIMS for all accepted participants. Accommodation expenses will also be covered by PIMS for out of town participants. For more information, please visit the website at http://www.stat.ubc.ca/~raph/BayesCRG/Activities/SummerSchool/SummerSchool.html.

World Meeting of the International Society for Bayesian Analysis, Hamilton Island, Australia, 21-25 July, 2008.

You are warmly invited to join us for the 9th

World Meeting of the International Society for Bayesian Analysis (ISBA), to be held on Hamilton Island Australia in 2008. The ISBA conferences are held every two years, with every second one held jointly with the Valencia meetings. These conferences have become one of the premier events in Bayesian statistics. ISBA 2008 will broadly follow the tradition of these meetings, combining an excellent scientific programme that includes 5 keynote speakers, 90 oral presentations run over 3 parallel sessions and two poster evenings, with an active social schedule aimed at allowing delegates time to explore this beautiful location. For additional details go to the website, http://www.isba2008.sci.qut.edu.au/, or e-mail isba08@qut.edu.au.

Sample Surveys and Bayesian Statistics: Workshop and Conference, Southampton, UK, 26-29 August, 2008.

The aim of this meeting is to highlight the potential advantages of Bayesian methodology and discuss and illustrate its possible applications in diverse areas of sample survey design and inference. The meeting will begin with a 1.5 days workshop, given by Professor Malay Ghosh (University of Florida, U.S.) and Professor Rod Little (University of Michigan, U.S.). It will be followed by a 2.5 days conference, consisting of invited and contributed research and applied papers, and a special panel discussion. Information on registration to the workshop and conference and submission of abstracts of contributed papers can be found on the conference website www.s3ri.soton.ac.uk/ssbs08/.

Sixth Workshop on Bayesian Inference in Stochastic Processes, Bressanone/Brixen (BZ), Italy, 18-20 June, 2009.

In this workshop, we will bring together experts in the field to review, discuss and explore directions of development of Bayesian Inference in Stochastic Processes and in the use of Stochastic Processes for Bayesian Inference. There will be sessions on Markov processes, state-space models, spatial, empirical, birth-death and branching processes. Theoretical and applied contributions (for example queueing, population modelling, signal processing) are both welcome. The workshop will thus be of interest to workers in both Bayesian Inference and Stochastic Processes. The workshop will be held in an informal environment (Accademia Cusano), to encourage discussion and promote further research in these fields. The workshop will be held in the city of Bressanone (Brixen in German), in the Italian Alps, close to the Austrian border. Additional information is available on the workshop website http://www.mi.imati.cnr.it/conferences/bisp6.html.

2009 Bayesian Biostatistics, Houston TX, January 26-28, 2009.

Current and prospective users of Bayesian biostatistics are invited to join experts in the field for a three-day conference sponsored by the Department of Biostatistics at The University of Texas M. D. Anderson Cancer Center in Houston, Texas, USA. Attendees will have the opportunity to attend two courses on the first day of the conference (Monday). The Use of Bayesian Statistics in Clinical Trials, and Applications of Bayesian Methods to Drug and Medical Device Development. On Tuesday and Wednesday, invited presentations will cover a variety of topics, possibly including comprehensive decision modeling; prior distributions in clinical studies and drug development; what Bayesian methods can provide that traditional methods cannot provide; Bayesian methods in medical journals; Bayesian methods in epidemiology; Bayesian methods and medical ethics; how to build a cadre of Bayesian experts; why Bayesian methods are not more widely used; how to assure good quality in Bayesian methods; and guidelines for publishing Bayesian analyses. Registration fees will be modest. Program co-chairs: Donald A. Berry, Ph.D., The University of Texas M. D. Anderson Cancer Center, and Telba Z. Irony, Ph.D., Center for Devices and Radiological Health, Food and Drug Administration. More information is available at http://www.mdanderson.org/departments/biostats