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A MESSAGE FROM THE PRESIDENT

by Peter Green
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It often seems that the main function of the president is to thank people, and this quarterly message is no exception. After an incredible 10 years as Webmaster, Mike Evans is stepping down, and certainly deserves all of our thanks for maintaining the site so well for so long. The website really is vital as both a channel of communication and a record of our activities, so its importance to ISBA can hardly be overstated. The website has recently been give a new look and feel, and this should be live by the time you read this. I am please to say that Robert Wolpert has undertaken to look after it - but, he says, not for 10 years!

I also want to sincerely thank J Andrés Christen for so ably editing and producing this Bulletin for the last three years. As I write, this vacancy is yet unfilled, and - as I frequently say - volunteers are always welcome!

The September 2006 newsletter mentioned that some work was underway to clarify and unify the structure of the various prizes that ISBA administers (DeGroot, Lindley, Mitchell, and Savage). That work is now complete, thanks to the leadership of Jay Kadane, and contributions from many: the revised rules form part of our Bylaws, and can be seen on the web. *Continue in page* 2.

A MESSAGE FROM THE EDITOR

by J. Andrés Christen
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This June issue of the Bulletin contains very interesting sections, starting with the Applications section with a report on "Bayesian Modeling of Epilepsy Disparities", by David Wheeler and Lance Waller. Also An Annotated Bibliography on "Bayesian Methods for Case-Control Studies", by Samiran Sinha, and also a couple of very interesting Bayesian software reviews.

It has been a great honor to serve as Editor of this Bulletin. I edited 12 ISBA Bulletin numbers and I hope you did find some of the articles in these issues interesting. This is my last issue as Editor, and a new Editor will be appointed soon. I wish to express my gratitude to the AE's that collaborated while I was Editor: Catherine Calder, Robert Gramacy, Gabriel Huerta, Brunero Liseo, Ramsés Mena, Antonio Pievatolo, Bruno Sansó, Alexandra M. Schmidt and Marina Vannucci. Thank you very much indeed, it was you that did the heavy work. The new editor will need help in establishing his/her editorial board. Please try to cooperate with the Bulletin by becoming an AE or suggesting names to the new Editor. Thank you all and bye for now. ▲

Contents

Continued from page 1.

The previous issue of this Bulletin carried tributes to Pilar Iglesias, chair of the Chilean chapter of ISBA, who died in March. I am very pleased to say that at the initiative of Alicia Carriquiry, Fabrizio Ruggeri and Jay Kadane, the Board has agreed to increase significantly the recently-started fund to support young researchers' travel to ISBA meetings, and name this in honour of Pilar. You can add your contributions to the fund by visiting the website, and I hope you will.

Finally, an item of interest for those of you for whom physical memorials are important - previous newsletters mentioned our interest in having the tomb of Thomas Bayes restored and cleaned. That work is now complete and visitors to London should include it in their sightseeing. The work was paid for by a generous donation from BEST LLC of New Jersey. ISBA members' donations to restoring the tomb will be put towards future cleaning - something that will be soon needed given London weather!

For those of you in the northern hemisphere - all the best for the summer.▲

BAYESIAN MODELING OF EPILEPSY DISPARITIES

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Previous research has suggested that the incidence rate for the disease of epilepsy is positively associated with various measures of social and economic disadvantage (Heaney *et al.*, 2002). The Centers for Disease Control and Prevention (CDC) defined epilepsy as an emerging public health issue in its 2003 report "Living Well with Epilepsy" and emphasized the importance of epilepsy studies in minorities and people of low socioeconomic status. In response, a group of researchers at Emory University and The Ohio State University have utilized a hierarchical Bayesian model in a study to analyze health disparities in epilepsy rates among multiple races/ethnicities in the city of Philadelphia, Pennsylvania. Involved in the study are David Wheeler and Lance Waller from the Department of Biostatistics at Emory University and John Elliot from the Department of Neurology at The Ohio State University. The goals of the project were to highlight any overall significant disparities in epilepsy rates between the populations of Caucasians, African Americans, and Hispanics in the study area during the years 2002-2004 and to visualize the spatial pattern of epilepsy rates by ethnicity to indicate where certain ethnic populations were most adversely effected by epilepsy within the study area. The terms ethnicity and race are often used synonymously in practice, and for convenience we use the term ethnicities to refer to the population groups in the study.

The researchers implemented a hierarchical Poisson Bayesian model to estimate epilepsy rates in small-area units to account for the instability of crude rate estimates, where a small number of observed cases or a small ethnic population count in an area would result in an unreliable rate with a large variance. The model required as input the crude relative risk of epilepsy (standardized patient ratio), which was estimated using the overall rate of epilepsy in the study data. The hierarchical Bayesian model jointly estimated the smoothed relative risk of epilepsy for the three ethnicities of interest using an intrinsic multivariate conditional autoregressive (CAR) prior (see, for example, Banerjee *et al.*, 2004) for the area-specific log relative risks. The Bayesian model estimates smoothed rates of epilepsy by borrowing strength for areas with small populations from the neighboring areas to produce more reliable rates. It also includes an age covariate to account for potential differences in population age structure among the areas. Outputs of the model include posterior estimates of overall epilepsy risk by ethnicity, local risk by ethnicity, and the overall correlation between the rates of different ethnicities. Markov chain Monte Carlo methods were used to provide samples of model parameter values from their joint posterior distribution.

Current smoothed rate estimates are at the ZIP Code level, as researchers were interested in a comparison of rates from two datasets, one of which, from the Pennsylvania Health Care Containment Council (PHC4) system, contained patient records with locational information available only at the ZIP Code level. The other dataset, from the five hospitals in the Temple University Health System (TUHS), contained epilepsy patient contact records with complete address information. The TUHS database is administrative in nature, while the PHC4 database is an aggregation of multiple reporting sources, and therefore has the potential for more complete and larger coverage. How-

ever, 37% of the PHC4 data for areas extending beyond the city of Philadelphia contain ZIP Codes listed as "private". These are thought to be primarily psychiatric or HIV patients. Given that there were some differences in the proportion of records with missing ZIP Codes by ethnicity, the researchers chose to use only the TUHS data to estimate epilepsy rates in Philadelphia in this example. To map individual epilepsy patient contacts from the TUHS, patient records were address matched, or geocoded, to a street network. Individual records for which an automatic match could not be made were located with Internet-based searches for an overall match rate of 96% of all patient records. Records of individual patient visits were combined to create unique patient records and then patients were aggregated by area and ethnicity to derive epilepsy patient counts

The estimated smoothed epilepsy rates for each ethnic group are plotted in Figure 1. The spatial patterns of epilepsy rates vary by ethnicity and are not explained entirely by the distribution of ethnic populations. The spatial distribution of epilepsy is more correlated between African Americans and Hispanics than it is for either of these groups with Caucasians. Results of the Bayesian model indicate that Hispanics have the highest epilepsy rate overall, followed by African Americans, and then Caucasians. There are significant increases in relative risk for both African Americans and Hispanics when compared with Caucasians, as indicated by the posterior mean estimates of 2.09 with a 95% credible interval of (1.67, 2.62) for African Americans and 2.97 with a 95% credible interval of (2.37, 3.71) for Hispanics.

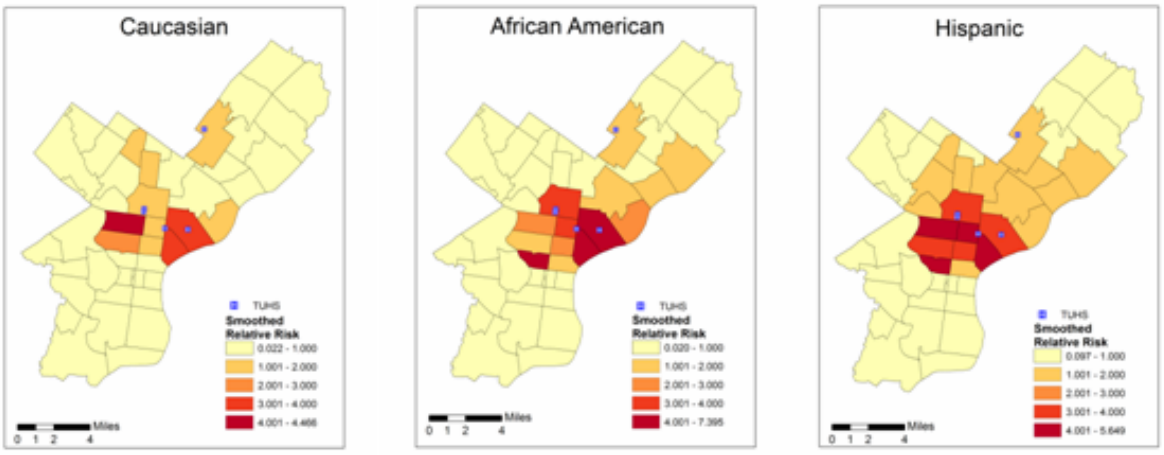
Our experience in analyzing epilepsy data demonstrates that using a Bayesian analysis in combination with geographic information system (GIS) technology can reveal spatial patterns in patient data and highlight areas of disparity in disease risk among subgroups of the population, in this case different ethnic groups. Furthermore, Figure 1 illustrates that these disparities vary within the study area in geographically distinctive ways. These patterns can be examined in various ways to improve outreach efforts and patient education programs, as well as for identifying community resources where such programs could be based. Future work will produce rate estimates at the census tract or neighborhood level and will incorporate hospital distance effects in the model.▲

References

- Banerjee, S., Carlin, B., and Gelfand, A. (2004). *Hierarchical Modeling and Analysis for Spatial Data*: Chapman & Hall/CRC: Boca Raton, Florida.

- Heaney, D., MacDonald, B., Everitt, A., Stevenson, S., Leonardi, G., Wilkinson, P., and Sander, J. (2002), "Socioeconomic variation in incidence of epilepsy: prospective community based study in south east England", *British Medical Journal*, **325**, 1013-1016.

Figure 1: Smoothed relative risk for epilepsy by ZIP Code for Caucasians, African Americans, and Hispanics with TUHS hospital locations.



BFRM: Software for Bayesian Factor Regression Models

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Overview

BFRM is a comprehensive implementation of sparse statistical models for high-dimensional data analysis, structure discovery and prediction.

The framework of sparse latent factor modelling coupled with sparse regression and ANOVA for multivariate data is relevant in many exploratory and predictive problems with high-dimensional multivariate observations. Bayesian analysis utilising sparsity-inducing models, and computational methods able to efficiently explore and fit large-scale models, now allow these approaches to be used in increasingly complex and high-dimensional problems.

The statistical methods and computational analysis represented in BFRM are generic and suited to many areas of application. A range of recent applications – and a core set of motivating problems for some of the recent modelling and computational developments – are biological studies using gene expression data. A number of these studies are represented in examples in the papers below. These illustrate exploratory and predictive analyses of gene expression data coupled with outcomes (phenotypes) to be predicted, and related studies in biological pathway analysis.

The main methodological aspects of BFRM are described in Carvalho *et. al.* (2007) [1]. Sparse factor modelling developments there build on and develop earlier ideas and methods from West (2003) [4]. BFRM is written in C++ and freely available to interested researchers. The BFRM executables for multiple platforms and operating systems, together with detailed descriptions for installing and running the code and a number of examples, are available at:

`http://xpress.isds.duke.edu:8080/bfrm/`

Examples and Case Studies

The examples in [1], [2] and [3] illustrate the use of BFRM in the following case studies:

[1] Based on the analogy of latent factors representing biological "subpathways" structure, this paper explores connections between factors and multiple biological aspects of cancer genomics. The studies discuss the discovery use of this approach in expanding the existing knowledge of oncogenic pathways along with the illustration of the predictive ability of aggregate patterns of gene expression profiles in prognostic clinical contexts.

[2] This paper discusses the use of sparse anova models in gene expression experiments designed to investigate the transcriptional responses to interventions that up-regulate a series of key oncogenes, and includes a number of practical model developments relevant to modern gene expression array technologies.

[3] This paper describes case studies that use BFRM for the creation of gene expression signatures of cardiovascular disease states, linking to risk factors from designed experiments in mice models. Analysis investigates cross-species extrapolation of risk signatures by projection to human observational data with the latter modelling via sparse latent factor analysis using BFRM.

Example summaries from the cardiovascular genomics studies are in Figure 1. Exploration of these and other graphical and numerical summaries – in designed experiments and observational data sets from cancer and cardiovascular genomics – are developed in the referenced papers. ▲

References

[1] Carvalho, C., Chang, J., Lucas, J., Wang, Q., Nevins J. and West, M. (2006). "High-dimensional sparse factor modelling: Applications in gene expression genomics." (Submitted). `http://ftp.stat.duke.edu/WorkingPapers/05-15.html`

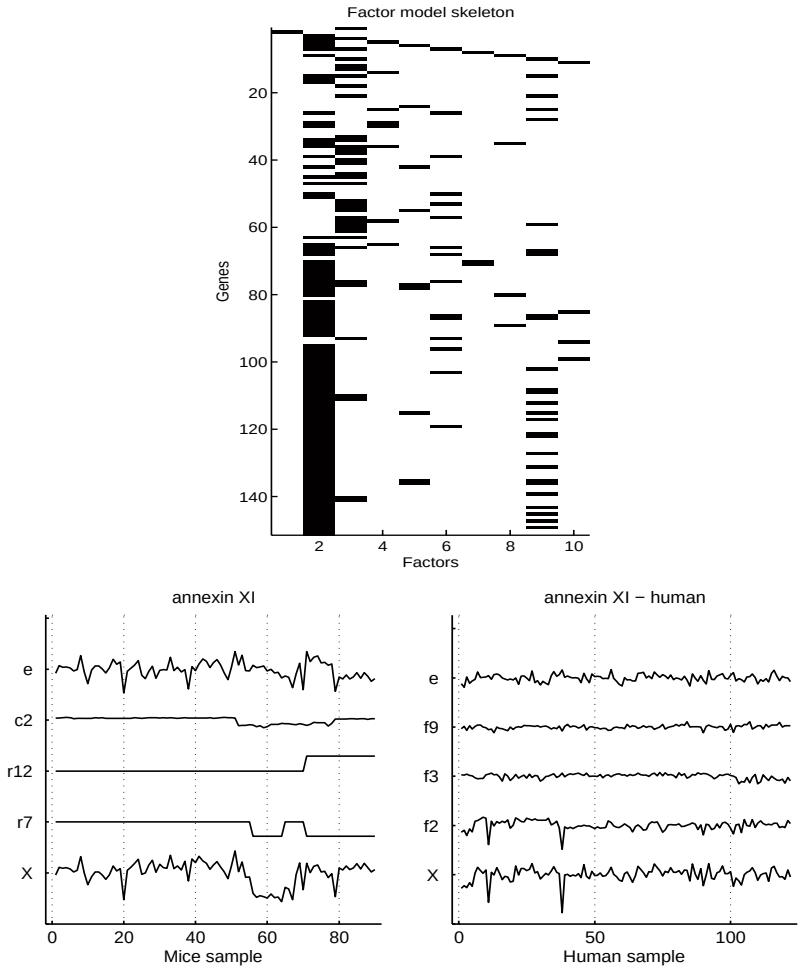
[2] Lucas, J., Carvalho, C., Wang, Q., Bild, A., Nevins J. and West, M. (2006). "Sparse statistical modelling in gene expression genomics." In *Bayesian Inference for Gene Expression and Proteomics*, (eds. K.A. Do *et al*), CUP, 155-176. `http://ftp.stat.duke.edu/WorkingPapers/06-01.html`

[3] Seo, D., Goldschmidt-Clermont P. and West, M. "Of mice and men: Sparse statistical modelling in cardiovascular genomics." (2007). *An-*

nals of Applied Statistics **1**, http://ftp.stat.duke.edu/WorkingPapers/07-05.html

[4] West, M. "Bayesian factor regression models in the "large p, small n" paradigm." (2003). *Bayesian Statistics* **7**, 723-732. http://ftp.isds.duke.edu/WorkingPapers/02-12.html

Figure 2: Examples from BFRM analyses of gene expression in designed experiments on mice coupled with human observational data, developed in a cardiovascular genomics project. The top frame is a "skeleton" of a latent factor model – fitted to 150 genes (rows) and involving 10 latent factors (columns) – in the human cardiovascular study, showing the sparsity pattern of gene-factor associations based on thresholding posterior probabilities of such associations (black="on", white="off"). The lower left frame shows a BFRM estimated decomposition of gene expression (X) of mouse gene annexin XI across mouse samples, illustrating estimated contributions to expression of this gene related to two design variables (r7, r12), a microarray experimental artifact correction regressor (c2), and the residual (e). The lower right frame shows a similar decomposition of the same gene but now assayed in the human data, and where the expression fluctuations across human samples relate to estimated latent factors 2,3, and 9.



BAYESIAN METHODS FOR CASE-CONTROL STUDIES

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Case-control study is a widely used retrospective design to collect epidemiological data. Let Y be the disease variable which takes value 1 or zero according as a subject has a disease or not, and X be the exposure variable of interest. Case-control study, in its simple form, collects a random samples of size n_0 from the target population with $Y = 0$, which

are called controls, and a random sample of size n_1 from the target population with $Y = 1$, which are called cases. Then the information on the exposure variable is collected retrospectively from the sampled individuals. The disease incidence model is

$$P(Y = 1|X) = H(\beta_0 + X\beta), \tag{1}$$

where $H(u) = 1/\{1 + \exp(-u)\}$. The concern is how to estimate β, the parameter associated with X. In general, β is the log-odds ratio associated with X, i.e.,

$$\beta = \log\left\{\frac{P(Y = 1|X + 1)P(Y = 0|X)}{P(Y = 1|X)P(Y = 0|X + 1)}\right\},$$

and for rare diseases, β represents the relative risk.

In a case-control setup, matching is often used for selecting "similar" controls to eliminate bias due to confounding factors. Statistical techniques for analyzing matched case-control data were first developed in Breslow et al. (1978). In the simplest setting, the data consist of n matched sets and there are $M_i(\geq 1)$ controls matched with a case in each matched set or stratum. We denote the i-th matched set by S_i, $i = 1, \cdots, n$. For the disease incidence model, one assumes

$$P(Y = 1|X, S_i) = H\{\beta_{0i} + X\beta\} \tag{2}$$

where β_{0i}'s are the stratum-specific intercept terms. The stratum parameters β_{0i}'s are eliminated by conditioning on the unordered set of exposures for the cases and controls in each stratum.

The bibliography is restricted mainly to Bayesian contributions to case-control studies, and due to space restriction it is not exhaustive.

General Aspect

- Altham, P. M. E. (1971), "The analysis of matched proportions", *Biometrika*, **58**, 561–576. This article considered Bayesian test of association for a common log odds-ratio parameter for several 2×2 contingency tables.

- Zelen, M. and Parker, R. A. (1986). "Case-control studies and Bayesian inference". *Statistics in Medicine*, **5**, 261–269. This article considered simple Bayesian analysis of case-control data with a binary exposure variable. The authors expressed the log odds-ratio parameter in terms of probabilities of exposure in control and case populations, and then they used *Beta* prior on the unknown parameters. The inference was based on the posterior mean and credible set.

- Seaman, S. R. and Richardson, S. (2001). "Bayesian analysis of case-control studies with categorical covariates". *Biometrika*, **88**, 1073–1088. This article dealt with case-control study with categorical exposure variable. The model parameters were estimated in a Bayesian framework by adopting full likelihood of the data.

- Müller, P., Parmigiani, G., Schildkraut, J. and Tardella, L. (1999). "A Bayesian hierarchical approach for combining case-control and prospective studies". *Biometrics*, **55**, 858–866. Here the authors proposed a Bayesian hierarchical model to estimate model parameters for a combined case-control and prospective studies. Instead of working with model 1, they modeled the conditional distribution of the exposure variable given the disease status, and carried out Bayesian analysis. They dealt with categorical and quantitative variables simultaneously.

- Seaman, S. R. and Richardson, S. (2004). "Equivalence of prospective and retrospective models in the Bayesian analysis of case-control studies". *Biometrika*, **91**, 15–25. This article showed that posterior distributions of the log odds-ratio parameter for prospective and retrospective data are equivalent under Poisson-multinomial model. This result is analogous to the result of Prentice and Pyke (1979)'s result, in the Bayesian framework.

- Rice, M. K. (2004). "Equivalence between conditional and mixture approaches to the rasch model and matched case-control studies, with application". *Journal of the American Statistical Association*, **99**, 510–522. Generally the inference of matched case-control study is based on the conditional likelihood obtained after conditioning on the sufficient statistic of the matched set specific nuisance parameter. The author derived the necessary and sufficient condition for equivalence between the conditional likelihood and the marginal likelihood obtained by integrating out the nuisance parameters with respect to some mixing distribution for a categorical exposure variable.

- Diggle, P. J., Morris, S. E. and Wakefield, J. C. (2000). "Point-source modeling using matched case-control data". *Biostatistics*, **1**, 89–105. This article considered Bayesian analysis for matched case-control study, where the exposure of primary interest is defined by the spatial location of an in-

dividual relative to a point or line source of pollution.

- Ghosh, M. and Chen, M-H. (2002). "Bayesian inference for matched case-control studies". *Sankhyā, B*, **64**, 107-127. This article presented Bayesian analysis for matched case-control data with one or more binary exposure variable. The article considered unconditional likelihood of the data, and studied posterior proprieties under different scenarios.

- Mukherjee, B., Sinha, S., and Ghosh, M. (2005). "Bayesian analysis for case-control studies: A review article". *Handbook of Statistics*, **25**, *Bayesian Thinking: Modeling and Computation*, 793–819. This is a review article, where the authors reviewed most of the Bayesian works related to this field, and some classical work in frequentist setup.

Missing Exposure Variable

The Bayesian inference for case-control study with partially missing exposure variable requires to model the distribution of the partially missing exposure variable. Special effort has been made on how to model the distribution in a flexible manner.

- Sinha, S., Mukherjee, B. and Ghosh, M., Mallick, B. K. and Carroll, R. (2005a). Semiparametric Bayesian modeling of matched case-control studies with missing exposure. *Journal of the American Statistical Association*, **100**, 591–601. This article dealt with partially missing exposure variable in matched case-control studies. The novelty of this work is how the stratum specific heterogeneity on the distribution of the partially missing exposure variable is handled by using Dirichlet process prior.

- Sinha, S., Mukherjee, B. and Ghosh, M. (2004). "Bayesian semiparametric modeling for matched case-control studies with multiple disease states". *Biometrics*, **60**, 41–49. This paper described a method for handling partially missing exposure variable in matched case-control setup. However, instead of binary disease status, the paper dealt with diseases with multiple categories. Semiparametric Bayesian method has been developed to estimate the model parameters.

Errors in Covariate

Following references concern how to estimate the risk parameter when the exposure variable is measured with error.

- Müller, P. and Roeder, K. (1997). "A Bayesian semiparametric model for case-control studies with errors in variables". *Biometrika*, **84**, 523–537. This article dealt with the problem of measurement error in the exposure variable. The proposed approach was very flexible in terms of the distribution of the exposure variable as well as in terms of the relationship between the surrogate variable and the unobserved exposure variable. The proposed method used Dirichlet mixture of multivariate normal prior on the joint distribution of the surrogate variable, unobserved exposure variable, and the variable which is measured without any error. The authors proposed an MCMC scheme to estimate the model parameters.

- Gustafson, P., Le, N. D., and Vallee, M. (2002). A Bayesian approach to case-control studies with errors in covariables. *Biostatistics* **3**, 229–243. This article proposed a Bayesian method for handling errors in covariate in case-control studies. The authors approximated the distribution of the true covariate by a discrete distribution over a fixed grid points, and then used uniform Dirichlet prior on the probability masses.

Gene-Environment Interaction

Following references deal with gene-environment interaction effect on the risk of a disease in case-control studies.

- Mukherjee, B., Zhang, L., Ghosh, M., and Sinha, S. (2007). "Semiparametric Bayesian analysis of case-control data under conditional gene-environment independence". *Biometrics* **63**. This article developed a semiparametric Bayesian method for estimating effect of genetic factor, environmental factor, and their interaction on the risk of a disease for a stratified case-control study. The authors used Dirichlet process prior to model the stratification effects on the distribution of the environmental covariate under the assumption of gene-environment independence in the control population.

- Zhang, L., Mukherjee, B., and Ghosh, M. (2007). Accounting for error due to misclas-

sification of exposures in case-control studies of gene-environment interaction. *Statistics in Medicine* to appear. This article dealt with misclassified genetic factor in case-control studies under the gene-environment independence assumption. ▲

Other References

Following articles and the book present pioneering work in case-control studies.

- Breslow, N. E., Day, N. E., Halvorsen, K. T., Prentice, R. L., and Sabai, C. (1978). "Estimation of multiple relative risk functions in matched case-control studies". *American Journal of Epidemiology*, **108**, 299–307.
- Prentice, R. L. and Pyke, R. (1979). "Logistic disease incidence models and case-control studies". *Biometrika*, **66**, 403–411.
- Breslow, N. E. and Day, N. E. (1980). *Statistical Methods in Cancer Research*, Volume 1. Lyon, International Agency for Research on Cancer.

SSS: SOFTWARE FOR HIGH-DIMENSIONAL BAYESIAN REGRESSION MODEL SEARCH

by Chris Hans, Quanli Wang, Adrian Dobra and Mike West

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Overview

SSS is a suite of software suite implementing "shotgun stochastic search" for "large p" regression variable uncertainty and selection. The SSS theory and methodology for regression models is described and exemplified in Hans, Dobra and West (2007) [1]. The general framework is that of regression with uncertainty about which predictors are in the model; model uncertainty is represented in terms of a prior variable inclusion probability to penalise model dimension. SSS explores the space of potentially very many models defined by subsets of predictor variables, guided by the (unnormalised) posterior model probabilities, and ranks and summarises sets of "top models" for assessment and prediction. The parallel implementation also provides some basic support for leave-one-out cross-validation analysis.

The current program includes both serial and parallel versions, implementing SSS for linear, binary (logistic) and survival (Weibull) regression model frameworks. Examples and case studies in [1], [2] and [3] illustrate the approach. SSS is freely available and written in C++. Executables, examples and detailed descriptions of the programs can be downloaded from:

`http://www.stat.osu.edu/~hans/sss/`

or

`http://xpress.isds.duke.edu:8080/sss/`

Serial Versions

Several versions of the serial-computing implementation of SSS are provided and can be run directly in Windows or Unix by taking text file inputs and producing summary text file outputs. Additionally, a Java graphical user interface (GUI) allows SSS to be run smoothly as a standalone program in Matlab version 7 and higher (see Figure 3). Provided in the serial suite are:

- a Windows executable;
- a Java GUI program for easy Matlab interface;
- 32- and 64-bit Linux executables;
- example input files and data;
- Matlab script files providing examples for running SSS using the GUI; and
- Matlab and R script files providing examples for summarizing SSS output.

Parallel Version

The parallel-computing version of SSS is also provided, along with source code, for use on a Unix cluster. The parallel program is similar to the serial version but takes advantage of parallelizable aspects of SSS, leading to a more efficient implementation for very high-dimensional problems. The parallel program uses the MPI (Message-Passing Interface) application programming interface to facilitate communication between nodes in the cluster. No other special libraries are required. Included in the download are:

- C++ source code and compiling instructions;

- Example input files and data; and
- Matlab and R script files providing examples for summarizing SSS output. ▲

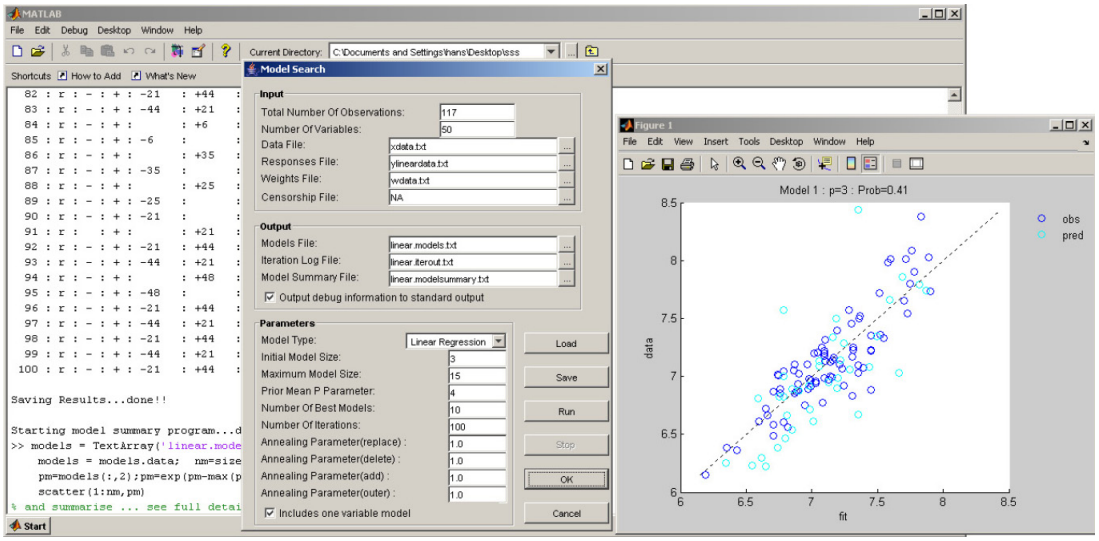
References

[1] Hans, C., Dobra, A. and West, M. (2007). "Shotgun stochastic search for "large p" regression." *Journal of the American Statistical Association*, to appear.

[2] Hans, C. and West, M. (2006). "High-dimensional Regression in Cancer Genomics." *ISBA Bulletin*, **13**(2), 2–3.

[3] Rich, J., Hans, C., Jones, B., Iversen, E., McClendon, R., Rasheed, B., Dobra, A., Dressman, H., Bigner, D., Nevins, J. and West, M. (2005). "Gene expression profiling and genetic markers in glioblastoma survival." *Cancer Research*, **65**, 4051–4058.

Figure 3: SSS Matlab GUI



Events

Construction and Properties of Bayesian Non-Parametric Regression Models.

Isaac Newton Institute for Mathematical Sciences, Cambridge, UK, 6-10 Aug. 2007, `http://www.newton.cam.ac.uk/programmes/BNR/bnrw01.html`. If you are interested in NP Bayes, please consider joining the fun at this workshop. We have an exciting program shaping up. Please visit the workshop homepage to sign up online, open until June 30. (Message to the Editor by Peter Müller, *pm@wotan.mdacc.tmc.edu*.)

New Awards

BEST Award: Duke Student Research Prize

ISBA member José M. (Pepe) Quintana presented the closing seminar of the academic year at ISDS, Duke University, on 20 April 2007. In an announcement at the reception following Pepe's talk, the BEST Award for Student Research was announced. Established by the BEST Foundation, a non-profit corporation whose primary mission is to make gifts, grants and contributions to educational, scientific and charitable institutions or organizations, the new prize will be awarded annually to a Duke student or students on the basis of a research project in Bayesian statistical modeling related to time series and other methods in financial applications. Full details are available at `http://www.stat.duke.edu/research/BEST/`. (Message to the Editor by Mike West, *mike@isds.duke.edu*.)

Pilar Iglesias' Fund

As you probably know, Pilar Iglesias, who organized the superb ISBA World Meeting at Viña del Mar, Chile in 2004, recently passed away. Pilar was a research leader in Latin America in the areas of Bayesian theory and analysis and an outstanding educator. She contributed to the profession through service in ISBA and in the Chilean Statistical Association and was a dedicated mentor of

students and young researchers.

A fund in memory of Pilar has now been established by ISBA. The goal is to raise 20,000 USD to endow an award in her name, to be given in perpetuity. The award would provide travel grants for one or two graduate students or young researchers from a developing nation so that they can participate in an ISBA World Meeting or a Valencia meeting. The funds will be managed by ISBA. The Pontifical Catholic University of Chile, Pilar's home institution, provided the initial 5,000 USD to the fund.

We ask that you consider making a contribution to the fund. Any amount, even if small, will help ISBA reach its goal.To make a contribution please visit the web site `http://www.ams.ucsc.edu/~bruno/cgi-bin/iglesias.cgi`. Using the secure online system is strongly encouraged.

We thank you in advance, Alicia Carriquiry, Jay Kadane, Fabrizio Ruggeri and Peter Green, President, ISBA. (Message to the Editor by Fabrizio Ruggeri, *fabrizio@mi.imati.cnr.it*.)

ISBA Bylaws

ISBA is pleased to announce that on 25 May 2007 the ISBA Board approved a Bylaw amendment to improve the way the DeGroot, Lindley, Mitchell, and Savage prizes are administered. These prizes will be announced, the nominations collected by, and appointments to ad-hoc award committees made by, a new ISBA Prize Committee, to be appointed by the ISBA President. It is hoped that the reformed structure will be more efficient than before, and will be less vulnerable to conflicts-of-interest. The details will be found on the ISBA website. Jay Kadane, Chair, Constitution and Bylaws Committee. (Message to the Editor by Robert Wolpert, *wolpert@STAT.Duke.edu*.) ▲

INTERNATIONAL SOCIETY FOR BAYESIAN ANALYSIS