

Completion Report for BSAS Scholarships

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Award Name and value of the award: The Murray Black award, £750

Was any additional funding secured to support the activity?

Yes: The International Society for Bayesian Analysis Young Researchers travel award, gave US \$500,
Scottish Agricultural College Trust Fund awarded £500.

Start/end date of the award:

26th-29th of June, 2012

Summary of the award (Briefly describe the objectives and how was it undertaken):

(approximately 300 words)

The objective of the project that was awarded money was to attend the international Society for Bayesian Statistics bi-annual meeting in Kyoto, Japan; attend tutorials, presentations and poster sessions; and present a poster of my own work sessions on the hindcasting of epidemics using paired sample data.

The conference went well overall. There were about 500 participants covering a range of fields from econometrics, via theoretical methodology, to game theory. I attended about 20 presentations on subjects of more or less relevance to animal health; geographical analyses of diseases, analysis of microarray data, spread of diseases across networks, and stochastic simulations of epidemics.

Apart from the things that was of more immediate relevance to my research, there was a lot to gain from seeing all the things and developments that is going on in Bayesian methodology, and getting a feel for where my own knowledge and approaches needs to be improved in order to reach a world-class standard.

My poster presentation was also well received; there were several appreciative comments both on the immediate usefulness of the research, and on the innovate approach to exploiting data. I also received some concrete and helpful feedback on what should be incorporated in future work, how the poster content could have been improved to better suit the more theoretical among the conference participants.

From the poster session and from the overall conference, there was a multitude of people doing interesting work that I'll be keeping an eye on in the future, and a fair few where we'll keep in contact after the conference because of aligning research interests. The networking aspect of the conference was probably the most beneficial outcome of all.

Benefits of the Award:

This is the main part of the report and the two sections below should be approximately 1000 words in total. You may focus on benefits to yourself, to the animal science community, or both – depending on the nature of the activity undertaken.

Benefit of the award to you (e.g. new knowledge or skills, new contacts and collaborations):

I feel that the benefits from attending the conference are far-reaching, and will probably affect my work for at least the coming year or two. The benefits can be split up into three or so categories: overview over current methodological research; picking up techniques that I will be incorporating into my every day work; and connections and awareness of persons doing interesting work.

Regarding the current research, a strong trend was a move away from the current practice in the field of using computationally intensive but theoretically exact Markov-Chain Monte Carlo procedures, to using more approximate methods known as “Approximate Bayesian Computation/ABC” and “Integrated Nested Laplace Approximation/INLA” (to mention the two foremost contenders), which are much faster, theoretically inexact and biased, but in practical use often giving answers that are closer to reality. There were 10 talks, and 5 to ten posters on this topic. This movement is important because if it continues, it promises to make a lot more statistical analyses, such as disease mapping, tractable, and furthermore much more accessible to non-statistician analysts.

A tool that was presented by James Flegal (Uni. of California), that will make its way directly into my current practice is an R statistical computational package for the calculation of standard errors from

Bayesian MCMC estimates; this is a huge practical breakthrough, because previously the uncertainty of the estimates was a mix of random variation and convergence failure; the new approach eliminates the convergence consideration.

I'm now planning to employ the above mentioned approaches of ABC and INLA for my work on wildlife disease mapping in the coming year; while I knew about INLA before the conference, its full importance was not apparent to me; and ABC was a completely new acquaintance.

I mentioned in my summary that connecting with new researchers was probably the most far-reaching consequence of the conference for me. Some of the researchers that might prove interesting to non statisticians were the following:

Julia Palacios, of the University of Washington, Seattle, USA. She is doing work on using the genetic variation of pathogens to identify by timing and extent, previous population bottle necks and widening events. Such events signify times of high spread and/or outbreaks, and an example of being able to recover a period of epidemic spread of Hepatitis C in Egypt in the late 1980s from pathogen data collected recently. While the work is in its early stages, in the long run this could prove very useful in getting a picture of how newly detected emerging infections (such as the Schmallenberg Virus in Sheep) have developed up until the time of detection.

Gabriela Cybis, of UCLA, California, USA. Gabriela is doing work on how to model the connection between antigenic variation and phylogenetic structure in a pathogen population, using the example of Influenza. By using clustering methods, one is able to predict antigenic shifts based on shifts in the genetic code, and possibly (in the very long run) predict the likelihood of new antigenic groups of pathogens occurring – something that is very important for vaccine development against a wide range of human and animal diseases.

Leonhard Held, of the University of Zurich, Switzerland. Leonhard is working on disease mapping and analysis of livestock diseases. He presented an example of using INLA to estimate the impact that cattle trade between farms on the spread of Coxiellosis in Swiss cows. The ease and simplicity of fitting an INLA model was very impressive.

Ioanna Manolopoulou, of Duke University, North Carolina, USA. Ioanna was presenting some very interesting work on classifying and modeling animal movements using a combination of diffusion models from physics for an underlying "force field" that affects ease of movement with a Bayesian circular regression type analysis, exemplifying with an analysis of how temperature differentials affect toucan movements in Central America. This approach has obvious applications, both for the analysis of wildlife movements, but also for things such as classifying movement behavior in livestock.

Benefit of the award to the animal science community, academic and industrial:

I hope to bring back some benefit of the award to the animal science community by discussing and disseminating my experience at ISBA, in the form of an overview presentation to my statistics colleagues at Biomathematics and Statistics Scotland, as well as giving tips of useful methodological approaches from a Bayesian perspective during research team meetings to my animal science colleagues at Scottish Agricultural College.

I've mentioned several times how valuable it was to meet and connect with colleagues from across the world – the number of applied statisticians working with infectious diseases in animals is pretty small, overall, and to be able to get to know so many people with interesting and stimulating viewpoints is bound to expand the international aspect of this kind of research, and create further collaborations across borders – there has already been quite a number of post-conference mails being exchanged, and a couple with potential for future collaborative work.

However, what I feel is the most important impression I'm bringing with me from this trip, is that attending ISBA has raised an awareness that there is a lot more advanced and useful theory and methods out there than what is currently in use by myself or by the British animal science field as a whole; this awareness has brought with it an ambition to raise my own level, and hopefully help raise the level of others, to be able to conduct research that is on the cutting edge, not only from a general science perspective, but also from a methodological perspective. There is a lot to be done!

Other supporting information:

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