Bayes on the Beach is an intentionally small international forum for discussing and exploring developments in Bayesian Statistics and its applications. This three day conference will take place in the world-famous Surfers Paradise on the Gold Coast and is designed to have a diverse format including presentations, contributed sessions, workshops, a poster session and tutorials.

This conference is supported by the Bayesian Statistics Section of the Statistical Society of Australia (SSA), Australasian Chapter of the International Society for Bayesian Analysis (ISBA); ARC Centre of Excellence for Mathematical & Statistical Frontiers (ACEMS) and Queensland University of Technology (QUT).
Sponsors and participating organisations

www.bragqut.wordpress.com

www.qut.edu.au

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Conference organisers:

Kerrie Mengersen
Jessica Cameron
Jagath Senarathne
Jacinta Holloway
Cheryle Blair
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<td><em>Title:</em> Understanding the behavior of complex cellular processes:</td>
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### Conference program: Poster session 1, Monday 13th November 2017, 20:00-22:00

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<td>Khue-Dung Dang, University of New South Wales Business School</td>
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<td>Brigitte Colin, Queensland University of Technology</td>
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<td>Bayesian modelling of temporal dependence for bivariate survival data using copulas</td>
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<td>Spectral density estimation of LIGO gravitational wave data using an AR-enhanced Whittle likelihood</td>
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<td>Miles McBain, Queensland University of Technology</td>
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| 08:30-09:30| **Keynote presentation 2**: Mark Girolami  
*Title: Stochastic modelling of urban structure - A Bayesian perspective* | Christopher Drovandi           |
| 09:30-11:00| **Tutorial 2**: Mark Girolami  
*Title: Probabilistic numerical computation: A role for (Bayesian) statisticians in numerical analysis?* |                                |
| 11:00-11:15| **Morning tea**                                                                                         |                                |
| 11:15-12:15| **Invited Presentation Session 2**  
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**Invited presentation**: Shunsuke Horii  
*Title: Bayesian sparse-smooth modeling and variational inference*  
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*Title: greta: simple and scalable statistical modelling in R*  
**Invited presentation**: Christopher Drovandi  
*Title: New insights into history matching via sequential Monte Carlo* | Matthew Sutton                  |
| 12:15-14:15| **Lunch**                                                                                                |                                |
| 14:15-15:30| **Keynote presentation 3**: Gael Martin  
*Title: Computing Bayes: Bayesian computation from 1763 to 2017!* | Shovanur Haque                 |
| 15:30-15:45| **Afternoon tea**                                                                                       |                                |
| 15:45-17:00| **Tutorial 3**: Gael Martin  
*Title: Recent advances in Approximate Bayesian Computation: Inference and forecasting* | Shovanur Haque                 |
| 17:00-18:15| **Workshop 2**                                                                                          | Jagath Senarathne              |
| 18:15-20:00| **Dinner**                                                                                                |                                |
| 20:00-22:00| **Poster session 2**                                                                                     |                                |
### Conference program: Poster session 2, Tuesday 14th November 2017, 20:00-22:00

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| 08:30-09:30  | **Keynote presentation 4**: Scott Sisson  
*Title: Modelling big data fast and on your laptop via symbolic data analysis* | Leah Price    |
| 09:30-11:00  | **Tutorial 4**: Scott Sisson  
*Title: "Phew, what a scorcher!" A short introduction to modelling extremes* |             |
| 11:00-11:15  | **Morning tea**                                                                    |              |
| 11:15-12:15  | **Invited Presentation Session 3**  
*Invited presentation*: Earl Duncan  
*Title: A-Z: 20 years of progress on the label switching problem* | Earl Duncan   |
|              | **Priors**                                                                         |              |
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| 14:00-15:00  | **Invited Presentation Session 4**  
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*Title: A study on analytical properties of Bayesian experimental design model based on an orthonormal system* | James McGree |
|              | **Invited Presentation**: Pubudu Thilan  
*Title: Model-based adaptive design methods for improving the effectiveness of reef monitoring* |             |
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*Title: Dual-purpose Bayesian design for parameter estimation and model discrimination of models with intractable likelihoods* |             |
| 15:00-16:00  | **Workshop 3**                                                                     | Jacinta Holloway |
| 16:00-16:15  | **Conference close**                                                               | Kerrie Mengersen |
| 16:15-16:30  | **Afternoon tea**                                                                  |              |
Trained in the French school of Data Analysis in Montpellier, Professor Susan Holmes has been working in non parametric multivariate statistics applied to Biology since 1985. She has taught at MIT, Harvard and was an Associate Professor of Biometry at Cornell before moving to Stanford in 1998. She teaches the Thinking Matters class: Breaking Codes and Finding patterns and likes working on big messy data sets, mostly from the areas of Immunology, Cancer Biology and Microbial Ecology. Her theoretical interests include applied probability, MCMC (Monte Carlo Markov chains), Graph Limit Theory, Differential Geometry and the topology of the space of Phylogenetic Trees.

**Keynote Presentation**

*Statistical challenges for microbial ecology*

The human microbiome is a complex assembly of bacteria that are sensitive to many perturbations. We have developed specific tools for studying the vaginal, intestinal and oral microbiomes under different perturbations (pregnancy, hypo-salivation inducing medications and antibiotics are some examples). We will show tools we have developed for analysing longitudinal multi-table data composed of 16s rRNA reads combined with clinical data, transcriptomic and metabolomic profiles. Challenges we have addressed include information leaks, the integration of phylogenetic information, longitudinal dependencies and uncertainty quantification. Our methods enable the detection of ecological gradients and their uncertainty quantification as well as the integration of tree-aware multivariate representations.

This contains joint work with Joey McMurdie, Lan Huong Nguyen, Pratheepa Jeganathan, Sergio Bacallado, Ben Callahan, Julia Fukuyama, Kris Sankaran and David Relman’s Lab members from Stanford.

**Tutorial**

*Waste not want not: how to use all the data available: a lesson from Next Generation Sequencing*

This tutorial will cover methods for including important information provided by frequencies in NGS data. We will show how we use these frequencies in mixture models to

− denoise the data and provide precise strain variant information
− find the "right" data transformations for read data that enable the use of statistical models on the downstream analysis.

This tutorial will involve practical tutorials on the use of the dada2 and phyloseq Bioconductor packages. These enable easy denoising, normalization, visualization and testing of Next Generation Sequencing data.
Keynote Speaker: Professor Mark Girolami, Imperial College London; Adjunct, University of Warwick

Mark Girolami is Chair of Statistics in the Department of Mathematics at Imperial College London and Associated Professor in the Department of Computing at Imperial College. He also holds an Adjunct appointment in the Department of Statistics at the University of Warwick. He is an Engineering and Physical Sciences Research Council (EPSRC) Established Career Research Fellow – Mathematics – (2012-2018), and previously an EPSRC Advanced Research Fellow – ICT – (2007-2012). In 2011 he was elected to the Fellowship of the Royal Society of Edinburgh and awarded a Royal Society Wolfson Research Merit Award. From 2015 to 2016 he was seconded to the Executive Board of the Alan Turing Institute (ATI) as one of the Founding Executive Directors. From January 2017 he is the Director of the £10M Lloyds Register Foundation Programme on Data Centric Engineering at the Alan Turing Institute. He is Editor-in-Chief Statistics and Computing and led the EPSRC UK Research Network on Computational Statistics and Machine Learning.

Keynote Presentation

Stochastic Modelling of Urban Structure – A Bayesian Perspective

Urban systems are complex in nature and comprise of a large number of individuals that act according to utility, a measure of net benefit pertaining to preferences. The actions of individuals give rise to an emergent behaviour, creating the so-called urban structure that we observe. In this talk, I develop a stochastic model of urban structure to formally account for uncertainty arising from the attendant complex behaviour. We further use this stochastic model to infer the components of a utility function from observed urban structure. This is a more powerful modelling framework in comparison to the ubiquitous discrete choice models that are of limited use for complex systems, in which the overall preferences of individuals are difficult to ascertain. We model urban structure as a realization of a Boltzmann distribution that is the invariant distribution of a related stochastic differential equation (SDE) that describes the dynamics of the urban system. Our specification of Boltzmann distribution assigns higher probability to stable configurations, in the sense that consumer surplus (demand) is balanced with running costs (supply), as characterized by a potential function. We specify a Bayesian hierarchical model to infer the components of a utility function from observed structure. Our model is doubly-intractable and poses significant computational statistical challenges that we overcome using recent advances in Markov chain Monte Carlo (MCMC) methods. We demonstrate our methodology with case studies on the London retail system and airports in England.
Consider the consequences of an alternative history. What if Leonhard Euler had happened to read the posthumous publication of the paper by Thomas Bayes on “An Essay towards solving a Problem in the Doctrine of Chances”? This paper was published in 1763 in the Philosophical Transactions of the Royal Society, so if Euler had read this article, we can wonder whether the section in his three volume book Institutionum calculi integralis, published in 1768, on numerical solution of differential equations might have been quite different.

Would the awareness by Euler of the “Bayesian” proposition of characterising uncertainty due to unknown quantities using the probability calculus have changed the development of numerical methods and their analysis to one that is more inherently statistical?

Fast forward the clock two centuries to the late 1960s in America, when the mathematician F.M. Larkin published a series of papers on the definition of Gaussian Measures in infinite dimensional Hilbert spaces, culminating in the 1972 work on “Gaussian Measure on Hilbert Space and Applications in Numerical Analysis”. In that work the formal definition of the mathematical tools required to consider average case errors in Hilbert spaces for numerical analysis were laid down and methods such as Bayesian Quadrature or Bayesian Monte Carlo were developed in full, long before their independent reinvention in the 1990s and 2000s brought them to a wider audience.

Now in 2017 the question of viewing numerical analysis as a problem of Statistical Inference in many ways seems natural and is being demanded by applied mathematicians, engineers and physicists who need to carefully and fully account for all sources of uncertainty in mathematical modelling and numerical simulation.

At present we have a research frontier that has emerged in scientific computation founded on the principle that error in numerical methods, which for example solves differential equations, entails uncertainty that ought to be subjected to formal statistical analysis. This viewpoint raises exciting challenges for contemporary statistical and numerical analysis, including the design of statistical methods that enable the coherent propagation of probability measures through a computational and inferential pipeline. This tutorial will present the key developments in the area of Probabilistic Numerics and the research opportunities it presents.
Keynote Speaker: Professor Gael Martin, Monash University

Gael Martin is a Professor of Econometrics in the Department of Econometrics and Business Statistics at Monash University, Melbourne, Australia, and was an Australian Research Council Future Fellow from 2010 to 2013. Her primary research interests have been in the development of simulation-based inferential methods for complex dynamic models in economics and finance. Time series models for long memory, non-Gaussian – including discrete count – data have been a particular focus, with state space representations being central to much of that work. The development of Bayesian simulation-based methods has formed a very important part of her research output, and provides the background for the presentations at Bayes on the Beach. She is currently an Associate Editor of Journal of Applied Econometrics, International Journal of Forecasting (IJF) and Econometrics and Statistics, was a guest editor for a special issue of IJF on Bayesian Forecasting in Economics.

Keynote Presentation

Computing Bayes: Bayesian computation from 1763 to 2017!

From Richard Price’s 1763 presentation to the Royal Society of ‘An Essay Towards Solving a Problem in the Doctrine of Chances’ by the Reverend Thomas Bayes, to 2017 papers on: pseudo-marginal Markov chain Monte Carlo, approximate Bayesian computation, variational Bayes and synthetic likelihood, we take a wild romp through two and a half centuries of Bayesian computation! From Martin Luther and the Protestant Reformation, through to the birth of the Dutch mercantile state, and finishing with an analogy between Bayesian statistics and the French language, get ready for a ride!

Tutorial

Recent advances in Approximate Bayesian Computation: Inference and forecasting

Approximate Bayesian computation (ABC) is becoming an accepted tool for statistical analysis in models with intractable likelihoods. With the initial focus being on the practical import of this algorithm, exploration of its formal statistical properties has begun to attract more attention. After a short review of the technique, I begin by outlining current results on the asymptotic behaviour of posterior distributions obtained by this method, namely: (i) conditions required for Bayesian consistency; (ii) the limiting shape of the posterior; and (iii) the asymptotic distribution of the ensuing posterior mean. Important implications of the theoretical results for practitioners are noted. I then proceed to discuss recent work on the use of ABC as a means of generating probabilistic forecasts, or for conducting what we refer to as ‘approximate Bayesian forecasting’. The four key issues explored are: i) the loss of forecast accuracy incurred when using an approximate rather than an exact forecast distribution; ii) the role played in approximate Bayesian forecasting by Bayesian consistency; iii) the importance of (particle) filtering in latent variable models; and iv) the use of forecasting criteria to inform the selection of ABC summaries in an empirical setting.
Keynote Speaker: Professor Scott Sisson, University of New South Wales

Scott is a Professor in Statistics at the School of Mathematics and Statistics, UNSW, and President of the Statistical Society of Australia. He is interested in computational and Bayesian statistics, particularly for computationally or analytically intractable problems, environmental and climate extremes and applied science. He is not interested in romantic comedies, window shopping or listening to Katy Perry.

Keynote Presentation

Modelling big data fast and on your laptop via symbolic data analysis

Symbolic data analysis (SDA) offers an alternative to divide-and-recombine methods for the analysis of big datasets. It can offer very fast computational speeds, that can easily be run on your laptop on a single core, at the cost of some inferential approximation. The basic idea is to summarise your large dataset into a smaller number of distributional summaries. I will outline some (new) SDA methods for data analysis and illustrate this with a number of toy and real analyses.

Tutorial

"Phew, what a scorcher!" A short introduction to modelling extremes
Many biological problems are concerned with understanding the behaviour of cells, both individually and as part of a larger ensemble. For example, in the developing mammalian embryo, individual cells need to integrate local signals in order to make decisions as to what type of cell they will differentiate into. These individual cell decisions need to be coordinated in such a way as to ensure the development of a functional organism, with its collection of cell types, tissues, and organs, not only in the right proportions but in precisely the correct spatial arrangement. Modern experimental methods now allow for the generation of huge amounts of data from these developing systems. Traditional approaches have typically focussed on modelling this behaviour as an emergent property of the interactions between low-level particles (genes, proteins, receptors, etc.). However, the huge variety and variability of these particles often results in these ‘bottom-up’ approaches becoming extremely difficult, or arguably even impossible, as their scope increases to accommodate the wealth of available data and phenomena. Recent work has shown that many of these problems can be reformulated in an equivalent way that can be recognised as one of Bayesian inference. This provides a framework for the paradigm of ‘top-down’ approaches which enables the application of concepts from Bayesian variational methods in furthering our understanding of these complex systems. The talk will illustrate the challenges, and briefly review the competing methodologies.
Modelling

Bayesian Effect Fusion for Categorical Predictors
Presenter: Helga Wagner
E-mail: Helga.Wagner@jku.at
Author: Helga Wagner
Affiliation: Department of Applied Statistics, Johannes Kepler University Linz

Sparse modelling and variable selection is one of the most important issues in regression type models, as in applications often a large number of covariates on comparably few subjects are available. To identify those regressors which have a non-negligible effect, many methods have been developed, which typically allow selection of single regression coefficients.

However, these methods are not appropriate to achieve a sparse representation of the effect of a categorical covariate, which is captured by a group of level effects. Hence, for a categorical covariate sparsity cannot only be achieved by excluding single irrelevant effects or the whole group of level effects but also by fusing levels which have essentially the same effect on the response.

In a Bayesian approach a sparse representation of the effect of a categorical predictor can be achieved by specifying appropriate prior distributions. We present two different specifications of the prior on level effects: The first is a multivariate Normal distribution with a precision matrix that allows for either almost perfect or almost zero dependence of level effects.

As an alternative we consider a sparse finite mixture prior where a spike at zero is combined with a location mixture of spiky components to allow clustering of level effects. For both priors Bayesian inference is feasible by MCMC methods. Performance of the methods is illustrated on simulated as well as real data from EU-SILC.
**Modelling**

**Bayesian Robustness for Fault Tree Analysis**

Presenter: **Chaitanya Joshi**  
E-mail: cjoshi@waikato.ac.nz  
Authors: **Chaitanya Joshi**¹, Fabrizio Ruggeri² and Simon P. Wilson³  
Affiliations: ¹University of Waikato, Hamilton, New Zealand  
²CNR-IMATI, Milano, Italy  
³Trinity College Dublin, Dublin, Ireland

We propose a prior robustness approach for the Bayesian implementation of the fault tree analysis (FTA). FTA is often used to evaluate risk in large, safety critical systems but has limitations due to its static structure. Bayesian approaches have been proposed as a superior alternative to it, however, this involves prior elicitation, which is not straightforward. We show that minor mis-specification of priors for elementary events can result in a significant prior mis-specification for the top event. A large amount of data is required to correctly update a mis-specified prior and such data may not be available for many complex, safety critical systems. In such cases, prior mis-specification equals posterior mis-specification. Therefore, there is a need to develop a robustness approach for FTA which can quantify the effects of prior mis-specification on the posterior analysis.

Here, we propose the first Bayesian robustness approach specifically developed for FTA. We not only prove a few important mathematical properties of this approach, but also develop easy to use Monte Carlo sampling algorithms to implement this approach on any given fault tree with AND and/or OR gates. We then implement this Bayesian robustness approach on two real life examples: a spacecraft re-entry example and a feeding control system example.
We present a Bayesian statistical approach for detecting climate regime shifts. The proposed algorithm uses Bayesian computational techniques that make time-efficient analysis of large volumes of data possible. Output includes probabilistic estimates of the number and duration of regimes, the number and probability distribution of hidden states, and the probability of a regime shift in any year of the time series. Analysis of the Pacific Decadal Oscillation (PDO) index is provided as an example. Two states are detected: one is associated with positive values of the PDO and presents lower interannual variability, while the other corresponds to negative values of the PDO and greater variability. We compare this approach with existing alternatives from the literature and highlight the exciting prospects for ours to unlock features hidden in climate data.
**Invited Presentation, Monday 13th November, 16:00 - 16:45**

**Professor Peter Donnelly:** Director of the Wellcome Centre for Human Genetics and Professor of Statistical Science at the University of Oxford.

Peter grew up in Australia and on graduating from the University of Queensland he studied for a doctorate in Oxford as a Rhodes Scholar. He held professorships at the Universities of London and Chicago before returning to Oxford in 1996. Peter’s early research work concerned the development of stochastic models in population genetics, including the coalescent, and then the development of computational statistical methods for genetic and genomic data, several of which have been used extremely widely. His current research focuses on understanding the genetic basis of human diseases, human demographic history, and the mechanisms involved in meiosis and recombination.

Peter is a Fellow of the Royal Society and of the Academy of Medical Sciences, and is an Honorary Fellow of the Institute of Actuaries. He is a Fellow of St Anne’s College, and an Honorary Fellow of Balliol College, in Oxford. He has received numerous awards and honours for his research. His TED talk has been downloaded over a million times. Peter also led the Royal Society’s recently released policy study on Machine Learning and its potential for and impact on society.

**Invited Presentation**

*Genomics and big data analytics: routes to improved drug development and better healthcare*

The drug development process is facing major challenges. Only 10% of drug targets taken into clinical trials come through the process to prove efficacious and safe, and gain regulatory approval. The need for pharmaceutical companies to recoup the costs of all the failed trials is one of the reasons behind the large cost of the few successful drugs. One reason given for the high failure rate is that most proposed drug targets arise from studies of non-human systems, with the findings not transferring perfectly across to humans. Human genetic data offers the opportunity to study human biology in humans. The explosion in such data, first from large scale research studies, and then increasingly from healthcare systems, promises to make this a powerful tool for improving drug development pipelines and providing decision support in clinical medicine. The talk will explain how genomics can be useful in this context, outline some of the analytical challenges, and give examples of how largescale genetic data, coupled with health outcomes and other phenotypes, can be used in this way.
Bayesian Sparse-Smooth Modeling and Variational Inference

Presenter: Shunsuke Horii
E-mail: s.horii@aoni.waseda.jp
Author: Shunsuke Horii
Affiliation: Waseda University, Japan

In this work, we present a general hierarchical Bayesian modeling for sparse and smooth signal estimation problem. The point estimation method based on convex programming for the problem is known as fused lasso. Fused lasso and its variants such as graph-guided fused lasso have a wide range of applications such as total variation denoising. Kyung et al. (2010) proposed a hierarchical Bayesian modeling for the lasso problem and developed an estimation procedure based on the Gibbs sampler. Our proposed model is a generalization of the previous work. That deals with more general priors and applicable to the problem of the graph-guided fused lasso. Furthermore, we derive the estimation procedures for the proposed model using variational inference, which is more efficient than the methods based on the Gibbs sampler. Simulation studies and real data analyses show that the proposed method has superior performance to the previous works.
greta: simple and scalable statistical modelling in R
Presenter: Nick Golding
E-mail: nick.golding.research@gmail.com
Author: Nick Golding
Affiliation: University of Melbourne

General purpose MCMC software packages like WinBUGS, JAGS, and STAN enable users to define and fit almost any statistical model without having to worry about implementation details and have enabled significant progress in applied Bayesian modelling. However these existing tools are largely unable to make use of recent advances in hardware and software for high performance computing so they often scale very poorly to large datasets. In addition, the need to specify models using a compiled, domain-specific language is a significant hurdle to potential users and makes it hard for the wider community to extend and build upon these tools.

greta is a new software package for flexible statistical modelling that aims to overcome these limitations. greta uses Google’s TensorFlow high-performance automatic differentiation library, so it scales well to massive data sets (millions of observations), can run across many CPUs or on GPUs. greta models can be fitted using efficient gradient-based MCMC samplers like Hamiltonian Monte Carlo, black-box variational Bayes methods, or maximum likelihood/empirical Bayes methods. greta models are written directly and interactively in R, so greta is easy to learn and straightforward to extend with new R packages or use as a backend for more specific software.

I will demonstrate greta and some extension packages for modelling with Gaussian processes, generalised additive models and dynamical systems. If you want to know more now, see the website: https://greta-dev.github.io/greta
New Insights into History Matching via Sequential Monte Carlo

Presenter: Christopher Drovandi
E-mail: c.drovandi@qut.edu.au
Author: Christopher Drovandi
Affiliation: School of Mathematical Sciences, Science and Engineering Faculty, Queensland University of Technology, Brisbane, Queensland, Australia

The aim of the history matching method is to locate non-implausible regions of the parameter space of complex deterministic or stochastic models by matching model outputs with data. It does this via a series of waves where at each wave an emulator is fit to a small number of training samples. An implausibility measure is defined which takes into account the closeness of simulated and observed outputs as well as emulator uncertainty. As the waves progress, the emulator becomes more accurate so that training samples are more concentrated on more promising regions of the space and poorer parts of the space are rejected with more confidence. Whilst history matching has proved to be useful, existing implementations are not fully automated and some ad-hoc choices are made during the process, which involves user intervention and is time consuming. This occurs especially when the non-implausible region becomes small and it is difficult to sample this space uniformly to generate new training points. In this article we develop a sequential Monte Carlo (SMC) algorithm for implementation which is closer to being fully automated. Furthermore, our novel SMC approach reveals that the history matching method yields a non-implausible distribution that can be multi-modal, highly irregular and very difficult to sample uniformly. Our SMC approach offers a much more reliable sampling of the non-implausible space, which requires additional thought and computation compared to other approaches used in the literature. This is joint work with David Nott and Dan Pagendam.
Mixture models provide a convenient way to describe non-standard densities and model heterogeneous data. However, under certain conditions, inference on Bayesian mixture models becomes impossible due to a phenomenon known as label switching. Therefore, in order to be able to make sensible inference, either label switching must be avoided, or its effects must first be reversed. The former was one of the earliest proposed methods for dealing with label switching, and is sometimes still used today, despite more recent research which exposes the flaws of this method. The ideal approach is to allow label switching to occur and reverse the label switching by means of a relabelling algorithm. In this presentation, a brief history of proposed solutions to the label switching problem is presented, and several long-standing misconceptions are laid to rest. The key contribution of this research is a new relabelling algorithm which makes improvements on two existing state-of-the-art solutions.
Scale-Dependent Priors for Variance Parameters in Structured Additive Distributional Regression
Presenter: Nadja Klein
E-mail: n.klein@mbs.edu
Authors: Nadja Klein\textsuperscript{1} and Thomas Kneib\textsuperscript{2}
Affiliations: \textsuperscript{1}Dr. Nadja Klein, University of Melbourne, Melbourne Business School, 200 Leicester Street, Carlton, VIC, 3053, Australia
\textsuperscript{2}Professor Thomas Kneib, University of Göttingen, Humboldtallee 3, 37073 Göttingen, Germany

The selection of appropriate hyperpriors for variance parameters is an important and sensible topic in all kinds of Bayesian regression models involving the specification of (conditionally) Gaussian prior structures where the variance parameters determine a data-driven, adaptive amount of prior variability or precision. We consider the special case of structured additive distributional regression where Gaussian priors are used to enforce specific properties such as smoothness or shrinkage on various effect types combined in predictors for multiple parameters related to the distribution of the response. Relying on a recently proposed class of penalised complexity priors motivated from a general set of construction principles, we derive a hyperprior structure where prior elicitation is facilitated by assumptions on the scaling of the different effect types. The posterior distribution is assessed with an adaptive Markov chain Monte Carlo scheme and conditions for its propriety are studied theoretically. We investigate the new type of scale-dependent priors in simulations and two challenging applications, in particular in comparison to the standard inverse gamma priors but also alternatives such as half-normal, half-Cauchy and proper uniform priors for standard deviations.
Eliciting and encoding pairwise comparisons: Accounting for exhaustion, incoherence and accuracy

Presenter: Samantha Low-Choy
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Sometimes it’s quite difficult to ask an expert to rate a long list of items. Instead, it may be easier for them to compare the items, one pair at a time. This provides a set of pairwise comparisons. Mathematically we can analyse the comparisons to recover the expert’s underlying mental model: ratings for individual items. Traditionally, the Analytical Hierarchy Process (AHP) has been used to do this in a deterministic fashion. However, we note that AHP places high demands on the expert. (1) They must be exhaustive: and provide a full set of comparisons. With 14 items, we require 91 comparisons! (2) The expert must be coherent, e.g. avoid mistakes like reversing comparisons. (3) The expert must consistently be accurate. Interestingly, very little work has considered relaxing these stringent demands. Here we show how a hierarchical Bayesian model with an extreme-value sampling distribution can help address these issues. We compare the encoded expert’s mental model as more comparisons are used as input. Using posterior predictive checks, we find that models with too few or too many comparisons lead to poorer overall performance: evidence that exhaustive elicitation of pairwise comparisons may be too exhausting! In addition, we can identify any signs of incoherence, and show inaccuracy was non-negligible. This approach provided input to RP’s PhD, on a case study where an ecological expert on a tree species was asked to evaluate relevance of 14 groups of new soil variables, to the species’ geographic distribution.
A Study on Analytical Properties of Bayesian Experimental Design Model based on an Orthonormal System
Presenter: Yoshifumi Ukita
E-mail: ukita@shodai.ac.jp
Authors: Yoshifumi Ukita¹, Shunsuke Horii², Toshiyasu Mtsushima²
Affiliations: ¹Yokohama College of Commerce
²Waseda University

The experimental design is a statistical method to analyze which factors are affecting the results of the target, and what kind of value should be set for the factor to improve the results. As it is quite likely that the researcher has prior knowledge of some aspect of the planned experiment, the Bayesian experimental design has received much attention over the last two decades. In machine learning fields, Bishop [1] introduced some analytical properties of Bayesian methods through models made from linear combinations of basis functions. As for the model of the experimental design, the traditional models are often expressed through the effect of each factor. On the other hand, it was also shown that the models can be expressed in terms of orthonormal basis functions by using complex Fourier coefficients, making all parameters independent. In this paper, analytical properties of Bayesian experimental models based on an orthonormal system is presented. Using the results of [1], it is shown that the posterior distribution and predictive distribution can be analytically derived within a Bayesian framework.

Model-Based Adaptive Design Methods for Improving the Effectiveness of Reef Monitoring

Presenter: Thilan AWLP  
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Authors: Thilan AWLP, McGree JM, Peterson EE, and Drovandi CC  
Affiliation: School of Mathematical Sciences, Science and Engineering Faculty, Queensland University of Technology, Brisbane, Queensland, Australia

This study aims to develop an innovative adaptive modelling and sampling framework to improve the effectiveness of monitoring the Great Barrier Reef (GBR). An indicator of reef health is coral cover, and we consider a Beta regression model for this response where the linear predictor for the mean includes a spatial random effect. In adaptive monitoring, one needs to decide which location should be visited next in order to collect highly informative data as measured by a utility function. In our work, such a utility function measures the precision of predictions of coral cover at unobserved locations. In general, estimating the expectation of this utility function is challenging as it requires sampling from or approximating a large number of posterior distributions. Thus, computationally efficient methods are needed, and we propose the Laplace approximation for this purpose. To find the next location which maximizes our utility function, we use the approximate coordinate exchange algorithm. Our work focuses on developing a design that compromises between the parameter estimation and spatial prediction. The effectiveness of our adaptive sampling design is evaluated against the Long Term Monitoring Program of the GBR which has been running for the last 20 years.

**Keywords:** Adaptive sampling, Approximate Coordinate Exchange, Beta Regression, Gaussian kriging, Reef monitoring
Design

Dual-purpose Bayesian design for parameter estimation and model discrimination of models with intractable likelihoods
Presenter: Mahasen B. Dehideniya
E-mail: d.mahasen@hdr.qut.edu.au
Authors: Mahasen B. Dehideniya, Christopher C. Drovandi, James M. McGree
Affiliation: School of Mathematical Sciences, Science and Engineering Faculty, Queensland University of Technology, Brisbane, Queensland, Australia

In this work, we propose a methodology based on total entropy to design dual-purpose experiments for parameter estimation and model discrimination for epidemiological models with computationally intractable likelihoods. Our methodology is based on a novel synthetic likelihood approach to approximate the likelihood of discrete observations of a stochastic process and to approximate the total entropy utility function. We consider two stochastic processes namely the Susceptible-Infected-Recovered model and the Susceptible-Exposed-Infected-Recovered which are used to model the foot and mouth disease. The model discrimination and parameter estimation properties of the designs were compared against optimal choices under the mutual information utility for model discrimination and the Kullback-Leibler divergence utility for parameter estimation. The results suggest that these dual-purpose designs perform efficiently under both experimental goals.

Keywords: Foot and mouth disease, Kullback–Leibler divergence, Mutual Information, Synthetic likelihood, Total entropy
The Block Pseudo-Marginal Sampler
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The Pseudo-Marginal (PM) approach is increasingly used for Bayesian inference in models where the likelihood is intractable but can be estimated unbiasedly. Deligiannidis et al. (2017) show how the PM approach can be made much more efficient by correlating the underlying Monte Carlo random numbers used to form the estimate of the likelihood at the current and proposed values of the unknown parameters. Their approach greatly speeds up the standard PM algorithm, as it requires a much smaller number of samples or particles to form the optimal likelihood estimate. Our paper presents an alternative implementation of the correlated PM approach, called the block PM, which divides the underlying random numbers into blocks so that the likelihood estimates for the proposed and current values of the parameters only differ by the random numbers in one block. We show that this implementation can be more efficient for some specific problems than the implementation in Deligiannidis et al. (2017); for example when the likelihood is estimated by subsampling or the likelihood is a product of terms each of which is given by an integral which can be estimated unbiasedly by randomised quasi-Monte Carlo. Our article provides methodology and guidelines for efficiently implementing the block PM. A second advantage of the block PM is that it provides a direct way to control the correlation between the logarithms of the estimates of the likelihood at the current and proposed values of the parameters than the implementation in Deligiannidis et al. (2017).

Hamiltonian Monte Carlo with Energy Conserving Subsampling
Presenter: Khue-Dung Dang
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Authors: Khue-Dung Dang\textsuperscript{1,2}, Matias Quiroz\textsuperscript{1,2}, Robert Kohn\textsuperscript{1,2}, Minh-Ngoc Tran\textsuperscript{1,2} and Mattias Villani\textsuperscript{4,2}
Affiliations: \textsuperscript{1}School of Economics, University of New South Wales Business School
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Hamiltonian Monte Carlo (HMC) has recently received considerable attention in the literature due to its ability to overcome the slow exploration of the parameter space inherent in random walk proposals. In tandem, data subsampling has been extensively used to overcome the computational bottlenecks in posterior sampling algorithms that require evaluating the likelihood over the whole data set, or its gradient. However, while data subsampling has been successful in traditional MCMC algorithms such as Metropolis-Hastings, it has been demonstrated to be unsuccessful in the context of HMC, both in terms of poor sampling efficiency and in producing highly biased inferences. We propose an efficient HMC-within-Gibbs algorithm that utilizes data subsampling to speed up computations and simulates from a slightly perturbed target, which is within $O(m^{-2})$ of the true target, where $m$ is the size of the subsample. We also show how to modify the method to obtain exact inference on any function of the parameters. Contrary to previous unsuccessful approaches, we perform subsampling in a way that conserves energy but for a modified Hamiltonian. We can therefore maintain high acceptance rates even for distant proposals. We apply the method for simulating from the posterior distribution of a high-dimensional spline model for bankruptcy data and document speed ups of several orders of magnitude compare to standard HMC and, moreover, demonstrate a negligible bias.
**Using Boosted Regression Trees and remotely sensed data to drive decision-making**
Presenter: Brigitte Colin  
E-mail: b.colin@qut.edu.au  
Authors: Brigitte Colin, Samuel Clifford, Paul Wu, Samuel Rathmanner, Kerrie Mengersen  
Affiliation: ARC Centre of Excellence for Mathematical and Statistical Frontiers, School of Mathematical Sciences QUT, Brisbane, Australia

Analysing Big Data is challenging due to the way they stored, maintained and processed and recorded. For our modelling approach it was required to bring all the data together in order to create one common data basis. This resulted in a structured but noisy dataset showing inconsistencies and redundancies. Here we show that BRT’s can process different data granularities, heterogeneous data and in general data showing Big Data properties with satisfying results and an acceptable processing time. We found in using a flexible, hierarchical, multivariate statistical machine learning algorithm, namely Boosted Regression Tree (BRT), there is a remarkable capability of addressing Big Data challenges. BRT have the advantage of dealing with missing data by default. Most importantly, BRT offers a wide range of possibilities to interpret results and make the performance more transparent and the explanatory variables can be tracked along the tree branches based on the splitting rules. Our results demonstrate that BRT are flexible in dealing with missing data, provide satisfying results in an acceptable processing time, as well as provide beneficial interpretation tools which will ultimately assist in a more confident decision making. A comparison with two similar regression models namely Random Forest and Least Absolute Shrinkage and Selection Operator (LASSO) show less flexibility and less satisfying performance using the same data input. We anticipate BRT to be a starting point for sophisticated hierarchical modelling in real world scenarios assisting decision makers around the world.

**Keywords:** Boosted Regression Trees, remotely sensed data, Big Data modelling approach, missing data.

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**Bayesian Multivariate Detection Limit and its Associated Uncertainty**
Presenter: Basim Saleh O Alsaedi  
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Authors: Basim Saleh O Alsaedi, Peter Dillingham, Christina McGraw, Timothy Schaerf  
Affiliations: 1University of New England; Australia  
2University of Otago; New Zealand  
3University of Tabuk, Saudi Arabia

Detection capability represent an important characteristic of the instrumental measurement process. However, detection limit suffers from inconsistency in its definitions and calculations due to decades-long debate of how the calibration problem should be solved. Recently, several groups have argued for consistent and probabilistic definitions for LOD, and developed estimation procedures for univariate and relatively simple multivariate data structures. In this work, the Bayesian methods are used to calculate detection threshold and detection limit for non-linear or multivariate data structure. We will show how Bayesian calibration methods provide a natural approach to estimating LOD for a multi-sensor array, demonstrating our approach using an array of ion-selective electrodes measuring lead in soil.
Accelerating Bayesian Synthetic Likelihood with the Graphical Lasso
Presenter: Ziwen An
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Authors: Ziwen An1,2, David J. Nott3 and Christopher C. Drovandi1,2
Affiliations: 1School of Mathematical Sciences, Queensland University of Technology, Australia
2Australian Research Council Centre of Excellence for Mathematical and Statistics Frontiers
3Department of Statistics and Applied Probability, National University of Singapore

As a simulation-based method, approximate Bayesian computation (ABC) can be used for problems where model simulation is available, without the evaluation requirement of the likelihood function. ABC keeps parameter values that guide the simulated data close to the observed data on the basis of a carefully chosen summary statistic. Despite having wider usage, ABC does encounter problems such as low efficiency, the curse of dimensionality with respect to the size of the summary statistic and requiring a lot of tuning parameters. One of the methods that tackle these problems is called Bayesian synthetic likelihood (BSL) (Price et al 2017). The main idea of BSL is to assume the summary statistic to be Gaussian. As a consequence, we only need to estimate the mean and covariance of the summary statistic at each iteration to approximate the Gaussian likelihood. The only tuning parameter required is n, the number of simulations per iteration to estimate the mean and covariance. However, the value of n still needs to be large depending on the size of the summary statistic because the sample covariance performs poorly as an estimator when n is small. Motivated by this, we propose to use the graphical lasso to estimate the covariance as it can have a significantly smaller risk for small to moderate n. In addition, the sparsity assumption of the graphical lasso is likely to be reasonable in many likelihood-free applications. In this talk, I will demonstrate how our method BSLasso improves the computational efficiency comparing to standard BSL with only one additional tuning parameter, the penalty parameter of the graphical lasso. This is joint work with David J. Nott and Christopher C. Drovandi.

Bayesian modelling of temporal dependence for bivariate survival data using copulas
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2Department of Statistics, University of Auckland, New Zealand

Copula models have become increasingly popular for modelling the dependence structure in multivariate survival data. In this work we explore a Bayesian approach to estimate the temporal association between bivariate survival times. We consider models belonging to the Archimedean family of copulas as dependence structure and piecewise exponential distributions for modelling the marginal distributions. The temporal dependence is defined so that the copula association parameter varies in time. For the estimation, we assume a two-step procedure. In a first step, from a Bayesian approach, we estimate the marginals survival function considering the bivariate lifetimes independents and following piecewise exponential distributions. Next, the estimation of the copula dependence parameter is carried out using a temporal factorization of the likelihood function and an autoregressive distribution of first order as prior distribution. The dynamic dependence is quantified through the Kendall’s tau coefficient. We illustrate the methodology using paired data from a study of laser photocoagulation therapy for retinopathy in diabetic patients.
Efficient Use of Derivative Information within SMC Methods for Static Bayesian Models

Presenter: Leah Price
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Affiliation: ¹School of Mathematical Sciences, Queensland University of Technology, Australia
²Australian Research Council Centre of Excellence for Mathematical and Statistics Frontiers
³School of Mathematical Sciences, University College, Dublin, Belfield, Ireland
⁴The Insight Centre for Data Analytics

Sequential Monte Carlo (SMC) is a powerful method for sampling from the posterior distribution of static Bayesian models and estimating the evidence for model choice. SMC applies reweighting, resampling and mutation steps to transition a population of particles through a sequence of distributions. The mutation step has the most impact on the computational and statistical efficiency of SMC and is often performed via several iterations of a Markov chain Monte Carlo (MCMC) kernel. We propose to make efficient use of the derivatives of the log posterior with respect to the parameters, which are available either in closed form or can be unbiasedly estimated for a large class of problems. Derivative information is used in the move step through Metropolis adjusted Langevin algorithm (MALA) moves, and we develop a new approach to adapt the tuning parameters of MALA based on the population of particles. We apply post-processing steps using zero-variance control variates to lower the variance of expectations with respect to the posterior and of two alternative evidence estimators. We demonstrate that our approach can lead to more precise estimates of the evidence and improved posterior expectations when compared to a more standard implementation of SMC.

This is joint work with Tony Pettitt, Nial Friel and Christopher Drovandi.

Bayesian methods for sensors with non-linear responses

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Authors: Peter Dillingham¹,², Basim Saleh O Alsaedi²,³, Christina McGraw¹,²
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²University of New England; Australia
³University of Tabuk, Saudi Arabia

Modern, deployable sensors often push the boundaries of traditional analytical methods. These sensors and the larger sensing systems that incorporate them are likely to be noisy, be deployed in challenging environments, and operate outside the linear range. As such, standard analytical techniques developed for laboratory-based sensors operating in the linear range do not adequately describe uncertainty in key measurands, e.g. analyte concentration, for these devices. Ion-selective electrodes (ISEs) are chosen as a model device to demonstrate these issues. Many ISEs, such as the pH probe, are well described and typically operate in the linear range of their response. However, recently developed ISEs often measure samples in complex chemical matrices, e.g. blood or soil, and operate near detection boundaries requiring analysis using the non-linear Nikolskii-Eisenman Equation. This becomes further complicated when coupled with standard addition techniques to combat electrode drift or when combining information from multiple sensors. We demonstrate the benefit of Bayesian methods for analysis of these next-generation sensors, both in terms of gaining an appropriate understanding of uncertainty in measurands and for their flexibility in accommodating different data structures.
Bayesian sequential design for Copula models: a comparison of designs selected under different Copula models
Presenter: Senarathne SGJ
E-mail: j.gedara@qut.edu.au
Authors: Senarathne SGJ, Drovandi CC, and McGree JM
Affiliation: School of Mathematical Sciences, Science and Engineering Faculty, Queensland University of Technology, Brisbane, Queensland, Australia

Copula models provide flexible structures to derive the joint distribution of multivariate responses. However, they are rarely considered in the experimental design context, particularly in a Bayesian framework where model and parameter uncertainty are considered. Here, we explore a variety of such models which explain dependence structures in experiments where bivariate mixed responses are observed. The sequential Monte Carlo algorithm is adopted to reduce the computational effort required in deriving efficient sequential designs. Moreover, the performance of the total entropy utility function is evaluated under different Copula models, which allows us to derive designs for the dual objectives of parameter estimation and model discrimination for Copula models. We illustrate our findings by considering an application in pharmacology with mixed outcomes.

Keywords: Model discrimination, Parameter estimation, Sequential design, Sequential Monte Carlo, Total entropy, Utility function.

To be or not to be (Bayesian) Non-Parametric: A tale about Stochastic Processes
Presenter: Roy Costilla
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Authors: Roy Costilla1, Ivy Liu2, and Richard Arnold2
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2Victoria University of Wellington, Wellington, New Zealand

Thanks to the advances in the last decades in theory and computation, Bayesian Non-Parametric (BNP) models are now use in many fields including Biostatistics, Bioinformatics, Linguistics and many others. Despite its name however, BNP models are actually massively parametric. A parametric model uses a function with a finite dimensional parameter vector as prior. Bayesian inference then proceeds to approximate the posterior of these parameters given the observed data. In contrast to that, a BNP model is defined on an infinite dimensional probability space thanks to the use of a stochastic process as a prior. In other words, the prior for a BNP model is a space of functions with an infinite dimensional parameter vector. Therefore, instead of avoiding parametric forms, BNP inference uses a large number of them to gain more flexibility.

To illustrate this, we present simulations and also a case study where we use life satisfaction in NZ over 2009-2013. We estimate the models using a finite Dirichlet Process Mixture (DPM) prior. We show that this BNP model is tractable, i.e. is easily computed using Markov Chain Monte Carlo (MCMC) methods; allowing us to handle data with big sample sizes and estimate correctly the model parameters. Coupled with a post-hoc clustering of the DPM locations, the BNP model also allows an approximation of the number of mixture components, a very important parameter in mixture modeling.
A Review of Bayesian Statistical Methods Applied to Big Data
Presenter: Farzana Jahan
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Authors: Farzana Jahan and Kerrie Mengersen
Affiliations: 1PhD Student, Science and Engineering Faculty, Queensland University of Technology
2Australian Laureate Fellow and Distinguished Professor, Science and Engineering Faculty, Queensland University of Technology

The Modern era is characterized as an era of information or Big Data. Big data in different fields such as health, sociology, science, engineering, business, information Technology, Law and Policy making etc. are being analysed to assist in better decision making. In a review of the literature, we have found that most articles are focused on computational algorithms, optimization and machine learning, with much less emphasis on the development of statistical models, in particular Bayesian approaches. We present a review of published studies that present Bayesian statistical models specifically for Big Data and discuss the reported and perceived benefits of these approaches. We conclude by addressing the question of whether focusing only on improving computational algorithms and infrastructure will be enough to face the challenges of big data.

What does NAPLAN mean to stakeholders? An exercise in elicitation
Presenter: Daniela Vasco
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Authors: Daniela Vasco, Judy Rose, Parlo Singh, Samantha Low-Choy
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2Griffith Institute of Educational Research, Griffith University
3Griffith Behavioural and Social Statistics Unit, Griffith University

Large quantities of data on educational performance are now routinely produced, analysed and used to inform policy and decision-making at different scales by schools, governments and international organisations. This is not only transforming the ways in which schooling gets done, but affects the production of knowledge about schools and systems. National and international educational testing regimes, such as NAPLAN and PISA, are important because they enable an overview of students’ and schools’ performance within and across countries. They also help identify schools and students that require more funding, resources or extra support. However, these reported statistics have been criticised regarding their use as a measure of performance, particularly affecting schools and students in disadvantaged areas. This study aims to find out how the results of the NAPLAN test are being interpreted by different stakeholders, such as academics, principals, teachers and parents. In order to capture this information we will apply expert elicitation techniques, being careful to manage heuristics and biases identified in the relevant cognitive psychology literature. The cognitive psychology is considered as it applies to how individuals are interpreting numeric information, for example whether proportions are more accurately interpreted when expressed in terms of their numerator and denominator or directly, as a proportion. This study reports on initial findings after interviewing academics that are also principals, teachers and/or parents of students that have done NAPLAN tests. This approach will enable a deeper understanding of the strengths and limitations of the NAPLAN reports provided to schools and parents.
Cell-type specific methylation analysis of heterogeneous methylation signal
Presenter: Daniel W. Kennedy
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Epigenome-wide association studies are often performed using heterogeneous methylation samples, especially when there is no prior information as to which cell-types are disease associated. While much work has been done on estimating cell-type fractions and removing cell-type heterogeneity variation, relatively little work has been done on identifying cell-type specific variation in heterogeneous samples. We present a Bayesian model-based approach for making cell-type specific inferences in heterogeneous settings, by using a logit transform to properly constrain parameters, and incorporating a prior knowledge of cell-type lineage via prior covariance structure. The approach was applied to the determination of sex-specific cell-type effects in methylation, where cell-type information was present as an independent verification of the results. The approach showed significant improvement in performance over previously used methods, particularly for detecting association in several rare cell-types.

Age dependent network dynamics via Bayesian hierarchical models reveal spatio-temporal patterns of neurodegeneration
Presenter: Marcela Cespedes
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Authors: Marcela Cespedes 1,2, James McGree 3, Chris Drovandi 1, Kerrie Mengersen 1, James Doecke 2, Jurgen Fripp 2
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The degeneration of the cerebral cortex is a complex process which often spans decades. This degeneration can be evaluated on regions of interest (ROI) in the brain through probabilistic network analysis. However, current approaches for finding such networks have the following limitations: 1) analysis at discrete age groups cannot appropriately account for connectivity dynamics over time; and 2) morphological tissue changes are seldom unified with networks, despite known dependencies. To overcome these limitations, a probabilistic dynamic wobbled model is proposed to simultaneously estimate ROI cortical thickness and network continuously over age, and was compared to an age aggregated model. The inclusion of age in the network model was motivated by the interest in investigating the point in time when connections alter as well as the length of time required for changes to occur. Our method was validated via a simulation study, and applied to healthy controls (HC) and clinically diagnosed Alzheimer’s disease (AD) groups. The probability of a link between the middle temporal (a key AD region) and the posterior cingulate gyrus decreased from age 55 (posterior probability > 0.9), and was absent by age 70 in the AD network (posterior probability < 0.12). The same connection in the HC network remained present throughout ages 55 to 95 (posterior probability ≥ 0.75). The analyses presented in this work will help practitioners choose suitable statistical methods to identify key points in time when brain covariance connections change, in addition to morphological tissue estimates, which could potentially allow for more targeted therapeutic interventions.
Bayesian modelling of transpiration rate response to atmospheric stress of 27 mature sorghum lines
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Sorghum is a crop well adapted for dryland grain production in the tropics. The stress physiology of Queensland and international lines has been studied in lysimeters at Gatton. Twenty seven lines were grown and data was collected on total hourly evaporation of green leaf area on two completely sunny days from 6:00 am to 1:00 pm. A nonlinear relationship in transpiration response to environmental stress was observed for increasing vapour pressure deficit (kPa) of the atmosphere. It is hypothesised that the relationship follows two linear phases. The first linear phase is a response of transpiration per green leaf area to increasing environmental stress (VPD) while the second appears to be where transpiration is possibly limited by radiation.

The hypothesised broken stick relationship was analysed using nls, rjags and rstan in R. To stabilise the variance, the log of the hourly transpiration response variable was employed. A series of models were fitted to assess differences in model parameters across genotypes. Several parameters (changepoint, intercept and slope of the first segment slope slope1) varied across sorghum lines while the slope of the second segment was common across all genotypes.

A Bayesian approach modelled the relationship using hierarchical models to examine the changepoint, intercept and slope1 across genotypes. A mixture model was also employed to ascertain evidence of genotype grouping. However, the results were not clear.

In addition to presentation of methods and results, several issues will be outlined including convergence, computational efficiency, back-transforming the mean response and model comparison.

Assessing record linkage accuracy using similarity weight matrix with Markov chain based Monte Carlo simulation approach
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Record linkage is the process of finding matches and linking records from different data sources so that the linked records belong to the same entity. There is an increasing number of applications of record linkage in statistical, health, government and business organisations to link administrative, survey, population census and other files to create a complete set of information for more complete and comprehensive analysis. Despite this increase, there has been little work on developing tools to assess the quality of linked files. Ensuring that the matched records in the combined file actually correspond to the same individual or entity is crucial for the validity of any analyses and inferences based on the combined data. In our last paper, we proposed a Markov Chain based Monte Carlo simulation method for assessing linkage accuracy and illustrates the utility of the approach using the ABS (Australian Bureau of Statistics) synthetic data in realistic data settings. In our method, an agreement matrix is created from all linking variable across all records in the two linked files and then simulates for generating re-sampled versions of the agreement matrix. In this paper, with the aim of improving our existing method, we used similarity weight in the agreement matrix. This weight allows partial agreement of the linking variable values for record pairs in the form of similarity weight. To assess the average accuracy of linking, correctly linked proportions are investigated for each record. Test results show strong performance of the improved method of assessment of accuracy of the linkages.
Prediction of QUT HDR Student Outcomes
Presenter: Hugh Andersen
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Significant time, money and resources are invested in HDR degrees by both students and QUT so it is beneficial to understand how students interact with QUT and what influences whether they pass or fail. Factor analysis, K means clustering and classification methods have been used in the research.

Spectral density estimation of LIGO gravitational wave data using an AR-enhanced Whittle likelihood
Presenter: Renate Meyer
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Author: Renate Meyer¹, Claudia Kirch², Matthew Edwards¹, Alexander Meier²
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The detection of gravitational waves by the advanced LIGO detectors on September 14, 2015, was a landmark moment for science, a testament to both theoretical and experimental physics, and came about 100 years after the prediction of gravitational waves by Albert Einstein in 1916. Sophisticated MCMC techniques have been used to compute the posterior distribution of the gravitational wave signal parameters, see e.g. Abbott et al. (2016), Meyer and Christensen (2016). The interferometer measurements are subject to various noise components, incl. seismic, thermal, and shot noise. So far, the noise has been assumed to be stationary Gaussian with known power spectral density, estimated by Welch method from a separate stretch of data, close to but not including the observations that contain the signal. However, this is unrealistic as the LIGO spectral density is time-varying and contains sharp peaks and high power, narrow band spectral noise lines.

Here we suggest a novel Bayesian nonparametric approach to spectral density estimation that is based on a generalization of Whittle’s likelihood approximations. It makes use of a parametric AR model via a nonparametric correction of the Whittle likelihood in the frequency domain. We prove contiguity and posterior consistency for Gaussian stationary time series and demonstrate in a simulation study that this technique takes advantage of the efficiency of parametric models while mitigating sensitivities, making it robust against model misspecifications. For the LIGO data, this AR-enhanced nonparametric spectral density estimate is able to estimate the sharp peaks and spectral lines.
Scalable Dirichlet process mixture models for analysis of big data
Presenter: Insha Ullah
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Author: Insha Ullah, Kerrie Mengersen
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Due to their conceptual simplicity and flexibility, non-parametric mixture models are widely used to identify latent clusters in data. However, when it comes to Big Data, such as Landsat imagery, such model fitting is computationally prohibitive. To overcome this issue, we fit Bayesian non-parametric models to pre-smoothed data, thereby reducing the computational time from days to minutes, without disregarding much of the useful information. Tree based clustering is used to partition the clusters into smaller and smaller clusters in order to identify clusters of high, medium and low interest.

The method is applied to Landsat images from the Brisbane region, which were also the original motivation for the development of the method. The images are taken as a part of the red imported Fire ants eradication program that was launched in September 2001 and is funded by all Australian states and territories, along with the federal government. To satisfy budgetary constraints, modelling is performed to estimate the risk of incursion in each region so that the eradication programme focuses on high risk regions. The likelihood of containment is successfully derived by combining the fieldwork survey data with the results obtained from the proposed method.

Sparse estimates from dense precision matrix posteriors
Presenter: Beatrix Jones
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Author: Beatrix Jones and Amir Bashir
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A variety of computationally efficient Bayesian models for the covariance matrix of a multivariate Gaussian distribution are available. However, all produce a relatively dense estimate of the precision matrix, and are therefore unsatisfactory when one wishes to use the precision matrix to consider the conditional independence structure of the data. This talk considers the posterior of model fit for these covariance models. We then undertake post-processing of the Bayes point estimate for the precision matrix to produce a sparse model whose expected fit lies within the upper 95% of the posterior over fits. The impact of the method for selecting the zero elements of the matrix, and the initial covariance model, are considered. Model selection based on credible intervals for the elements of the precision matrix is typically the preferred method, although using relatively low credible levels. Bayesian Adaptive Lasso, inverse Wishart, and Bayesian factor models were considered for generating the posterior, with Bayesian Adaptive Lasso leading to the sparsest results. We illustrate our findings with moderate dimensional data examples from finance and metabolomics.
Focused Econometric Estimation: The interplay between the Bayesian and frequentist approaches
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Central to many econometric inferential situations is the estimation of non-linear functions of parameters. The mainstream in econometrics estimates these quantities based on a plug-in approach without consideration of the main objective of the inferential situation. We propose the Bayesian Minimum Expected Loss approach focusing explicitly on the function of interest, and calculating its frequentist variability. Simulation exercises show that our proposal outperforms competing alternatives in situations characterized by small sample sizes and noisy models. In addition, we observe in the applications that our approach gives lower standard errors than frequently used alternatives.

Model-based socio-economic health measures using causal modelling
Presenter: Fui Swen Kuh
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This research attempts to develop model-based socio-economic health measures using statistical causal inference and modelling. There is a growing consensus for an alternative measure to Gross Domestic Product (GDP) for a country’s socio-economic health. Many conventional ways of constructing the health indices involve combining different observable metrics to form an index. However, the ‘health’ of a society is inherently latent, with the metrics being observable indicators of health. Much effort has been attempted to provide this alternative measure but none to our knowledge so far that uses a model-based approach to reflect the latent health. To take this into account, we adopt the latent health factor index (LHFI) approach that has been used in assessing ecological health. This framework integratively models the relationship between metrics, the unobservable latent health, and the covariates that drive the notion of health. Moreover, we are extending the LHFI approach by integrating it with statistical causal modelling to investigate the causes and effects embedded in the factors influencing health and the metrics. We implement our model using data pertaining to different aspects of societal health and potential explanatory variables. The approach is structured in a Bayesian hierarchical framework and the results obtained by applying Markov Chain Monte Carlo (MCMC) techniques. The resulting health measures aim to provide a holistic quantification of the overall ‘health’ of a society.
Automated Sensitivity Computations for MCMC Gibbs Output
Presenter: Liana Jacobi
E-mail: ljacobi@unimelb.edu.au
Authors: Liana Jacobi, Mark Joshi, Dan Zhu
Affiliation: Department of Economics, University of Melbourne

While recent advances in computational power have made the Bayesian approach a feasible and attractive alternative tool to the classical estimation approach to investigate a diverse range of empirical problems in economics and other areas, it is often applied hesitantly. The main reason aside from the computational complexity is the element of subjectivity involved through the required specification of prior beliefs for all model parameters. The researcher has to specify prior distributions for all model parameters and their associated parameters, so-called hyper-parameters. The extra information is often difficult to specify reliably. Knowledge about sensitivity of the MCMC output contains important information regarding the robustness of the estimation results. While the importance of a comprehensive local sensitivity analysis is often acknowledged, it is a non-trivial task given the complex form of the posterior distribution and currently not part of standard Bayesian analysis. If any sensitivity analysis is undertaken in current work, it typically is done via a bumping-type approach by rerunning the model with a small set of different inputs and observing whether or how the outputs change. This is a computationally very costly and problematic when we have discontinuities in the sampler.

In this paper we introduce a general and flexible approach to undertake a comprehensive prior input sensitivity analysis for output from Bayesian MCMC analysis to assess the robustness of (i) posterior estimates to all prior hyper-parameters and (ii) MCMC parameter draws with respect to all starting values (chain convergence). The sensitivities are computed via embedded sensitivity algorithms that build on recent developments in sensitivity analysis of high-dimensional numerical integrals based on automatic numerical differentiation methods for output obtained via classical simulation methods. The basic idea consists of using automatic algorithms to differentiate the MCMC algorithm to evaluate the integral to obtain the posterior distribution. A key requirement of algorithmic differentiation is the continuity of the algorithm. We show how to address issues of discontinuities that arise in the context of common random variable updates in Gibbs algorithms, the Gamma and Wishart updates. Different from existing methods, the approach enables researchers to compute sensitivities with respect to both the complete set of prior hyper-parameters as well as the complete set of starting values required to initiate the MCMC chain. Further, as part of the algorithmic differentiation the complete set of partial derivatives (all inputs) is computed for all parameters (draws) at every iteration of the chain. The latter contain important information to monitor the convergence behaviour of the chain.

The paper introduces a new set of direct measures of chain convergence based on the starting value sensitivities of all parameters that will help to assess chain convergence directly and set a reasonable burn-in period. The measures will complement existing measures of algorithm efficiency based on the autocorrelations of the draws.

To test and illustrate the new methods, we have implemented sensitivity analysis both with respect to the prior hyper-parameters and MCMC chain starting values in the context of the Gibbs estimation of linear and student-t regression models as well as joint models in simulated and real data experiments. While overall prior parameters sensitivities are small in our real data applications, partially a results of large sample sizes, the sensitivities vary both across parameters within a model and across models. The developed convergence measures show the fastest convergence of the Gibbs sampler for the linear model and the slowest convergence for the Gibbs sampler of the Joint Model. The latter has a particularly slow convergence if a full covariance matrix is chosen to start of the chain, requiring 10,000 iterations as a burn-in period. We also show that our sensitivity estimates of the posterior means with respect to the hyper-parameters are comparable to those obtained via the likelihood ratio approach, but are faster to converge and more stable.

Keywords: automatic differentiation, Gibbs sampler, local sensitivity analysis, MCMC analysis, prior hyper-parameters, robustness analysis, starting values

JEL Codes: C11, C02, C50, C60
Modelling developmental trajectories of children with disabilities
Presenter: Patricia Gilholm
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Author: Patricia Gilholm
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As part of my PhD project I am investigating methods for clustering developmental milestones of children with rare and heterogeneous disabilities, to identify children with similar developmental trajectories. The motivation for conducting this research is that there is often differences in treatment response and symptom expression amongst children with identical diagnoses. Therefore, by clustering developmental milestones in the early years of life, we hope to identify the similarities and differences in development between and within diagnoses. My poster will outline the statistical methods used for modelling mixtures of multivariate longitudinal data. The poster will describe my research problem which involves clustering of small heterogeneous samples, temporal dependency and dependency between outcomes. I will outline the difficulties associated with modelling this complex data structure and will present the possible solutions to these problems, including the use of Bayesian estimation methods for inference.

ABC model selection for spatial max-stable models applied to South Australian maximum temperature data
Presenter: Marus Hainy
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Max-stable processes are a common choice for modelling spatial extreme data as they arise naturally as the infinite-dimensional generalisation of multivariate extreme value distributions. Statistical inference for such models is complicated by the intractability of the multivariate density function. Nonparametric and composite likelihood-based approaches have been proposed to address this difficulty. More recently, a simulation-based approach using approximate Bayesian computation (ABC) has been employed for estimating parameters of max-stable models. ABC algorithms rely on the evaluation of discrepancies between model simulations and the observed data rather than explicit evaluations of computationally expensive or intractable likelihood functions. The use of an ABC method to perform model selection for max-stable models is explored. Four max-stable models are considered: the extremal-t model with either a Whittle-Matérn, Cauchy or powered exponential covariance function, and the Brown-Resnick model. The method is applied to annual maximum temperature data from 25 weather stations dispersed around South Australia.
Now you see it? Now you don’t? The role of graphics in identifying MCMC convergence
Presenter: Nicholas Tierney
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Traceplots and density plots are often used to determine convergence of an MCMC chain in a Bayesian model. There are, however, many ways to describe convergence, and not all of them are graphical. In this truly interactive poster we live-test whether people can visually identify convergence using a lineup approach to answer the questions:

1. Can individuals visually identify convergence?
2. Are some visualisations better than others for identifying convergence?
3. Are there other methodologies for identifying convergence that are better than others?
4. Is being able to identify convergence dependent upon a person’s experience with Bayesian statistics?

Multivariate Bayesian Sparse Group Selection with Spike and Slab
Presenter: Matthew Sutton
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We propose two multivariate extensions of the Bayesian group lasso for variable selection and estimation for data with high dimensional predictors and multi-dimensional response variables. The methods utilize spike and slab priors to yield solutions which are sparse at either a group level or both a group and individual feature level. The incorporation of group structure in a predictor matrix is a key factor in obtaining better estimators and identifying associations between multiple responses and predictors. The approach is suited to biological studies where the response is multivariate, and each predictor is embedded in some biological grouping structure such as gene pathways. Our Bayesian models are connected with penalized regression, and we prove both oracle and asymptotic distribution properties under an orthogonal design. We derive efficient Gibbs sampling algorithms for our models and provide the implementation in a comprehensive R package called MBGSGS available on the CRAN. The performance of the proposed approaches is compared to state-of-the-art variable selection strategies on simulated data sets. The proposed methodology is illustrated on a genetic dataset in order to identify markers grouping across chromosomes that explain the joint variability of gene expression in multiple tissues.
Effective online Bayesian phylogenetics via sequential Monte Carlo with guided proposals
Presenter: Mathieu Fourment
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Modern infectious disease outbreak surveillance produces continuous streams of sequence data which require phylogenetic analysis as data arrives. Current software packages for Bayesian phylogenetic inference are unable to quickly incorporate new sequences as they become available, making them less useful for dynamically unfolding evolutionary stories.

This limitation can be addressed by applying a class of Bayesian statistical inference algorithms called sequential Monte Carlo (SMC) to conduct online inference, wherein new data can be continuously incorporated to update the estimate of the posterior probability distribution.

In this paper we describe and evaluate several different online phylogenetic sequential Monte Carlo (OPSMC) algorithms.

We show that proposing new phylogenies with a density similar to the Bayesian prior suffers from poor performance, and we develop ‘guided’ proposals that better match the proposal density to the posterior.

Furthermore, we show that the simplest guided proposals can exhibit pathological behavior in some situations, leading to poor results, and that the situation can be resolved by heating the proposal density.

The results demonstrate that relative to the widely-used MCMC-based algorithm implemented in MrBayes, the total time required to compute a series of phylogenetic posteriors as sequences arrive can be significantly reduced by the use of OPSMC, without incurring a significant loss in accuracy.

Bayesian spatio-temporal estimation of dengue fever: when areas are few
Presenter: Aswi Aswi
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Authors: Aswi Aswi, Susanna Cramb, Kerrie Mengersen
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Introduction: Spatio-temporal modelling when there are few (<20) small areas can be challenging. Bayesian methods can be beneficial in this situation due to the ease of specifying structure and additional information through priors. However, care is needed as there are often fewer neighbours and more edges, which may influence results. Here we investigate Bayesian spatial and spatio-temporal model specification when there are few areas.

Methods: Annual dengue fever incidence data for Makassar, Indonesia (14 geographic areas) during 2002-2015 were obtained from the City Health Department of Makassar. A range of Bayesian model specifications were considered: independent model, BYM model, linear temporal trend model and nonparametric dynamic trend model.

Models were run using R-INLA and compared using goodness-of-fit measures, such as Deviance Information Criterion (DIC) and Conditional Predictive Ordinate (CPO), as well as comparing the obtained estimates and their precision for each area.

Results: Across all models, the highest relative risk (RR) was observed in Rappocini in 2002 and the estimate ranged from 2.12 to 7.07 between models. The lowest DIC and -mean (log (CPO)) was seen for the nonparametric dynamic trend spatio-temporal model. The RR in each area and year from the dynamic model had wider 95% CIs than the linear time trend spatio-temporal model.

Conclusion: Model choice had a large impact on results, and the nonparametric dynamic trend spatio-temporal model had much better fit than other options. To ensure results are valid and reliable, careful exploration of a range of models is important, especially when there are few areas.
Parameter Inference and Forecasting for Dynamic Queueing Networks
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Queueing systems can be joined together to form queueing networks to model systems such as hospitals, web-servers, or even biological pathways. Likelihood-based parameter inference, when it is performed at all, requires restrictive assumptions such as time invariance. However we must drop this assumption and build dynamic queueing networks (DQNs) if we are to model highly dynamic systems such as airport passenger terminals.

We provide a general approach for simulation, parameter inference and forecasting for DQNs. The computational efficiency of a new queueing simulation algorithm allows for queueing simulations to be embedded completely within an Approximate Bayesian Computation (ABC) estimation procedure for the purposes of parameter inference. To forecast with DQNs we adapt methods developed in Numerical Weather Prediction (NWP), where streaming data is assimilated into ensemble forecasts to provide real-time updates. We demonstrate the application of this approach with an international airport passenger terminal.

Decomposition of wetland plants: a non-linear hierarchical Bayesian approach
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Freshwater wetlands are very effective at storing carbon, primarily due to plant CO2 uptake during photosynthesis and deposition as litter. Plant species’ attributes, termed ‘traits’, can be used to generalise species’ contribution to soil carbon. In this study, we set up a decomposition experiment of 29 wetland plants to explore the predictive capacity of traits on litter decomposition. We combined traits associated with photosynthetic rate (‘leaf’ traits) with traits related to leaf chemistry (‘biomass’ traits). Biomass traits were estimated by modelling a three-part mixture model of combustion rate.

We implemented a Bayesian trait-based non-linear hierarchical model in Stan to test the impact of traits on decomposition of a suite of wetland species. We used the non-linear Weibull function in order to further test the effect of traits on two distinct decay parameters: shape and scale. Our aim was to determine how well traits alone could predict species’ decay, so the model evaluation criterion was a cross-validation estimate of predictive performance.

Model comparison identified that models containing biomass traits better predicted decay rate than those with leaf traits, on either parameter. We also found that trait effects on the scale parameter had a stronger impact on prediction. MCMC made the model parameterisation to test this hypothesis tractable. Compared to typical negative exponential or log-linear models for decay, this work has pushed the boundary for how we model decomposition.
Antagonising the echo chamber: Can a social network counteract cognitive bias with Bayesian rationality?

Presenter: Kate Devitt
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Authors: Kate Devitt, Tamara Pearce, Alok Chowdhury, Kerrie Mengersen
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Discussion forums (e.g. Reddit) and social media (e.g. Facebook) allow fast dissemination and analysis of ideas. However, because individuals curate content aligned to values and beliefs, such forums can become echo chambers—existing beliefs are confirmed and disconfirming evidence ignored. Research in cognitive biases has shown that increasing the number and diversity of hypotheses considered by individuals can improve decision making.

This presentation presents collaborative research between QUT and a global online travel agency (OTA) to generate, present and evaluate hypotheses in a social platform to counteract cognitive bias and improve scientific organisational culture. The platform explicitly links hypotheses ‘posts’ (pertinent to strategic business goals) to evidence ‘comments’ (e.g. news articles or technical updates). Each piece of evidence is weighted objectively and subjectively by users and outside experts to produce a hybrid weighting fed into an algorithm to output a likelihood that a hypothesis is true. The algorithm takes both the quantity and quality of user interactions on the system into consideration. Incorporating Bayesian rationality, the algorithm weights evidence differently depending on context and purpose to reduce biases amplified within existing social media ‘echo-chambers’.

This research initially investigates whether using the platform will increase number of relevant hypotheses generated and whether using the platform increases the amount and quality of evidence used to justify hypotheses. We will then evaluate impacts on strategic decision making such as whether using the platform improves closed innovation within the OTA, facilitate increased scientific behaviours and/or intellectual humility amongst employees.

Absorbing Markov Chains and Persistence in Complex Ecosystem Models

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Predicting the persistence of species under anthropogenic and environmental disturbances is a key task in the management of complex ecosystems. One way to capture the various ecological, biological and environmental processes and their interactions under uncertainty is to use a probabilistic state space model. Dynamic Bayesian Networks (DBNs), which are considered general forms of Hidden Markov Models and Kalman filters, provide a method for forwards and backwards inference on such state space models. Thus, it is possible to compute the probability of persistence under different disturbance regimes, or alternatively, predict the regimes under which persistence or a desired population level is achieved.

However, due to interdependencies between variables, absorbing states or even absorbing classes (sets of states) can arise. When the system enters an absorbing state, it can never leave that state, such as if an individual organism enters a deceased state. In an ecosystem, there can be more complex relationships between population, loss and recovery (such as with recruitment and growth) resulting in a zero absorbing class. As a result, following changes to the population arising from disturbances, the modelled system is unable to transition out of the zero states even with positive recovery. The poster illustrates the problem with an example seagrass ecosystem DBN model. Through the introduction of variable transition probabilities, effectively producing an inhomogeneous Markov Chain, it is possible to overcome the challenge of absorbing states. Consequently, it is possible to more accurately capture loss and recovery and thus the probability of persistence of an ecosystems for the purposes of decision support.
A comparison of approaches for benchmarking service organisations
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Organisational benchmarking is widely applied across a range of industries including health, education and government. Benchmarking typically compares organisations with their peers such as through ranking and to determine performance standards. However, there can be differences in the context for individual organisations that need to be accounted for in order to make reasonable comparisons. In schools for example, the socio-economic characteristics of students and their parents can affect their expected level of performance on assessment tasks. Regression and multilevel models have been extensively applied for benchmarking in the hospital and education sectors. These models score the level of performance of an organisation whilst incorporating the innate variability and uncertainty in an organisation’s client base.

Using findings from the literature and a study of social service organisations, this poster compares regression and multilevel modelling approaches to benchmarking and ranking. Also referred to as hierarchical models, multilevel models provide a means to encode structure in the data such as students nested within a school, and schools within a region. Using the social services dataset, we compare approaches using response metrics including the number of sessions of service provided, the number of clients served and the number of clients from specific demographics. The outputs of the regression, multilevel model, and multilevel model fitted with Markov Chain Monte Carlo (MCMC) are compared. The latter Bayesian approach has an additional advantage in that uncertainty in both model parameters and model predictions are captured explicitly with probability distribution, which helps to assist decision making.

Stochastic Patching Process
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Stochastic partition models tailor a product space into a number of rectangular regions such that the data within each region exhibit certain types of homogeneity. Due to constraints of partition strategy, existing models may cause unnecessary dissections in sparse regions when fitting data in dense regions. To alleviate this limitation, we propose a parsimonious partition model, named Stochastic Patching Process (SPP), to deal with multi-dimensional arrays. SPP adopts a “bounding” strategy to attach rectangular patches to dense regions. SPP is self-consistent such that it can be extended to infinite arrays. We apply SPP to relational modeling and use MCMC sampling for approximate inference. In particular, Conditional-SMC is adopted to sample new patches. The experimental results validate the merit of SPP compared to the state-of-the-arts.
Bayesian Demand Analysis of Virtual Supermarket Experiment
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Food price elasticities are essential in evaluating impacts of pricing interventions in the public health sector. For example, assessing the highly debated introduction of a sugary drink tax requires knowledge on how consumers adjust their consumption in response to a price increase in sugary drinks to understand the both intended and unintended consequences from such an intervention. However, econometric estimates of food price elasticities based on observational data are typically not based on data with much variation in prices, making the reliability of the estimates questionable. In this paper, we analyse data from a unique data set obtained from a “Virtual Supermarket Experiment” undertaken in New Zealand (NZ) in 2016, which simulates the real supermarket setting in NZ. The experiment, which involved 1000 households and 1400 products, was designed specifically to allow multiple food tax and subsidy policies to be assessed with experimental variations in price.

We investigate consumption decisions of consumers using a Linear Almost Ideal Demand System (AIDS) initially with 21 food groups. A common issue in the empirical literature is the identification of the large matrix of price elasticities. We employ a Bayesian estimation approach to incorporate prior knowledge about price elasticities that is available from previous studies but typically ignored in the standard frequentist demand analysis. We estimate a Tobit-type model that meets the theoretical requirements of budget-balancedness and symmetry in a demand system via a Gibbs sampler on the model parameters. The empirical analysis presents price elasticity initial estimates for 21 food groups in NZ.

Visualization of random effects in Bayesian hierarchical models
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Communication of parameter values and predictions is an important part of presenting the results of statistical modelling, whether via graphical means or numerical summaries. With the popularity of Bayesian modelling software such as WinBUGS, JAGS and STAN, it has become common to show trace plots and density plots when presenting analysis as these are the default visualisations shown by the coda package in R. Those writing their own samplers, whether in R, MATLAB, C++ or some other language must also make choices about how to present their results and are no doubt influenced by common approaches from other software. The more complex the model, the more complex the visualisation task, particularly when considering hierarchical models with mixed effects across multiple levels.

The rise of the tidyverse package family has resulted in the ggmcmc package, an implementation of coda style visual summaries in the ggplot2 grammar of graphics framework. While this results in a more elegant framework for visualisation, such a framework does not guarantee easily interpretable presentation of complex information. In this poster we provide some criticisms of current visualisations of model parameters and invite attendees to discuss and suggest alternative approaches to visualisation of model parameters and predictions for mixed effects models, particularly when communicating with non-statistician audiences.
**Modular Shiny apps for reproducible data communication**

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Interactive visualisation is an effective way to gain insights from complex data analyses in many areas including data exploration and model interpretation. Visualisation elements in interactive applications (apps) are often recycled in different contexts to provide insights into various aspects of an overall analysis. However, app complexity typically increases with the number and nature of included features. The *shiny* R package is a powerful tool for interactive data science communication as it connects the underlying analytical platform to the end users via a responsive web interface. This package also features a built-in modularisation framework to mitigate app development complexity. Our poster presentation provides an overview of the important concept of modular software design as a foundation for interactive data-driven apps. These ideas are presented in the context of the substantive real world problem of inbound airport passenger management captured as an interactive *shiny* web app. The results of our work demonstrate that the *shiny* platform is an excellent deployment tool to present data-driven solutions implemented in R to broad audiences as it facilitates rapid prototyping and development, and modular app architecture without the need to re-implement core analytics components.