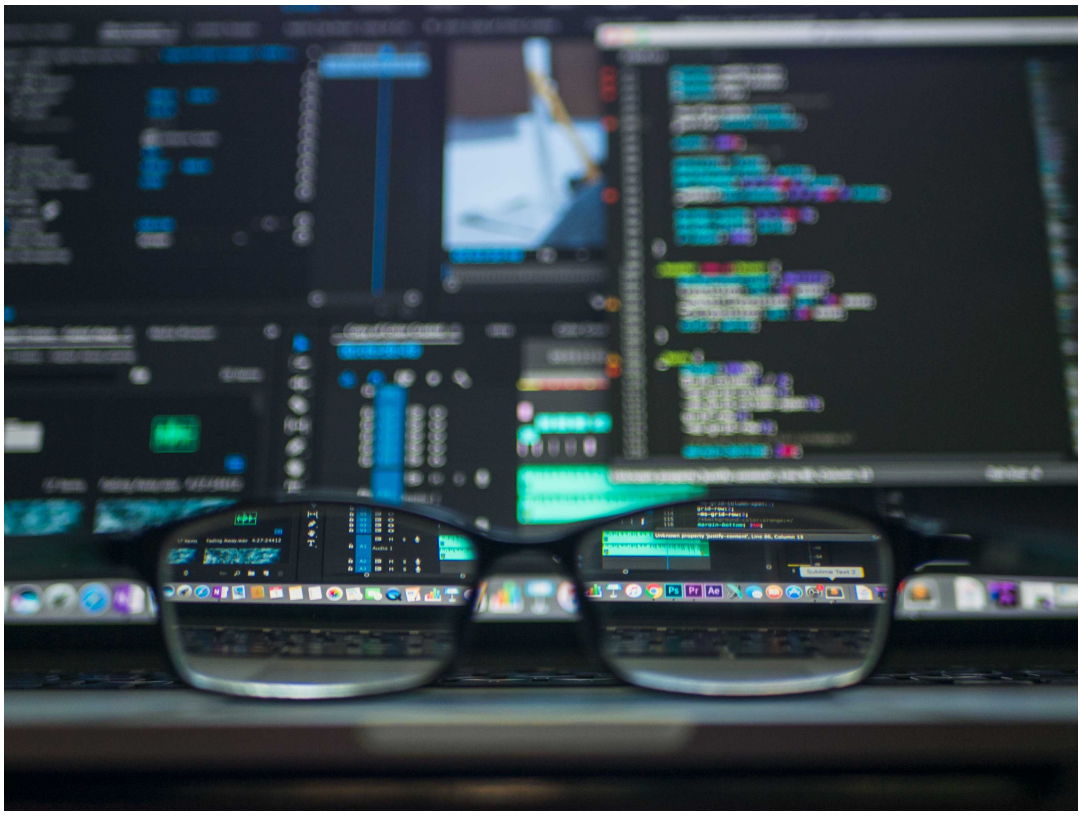
THE UNIVERSITY *of* EDINBURGH
Centre for Statistics

CFS Annual Conference 2022

June 14, 2022
James Clerk Maxwell Building (JCMB), Lecture Theatre A + Teaching Studio 3217
University of Edinburgh, King's Buildings, EH9 3FD



Hosted by the **Centre for Statistics**
THE UNIVERSITY *of* EDINBURGH
Edinburgh, UK
https://centreforstatistics.maths.ed.ac.uk
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Organized by Sara Wade (sara.wade@ed.ac.uk), Cecilia Balocchi (cecilia.balocchi@ed.ac.uk), Ozan Evkaya (oevkaya@ed.ac.uk), and Victor Elvira (victor.elvira@ed.ac.uk).

CFS Annual Conference 2022

The **Centre for Statistics (CFS) Annual Conference** showcases the most innovative interdisciplinary research / applications and brings together researchers from across the University of Edinburgh and Associated Institutions. The one day conference features a number of **invited speakers**, a **poster session** and plenty of time for **networking**.

Programme:

- **09:00-09:30:** Registration with coffee/tea.
- **09:30-09:45:** Welcome (Victor Elvira, Director of Centre for Statistics).
- **09:45-10:15:** Valeria Skafida (Social Sciences) *Growing up with domestic abuse: insights from a Scottish birth cohort study and ethical reflections*
- **10:15-10:45:** Diego Oyarzun (School of Informatics & School of Biological Sciences) *Computational methods for biotechnology and biomedicine*
- **10:45-11:15:** Coffee.
- **11:15-11:45:** Joe Zuntz (Astrophysics) *Statistical Challenges for Upcoming Cosmology Surveys*
- **11:45-12:15:** Simon Wood (Statistics, School of Mathematics) *Functional inference and Covid dynamics*
- **12:15-14:15:** Posters and Lunch.
- **14:15-14:45:** Riccardo Marioni (Centre for Genomic and Experimental Medicine) *How much about human health can we learn from a single blood test?*
- **14:45-15:15:** Sotirios Tsaftaris (Engineering) *The pursuit of generalisation with real data*
- **15:15-15:45:** Coffee (+ Group Photo).
- **15:45-16:15:** Steven Hancock (Geosciences) *Lidar signal processing to increase the coverage and accuracy of global vegetation maps*
- **16:15-16:45:** Maria Valdes Hernandez (Edinburgh Imaging/Clinical Brain Sciences) *Voxel-based statistics of brain imaging data*
- **16:45-16:50:** Closing (Victor Elvira, Director of Centre for Statistics).

Invited talks are 25 min + 5 min Q&A and changeover.

The full programme including titles and abstracts of talks and posters can be found on:

https://centreforstatistics.maths.ed.ac.uk/cfs/events/upcoming-events/cfsc-2022

Invited talks feature speakers from the **University of Edinburgh**, across **8** Schools and Institutes, including the School of Social and Political Sciences, School of Informatics, Institute for Astronomy, School of Mathematics, Institute of Genetics and Cancer, Centre for Clinical Brain Sciences, School of Geosciences, and School of Engineering

Growing up with domestic abuse: insights from a Scottish birth cohort study and ethical reflections

Valeria Skafida (valeria.skafida@ed.ac.uk)

School of Social and Political Sciences, University of Edinburgh

Abstract: Using a Scottish longitudinal birth cohort study, this talk showcases some recent research on domestic abuse prevalence, and outcomes for children living with domestic abuse. We will look at the extent to which experiences of abuse among mothers of young children are socially stratified and at how living with domestic abuse relates to children being victims of violence themselves. We also explore whether there are protective factors which can shield a child from the detrimental effects of domestic abuse. Finally, delving into more ethical matters, this talk will question what researchers can and what they should do when dealing with missing data in surveys covering sensitive topics such as this one.

†**Time slot**: 09:45-10:15

Computational methods for biotechnology and biomedicine

Diego Oyarzun (d.oyarzun@ed.ac.uk)

School of Informatics & School of Biological Sciences, University of Edinburgh

Abstract: In this talk I will give an overview of our work at the Biomolecular Control Group. Our team works on computational methods to study molecular networks in living cells. We use a mix of mathematics and computation to understand the inner workings of natural systems, as well as to design new biological circuits for biotechnology. We employ a wide range of methods for mechanistic modelling (optimal control, nonlinear dynamics, stochastic analysis), as well as data-driven models with various flavours of applied machine learning. Large parts of our work are in collaboration with wetlabs in the UK and abroad. I will particularly focus on two data-driven projects on a) machine learning for drug discovery, and b) genotype-phenotype prediction for biotechnology, and highlight the various data and statistical challenges that arise in them.

†**Time slot**: 10:15-10:45

Statistical Challenges for Upcoming Cosmology Surveys

Joe Zuntz (joe.zuntz@ed.ac.uk)

School of Pyhsics and Astronomy, University of Edinburgh

Abstract: Upcoming astronomical surveys like the Rubin Observatory and Euclid space probe will map galaxy locations and gravitational distortion across a large fraction of the observable Universe. Processing and analysing data from these surveys requires a wide variety of statistical techniques, from classical inference fo final science exploitation to the latest machine learning methods to characterise our data. I will give a short overview of some of the more interesting statistical challenges in the field and the methods being used to address them.

†**Time slot**: 11:15-11:45

Functional inference and Covid dynamics

Simon Wood (simon.wood@ed.ac.uk)

School of Mathematics, University of Edinburgh

Abstract: Statistical methods for inferring functions have been well studied in statistics for half a century, but, unlike other statistical methods, do not seem to have been widely adopted in epidemiological modelling. This talk will illustrate how inference about incidence rates and the pathogen reproductive number, R, can be accomplished using relatively standard statistical functional inference methods. This includes cases in which the function of interest is embedded in a complex disease transmission model. Applying such methods to health service and daily mortality rate data indicated that UK Covid daily new infections were in decline, and R<1, some time before each national lockdown. These results were first available in April 2020 and were confirmed by subsequent reconstructions from randomized surveillance sampling studies.

†**Time slot**: 11:45-12:15

How much about human health can we learn from a single blood test?

Riccardo Marioni (Riccardo.Marioni@ed.ac.uk)

Centre for Genomic and Experimental Medicine, University of Edinburgh

Abstract: We know that both genes and the environment can influence our risk of developing diseases as we age. Whereas our genetics are fixed, our environment and lifestyle can be altered. One way we can track the influence of the environment is by studying chemical additions to our DNA that turn genes on and off. These additions, termed epigenetic modifications, can help us objectively measure factors such as alcohol consumption and smoking behaviour and build a picture of someone's overall health. Using data from the Generation Scotland study, I will show how these patterns can help to improve prediction of disease, leading to healthier ageing.

†**Time slot**: 14:15-14:45

The pursuit of generalisation with real data

Sotirios Tsaftaris (S.Tsaftaris@ed.ac.uk)

School of Engineering, University of Edinburgh

Abstract: Modern machine learning has shown tremendous potential in a variety of domains including healthcare. For example, the interpretation of radiological images has seen considerable growth thanks to AI. No matter the domain the holy grail is to devise models that can generalise: i.e. perform well on data beyond the training set. However spurious correlations exist in the datasets that we train with. Some may be frequent and omnipresent and some less so. And in some cases their existence is not readily visible or identifiable. I will review recent theory inspired by a causal view to machine learning that can formalise spurious correlations and generalisation. I will then proceed to discuss several approaches from our team that can detect if models are susceptible to rare spurious correlations in real data, can build models that are invariant to correlations (e.g. scanner differences in medical images or differences between populations) thanks to disentangled representations, and can generate counterfactual data as means to correct for spurious correlations. I will conclude with limitations to hopefully inspire new solutions that traverse the world of causality, learning representations, and privacy/fairness. (All the work presented is joint with students, postdocs, collaborators and other members of VIOS https://vios.science

†**Time slot**: 14:45-15:15

Lidar signal processing to increase the coverage and accuracy of global vegetation maps

Steven Hancock

School of Geosciences, University of Edinburgh

Abstract: Satellite lidar is the only way to directly measure tree height and canopy cover profile from space. These measurements enable the accurate modelling of essential climate variables like biomass and biodiversity. Lidar measurements require the ground to be accurately detected which requires there to be sufficient lidar signal to distinguish these returns from noise and canopy. This sets the limit on the minimum amount of laser energy that a satellite must emit to allow an accurate measurement, which in turn sets the coverage that a lidar satellite can achieve. Because of the energy requirements, the highest coverage satellite lidar will only directly image around 2-4 % of the Earths surface within a 3 year mission. The UK Space Agency funded Global Lidar Altimetry MISsion (GLAMIS) project has been investigating how signal processing, photonics and development in small-sats could reduce the energy requirements for an accurate measurement and so increase the coverage of satellite lidar. Increased coverage would open up many new applications; particularly precise biomass change estimation and global flood modelling.

†**Time slot**: 15:45-16:15

Voxel-based statistics of brain imaging data

Maria Valdes Hernande (M.Valdes-Hernan@ed.ac.uk)

Edinburgh Imaging/Clinical Brain Sciences, University of Edinburgh

Abstract: TBA

†**Time slot**: 16:15-16:45

Contributed posters feature presenters from the **University of Edinburgh** across Schools and Institutes, including the School of Mathematics, MRC Institute of Genetics and Molecular Medicine, School of Geosciences, School of Health in Social Science, Institute of Genetics and Cancer and The Roslin Institute. Totally, **15** contributed posters to share from diverse disciplines

(3) Functional covariate–adjusted extremal dependence

Anwar Alabdulathem (s1794726@ed.ac.uk)

University of Edinburgh

Abstract: Propose a method that learns how the dependence between the extreme values of a random vector may change conditionally on a random function. Our model can be regarded as a functional covariate regression model for a bivariate extreme response. The main target of interest is what we define as the angular manifold, which is a family of angular densities indexed by a functional covariate. The simulation study suggests that the proposed methods perform well in a wealth of simulation scenarios.

(4) Parameter Estimation in Sparse Linear-Gaussian State-Space Models via Reversible Jump Markov Chain Monte Carlo

Benjamin Cox (Benjamin.Cox@ed.ac.uk)

University of Edinburgh

Abstract: State-space models (SSMs) are a powerful statistical tool for modelling time-varying systems through a latent state. In these models, the state is not directly observed, and a sequence of observations relating to the state are obtained. In real-world applications, the model parameters are not known and must be estimated. The estimation of these parameters is a very challenging but essential task to perform inference and prediction. A relevant and highly used model is the linear-Gaussian state-space, since it allows for exact inference when all model parameters are known. In this model, the state dynamics are described via a state transition matrix, which is often unknown. This model parameter is known to be particularly hard to estimate, since it encodes the between-step relationships of the state elements, which are never observed. In real systems, this transition matrix is often sparse, as not all states will directly affect every other state. However, most contemporary parameter estimation methods do not exploit this feature. In this work, we propose SpaRJ, a novel, fully Bayesian method to obtain sparse estimates of the transition matrix of a linear-Gaussian state-space model. We exploit the sparsity of the latent space by uncovering its underlying structure. Our approach allows for improved interpretability, more efficient inference, and a fully Bayesian uncertainty quantification. SpaRJ is based on reversible jump Markov chain Monte Carlo and allows an efficient exploration of sparse subspaces, adapting to the implicit model dimension. The novel methodology has strong theoretical guarantees, has minimal computational overhead when compared to standard Markov chain Monte Carlo methods, and exhibits good performance in numerical experiments, recovering known relationships from real data.

(11) Longitudinal dynamics of clonal haematopoiesis identifies gene-specific fitness effects

Eric Latorre (elatorre@ed.ac.uk)

University of Edinburgh

Abstract: "Clonal Haematopoiesis of Indeterminate Potential (CHIP) is defined as the expansion of haematopoietic stem cells (HSCs) in healthy aged individuals that results from genetic alterations. Although mostly inconsequential, the constant rate of the acquisition of mutations in HSCs (17 mutations/year) leads to an increasing probability, with respect to age, of a variant occurring in a gene that may alter the complex homeostasis of cell division and lead to the subsequent expansion of somatic clones. As a result, CHIP has been shown to be a condition affecting more than 10% of the population over 65 years of age, with a prevalence that increases dramatically over subsequent decades. Further, CHIP is a pre-malignant state linked with a ten-fold increase in the later onset of haematological cancers highlighting the importance of detecting fit clones and predicting their growth at an early stage. CHIP is also associated with an increased risk for all-cause mortality, heart disease and ischemic stroke – pathologies where age is a primary risk factor. Unprecedented access to longitudinal data following the dynamics of clonal haematopoiesis in time has allowed us to develop novel mathematical methods, relying on the theory of branching processes and Bayesian analysis, to detect and analyse the behaviour of rapidly expanding mutations. First, our novel likelihood-based filter for time-series data (LiFT) allows us to accurately detect fast-growing mutations with before they grow large. LiFT surpasses the current standard of clinical diagnosis of CHIP by detecting highly pathogenic mutations at an early stage of their clonal expansion that would have been missed otherwise. Further, longitudinal data allows us to infer stem cell fitness, or clonal growth speed, associated to cells carrying any mutation or combination of mutations that are unique to each individual. This in stark contrast with previous attempts where the fitness associated to CHIP mutations could only be associated to highly recurrent mutations and was assumed to be uniform across individuals. Our longitudinal approach therefore opens the possibility of personalised clinical management. Finally, we find that there exist gene-specific fitness effects that overcome individual variation. This crucial insight can serve as a basis to inform the screening of CHIP in a clinic.

(13) Bayesian Hawkes process approximation with Inlabru

Francesco Serafini (s1898281@ed.ac.uk)

School of Geosciences, University of Edinburgh

Abstract: Hawkes process are very popular mathematical tools for modelling phenomena exhibiting a self-exciting behaviour. Typical examples are earthquakes occurrence, wild-fires, crime violence, trade exchange, and social network activity. The widespread use of Hawkes process in different fields calls for fast, reproducible, reliable, easy-to-code techniques to implement such models. We offer a technique to perform approximate Bayesian inference of Hawkes process parameters based on the use of the R-package Inlabru. Inlabru, in turn, relies on the INLA methodology to approximate the posterior of the parameters. The approximation is based on a decomposition of the Hakwes process likelihood in three parts, which are linearly approximated separately. The linear approximation is performed with respect to the mode of the posterior parameters distribution, which is determined with an iterative gradient-based method. The approximation of the posterior parameters is therefore deterministic, ensuring full reproducibility of the results. The proposed technique only required the user to provide the functions to calculate the different parts of the decomposed likelihood, while the optimization is performed through the R-package Inlabru. The limitations of this approach include the functional form of the different likelihood parts, which needs to be as linear as possible with respect to the parameters of the model. Moreover, care should be taken of the numerical stability of the provided functions

(6) Differential privacy and synthetic data

Gillian Raab (gillian.raab@ed.ac.uk)

University of Edinburgh

Abstract: Differential privacy (DP) is a method of safeguarding results obtained from databases by guaranteeing that any individual record will have only a very small influence on the answer. Synthetic data allow microdata to be released where no record corresponds to a real person or entity. The R package synthpop for synthetic data has been extended to make the microdata DP. Results will show how the DP parameter relates to a traditional disclosure contro; measure and how the DP parameter affects the utility of the data.

(8) Storyboarding and statistics

Glenna Nightingale (Glenna.Nightingale@ed.ac.uk)

School of Health in Social Sciences, University of Edinburgh

Abstract: My presentation showcases the incorporation of storytelling and storyboarding in the development of resources for teaching statistics. I will present seven digital resources (3 animations, 3 R Shiny apps, and one short film) that I have developed and will indicate areas that I am interested in collaborating with colleagues.

(10) Comparing genome size and composition using k-mers

Hannes Becher (H.becher@ed.ac.uk)

IGC, University of Edinburgh

Abstract: K-mers of genomic sequencing data are commonly used to assess genome size and the completeness of genome assemblies by means of the k-mer spectrum. As an extension, a joint k-mer spectrum can be used to compare the genome composition of pairs of individuals and to identify the sequences underpinning genome size differences. To reduce the size of joint k-mer matrices, k-mer counts can be binned without loosing relevant information. The joint k-mer spectrum is a useful tool for studying phenomena such as intra-specific genome size variation, genomic repeats, aneuploidy, and polyploidy.

(5) Bayesian modelling of transcriptional dynamics

Huizi Zhang (H.Zhang-144@sms.ed.ac.uk)

School of Mathematics, University of Edinburgh

Abstract: Single-cell RNA-sequencing (scRNA-seq) is a powerful tool that enables measurements of transcriptome profiles for individual cells across thousands of genes. It has led to various downstream analysis such as clustering and trajectory inference to identify new cell types and investigate biological processes. However, it only provides a snapshot of cell status as cells are killed when measurements are taken. A recent RNA velocity model is proposed to study the cellular dynamics using nascent and mature mRNA abundance, which relies on frequentist method for parameter inference. Based on this model, our goal is to construct a Bayesian RNA velocity model to quantify the uncertainty in the cell velocities as well as their associated latent time.

(2) Optimised core subset construction for the APY model

Ivan Pocrnic (ivan.pocrnic@roslin.ed.ac.uk)

The Roslin Institute, University of Edinburgh

Abstract: We are entering the era of mega-scale genomics, which is causing computational issues for standard genomic evaluation models due to their cubic computational complexity. A number of scalable genomic evaluation models have been proposed, like the APY model, where genotyped animals are randomly partitioned into core and noncore subsets. While the APY model is a good approximation of the full standard model, the random partitioning can make results unstable, possibly affecting accuracy or even reranking individuals. In this contribution, we present alternative optimised constructions of the core subset and show how to use them to update the core subset with the arrival of new data. We compared constructions that were either (1) random; (2) optimised based on the value of diagonals of genomic relationship matrix; (3) optimised via random sampling with weights from (2); and (4) optimised using conditional sequential sampling algorithm. We have compared proposed constructions with the GBLUP setting and assessed their effect on accuracy and continuous rank probability scores (CRPS) of predictions. To understand the different constructions we have visualised the core subsets using non-linear dimension reduction technique UMAP - uniform manifold approximation and projection for dimension reduction. While the accuracy and CRPS of the proposed core subset constructions were mainly governed by the size of the core subset, the optimisation reduced variation compared to the standard random sampling construction. In addition to addressing the challenges caused by random sampling, sequential sampling algorithm was equally accurate when applied to the reduced-rank genotype matrix instead of the full one, and was easily expandable with the arrival of new data. Furthermore, there is an indication that the sequential sampling strategy is capturing the fine-scale population structure (e.g., paternal half-sib families in our study) as visualised by UMAP, spreading the core individuals across the given genotype space. We are further exploring the benefits of the proposed core subset constructions in non-homogeneous populations or populations with the unbalanced structure.

(15) Impact of climate and local environment on Dengue and Zika dynamics in Brazil: A joint Bayesian spatio-temporal model

Man Ho Suen (s1872841@ed.ac.uk)

Statistics, University of Edinburgh

Abstract: Arboviral diseases pose a major challenge for public health in Brazil. This project focuses on Dengue and Zika virus, which share the same virus family and vector. Thanks to the multiple data sources, this study aims to deliver a spatio-temporal Bayesian hierarchical model for examining the interactions among climate, diseases distribution and environmental conditions. Hence, the objectives are to (i) to jointly examine the spatial distribution and temporal variability of the arboviral diseases in relationship to climatological factors, in presence of changes in the local environmental conditions, and (ii) to predict the probability of outbreak of the diseases with quantified uncertainty. The data are fitted with fixed or random effects M model. Intrinsic conditional autoregressive prior (iCAR), Leroux prior (LCAR) and proper conditional autoregressive prior (pCAR) are considered to account for the spatial dependence. Random walk of first order (RW1) is applied for the temporal dependence. Here we present preliminary results obtained from monthly data in the state of Bahia in Brazil during Jan 2015 - Jun 2019. The posterior mean of the spatial risk shows different clustering for the diseases. This study provides insights into the discussion of the interactions between global climate changes and arboviral diseases epidemics.

(14) Discretising a Continuous World: Accelerated Inference for State-Space Models via Hidden Markov Models

Mary Llewellyn (mary.llewellyn@ed.ac.uk)

University of Edinburgh

Abstract: State-space models (SSMs) are often used to model time series data where the observations depend on an unobserved latent process. However, inference on the process parameters of an SSM can be challenging, especially when the likelihood of the data given the parameters is not available in closed form. In the Bayesian framework, a variety of approaches to model fitting have been applied, including MCMC using Bayesian data augmentation, sequential Monte Carlo (SMC) approximation, and particle MCMC algorithms, which combine SMC approximations and MCMC steps. However, such methods can be inefficient because of sample impoverishment in the sequential Monte Carlo approximations and/or poor mixing in the MCMC steps. This poster details an approach that borrows ideas from discrete hidden Markov models (HMMs) to provide an efficient MCMC with data augmentation approach, imputing the latent states within the algorithm. Our approach deterministically approximates the SSM by a discrete HMM, which is subsequently used as an MCMC proposal distribution for the latent states. We illustrate our approach with several examples.

(12) Bayesian scalar-on-image regression via random image partition models: Automatic identification of regions of interest

Mica Teo (mica.teo@ed.ac.uk)

University of Edinburgh

Abstract: Scalar-on-image regression aims to investigate changes in a scalar response of interest-based on high-dimensional imaging data. These problems are increasingly prevalent in numerous domains, particularly in biomedical studies. For instance, they aim to utilise medical imaging data to capture the complex pattern of changes associated with disease and improve diagnostic accuracy. However, the massive dimension of the images, which can often be in the millions, combined with modest sample sizes, typically in the hundreds in most biomedical studies, pose serious challenges. Specifically, scalar-on-image regression belongs to the "large p, small n" paradigm, and hence, many models utilise shrinkage methods. However, neighbouring pixels in images are highly correlated, making standard regression methods, even with shrinkage, problematic due to multicollinearity and the high number of nonzero coefficients. We propose a novel Bayesian scalar-on-image regression model that utilises the spatial coordinates of the pixels to group pixels with similar effects on the response to have a common coefficient, thus, allowing for automatic identification of regions of interest in the image for predicting the response of interest. We explore two classes of priors for the spatially-dependent partition process, namely, Potts-Gibbs random partition models (Potts-Gibbs) and Ewens-Pitman attraction (EPA) distribution and provide thorough comparison of the models. In addition, Bayesian shrinkage priors are utilised to identify the covariates and regions that are most relevant for the prediction. The proposed model is illustrated using the simulated data sets.

(9) Optimized Auxiliary Particle Filters: adapting mixture proposals via convex optimization

Nicola Branchini (n.branchini@sms.ed.ac.uk)

School of Mathematics, University of Edinburgh

Abstract: Auxiliary particle filters (APFs) are a class of sequential Monte Carlo (SMC) methods for Bayesian inference in state-space models. In their original derivation, APFs operate in an extended state space using an auxiliary variable to improve inference. In this work, we propose optimized auxiliary particle filters, a framework where the traditional APF auxiliary variables are interpreted as weights in a importance sampling mixture proposal. Under this interpretation, we devise a mechanism for proposing the mixture weights that is inspired by recent advances in multiple and adaptive importance sampling. In particular, we propose to select the mixture weights by formulating a convex optimization problem, with the aim of approximating the filtering posterior at each timestep. Further, we propose a weighting scheme that generalizes previous results on the APF (Pitt et al. 2012), proving unbiasedness and consistency of our estimators

(7) Randomized Time Riemannian Manifold Hamiltonian Monte Carlo

Peter Whalley (s2110992@ed.ac.uk)

University of Edinburgh

Abstract: Efficient sampling of high dimensional probability distributions is required for Bayesian inference and is a challenge in many fields. In the last decade several sampling methods have been proposed which rely on piecewise deterministic Markov processes (PDMPs). PDMPs are based on following deterministic trajectories with stochastic events which correspond to jumps in the state space. I will discuss the wish to implement constraints into this structure to potentially exploit geometries of high-dimensional problems. Efficient sampling on constrained spaces is also needed in many applications including protein conformation modelling, directional statistics and free energy computations. I will introduce a PDMP version of Riemannian Hamiltonian Monte Carlo, which we call randomised time Riemannian Hamiltonian Monte Carlo. I will show how randomizing the duration parameter for Hamiltonian flow can improve the robustness of Riemannian Hamiltonian Monte Carlo methods. I will then compare the two methods on some example distributions which arise in application.

(1) Trace-class Gaussian priors for Bayesian learning of neural networks with MCMC

Torben Sell (torben.sell@ed.ac.uk)

School of Mathematics, University of Edinburgh

Abstract: The poster introduces a new neural network based prior for real valued functions on $\mathbb{R}d$ which, by construction, is more easily and cheaply scaled up in the domain dimension d compared to the usual Karhunen-Loève function space prior. The new prior is a Gaussian neural network prior, where each weight and bias has an independent Gaussian prior, but with the key difference that the variances decrease in the width of the network in such a way that the resulting function is almost surely well defined in the limit of an infinite width network. The poster provides a high-level overview of the prior, and presents theoretical results as well as numerical examples.

(.) represents the screen location of the posters in Teaching Studio 3217

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