



## NCSE Summer Meeting @ Kent 26<sup>th</sup> – 29<sup>th</sup> June 2017 Abstracts

### Monday pm

- **Efficient state-space model-fitting for ecological data**  
*Ruth King* - University of Edinburgh

State-space models are commonly used to describe ecological data. They are a very useful representation, separating the underlying true system process (of biological interest) from the observation process (conditional on the true states). However, in many cases, the associated likelihood for the state-space model is analytically intractable. To deal with this, different approaches have been used, including using simplifying assumptions so that the model reduces to be of linear Gaussian form (or approximately) and using the Kalman filter; or using a Bayesian data augmentation approach which can be computationally intensive, with standard, vanilla MCMC approaches performing poorly due to high autocorrelation. In this talk I will describe ongoing research that aims at developing general efficient Bayesian model-fitting algorithms for common ecological models. The new model-fitting techniques will be applied to real count data (integrated with capture-recapture-type data) to demonstrate the improved computational efficiency.

- **Efficient occupancy model-fitting for extensive citizen-science data**

*Emily Dennis - Butterfly Conservation, Byron Morgan - University of Kent, Stephen Freeman - CEH, Martin Ridout - University of Kent, Tom Brereton, Richard Fox - Butterfly Conservation, Gary Powney, David Roy - CEH*

Large-scale citizen-science data present important new opportunities for biodiversity modelling. Recently proposed occupancy modelling approaches naturally incorporate random effects to account for annual variation in the composition of sites surveyed, however associated these Bayesian analyses are typically extremely time consuming.

We present an alternative approach, where site variation is described in a standard way through logistic regression on relevant environmental covariates. This allows efficient occupancy model-fitting using classical inference, which is easily achieved using standard computers. This is especially important when models need to be fitted each year, typically for many different species. In addition, the covariates used might provide insights into the ecology.

In this talk we apply the two approaches, with and without random effects, to records for a sample of species from the UK Butterflies for the New Millennium data base and to a large number of Scottish moth species, using records from the National Moth Recording Scheme.

We demonstrate that the two approaches can result in similar conclusions regarding trends, discuss the advantages and disadvantages associated with each approach, and also show the use of the classical approach for simply constructing regional indices and for producing dynamic occupancy maps.

Dennis EB, Morgan BJT, Freeman SN, Ridout MS, Brereton TM, Fox R, et al. (2017) Efficient occupancy model-fitting for extensive citizen-science data. PLoS ONE 12(3): e0174433.

- **A stochastic dynamic model for longitudinal butterfly data**

*Takis Besbeas* - Universities of Athens and Kent, *Emily Dennis* - Butterfly Conservation, *Byron Morgan* - University of Kent

The UK Butterfly Monitoring Scheme (UKBMS) has been running for over just 40 years, and has resulted in a data set that is acknowledged to be the best of its kind in the world. These long-term data are an invaluable resource; in particular they allow investigation of the effects of climate change, as butterflies are particularly sensitive to the consequent effects. A dynamic model proposed by Dennis et al (2016), applied to UKBMS data was the first to allow the estimation of productivity, from year to year and, when appropriate, brood to brood, and how this varies with temperature and longitude. A simplifying feature of the model was a deterministic auto-regression describing temporal changes involving productivity. In this talk we revisit that model, and show how it can be made fully stochastic by reformulating it as a hidden Markov model (HMM). This allows much greater flexibility, eg., with regard to choice of distributions in the model. It is then possible to investigate the effect of the deterministic simplification on estimation of bias and precision. Complicating factors are the need to categorise the counts, due to the very large numbers of states that are typically involved (see Zucchini et al (2016, p158) and Cowen et al (2017)), and also the use of different HMMs for each site at which data are collected. Illustrations are provided through simulations, and in describing UKBMS data on Adonis blue, which is bivoltine and Small skipper, which is univoltine. In addition, we indicate how the stochastic model may be used to describe data on other stages of the life cycle, such as egg counts and counts of larval webs.

Cowen, L.L.E., Besbeas, P., Morgan, B.J.T. and Schwarz, C.J. (2017) Hidden Markov Models for extended batch data. *Biometrics*, in press.

Dennis, E.B., Morgan, B.J.T., Freeman, S.N., Roy, D. B. and Brereton, T. (2016) Dynamic models for longitudinal butterfly data. *JABES*, 21,1, 1-21.

Zucchini, W., MacDonald, I.J. and Langrock, R. (2016) Hidden Markov Models for Time Series, An Introduction Using R, Second Edition, Chapman & Hall/CRC.

- **The use of penalised likelihood to improve estimation in removal models**

*Ming Zhou, Eleni Matechou, Rachel S. McCrea, Diana J. Cole, Richard A. Griffiths* - University of Kent

Classical removal experiments – the movement of protected animals or plants out of the path of development projects as a wildlife management tool – can be used to estimate the abundance of a population within a closed area. The classic removal model (Moran, 1951) assumes a constant capture probability and all animals are available for detection throughout the study, which results in a simple geometric decline of removed counts of individuals over time. However, the real data collected from some species exhibit unexpected fluctuations in the number of captured animals. This is because arrival of animals takes place during removal sampling. Our work is driven by real data on slow worms, *Anguis fragilis*, common lizards, *Zootoca vivipara* and great crested newts, *Triturus cristatus*, where existing approaches may give rise to misleading conclusions.

The estimation of temporary emigration or population renewal for removal data relies on the use of the robust design (Zhou et al.) However, there are many removal data which lack the robust

design structure. Regularisation methods have been a popular tool, in particular for scenarios where the number of variables is greater than the number of observations (Tibshirani, 1996). These work by maximising an objective likelihood function which additionally enforces a roughness penalty function. We investigate the use of maximum penalised likelihood estimation to overcome the issues of parameter redundancy for removal data collected without the use of the robust design using simulations and a data set of common lizards.

Moran, P.A.P. (1951) A mathematical theory of animal trapping, *Biometrika*, 38, 307-311.

Tibshirani, R. (1996) Regression Shrinkage and Selection via the LASSO, *Journal of Royal Statistical Society B*, 58 (1), 267-288.

Zhou, M., McCrea, R. S., Matechou, E., Cole, D. and Griffith, R. A. (2017) Removal Models Accounting for Temporary Emigration, in submission.

- **A Polya Tree based model for counts of unmarked individuals in an open population**

*Alex Diana, Eleni Matechou, Jim Griffin - University of Kent*

Many ecological sampling schemes do not allow for individual marking, as opposed to, for example, capture-recapture schemes, but provide instead only the total count of individuals detected at each sampling occasion.

In this paper, we propose a novel approach to model count data in a population with size that is not assumed to be constant since individuals can arrive and depart from the site during the sampling period. A Bayesian nonparametric prior known as Polya Tree is used for modelling the bivariate density of arrival and departure times. Thanks to this choice, we can easily incorporate prior information on the density while still allowing

the model to flexibly adjust the posterior inference according to the observed distribution of the counts. The model provides moreover great scalability as the complexity does not depend on the population size but just on the number of sampling occasions, making it particularly suitable for data-sets with high number of detections. We apply the new model to count data of newts collected from the Durrell Institute of Conservation and Ecology.

- **Modelling temporary emigration using a Bayesian nonparametric changepoint process for capture-recapture data**  
*Eleni Matechou* – University of Kent, *Raffaele Argiento* – University of Torino

Motivated by data on anglers in Norway, we present novel capture-recapture models that account for temporary emigration without relying on the robust design sampling approach. Anglers fishing on a given day in the season are detected only if they catch a salmon, and otherwise remain undetected. Hence the number of anglers that visit the site to fish as well as the number of visits and the dates of these visits for each angler are unknown.

We treat the individual visits as changepoint processes and hence can infer the number of visits and their dates for all individuals, detected and undetected, in the population of anglers. We consider a Bayesian nonparametric approach to account for individual heterogeneity in terms of number and duration of visits as well as of detection probability.

## Tuesday am

- **UK and European Marine Litter Monitoring**  
*Jon Barry* - Cefas

Ecological problems associated with marine litter and, in particular, plastic litter are becoming increasingly prevalent. I describe the beach and trawl monitoring surveys that have been put in place in recent years. I show spatial and temporal results of these surveys and describe some of the potential research problems associated with litter monitoring.

- **Combining ecosystem models**

*Mike Spence* – University of Sheffield

When making predictions about marine ecosystems, we often have available a number of different complex models that attempt to represent their dynamics in a detailed mechanistic way. Each of these models can be used to simulate large-scale experiments and make forecasts about the fate of marine ecosystems under different scenarios in order to advise management decisions. However, structural differences, systematic discrepancies and uncertainties lead to different models giving different predictions under these scenarios. This is further complicated by the fact that the complex models may not be run with the same species or functional groups, spatial structure or time scale. That said, it is often the case that these models have shared biases as well as their individual biases. Rather than simply try to select a 'best' model, or take some weighted model average, it is important to exploit the strengths of each of the available models, while learning from the differences between them. To achieve this, we construct a flexible statistical model of the relationships between a collection or 'ensemble' of mechanistic models and their biases, allowing for structural and parameter uncertainty and for different ways of representing reality. Using this statistical meta-model, we can combine prior beliefs, model estimates and direct observations using Bayesian methods, and make coherent predictions of future outcomes under different scenarios with robust measures of uncertainty. In this talk we will present the modelling

framework and discuss results obtained using a diverse ensemble of models in scenarios involving future changes in fishing levels.

- **Counting something that's almost gone: combined visual-acoustic abundance estimate of the vaquita**

*Len Thomas* - University of St Andrews

The vaquita is the world's most endangered cetacean - now almost extinct due to bycatch in an illegal fishery in its native Gulf of California, Mexico. Reliable estimates of population size and trend are key to prompting conservation action; ironically these are harder to obtain as population size decreases. We describe a combined visual line transect and passive acoustic population survey that took place in autumn 2015. We focus on the analysis, which involved combining (1) a Bayesian line transect model of variation in detectability as a function of sighting conditions and variation in density over geographic space (using previous, as well as current survey data); (2) a simulation model of detectability under perfect sighting conditions; (3) a spatial model of spatial variation in acoustic detection rate. The resulting abundance estimate was 59 (95% CRI 22-145). Despite the complications, analysis was undertaken by an Expert Panel, using BUGS and R, in just a few days - illustrating the power of modern approaches to obtain useful estimates with relative ease. The abundance estimate, combined with separate acoustic monitoring that shows an ongoing precipitous decline, has prompted planning to catch the last remaining vaquita and try to preserve the species in captivity.

- **Comparing methods for estimating abundance from passive acoustic monitoring data using the example of bowhead whales**

*Cornelia S. Oedekoven, Tiago Marques, Danielle Harris, Len Thomas, Aaron Thode, Susanna Blackwell, Alexander Conrad, Katherine Kim* - University of St Andrews

Recent developments in analysing passive acoustic monitoring data have demonstrated that various methods for estimating abundance from visual data can be extended to be applicable to acoustic data. These include distance sampling (DS) and spatially explicit capture recapture (SECR). For acoustic data, additional challenges exist in that we do not detect individual animals or groups of animals but the cues (sounds) that the animals produce. Furthermore, determining the location of the detected animals using acoustic data is often difficult and in some cases, impossible. Distance sampling methods, for example, rely on accurate measurements of the distance between the animals producing the cues and the detector. SECR relies on being able to detect the same cues on more than one detector and matching them between detectors. Here we summarise various methods available including direct census, DS (using estimated distances from beamforming or sound propagation models), and SECR, and present a comparison on the performance of these methods applied to bowhead whale call data collected with DASARs in the Beaufort Sea.

- **Measuring and modelling large-scale population dynamics at the interface between statistics and applied ecology**  
*Rob Freckleton - University of Sheffield*

Ecological systems are enormously variable at almost every scale at which we observe them. This variability is a challenge to our understanding of these systems as well as our ability to predict them. Conventionally ecological demographic monitoring has been focussed on detailed measurements at fine scales, with the consequence that data on large-scale variability in population dynamics is relatively rare. In this talk I will discuss this challenge in ecology and how it can be overcome. I will use arable weeds in the UK as a case study in how we link from ecological observation to understanding and forecasting future

management. I will show how models can be used to generate predictions that are relevant to understanding long-term management as well as potentially informative to individual managers. I will highlight that successful integration of novel tools for measuring populations and analysing data are the key to this and that there is unrealised potential for ecological modelling in applied ecology.

- **Problems with Using Data Cloning to Investigate Identifiability**

*Diana Cole, University of Kent*

In some models parameters are confounded so that it is not possible to estimate all parameters; this could be caused by the model structure or a specific data set. This is known as parameter redundancy or non-identifiability. Formal algebraic methods exists to investigate this problem (see for example Cole et al, 2010), however these can be complex to use. An alternative method that is currently popular involves data cloning (Lele et al, 2007, Lele et al, 2010). However we demonstrate that it is possible for data cloning to produce misleading or inaccurate results.

Cole, D. J., B. J. T. Morgan and D. M. Titterington (2010), The parametric structure of models. *Mathematical Biosciences* 228, 16–30.

Lele, S. R., B. Dennis and F. Lutscher (2007), Data Cloning: Easy Maximum Likelihood Estimation for Complex Ecological Models Using Bayesian Markov Chain Monte Carlo Methods. *Ecology Letters* 105, 551–563

Lele, S. R., K. Nadeem and B. Schmuland (2010), Estimability and Likelihood Inference for Generalized Linear Mixed Models

## Wednesday am

- **Integrated Population Models incorporating Spatial Information**

*Marina Jimenez-Munoz, Diana Cole, Eleni Matechou, University of Kent, Stephen Baillie, Rob Robinson, British Trust for Ornithology*

To reverse biodiversity loss we need to understand the environmental and demographic causes of changes in distributions and abundances. Several independent studies and models exist that allows us to estimate demographic parameters, such as survival rates. However, the results of these separate analyses may be sometimes inaccurate, misleading or incomplete.

We develop an integrated population model for ring-recovery and count data that incorporates spatial information including geographical coordinates and habitat type. We illustrate this model using BTO Starling data.

- **Modelling the spatial distribution of non-breeding seabirds using multiple data sources**

*Adam Butler -BioSS, Ewan Wakefield - University of Glasgow, Kate Searle - CEH, Matthew Carroll, Mark Bolton - RSPB, Sarah Burthe, Francis Daunt - CEH*

There is considerable policy interest in modelling the spatial distribution of seabirds within the waters around the British Isles, in order to quantify the likely impacts of human activities (e.g. offshore wind farms) and to identify key areas for protection. Recent work (Wakefield et al., submitted) has used GPS data to model the distribution of four species - kittiwake, guillemot, razorbill and shag - in relation to a range of covariates (relating to accessibility, competition, and environmental suitability).

These distributions relate solely to breeding birds, however, and there is also interest in quantifying the spatial distribution of non-breeding birds. Direct data on non-breeding birds are rarely available, but spatial survey data (collected using boat-based or aerial line transects) will include a mixture of breeding and non-breeding birds. We propose a model for the spatial distribution of non-breeding birds that is a direct extension of the recently developed model for breeding birds (Wakefield et al., submitted), and propose a mechanism for inferring the additional parameters of this model by maximizing the association between spatial survey data and the predictive spatial distribution from the model. We apply the model to three species - kittiwake, guillemot and razorbill - using data from the entire UK Economic Exclusion Zone, and compare the inferred distributions of non-breeding birds against those of breeding birds. Possibilities for further work - especially in relation to the quantification of uncertainty within the model - will also be discussed.

- **Estimation of roe deer population density in a mountainous Mediterranean area using hierarchical distance sampling**  
*Costas-Simos Nisiotis* - Athens University of Economics and Business, *Takis Besbeas* - Athens University of Economics and Business, NCSE, University of Kent

Distance sampling refers to a suite of methods for estimating animal density or abundance from a sample of distances to detected individuals. The main methods are based on line or point transects and Hierarchical Distance Sampling (HDS) provides an elegant and general framework for analysing data from these sampling methods. We show analytically that HDS is equivalent to Conventional Distance Sampling under a Poisson assumption of abundance but the hierarchical framework allows more flexibility in general. In the context of an incredibly rich data set on roe deer living in Mountain Parnitha collected by WWF Greece in 2008, we develop new models for HDS involving alternative abundance distributions and perform an extensive model selection for both the observation (detection function) and latent (abundance) processes of the framework. The analysis of the real data is made interesting by the fact that 62% of the habitat was burnt by destructive forest fires in 2007 and the model selection procedure reveals that different latent models are functioning at the two habitats. In addition to density, WWF were also interested in investigating issues related to survey design, and we use simulation methods to give guidance on the sample size required to provide specified levels of precision. The work is joint with WWF Greece.

- **Incorporating animal movement with distance sampling and spatial capture-recapture**

*Richard Glennie, Stephen T. Buckland - University of St Andrews,  
Roland Langrock - Bielefeld University*

Distance sampling and spatial capture-recapture (SCR) methods are used to infer the density and distribution of wild animal populations. Both approaches model encounters between detectors and animals where the probability of detection depends on the animal's location. For mobile animal populations, this probability is determined by the unobserved path the animal travels during the survey. Yet neither approach explicitly

accounts for this movement. We describe a continuous-spacetime model that incorporates a hidden animal movement process, informed by independently obtained movement data, such that the probability of detection depends explicitly on the entire path taken by the animal. Spatial hidden Markov model methods are used to approximately calculate the average probability of detection over all possible animal trajectories.

For distance sampling, we show that accounting for movement can improve the accuracy of density estimates and can widen applicability to fast-moving species (e.g. cetaceans and seabirds). For SCR, we show that an explicit movement model can account for correlations in detections caused by contiguous movement paths and that animal location over time can be inferred from observed encounters. Furthermore, we demonstrate the flexibility of our approach by including animal behaviour, landscape connectivity and varying effort. Finally, we discuss the potential for models that incorporate movement data and population abundance survey data to provide wider inference on population distribution over time.

- **Bayesian Inference for animal habitats from movement in continuous time**

*Hajar Alkhezi, Paul G. Blackwell - University of Sheffield*

Our goal is to develop an extension to methods for exact Bayesian inference for animal movement in continuous time, which will make modelling animal movement in continuous time more widely applicable because the new method will be more flexible and efficient. The basic idea is to estimate the boundaries of unknown habitat regions, using animal movement to learn about the environment. It is usual to understand the regions to be known as corresponding to observable features of a habitat. If the boundaries of the regions are unknown, we can estimate them by assuming the different regions are associated with different

movement behaviours, with each region corresponding to one behavioural state. Moreover, a shift in behaviour means the animal has encountered the boundary of another region. We use the exact Bayesian statistical analysis for movement models with behavioural switching in continuous time, without need for time-discretisation error. To make the estimated boundary idea work with the exact method, we must assume that the transition rate has an upper bound, which means that instantaneous changes in behaviour do not occur when the animal moves from one region to the next. This enables us to carry out inference for the boundary by adding an extra MCMC step to vary the boundary.

- **Inferring animal movement and behaviour in continuous time from irregular and noisy GPS observations**

*Alison Parton, Paul G. Blackwell-University of Sheffield*

Observations of animal movements from GPS trackers are typically sampled at irregular times and in the presence of spatial error. Mechanistic modelling of movement often ignores observation error and is formulated in discrete time, despite the inevitable problems with time scale invariance. A natural solution is to define movement in continuous time, yet the uptake of such modelling has been slower than that of its discrete counterparts.

The lack of continuous time implementation is often excused by a difficulty in comprehension. We aim to bolster this usage by presenting a continuous time movement model with interpretable parameters, similar to those of popular discrete time models that use turning angles and step lengths. Movement is defined by a joint bearing and speed process, with parameters dependent on a continuous time behavioural switching process, creating a flexible class of movement models.

Inference is carried out using Markov chain Monte Carlo, augmenting observed locations with a reconstruction of the

underlying, unobserved movement process. This method is presented using GPS data from reindeer (*Rangifer tarandus*) to identify and make inference about multiple movement behaviours.

- **Multiple movement behaviours with wrapped normally distributed turning angles can lead to mis-classification as a single movement strategy with a wrapped Cauchy distribution.**

*Joseph Bailey* – University of Essex

Modelling the way in which animals move through their landscape is a vital and active area of research in movement ecology. Analysis of such movement data often results in various parameters which can be used to reconstruct and interpret the movement behaviour, such as step lengths, turning angles, bout lengths etc. When considering the distribution of the turning angles, one would expect to find a near normal distribution centred around some preferred direction in non-random movement, corresponding to a high number of turns with small deviations from the preferred direction and few larger turns. However, the analysis of data can return heavy tailed distributions, indicating a propensity for highly directed movement with occasional medium and large turns, a result which appears counter intuitive to sensible movement strategies. This type of behaviour has been noted in harbour seals [1], cow elk [2] and panthers [3]. In this presentation, I demonstrate how the mixing of two normally distribution random processes can lead to misclassification as a single heavy-tailed distribution (in this case a wrapped Cauchy distribution) when selected using best-fit model methods. This in turn leads to a method for separating and identifying different movement behaviours from movement data.

[1] McClintock, B. T., Russell, D. J. F., Matthiopoulos, J. and King, R. (2013), Combining individual animal movement and ancillary

biotelemetry data to investigate population-level activity budgets. *Ecology*, 94: 838–849.

[2] Morales, J. M., Haydon, D. T., Frair, J., Holsinger, K. E. and Fryxell, J. M. (2004), Extracting more out of relocation data: Building movement models as mixtures of random walks. *Ecology*, 85: 2436–2445.

[3] van de Kerk, M., Onorato, D. P., Criffield, M. A., Bolker, B. M., Augustine, B. C., McKinley, S. A. and Oli, M. K. (2015), Hidden semi-Markov models reveal multiphasic movement of the endangered Florida panther. *Journal of Animal Ecology*, 84: 576–585.

- **Can animals do MCMC? Integrating resource selection and step selection**

*Théo Michelot, Paul Blackwell* -University of Sheffield, *Jason Matthiopoulos*- University of Glasgow

Linking animal movement to environmental conditions is a crucial step to understand how animals will be affected by a changing environment. Resource selection functions aim to model the spatial distribution of an animal's locations in terms of the distribution of resources. Step selection approaches extend the framework to incorporate movement, by modelling the animals' displacements in terms of the distribution of resources. However, step selection methods do not generally make it possible to estimate the resource selection function, such that the two approaches are usually incompatible. We will describe a new model for step selection, for which the distribution of the animal's locations coincides with the resource selection function. Our method uses an analogy between the movements of an animal in the plane and the movements of an MCMC sampler in 2D parameter space, to guarantee convergence to the utilisation

distribution. We will compare our model to other resource selection and step selection approaches on simulated data with known distributions and, if time permits, on real data.

## **Wednesday pm**

- **Using GAMs to estimate fishing gear efficiency in the North Sea**

*Nicola Walker, David Maxwell, CEFAS*

There is a need to better quantify the effects of fishing on some target and many non-target species taken as bycatch in trawl fisheries. However, this is complicated by the fact that only a proportion of fish are caught by the different fishing gears. Gear efficiency is the probability that fish in the path of a trawl will be caught and retained, but varies by species and length, and between the different fishing gears. We present a method that applies generalised additive models (GAMs) to catch-at-length data to estimate catch-ratios between trawl gears by species and size class. We then demonstrate how these catch ratios can be manipulated to obtain estimates of absolute gear efficiency and discuss their utility in fisheries management.

- **How much effort is needed to detect population changes in amphibians? A test using a bromeliad-inhabiting frog**

*Izabela M. Barata, Richard A. Griffiths, Martin Ridout* – University of Kent

Rare amphibians are often cryptic and difficult to detect in the field, and this presents challenges in designing surveys to detect population changes. We combined power analysis and occupancy modelling to determine the survey effort needed to detect population change in *Crossodactylodes itambe* – a frog endemic to Brazilian highlands and found only in a single species of bromeliad. Treating individual bromeliads as occupied or unoccupied ‘sites’, we surveyed the study area in 2014 (123 sites, 3 surveys) and 2015 (147 sites, 21 surveys), applying visual encounters in both years. Detection probabilities were high ( $0.57 \pm 0.05$  in 2014,  $0.54 \pm 0.01$  in 2015), and there was no significant change between years. Overall, 30-48% of bromeliads were estimated to be occupied by frogs in both years. Model selection shows consistency within years, with occupancy estimates positively correlated with elevation. For *C. itambe*, 3-6 visits was sufficient for 95% confidence in detection, and two visits resulted in 80% certainty that the species could be detected if present. Increasing the number of sites and number of visits improved statistical power for detecting change from one year to the next. Current survey effort can detect a decline of 36% in the population, with 80% power. Increasing the number of sites is the only option to improve statistical power. In order to have 80% power to detect a decline of 15%, a suitable design would require four visits at 565 sites. Although our sampling design has good precision for occupancy estimates, if the main goal is detecting small changes in the population, we need to increase the total number of monitored sites. Power analysis should be routinely applied to amphibian population assessments to improve design and determine whether survey effort is sufficient.

- **Incorporating statistical models into conservation practice: challenges and opportunities**

*Richard A. Griffiths* - University of Kent

Despite considerable advances in statistical models for the assessment of animal populations in recent years, uptake by conservation practice has been patchy at best. Indeed, for certain animal groups - such as amphibians, reptiles and some mammals - conservation decision-making is often based on archaic methods and analysis based on traditional practice that has not changed for several decades. This can result in unreliable status assessments and poor management decisions that are cost-ineffective. The reasons for this situation include: (1) a poor appreciation and understanding of statistical modeling by many conservation professionals; (2) low incentives for statistical modelers to enter conservation practice; (3) failure of legislation, policy and guidance to embrace sound design and analysis; (4) timeframes for population assessments that are driven by commercial and development agendas; and (5) very poorly integrated data management and data flow systems within the sector. Bridging the divide between the science and practice will therefore require an integrated approach that will need to combine improved awareness, training, advocacy and incentives.

- **An alternative improved Chao estimator**

*Ratchaneewan Kumphakarm* - Maejo University of Chiangmai,  
*Martin Ridout*, University of Kent

The Chao estimator is a popular nonparametric estimator of species richness, the number of species present in a population. It is derived from a random sample of individuals from the population, but uses only the number of observed species ( $K$ ), and the number of species seen exactly once ( $f_1$ ) and exactly twice ( $f_2$ ). The Chao estimator provides an estimated lower

bound for species richness. Recently Chiu et al. (2014) described an improved estimator, termed the iChao1 estimator, which attempts to reduce the bias of the original Chao estimator by using additional data on the number of species seen three or four times in the sample ( $f_3, f_4$ ).

Here, we describe an alternative estimator that is intended to perform similarly to iChao1 but using only the same data ( $K, f_1, f_2$ ) as the original Chao estimator. The different estimators are compared using simulation and applied to several real data sets. We find that the new estimator is generally similar to iChao1, but sometimes gives improved performance. However, more work is needed to determine when these "improved" estimators offer a genuine improvement over the original Chao estimator.

Chiu C-H, Wang Y-T, Walther BA, and Chao A (2014). An improved nonparametric lower bound of species richness via a modified Good-Turing frequency formula *Biometrics*, 70(3), 671-682.

- **Will you walk a little faster...? Prospects for efficient inference for continuous-time movement models**

*Paul Blackwell* - University of Sheffield

Models of movement that are formulated in continuous time are increasingly being recognised as important, for both theoretical and practical reasons. However, unless rather simplistic approximations are used, fitting continuous-time models to data can be computationally demanding, especially when the models incorporate switching between different behavioural states. One current strand of my research involves trying to improve the efficiency of fitting such models, taking inspiration from the very fast algorithms widely used to fit Hidden Markov models. This is definitely work in progress, but in this talk I will try to say

something about what can be done, and show some re-analysis of one or more examples from the literature.

- **Design and analysis of experiments testing for biodiversity**

*Rosemary A. Bailey* - University of St Andrews

It is now widely believed that biological diversity is good for the environment. One way that ecologists test this is to place random collections of species in mini-environments and then measure some outcome. I have been working with a group of fresh-water ecologists to improve this in two ways. The first is that our subsets of species are carefully chosen, not random. The second is that we fit a nested family of plausible models. Our results suggest that the underlying model is not diversity at all. My talk will concentrate on ways of understanding a complicated family of plausible models.

- **Monitoring the biodiversity of regions**

*Stephen T. Buckland*- University of St Andrews, *Alison Johnston*-BTO

Through the CBD 2010 and 2020 biodiversity targets, nations committed to reducing the rate of loss of biodiversity. This requires calculating the biodiversity trends in nations, whereas previously, most academic research on quantifying biodiversity concerned communities within relatively small sites. We consider design and analysis issues that CBD targets raise and explore the potential pitfalls for managers of monitoring schemes when statistical principles yield to practical constraints. We list five main criteria that well-designed monitoring programmes

should meet: representative sampling locations, sufficient sample size, sufficient detections of target species, a representative sample of species, and a sound temporal sampling scheme. We examine the implications of biodiversity assessments that fail to meet these criteria and suggest ways to alleviate these implications through analytical approaches. We discuss the remarkable potential for wide-scale biodiversity monitoring offered by technological advances and by the rise of “citizen science”.