NCSE Summer Meeting, 2015

Abstracts

Multistate modelling of guppy data

RACHEL McCREA

Collaborators: Tim Coulson, Ruth King, David Reznick, Andres Lopez-Sepulcre and Joe Travis

Abstract:

Guppies inhabit streams in Trinidad and habitats can be categorised into high and low predation areas. Experimental transplants of guppies from high to low predation streams were performed in 2008 and 2009. All introduced fish were adult and individually marked at introduction and mark-recapture data is collected each month, along with individual level data is also collected as well as location in the steam data.

I am going to discuss the challenges of analysing these data and will present our modelling approaches for answering key ecological questions.

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Predicting malaria susceptibility using antibody levels

JOHN JOSEPH VALLETTA

Abstract:

Despite progress in malaria control, over half a million children die every year from severe complications. Naturally acquired immunity to malaria is complex and still a poorly understood process, with increasing evidence pointing towards an orchestration of multiple immune mechanisms triggered by different antigens. Discovering which group of antigens induce antibody responses that confer protection from malaria would elucidate on this complex immunological response, but also direct vaccine development. I will present the current state of the literature, specifically on statistical methods used to assess putative correlates of protection, and discuss their shortcomings. I will then discuss the challenges of modelling malaria epidemiological data and propose techniques that can alleviate current shortcomings.

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Modeling spatio-temporal dependency with multispecies data

CHARLOTTE JONES-TODD

Abstract:

I consider a spatio-temporal modelling technique which handles complex dependency structures in space and over time, and focus on how such an approach can be used to infer about dependency between the latent spatial processes which drive the spatial distribution of multiple response variables, hence avoiding building a common ``response-covariate'' model usually used to infer such relationships.

Using Integrated Nested Laplace Approximation (INLA) I demonstrate on how such an approach can be used to infer the latent spatial processes which drive the spatial distribution of both an avian predator and a species upon which it predates, and how they change over time, whilst also dealing with the zero inflation inherent in many multi-species ecological datasets.

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Spatial point process models for distance sampling data

JOYCE YUAN

Abstract:

Distance sampling is a widely used approach for wild life surveys. Traditional design-based approaches assume a uniform distribution of animals in space and do not account for the underlying spatial structure of population density. We interpret distance sampling data as a filtered spatial point pattern and propose a model-based approach to fitting a spatial log-Gaussian Cox process model to the data. Such model uses the flexible Stochastic Partial Differential Equation (SPDE) approach to account for the spatial autocorrelation, and the Integrated Nested Laplace Approximation (INLA) approach for Bayesian inference. We illustrate the method using line transept data from the shipboard cetaceans surveys in the eastern tropical Pacific (ETP).

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SECR methods for cue directionality and strength heterogeneity

BEN STEVENSON

Abstract:

Spatially explicit capture-recapture (SECR) methods can be used to estimate animal density from cue detection data collected across an array of fixed detectors. Recent applications have involved a wide variety of taxa, including birds, frogs, primates, and whales. These methods typically model detection probabilities via a detection function, whereby the probability of a cue being detected by any given detector depends only on the distance between their respective locations. This implies that cues are equally detectable in all directions, and if individuals emit cues in a particular direction then this may not hold. Additionally, given a cue's source location, it is assumed that detections across the array are independent. This assumption is violated if there is variation in cues' source strengths, with some cues being more detectable than others at any given distance. In this talk I will outline new SECR methods that provide appropriate density estimators for surveys subject to either cue directionality or cue source strength heterogeneity. Acoustic surveys are a common source of cue detection data, however small microphone arrays collect very little information about call directions and call source strengths. These detection data can be augmented by received signal strengths and times of arrival, allowing for estimable cue directionality and source strength parameters.

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Quantifying temporal trends in biodiversity, and how they vary spatially

STEVE BUCKLAND

ST Buckland, PJ Harrison and Y Yuan

Abstract:

We consider methods for quantifying biodiversity changes in time, and how those changes vary spatially, using data from the UK Breeding Bird Survey. We discuss measures based on the geometric mean of relative abundances, on departures from evenness, and on the differential rates of change of different species. We find evidence of detrimental changes in the south-east of England perhaps related to habitat loss, and evidence of increased diversity in the West of Scotland, possibly resulting from climate change.

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Emon: An R package for environmental monitoring and survey design

JON BARRY

Abstract:

I will describe a recently-developed (with David Maxwell at Cefas) R package ((https://r-forge.r-project.org/projects/emon/) designed to aid survey designs for marine environmental and ecological monitoring. The package is a collection of functions that are in six main areas: calculation of statistical power for three common designs (comparing two areas, looking for trends, Before and After Control Impact studies), spatial designs to detect items of interest (e.g. invasive species), Generalised Visual Fast Count estimation methods for underwater video surveys, and a measure of spatial correlation. I will describe these functions using examples from the creation of the Hythe Marine Conservation Zone and a national sampling programme to detect invasive species. All power functions work using simulation â€" which gives the flexibility to allow a number of distributions for data together with parametric and non-parametric assessment of p-values.

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The use of electronic books for teaching statistical ideas with application to statistical ecology

PROFESSOR WILLIAM BROWNE

Abstract:

In this talk I will describe some of the developments at the Centre for Multilevel Modelling with regard to our recent Stat-JR software package. In particular I will talk about its electronic book interface and the use of workflows in statistics. This will lead on to discussion of our ideas around a statistical analysis assistant (SAA) which will assist non-statisticians to perform statistical analysis. I will illustrate the software developments with statistical ecology applications. The talk will be interactive and I will canvas opinion of the audience on what aspects of research in statistical ecology could benefit from some form of SAA.

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Abundance estimation using integrated modelling of unmarked animal data from camera traps.

NATOYA JOURDAIN

Natoya Jourdain, Diana Cole, Martin Ridout and Marcus J. Rowcliffe

Abstract:

The use of camera traps to estimate animal density has so far been restricted to capture-recapture analysis of species with unique identifiable markings. The Random Encounter Model (REM) developed by Rowcliffe et al., (2008) estimates animal abundance without the need for individual recognition of the animals. The REM describes rates of contacts between animals and camera traps from which an estimator for animal density can be derived. To obtain an estimate of population density, the REM considers two distinct and independent sets of data: 1) trap rate data, and 2) an estimate of animal speed of movement, which is a fixed average. We extend the REM by developing an integrated likelihood. The extended Random Encounter Model (eREM) adopts maximum likelihood estimation, modelling simultaneously camera trap and animal speed of movement data. We modelled the camera trap data by a Poisson distribution and animal speed by a gamma distribution. Testing the reliability of this approach through simulation, we found that eREM is an improvement over REM. Our analyses confirm that the REM provides approximately unbiased estimates of the parameters themselves but underestimates their variances, whereas the eREM is unbiased and estimates variance correctly. The eREM was extended to include covariates such as habitat type and camera. In the analysis of a real data set, the study site was divided into four areas of contrasting habitat. The results showed that density varied with habitat. Also, what is striking is the estimation of non-zero densities for some species in habitats where there were no census observations.

References:
Rowcliffe, M.J. et al. (2008), Estimating animal density using camera trap methods without the need for individual recognition, Journal of Applied Ecology 45, 1228-1236.

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Modelling meerkats

BYRON MORGAN

Martin Ridout, Takis Besbeas, Byron Morgan, University of Kent
Stuart Sharp, Lancaster University

Abstract:

Meerkats, *Suricata suricatta*, have been studied intensively in the Kalahari for many years; see Clutton-Brock (2002, 2008). This has resulted in a wealth of data, recently analysed by Bateman et al (2011) and Ozgul et al (2014), who used individual-based modelling (see Grimm and Railsback, 2005).

Interesting features include the facts that the animals live in social groups, and are cooperative breeders: usually only the dominant female in each group reproduces, and other females assist the dominant female. There is a remarkable discrepancy in lifespans, with the dominant females greatly outliving other females.

This talk presents the results from a multi-state analysis of the data (see Willekens, 2014), and comparisons will be drawn between the two modelling approaches.

References

Bateman, A.W., Coulson, T. and Clutton-Brock, T.H. (2011) What do simple models reveal about the population dynamics of a cooperatively breeding species? *Oikos*, **120**, 787-794.

Clutton-Brock, T. (2002) Behavioural ecology – breeding together: kin selection and mutualism in cooperative vertebrates. *Science*, **296**, 69-72.

Clutton-Brock, T. (2008) Meerkat manor: Flower of the Kalahari, Phoenix.

Grimm, V. and Railsback, S.F. (2005) *Individual-based modelling and ecology* (2005) Princeton University Press, Princeton, NJ.

Ozgul, A., Bateman, A.W., English, S., Coulson, T. and Clutton-Brock, T.H. (2014)

Linking body mass and group dynamics in an obligate cooperative breeder.

J. Animal Ecology, **83**, 1357-1366.

Willekens, F. (2014) *Multistate analysis of life histories with R*, Springer, Cham.

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Detecting heterogeneity in capture-recapture models: diagnostic goodness-of-fit tests

ANITA JEYAM

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Abstract:

Capture-recapture models have increased in complexity in order to be more biologically realistic. It is possible to fit many models to the same dataset, and the best model is generally chosen using information criteria, which will select the least worst model among the subset of tested models. Hence, it is important to check that candidate models fit the data adequately.

Specific diagnostic goodness-of-fit tests exist for capture-recapture models (Pradel et al, 2003). These tests not only assess the fit of the model, subcomponents of them provide biologically interpretable results which diagnose why the model does not fit. For the time-dependent Cormack-Jolly-Seber (CJS) model, these tests can detect trap-dependence and transience. However, those are not the only reasons a time-dependent CJS model would provide an inadequate fit to the data. We focus on the case where the data exhibits heterogeneity in capture, which is taken into account using mixture models (Pledger et al, 2003).

We investigate the use of diagnostic goodness-of-fit tests to find out whether this type of heterogeneity can be detected and specifically identified: for instance, does heterogeneity in capture affect the tests differently from a combination of trap-dependence and transience? We derive a specific diagnostic test for heterogeneity in capture and use simulation to assess its performance, as well as the performance of the approach proposed in Péron et al. (2010).

References

Péron, G. , Crochet, P.-A. , Choquet, R. , Pradel, R. , Lebreton, J.-D. and Gimenez, O. (2010) Capture-recapture models with heterogeneity to study survival senescence in the wild. Oikos, 119(3): 524-532.

Pledger, S., Pollock, K. H. and Norris, J. L. (2003) Open capture-recapture models with heterogeneity: I. Cormack-Jolly-Seber model. Biometrics, 59: 786-794.

Pradel, R., Wintrebert, C., and Gimenez, O. (2003) A proposal for a goodness-of-fit test to the Arnason-Schwarz multisite capture-recapture model. Biometrics, 59(1), 43-53.

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Efficient model-fitting for N-mixtures

TAKIS BESBEAS

Athens University of Economics and Business, Athens, Greece
University of Kent, Canterbury, UK

Abstact:

Estimating population abundance is an important component of ecological research. N-mixture models can be used to estimate animal abundance from counts with both spatial and temporal replication without requiring individuals to be indentified. The original N-mixture model (Royle, 2004) was developed for closed populations but the model has been recently extended to open populations by including population dynamics parameters (Dail and Madsen, 2011). The models offer great potential but require an upper bound to be set, which complicates computations. We discuss efficient methods for fitting N-mixtures based on latent-state modelling. We illustrate the new approach using real and simulated data and compare it with existing methodology.

References

Dail, D. and Madsen, L. (2011). Models for estimating abundance from repeated counts of an open metapopulation. Biometrics 67, 577–587.

Royle, J. A. (2004a). N-mixture models for estimating population size from spatially replicated counts. Biometrics 60, 108–115.

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DAVID ELSTON

Some adventures in statistical ecology

Abstract:

Statistical methods are central to the collection and assessment of evidence by ecologists. The range of issues to be addressed is wide and continues to expand as technological advances lead to new types and growing volumes of data. Hence a career as a statistical ecologist is a voyage of discovery into the properties and potential uses of familiar methods as well as the development of new approaches. I will describe some of my own forays into the jungle of (personally) unchartered territory, what these have taught me, and some general points that may be of relevance to others.

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EMILY DENNIS

Dynamic models for longitudinal butterfly data

Emily B. Dennis[1,2], Byron J.T. Morgan[1], Stephen N. Freeman[3], David B. Roy[3] and Tom Brereton[2]

[1]*School of Mathematics, Statistics and Actuarial Science, University of Kent, Canterbury, Kent*
[2]*Butterfly Conservation, East Lulworth, Dorset*
[3]*Centre for Ecology & Hydrology, Wallingford, Oxfordshire*

Abstract:

Butterfly populations are undergoing changes in abundance, phenology and voltinism. As they respond sensitively and rapidly to changes in habitat and climate, their population status is a valuable indicator for changes in biodiversity and phenology. Butterflies have multi-stage life cycles and hence count data of the adult stage fluctuate within each year in response to their emergence as adults. A range of models have been proposed to describe this seasonal variation (Dennis et al. 2013, 2014, Matechou et al. 2014), but do not impose a relationship between counts from one year to the next.

We present models which provide succinct descriptions of seasonal insect count data from consecutive years. This approach produces novel estimates of the key parameters of brood productivities, making the data from each brood a function of those in the previous brood. It may be applied to univoltine and bivoltine species. For the latter, the productivities of each brood are estimated separately, which results in new indices for different generations.

A concentrated likelihood results in appreciable efficiency gains (Dennis et al. 2014). We illustrate the methods using data from the UK Butterfly Monitoring Scheme. Both phenomenological and stopover models are used, including weather and site-specific covariates. Comparisons are drawn with the performance of existing models.

The predictions of fitted dynamic models have the potential to improve our understanding of underlying demographic processes. This will be important for insects such as UK butterflies, many species of which are in decline.

References

Dennis, E.B., Freeman, S.N., Brereton, T. & Roy, D.B. (2013) Indexing butterfly abundance whilst accounting for missing counts and variability in seasonal pattern. *Methods in Ecology and Evolution*, 4, 637-645.

Dennis, E.B., Morgan, B.J.T, Freeman, S.N., Roy, D.B. & Brereton, T. (2014) A generalised abundance index for seasonal invertebrates. Technical report UKC/SMSAS/14/006, University of Kent.

Matechou, E., Dennis, E.B., Freeman, S.N. & Brereton, T. (2014) Monitoring abundance and phenology in (multivoltine) butterfly species; a novel mixture model. *Journal of Applied Ecology*, 51, 766-775.

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How to get the best out of distance sampling using model selection

ROCIO PRIETO GONZALEZ

Rocio Prieto Gonzalez, Tiago A. Marques, Len Thomas

Abstract:

Many simulations have been done for testing the properties and robustness of distance sampling estimators. When data is generated from a particular model and fitted using the same model they seem to perform well. However, in a real life situations the true model is unknown. Therefore, the standard methods for fitting detection functions to distance sampling data (as described by Buckland et al. 2001) involve selecting among several classes of semi-parametric models, and it is recommended that this selection is performed using standard model selection techniques such as AIC.

Here, we check the performance of distance sampling estimators when data was analysed using model selection, comparing line and point transect estimators in a reasonable number of scenarios. As has been shown, point transect estimation is more difficult and model selection more critical, since the fit of the model to the distance data near the line or point is the most important and in point transects fewer distances are recorded. Our simulation study show that, point transect sampling can be highly biased ($>15\%$) if the sample size is under the 75-100 observations recommended (Buckland et al. 2001). Moreover, under realistic circumstances and an adequate sample size, in some situations we still find around 10% bias, unless the sample size is very high.

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The use of likelihood-free inference techniques in designing complex sensor-based studies

ADAM BUTLER

Coauthors: Sarah Brocklehurst (BioSS), Maria Bogdanova (CEH), Kate Searle (CEH), Mark Brewer (BioSS), Mark Newell (CEH), Sarah Wanless (CEH), Catarina Rei (EDPR), Paula Low (EDPR), Francis Daunt (CEH)

Abstract:

One of the key trends within modern biology has been a rapid rise in the use of automated sensors to study the behaviour, movement, physiology and state of individual organisms, as well as interactions with their environment and with other organisms. It is now relatively cheap and straightforward to collect large amounts of data using automated sensors, but there continue to be important bottlenecks that restrict data collection. In seabird ecology, for example, there are typically bottlenecks relating to the number of individuals that can be tagged and the total number of observations that can be collected. There are aspects of sensor operation that can be controlled, however, including the frequency at which records are collected.

A crucial issue when designing studies using this type of data is to decide what the optimal values for these controllable parameters are, given the constraints imposed by the bottlenecks. Such questions relate to general statistical issues of experimental design, but the complex nature of the data involved (hierarchical, with strong autocorrelation in both space and time and potentially complicated patterns of missing data) mean they cannot be addressed using standard methods. We propose a framework based on simulation, which is motivated by techniques developed in the context of likelihood-free inference, and demonstrate this approach using both simulated data and real seabird tracking data from three colonies in SE Scotland.
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"What's missing from Movement Ecology?" / "Is movement analysis too complicated?"

EDD CODLING

Abstract:

In my presentation I will discuss two open questions:

"What's missing from Movement Ecology?" Recent advances in tracking technology have allowed us to collect huge amounts of animal movement data. However, the shift towards a more complete study of "movement ecology", rather than simply studying "movement", has not yet been fully realised. I will highlight the key data requirements and methodological features that may be required for a full movement ecology framework and suggest some ways forward to overcome current problems.

"Is movement analysis too complicated?" Methods and tools for analysis of movement data have become increasingly more sophisticated over the past few years. However, many of these tools are now highly complex requiring significant expertise to understand and implement correctly, or are computationally intensive. Although these tools are often more statistically rigorous they may not always outperform more simple methods when used in a practical way. I will discuss a number of reasons why simple tools are still important as part of a general toolkit for movement analysis.

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JORGE ALBERTO VÁZQUEZ DIOSDADO

Differences in space use patterns between lame and non-lame dairy cows

Jorge A. Vázquez Diosdado[1], Zoe E. Barker[2], Jonathan R. Amory[2], Darren P. Croft[3], Nick J. Bell[4], Edward A. Codling[1].

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Abstract:

Advances in sensor technology and novel statistical methodologies have made it possible to accurately derive space-use patterns of movement in both wild and domesticated animal species. Until now, space-use patterns have not been directly linked to differences in the health status of animals. In this study, cows from a high yielding group on a commercial farm were scored for lameness using the DairyCo mobility score. 10 non-lame (score 0) and 10 lame (score 2) cows were subsequently fitted with novel local positioning wireless sensors (Omnisense 500®) mounted on a neck collar. The sensors were used to track the position of each cow within their normal management group in a cubicle shed for 5 days. We investigated space use intensity of different zones of the barn and transitions between them. The results showed significant differences on both space use intensity and transitions between zones between lame and non-lame cows. Difference in space use intensity indicates that lame cows spent more time in zones close to the milking parlour. In addition, non-lame cows have significantly more transition between zones that are far away from the milking parlour. Repeated visits between the farthest zones of the barn were also significantly higher for non-lame cows. Differences in space-use patterns could potentially be used to build a predictive model for early detection of lameness in dairy cows, leading to faster treatment and improved welfare. The methodology could be extended to explore space-use patterns in other animal species.

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Likelihood Profiles and Parameter Redundancy

DIANA COLE

Abstract:

If two parameters are confounded so that they only ever appear in the model as a product, then it is not possible to estimate the two parameters individually – only their product. Such a model is termed parameter redundant. In more complex models the confounding it is not always as obvious. In such cases symbolic methods can be used to detect parameter redundancy and also give combinations of parameters that can be estimated (see for example Cole *et al,* 2010). Symbolic methods are not straightforward to use, and require the use of a symbolic algebra package such as Maple. But they are not the only way to detect parameter redundancy, numeric methods exist as well. However numeric alternatives can be inaccurate. A hybrid-numeric method has been developed that is simpler to use and more accurate (Choquet and Cole, 2012). However unlike the symbolic method this cannot be used to find combinations of parameters that can be estimated. Here we consider an alternative method which examines the likelihood.

A parameter redundant model will not have a unique maximum likelihood estimate as there will be a flat ridge in the likelihood surface (Catchpole and Morgan, 1997). In practise, most ecology models are fitted using numerical methods so the flat ridge might not be obvious. One way to detect this is using a likelihood profile. The likelihood profile will be flat for a parameter that cannot be estimated due to parameter redundancy. The information used to create a likelihood profile can also be used to examine which combinations of parameters that can be estimated, see Eisenberg and Hayashi (2014). This talk explores how this method applies to ecological models.

References

Catchpole E. A. and Morgan, B. T. J. (1997) Detecting parameter redundancy. Biometrika, 84, 187–96.

Choquet, R. and Cole, D.J. (2012) A Hybrid Symbolic-Numerical Method for Determining Model Structure. Mathematical Biosciences, 236, 117-125.

Cole, D. J., Morgan, B. J. T and Titterington, D. M. (2010) Determining the Parametric Structure of Non-Linear Models. Mathematical Biosciences, 228, 16-30.

Eisenberg, M.C. and Hayashi, M. A. L. (2014) Determining identifiable parameter combinations using subset profiling. Mathematical Biosciences, 256, 116–126.

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Approximate pseudo likelihood estimation of species richness

RATCHANEEWAN KUMPHAKARM

Abstract:

The distribution of the number of distinct species in a random sample of individuals from a population, where different species have unequal probabilities of selection, is known exactly, but the exact form is computationally intractable except for small samples. Hidaka (*Biometrika,* 2014) gives the asymptotic distribution as the sample size tends to infinity, and suggests how this can be used to construct approximate (pseudo-) likelihood for estimating the number of species in the population. In this talk an improved approximation is proposed and the performance of Hidaka's method is explored.

Reference
Hidaka, S. (2014). General type-token distribution. Biometrika, 101(4), 999-1002.

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The development of removal models with a hidden state: A case study for reptile and amphibian data

MING ZHOU

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Abstract:

Classical removal experiments can be used to estimate the abundance of a population within a closed area, by successively sampling the area for particular animal species and relocating captured individuals to other sites (Zippin, 1956). In the simple case of constant capture probability, removal models result in geometric declines of predicted counts of individuals over time. However, when removals are conducted on reptiles and amphibians, the animals sometimes become undetectable as they hide below ground, and then emerge into the study area from underground when climatic conditions are suitable. Thus we propose a new class of removal models which incorporate a hidden state, allowing the modelling of movement into and out of the observable study area.

The work is motivated by removal data on slow worms, *Anguis fragilis* and common lizards, *Zootoca vivipara*. Removal sampling of these protected species is often undertaken prior to land development. We consider two model developments: (1) a flexible multievent framework (Pradel, 2005) to allow for individuals becoming temporarily unavailable for detection, and (2) accounting for seasonal/climatic variations in detectability and transition probabilities.

We evaluate the performance of the proposed model and consider limitations of our approach by applying it to data from simulations.

Reference
Pradel, R. (2005) Multievent: an extension of multistate capture-recapture models to uncertain states. Biometrics. 61:442-447

Zippin, C. (1956) An evaluation of the removal method of estimating animal populations. Biometrics, 12, 163-189.

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Does body size accurately predict movement rates in fish? An analysis of marine telemetry data.

CHRISTOPHER GRIFFITHS

Griffiths C.[1,2], Blanchard, J.[2], Blackwell, P.[3], Righton, D.[4], Law, R.[5], J. Pitchford.[5], G. Delius.[5]

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Abstract:

Marine ecosystems are highly size-structured. Fish grow several orders of magnitude in their lifetime, feeding on organisms that are a fraction of their own size. As a predator consumes a smaller prey item, the prey item will die and the predator will grow based on some value of assimilation. This produces a continuous size gradient or size spectrum that is indicative of marine food webs. In general terms, a predator's ability to catch its prey depends on three rules: (1) the availability of prey, (2) the size suitability of prey and (3) the volumetric search rate. Commonly referred to as a 'search volume' the volumetric search rate of an individual or population is a function of the distance travelled per unit time and a search radius in three-dimensional space. Currently size spectrum models assume that search volume scales allometrically with body size on a log-log scale however no work has attempted to quantify this relationship at the interspecific or community level. Our study introduces the idea of using individual based to test such assumptions by analysing the movement characteristics of tagged fish across a range of body sizes. Beginning with detailed information on several marine fish we compute approximations of movement on the horizontal and vertical axes then combine them to produce a measure of distance travelled per day. In this presentation I will discuss the methodology behind our approximations and show how both types of movement vary throughout the year as individuals move between habitats. I will then briefly explore how distance travelled per day scales with body size with the ultimate aim of incorporating more biological realistic movement into size spectrum community models.

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The `Step and Turn' Animal Movement Model in Continuous-Time

ALISON PARTON

Abstract:

Understanding how wildlife paths evolve has the potential to affect a range of areas within ecology. Yet the questions of why, when and where animals move are still unanswered in many areas of ecology. Due to their intuitiveness and accessibility to non-statisticians, the current group of statistical animal movement models with the most widespread use by ecologists are those based on Morales et al. (2004) using 'turning angles' and 'step lengths'. However, these models are based in a discrete-time setting in which the animal's location is only defined at pre-determined discrete time-points.
This talk will discuss the need for movement models formulated in continuous-time, introducing an `equivalent' continuous-time version of the Morales et al. (2004) model. Work is still in progress to develop techniques for full Bayesian inference for movement data under this model, however, current progress on this work will be presented and discussed.

J.M. Morales, D.T. Haydon, J. Frair, K.E. Holsinger, and J.M. Fryxell. Extracting more out of relocation data: Building movement models as mixtures of random walks. Ecology, 5(9):2436-45, 2004. doi: 10.1890/03-0269.

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Continuous-time movement modelling

HAJAR ALKHEZI

Abstract:

I am currently at the beginning of my PhD programme, looking at new methods of Bayesian inference for animal movement in continuous time. For a range of continuous-time models, there are existing methods which are exact, but which require complex algorithms to implement. Our goal is to develop new methods which are good approximations, motivated by exact methods but easier to implement and more efficient. We hope that these approximations will make modelling animal movement in continuous time more widespread. The methods are expected to be simulation based and to make use of Markov Chain Monte Carlo algorithms.

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Exact Bayesian statistics for continuous-time movement

PAUL BLACKWELL

Realistic models of animal movement need to take account of variations in behaviour, in response to local habitat type, time of day, etc. Even though an animal's location is typically observed only at discrete times, there are many advantages to formulating movement models in continuous time, allowing coherent interpretation and comparison as well as natural handling of missing or irregular observations. A rich class of models can be defined by representing an animal's behaviour as a continuous-time Markov chain, with transition rates that may depend on time and on the animal's location, and representing its movement as a diffusion process, with parameters determined by its behaviour.

In this talk I will describe some recent progress in Bayesian inference for such models using a Markov chain Monte Carlo approach, exploiting an exact simulation technique to avoid any time-discretization error, despite the complex relationship between location, behaviour and movement. This is joint work with Mu Niu.

These ideas will be illustrated using data on individual fishers, Martes pennanti, (courtesy of Scott LaPoint, Max Planck Institute for Ornithology, Konstanz) and wild boar, Sus scrofa, (courtesy of Mark Lambert, Animal and Plant Health Agency, York). If time permits, I will also look at extensions to multiple animals, using data on a group of simultaneously tracked reindeer, Rangifer tarandus, (courtesy of Anna Skarin, Swedish University of Agricultural Sciences, Uppsala).

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How many fish are in the sea?

MICHAEL SPENCE

Abstract:

The need to understand marine ecosystems has led to the development of a number of different complex models. These models can be used to make forecasts about the fate of marine ecosystems under different past and future scenarios.

Biasses and uncertainties lead to different models giving different predictions under these scenarios. By examining the structural and parameter uncertainty of these models we are able to build a multi-model ensemble that allows us to make probabilistic statements about the true prediction.

In this talk we will describe the general framework we are using to build a model ensemble and demonstrate this with a case study of the North Sea.

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Improved trend estimation of European spatio-temporal forest health monitoring data

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Abstract:

Forests are economically, recreationally and ecologically important, providing timber and wildlife habitat and acting as a carbon sink, among many ecosystem services. They are therefore extremely valuable to society, and it is crucial to ensure that they remain healthy. For these reasons forest health is monitored in Europe by The International Co-operative Programme on Assessment and Monitoring of Air Pollution Effects (ICP Forests) in cooperation with the European Union. ICP Forests was launched in 1985 due to the growing public awareness of possible adverse effects of air pollution on forests and is operating under the UNECE Convention on Long-range Transboundary Air Pollution. More recently climate change has contributed to the decline in forest health. Part of the ICP are around 6000 observation plots on a systematic transnational grid of 16 x 16 km throughout Europe. The yearly Report on the Forest Condition in Europe, e.g (Michel et al 2014), presents mostly descriptive statistical analyses of European forest health monitoring data. Based on (Augustin et al 2009) we propose a unified modelling approach for the European forest health data enabling to model several countries combined for certain species.

In the modelling it is necessary to consider the possibility of spatial and temporal correlations between survey plots, a differing temporal trend of defoliation between areas because of site characteristics, pollution levels and transnational inconsistencies and gaps in the data.

References
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