



# SEEM CONFERENCE

## 2-4 DECEMBER 2019



# VICTORIA UNIVERSITY OF WELLINGTON

## Detailed Programme and Abstracts



Photo credit: Associate Professor Isabel Castro, Massey University

### Contents

Monday 2 December .....	2
Tuesday 3 December .....	3
Wednesday 4 December .....	4
Abstracts .....	5

All sessions will be held in Lecture Theatre 1 in the Te Toki a Rata Building (see the [Kelburn Campus Map](#))

## Monday 2 December

- 8:00** Registration
- 8:45** Welcome, opening address
- 9:00** Keynote speaker – Shirley Pledger  
[\*The symbiosis between ecologists and statisticians\*](#)
- 10:00** Morning tea
- 10:30** Anthony Charsley  
[\*Modelling the probability of capture for New Zealand's longfin eels and shortfin eels\*](#)
- 10:55** Malyon Bimler  
[\*Interaction networks to reveal the structure of complex plant communities\*](#)
- 11:20** Gordana Popovic  
[\*Hierarchical clustering with fused mixtures\*](#)
- 11:45** Russell Millar  
[\*Evaluating predictive loss of models for over-dispersed count data\*](#)
- 12:10** Lunch
- 13:00** Invited speaker – Jim Thorson  
[\*Improved realism in model-based community ecology: identifying nonlocal associations in multivariate spatio-temporal models\*](#)
- 13:40** Break
- 13:45** Zach Goeden  
[\*Likelihood-based clustering of commercial fisheries data\*](#)
- 14:10** Kyuhan Kim  
[\*A two stage-structured Schaefer model in a state-space framework, with application to the Korean pollock population\*](#)
- 14:35** Charlotte Jones-Todd  
[\*Continuous-time discrete-space models of marine mammal exposure to Navy sonar\*](#)
- 15:00** Afternoon tea
- 15:20** Robin Aldridge-Sutton  
[\*New methods for estimating population size based on close-kin genetics and extensions\*](#)
- 15:45** Wen-Han Hwang  
[\*Right-censored negative binomial models with detection times\*](#)
- 16:10** Peter Caley  
[\*On inferring population trends of mobile waterbirds from transect surveys in variable environments\*](#)
- 16:35** Break
- 16:40** Invited speaker – Danielle Shanahan  
[\*Conservation in cities: does it make sense?\*](#)
- 17:20** Break
- 17:30** Poster + Pizza Session
1. Alberto De Rosa: [\*Hey, R. U. There? Autonomous Recording Units - ARUs - as means to monitor sounds in a spatially explicit fashion\*](#)
  2. Heather Jenkins: [\*Comparative analysis of farms across the New Zealand landscape\*](#)
  3. Julius Juodakis: [\*Evaluating acoustic monitoring surveys via spatial capture-recapture\*](#)

4. Lindsay Morris: [Goodness-of-fit of Bayesian spatial models using pivotal discrepancy measures](#)
5. Zihao Wen: [Variable Selection for Inhomogeneous Poisson Point Process Using Minimum Message Length: an Ecological Case Study](#)

## Tuesday 3 December

<b>9:00</b>	Keynote speaker – Simon Upton <a href="#"><u>Environmental Reporting in New Zealand</u></a>
<b>10:00</b>	Morning tea
<b>10:30</b>	Sonja Miller <a href="#"><u>Increasing the reach: 'Re-use' of research in environmental reporting</u></a>
<b>10:55</b>	David Harris and Camden Howitt <a href="#"><u>From cleaning the beach to developing litter statistics - a model for community, NGO, and government collaboration</u></a>
<b>11:20</b>	Lilian Morrison <a href="#"><u>Time Series Trends in Environmental Monitoring</u></a>
<b>11:45</b>	Break
<b>11:50</b>	Invited speaker – Graham McBride <a href="#"><u>All this debate about p-values misses the point: test sensible hypotheses, or simply make an assessment</u></a>
<b>12:30</b>	Lunch
<b>13:00</b>	Excursions

## Wednesday 4 December

<b>9:00</b>	Keynote speaker – Rachel Fewster <a href="#"><i>How to count the unseen when we can't count the seen: new methods for dealing with uncertain identity in capture-recapture studies</i></a>
<b>10:00</b>	Morning tea
<b>10:30</b>	David Chan <a href="#"><i>Spatial capture-recapture: Applications to acoustic surveys of cetacean populations</i></a>
<b>10:55</b>	Rishika Chopara <a href="#"><i>That's not the Mona Lisa! How to interpret spatial capture-recapture density surface estimates</i></a>
<b>11:20</b>	Nick Mulgan <a href="#"><i>Estimating the size of a very low density population</i></a>
<b>11:45</b>	Ben Stevenson <a href="#"><i>New point processes for spatial capture-recapture models</i></a>
<b>12:10</b>	Lunch
<b>13:00</b>	Invited speaker – Res Altwegg <a href="#"><i>Mapping biodiversity in remote areas</i></a>
<b>13:40</b>	Break
<b>13:45</b>	Elliot Dovers <a href="#"><i>Combining sources of data in species distribution models</i></a>
<b>14:10</b>	David Wilkinson <a href="#"><i>Defining and evaluating the predictions of joint species distribution models</i></a>
<b>14:35</b>	Helene Thygesen <a href="#"><i>Spatial trends in DOCs National Monitoring Programme biodiversity data</i></a>
<b>15:00</b>	Afternoon tea
<b>15:20</b>	Maeve McGillicuddy <a href="#"><i>Adding latent variables to glmmTMB for parsimonious high dimensional modelling</i></a>
<b>15:45</b>	David Hodge and Bonnie Farrant <a href="#"><i>'R' for Environmental Reporting</i></a>
<b>16:10</b>	John Forne <a href="#"><i>Spatial statistics for Environmental Reporting</i></a>
<b>16:35</b>	Break
<b>16:40</b>	Invited speaker - Nick Golding <a href="#"><i>Fitting demographic models to species distribution data</i></a>
<b>17:20</b>	Closing remarks
<b>18:00</b>	Dinner - Wellesley Boutique Hotel

## Abstracts

### Keynote and Invited speaker abstracts

#### Mapping biodiversity in remote areas

*A/Prof Res Altwegg, University of Cape Town*

When the South African government considered developing the vast arid interior of the country for shale gas extraction in 2016, a group of scientists teamed up to collect much-needed distribution data for hundreds of species with the view to guide later impact assessments. This project raised a number of questions that typically need to be addressed when designing biodiversity surveys in remote areas, and during the subsequent data analysis. How do we select sampling sites and how many of them do we need? How do we design a sampling protocol that allows us to get robust estimates of occupancy probability while still being practical in the field? How do we adapt the protocol for each taxonomical group (including plants, insects, scorpions, mammals, reptiles, birds and others)? How do we make best use of sparse data? We used a probabilistic design that sampled the important environmental gradients efficiently and also took into account costs of reaching each site. We found that each taxonomic group needed a slightly different data-collection protocol but in general, a combination of spatially repeated sampling and recording time to first detection of each species proved workable. We analysed the data using hierarchical multi-species occupancy models that used time-to-detection information. The time-to-detection information improved occupancy estimates even though some replication was still necessary to get reliable estimates. For most taxa, we had additional distribution information from opportunistically collected presence-only records. We included this information in our analyses using recent data fusion techniques and found that it improved our occupancy estimates substantially for most species. Mapping biodiversity in remote areas is challenging but recent developments in data collection techniques, sampling protocols and data analysis tools offer exciting new possibilities.

#### How to count the unseen when we can't count the seen: new methods for dealing with uncertain identity in capture-recapture studies

*Professor Rachel Fewster, University of Auckland*

Capture-recapture is one of the most popular methods for estimating population size and trends. However, physically capturing and tagging animals can be a dangerous and stressful experience for both the animals and their human investigators - or if it transpires that the animals actually enjoy it, biased inference may result. Consequently, researchers increasingly favour non-invasive sampling using natural tags that allow animals to be identified by features such as coat markings, dropped DNA samples, acoustic profiles, or spatial locations. These innovations greatly broaden the scope of capture-recapture estimation and the number of capture samples achievable. However, they are imperfect measures of identity, effectively sacrificing sample quality for quantity and accessibility. As a result, capture-recapture samples no longer generate capture histories in which the matching of repeated samples to a single identity is certain. Instead, they generate data that are informative - but not definitive - about animal identity.

I will describe two ways of dealing with capture-recapture data in the face of uncertain identity. The key characteristic of these methods is that they do not make any attempts to explicitly match samples to the same animal. This means that computation speeds remain fast even for very large sample sizes. Analysing data with millions of samples takes much the same time as analysing hundreds.

The first approach is a new analysis framework termed Cluster Capture-Recapture (CCR). For CCR analyses, we assume that repeated samples from the same animal will be similar, but not necessarily identical, to each other. We treat the sample data as a clustered point process, and derive the necessary properties of the process to estimate abundance and other parameters. I will describe a preliminary application of CCR for acoustic monitoring.

The second approach concerns a broad class of models known as latent multinomial models. These include two-source capture-recapture models - where animals are captured by two different protocols such as photo-ID and DNA samples that cannot be matched to each other - and related multi-list models in the context of medical and social statistics, as well as more general models where data are summarized before reporting. Previous approaches to model-fitting largely use simulation-based methods such as data-augmentation via MCMC. I will show how a likelihood based on the saddlepoint approximation method can deliver remarkably fast and accurate inference for these models.

## Fitting demographic models to species distribution data

*Dr Nick Golding, University of Melbourne*

Correlative species distribution models are good at describing species' current distributions, and inferring their environmental drivers. However they are pretty bad predicting what will happen if we change something, like fragmenting habitat, introducing other species, or implementing a control or conservation action. Replacing the statistically convenient (but ecologically meaningless) internal structure of these models with demographic models should enable us to make much better predictions of how distributions will change.

I will present recent work developing demographic species distribution models that extend matrix population models to explicitly consider how vital rates vary through space (like spatial integral projection models) but are fitted to commonly available species distribution data (like dynamic range models). Combining these approaches enables us to fit ecologically-realistic species distribution models without the need for detailed demographic data. We can include density dependence, dispersal, biotic interactions and prior knowledge of species' population dynamics and ecology.

Asking for more information from the same data means we have to deal with a number of potential issues, including poorly-identified parameters and more computationally intensive statistical inference. I'll argue that non-identifiability is actually a good thing (in this context) and show how the computational issues can be resolved using the Bayesian inference package greta, and some new extensions for modelling dynamical systems.

## All this debate about p-values misses the point: test sensible hypotheses, or simply make an assessment

*Graham McBride, NIWA, Hamilton*

In 2016 a group of senior international epidemiologists and statisticians published commentary on 25 contentious issues relating to the use of  $p$ -values. These included inferences that "Statistical significance indicates an important relation has been detected", or "...  $p$ -value greater than 0.05 means that no effect was observed". A premiere science journal ( *Nature* ) has this year published five commentaries on shortcomings and defences of  $p$ -values. Yet most applied science authors and editors seem not to be aware of the issues; vast numbers of  $p$ -values are reported as the norm in science journals.

I argue that's because it is seldom explained that these  $p$ -value difficulties arise from testing hypotheses that are a priori false-so we learn very little from the results. If it really is necessary to test, then do so for hypotheses that may be true, i.e., interval or one-sided tests. Or simply make an assessment. For example, we have developed a trend assessment procedure aligned with a requirement of the National Policy Statement for Freshwater Management (Objective A2) that overall water quality in a 'Freshwater Management Unit' is improved or maintained. It abandons testing altogether and instead considers two questions directly related to these requirements: (i) what is the direction of change? (ii) if that can be inferred, is that trend environmentally significant? The key postulate-in place of a hypothesis-is that there is always a trend, of whatever magnitude (but you may not have enough data to decide on its direction).

This approach has recently found favour with water quality monitoring and management agencies. An example is given of a country-wide assessment that, for the first question, reports more meaningful information on trend direction than the traditional testing approach. The case of environmental significance is rather more complex (and is ignored altogether in point-hypothesis tests). Some ideas are proposed for how that may be addressed.

## The symbiosis between ecologists and statisticians

*Professor Shirley Pledger, Victoria University of Wellington*

Useful scientific advances are often made in interdisciplinary research. One classical example is so-called "Applied Mathematics" which blends physics and mathematics to provide formulae for topics as disparate as bridge design and planetary motion. Another far-reaching example is the development of applied statistics by R. A. Fisher and others for the design and analyse agricultural trials, leading to more efficient provision of food.

Applied statisticians are fortunate in being able to work with researchers in many different disciplines, learning their jargon, finding what they need to know, linking it with existing statistical models and/or developing new study designs or models to approximate the reality of the situation.

The interplay of ideas between ecologist and statistician will be illustrated by examples from capture-recapture and ecological community analysis. In these examples, chains of ideas over time have refined the models, made them more useful for description and prediction, given insights for generating more studies, and provided methods which are also useful in other disciplines. Topics touched on will include heterogeneity, over-dispersion, spatial distributions, pattern detection, under-dispersion and "Big Data".

(There will be quite a lot about underdispersion, which may even culminate in a theorem, but very little indeed on big data.)

It is to be hoped that the relationship between ecologist and statistician is always symbiotic, mutualistic in a positive way, and not parasitic.

## Conservation in cities: does it make sense?

*Dr Danielle Shanahan, Director Centre for People and Nature, Zealandia*

Conservation is extremely challenging in urban landscapes, yet cities continue to invest significant resources into managing and promoting biodiversity in these highly altered environments. Does this make sense where global resources for conservation are scarce? In this talk I will discuss key motivations for carrying out conservation in cities, drawing on policy and planning statements from across the Oceania region. I will highlight the transformation of Wellington's birdlife, which is perhaps the only city in the world where bird biodiversity is on the rise, not the decline. Finally, I will talk about what becoming nature-rich means for people, focusing on key research outcomes that have begun to quantify the health and wellbeing benefits that people receive from nature experiences.

## Improved realism in model-based community ecology: identifying nonlocal associations in multivariate spatio-temporal models

*Dr James Thorson, Alaska Fisheries Science Center, National Marine Fisheries Service, NOAA, Seattle, WA, USA*

Community ecology is central to understanding global change in the Anthropocene, including (to choose a few examples) the impact of invasive earthworms on Boreal carbon cycling, trends in fish migration in response to melting sea ice, and changing fire regimes in high-latitude forests. These examples all include complex linkages between multiple physical and biological variables operating at both local and regional scales. I begin by claiming that community ecology can address these problems by treating each variable as a function defined across continuous space and discrete time, where expected change is represented by a multivariate functional. I summarize efforts to approximate this problem using localized dynamics, where previous research has addressed four "big-N" problems posed by spatial correlations, correlated process errors across species, advective-diffusive movement, and asymmetric species interactions. I then discuss new avenues to represent nonlocal effects, representing e.g. behavioral adaptation to changing landscape conditions. To do so, I first show that multivariate spatio-temporal models can generalize the "empirical orthogonal function" (EOF) analysis commonly used in atmospheric science and oceanography, and can extract dominant "features" from spatially distributed physical measurements. I then explore variable-coefficient models as a way to estimate changes in biological processes resulting from dominant physical features. Finally, I introduce "empirical orthogonal regression," where EOF analysis is conducted simultaneously with a time-series biological model, to estimate the rotation of physical features that has maximal explanatory power for a regional biological process. I end by discussing why this class of nonseparable spatio-temporal models is likely to be useful to account for behavioral adaptation to changing physical conditions.

## Environmental Reporting in New Zealand

*Simon Upton, NZ Parliamentary Commissioner for the Environment*

The Parliamentary Commissioner for the Environment has a statutory role under the Environmental Reporting Act 2015 to comment on NZ's environmental reporting system. With the completion of the first full cycle of five domain reports and a synthesis report under the Act, the Commissioner has decided to review its efficacy. The review is due for completion in late 2019.

The scope of the review covers the Environmental Reporting Act itself, the structure and implications of the current reporting framework, the wider environmental 'data' system and the roles of different central and local government agencies in that system. The review is guided by three key questions:

1. What is the purpose of environmental reporting and how do the reports currently being undertaken contribute to that purpose?
2. What sort of information is needed to support environmental reporting, what underlying research is needed to inform the collection of information and what analytical framework is required to present the results of data collection?
3. What contribution do environmental reports make to improving environmental outcomes and well being?

Environmental reporting in NZ has come a long way in twenty years, and is still evolving today. In his presentation, Simon Upton will present the key conclusions of his review, and will discuss his recommendations for improvement to New Zealand's environmental reporting system.

## Contributed presentation abstracts

### 1. (O) New methods for estimating population size based on close-kin genetics and extensions

Robin Aldridge-Sutton, Emma Carroll, Rachel Fewster  
University of Auckland, Department of Statistics  
[rald898@aucklanduni.ac.nz](mailto:rald898@aucklanduni.ac.nz)

Close-kin genetics is an emerging approach to estimating population size and demographics, based on family relationships elicited from samples of genotyped animals. The field is still in its infancy but is generating considerable interest, partly due to recent advances in genomics providing high-resolution genotype datasets. Some flagship studies have already been completed, including estimates of population demographics for white sharks in Australia and New Zealand. We are interested in applying the method to the New Zealand southern right whale population, which underwent a dramatic decline after an estimated 35,000 whales were slaughtered during 19th century whaling, and is now recovering. We investigate the accuracy and precision of close-kin genetics for estimating population size for this species, and present a Shiny interface for investigating the performance of the method by simulation under realistic population trajectories. We also present new ideas for extending close-kin genetics to a wider methodology for estimating population abundance and demographics. Instead of requiring the analyst to predetermine kinship between each pair of animals, and delete any pairs over which there is doubt, the new method is based on a pseudo-likelihood which incorporates multiple levels of kinship together with kinship uncertainty. We present preliminary results and compare the new approach with the standard close-kin genetics approach.

### 2. (O) Interaction networks to reveal the structure of complex plant communities

Malyon Bimler, Trace Martyn, Daniel B. Stouffer, Margaret M. Mayfield  
University of Queensland  
[malyonbimler@gmail.com](mailto:malyonbimler@gmail.com)

Understanding how ecological communities function and respond to change requires an understanding of how the different species within it relate to each other. Those relationships are difficult to quantify in complex plant communities because they cannot be directly observed as in food webs or other interaction networks, and must instead be inferred by other means. Current methods are inadequate for plant systems because they tend to rely on co-occurrence patterns (inaccurate) or intensive experimental designs (time-consuming, especially for diverse communities). I describe a general framework which allows us to estimate all pair-wise interactions in complex plant communities from empirical data and population dynamics models. This framework requires a multi-tiered approach to resolve all interactions. We first apply individual fitness models to each species in order to estimate interactions between species commonly observed to co-occur, then use a response-effect model to approximate unobserved interactions. We use a Bayesian statistical approach which allows us to estimate interaction coefficients despite high model complexity, as well as quantify the uncertainty around the resulting community matrix. We apply this method to annual plant communities measured under different levels of natural shade (canopy cover) from Western Australia. Open and shaded communities show marked differences in their competitive structure. The resulting interaction networks uncover relationships and processes which are not detected by co-occurrence methods yet fundamental to understanding coexistence dynamics. This environmental variation in both species interactions and coexistence outcomes must be accounted for in order to understand landscape-level patterns of species diversity.

### 3. (O) On inferring population trends of mobile waterbirds from transect surveys in variable environments

Peter Caley  
CSIRO  
[peter.caley@csiro.au](mailto:peter.caley@csiro.au)

Monitoring waterbird populations inhabiting eastern Australia is immensely challenging for reasons of counting logistics, population aggregation and movement in response to large spatio-temporal variation in resource availability. Here we develop a state-space model that in addition to explicitly incorporating both process noise and observation uncertainty, additionally uses random effects to model the variation in the proportion of the total population that is present on transects. The model infers that many waterbird species are at a substantially lower population now than at the start of monitoring c. 35 years ago. Very few, however, of the inferred long-term rates of increase for these species are negative with any great belief. So although we have strong belief some populations have declined, we are not as confident that the decline is a result of ongoing trend, as opposed to it simply being a result of process variation. This result, whilst intellectually interesting, is disappointing from a management perspective. A common response to lack of power in statistical studies is to increase sample size, or in the case of longitudinal monitoring, to monitor for longer. Here we demonstrate that monitoring for longer won't help power appreciably—the process noise is simply too great. Improving inference will not only require incorporating covariates for the transects subject to counting, but also those that are not (and make up c. 90%) of the range of these species, and suitably realistic dynamic models to link changes in waterbird numbers to environmental conditions.

### 4. (O) Spatial capture-recapture: applications to acoustic surveys of cetacean populations

David Chan, Ben C. Stevenson, Regina A. Guazzo, Tyler A. Helble  
The University of Auckland  
[dcha704@aucklanduni.ac.nz](mailto:dcha704@aucklanduni.ac.nz)

Acoustic surveys are rapidly becoming one of the most common ways to assess cetacean populations, and can be vastly cheaper than other alternatives, like visual surveys. This is because visual surveys have low detection rates, even under ideal conditions. However, acoustic surveys can detect large numbers of vocalising individuals, if the monitoring devices and survey design are appropriate for the target population. Acoustic spatial capture-recapture (ASCR) can estimate call density from these surveys. ASCR has not been widely applied to acoustic surveys of cetacean populations although it is acknowledged in the literature. In this talk I describe an application of ASCR to estimate call density of eastern North Pacific gray whales, and how it varies with environmental covariates like ocean depth and distance from coast. Our findings are broadly consistent with those of Guazzo et al. (2017), who described the data set and estimated homogeneous call density within the hydrophone array using a method that analysed a subset of calls that could be accurately localised. Our analysis highlights two considerable advantages of ASCR over other established methods in the literature: calls do not have to be localised to be included in the analysis, and it allows estimation of an inhomogeneous call density surface. Guazzo, R. A., Helble, T. A., Gerald, L. D., Weller, D. W., Wiggins, S. M., & Hildebrand, J. A. (2017). Migratory behavior of eastern North Pacific gray whales tracked using a hydrophone array. , (10), e0185585.

## 5. (E) Modelling the probability of capture for New Zealand's longfin eels and shortfin eels

Anthony Charsley<sup>1</sup>, Nokuthaba Sibanda<sup>1</sup>, Simon Hoyle<sup>2</sup>

<sup>1</sup>Victoria University of Wellington, <sup>2</sup>NIWA

[anthonyrcharsley@gmail.com](mailto:anthonyrcharsley@gmail.com)

Probability of capture models for New Zealand's endemic longfin eel and native shortfin eel allow conservation managers to understand how these species are distributed. The previously used regularized random forest models were repeated using the New Zealand Freshwater Fish Database (NZFFD) and compared against the vector autoregressive spatial-temporal (VAST) and Gaussian random field (GRaF) modelling approaches. Distribution maps from each of the modelling approaches tended to agree with one another and previously constructed maps. K-fold cross validation and spatial k-fold cross validation was used to measure how well the models predicted probability of capture in geographical locations which were spatially dependent to the training data and independent of the training data, respectively. Area under the receiver operator characteristic curve (AUC) analysis showed that VAST had improved predictive ability for probability of capture for both eel species in comparison to RRF models when the training data and test data were spatially dependent. When the training data and test data are spatially independent, RRF and VAST performed approximately the same. GRaF outperformed RRF when predicting probability of capture for longfin eels but not for shortfin eels. The VAST model showed a small improvement over the GRaF model at predicting the probability of capture for shortfin eels but performed approximately the same for longfin eels. Given that GRaF is more computationally intensive than VAST and that VAST improves upon the RRF models for both species, it is recommended that the VAST models are developed further for New Zealand eel species.

## 6. (O) That's not the Mona Lisa! How to interpret spatial capture-recapture density surface estimates

Rishika Chopara, David L. Borchers, Ian Durbach, Rachel Phillip, and Ben C. Stevenson

University of Auckland

[rcho900@aucklanduni.ac.nz](mailto:rcho900@aucklanduni.ac.nz)

Spatial capture-recapture (SCR) models use records of when and where animals were detected to estimate animal abundance and distribution throughout a survey region. An individual's detection probability is modelled using the unobserved distances between detectors and its 'activity centre', the centroid of the space it used during the survey. Two methods are commonly used to create animal density maps from a fitted SCR model. The first provides the expected activity centre density surface (EACDS), given by the intensity of an inhomogeneous Poisson process fitted to the data using spatially referenced environmental covariates. By contrast, the second do not require spatial covariates, instead summing conditional distributions of the activity centre's locations, given their capture histories, to estimate a realised activity centre density surface (RACDS). We present an extension of this approach, which estimates a realised space usage density surface (RSUDS). By simulating our own spatial capture-recapture data using a density surface based on a grayscale image of the Mona Lisa, we illustrate that the three methods estimate fundamentally different concepts of 'animal density'. An RACDS confounds animal clustering with precision of activity centre location estimates, inviting incorrect ecological inference if taken to represent species distribution. We emphasise that the choice of method should depend on the question being asked: an EACDS describes where animals in general are likely to have activity centers, an RACDS describes where some animals currently in the survey region are likely to have activity centres, and an RHUDES describes which locations are most frequently visited by animals.

## **7. (E) Hey, R. U. There? Autonomous Recording Units - ARUs - as means to monitor sounds in a spatially explicit fashion**

Alberto De Rosa, Isabel Castro, Janneke Klute, Lucas Mugnier, Stephen Marsland  
Massey University  
[a.derosa@massey.ac.nz](mailto:a.derosa@massey.ac.nz)

Conservation decision makers need comparable information regarding ecological communities in order to efficiently allocate resources. Thanks to their high mobility and susceptibility to environmental changes, birds (class: Aves) represent ideal approximates for monitoring ecosystems. Hence, it is necessary to accurately, objectively, and possibly with reasonable expenses, provide information regarding trends of avian populations. Passive acoustic monitoring can represent a competitive source of such information as it already complies with these requirements in terms of objectivity and affordability: thanks to recent technical and technological advancements, the tools to store and analyse large amounts of acoustic data are available, and autonomous recording units (ARUs) are not excessively expensive. However, compared to remotely deployed ARUs, human observers conducting point counts can provide additional information, crucial to infer avian population trends, such as distance and direction of the vocalising birds. Using acoustic playback, this experiment aimed at comparing the performances of a bi-dimensional array of ARUs, and a uni-dimensional array of microphones microarrays in inferring direction of arrival, height, distance, and direction of broadcast of a selection of avian vocalisations and pure tones.

This comparison furthers our ability to productively employ passive acoustic monitoring, which can in turn lead to more extended monitored areas, hence to more informed conservation decisions.

## **8. (O) Combining sources of data in species distribution models**

Elliot Dovers, David Warton, Gordana Popovic, Ian Renner  
University of New South Wales  
[e.dovers@unsw.edu.au](mailto:e.dovers@unsw.edu.au)

Species distribution models of presence probability or intensity can be improved by combining data from various sources. Presence/absence samples contain detailed information but are costly. Conversely, historic records of presence are often more readily available but can be biased due to the opportunistic nature of their collection. We would like to leverage information within the two by jointly fitting a model assuming the data sets share an underlying spatially inhomogeneous point process. Previous attempts to fit such models have made unrealistic independence assumptions, when we would expect missing covariates (for example) to induce correlation across data types. We develop a log-Gaussian Cox process (LGCP) approach using a shared latent random field to account for both potential missing environmental and bias covariates in the data, and as a mechanism to capture other sources of dependence across the two datasets. Like many hierarchical models, this extension comes with added computational complexity. Using our recently developed fast approximation methods, we are able to estimate the shared parameters of the joint likelihood of the combined data in a computationally efficient manner. We illustrate this through the example of a Eucalyptus tree species in the Greater Blue Mountains World Heritage Area.

## 9. (O) Spatial statistics for Environmental Reporting

John Forne  
Statistics NZ  
[john.forne@stats.govt.nz](mailto:john.forne@stats.govt.nz)

Heatmaps have become reasonably common for communicating various phenomena in Environmental Reporting. They have the advantage of being relatively simple and easy to grasp. However, some environmental patterns are complicated (noisy) and it could be/is valuable to help people identify where a pattern they're seeing is merely a random spatial distribution and is significant and where it is not. This paper explores using Getis Ord GI\* with a range of data and considers what types of data lend themselves to this type of statistic. Three datasets being considered, include

1. SST\_anomalies 1982-2017
2. By-catch of Hector's and Maui Dolphins
3. Livestock numbers.

## 10. (O) Likelihood-based clustering of commercial fisheries data

Zach Goeden, Louise McMillan, Shirley Pledger and Richard Arnold  
School of Mathematics and Statistics, Victoria University of Wellington  
[zach.goeden@gmail.com](mailto:zach.goeden@gmail.com)

Commercial trawl data present a valuable opportunity for fisheries stock assessment and for measurement of changes over time, such as may be seen as a result of climate change, when species may move. The data include trawl location, gear type, and biomass of fish caught by species, which we have initially coded as presence/absence for the 25 top occurring species. We use a likelihood-based method which clusters the trawls into groups with similar species patterns. The method uses finite mixture models, estimated by the EM algorithm, returning fuzzy membership indicators. The method is implemented in the new R package *clustglm*, which allows for interactions between gear, species type and cluster membership. It is, however, computationally intensive given the expected large number of clusters, and we have been investigating ways to make the method feasible at scale. These include an improved choice of starting points for the EM algorithm, and hierarchical top down splitting of clusters. This latter method allows for reallocations of events after splits to reduce the risk of misallocation. We will present some initial results from clustering of a trawl data set from NZ commercial fisheries.

## 11. (O) From cleaning the beach to developing litter statistics - a model for community, NGO, and government collaboration

David Harris, Camden Howitt  
Environmental Reporting, Statistics NZ; Sustainable Coastlines  
[David.Harris@stats.govt.nz](mailto:David.Harris@stats.govt.nz)

How do you go from volunteer beach clean-ups to developing a statistically robust, public-facing dataset? In New Zealand, citizen science is being used to provide data on beach litter. Citizen science, also known as 'community science', 'crowd science', or 'civic science', is carried out by members of the general public, often in collaboration with or under the direction of scientists. In this presentation we outline the partnerships, process and journey that started with a litter collection guideline for community use to becoming a robust public facing data set that informs on a waste issue where data had been missing for decades. The data is administered by Sustainable Coastlines (SC), a New Zealand

Charity with a mission to enable people to look after their coastlines and waterways. Their mission is achieved by coordinating and supporting large scale coastal clean-ups, educational programs, public awareness campaigns and riparian planting projects. Through partnering with central government agencies (the Ministry for the Environment, Department of Conservation and Stats NZ), SC works with communities towards the dual goals of raised community awareness and action, and cleaner beach environments. This project is a model of how, with scientific and statistical guidance, environmental information collected by local communities can meet statistical requirements. The litter data is available via the Litter Intelligence Programme <https://litterintelligence.org/data/survey?id=228>.

## 12. (O) 'R' for Environmental Reporting

David Hodge and Bonnie Farrant  
Statistics NZ  
[david.hodge@stats.govt.nz](mailto:david.hodge@stats.govt.nz)

Environmental professionals, academics and students are often required to work with tabular and spatial data. R is an open source code-based data science language that provides an extensive suite of packages for working with such data. Stats NZ has an Environmental Reporting team that uses R extensively for all of our tabular/spatial data cleaning, analysis, and visualisation. This talk will give a brief overview of our use of R in the Environmental Reporting team.

## 13. (E) An “adaptive” test for the parametrical mean function

Yih-Huei Huang  
Department of Mathematics, Tamkang University, Taiwan  
[yhuang@mail.tku.edu.tw](mailto:yhuang@mail.tku.edu.tw)

We consider the test if the mean function assumption is plausible in regression problems. Under the null hypothesis ( $H_0$ ) assumption, one can create unbiased estimation functions easily and make the model being over identifiable. It follows that there could be different but consistent estimators for regression parameters. These estimates will converge to the same value (the true parameter) under  $H_0$  and converge to different values otherwise. We utilize this property to construct a test statistic that is adaptive to which hypothesis holds. It results in a more powerful test than some traditional approaches. We shall give a simulation study to evaluate the performance of our adaptive test and a theoretical comparison with Sargan-Hansen test in a special case will also be discussed.

## 14. (O) Right-censored negative binomial models with detection times

Wen-Han Hwang, Rachel Blakey, Jakub Stoklosa  
National Chung Hsing University  
[wenhan@nchu.edu.tw](mailto:wenhan@nchu.edu.tw)

Conducting complete surveys on flora and fauna species within a sampling unit (or quadrat) of interest can be costly, particularly if there are several species in high abundance. A commonly used approach, which aims to reduce time and costs, consists of occurrence data reflecting the status of occupancy of a species e.g., rather than counting every individual, the survey is stopped as soon as one individual has been observed. Although this approach is cheaper to conduct than a complete survey, some statistical efficiency in model estimators is lost. In this study, we consider occurrence data as a special case of right-censored count data where the collecting process stops until some set threshold on the number of observed individuals is reached. We then propose a new class of regression estimation models for right-censored count data that incorporate information from detection times (or catch effort) collected during

sampling. First, we show that incorporating ancillary information in the form of detection times can greatly improve statistical efficiency over, say, right-censored Poisson or negative binomial models. Furthermore, the proposed models retain the same cost-effectiveness as censored-type models. We also consider zero-truncated and zero-inflated models for a variety of count data types. These models can be extended to a more general class of mixed Poisson models. We investigate model performance on simulated data and give two examples consisting of plant abundance data and bat acoustics data.

#### **15. (P) Comparative analysis of farms across the New Zealand landscape**

Heather Jenkins<sup>1</sup>, AJR. Godfrey<sup>1</sup>, SA. Trewick<sup>2,3</sup> VL. Vermeulen<sup>4</sup>

<sup>1</sup>School of Fundamental Sciences, Massey University, <sup>2</sup>NZ Centre for Planetary Ecology, <sup>3</sup>School of Agriculture and Environment, Massey University, <sup>4</sup>Pamu (formerly Landcorp Farming Ltd)

[Heather.K.Jenkins@gmail.com](mailto:Heather.K.Jenkins@gmail.com)

Agriculture provides our food and is a major contributor to the New Zealand economy, but it has a substantial environmental footprint. Modern agriculture is unfortunately a major contributor of greenhouse gases and freshwater pollutants, and is associated with extensive biodiversity reduction. It is increasingly accepted that changes to farming practices and crop types are required to balance production with long term environmental sustainability. In this project we are examining Pamu's on-farm data gathered via the Overseer tool from a wide range of farms across New Zealand in the context of available spatial and environmental information. The on-farm data includes a fertiliser model, eg. N/P lost to water and GHG Emissions, as well as variables that characterise the farms such as the effective farm area and catchment area. This initial expository project looks at dairy and livestock farms over a 3 year period. The work is directed at the formulation of "ecological" modelling that will enable development of more sustainable production choices and practice. By integrating standardised on-farm data across the New Zealand landscape and supplementing this with detailed land environment data the project will identify a) what additional farm data are required for effective predictive modelling and b) form the basis of an integrated ecosystem-wide approach to land use.

#### **16. (O) Continuous-time discrete-space models of marine mammal exposure to Navy sonar**

Charlotte Jones-Todd, Enrico Pirodda, Gregory S. Schorr, Erin A. Falcone, Robin W. Baird, Stephanie Watwood, Len Thomas

University of Auckland

[c.jonestodd@auckland.ac.nz](mailto:c.jonestodd@auckland.ac.nz)

Marine mammal species are increasingly being exposed to human activities that may cause individuals to change their natural behaviour. Military exercises (sonar) are, perhaps, the type of activity given the most media attention due to their potentially adverse effect on an individual's natural behaviour pattern. Using telemetry data, collected with uncertainty, this talk will discuss a discrete-space, continuous-time, model to estimate individual transition rates of cetaceans across the boundaries of US naval weapons ranges. This approach allows us to infer the progressive decay in response to sonar activity as well as allowing for differences in movement patterns between individuals. The model is fitted to data from a range of cetacean species with different movement behaviour and ecology, occurring over the Hawaii Range Complex (HRC), the Southern California Range Complex (SOCAL), and the Atlantic Undersea Test and Evaluation Center (AUTEK) range.

## 17. (P) Evaluating acoustic monitoring surveys via spatial capture-recapture

Julius Juodakis, Isabel Castro, Stephen Marsland  
Victoria University of Wellington  
[julius.juodakis@sms.vuw.ac.nz](mailto:julius.juodakis@sms.vuw.ac.nz)

Autonomous acoustic recording units provide a convenient way to survey animal populations and estimate their densities. However, the results depend on many design decisions, from survey protocol to manual or computational analysis of the recordings. When developing the survey design or analysis tools, researchers will typically modify a particular part of the pipeline to improve a metric that measures only that part of the process. There is no standard metric to quantify the impact of such changes on the overall workflow. We propose that the precision of call density estimated by spatially explicit capture-recapture is a suitable metric for evaluating acoustic survey methods. We investigate its properties using the recently proposed approximations, simulations, and survey data of little spotted kiwi, *Apteryx owenii*. We compare the metric to a similar approach using occupancy modelling, and to concordance measures that are commonly used for evaluating automatic call recognition, such as sensitivity and specificity. We find that in this framework, the optimal design can be identified without knowing the underlying animal density or certain other parameters, in contrast to occupancy modelling. The proposed measure accurately responds to changes in dataset size, so it allows evaluating tradeoffs which involve sampling cost. In particular, we compared manual vs. software-based call detection, and observed that the software misses some calls amounting to 8% loss of precision, but overall increases the precision by 31%, by decreasing analysis effort. We also demonstrate that concordance measures fail to identify optimal design choices, and can be artificially inflated by deleting data.

## 18. (O) A two stage-structured Schaefer model in a state-space framework, with application to the Korean pollock population

Kyuhan Kim<sup>1</sup>, Nokuthaba Sibanda<sup>1</sup>, Richard Arnold<sup>1</sup>, Teresa A'mar<sup>2</sup>  
<sup>1</sup>School of Mathematics and Statistics, Victoria University of Wellington; <sup>2</sup>National Institute of Water and Atmospheric Research Ltd., Wellington  
[Kyuhan.Kim@sms.vuw.ac.nz](mailto:Kyuhan.Kim@sms.vuw.ac.nz)

The Schaefer model is one of the simplest and least data-demanding stock assessment methods in quantitative fisheries. The model only requires time series of total catch (e.g., annual harvest) and a relative abundance index, such as catch-per unit effort (CPUE). An important underlying assumption of this simple model is that CPUE is proportional to abundance. However, in practice, such an assumption is often problematic because 1) most CPUE data are from commercial fisheries, and 2) fishing activities are strongly size selective. Under these circumstances, a single set of such fisheries-dependent CPUE cannot provide a reliable measure of population abundance, but it would roughly represent a relative population size of individuals in some particular range of body size. In this study, we developed a state-space, two stage-structured Schaefer model, to accommodate multiple sets of CPUE and catch collected from different size-selective fisheries of a single species. The model also incorporates process and observation errors. Our model is a simplification of the true situation, but is an improvement over the simple Schaefer model. One key advantage of our model is the ability to utilize the same prior information used in the standard Schaefer model, because our model contains the same biological parameters as the standard one. We apply our model to the Korean pollock population, a fishery that has been heavily exploited by targeting both juveniles and adults for more than two decades.

## 19. (O) Adding latent variables to glmmTMB for parsimonious high dimensional modelling

Maeve McGillicuddy, David Warton, Gordana Popovic  
The University of New South Wales, Sydney, Australia  
[m.mcgillicuddy@unsw.edu.au](mailto:m.mcgillicuddy@unsw.edu.au)

Many studies use observational or experimental data which can be highly correlated, violating the assumption of statistical independence required in many modelling approaches. Generalised linear mixed models (GLMMs) provide a flexible approach to model data, including multivariate data, with clustered or correlated outcomes via random effects. This may require estimating many parameters for the variance-covariance matrix of the random effects, which becomes a problem when the random effects are of high dimension and there is not enough data. This often happens when modelling multivariate abundance data in ecology. Our motivating example is a study investigating the effect of an offshore wind farm on fish abundance with 20 fish taxa. Along with fixed effects, we would like to capture correlation across taxa using an observation-level multivariate random effect, but its variance-covariance matrix would have 136 parameters, to be estimated from a sparse dataset with only 179 observations. Another way to model correlation is to use a factor analytical approach, sometimes called a generalised latent variable model (GLVM). A latent variable can be understood as a reduced rank covariance structure for the random effects, with potentially many fewer parameters. While there are several software packages available that can fit a multivariate GLVM, they are not very flexible when it comes to adding additional random effects, for example, a random effect for clustering. We aim to add latent variables to the flexible package, *glmmTMB*, to create a reduced rank covariance structure for latent variables which can be used for a broad range of problems in ecology and other areas.

## 20. (O) Evaluating predictive loss of models for over-dispersed count data

Russell Millar  
Department of Statistics, University of Auckland  
[r.millar@auckland.ac.nz](mailto:r.millar@auckland.ac.nz)

The widely applicable information criterion (WAIC) and leave-one-out cross-validation loss (LOO-CVL) provide, under weak regularity conditions, approximately unbiased estimators of the expected predictive loss of Bayesian models. In models for over-dispersed count data the regularity condition will typically be satisfied if the likelihood is marginalized over observation-level latent variables, but not if the likelihood is conditioned on the latent variables. The predictive loss targeted by LOO-CVL is the same using either level of likelihood, but importance sampling estimators of this loss are much more vulnerable to numerical problems when using conditional likelihood. In contrast, the loss targeted by WAIC is different at the conditional level. The literature contains several examples where, for convenience, conditional-level WAIC has been used for comparing models for over-dispersed count data. It is shown that this does not provide a reliable estimator of its target loss, and simulations show that it can favour the incorrect model. It is recommended that WAIC and LOO-CVL be evaluated using the marginalized likelihood.

## 21. (O) Increasing the reach: 'Re-use' of research in environmental reporting

Sonja Miller

Environmental Reporting Team, Statistics NZ

[Sonja.Miller@stats.govt.nz](mailto:Sonja.Miller@stats.govt.nz)

One of the objectives of environmental reporting is for our understanding of the environment to be evidence based. While much of the data underpinning our indicators is collected by entities such as crown research institutes and regional councils, we do look to research to fill gaps. We describe the data quality criteria we use to assess the data underpinning our indicators in environmental reporting. We also briefly describe a number of ecological studies that didn't meet our data quality criteria as indicators but were developed as case studies to fill information gaps in environmental reports.

## 22. (O) Goodness-of-fit of Bayesian spatial models using pivotal discrepancy measures

Lindsay Morris, Nokuthaba Sibanda Victoria University of Wellington

[morrislind2@myvuw.ac.nz](mailto:morrislind2@myvuw.ac.nz)

Within the field of geo-statistics, Gaussian processes are a staple for modelling spatial and spatio-temporal data. Statistical literature is rich with definitions and estimations of the mean and covariance structures of these processes (in both frequentist and Bayesian contexts). However, considerably less attention has been paid to developing goodness-of-fit tests that allow for assessment of model adequacy. Jun et al. (2014) introduced a statistical test that uses pivotal discrepancy measures to assess the goodness-of-fit in the Bayesian context. We present a modification and generalization of their statistical test. The initial method involves spatial partitioning of the data, followed by evaluation of a pivotal quantity at each posterior draw to obtain a posterior distribution of pivotal statistics. Order statistics from this distribution are used to obtain approximate p-values. Jun et al. (2014) use arbitrary partitions based on pre-existing spatial boundaries. The partitions are made to be of equal size. Our method uses a novel approach to partitioning based on K-means clustering and generalises Jun et al.'s approach to incorporate unequal partition sizes. Observations from a spatial or spatio-temporal process are partitioned using an appropriate feature vector that incorporates the geographic location of the observations into subsets (not necessarily of the same size). The method's viability is illustrated in a simulation study, and in an application to hoki (*Macruronus novaezelandiae*) catch data from a survey of the sub-Antarctic region.

## 23. (O) Time Series Trends in Environmental Monitoring

Lilian Morrison, Statistics NZ

[lilian.morrison@stats.govt.nz](mailto:lilian.morrison@stats.govt.nz)

The importance of trend assessment to tell the story about our environment cannot be underestimated in either ecology or environmental monitoring. For example, to know whether actions to combat climate change have had an effect, we will need the ability to determine when the trend(s) change direction. However, time series are composed of short-term irregularities and seasonal patterns as well as medium-term trend cycles and/or long-term trends. Any dataset is likely to include more than one time series component. The medium/long term trends do not have to be monotonic in time and many series contain turning points when a component switches direction(s). At Stats NZ we use the X-13 methodology, an Unobserved Components Model (UCM) to analyse time series. The UCM paradigm allows the estimation of each of the components making up the series. While we cannot observe the individual components separately, we can decompose the time series into these components and

analyse them. Terms to estimate / model the effects of changes in policy or behaviour can be added. The UCM also allows us to acknowledge that the closer the data points are in time the more likely there is a correlation. I will use an environmental dataset to demonstrate these components. I will also show why it is not necessarily easy to determine that a true change of direction has occurred until sometime after the event.

#### 24. (O) Estimating the size of a very low density population

Nick Mulgan, James Russell, Helen Nathan, Margaret Nicholls  
Zero Invasive Predators (ZIP)  
[nick.mulgan@gmail.com](mailto:nick.mulgan@gmail.com)

The Predator Free 2050 initiatives require removal of rats, possums and stoats from the New Zealand mainland. As a step towards this Zero Invasive Predators (ZIP) has been trialling the adaptation of aerial suppression operations to eradication by using multiple non-toxic pre-feeds and two 1080 toxin applications. The current site is a 9000 ha forest and alpine block in the Perth River valley, South Westland. Predator detection is via chew cards and a network of trail cameras trained on automatic lure dispensers. One modelling challenge that arises is estimating the size of a very low-density unmarked population between the two toxin applications. Some of the behavioural difficulties involved are bias associated with training a fraction of the population to a lure, possible changes in behaviour when most nearby animals have been killed, and detecting rats at landscape scale. Spatially explicit capture-recapture (SECR) models determine the expected number of detections  $E(C)$  in terms of the population density  $D$ , hazard of detection  $\lambda_0$  and predator movement scale  $\sigma$ .  $E(C)$  is approximately proportional to  $D\lambda_0\sigma^2$  with the three variables not separable. We solve for the unknown density by scaling an index of predator distribution before the operation to match the detection count after the toxin drop. This estimator  $\hat{D}$  is unbiased, given the assumptions, and has minimum variance. We discuss its sensitivities to  $\lambda_0$  and  $\sigma$  and illustrate the method with the three target species in the Perth block.

#### 25. (O) Hierarchical clustering with fused mixtures

Gordana Popovic, David Warton, Trevor Hastie  
UNSW Sydney  
[g.popovic@unsw.edu.au](mailto:g.popovic@unsw.edu.au)

Clustering data has many applications, including grouping related genes, customers and stocks, to better understand the patterns in these data. In ecology, grouping sites by species composition or abundance can help us understand communities of species, and assist in monitoring and management. While many existing clustering methods are algorithmic, mixture models fit by maximum likelihood have recently gained popularity for clustering, including in ecology, because they are better able to account for the highly discrete nature of these data. However, unlike many algorithmic methods, mixture model clusters are not hierarchical. For Gaussian responses, a fused lasso penalty on the distance between cluster centres can create a hierarchical path of models with nested clusters. We will extend these models to discrete data with discrete mixtures, with applications for hierarchical clustering in ecology.

## 26. (O) New point processes for spatial capture-recapture models

Ben Stevenson, Andrew E. Seaton, Callum K. Y. Young University of Auckland  
[ben.stevenson@auckland.ac.nz](mailto:ben.stevenson@auckland.ac.nz)

Spatial capture-recapture (SCR) generalises traditional nonspatial CR models by introducing a point process for animals' unobserved activity centres. Each activity centre represents the location around which an animal based its movement during the survey period. To date, all but one application of SCR has modelled activity centres with a Poisson point process, which implicitly assumes that each animal's location is independent of all others. Although this assumption ensures estimation is tractable and that computational demands are sufficiently inexpensive to allow model fitting within manageable time frames, it does not realistically represent the way animals are distributed throughout a survey region. Animals cluster together due to social dynamics and in response to environmental factors like heterogeneous resource availability. SCR methods have been proposed to model clustering related to observed environmental covariates—but often these covariates alone are insufficient, and animals can respond to unobserved or unobservable factors. In this talk I present two SCR models, each incorporating a non-Poisson point process for activity centres. The first comprises stacks of activity centres sharing the same location, and is relevant to species that live in groups and to applications of SCR to acoustic data. The second uses a log-Gaussian Cox process, inducing clustering via latent spatial heterogeneity in animal density.

## 27. (O) Spatial trends in DOC's National Monitoring Programme biodiversity data

Helene Thygesen  
Department of Conservation  
[hthygesen@doc.govt.nz](mailto:hthygesen@doc.govt.nz)

The Department of Conservation's National Monitoring Programme is a rich data resource, based on repeated surveys of New Zealand's biodiversity. The statistical analysis of the Programme's data have primarily been aimed at making inference about national trends in abundance, occupancy and species richness, while information at the local level has primarily been descriptive. There is a demand for regional-level reporting on statistical inference, which is challenging as the models are quite complex (for example separating zero-inflation related to detectability to zero-inflation related to occupancy), which requires a large sample size. I discuss how generalized additive models or density-ratio analysis could be integrated in the existing modelling framework.

## 28. (O) Variable Selection for Inhomogeneous Poisson Point Process Using Minimum Message Length: an Ecological Case Study

Zihao Wen, David Dowe  
Monash University  
[zihao.wen1@monash.edu](mailto:zihao.wen1@monash.edu)

The inhomogeneous Poisson Point Process (IPPP) is widely used in species distribution modeling. Since species data is generally less accessible than environmental data, and the number of predictors possible in models therefore limited, variable selection is often needed to help identify relevant and irrelevant variables in species distribution modeling. The Akaike information criterion (AIC) and its small-sample-size corrected version, AICc, are usually used for variable selection in ecology, as well as Schwarz's Bayesian information criterion (BIC). In this study we propose the use of an alternative Bayesian information-theoretic principle, minimum message length (MML), that has not previously been applied as a variable selection criterion for IPPP. In the common ecological case of many potential explanatory

variables and relatively small numbers of species presence points, MML performs particularly well compared to the alternative methods mentioned above according to the results of our simulations. We also use the above criteria to study the spatial distribution of the tropical rainforest plant species located in Barro Colorado Island, Panama, MML identified the variables deemed important by ecologists. Our results suggest that in most cases MML has a higher probability of selecting the correct explanatory variables.

## 29. (O) Defining and evaluating the predictions of joint species distribution models

David Wilkinson, Nick Golding, Gurutzeta Guillera-Arroita, Reid Tingley, Michael McCarthy  
The University of Melbourne  
[davidpw@student.unimelb.edu.au](mailto:davidpw@student.unimelb.edu.au)

Joint species distribution models (JSDMs) extend the standard single species distribution model (SDM) approach by allowing multiple species to be modelled simultaneously. This approach accounts for species correlations not explained by available environmental predictors. Despite increasing adoption of JSDMs in the literature, it remains unclear how JSDM predictions differ from those of standard SDMs. By stacking multiple SDMs together we can predict community assemblage or species richness, but this does not account for species correlations. JSDMs, however, allow us to perform predictions in a variety of different ways: environment-only predictions akin to the stacked SDM approach, community assemblage predictions accounting for species correlations, and species or community level predictions conditional on known occurrence states of one or more species in the community. Predictions need to be evaluated and there is a wide array of potential metrics for JSDMs and their different prediction types. These include common SDM metrics evaluated at the species level, like AUC, and metrics that operate at the community level like community dissimilarity metrics or species richness. For a case study of frog species in Melbourne, Australia, preliminary results suggest that despite likelihood-based metrics indicating JSDMs are better fit to the data than stacked SDMs, JSDM predictions accounting for species correlations are prone to overprediction. JSDMs overpredicted species richness by ~10% and had higher rates of both true and false positive predictions than stacked SDMs. The community dissimilarity metrics returned mixed results where the JSDMs simultaneously performed better and worse community assemblage predictions depending on the metric.