1. Landscape adaptation for biodiversity conservation in a changing climate
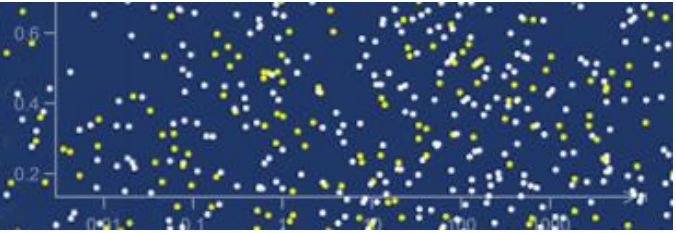
Nigel Andrew

University of New England

Co-authors: Ian Oliver, Josh Dorrough and Helen Doherty

We address the issue of adapting landscapes for improved biodiversity conservation in a changing climate, by assessing the importance of additive (main) and multiplicative (interaction, or synergistic) effects of land cover and land use with climate. We used a 1000 m elevation gradient in eastern Australia; sampling from 121 sites with variable land cover and land use intensity. We used generalised linear mixed modelling to test the hypotheses that ant richness (species and genus), abundance and diversity would vary according to land cover and land use intensity but that these effects would vary according to climate. Our findings suggest that the impacts of climate change on insect biodiversity may be mitigated to some degree through landscape adaptation by increasing woody native vegetation cover and by reducing the cover of exotic vegetation and of bare ground.

Key words: synergistic effects, biodiversity, insects, ants, species richness, species turnover

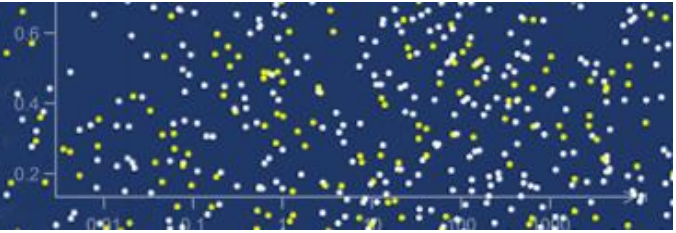## 2. Response of Australian Grassland Thysanoptera to a Changing Climate

Matthew Binns

University of New England

Co-authors: Nigel Andrew, Heloise Gibb, David Warton

Changes in climate over the coming century are expected to have a major influence on the structure of insect communities. Sweep net sampling was used to collect Thysanoptera from Themeda triandra grassland across a climatic gradient in NSW and Victoria, Australia. Thysanoptera were identified to species or morphospecies and a range of morphological measurements were taken using computer software and an imaging microscope. A multivariate GLM was used to determine how different species are associated with different environmental variables. A model based implementation of the 'fourth corner problem' was used to determine the interaction between environmental variables (matrix 'R') and morphological measurements (matrix 'Q') in determining abundance (matrix 'L'). We also simulate a warmer, drier climate by performing a transplant experiment across three different sites using both diploid and tetraploid Themeda triandra plants.

Key words: Thysanoptera, Climate, mvabund, Transplant

3. Ergodic properties of a Markov chain used for inferring genotype from corrupted DNA

Paula Bran

Student

Co-authors: Richard Barker, Matthew Schofield

The use of Markov chain Monte Carlo (MCMC) has been increasing in several areas, including ecology. We study the convergence properties of the Markov chains generated by a Gibbs sampler implemented in order to estimate animal abundance using non-invasive DNA samples. Convergence is important because we need to ensure that a stationary distribution exists and that it coincides with the target (posterior) distribution. A necessary condition for convergence is irreducibility which is the freedom to move between any pair of states of the chain. The positivity condition is a sufficient condition for irreducibility of a Gibbs Markov chain, however it does not hold in this case. We discuss these issues and show how to prove irreducibility of the Markov chain for models in this class.

Key words: Gibbs sampling, population estimation, irreducibility, ergodicity, non-invasive genetic sampling, positivity condition
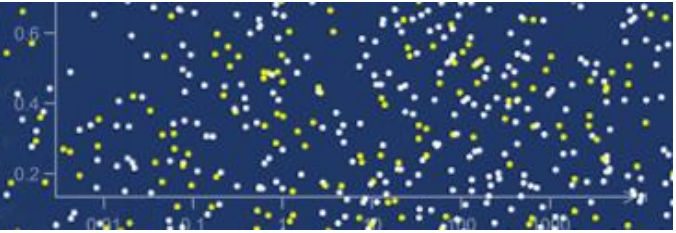
4. Meta-barcoding of terrestrial biodiversity from soil DNA: methodological considerations and application to an island ecosystem

Andrew Dopheide

University of Auckland

Meta-barcoding and metagenomic techniques enable sampling and analysis of a much broader range of taxa in ecosystems than is feasible using traditional methods. We investigated methodological factors that may influence the outcomes of meta-barcoding studies of terrestrial biodiversity from soil DNA, including variability of PCRs and spatial discrimination of samples. We applied these techniques to the analysis of biodiversity on a forested island, based on PCR and sequencing of prokaryote and eukaryote targets from soil DNA. We also established a reference database of barcode sequences from invertebrate specimens using traditional methods. Meta-barcoding resulted in the detection of a much wider range of biodiversity than the traditional methods, however, including fungi, protists, and small invertebrate groups. However, broadly similar relationships between samples and communities were observed for both the traditionally-collected specimens and the soil meta-barcoding data.

Key words: meta-barcoding, PCR variability, terrestrial biodiversity, invertebrates, eukaryotes

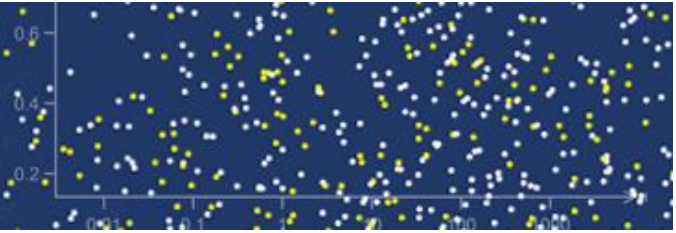## 5. Biodiversity Impacts and Adaptation to Climate Change at a sub-continental scale

Dr Michael Drielsma

OEH NSW; University of New England

Co-authors: Jamie Love, Glenn Manion, Hanieh Saremi, Tom Harwood, Kristen Williams

Climate change poses a significant but uncertain threat to biodiversity across the world and certainly to south-eastern Australia. However, communities and government agencies need clear, rigorously derived messages regarding risks and how to optimise adaptation efforts. We are implementing a program of intersecting global and regional climate futures with contemporary and potential landscape scenarios. We then create static and interactive maps for engaging and informing the community into developing their own adaptation responses.

Key words: climate scenarios biodiversity spatial community modelling

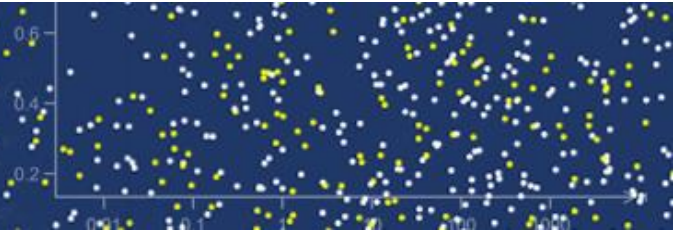# 6. Bayesian spatio-temporal modeling and mapping of Dengue Fever The Case of the City of Bandung, Indonesia

I Gede Nyoman Mindra Jaya

Padjadjaran University

Co-authors: Henk Folmer and Budi Nurani

Dengue fever is an acute febrile disease caused by the dengue virus which is transmitted by the Aedes mosquito. The WHO (2009) noted that Asia has the highest incidence of dengue fever in the world and Indonesia the highest in Southeast Asia. Local variation in risk is influenced by rainfall, temperature, humidity and human behavior. Spatio-temporal modeling and mapping have been widely applied to analyze the spatial distribution of dengue fever incidence and its trend, notably to detect hot spots. The most common approach is based on the assumption that there is a log-linear relationship between relative risk and calendar time within areas, that the time-trend varies from area to area while covariates are ignored. However, adequate modeling and mapping of dengue fever also require that spatio-temporally varying covariates and spatial spillover effects are taken into account.

Key words: Dengue Fever, Spatio Temporal Modeling, INLA, Varying Coefficient

7. Statistics for studying abundance and distribution of marine mammals using Unmanned Aerial Vehicles (UAVs)
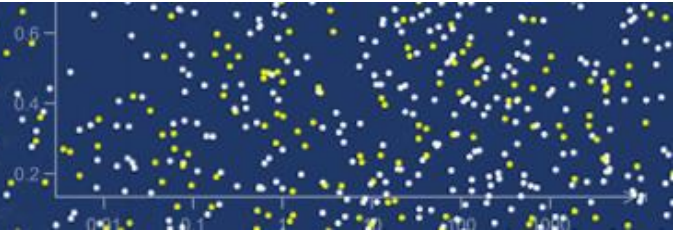
Natalie Kelly

CSIRO

Co-authors: Amanda Hodgson, David Peel

Advancements in imaging technology, and the rapid emergence of Unmanned Aerial Vehicles (UAVs, or drones) in civil applications, offer an opportunity to improve aerial surveys of large fauna. Despite UAVs being recognised as a promising method for surveying fauna, little attention has been given to understanding and quantifying biases in this method, and comparing UAV to traditional human observers: quantities that are fundamental for returning accurate and precise abundance and distribution results, and for ensuring continuity in series of abundances. Here we present thoughts on how to quantify biases introduced either because animals are diving (availability bias), or which are at the surface, but missed by observers (perception bias), when using image data from UAVs; this is demonstrated using a case study of a UAV survey for humpback whales. We also consider the differences in results from concurrent human- and UAV-based aerial surveys using a dugong survey as a case study.

Key words: UAVs; marine mammals; abundance and distribution; line transect

8. Improving prediction power of Species Distribution Models: Combining presence-only data with limited presence-absence data
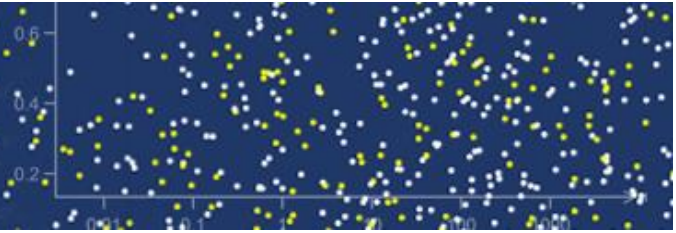
Vira Koshkina

RMIT University

Co-authors: Yan Wang, Ascelin Gordon, Matt White, Lewi Stone

The main objective of this work is to expand on works of [Dorazio, 2014] and [Fithian et al., 2015] in combining presence-only dataset with data from planned surveys in order to increase predictive power of the model. Our proposed model takes into account imperfect detection during presence-absence surveys (unlike [Fithian et al., 2015]) and does not require point count data (unlike [Dorazio, 2014]). We com- bine a point process spatial model with Mackenzie et al.s presence-absence model [MacKenzie et al., 2002] which makes it possible to determine the true (non-relative) rate λ over a large area of opportunistic surveys.

Results of simulations show that even a small presence-absence dataset can improve the prediction power of the model significantly. We conduct a thorough investigation of the effects that presence- absence data have on the model depending on the number of repeated surveys, number of sites, and the area that was covered by the surveys.

Key words: sdm, presence-only, presence-absence

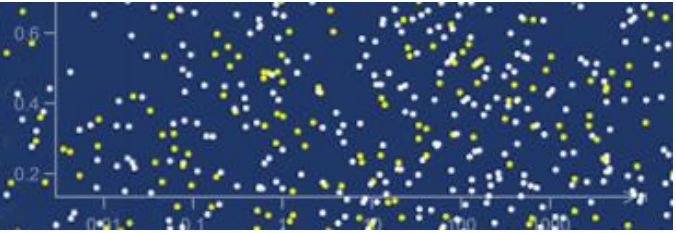## 9. The landscape of turnover: a spatially explicit mapping of species turnover using zeta diversity

Guillaume Latombe

Monash University

Co-authors: Guillaume Latombe, Cang Hui, Mariona Roige & Melodie A. McGeoch

Zeta diversity measures the spatial turnover in species composition by computing the average number of species shared across multiple assemblages. It more comprehensively represents the spatial structure of multi-species distributions than other measures of turnover such as beta diversity. However, current measures of zeta diversity are spatially implicit, and still do not fully take into account the spatial heterogeneity of species assemblages. We use a combination of zeta diversity indices to generate a landscape of species turnover that can be visualised as a spatial map. We apply this technique at a continental scale at different levels of spatial resolution to unveil the spatial structure of bird communities across Australia using occurrence records from the Australian Bird Atlas. Regions with different levels and structures of community turnover naturally emerge across the landscapes, suggesting spatial heterogeneity in the local processes that structure these communities.

Key words: spatial turnover, zeta diversity, beta diversity, birds, map

10. Where Did They Come From? Visualizing Population Genetics
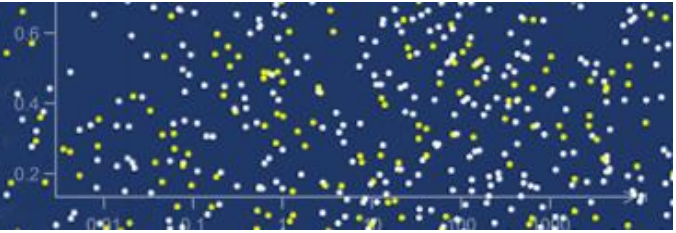
Louise McMillan

Department of Statistics, University of Auckland

Co-authors: Rachel Fewster

Rats are one of many invasive pests in New Zealand. Rats were eradicated from the Broken Islands off Aotea/Great Barrier Island (GBI) in 2009, but more were found in subsequent years. We used genetic methods to check if the new rats survived the eradication or swam over from mainland GBI.

The genetic method used improves on the method of Rannala & Mountain (1997). We take samples from multiple populations, and then compare the genetic data from new samples to the population data, to see which population is the best fit. The populations are the rats captured on the Broken Islands and Great Barrier Island before the eradication in 2009, and the new samples are rats captured on the Broken Islands after the eradication. We provide a way of processing samples which have some missing genetic data so they can be visualized on a graph alongside samples with full data. Visualizing population structure, and detecting the origin of new animals, can improve the management of invasive pests.

Key words: population genetics, assignment, saddlepoint, invasive pests

11. Sampling and analysis of microbial communities using 16S rRNA gene surveys – characteristics of the generated data
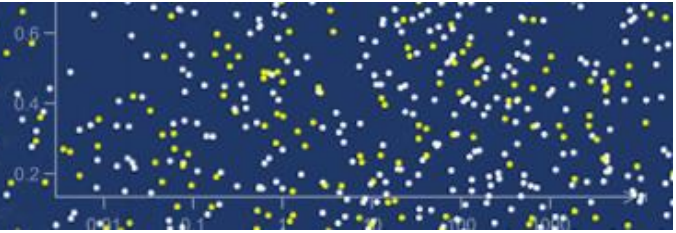
Shaun Nielsen

Centre for Marine Bioinnovation, Univeristy of New South Wales

Co-authors: Ezequiel M. Marzinelli and Torsten Thomas

Cellular microorganisms play fundamental ecological roles on Earth. Investigating their abundance, diversity and function is critical to our understanding of the Earths biosphere. Surveys the 16S rRNA gene diversity are the first approach in sampling microbial communities. Technological advances in DNA sequencing has led to the generation of large gene surveys, typically generating millions of gene counts per survey, tens of thousands of gene counts per sample and thousands of operational taxonomic units (OTUs; a proxy of taxonomic or functional groups). Serious methodological issues are associated with generating this type of data from sample preparation to bioinformatics analysis. Ultimately the surveys can only represent the relative abundance of OTUs among samples. Despite this, these data appear to be suitable for modern statistical methods. In this poster we present various characteristics of the data generated in 16S rRNA gene surveys and analysis solutions for discussion.

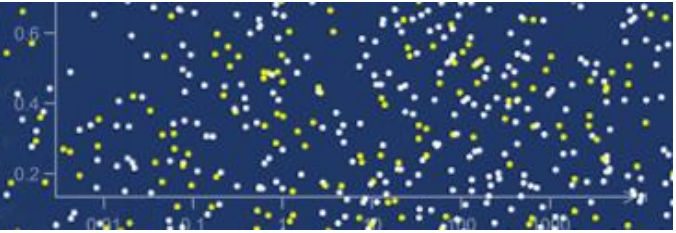*Key words: Microbes Sequencing Community 16S*

12. A general framework for measuring biodiversity based on rarefaction curves

David Nipperess

Macquarie University

Rarefaction curves plot the relationship between diversity and sampling effort and are commonly used to estimate sampling sufficiency and to correct for variance in sampling effort. What is not as widely appreciated is that rarefaction curves also contain rich information on the entropy (or evenness), beta-diversity and disparity of ecological communities. I present a very flexible framework for measuring all these aspects of biodiversity, derived from the initial slope of the rarefaction curve. This initial slope, which I call delta-D, is the expected gain in diversity when increasing sampling effort from one to two individuals, sampling units or species, and has a direct relationship to the Gini-Simpson index, Rao's Quadratic Entropy and the PIE (Probability of Interspecific Encounter) index. I demonstrate the application of the framework using a dataset of bird observations from Barrington Tops National Park.

Key words: rarefaction, entropy, evenness, beta-diversity, phylogenetic diversity, functional diversity
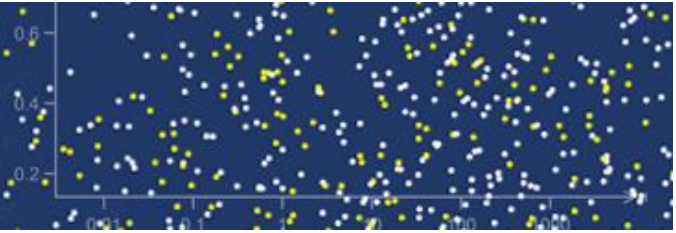
13. Analyzing community data – how well do different statistical frameworks predict species occurrence and community patterns?

Anna Norberg

Department of Biosciences, University of Helsinki

A large array of statistical frameworks has been developed for analyzing community ecological data sets describing the occurrences or abundances of species in a number of sampling units and the environmental attributes of those sampling units. We compare various statistical frameworks (species distribution models and joint species distribution models) in terms of their predictive performance. We parameterize the statistical frameworks with training data, and then use them to predict independent validation data representing both similar and different environmental conditions under which the training data were acquired. We consider both real and simulated data. We compare the model predictions to the validation data both at the species and community levels, the latter including measures of species richness, community dissimilarity, and co-occurrence.

Key words: species distribution model, community, model comparison, prediction

14. Molecular mark-recapture using relationship estimates from genome-wide SNPs
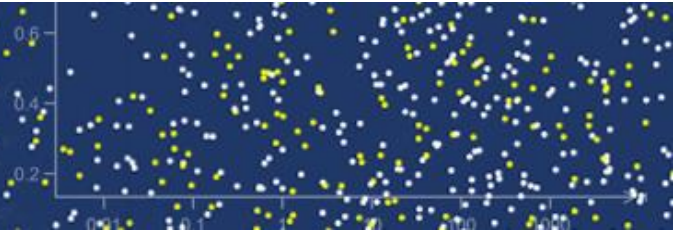
Gordana Rasic

University of Melbourne

Co-authors: Ary A Hoffmann

There are very few insects for which we have a good understanding of movement patterns. In small insects, such as the dengue fever mosquito Aedes aegypti, traditional mark-release-recapture techniques using fluorescent dust are challenging and have produced estimates of dispersal that differ greatly among studies. This is particularly problematic for the Wolbachia-based strategies to control Ae. aegypti, because the form of the dispersal kernel can have a large effect on predicting the speed of Wolbachia spread through a mosquito population. Here, we explore the utility of spatially referenced relationship estimates from genome-wide SNPs among mosquito larvae for constructing dispersal kernels. We also use individual-based simulations of mosquito movement and population dynamics in landscapes to test sensitivity of our approach to different dispersal functions.

Key words: dispersal kernel, genome-wide SNPs, relationship, individual-based simulations, heterogeneous landscapes

15. Water temperature variation due to Indian Ocean dipole impact on purse seine fisheries dynamics in Prigi Bay, Indonesia: a statistical approach
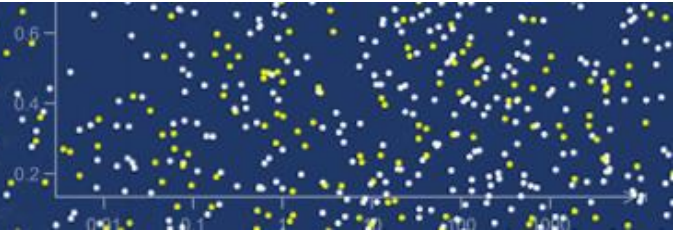
Aida Sartimbul

Department of Marine Sciences, Brawijaya University

Co-authors: Hideaki Nakata, Nurin Hidayati, Zulfan Khaidar

IOD played an important role in water temperature variability of Indian Ocean. Water temperature variability supports commercial fisheries along south Java Water. Daily of six-month in situ tidbit water temperature data (Jun-Dec 2012) were used to test their correlation with satellite sea surface temperature data. The result showed highly correlation between two data series, and no different between both data (Sakaronov-Smirnov). Thus, satellite temperature data can substitute the lack of tidbit water temperature data series. Together with chlorophyll-a and climatic index (Indian Ocean Dipole), factor loading of PCA showed that fisheries catch at Prigi Bay was driven by Satellite temperature, Chlorophyll-a, and Indian Ocean Dipole (PC1), and they contributed 16.2, 22.3, 17.0 % of total variables, respectively. Furthermore, fisheries catch, such as Bali Sardine, Mackerel Tuna and Skipjack Tuna contributed 19.0, 11.9, and 9.1 % respectively, while Indian Scad only 4.5 %.

Key words: Water temperature, Indian Ocean Dipole, fisheries catch, PCA, Prigi Bay

16. Misidentification in mark-recapture: connecting the latent multinomial
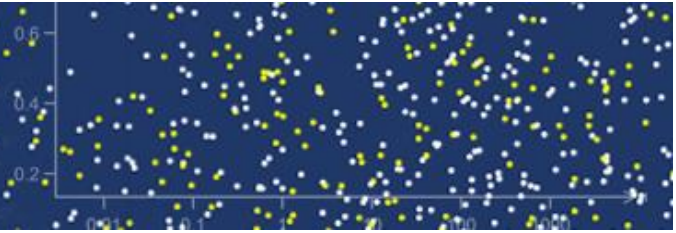
Matthew Schofield

University of Otago

Co-authors: Simon Bonner

Misidentification in mark-recapture studies can lead to biased estimation and inaccurate decision making. One proposed solution is to use a latent multinomial model. This involves expressing the capture histories counts, potentially observed with error, as a linear function of true capture history counts. The model can then be fitted using MCMC where the unknowns include the true capture history counts. This is challenging as we need to ensure that these true counts are consistent with the observed data (i.e. satisfy the linear constraint). One proposed solution is to use elements of a basis for a null space to generate candidate true counts. We explore this approach and show that it is not sufficient to produce an irreducible Markov chain. To solve this problem, we consider the notion of a Markov basis; a larger set of vectors ffrom the null space that ensures irreducibility of the Markov chain.

Key words: mark-recapture; misidentification; latent multinomial; Markov basis; irreducibility

17. Quantifying aggregation and zero inflation in faecal egg counts of sheep and goats.
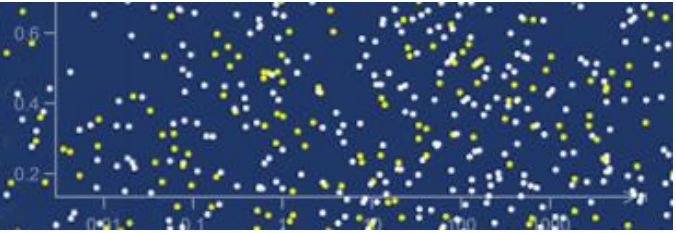
Phuti Sebatjane

University of South Africa

Co-authors: Peter Njuho

A Poisson distribution is usually an initial step in analyzing count data.   When the Poisson distribution cannot explain the extra variation around the mean, the negative binomial distribution better explain the overdispersion since it assumes a quadratic mean-variance relationship. In this study egg counts of fifteen internal parasite species in sheep & goats indicate not only overdispersion but also possible zero inflation due to high proportion of zeroes. Two measures of aggregation are calculated; the index of discrepancy & the variance to mean ratio, and their accuracy in measuring aggregation is investigated. The Poisson and the negative binomial model are fitted to the data. To test for zero inflation, the zero inflated counterparts of the standard count models are also fitted. All the fifteen egg counts are found to be zero inflated not only due to the high proportion of zeroes but also the covariate structure employed.

Key words: overdispersion, zero inflation, Poisson distribution, negative binomial distribution, faecal egg counts

18. Novel Parallel Markov Chain Monte Carlo Design for Random Sampling in Challenging Densities
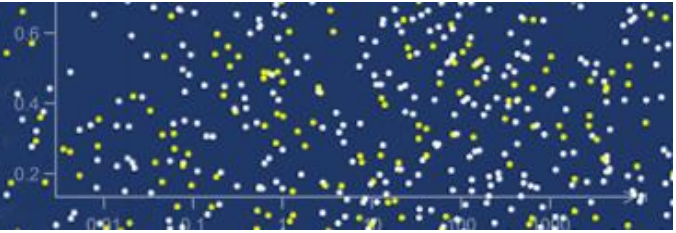
Khoa T. Tran

University of Newcastle

Co-authors: Brett Ninness

A generalised framework for Metropolis–Hastings admits many algorithms as specialisations and allows for synthesis of multiple methods to create a parallel algorithm, with no tuning required, to efficiently draw uncorrelated samples, from the posterior density in Bayesian inference, at lower computational cost in comparison with conventional samplers. Two automatic annealing schemes demonstrate complementary robustness in detecting multi-modal distribution.

Key words: MCMC, Bayesian Statistic

19. Is it a bug or a pest? Inferring reporting probabilities of pests from citizen science records.
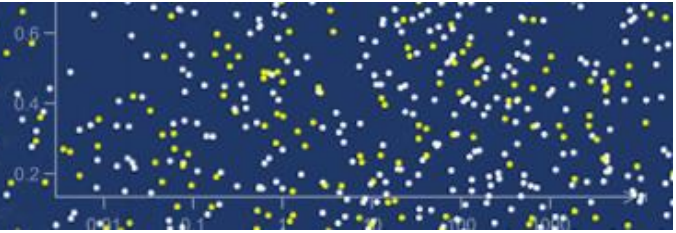
Marijke Welvaert

CSIRO

Co-authors: Peter Caley

Up until now, citizen science has been primarily focused on biodiversity and ecological monitoring, but it has been argued that citizen science could also provide added value to biosecurity surveillance. Indeed, while existing citizen science platforms (e.g.\ Atlas of Living Australia) do not necessarily contain biosecurity related information, these growing datasets can inform us about the type of species that are typically reported by citizen scientists, and whether they are likely to include exotic pests and/or pathogen species.

Given that we know what species families are typically reported by citizen scientists, we can cross reference those to the species families that are of high pest concern. Using a feature-based modelling approach, we identified which features in the Coleoptera and Hemiptera order correlate with reporting of those species. These results help us understand in more detail how the general public can be incorporated in general surveillance for biosecurity.

Key words: Citizen science, biosecurity risk, detection probability, sampling bias

20. Fox Control Program and Remote Camera Monitoring in Great Otway National Park

Kally Yuen

Australian Mathematical Sciences Institute

Co-authors: Mark J Antos, Gary Summers, Emma Danby, Sylvia van der Peet and Carlie Bronk

In 2009, a camera monitoring program was set up in the western region of Great Otway National Park to address specific management questions: Is fox baiting successful in reducing Red Fox activity? Is there a subsequent positive response from potential prey species?

Cameras operated for 24 hours on consecutive days each year – 20 cameras in fox baiting area and 20 in an unbaited area. Monitoring was conducted annually, starting in winter of 2009. Dynamic occupancy models were used to examine the effect of fox baiting and possible changes of site occupancy rate over time for each key species.

Although there was no suggestion of an effect of fox baiting on the occupancy rates of both Red Fox and critical weight range mammal, fox baiting had a positive influence on the occupancy rates of Bassian Thrush, a ground-dwelling bird.

The data have provided information about the distribution of species of conservation concern and introduced predators which can help with future management.

Key words: dynamic occupancy models, remote camera monitoring