Australasian Bayesian Network Modelling Society

November 14-15, 2022: Workshops (University of Sydney)
November 16-17, 2022: Conference (University of Sydney)
abnms2022@abnms.org

Fourteenth Annual Conference of the Australasian
Bayesian Network Modelling Society
(ABNMS2022)

Sydney, Australia

Special Thanks to our Conference Partners and Sponsors

Bayesian Intelligence specialises in consulting on Bayesian network technology. Located in Melbourne, Australia, Bayesian Intelligence was created in 2007 by directors Ann Nicholson and Kevin Korb, each having over two decades of experience in Bayesian networks and co-authors of the textbook Bayesian Artificial Intelligence.

Bayesian Intelligence has supported ABNMS since the very first conference in 2009 and helped with the organisation of this year's conference.

The University of Sydney is globally recognised as a leading institution in research and teaching. The University excels across an incredible range of disciplines and is constantly pushing new boundaries in the pursuit of knowledge. Some of Australia's brightest researchers and most promising students work together to answer tomorrow's big questions and affect positive change in people's lives.

The University is partnering with ABNMS to host the 2022 conference in Sydney.

DST is the Australian government's lead agency responsible for applying science and technology to safeguard Australia and its national interests. They work closely with industry, universities and the scientific community to enhance our combined ability to support Australia's defence and national security capabilities and to contribute to national wealth.

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Workshop Program

Study Room 3, Chau Chak Wing Museum, University Place, The University of Sydney, Camperdown, Sydney, NSW

Monday, November 14th: Intro to BNs Day 1

9:00	Arrival, registration and setup	
9:30	Welcome and introduction	Owen Woodberry &
9:45	BN basics	Steven Mascaro
	Introduction to BNs – probabilities, Bayes Theorem, nodes, arcs, CPTs, reasoning	*Bayesian Intelligence*
10:45	Morning tea	
11:15	BN software introduction	Owen Woodberry &
	Introduction and overview of commonly used BN software, e.g., Netica and GeNIe	Steven Mascaro
		Bayesian Intelligence
12:30	Lunch	
13:30	BN software introduction (cont.)	Owen Woodberry &
14:15	Decision networks	Steven Mascaro
		Bayesian Intelligence
15:00	Afternoon tea	
15:30	GIS integration	Owen Woodberry &
		Steven Mascaro
		Bayesian Intelligence
17:00	Finish	

Notes?

Tuesday, November 15th: Intro to BNs Day 2

9:00	Arrival and setup	
9:15	Elicitation	Owen Woodberry & Steven Mascaro *Bayesian Intelligence*
11:00	Morning tea	
11:30	Learning BNs from data	Owen Woodberry & Steven Mascaro *Bayesian Intelligence*
12:30	Lunch	
13:15	Case study: Modelling COVID-19 disease progression (Part 1)	Yue Wu, Steven Mascaro & Owen Woodberry *University of Sydney* & *Bayesian Intelligence*
15:00	Afternoon tea	
15:15	Case study: Modelling COVID-19 disease progression (Part 2)	Yue Wu, Steven Mascaro & Owen Woodberry *University of Sydney* & *Bayesian Intelligence*
17:00	Finish	

Notes?

Conference Program

Auditorium, Chau Chak Wing Museum, University Place,
The University of Sydney, Camperdown, Sydney, NSW

Wednesday, November 16th: Conference Day 1

8:40	Registration & setup	
9:00	Welcome and conference opening	
Session 1: Health		
9:10	Updates from COVID-19 Projects	Thomas Parr, Steven Mascaro, Helen Mayfield
9:55	Urinary tract infections in children: building a causal model-based decision support tool for diagnosis with domain knowledge and prospective data	Jessica Ramsay, Steven Mascaro, Anita Campbell, David Foley, Ariel Mace, Paul Ingram, Meredith Borland, Christopher Blyth, Nicholas Larkins, Tim Robertson, Phoebe Williams, Tom Snelling and Yue Wu
10:15	Eliciting expert knowledge to build a causal model of infection in children	Ariel Mace, Yue Wu, Andrew Martin, Peter Richmond, Steven Mascaro and Thomas Snelling
10:35	A Bayesian network to facilitate detection and management of chronic wet cough in primary care clinics	Steven Mascaro, Pamela Laird, Gloria Lau, Anne Chang, Maree Toombs, Roz Walker, Peter Morris, Gabrielle McCallum, Richard Norman and Andre Schultz
10:55	Morning Tea	

Session 2: Environment Hazards and Climate Change		
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11:20	RiverWatch: 'nowcasting' recreational water quality in urban estuaries using Bayesian Networks	Simon Lloyd, Guido Carvajal, Nerida Taylor, Paul Osmond, David Roser and Stuart Khan
11:40	Modelling historical shoreline changes using Bayesian network model in Nanumea, Tuvalu.	Shannon Bengtson, Elizabeth Keller, Annemarie Christophersen, Moritz Wandres, Antonio Espejo and Herve Damlamlian
12:00	Predicting Effects of Climate Change and Sea-Level Rise on Wetlands of the Pacific Coast, USA	Bruce Marcot, Karen Thorne, Joel Carr and Glenn Guntenspergen
12:20	Achieving human and ecosystem health benefits through integrated watershed management: improving disease prevention and marine environments in Fiji	Ama Wakwella, Carissa Klein, Amelia Wenger, Stacy Jupiter, Helen Mayfield, Aaron Jenkins and Collen Lau
12:40	Lunch	
Invited Speaker		
13:40	Active Inference	Thomas Parr
Session 3: Tool Developments (part 1)		
14:40	CAT: The Causal Attribution Tool	Kevin Korb, Steven Mascaro, Erik Nyberg and Yang Li
15:00	Afternoon Tea	

Session 4: Defence		
15:20	A stochastic model for assessing Defence capability options	Minh-Tuan Nguyen, James Peacock and Andrew Coutts
15:40	An Overview of the Bayesian Elicitation Support Tool	Timothy Heseltine, Hannah Gallant, Ivo Widjaja, Kerryn Owen, James Peacock, Michael Galister and Minh-Tuan Nguyen
ABNMS		
16:00	Annual General Meeting	
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18:30	Conference Dinner

Notes?

Thursday, November 17th: Conference Day 2

8:40	Day Start	
Tool Developments (part 2)		
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Session 5: Environment		
9:00	Predicting invasiveness of a global pathogen	Peter Scott, Bruce Marcot and Treena Burgess
9:20	Exploring volcanic monitoring and eruption data with Uninet	Annemarie Christophersen, Anca Hanea, Yannik Behr and Craig Miller
9:40	A modified Bayesian Network model of a scenario study for risk management related to shark-human interactions	Gang Xie, Peter Simmons, Michael Mehmet, Belinda Curley, Nicola Ivory, Kane Callaghan and Kim Wolfenden
10:00	Where the bee sucks, there suck I An integrating decision support system for pollinator abundance	Martine Barons and Aditi Shenvi
10:20	Green fire breaks, can they work?	Erica Marshall, Kate Parkins, Trent Penman
10:40	Morning Tea	
Session 6: Methods		
11:10	Making equivalent sample size an integral part of Bayesian network modelling practices	Steven Mascaro

11:30	Are bibliometric characteristics of a paper and of its authors good predictors of a paper's citation score? An application of learning and validating continuous BNs for highly skewed distributions.	Tina Nane and Anca Hanea
11:50	Structure Elicitation Approaches for Bayesian Networks: A Survey	Ross Pearson, Steven Mascaro and Ann Nicholson
12:10	A Framework for fake news detection on Social Media: A Probabilistic Reasoning Approach	Mehreen Rashid, Fabliha Anber, and Md Samiullah
12:30	Lunch	
Session 7: Health		
13:30	Evaluating complementary diagnostic markers for lymphatic filariasis surveillance in American Samoa	Helen Mayfield, Patricia Graves and Colleen Lau
13:50	Can we control antimicrobial resistance through effective education and better diagnosis?	Yue Wu, Tom Snelling and Mark Tanaka
14:10	Data Driven modelling of antimicrobial resistance using Bayes Nets, regression and primary statistical analyses	David Roser, Henrietta Venter, Sylvia Sapula and Michael Short
14:30	Designing clinical trials using causal models	Tom Snelling, Yue Wu, Charlie McLeod, Andre Schultz, Steven Mascaro, Owen Woodberry
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How to get there

Workshops venue (Monday 14th & Tuesday 15th)

Study Room 3, Chau Chak Wing Museum,
University Place, The University of Sydney,
Camperdown, NSW 2006

Conference venue (Wednesday 16th & Thursday 17th)

Nelson Meers Auditorium, Chau Chak Wing Museum,
University Place, The University of Sydney,
Camperdown, NSW 2006

Dinner venue (Wednesday 16th 18:30pm)

Rubyos, 18-20 King Street
Newtown, NSW 2042
Dress code: as casual or formal as you wish
BYO or purchase drinks on site

Transport Information

Travelling to the University of Sydney:
There are two main entrances – the most convenient to the Chau Chak Wing Museum is the one on Parramatta Rd.

By train: Redfern is a 10-minute walk to the campus. Many students walk this route, and a free shuttle bus runs between Fisher Library and Redfern Station in the evening (4pm-10.30pm) during semester.

Central is a 15-minute walk along City Rd and George St. There are frequent buses from Railway Square to Parramatta Rd and City Rd. The airport train is around a 5-10 min journey to Central Station.

By bus: If you are arriving by bus, there are stops at our main entrances on Parramatta Rd and City Rd. Use the map below to locate the closest bus stop to your destination.

By car: The University is 3km from the centre of the CBD and roughly a 20m drive in peak traffic. If you are coming directly from the Sydney Airport, the University is a 30min drive, roughly 7.5km.

Parking on campus: There is limited parking on the Camperdown/Darlington Campus and we encourage people to use public transport, walk or cycle in by using bicycle parking, safe pedestrian routes, and the campus bus.

The University is a paid parking area at all times at a rate of $4 per hour, up to a maximum charge of $24 per day. We have a paperless system, using licence plate recognition technology. No parking tickets are required. No paper receipts are provided. You will need to take a photo of the final screen showing a URL address to contact to obtain a parking receipt.

Parking Meter Machines accept EFT payments, cash and coins or you can download the CellOPark app onto your phone. Machines do not offer refunds.
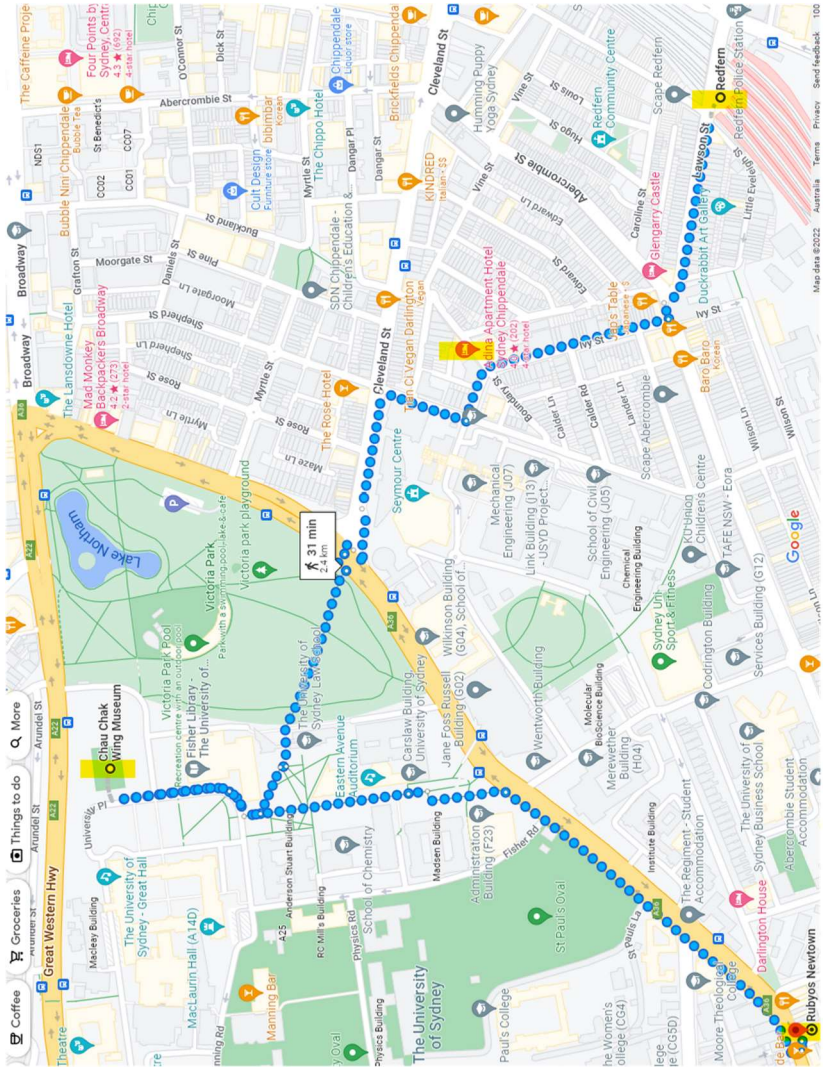
Suggested Accommodation

There are many accommodation options available near the University of Sydney's Camperdown Campus.

A full list can be found at
https://www.abnms.org/conferences/abnms2022/travelAndAccommodation

Maps

Keynote Speaker

Thomas Parr is a theoretical neurobiologist and honorary research fellow at the Wellcome Centre for Human Neuroimaging (WCHN) in the University College London (UCL) Queen Square Institute of Neurology. He completed his MBBS at UCL Medical School, additionally completing his PhD at in the Theoretical Neurobiology group of the WCHN under the supervision of Professor Karl Friston. During this time, he developed an interest in active inference — a framing of brain function in terms of the internal (probabilistic) models our nervous systems rely upon to guide perception and action. He is an author of the first comprehensive book on active inference (Active Inference: The Free Energy Principle in Mind, Brain, and Behavior). In addition to his work developing the theoretical foundations of this approach, he has an interest in the application of active inference to understanding neurological disorders. This relies upon treating neuronal computation as inference and seeks to identify the forms of internal models that lead to pathological false inferences.

Abstracts

Day 1 – 9:10 COVID Project Updates

Thomas Parr, Steven Mascaro, Helen Mayfield

Three teams have been invited to present updates about their research on COVID-19.

Day 1 – 9:55 Urinary tract infections in children: building a causal model-based decision support tool for diagnosis with domain knowledge and prospective data

Jessica Ramsay, Steven Mascaro, Anita Campbell, David Foley, Ariel Mace, Paul Ingram, Meredith Borland, Christopher Blyth, Nicholas Larkins, Tim Robertson, Phoebe Williams, Tom Snelling and Yue Wu

Background: Urinary tract infections (UTIs) in children can be difficult to diagnose due to variable clinical presentations and the difficulties in obtaining a urine sample. Within the emergency department (ED), clinical decisions require consideration of several complex factors and interactions for effective management. Directed acyclic graphs (DAG) and causal Bayesian networks (BN) offer a unique way to describe disease pathophysiology, laboratory testing processes and management decisions that infers quantitative inference and can therefore offer a tool for clinical decision support.

Methods: We held knowledge elicitation workshops and one-on-one meetings with clinical domain experts to establish a UTI DAG (the Expert DAG). We also collected data prospectively from the ED of a large children's hospital on patients presenting with a suspected UTI. The Expert DAG, prospective data and further expert knowledge were combined to produce an application-oriented BN (the Applied BN) to support the diagnoses of paediatric UTIs. Qualitative and quantitative methods were then used to assess the performance of the Applied BN.

Results: 431 episodes of suspected UTIs were collected from May 2019 to November 2020. The Expert DAG elucidated relationships between infection, specimen contamination and clinical management in paediatric UTIs. Parameterised using prospective

data and expert-elicited parameters, the Applied BN achieved an excellent and stable performance in predicting Escherichia coli culture results. The mean area under the receiver operating characteristic curve was 0.86 and the mean log loss was 0.48 based on 10-fold cross-validation. We illustrate how the BN can be presented for decision support using three hypothetical clinical scenarios.

Conclusion: Causal BNs created from expert elicited DAGs and prospective clinical data can integrate case-specific information to provide individual decision support for the diagnosis of paediatric UTIs. Such models support the interpretation of urine culture results and could improve patient care and antibiotic prescribing.

Day 1 – 10:15 Eliciting expert knowledge to build a causal model of infection in children

Ariel Mace, Yue Wu, Andrew Martin, Peter Richmond, Steven Mascaro and Thomas Snelling

Aims: Fever is a common, and often complex, problem in children. The signs and symptoms of childhood infection are frequently non-specific; differentiating benign, self-limiting infections from serious infections with potentially severe outcomes can be difficult, even for experienced clinicians. Existing tools to aid the diagnosis of serious infections are affected by variable performance, narrow scope of clinical application, poor transparency and usability, and ultimately low uptake. Causal Bayesian networks (BNs) provide a framework for understanding complex diagnostic problems like the child with undifferentiated fever. We describe the process of creating a highly generic causal model of infection, derived through expert elicitation, that aims to address the limitations of existing diagnostic tools.

Methods: Domain experts in the field of childhood infection (paediatric, emergency and infectious disease physicians) were identified and invited to participate in knowledge elicitation sessions facilitated by BN modelling experts. Their knowledge was elicited via structured surveys, written feedback and face-to-face (Zoom) workshops. Ethics approval (Sydney Children's Health Network) was

obtained to utilise a large dataset (>10,000 febrile children) for BN structure development, parameterisation and validation.

Results: Four knowledge elicitation workshops were held between September 2020-October 2021; 21 experts participated in one or more sessions. Four submodels have been incrementally and iteratively built, including three system-specific models (urinary tract, gastrointestinal and central nervous systems) and a submodel of systemic inflammatory/sepsis responses arising from localised infection.

Conclusions: To our knowledge, ours is the first expert-informed causal model of infection and sepsis in children. We demonstrate how a complex clinical problem can be fragmented into smaller, tractable causal subcomponents, validated and then recompiled into an integrated model to aid clinical reasoning. We anticipate that parameterisation our BN model will enable the creation of clinical decision support tools for childhood infection that are not only accurate, but also transparent, understandable, and generalisable.

Day 1 – 10:35 A Bayesian network to facilitate detection and management of chronic wet cough in primary care clinics

Steven Mascaro, Pamela Laird, Gloria Lau, Anne Chang, Maree Toombs, Roz Walker, Peter Morris, Gabrielle McCallum, Richard Norman and Andre Schultz

Chronic wet cough (CWC) in children is a symptom commonly encountered in primary care clinics and could reflect serious underlying disease. However, CWC is often not managed according to best practice clinical guidelines and even goes undetected. The barriers and enablers to the detection and optimal management of CWC in primary care clinics are many and complex. Implementation of a multi-faceted program to facilitate detection and management of CWC in a large regional Aboriginal medical service has been shown to be effective, ultimately resulting in improved health outcomes. However, the implementation was time and resource intensive. Implementation of all components of such a multi-faceted program might not be necessary at every clinic.

Here, we explore the use of Bayesian networks (BNs) to help reduce the resources required during implementation. We build upon our existing research with stakeholders that identified key barriers and enablers, and place these, along with the proposed components of the implementation program, into a quantitative causal model. We present a causal structure that was developed via workshops with three experts and was parameterised in two phases: a first phase in which the same three experts participated in a quantitative Delphi elicitation, and a second phase in which a diverse group of stakeholders provided responses to a qualitative survey. Stakeholder surveys are also used to validate the model, both in terms of its structure and parameterisation.

The approach allows us to quantitatively estimate the relative impact of each component of the program prior to roll-out and to identify the most important and propitious components to implement at individual clinics. This work also suggests methods for streamlining and scaling implementation processes that may eventually be of value to implementation science more broadly.

Day 1 – 11:20 RiverWatch: 'nowcasting' recreational water quality in urban estuaries using Bayesian Networks

Simon Lloyd, Guido Carvajal, Nerida Taylor, Paul Osmond, David Roser and Stuart Khan

Current methods for monitoring the microbiological quality of recreational waters require 18-24 hours to process, so the World Health Organisation recommends predictive modelling in support of pollution control and public communication of bathing safety. We assessed the use of Bayesian Networks for predicting the likelihood of the key faecal indicator bacteria, Enterococci, exceeding guideline benchmarks at estuarine locations in Sydney's Parramatta River. Hydro-meteorological data, including rainfall, solar exposure, tidal flows and wind were matched to water quality records taken at 3 to 6 day intervals and spanning 25 years, to issue daily predictions of bathing water quality. Enterococci estimates were further employed

to infer gastrointestinal illness risk, using algorithms developed originally for estimating long term bathing site risk.

Construction, training and cross-validation of a semi-naïve 'RiverWatch' BN were undertaken using 1300 datapoints from Dawn Fraser Baths. Data from the two most recent swimming seasons were then used for independent verification. Classification accuracy was benchmarked against a spreadsheet method currently used by Beachwatch NSW for daily pollution predictions at the same location. Comparing pollution events of public health concern, prediction reliability improved from 75% (6 of 8 events) Beachwatch to 100% (8 of 8 events) RiverWatch. To assess transferability of the modelling approach the 'RiverWatch' BN was applied to four further locations. Two data rich locations correctly classified 91% (10 of 11) and 89% (8 of 9) pollution events. Two data poor locations were evaluated using nested cross-validation within the training process and correctly classified 63% (12 of 19) and 80% (12 of 15) pollution events. Characterisation of rainfall patterns and salinity variation proved central to model development. Confidence in model outputs should be improved by training with more frequent measurements. Model outputs are being linked to an online 'nowcast' dashboard for communicating real-time water quality to the Sydney bathing public.

Day 1 – 11:40 Modelling historical shoreline changes using Bayesian network model in Nanumea, Tuvalu.

Shannon Bengtson, Elizabeth Keller, Annemarie Christophersen, Moritz Wandres, Antonio Espejo and Herve Damlamlian

Shoreline erosion can have deleterious effects on coastal communities, yet shoreline changes remain poorly constrained on many atolls across the Pacific. Here, we aim to develop a Bayesian network model (BN) that can be used by decision-makers to estimate the probability of erosion and accretion on the main islet of Nanumea, Tuvalu. We use snapshots of shoreline locations based on three proxies digitised from satellite images from 1974 to 2020: vegetation line, beach toe, and high water mark, with 16, 13, and 14 snapshots respectively. We divide the shoreline into 250 segments

and calculate the shoreline change for each segment along perpendicular transects compared to a baseline (year 2003). We group the shoreline segments into regions using a k-mean algorithm trained on shoreline change, location, and mean wave energy from XBeach simulations. The number of clusters is optimised using the elbow method. We then develop a BN using the SMILE engine which models each shoreline group for each proxy with individual nodes. The data are binned into erosion and accretion. We include nodes for mean wave energy, tide, precipitation, and building density to constrain shoreline changes in the model. The conditional probability tables are estimated using expectation-maximisation. Our preliminary results suggest some capability of the model to estimate shoreline change, however further work is needed to incorporate large wave events which can cause significant and sudden changes in shoreline location.

Day 1 – 12:00 Predicting Effects of Climate Change and Sea-Level Rise on Wetlands of the Pacific Coast, USA

Bruce Marcot, Karen Thorne, Joel Carr and Glenn Guntenspergen

As climate change causes a rise in sea level, some of the most threatened ecosystems are coastal tidal saline wetlands (TSWs), including marshes and estuaries. Studies generally suggest significant losses over coming decades, but what are needed are projections of site-specific TSWs, particularly along the Pacific Coast USA. We present a Bayesian network (BN) model that we developed based on literature review and direct research experience, and parameterized from on a database we compiled of 26 sample TSWs, to predict changes (declines) in the resilience of specific TSWs to projected sea-level rise. We modeled resilience in two dimensions along wetland vertical elevation capital and wetland lateral migration capital. We found that all sites would lose at least 50% of their elevation capital resilience between 2060 and 2100, and 100% by 2070 to 2130, depending on the site. Under a 1.5-m sea-level rise scenario, nearly all sites in California will lose most or all of their lateral migration resilience. Our model can be useful in risk analysis and risk

management to prioritize sites needing more immediate conservation action.

Day 1 – 12:20 Achieving human and ecosystem health benefits through integrated watershed management: improving disease prevention and marine environments in Fiji

Ama Wakwella, Carissa Klein, Amelia Wenger, Stacy Jupiter, Helen Mayfield, Aaron Jenkins and Collen Lau

Degradation of watersheds from land-based human activities alters the provisioning of water, impacting critical processes for both downstream coastal ecosystems and humans such as the spread of pollutants and water-related infectious diseases. In many Pacific Island countries, such as Fiji, this link is particularly critical as people rely on marine ecosystems for food and livelihoods, and water-related diseases such as leptospirosis are endemic.

While the links between watershed condition, water quality, and impacts onto downstream coastal ecosystems are known and well researched, there is limited research into the environmental drivers of water-related infectious diseases, particularly at the watershed-scale. There is even fewer examples of cross-disciplinary research or effort to manage these aspects of human and ecosystem health.

An opportunity exists to combine knowledge, resources, and funding from across different sectors in public health and ecosystem management to better understand the watershed system and optimise watershed management. Working in close collaboration with the Watershed Interventions for Systems Health (WISH) Fiji project, this research uses a cross-sectoral Bayesian Belief Network approach to optimise management of watersheds in Fiji when considering both human and ecosystem health. We aim to identify how human driven land-use change in Fijian watersheds impacts both the risk of water-related infectious diseases in humans and the health of downstream coral reefs.

Specifically, we will assess the influence of land-use variables on predictions of levels of leptospirosis and typhoid, as well as the contribution of sediment to downstream coral reef condition. These

models can help us understand the impacts of environmental interventions on both human disease risk and coral reef health, with a view to prioritising for management interventions. Preliminary conceptual models indicate that environmental interventions targeting flood risk could potentially provide some of the greatest co-benefits to both human and ecosystem health.

Day 1 – 14:40 CAT: The Causal Attribution Tool

Kevin Korb, Steven Mascaro, Erik Nyberg and Yang Li

Causal Bayesian Networks (CBNs) are a popular way of modelling causal and probabilistic dependencies between important variables across many sciences. However, standard interfaces and measures for exploring these relationships only show how observations of some variables update the probability distributions over others. This does not adequately distinguish between correlation and causation, which is liable to mislead many users, who are often interested in causal influence and the possibilities for making things happen. To address this shortcoming, we have developed a new tool specifically for the causal investigation of CBNs. It answers "What if?" questions, by showing how external interventions on some variables would update the probability distributions over others.

Our Causal Attribution Tool (CAT) allows you to explore different causal scenarios, entertaining and testing different hypotheses about what is causing what. For example, CAT allows you to look at any number of hypothetical randomized controlled experimental interventions on possible causes of an effect variable (or variables) of interest, and measure the outcomes by comparing posterior distributions of the effect variable. CAT also supports arbitrary observational contexts, by allowing you to set values for any context variables.

In addition, CAT will issue a verdict about what causes are more, or less, responsible for either particular outcomes or for general influence on an outcome variable or variables. To be sure, how best to judge causal attribution is a contested problem. So far, CAT implements three leading contenders for such a method: Fraction of

Attributable Risk (FAR; see Stott, et al., 2016), Cheng's Causal Power measure (Glymour and Cheng, 1998), and ours, using Causal Information Theory (Korb, et al., 2011). Other criteria will be implemented by us or can be implemented by you.

CAT is open source. We propose to to integrate it into the ABNMS Bayesian Network database, and it is currently supported at https://causalattribution.org (open for Beta testing).

Glymour, C. and P. Cheng (1998). Causal mechanism and probability: a normative approach. In M. Oaksford and N. Chater (Eds.), Rational models of cognition. Oxford: Oxford Univ. Press.

Korb, K. B., Nyberg, E. P., & Hope, L. (2011). A new causal power theory. In Illari, Russo and Williamson (Eds) Causality in the Sciences, Oxford University Press, pp. 628-652.

Stott, P. A., Christidis, N., Otto, F. E., Sun, Y., Vanderlinden, J. P., Van Oldenborgh, G. J., … & Zwiers, F. W. (2016). Attribution of extreme weather and climate-related events. Wiley Interdisciplinary Reviews: Climate Change, 7(1), 23-41.

Day 1 – 15:20 A stochastic model for assessing Defence capability options

Minh-Tuan Nguyen, James Peacock and Andrew Coutts

Bayesian network (BN) models are used to support decision-makers (DMs) with regards to capability acquisition in military organisations1. However, various forms of uncertainty exist when using BNs as a decision- support tool. Firstly, BNs represent the aleatoric uncertainty (i.e. natural variation) of the system being modelled. Secondly, approximate inference introduces errors in the estimate of calculated values. Thirdly, eliciting model parameters from subject matter experts (SMEs) introduces epistemic (knowledge) uncertainty. As such, uncertainty must be accepted as a feature of the evaluation process. This study outlines a BN modelling approach with simulation and proposes a stochastic model for quantitatively analysing the uncertainty associated with eliciting data from SMEs.

Epistemic uncertainty can be captured explicitly via elicitation processes2. This might be represented as a probability distribution (e.g. normal, triangular, discrete). Once captured, Monte-Carlo simulation is then performed to produce multiple instances of the BN whereby distinct conditional probability tables are produced by sampling from the elicited bounds. For each BN, outcome statistics (e.g. posterior probability of a mission success) are inferred and then aggregated via summary statistics (e.g. mean and variance) across all instances of the BNs. Instead of obtaining single- point estimates from the evaluation model, a distribution of the decision variables and hence, a range of assessment values for each decision variable can be presented to the DMs.

The use of an exact inference algorithm to analyse the BNs is crucial to not conflate the types of uncertainty. If an approximate inference algorithm is used, the uncertainty between epistemic uncertainty and estimated outcome variables will be combined in the evaluation process. Further, the use of approximate algorithms that require Monte- Carlo sampling might increase the computational burden to unacceptable levels (e.g. time constraints). We present the application of an exact inference algorithm using variable elimination method to explore epistemic uncertainty. The proposed approach provides BN models an ability to deal with the uncertainty in data collection and gives the flexibility to DMs in option comparison and sensitivity analysis.

Day 1 – 15:40 An Overview of the Bayesian Elicitation Support Tool

Timothy Heseltine, Hannah Gallant, Ivo Widjaja, Kerryn Owen, James Peacock, Michael Galister and Minh-Tuan Nguyen

Defence Science and Technology Group (DSTG) uses Bayesian networks (BNs) to analyse Defence capabilities for strategic planning purposes, such as force-structure design. The Bayesian Reasoning Value Model (BRVM) utilises Bayes' theorem to represent strategic planning entities and their relationships as interconnected nodes within a BN, to estimate the probability of mission success given

contributing Defence elements, various operational scenarios and threats.

In collaboration with the University of Melbourne, Defence has developed the Bayesian Elicitation Support Tool (BEST). BEST is designed to create a BRVM during workshops with subject matter experts, capture data and construct the network in real time. Previously, spreadsheets and offline facilitated discussions achieved this with the following consequences:

• Data processing introduced significant time delays and reproducibility errors

• Collected data was accidentally lost or corrupted

• Data inconsistencies required manual intervention, exacerbating data processing delays.

In contrast, BEST offers these advantages:

• Establishes an integrated data storage and management platform, aids data organisation and provides secure access to the subject matter experts.

• Facilitates automated data collection, online survey distribution to multiple participants to provide timely responses and allows the flexibility to allocate subsections of the model to match participants' expertise. As BEST allows for distributed, asynchronous survey completion, it enhances productivity of time-poor people such as military decision makers.

• The conditional probability tables (CPTs) can be calculated using the appropriate method for a given problem, such as an indirect elicitation or Cain method. Further, BEST reduces bias by aggregating the responses from multiple participants and supports provision of qualitative opinions.

This presentation will outline our Bayesian approach in the Defence context and will demonstrate how BEST is used to design a BN and collect data for CPT estimation. It will also elaborate on the methods used to complete CPTs and further Bayesian analysis techniques that are currently in development.

Day 2 – 8:40 Tools for Elicitation of Continuous Probability Distributions for Bayesian Networks

Marek Druzdzel

It is often forgotten that there is nothing in the theory underlying Bayesian networks that prevents them from having continuous variables and continuous distributions. I have been involved in building a Bayesian network modeling system that offers unlimited flexibility and does not limit modelers to special cases, such as multivariate Normal distributions with all noise being Normal and all interactions being modeled by linear functions. In this talk, I will show two useful tools recently added to GeNIe (http://www.bayesfusion.com/) for constructing equations involving continuous probability distributions: (1) Metalog Builder, and (2) Distribution Visualizer.

Metalog distributions (Keelin 2016) are a family of continuous probability distributions that show remarkable shape flexibility, a choice of bounds, including infinite bounds, and capability to fit data. They are also efficient in sample generation, which directly supports environments based on simulation. I will introduce the metalog distributions and show some of their phenomenal properties that have useful practical applications. The Metalog Builder is an interactive tool that allows for fitting a metalog distribution to data or to any number of percentiles specified by an expert. The resulting distributions can be visualized and chosen based on a compromised between their fit to data and complexity.

Choosing the right probability distribution over continuous data is a skill that requires considerable statistical insight. When the distribution is transformed by an equation expression, the task is daunting even for an experienced decision analyst. Distribution Visualizer is an interactive tool for visualizing expressions with probability distributions through Monte Carlo simulation. This helps with selecting an expression that is most appropriate for the task at hand.

Day 2 – 9:00 Predicting invasiveness of a global pathogen

Peter Scott, Bruce Marcot and Treena Burgess

The Phytophthora genus is associated with significant plant diseases in natural ecosystems, production, and urban environments globally. Phytophthora pathogens pose formidable biosecurity challenges as they are increasingly spread globally and often cause major diseases within newly invaded environments. Many significant new diseases, including Kauri dieback and Sudden Oak death, are caused by species that were only identified after the discovery of the disease. Based on the rate of identifying new species, models suggest there may be up to four times more Phytophthora species than are currently described. These new species may have serious impacts, even if they are not currently associated with serious diseases. Therefore, it is difficult to determine the management requirements of these new species when they are initially identified. A multivariate Bayesian traits analysis was conducted to determine if biological traits, that can be easily measured within the laboratory, may be used to develop models to predict the impact of these newly identified species. These Bayesian models effectively predict the invasion risk of Phytophthora species and can effectively be used for new species. This approach could be used to develop risk models for other genera of plant pathogens.

Day 2 – 9:20 Exploring volcanic monitoring and eruption data with Uninet

Annemarie Christophersen, Anca Hanea, Yannik Behr and Craig Miller

Bayesian Networks (BNs) have been promoted in the scientific literature for more than a decade as a framework for combining different volcano monitoring data and linking them to the underlying driving processes. Best practice recommendations for volcano observatories propose using probabilistic methods with uncertainties to forecast eruptions. However, applications of BNs in real-time monitoring are rare. We recently developed a discrete BN to forecast volcanic eruption on Mt Ruapehu, Aotearoa New Zealand. The model automatically updates daily, using the latest monitoring

data. The results are displayed on a dashboard for the members of the volcano monitoring group to see and include in their discussions. The model structure was defined by experts, based on the conceptual understanding of the volcanic processes at Mt Ruapehu. The conditional probability tables were estimated from the long monitoring records, supplemented by expert elicitation. Here we use the same model structure and data to explore continuous methods of model parameterisation. We model the probability distribution of each variable separately from the dependence and parametrise the dependence using (conditional) rank correlations. This approach is implemented in the Uninet software. Uninet is a dependence modelling software package with a focus on continuous distributions. It has great features for data analysis that help us present the data in novel ways. Uninet is available from https://lighttwist-software.com/uninet/.

Day 2 – 9:40 A modified Bayesian Network model of a scenario study for risk management related to shark-human interactions

Gang Xie, Peter Simmons, Michael Mehmet, Belinda Curley, Nicola Ivory, Kane Callaghan and Kim Wolfenden

In our recently published article "A scenario study of the acceptability to ocean users of more and less invasive management after shark-human interactions", Bayesian Network (BN) was chosen as the principal analysis tool for identifying patterns from a survey study of 1769 valid responses. A modified BN model (26 nodes, 54 links) was proposed in this poster to improve the prediction performance of those four risk management policy/strategy variables in the original BN model (26 nodes, 44 links). At the cost of substantive increase in number of model parameters (7200 conditional probabilities estimated for the original model versus 19872 for the modified model), the modification was justified by the consistently lower error rate results in predicting the outcomes of the four focus strategy variables. The modified BN model has showed a higher sensitivity in quantifying the impacts of predictor variables (e.g., Scenarios and the characteristics of respondents) on the response variables

(preference levels for four types of risk management strategies). The overall patterns of the much higher proportions of support for the Education and Noninvasive strategies versus the much lower proportions of support for the Invasive and Population Reduction strategies remained the same for both BN models but to a slightly lesser extent in the modified model. Since the modified model counted for both the direct and indirect effects of the predictor variables on the response variables, the changes of the proportions of support for each of the four possible risk management strategies were more sensitive to the changes in the predictor variable such as Scenario, Age, Gender, or Frequency of Beach Visit. Hence the modified model was deemed to be an improved version of the original BN model.

Day 2 – 10:00 "Where the bee sucks, there suck I" An integrating decision support system for pollinator abundance

Martine Barons and Aditi Shenvi

The world's dependence on pollinators for food production and the serious nature of the decline in insect pollinators (especially bees and hoverflies) has recently been recognised, with the UK Government issuing its first National Pollinator Strategy in 2014. Whilst much work exists in the ecology domain in understanding supportive and unsupportive environments, the rigorous quantification of this, such that policymakers can decide between competing policy action, has yet to be developed. Building on success working with The National Archives on risk management for digital archives (another relatively recent problem), we are developing a bespoke decision support tool, tailored the Australian context, to allow policymakers to compare the cost effectiveness of candidate policy options. This is particularly timely since, despite the careful biosecurity risk control at Australia's borders for which it is renowned, the Varroa mite has made a recent incursion into Australia and is causing the destruction of many managed honeybee hives. Moreover, unusually, Australia has a large population of feral honeybee colonies living wild, and these provide a substantial proportion of the country's food crop pollination.

Without the intervention of beekeepers available to managed colonies, these feral colonies are likely to be eliminated by the Varroa mite, with consequent impacts on Australia's food security.

Where The Bee Sucks (There Suck I) This song from The Tempest by William Shakespeare is sung by Ariel, a sprite who is in the service of the sorcerer Prospero. Act Five, Scene 1, Lines 88-95

Day 2 – 10:20 Green fire breaks, can they work?

Erica Marshall, Kate Parkins, Trent Penman

Under a changing climate we are likely to experience larger, more frequent, and more severe fires in many parts of the world. Traditional methods of managing wildfire risk can exacerbate impacts on carbon and biodiversity, without reducing wildfire risks to people on high fire danger days. Feedbacks between increased fire risk and the environment, particularly because fires release large amounts of carbon, mean that this problem is likely to worsen going forward. Green firebreaks are defined as planted strips of low flammability vegetation which are strategically placed to reduce fire spread in the landscape. In theory, green firebreaks can reduce wildfire risk to property and houses while producing co-benefits to biodiversity and carbon sequestration. Despite the extensive use of green firebreaks in China, Europe, North America, and New Zealand, they have yet to be tested as a scalable solution in Australia. One aspect of the testing required to validate the use of green firebreaks in Australia is identifying key elements of planting designs which increase carbon and biodiversity values, without increasing risk to people and property. Here we use a Bayesian Network analysis to test green firebreak planting designs and identify key elements which deliver optimal outcomes for biodiversity, carbon sequestration, and wildfire risk. We developed separate sub-models for biodiversity, carbon and fire risk and combined those sub-models into a comprehensive network. We populated this network with a variety of data including field data, equations gathered from the literature

and expert knowledge. We tested this network on six sites across Victoria and New South Wales to determine how implementing green firebreaks on private property might change the risk profile for those properties. We also prioritised planting designs which produced the greatest increases in carbon sequestration and biodiversity, without increasing risk to people and property.

Day 2 – 11:10 Making equivalent sample size an integral part of Bayesian network modelling practices

Steven Mascaro

A key advantage of Bayesian networks (BNs) is their ability to integrate uncertain information from a wide and diverse array of sources, translating all such information into the common language of probability. The focus on probability (along with the power to represent complex multivariate causal problems) has made BNs one of the leading candidates for modelling, and making decisions under, uncertainty. Unfortunately, one kind of uncertainty that is often missing from BN modelling --- at least when working with traditional discrete BNs --- is second order uncertainty, i.e., probabilities over probabilities. While second (and higher) order uncertainties are the bread and butter of hierarchical Bayesian models and often equation-based BNs, such models are not as convenient to work with and are often unintuitive for domain experts, and are hence not always a viable option. In the case of discrete BNs, second order uncertainties are used when learning parameters in the form of an equivalent sample size (ESS, sometimes called "confidence" or "experience") or when performing sensitivity analyses on a BN using techniques such as variance-based sensitivity analysis. However, they are generally ignored in most BN modelling processes, and the potential implications of this kind of uncertainty on reasoning and decision-making are rarely considered.

Here, we provide a simple method for estimating the ESS of the conditional posterior distribution of a node in a discrete BN given unconditional ESS estimates for each node --- a method which can be readily integrated into any BN software package. We examine how

the estimated ESS using this method may match or differ to the real sample size in bespoke data trained models, and how well the estimates accord with our expectations in purely expert-knowledge driven BNs. We also demonstrate how ESS estimates can impact our interpretation of the posterior distributions produced by BNs under various evidence conditions, and ultimately what conclusions we can draw from our BN models. We argue that estimated ESS is a natural, simple and intuitive way to represent second order uncertainty, not just as an incidental part of parameter learning, but also as a key feature of reasoning and validation, from where it has thus far been missing.

Day 2 – 11:30 Are bibliometric characteristics of a paper and of its authors good predictors of a paper's citation score? An application of learning and validating continuous BNs for highly skewed distributions.

Tina Nane and Anca Hanea

The aims of this research are twofold: 1) find good predictors of a paper's mean citation score, and 2) investigate learning and validating continuous BNs when the distribution of the variable of interest (the mean citation score) and some of its predictors are highly skewed and potentially zero inflated.

We use a rich dataset of bibliometric information about 10,725 journal articles, published between 2010 and 2014 in journals indexed for Web of Science and for which at least one author was affiliated to the Technical University of Delft. Citations received by each of these articles up to and including 2017 are then averaged to a mean citation score (the variable of interest). Information about the number of authors, references, as well as a journal citation score is registered for each publication. Moreover, data on the co-authors, e.g., the largest academic age, the largest number of publications, and the largest two citation performance scores among all co-authors, are also available.

We expect some of these covariates to be good predictors of the mean citation score of a paper, based on known correlations, e.g.,

the journal score correlates well with the number of citations. However, how bibliometric information about a paper and its authors jointly influence its citation performance has not yet been studied. We investigate that by learning and validating a BN (with Uninet and the bnlearn R package). We perform a k-fold cross-validation, compare results for several values of k, and discuss k optimality in light of recent publications on the subject.

This research is still in its infancy and, at this stage, is exploratory, hence conclusions are yet to be formulated.

Day 2 – 11:50 Structure Elicitation Approaches for Bayesian Networks: A Survey

Ross Pearson, Steven Mascaro and Ann Nicholson

Bayesian Networks (BN) provide a graphical and probabilistic approach for modelling real world problems. Knowledge Engineering for Bayesian Networks (KEBN) is the process of sourcing information and representing that information compactly within a BN. Information is typically sourced from literature, experts, data, and in some cases, existing models. Extracting information from experts is referred to as the process of expert elicitation and is a common approach for encoding variables, structure and parameters within a BN.

Research regarding the elicitation of probability estimates from experts is well represented in the literature even specifically when those probability distributions are for BNs. However, eliciting the qualitative elements of the BN (structure) has received much less attention. We conducted a semi systematic literature review to survey the current state of play in regards to BN structure elicitation methodology.

Day 2 – 12:10 A Framework for fake news detection on Social Media: A Probabilistic Reasoning Approach

Mehreen Rashid, Fabliha Anber and Md Samiullah

The Internet has become an ideal breeding ground for rapid dissemination of fake news with the increasing popularity of rapidly

growing online social media networks such as Facebook and Twitter. Targeted readers are persuaded by distorted facts creating biased opinions which has the potential of affecting the individuals and society negatively as a whole. Thus, a massive amount of recent work is dedicated to detect the fake news which is widely propagated on social media networks. However, very few studies on probabilistic models (PMs), other than Naive Bayes, have been conducted in order to detect fake news on social media. More complex PMs, e.g., Bayesian Networks can be very handy and useful in this case that can predict the likelihood of news being fake, rather than directly labelling it as fake or true. Our goal in this paper is to create a Bayesian Network-based framework by mimicking the process of detecting fake news by a reasonable human being. In particular, a human makes attempt to know demographics details of the news and anticipate its truthfulness. In the process, various questions can be asked about a news, but in this study, we handle three major questions: "who" spread the news and "who" are involved; what is said in the news (content) and if it is reasonable; and "when" is the news published and if there is any contemporary issue that is remarkable. The framework has separate modules for different such questions for which we perform reasoning on the credibilities of the modules based on their respective features. The modules' inherent BNs can be constructed/modified by expert elicitation, existing knowledge-base or data. We have collected a set of real-life annotated data to train the modules and left scope for incorporating expert knowledge. Our framework computed the credibility of the individual module and then decide on the authenticity of the news by combining the credibility information of the modules. The proposed framework is capable of adapting various changes e.g., increasing the number of questions or modules, dealing with different sets of questions, dividing the modules into submodules to create a more complex structure while running the existing system. We are planning to conduct extensive

analysis of the performance of our framework with the available real-life data as well as making synthetic datasets.

Day 2 – 13:30 Evaluating complementary diagnostic markers for lymphatic filariasis surveillance in American Samoa

Helen Mayfield, Patricia Graves and Colleen Lau

Lymphatic Filariasis (LF) is a major public health burden, with an estimated 51 million people infected across 47 countries, and a further 863 million people at risk of infection. Elimination programs aim to eliminate LF as a public health problem by reducing transmission and the impacts of morbidity in those people already affected by elephantiasis or scrotal hydroceles. Reliable sero-diagnostic tools are crucial for making programmatic decisions to guide these efforts. Anti-filarial antibody responses may be detectable earlier than antigen (Ag) or circulating microfilaria (Mf) and provide an earlier indicator of infection as well as decline in prevalence after interventions such as mass drug administration. This would mean that antibody responses might offer opportunities for more timely surveillance. The aim of this study was to compare the utility of antigen and antibodies (and combinations of these) as indictors of LF infection for post-mass drug administration and post-elimination surveillance.

Bayesian networks were constructed using data from American Samoa collected in 2010, 2014 and 2016 (n = 11,662). Blood samples were tested for antigen and antibodies (Wb123, Bm14, and Bm33). The effectiveness of different combinations of these four indicators for identifying infection was explored through scenario analysis. The mean Area Under Curve results for BNs tested using cross-validation were highest for the antigen (0.92, Standard deviation - SD=0.02) and Bm14 (0.88, SD=0.01) models, and lowest for Bm33 models (0.74, SD=0.01). Among the 5616 antigen-negative participants, the relationship with antibodies varied with 14.6% being Wb123-positive, 8.6% Bm14-positive and 32.5% Bm33-positive. The concordance between markers was lower for antibody-positive participants, with antigen-positive results in 1.1% of Wb123-negative

and 1.3% of Bm14-negative participants. The results show that concurrent testing of antigen and antibodies for LF can increase the sensitivity of detection. Incorporating additional antibody diagnostic measures into existing antigen testing regimes would potentially be of benefit.

Day 2 – 13:50 Can we control antimicrobial resistance through effective education and better diagnosis?

Yue Wu, Tom Snelling and Mark Tanaka

Aims: Excessive use of antibiotics has been considered to directly cause the spread of resistant bacteria and the worldwide public health problem of antimicrobial resistance (AMR). Effective control of AMR is challenging due to the complex nature of the problem, where evolutionary, microbiological, epidemiological, clinical and behavioural factors interact to form a dynamic system. This study aims to investigate how different interventions for reducing inappropriate antibiotic use in clinical practice may contribute to the control of AMR.

Methods: We use Bayesian network (BN) to model the problem of AMR as an intersection of microbial evolution, population health, infection management, and clinical decision making. Variables definition and parameters selection will be informed by both domain expert knowledge and literature. We will simulate the impact of different intervention strategies on the AMR evolution and the utility of antibiotic use under disease scenarios with realistic clinical implications. We will conduct sensitivity analysis to explore uncertainties in the parameter space.

Results: While this study is in its early phase, we have established a dynamic BN which describes the interactions among key events in the problem domain of interest, including the emergence and spread of AMR in commensal and pathogenic bacteria, the healthcare presentation of infection episodes, the intervention strategies for promoting appropriate clinical antibiotic use, and the potential consequence or utility of antibiotic use. Based on this framework, we have identified a series of scientific, clinical and methodological

questions for further investigation. In particular, we highlight the importance of well-defined variable parameters which should serve as the theoretical basis of subsequent simulation outcomes.

Conclusions: BN provides an intuitive and practical framework for studying the problem of AMR. This study may contribute to the theoretical understanding of the potential impact and utility of clinical interventions on the problem of AMR.

Day 2 – 14:10 Data Driven modelling of antimicrobial resistance using Bayes Nets, regression and primary statistical analyses

David Roser, Henrietta Venter, Sylvia Sapula and Michael Short

Antimicrobial resistance (AMR) is among the United Nations Environment Program's top five emerging environment and health concerns. Particularly vulnerable to AMR bacteria are residential age care facility (RACF) residents with their high density living, high antibiotic use and impaired immune systems. Previous models applied to this problem include dynamic 'Susceptible, Infected, Resistant' and regression style analyses. We describe the results of Data Driven modelling of RACF AMR using semi-naïve Bayes Nets, regression and basic statistical analyses in a complementary fashion in support of better facility management. Three RACF and one independent aged populations (n=113) were screened for single and multiple drug resistant Escherichia coli, Staphylococcus aureus and Vancomycin Resistant Enterococci. Candidate factors driving AMR bacteria frequency and diversity explored included antibiotics prescribed, treatment course numbers and durations, and hospital visit rates and stays. The models were employed to assess the relative contribution of each factor, statistical significance and model predictive potential.

No single modelling approach provided a comprehensive picture. But together they generated and explored various hypotheses. Semi-naive Bayes Nets and (backward) regression analyses indicated that candidate drivers could account for ca 35%, 30% and 15% of the colonization by AMR bacteria overall, E. coli and MRSA respectively. Though no single variable appeared dominant, antibiotic prescription

rate and type variables appeared frequently. Bayes Nets were especially useful for quantifying relative contributions. Resistant E. coli isolates were most frequently isolated (39%). Only one VRE isolate was detected in the most intensively treated patient (6 antibiotics, 17 courses, over 141 days). There was no significant difference between E. coli colonization of RACF and independent volunteers. Hospital admission alone was not associated with AMR occurrence though extended stay was. These initial analyses indicate major gaps in understanding AMR drivers and variance. Using Bayes Nets in combination with other techniques greatly aided data interpretation.

Day 2 – 14:30 Designing clinical trials using causal models

Tom Snelling, Yue Wu, Charlie McLeod, Andre Schultz, Steven Mascaro, Owen Woodberry

Aims: Clinical trials are considered to provide gold-standard evidence of the causal effects of treatments. While elegant, traditional clinical trials generally only address clinical questions that can be distilled into a simple (and possibly overly simplistic) hypothesis. However, clinical management problems usually entail complex decisions in the context of multiple uncertainties. We aim to use causal inference to develop a coherent framework for designing trials to address, quantify and resolve these multiple 'decision-relevant' uncertainties.

Methods: We reframe trials as tools to generate evidence to inform clinical decisions rather than as classical experiments for testing hypotheses. We have worked with stakeholders (patients, clinicians, researchers) to develop consensus causal models that help define the clinical question, the population/s of interest, the intervention/s and comparator/s of interest, the outcome/s of interest, and therefore the specific causal effects (estimands) of interest. Building on this framework, we apply a Bayesian approach to pre-specify the strength of evidence required to affect one's decision, and thereby specify decision rules to determine when the study should stop.

Results: BEAT-CF (Bayesian Evidence-Adaptive Treatment of Cystic Fibrosis) is presented as an illustrative example of how causal models

are used for selecting treatments for evaluation, patient outcomes, and for defining relevant patient subgroups. The causal model was used to distinguish the de facto (intent-to-treat) from the de jure (per-protocol) treatment effects, and to identify the potential for bias from unblinded treatment. We also consider the heterogeneity in treatment effects based on a clinician's preferred treatment.

Conclusions: Although it is often assumed that clinical trials permit valid causal inference, they provide no guarantee of this, nor do trials ensure the results will be informative for decision-making. We propose a framework based in causal inference for ensuring trials are better suited to the goal of better decision-making.

List of Delegates

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Associate Professor	André	Schultz	Department of Respiratory Medicine
Ms	Ama	Wakwella	University of Queensland
Mr	Amarnath	D	IIIT Hyderabad
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Dr	Annalie	Dorph	University of New England
Dr	Annemarie	Christophersen	GNS Science
Mr	Anthony	Sunjaya	UNSW Sydney
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Dr	Bruce	Marcot	US Forest Service
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Miss	Grace	Currie	The University of Sydney
Mrs	Hannah	Gallant	Defence Science and Technology Group
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Dr	Marie	Estcourt	The University of Sydney
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