Phylomania 2014

University of Tasmania, 5-7 November

Program

Wednesday, 5 November

8.20am-9:00am	Registration and coffee
9:00am-9:10am	**Professor Paddy Nixon** Deputy Vice-Chancellor (Research), University of Tasmania *Welcoming remarks*
9:10am-9:50am	**Michael Charleston**, University of Sydney, Australia *Suite, suite phylogenetics*
9:50am-10:10am	**Greg Jordan**, University of Tasmania *Getting my hands dirty: Climates, phylogeny and ancestral ecologies in conifers*
10:10am-10:30am	**Saan Ketelaar-Jones**, University of Tasmania *Accuracy of ancestral state reconstruction on simulated phylogenies*
10:30am-11:00am	Morning tea
11:00am-11:20am	**Dorothy Steane**, University of Tasmania *Using genome-wide scans to detect adaptation to environment in a widespread eucalypt species*
11:20am-11:40am	**Matt Larcombe**, University of Tasmania *The strength of hybrid incompatibility snowballs with divergence between* Eucalyptus *taxa*
11:40am-12:00pm	**Anna Brüniche-Olsen**, University of Tasmania *Extensive population decline in the Tasmanian devil predates European settlement and Devil Facial Tumour Disease*
12:00pm-2:00pm	Lunch
2:00pm-2:20pm	**Tristan Stark**, University of Tasmania *Purity-dependent slippage models for microsatellite evolution*
2:20pm-2:40pm	**Bennet McComish**, University of Tasmania *Microsatelitte evolution in Adelie Penguins*
2:40pm-3:00pm	**Ben Halliwell**, University of Tasmania *Who cares? The evolution of parental care in squamate reptiles*
3:00pm-3:30pm	Afternoon Tea
3:30pm-4:10pm	**Jeremy Sumner**, University of Tasmania *The epic battle between Markov and phylogenetic invariants: equations*
4:10pm-4:30pm	**Barbara Holland**, University of Tasmania *The epic battle between Markov and phylogenetic invariants: graphs*
4:30pm-	**Phylomaniacs at the pub**: *Preachers*, 5 Knopwoods St, Hobart

Thursday, 6 November

8:30am-9:10am	Coffee
9:10am-9:50am	**David Bryant**, University of Otago, New Zealand *Taxicab diversities*
9:50am-10:10am	**Sangeeta Bhatia**, University of Western Sydney, Australia *Performance of genome rearrangement distance metrics under variable inversion length*
10:10am-10:30am	**Stuart Serdoz**, University of Western Sydney, Australia *Bacterial genome rearrangements and expected distance*
10:30am-11:00am	Morning tea
11:00am-11:40am	**Steffen Klaere**, University of Auckland, New Zealand *How a blind man checks whether the fat man went into a lingerie store*
11:40am-12:00pm	**Daisy Shepherd**, University of Auckland, New Zealand *Detecting heterogeneity in phylogenetic inference*
12:00pm-2:00pm	Lunch
2:00pm-2:40pm	**Ben Rorhlach**, University of Adelaide, Australia *Data-driven model selection for approximate Bayesian computation via multiple logistic regression*
2:40pm-3:00pm	**Michael Woodhams**, University of Tasmania *Looking for evidence of hybridization via simulated gene trees and ABC*
3:00pm-3:30pm	Afternoon Tea
3:30pm-3:50pm	**Jonathan Mitchell**, University of Tasmania *Distinguishing convergence on three-taxon phylogenetic networks*
3:50pm-4:10pm	**Monika Balvočiūtė**, University of Otago, New Zealand *Multidimensional scaling and flat split systems*
4:10pm-4:30pm	**Abby Harrison**, Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia *The population structure of* Plasmodium Falciparum *in Papua New Guinea*
7:30pm-	**Phylomaniacs dinner**: *Hope and Anchor Hotel* 65 Macquarie St, Hobart Wharf

Friday, 7 November

9:00am-9:30am	Coffee
9:30am-9:50am	**Yuliya Karpievitch**, University of Tasmania *Accurate regression parameters and summary statistics estimation in data with censored missing values*
9:50am-10:10am	**Stephen Crotty**, University of Adelaide, Australia *Oh, what a tangled web we weave, when first we practise to misspecify our evolutionary models*
10:10am-10:30am	**Malgorzata O'Reilly**, University of Tasmania *Markovian-modulated models and their application potential*
10:30am-11:00am	Morning tea
11:00am-11:20am	**Michael Woodhams**, University of Tasmania *Lie Markov DNA models: Consistent treatment of time-inhomogeneous mutation*
11:20am-11:40am	**Peter Jarvis**, University of Tasmania *Phylogenetics as quantum computation*
11:40am-12:00pm	**Andrew Francis**, University of Western Sydney, Australia *Tree-like Reticulation Networks*
12:00pm-	Lunch
2:00pm-	**Phylomaniacs excursion** (details TBD)

Abstracts

Monika Balvočiūtė
University of Otago, New Zealand

Multidimensional scaling and flat split systems
Joint work with David Bryant

We present a new algorithm for multimensional scaling (MDS). It is based on an agglomerative approach similar to the FlatNJ algorithm for computing planar split networks (published earlier this year). In the talk we will explain how MDS is related to the planar split networks, discuss different neighbor selection strategies and explain how agglomeration can be applied for positioning points in two-dimensional space.

Sangeeta Bhatia
University of Western Sydney, Australia

Performance of genome rearrangement distance metrics under variable inversion length

The design of algorithms for finding the reversal distance between genomes has focused on finding the minimal number of inversions and a sequence of inversions transforming one genome into another. Most of these algorithms do not take the length of the reversal into account. An accumulating body of evidence shows that not all reversals are equally likely in the genome and there is a propensity towards short reversals. Through computer simulation, we study the effect of the violation of assumptions about the reversal length on the performance of algorithms in recovering the true tree. We compare the performance of GRIMM (which implements Hannenhalli-Pevzner algorithm) which allows inversions of any length with an algorithm developed by us that only allows inversions of length 2. The simulations show that for deep phlyogenetic trees, ignoring the reversal length leads to losing all phylogenetic signal present in the sequence. If nature is indeed inclined towards shorter inversions, researchers would do well to pay heed.

Anna Brüniche-Olsen
University of Tasmania

Extensive population decline in the Tasmanian devil predates European settlement and Devil Facial Tumour Disease

The Tasmanian devil (*Sarcophilus harrisii*) was widespread in Australia during the late Pleistocene, but is now endemic to the island of Tasmania. Low genetic diversity combined with the spread of Devil Facial Tumour Disease has raised concerns for the species' long-term survival. Here we investigate the origin of low genetic diversity by inferring the species' demographic history using temporal sampling with summary statistics, full-likelihood and Approximate Bayesian Computation methods. Our results show extensive population declines across Tasmania correlating with environmental changes around the last glacial maximum (LGM) and following unstable climate related to increased 'El Niño?Southern Oscillation' (ENSO) activity.

David Bryant
University of Otago, New Zealand

Taxicab diversities

The work of Linial, London and Rabinovich on the Geometry of Graphs has had a significant and long-lasting impact on combinatorial optimization and data analysis. They showed how the mathematics of embedding metrics in L_1 (taxicab) spaces could help solve difficult computational problems, adding some powerful techniques to the algorithm designer's toolkit. I will show how much of this theory extends seemlessly to diversities, a generalization of metric spaces beyond pairwise comparisons which were first introduced at Phylomania many years ago.

Mike Charleston
University of Sydney, Australia

Suite, suite phylogenetics

There are over 100 different versions of Bach's 'cello suites, and they're all different in interesting, subtle and musically important ways. As they've been created from a single (lost) original and four hand-written versions, we may be left wondering what really was the intended manuscript? What is the relationship among all the versions? We use some simple techniques from phylogenetics in novel ways to attempt to uncover the phylogenetic history of this music.

Stephen Crotty
University of Adelaide, Australia

Oh, what a tangled web we weave, when first we practise to misspecify our evolutionary models

Given the complexity of the evolutionary process, attempts to model it for the purposes of phylogenetic analyses will invariably result in model misspecification. Phylogeneticists have always been aware of this source of error but relatively little has been done to examine in detail the impact of specific types of misspecification and their interactions. I'll present models and simulated datasets that have been carefully constructed to exhibit specific types of model misspecification, illuminating their effects on ML estimation.

Andrew Francis
University of Western Sydney, Australia

Tree-like Reticulation Networks
Joint work with Mike Steel

Hybrid evolution and horizontal gene transfer (HGT) are processes where evolutionary relationships may more accurately be described by a reticulated network than by a tree. In such a network, there will often be several paths between any two extant species, reflecting the possible pathways that genetic material may have been passed down from a common ancestor to these species. These paths will typically have different lengths but an 'average distance' can still be calculated between any two taxa. In this talk, I will show that in some circumstances this average distance is unable to distinguish reticulate evolution from pure tree-like evolution. That is, there are reticulated networks in which the average distances satisfy the four-point condition. Another way to say this is that a metric satisfying the four-point condition does not imply the taxa are from a tree: it merely gives the existence of a tree.

Ben Halliwell
University of Tasmania

Who cares? The evolution of parental care in squamate reptiles

Theory predicts that patterns of parental care within a species are the product of trade-offs between benefits for offspring fitness and parental costs. Thus, differences in care between species arise from interspecific differences in ecology, life history, or phylogeny that mediate the value of benefit and cost functions involved in the trade-off. Research increasingly suggests that the occurrence and complexity of care among reptiles is greater than previously suspected. Yet the causal factors driving emergence of parental care, and transitions between different modes of care, remain enigmatic. Studying the costs and benefits of care within a species is useful for inferring the causal relationships that maintain care states. However, comparative analyses of care traits across species are required to 1) identify the divergence in key ecological, life-history or phylogenetic characteristics responsible for transitions between modes of care; 2) elucidate the evolutionary pathways (i.e. most common transition) that have led to current diversity in reptilian care; and 3) understand the evolutionary constraints prohibiting the emergence of more sophisticated modes of care in reptiles. Here we present a preliminary phylogenetic analysis of parental care behavior in the squamates (lizards and snakes) as an introductory attempt to address the questions stated above.

Abby Harrison
Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia

The population structure of Plasmodium flaciparum *in Papua New Guinea*
Joint work with Natacha Tessier, Livingstone Tavul, Magnus Manske, Olivo Miotto, Dominic Kwiatkowski, Inoni Betuela, Peter M. Siba, Ivo Mueller, Melanie Bahlo, and Alyssa E. Barry

Papua New Guinea (PNG) has the highest burden of malaria outside of Africa with intense year round transmission ranging from hyper- to holo-endemic in the lowland and coastal areas to largely absent in the highlands. The country's extremely diverse biogeography contributes to variable parasite population dynamics and transmission, even across the highly endemic areas. Recently, we have shown that the population structure of *Plasmodium falciparum* on the north coast of Papua New Guinea (PNG) is fragmented. Should such population fragmentation and structure be observed throughout PNG then mapping of this geographical diversity will enable the monitoring of changes in populations, the identification of routes of migration, predict the spread of drug resistance, and pinpoint the source of outbreaks. Such knowledge will be valuable for the success of malaria elimination and control programmes as it will enable informed choices to be made. Using microsatellite markers, mitochondrial sequences, and genome wide SNP data, from three geographically distinct populations within PNG, we are investigating *P. falciparum*'s genome dynamic nature and demographic structure. We are working towards defining a high-resolution map of parasite population networks and migration patterns throughout PNG. Using state-of-the-art Fluidigm Integrated Fluidic Circuit SNP genotyping, a panel of geographically informative SNPs, and a national cross-sectional *P. falciparum* dataset of isolates covering all endemic areas of PNG. This unique perspective is possible due to countrywide screening conducted in PNG as part of the national malaria control program in which over 13000 individuals across the entire country were surveyed for malaria infections.

Barbara Holland
University Tasmania, Australia

The epic battle between Markov and phylogenetic invariants: graphs

I will follow up Jeremy's highfalutin (group-theoretic) ideals with some **real data**. (When I say real data, I mean real simulated data of course.) This talk will present the results of a simple simulation study comparing invariants that

a) do or don't know about leaf actions (Markov vs phylogenetic invariants)

b) do or don't use information about the expected sign of the invariant functions.

Peter Jarvis
University of Tasmania

Phylogenetics as quantum computation
Joint work with Demosthenes Ellinas

We present a novel application of the discipline of quantum computation-information to the field of evolutionary phylogenetics. The following results will be prefaced by a non-technical review of the idea of how simulation of stochastic models can be achieved by exploiting the behaviour of quantum systems.

Quantum simulation of phylogenetic evolution and inference, is proposed in terms of trace preserving positive maps (quantum channels) operating on quantum density matrices defined on Hilbert spaces encoding states of biological taxa with K characters. Simulation of elementary operations such as speciation (branching of trees, phylogenesis) and phyletic evolution along tree branches (anagenesis), are put forward utilizing conditional control-not unitary gates and quantum channels with unitary or complex matrix Kraus generators.

Basic evolutionary models are simulated and associated to quantum circuits. Specifically, the standard group-based phylogenetic models are associated to quantum random walks with unitary Kraus generators (random unitary channels), while more general models in the Lie-Markov class, such as the Felsenstein and strand symmetic models, are realized via post-measurement operations. Simulation of iterative cherry-growing and cherry-pruning basic processes in phylogenetic trees is formulated in the quantum setting, and their dual character is shown in terms of the state-observable duality. In this way the central problem of phylogenetics – the statistical estimation of free parameters of stochastic matrices implementing the stochastic evolution of characters along tree branches – is addressed by formulating an analogous quantum maximum likelihood estimation problem for the free parameters of quantum channels operating along branches.

Greg Jordan
University of Tasmania

Getting my hands dirty: Climates, phylogeny and ancestral ecologies in conifers
Joint work with Tim Brodribb

In this talk I investigate the evolutionary origins of conifers. The conifers are well known to be a group that has been heavily influenced by extinction, with reductions in both diversity and abundance since the Cretaceous or Paleogene. This poses significant problems for ancestral state reconstruction.

The conifers fall neatly into a set of essentially northern hemisphere clades ("northern conifers") and essentially southern hemisphere clades. The northern and southern conifers occupy strikingly different environmental spaces, even in the regions where the groups overlap, suggesting some strong phylogenetic influence on ecology (niche conservatism). Recent physiological evidence supports these inferences.

We therefore investigate the geographic distributions of the world's conifers, and how these relate to phylogeny and climate. Patterns of species richness and phylogenetic richness show differences that may be explained by historical influences, with conservation of ancestral ecologies in some now rare clades. We also consider the use of phylogenetic endemism in climatic space, rather than geographic space, as a tool for overcoming some of the problems with ancestral state reconstruction.

Yuliya Karpievitch
University of Tasmania

Accurate regression parameters and summary statistics estimation in data with censored missing values

Censored values are common in biological data. Censored values occur due to our inability to measure something of low concentration (left-censored) or saturation of the detector (right-censored). Here I will present statistical analysis of data that are left-censored for estimation of regression coefficients and descriptive statistics. I will show comparisons of several imputation methods including multiple imputation applied to left-censored values and compare with complete case analysis and substitution with 1/2 of the detection limit. I also note that if normalization is necessary, normalization should be done first before any imputation takes place.

Saan Ketelaar-Jones
University of Tasmania

Accuracy of ancestral state reconstruction on simulated phylogenies

Accurate methods of ancestral state reconstruction (ASR) are fundamental to our understanding of the process of evolution, as well as practical applications targeting specific sequences or morphological adaptations. Different ASR methods rely on different sets of implicit or explicit assumptions. Errors can be introduced into a reconstruction when these assumptions are violated. Four methods of ASR (maximum parsimony [MP], maximum likelihood [Mk2], constrained maximum likelihood [MkC] and binary state speciation and extinction [BiSSE]) were used to reconstruct binary characters on trees simulated under conditions designed to violate model assumptions. Trees were simulated to represent selective extinction, extreme extinction, state dependent character change and extreme character plasticity. The accuracy of each ASR method decreased as the trees were simulated with asymmetric and/or extreme rates. Extreme but symmetric rates of character change resulted in the largest decrease in accuracy. Similarly, extreme extinction rates resulted in reduced ASR accuracy. The three likelihood methods (Mk2, MkC and BiSSE) had similar accuracy reduction patterns, while MP was consistently less accurate. Node depth reduced accuracy for all methods of ASR under every evolutionary scenario; however this could only be observed after depth was binned to counter node scarcity.

Steffen Klaere
University of Auckland, New Zealand

How a blind man checks whether the fat man went into a lingerie store

Gatesy (2007) compared model selection with a fat man looking for suitable clothing in a women's lingerie store. Something will fit best, doesn't mean it will fit good. Gatesy added that people tend to turn a blind eye to the things that don't fit well. There have been few attempts at drawing the eye toward the misfits, but only one stuck partially because of the lack of diagnostic tools. Here, I will present some of the attempts at such tools that I have worked on over the last few years. We will take the idea of influence measures to a new level, and discuss omnibus tests for model-to-data goodness of fit.

Matt Larcombe
University of Tasmania

The strength of hybrid incompatibility snowballs with divergence between Eucalyptus *taxa*
Joint work with Barbara Holland, Dorothy Steane, Rebecca Jones, Dean Nicolle, René E. Vaillancourt, Brad M. Potts

The evolution of reproductive isolation between diverging populations is a fundamental characteristic of speciation. Intrinsic postmating barriers that prevent hybridisation between populations are particularly important because they are thought to be largely irreversible, and therefore provide a clear pathway to the evolution of complete reproductive isolation. Intrinsic postmating barriers arise when minor allelic changes develop between diverging populations that cause incompatibilities when brought together in inter-population hybrids – leading to hybrid inviability or sterility. This model is widely accepted as a primary mechanism in the evolution of reproductive isolation. However, evidence of one key prediction of this model, that incompatibilities should 'snowball' (accelerate) relative to the time since divergence due to epistasis, has been difficult to find. We investigated patterns in the strength of reproductive isolation in *Eucalyptus* by undertaking manipulated hybridisations between *Eucalyptus globulus* and 99 eucalypt species from 13 taxonomic sections. Data on hybrid incompatibility (the relative number of hybrids produced and their survival at nine months) was compared to genetic distances derived from 8350 genome wide DArT markers. We then took a modelling approach developed by others, and address some statistical problems identified by the original authors, to assess which of three possible mode-of-evolution-models (snowball, linear or slowdown) best fitted our data. The maximum likelihood approach we employed consistently found that the snowball model was best at explaining the relationship between the strength of incompatibility and genetic distance in *Eucalyptus*, whereas the previous least squares method could not find support for any one model over another. This is some of the first evidence that the *strength* of incompatibility can snowball as divergence increases, and is consistent with recent genetic mapping studies that show that the actual *number* of incompatibilities can snowball with divergence.

Bennet McComish
University of Tasmania

Microsatelitte evolution in Adelie Penguins

Microsatellites are short tandem repeat sequences that have been widely used as genetic markers in a variety of population genetic studies. The number of repeats at a locus is thought to change by slippage of DNA polymerases during replication, and these loci exhibit high levels of length polymorphism. Several models of microsatellite evolution have been developed, some of which take into account both replication slippage and point mutation. These models vary widely in complexity, but it is not clear that any of them succeed in capturing all of the relevant biological processes. I will present some results examining microsatellite loci of different phylogenetic ages in Adelie penguins, and discuss how these might be used in testing existing models of microsatellite evolution and developing new ones.

Jonathan Mitchell
University of Tasmania

Distinguishing convergence on three-taxon phylogenetic networks
Joint work with Barbara Holland and Jeremy Sumner

We determine whether two and three-taxon phylogenetic trees, both non-clock-like and clock-like, can be distinguished from more generalised networks which allow for convergence. Convergence is modelled with a convergence period, a period of time after divergence has occurred when the process of divergence is gradually reversed. We will call this model the "convergence/divergence" model. Examples of processes leading to convergence are hybridisation, horizontal gene transfer and convergence of morphological traits. We consider the network model of Sumner et al. [2012], restricted to the binary symmetric case. We start by computing the phylogenetic tensors, that is the probability distributions of character sequences, for each of the trees and networks. Noting that the phylogenetic tensors are functions of time parameters, we find the constraints on the tensors imposed by these time parameters. These constraints define the probability spaces of the trees and networks. For both the two and three-taxon cases, we compare the probability spaces for all competing trees and networks. Finally, we analyse binary morphological characters from a data set of cormorants and shags from Holland et al. [2010]. On groups of triplets, we compare BIC values for various three-taxon trees and networks, both with and without convergence.

Malgorzata O'Reilly
University of Tasmania

Markovian-modulated models and their application potential

I am going to talk about my work in the area of matrix-analytic methods (MAMs). MAMs is an area of applied probability which studies a range of Markovian-modulated models using numerically efficient methods. These models have a lot of application potential in many areas of science, where we are interested in modeling the evolution of a real life system with element of uncertainty.

Ben Rorhlach
University of Adelaide, Australia

Data-driven model selection for approximate Bayesian computation

Sometimes researchers are interested in reconstructing population sizes over time from a large sample of DNA sequences. Popular methods of calculating such estimates involve Approximate Bayesian Computation (ABC). ABC requires no knowledge of likelihood functions for any given model of population dynamics. However, to infer the historic population dynamics we must first select the model of population dynamics that best fits our data. In this talk I aim to introduce ABC and describe its use in population genetics. Following this, I will introduce our method of model selection that employs Multiple Logistic Regression. I will compare this method of model comparison to current popular methods of post hoc model comparison to show how both accuracy and efficiency can be improved.

Stuart Serdoz
University of Western Sydney, Australia

Bacterial genome rearrangements and expected distance

The aim of many rearrangement algorithms is to attempt to find the minimum number of rearrangements to explain the change between two genomes. These pairwise distances are used in methods such as NJ, UPGMA, and the Fitch-Margoliash method. Minimal distances underestimate the true length of the evolutionary path and this has pushed phylogeny construction away from distance based methods. Our approach takes into account the underlying group structure to provide a weighted average distance over all possible histories with the idea of providing an expected distance. This talk will introduce the development of the expected distance with a focus on walks on Cayley graphs.

Daisy Shepherd
University of Auckland, New Zealand

Detecting heterogeneity in phylogenetic inference

Heterogeneity presents a major challenge to the modelling process within phylogenetic analysis. Sitewise heterogeneity is commonly modelled by the gamma rate parameter, with the additional invariant sites parameter to improve model accuracy. However, the issues with the identifability of the invariant sites model cause it to be unreliable for accurate inference. A redefined gamma model was trialled, which aimed to incorporate the invariant sites parameter into the gamma rate parameter. This proposed a new approach to discretise the gamma distribution, with AIC indicating a preference toward the new model, due to the reduced complexity. Current research has extended these ideas, and focuses on the challenge of modelling heterogeneity on the genomic scale. Our primary interest concerns finding heterogeneous rates of heterogeneity along genomes. We wish to investigate where there is a change in rate along the sequence, through comparison with the rate for the full alignment. Preliminary fndings using both the sliding window and hierarchal methods will be reported.

Tristan Stark
University of Tasmania

Purity-dependent slippage models for microsatellite evolution

Microsatellites are an extremely useful source of genetic variation for studying recent evolutionary events. Currently, many population genetics studies are based on simple models of microsatellite evolution, however it is known from empirical studies that the evolution of microsatellites is a more intricate process which may warrent more complex modelling. There have been some efforts in the past to reconcile slipped-strand mispairing, which is regarded as the most important process in the evolution of microsatellites with the broader mutational process of point mutation; however these models have treated only the length-changing, and not the mutation-rate-changing effect of point mutation. This work introduces a model which reconciles existing models of slipped-strand mispairing with point mutation in a mathematically simple and practically robust way, accounting for rate-changing effects of impurities build-up by point mutation events. We use our model to test the hypothesis that impurity in microsatellites (brought about by point mutation) leads to a decrease in the rate at which the slipped-strand mispairing process occurs by fitting the model to Adelie penguin data.

Dorothy Steane
University of Tasmania and University of the Sunshine Coast, Australia

Using genome-wide scans to detect adaptation to environment in a widespread eucalypt species

In a time of rapid environmental change, an understanding of the adaptive capacity of foundation species, such as forest trees, is of increasing interest for both commercial and ecological purposes. Adaptive variation within plant species is best studied using common garden experiments, but these are expensive and time-consuming, especially for trees that have long generation times. We explored whether genome-wide scans could be used to detect adaptation to climate and provide an alternative to common garden experiments. As a case study, we sampled nine populations of a widespread forest tree species, *Eucalyptus tricarpa*, across an aridity gradient in southeastern Australia. Using a Bayesian analysis we identified a suite of 94 putatively adaptive (outlying) sequence-tagged markers distributed across the genome. Population-level allele frequencies of these outlier markers were strongly correlated with temperature and moisture availability at the site of origin, and with population differences in functional traits measured in two common gardens. Using the output from a canonical analysis of principal coordinates we devised a metric that provides a holistic measure of genomic adaptation to aridity, that could be used to guide revegetation projects, assisted migration or genetic augmentation. The metric provides a means of predicting the species' distribution under climate change, taking into account the present standing genetic variation.

Jeremy Sumner
University of Tasmania

The epic battle between Markov and phylogenetic invariants: equations
Joint work with Amelia Taylor, Barbara Holland, and Peter Jarvis

Our recent work critically assesses the statistical power of phylogenetic invariants in the simplest interesting case possible: binary characters on quartets. Our insight into the problem begins by demanding that any statistical measure built from phylogenetic invariants should behave sensibly under parameter changes at the leaves of the quartet trees. From this point of view, the ideal I of phylogenetic invariants provides a sequence of (high-dimensional) vector spaces stratified by polynomial degree. Luckily, these vector spaces have lower-dimensional subspaces invariant to changes of substitution process at the leaves. The most attractive case ensues when the invariant subspace is one-dimensional; such subspaces are spanned by our favourite group-theoretical quantities *Markov invariants*.

I will show how the Markov invariants provide a unique solution to the problem of finding a statistically powerful measure of tree support from an infinite continuum of potential choices. Barbara will follow my talk with a bunch of graphs that suggests our theoretical work is very much on the right track.

Michael Woodhams
University of Tasmania

Looking for evidence of hybridization via simulated gene trees and ABC
Joint work with Barbara Holland

I have created a simulator for generating gene trees in the presence of hybridization and lineage sorting. I use this simulator for an approximate Bayesian computation (ABC) analysis of several large data sets to attempt to discover whether hybridization has been important in these lineages.

Lie Markov DNA models: Consistent treatment of time-inhomogeneous mutation
Joint work with Jeremy Sumner and Jesús Fernández-Sánchez

A process for which the instantaneous rate matrix varies with time but is always in the general time reversible model (GTR) will none the less produce non-GTR Markov matrices. To model a time inhomogeneous process with differing GTR rate matrices on each edge is therefore mathematically inconsistent.

The Lie Markov DNA models are precisely those which can consistently model inhomogeneous mutation processes: if the rate matrix at all times lies within the model, the resulting Markov matrix can be derived from a single 'average' rate matrix which also lies in the model.

Within certain symmetry constraints (which allow for transitions to be distinguished from transversions) we derive a family of nearly 100 models. We test the models on a variety of real world data sets, to determine which of these Lie Markov models are promising.

List of participants

Monika Balvočiūtė
University of Otago, New Zealand

Sangeeta Bhatia
University of Western Sydney, Australia

Anna Brüniche-Olsen
University of Tasmania, Australia

David Bryant
University of Otago, New Zealand

Michael Charleston
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Stephen Crotty
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Dorothy Steane
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Jeremy Sumner
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Michael Woodhams
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