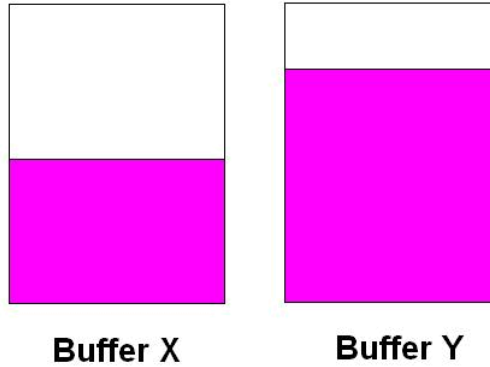


PhD Topics

Supervisor: Małgorzata O'Reilly

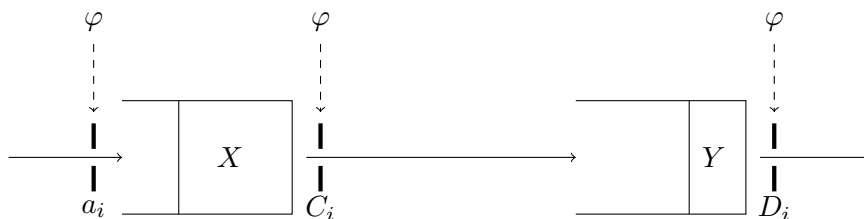
Stochastic Markovian Networks (potential topic)



Summary: Markov-modulated fluid queues, in which the amount of customers/data in a buffer is modelled using a continuous variable, have been studied extensively via matrix-analytic methods. In the analysis of networks of fluid queues however, the results for a few special two-node cases could only be obtained. However, the operator-analytic methods, a generalization of the matrix-analytic methods for single queues, is a promising approach that could lead to novel numerical schemes.

An example is a system of two fluid queues, with contents that are being driven by a background Markov chain in such a way that the content of the second queue also depends on the content of the first queue. The main questions in this context are: (i) how complex can we allow such models to be, while still being able to find the joint stationary distribution, and (ii) what approximations can be devised in cases where analytic solutions are not possible.

This project will focus on theory and algorithms for the analysis of stochastic fluid networks, and is an exciting opportunity to contribute to the advancements in this field. You will work on simulations, theoretical models, and algorithms. You will have an opportunity to interact with mathematicians in a rich international collaborative environment.



Stochastic Models for the Conservation of Endangered Species.

(Mr Habtu Kiros, PhD candidate, 2023-now)

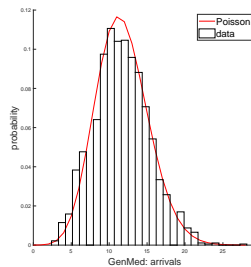


Summary: In populations of endangered species, management strategies referred to as *genetic rescue* have been advocated in order to help avoid extinction. An example of considerable concern in the Australian context is the conservation management of Tasmanian Devils suffering from the *Devil Facial Tumour Disease* (DFTD), which puts them in danger of extinction. An important factor in this context is the ability to assess the impact of conservation efforts. Conservation strategies have been used with the hope of increasing the genetic diversity of the wild population, but this remains a challenging problem.

An essential objective of conservation strategies is to increase the genetic diversity of a wild population, with the hope of increasing its chances of survival in the long term. This project will focus on developing stochastic simulation and theoretical models for the numerical assessment of conservation strategies, which will assist in these efforts. The techniques will be applied to the problem of conservation of the Tasmanian Devil population, suffering from the DFTD. This work will involve a collaboration with biologists, and communication with groups whose role is to maintain the *Insurance Population* gathering animals from areas where there had not been evidence of DFTD.

Models for hospital patient flow: Decision-making in a challenging environment.

(Mr M Abdullah Khokhar, PhD candidate, 2022-now)



Summary: A PhD student involved in this project will be part of a multidisciplinary team of healthcare professionals, computer scientists and mathematicians, working together on a range of stochastic models for patient flow and algorithms for the optimal patient care journey. This project aims to develop a better understanding of the practicalities of the real issues facing the managers of healthcare systems, which will lead to improved models and algorithms for patient flow. We anticipate practical outcomes in the form of better understanding of policies and rules of thumb that could be applied to improve the bed block and ambulance ramping issues at the regional hospitals. We will collaborate with the Tasmanian Department of Health and hospitals in Tasmania on this applications-driven project. Our overarching goal is a decision-support digital tool for patient-flow managers, to optimise the patient journey, contributing to patient safety and quality of care.

Stochastic Modeling of Patient Flow in Hospitals

(Mr Aregawi Abera, PhD candidate, 2018-2023)

Summary: Modern hospital is a highly complex and unpredictable system, which cannot be managed efficiently using intuitive methods. Instead, we require sophisticated tools in the form of efficient algorithms developed using appropriate mathematical modeling. Compelling clinical evidence indicates that when mathematical modeling is used in hospitals, significant savings can be made that have a positive outcome to the patients. The aim of this project is to develop modelling tools for the analysis of the patient flow and optimal bed allocation algorithm for the patients in the Emergency Department to the wards.

Mathematical models for the evolution of species

(Mr Albert Soewongsono, PhD candidate, 2019-2023)

Summary: Phylogenetics is the study of the evolutionary history of organisms. These organisms encompass biological entities such as viruses, genes, and also species. Their relationships can be visualised using a mathematical graph, known as a phylogenetic tree. In this thesis, our objects of interest are species trees. In particular, we develop various mathematical models for the evolution of species and their corresponding phylogenetic tree. These models can be used to understand underlying biological processes that drive past speciation and extinction events. Understanding these evolutionary dynamics is important since it can help with preserving present-day species and reconstructing how biodiversity has evolved through time.

Applications of the Phase-type Distribution and Related Results in Evolutionary Biology

(Mr Jiahao Diao, PhD candidate, 2018-2022)

Summary: Gene duplication has been identified as one of the key processes for driving functional change in the genome. Along with the duplication processes, point mutations may occur in a coding region or regulatory region of a gene. If a point mutation destroys the function of a coding region or regulatory region, it is known as a null mutation. The mechanics of these evolutionary processes can help us understand how genomes can maintain or modify the functions through the evolutionary time. This thesis introduces two main Markov models for the evolutionary processes of gene family duplication called the Detailed Binary Matrix (DBM) model and the Level Dependent Quasi-Birth-Death (LDQBD) model. Moreover, we developed two models for neofunctionalisation, in which we consider how genes can become associated to perform a joint function.

Markovian-modulated stochastic models and their applications

(Ms Aviva Samuelson, PhD candidate, 2015-2020)

Summary: Markovian-modulated models are a class of models with a two-dimensional state-space consisting of a phase and a level. The phase variable is often used to describe the state of some physical environment that we want to model. Simple two-phase examples are on/off mode of a switch in a telecommunications buffer, peak/off-peak period in a telephone network, or wet/dry season in reservoir modeling. The model assumes that the transitions between phases occur according to some underlying continuous-time Markov Chain. Furthermore, the rate of increase of the fluid level at time t depends on the phase at time t , and so the Markov Chain is the process that drives the fluid level at time t . The aim of the project is to develop novel models and methods in the area. Research will involve theoretical analysis using appropriate applied probability theory, development of numerical algorithms, and coding in MATLAB.

Mathematical Models for Microsatellite Evolution

(Mr Tristan Stark, PhD, 2014-2018)

Summary: Microsatellites are found in vastly greater density than that which would be implied by random allocation of nucleotides. They are found throughout the genome, in coding and non-coding regions and in organisms composed of cells of any structure. Many microsatellites are thought to evolve neutrally, experiencing no selective pressure, and polymerase chain reaction techniques lead to a high availability of microsatellite data by allowing for the production of many copies of DNA sequences. This, together with high levels of polymorphism resulting from frequent mutation, leads to microsatellites being highly favoured as genetic markers (sequences of DNA occurring at a known locus, used to identify an individual or species). Hence, microsatellites are of interest in a wide array of population genetics and evolutionary inference applications. In order to make inferences using microsatellite data, a biologically realistic model for the time evolution of microsatellites is required, however theoretical models have largely failed to explain observed allele frequency distributions. The aim of this project is to build appropriate mathematical models for more accurate and relevant way of representing the evolution of microsatellites.