

2014 Southwestern Ontario Graduate
Mathematics and Statistics Conference

May 20-21, 2014

UNIVERSITY
of GUELPH

2014 Southwestern Ontario Graduate Mathematics and Statistics Conference

Schedule of Talks

Tuesday, May 20, 2014.

- 8:30 **Registration and Breakfast**
- 9:00 **Nadia Bifolchi**, University of Guelph.
Improving the fit of individual-level models for incomplete infectious disease data.
- 9:25 **Diego Ayala**, McMaster University.
Extreme Vortex States and Singularity Formation in Incompressible Flows.
- 9:50 **Amenda Chow**, University of Waterloo.
Characterizing Hysteresis in Linear and Nonlinear Dynamical Systems.
- 10:15 **Kenneth Blahut**, Ryerson University.
Modeling the in vitro spread of hepatitis C virus to quantify the contribution of cell-to-cell and free virus infections.
- 10:40 **Coffee Break**
- 10:55 **Nuzhat Rafique**, University of Guelph.
Social Influence and Consumers Demand with Time Dependent Population.
- 11:20 **Richard Kohar**, Royal Military College of Canada.
How close were we? Why measuring the sum squared error falls short for timing prediction in real-time.
- 11:45 **Shiva Ashta**, University of Toronto.
Higher Order Asymptotics and Normal Coefficients of Variation.
- 12:10 **Lunch**
- 1:10 **Jeffrey Daniel**, University of Guelph.
Derivation of leverage and influence diagnostics for MAXENT models in ecology.
- 1:35 **Fei Wang**, Western University.
Using SDP and Geometric Involutive bases to compute the real radical ideal of a polynomial system.
- 2:00 **Behzad Nikzad**, University of Ontario Institute of Technology (UOIT).
Codimension two bifurcation in a low order model of Plane Couette flow.
- 2:25 **Coffee Break**
- 2:40 **Oksana Pichugina**, Brock University.
A Generalization of the Hypercube Graphs.
- 3:05 **Colin Phipps**, University of Waterloo.
A microscale mathematical model for metabolic symbiosis in tumours.
- 3:30 **Cristina Tortora**, University of Guelph.
Mixture of generalized hyperbolic for high dimensional data sets.

Wednesday, May 21, 2014.

- 8:30 **Registration and Breakfast**
- 9:00 **Sayantee Jana**, McMaster University.
A Bayesian approach to the High-dimensional problem in Growth Curve Model.
- 9:25 **Najma Amadou**, Royal Military College of Canada.
Forecasting Timing Event: “When” instead of “What”.
- 9:50 **Jun Yang**, Queen’s University.
Lower Bounds on the Probability of a Finite Union of Events.
- 10:15 **Safia Athar**, University of Guelph.
SIS Models and Network Migration: A Framework for Dynamic Models of Decision Making Under Infection.
- 10:40 **Coffee Break**
- 10:55 **Y. Nikita Zhang**, Western University.
Modelling Disability Using Mixtures of Markov Chains.
- 11:20 **Irena Papst**, McMaster University.
Equivalent dynamical effects of different seasonal forcing patterns in infectious disease transmission.
- 11:45 **Carolyn Augusta**, University of Guelph.
Estimating Parameters in Individual-Level Models of Infectious Disease.
- 12:10 **Lunch**
- 1:10 **Charles Keown-Stoneman**, University of Guelph.
Multi-state models for accommodating internal covariates in survival analysis.
- 1:35 **Nathalie Moon**, University of Waterloo.
The impact of prevalent cohort sampling on multistate transition probabilities in chronic disease processes.
- 2:00 **Utkarsh Dang**, McMaster University.
Mixtures of power exponential distributions.
- 2:25 **Coffee Break**
- 2:40 **Adrien Thierra**, McMaster University.
Double squares: An History.
- 3:05 **Pardis Noorzad**, Ryerson University.
Modelling the Facebook Social Network: The Memoryless GEO-P Graph Model.
- 3:30 **Preeti Mohindru**, University of Guelph.
The DJL conjecture for CP matrices over max-min semirings.

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Abstracts

Najma Amadou, Royal Military College of Canada.

Forecasting Timing Event: “When” instead of “What”.

We are interested in a particular form of time series: the event timing time series or binary time series that contains instantaneous events that occur over time. Unlike other forecasting binary time series methods, the forecasting timing event model proposed a new computational approach using interval timing. The idea of this approach, inspired by how animals learn, is to predict when an event will occur instead of what event will occur at every time step. We analyse the autoregressive AR(p) model and the long short term memory (LSTM) artificial neural network by applying them on the task of predicting when an event will occur and compare their performance with the forecasting timing event model.

Shiva Ashta, University of Toronto.

Higher Order Asymptotics and Normal Coefficients of Variation.

Krishnamoorthy and Lee (2013) compared three methods to study coefficients of variation of independent normal populations. A mean- and variance-corrected version of the signed likelihood root statistic and an approach using generalized pivotal quantities were compared, and shown to give very accurate inference. We propose the use of the r -star approximation (Barndorff-Nielsen 1991) constructed using the method of Fraser and Reid (1993) as an alternative method to compare normal coefficients of variation. Confidence intervals for the difference and ratios of two coefficients of variation are also developed. Finally, the relationship between the r -star approximation and generalized pivotal quantity approaches are studied numerically and analytically.

Safia Athar, University of Guelph.

SIS Models and Network Migration: A Framework for Dynamic Models of Decision Making Under Infection.

This talk studies the decision-making of a population as it changes under an epidemic spread in a closed geographic location. For this purpose we develop a hybrid dynamical system model that shows movement of the parts of the population (commuters) in the presence of a disease like influenza, and keeps track of the changes in the numbers of susceptible and infective individuals at each location. This model aims to monitor the effect of decision-making of the people moving on a daily basis between different cities that have attractive utilities, and how an epidemic may impact the travelling work force and primarily the local economy. This study shows how the choice of individuals (between missing work or going in sick, thus spreading the illness further) impacts the spread of disease and how it can be modelled to investigate the cost implied by these choices.

Carolyn Augusta, University of Guelph.

Estimating Parameters in Individual-Level Models of Infectious Disease.

Individual level models (ILMs) are flexible and elegant models of disease spread. We explore the ILM framework for modelling infectious diseases, and discuss parameter estimation via Bayesian Markov Chain Monte Carlo (MCMC) and Maximum Likelihood Estimation. We show these estimation methods on two population structures: a grid population and a bivariate normal population. Emphasis is given to the difficulty of estimating the infectious period.

Diego Ayala, McMaster University.

Extreme Vortex States and Singularity Formation in Incompressible Flows.

One of the most prominent open problems in mathematical physics is determining whether solutions to the incompressible three-dimensional (3D) Navier-Stokes system, corresponding to arbitrarily large smooth initial data, remain regular for arbitrarily long times. A promising approach to this problem relies on the fact that both the smoothness of classical solutions and the uniqueness of weak solutions in 3D flows are ultimately controlled by the growth properties of the H^1 seminorm of the velocity field \mathbf{u} , also known as the enstrophy.

In this context, the sharpness of analytic estimates for the instantaneous rate of growth of the H^2 seminorm of \mathbf{u} in two-dimensional (2D) flows, also known as palinstrophy, and for the instantaneous rate of growth of enstrophy in 3D flows, is assessed by numerically solving suitable constrained optimization problems. It is found that the instantaneous estimates for both 2D and 3D flows are saturated by highly localized vortex structures.

Moreover, finite-time estimates for the total growth of palinstrophy in 2D and enstrophy in 3D are obtained from the corresponding instantaneous estimates and, by using the (instantaneously) optimal vortex structures as initial conditions in the Navier-Stokes system and numerically computing their time evolution, the finite-time estimates are found to be uniformly sharp for 2D flows, and sharp over increasingly short time intervals for 3D flows. Although computational in essence, these results indicate a possible route for finding an extreme initial condition for the Navier-Stokes system that could lead to the formation of a singularity in finite time.

Nadia Bifulchi, University of Guelph.

Improving the fit of individual-level models for incomplete infectious disease data.

A simplification often made in the collection of infectious disease data is to observe disease spread on a discrete scale instead of the true continuous scale. In addition, few studies have the resources available to collect information on the full population. The proportion of the population observed and the length of each time-interval between observation have major implications on the quality of data collected and the amount of missing information reported. This study was undertaken to determine how different model parameterizations could best account for missing/unobserved infectious disease data. A simulation study was used to carry out this research, with infectious disease spread being observed within a virtual agricultural setting with farm-level data observed under various sampling/surveillance scenarios. This talk will focus on a class of discrete-time individual-level models (ILMs) which utilize individual level susceptibility/infectivity risk factors to model infectious disease spread through time and space. Several different ILMs, each incorporating

different functions for random unobserved behaviour and model components accounting for the length of each observation time interval, were fit to the observed data. Inclusion of a baseline random infection term in addition to an additive random infection term depending on the number of infective individuals observed within the ILM resulted in the best fit of all models tested. When modelling a real life infectious disease outbreak and specific disease system, the model parameterized should be tailored to both the type / amount of data collected and the underlying disease system and population. The fit of ILMs in cases of excessive missing/unknown information is optimized when the structure of each model incorporates some knowledge of the disease spread characteristics.

Kenneth Blahut, Ryerson University.

Modeling the in vitro spread of hepatitis C virus to quantify the contribution of cell-to-cell and free virus infections.

Mathematical and computer models that reproduce the spread of a viral infection within a cell culture (in vitro) provide unique, valuable information: the accurate quantification of key infection parameters (e.g., viral production rate, infectious cell lifespan). Changes in these parameters, in turn, can indicate how a mutation affects viral fitness or identify the mode of action and efficacy of novel antiviral drugs. There currently exists only one mathematical model describing the course of a hepatitis C virus (HCV) infection in vitro: a non-spatial ODE model. However, experiments have shown that the spread of HCV infection has an important spatial component: infection disseminates both distally via release and diffusion of virus through the medium, and locally via direct, cell-to-cell infection. Both infection modes appear to play an important role, yet could be differentially affected by antiviral therapy. Therefore, characterizing their relative contribution to infection kinetics has important implications for the control of HCV infections. We have developed a agent-based computer model which explicitly incorporates both distal and local modes of infection. The model consists of a two-dimensional, hexagonal grid in which each site corresponds to one, non-motile, hepatocyte (liver cell). Since experimental measures taken over the course of infection typically report both the concentration of extracellular infectious virus, as well as the count of intracellular viral RNA segments, our model also tracks both of these quantities. Within each cell, the concentration of HCV RNA is tracked and updated via an ODE model for intracellular viral replication. The intracellular concentration within each cell is, in turn, linked to the rates of extracellular release and cell-to-cell infection. In this presentation, I will showcase the range of kinetics exhibited by our model and its performance in reproducing data from experimental in vitro HCV infections.

Amenda Chow, University of Waterloo.

Characterizing Hysteresis in Linear and Nonlinear Dynamical Systems.

Hysteresis is a phenomenon that occurs frequently in nature and man-made processes. It often appears in nonlinear dynamical systems and is commonly identified by a looping behaviour in the input-output maps of the dynamical system. However, the existence of a loop is not sufficient to identify hysteretic systems, nor is hysteresis present solely in nonlinear systems. Approaches for characterizing hysteresis and examples of both linear and nonlinear models that exhibit hysteresis are presented.

Utkarsh Dang, McMaster University.

Mixtures of power exponential distributions.

A novel family of mixtures of multivariate power exponential distributions is introduced. We investigate the use of the power exponential distribution for dealing with varying tail-weight and peakedness of data in a model-based clustering context. A family of parsimonious models is proposed using an eigen-decomposition of the scale matrix. For parameter estimation, a generalized expectation-maximization algorithm is used. Lastly, the utility of this family of models is illustrated using both toy and benchmark data.

Jeffrey Daniel, University of Guelph.

Derivation of leverage and influence diagnostics for MAXENT models in ecology.

MAXENT is a statistical learning algorithm used to model the geographic distribution of species using presence-only data. Although it is very popular among ecologists, MAXENT currently lacks the diagnostic methods that are available for traditional regression models. A major step towards resolving this issue has been made by recent results demonstrating the equivalence of MAXENT and Poisson regression. In this talk, we describe the MAXENT algorithm and review these equivalence results. We then discuss how the relationship between MAXENT and Poisson regression can be used to derive methods for assessing the leverage and influence of observations in MAXENT models.

Syantee Jana, McMaster University.

A Bayesian approach to the High-dimensional problem in Growth Curve Model.

Traditional approaches of testing a linear hypothesis on the mean of the Growth Curve Model fail in high-dimensional scenarios (sample size \leq number of parameters: $n < p$) since such setup leads to singular sample covariance matrix. Previously, we suggested a simple approach to moderation: using the Moore-Penrose generalized-inverse of the sample covariance matrix. Although it worked well empirically, but its performance declined in the near singularity zone ($n \approx p$). Here, we propose a Bayesian growth, assuming Inverse Wishart prior for the unknown population covariance matrix. The posterior distribution is then used to provide a moderated estimator for the covariance matrix, and this new estimator is always positive definite unlike the sample covariance matrix. It is then used to develop a test statistic for testing the linear hypotheses in question. Simulation studies show that the test is unbiased, powerful, symmetric, monotone with respect to n and parameter matrix and has level close to the nominal value. This is true for different structures of the hyperparameter of the prior distribution, for example, autocorrelation structure, Toeplitz structure and also unstructured.

Charles Keown-Stoneman, University of Guelph.

Multi-state models for accommodating internal covariates in survival analysis.

Multi-state models are a useful way of investigating the relationship between events in discrete and continuous time. In this talk, we look at the application of multi-state models, and of traditional survival analysis, in the presence of internal covariates. Internal covariates are measurements of the subjects of interest that vary over time and may be affected by the event of interest. When internal covariates are present in semi-parametric models, the interpretation of the regression coefficients and hazard functions is still valid. However, the relationship between the hazard and the survival function is not as simple as with external covariates. In the literature, multi-state models have been recommended for analyzing covariates in continuous time. If the internal covariate is categorical, one can allow states of a multi-state model to account for changes in the internal covariate. Both non-parametric and parametric models are discussed with analysis using data on bipolar disorder.

Richard Kohar, Royal Military College of Canada.

How close were we? Why measuring the sum squared error falls short for timing prediction in real-time.

Predicting the future can be viewed as a time series forecasting problem. The usual method is to try and predict upcoming observations for one or more time steps ahead. Currently, computer algorithms that predict upcoming observations try to minimize a cost function, for example, the sum-squared error function, with a gradient-based approach. For the problem of predicting instantaneous events in a time series, the sum-squared error function is simply a poor choice. Instead, we propose a new alternative cost function that is suitable for predicting events in real-time, and show that it can measure different kinds of timing errors that are commonly seen in applications.

Preeti Mohindru, University of Guelph.

The DJL conjecture for CP matrices over max-min semirings.

A real matrix A is called completely positive (CP) if there exists a nonnegative matrix B such that $A = BB^T$. Completely positive matrices are clearly square symmetric matrices over the set of nonnegative numbers. Interest in work on nonnegative factorization comes from the theory of inequalities, the study of block designs in combinatorics, economic modelling and probability and statistics. The main problem in the theory of CP matrices is to find a smallest nonnegative matrix B such that $A = BB^T$. The minimum number of columns in a smallest nonnegative matrix B is called the CP-rank of A . Drew, Johnson and Loewy (DJL) conjectured that for $n \geq 4$, the CP-rank of every $n \times n$ completely positive matrix over nonnegative numbers is at most $\lfloor n^2/4 \rfloor$. Since the set of all nonnegative numbers forms a semiring, we can consider the DJL conjecture for matrices over max-min semirings. A max-min semiring is a totally ordered set with greatest and least element, where the sum of two elements is defined as their maximum and the product of two elements is defined as their minimum. We prove the DJL conjecture for CP matrices over max-min semirings. We also relate the special case of this result for Boolean matrices to a well-known graph theoretical result of Erdos, Goodman and Posa.

Nathalie Moon, University of Waterloo.

The impact of prevalent cohort sampling on multistate transition probabilities in chronic disease processes.

Prevalent cohort studies sample individuals from a population with a probability proportional to their survival time. Considerable attention has been given to the impact of this sampling scheme on inferences about survival, but relatively little work has been done on more general multistate models of complex disease processes. We derive the length-biased transition probability matrix for a K -state Markov disease process and compare various features to the population-level counterparts. The effect of length bias on several quantities of interest will be discussed along with suitable methods of analysis to address this problem.

Behzad Nikzad, University of Ontario Institute of Technology (UOIT).

Codimension two bifurcation in a low order model of Plane Couette flow.

The study of the onset of turbulence in the flow of fluids, which are governed by the Navier-Stokes equations, has produced some famous instabilities e.g. Kelvin Helmholtz instability. An important, and as of yet mysterious, flow is Plane Couette flow in which turbulence is observable. Another observable phenomenon in Plane Couette flow is a "bursting" process whereby along with the linear laminar profile, non-laminar coherent structures appear and dissipate regularly. Yet, surprisingly V.A. Romanov has proven that the linear laminar profile of Plane Couette flow is linearly stable for all Reynolds number. In order to reconcile these seemingly contradictory facts a search began for numerical periodic solutions to Plane Couette flow. Nagata produced the first such solution and since then many others have been found as well. In order to explain the "bursting" process Fabian Waleffe introduced a low order model of Plane Couette flow that exhibits the phenomenon. We study the bifurcation diagram of a periodic solution of the Waleffe model found by the method of Nagata.

Pardis Noorzad, Ryerson University.

Modelling the Facebook Social Network: The Memoryless GEO-P Graph Model.

Online social networks are ubiquitous. Social scientists and marketing teams can peruse the insight gained by studying the resulting social graph. In order to study these networks, we must design graph algorithms that scale well with the size and order of the corresponding graphs. To test these algorithms, random samples need to be generated. In this case the random samples are graphs. In this talk we go over several methods for generating random graphs. We are especially interested in the M-GEOP model, and in assessing the fit of these models to our sample Facebook dataset.

Irena Papst, McMaster University.

Equivalent dynamical effects of different seasonal forcing patterns in infectious disease transmission.

In modelling the spread of childhood infectious diseases, it is important to consider seasonal variation in contact rates among children. Models that include such "seasonal forcing" of the transmission process display more complex epidemic patterns than simpler models – patterns that are closer to those seen in real epidemic data. In an attempt to be as realistic as possible, many studies have used a "term-time forcing function" that yields high transmission when school is in session and low transmission otherwise. By contrast, theoretical studies aiming to understand the possible behaviours of seasonally forced epidemic models have typically used a simple sinusoidal forcing function. While the sinusoid seems to approximate the school term schedule only roughly, it turns out that, with a simple adjustment, a sinusoidally forced system can exhibit almost identical dynamics as a term-time forced system. Such a sinusoidal approximation may be useful in analytical work, and demonstrates that understanding real epidemics does not require finely detailed knowledge of the seasonal forcing function. In this talk, I discuss quantifying and explaining the adjustment that allows us to use simpler, sinusoidal forcing over term-time forcing in an SIR model with vital dynamics.

Colin Phipps, University of Waterloo.

A microscale mathematical model for metabolic symbiosis in tumours.

The metabolism of cancer cells differs significantly from that found in normal tissues. We will develop a mathematical model for nutrient concentrations in cancerous tissue surrounding a single cylindrical microvessel. We will analyze the interdependence between cell populations' metabolic behaviours on a microscopic scale, specifically the emerging paradigm of metabolic symbiosis that exists between aerobic and glycolytic cells. We will consider evidence that cells near the vessel preferentially utilize lactic acid produced by glycolytic cells far from the vessel which simultaneously consumes a waste product and conserves glucose for these anaerobic cells. Inhibiting metabolic pathways in cancer cells is a promising area of cancer treatment research. Effects that could be induced by treatments, such as altering vessel concentrations (e.g. increased oxygen or lactate concentration) or reducing ATP production by inhibiting glucose/lactate transport, will be analyzed by performing sensitivity analyses on the model.

Oksana Pichugina, Brock University.

A Generalization of the Hypercube Graphs.

We introduce and study a class of graphs which contain hypercubes and complete graphs as special cases. Let M be a set of partial n -permutations of η elements on a multiset $S \subseteq \{0, 1\}^\eta$ where $n < \eta \leq 2n$. We map M into the Euclidean space R^n to get Euclidean combinatorial set E . Consider the following generalization of the hypercube graph Q_n : the 1-skeleton G of a polyhedron $P = \text{conv}E$. On one hand, E is a special case of a partial permutation set on $S = \{0^m, 1^{\eta_2}\}$. On the other hand, it is a subset of $\text{vert} Q_k$. By combining the properties of both of these sets, we derive properties of E and P such as the non-redundant constraints system of P and the adjacency criteria. We determine the order, size, diameter, and the regularity of G via geometrical characteristics of E and corresponding combinatorial polyhedron.

Nuzhat Rafique, University of Guelph.

Social Influence and Consumers Demand with Time Dependent Population.

This work is centered on the study of adoption of new products introduced in markets examined through a continuous time dependent 2-dimensional partial differential equation (PDE) model and a discrete in time agent based model (ABM). In the PDE model, a diffusion process is used to model the spread of new ideas or product adoption over time. ABM are heterogenous and discrete in time, we incorporate heterogeneity through: individual intrinsic preference change, social influence vs. product popularity, and different weights on a products distance from the individuals preference. We propose to examine the effect of neighbours influence on adoption using preferential attachment networks. The PDE model was examined through parameters introduced, including price sensitivity, individual preferences, speed of adoption and social influence. Our PDE model supports the direct link between differentiated economic product market model and our parameters.

Adrien Thierra, McMaster University.

Double squares: An History.

This presentation is about the maximal number of squares in a string. We will first define the different problems and then give the audience a tour of the different methods used to tackle those problems. We will present the proof of Fraenkel and Simpson, and Ilie's technique to shorten and tighten that proof. We will have an insight on N'Guyen Huong Lam's result. Finally, we will have a look at the framework used in "How many squares can a string contains" to significantly lower the bound on the maximal number of squares in a word.

Cristina Tortora, University of Guelph.

Mixture of generalized hyperbolic for high dimensional data sets.

The most widely used model-based clustering technique for high-dimensional data is the mixture of factor analyzers model. It is based on a latent Gaussian mixture model, and the aim of this talk is to extend it to the mixture of generalized hyperbolic factor analyzers (MGHFA) model. The mixture of generalized hyperbolic distributions has been proposed in 2013 (Browne and McNicholas), it is able to handle skewness and heavy tails, and it has the Gaussian, Student- t , normal inverse Gaussian and variance-gamma distributions as special cases.

An alternating expectation-conditional maximization algorithm is used for parameter estimation and the Bayesian information criterion is used to select the number of factors as well as the number of components. The performance of our generalized hyperbolic factor analyzers is illustrated on real data sets, where it performs favorably when compared to its Gaussian analogue.

Fei Wang, Western University.

Using SDP and Geometric Involutive bases to compute the real radical ideal of a polynomial system.

Geometric involutive bases for polynomial systems of equations have their origin in the prolongation and projection methods of the geometers Cartan and Kuranishi for systems of PDE. They are useful for numerical ideal membership testing and the solution of polynomial systems.

We were motivated by some remarkable recent work by Lasserre and collaborators in the area of real algebraic geometry who employed our prolongation projection involutive criteria as a part of their semi-definite based programming (SDP) method for identifying the real radical of zero dimensional polynomial ideals. In this talk we begin an exploration of the interaction between our geometric involutive bases and SDP methods particularly in the positive dimensional case.

Jun Yang, Queen's University.

Lower Bounds on the Probability of a Finite Union of Events.

Lower bounds on the probability of a finite union of events are considered, *i.e.* $P\left(\bigcup_{i=1}^N A_i\right)$, in terms of the individual event probabilities $\{P(A_i), i = 1, \dots, N\}$ and the *sums* of the pairwise event probabilities, *i.e.*, $\{\sum_{j:j \neq i} P(A_i \cap A_j), i = 1, \dots, N\}$. The contribution of this work includes the following: (i) in the class of all lower bounds that are established in terms of only the $P(A_i)$'s and $\sum_{j:j \neq i} P(A_i \cap A_j)$'s, the *optimal* lower bound is given numerically by solving a linear programming (LP) problem with $N^2 - N + 1$ variables; (ii) a new analytical lower bound is proposed based on a relaxed LP problem, which is at least as good as the existing KAT bound; (iii) numerical examples are provided to illustrate the performance of the bounds.

Y. Nikita Zhang, Western University.
Modelling Disability Using Mixtures of Markov Chains.

Multi-state models provide a convenient way of representing disability processes. In the simplest case, the model involves three states: active (not disabled), disabled and dead. While calculations are easy if one assumes that the model is a Markov chain, this is rarely appropriate. It is more reasonable to assume that the future of the process is influenced by its history. This occurs when one uses a mixture of Markov chains. We consider how to construct mixture models and investigate how the intensities of these processes depend on their histories.