School of Mathematical and Statistical Sciences
Arizona State University

M E M O R A N D U M

DATE: 03/21/2024

TO: Faculty and Students

FROM: Professor(s) Dieter Armbruster
Chair/Co-Chairs of Camille Moyer
Defense for the PhD in Applied Mathematics
Committee Members
John Fricks
Richard Hahn
Rosemary Renaut
Sharon Crook
Zeliha Kilic

DEFENSE ANNOUNCEMENT

Candidate: Camille Moyer

Defense Date: Friday, April 05, 2024

Defense Time: 12:00 PM

Virtual Meeting Link: https://asu.zoom.us/j/5816037703?omn=86863119128
Live Attendance: WXLR Wexler Hall (Tempe) A307

Title: Bayesian Approach in Addressing Simultaneous Gene Network Model Selection and Parameter Estimation with Snapshot Data

Please share this information with colleagues and other students, especially those studying in similar fields. Faculty and students are encouraged to attend. The defending candidate will give a 40-minute talk, after which the committee members will ask questions. There may be time for questions from those in attendance. However, guests are invited to attend as observers and will be excused when the committee begins its deliberations or if the committee wishes to question the candidate privately.

ABSTRACT
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ABSTRACT

Gene expression models are key to understanding and predicting transcriptional dynamics. This thesis devises a computational method which can effciently explore a large, highly correlated parameter space, ultimately allowing the author to accurately deduce the underlying gene network model using discrete, stochastic mRNA counts derived through the non-invasive imaging method of single molecule fluorescence in situ hybridization (smFISH). An underlying gene network model consists of the number of gene states (distinguished by distinct production rates) and all associated kinetic rate parameters. In this thesis, the author constructs an algorithm based on Bayesian parametric and nonparametric theory, expanding the traditional single gene network inference tools. This expansion starts by increasing the effciency of classic Markov-Chain Monte Carlo (MCMC) sampling by combining three schemes known in the Bayesian statistical computing community: 1) Adaptive Metropolis-Hastings (AMH), 2) Hamiltonian Monte Carlo (HMC), and 3) Parallel Tempering (PT). The aggregation of these three methods decreases the autocorrelation between sequential MCMC samples, reducing the number of samples required to gain an accurate representation of the posterior probability distribution. Second, by employ- ing Bayesian nonparametric methods, the author is able to simultaneously evaluate discrete and continuous parameters, enabling the method to devise the structure of the gene network and all kinetic parameters, respectively. Due to the nature of Bayesian theory, uncertainty is evaluated for the gene network model in combination with the kinetic parameters. Tools brought from Bayesian nonparametric theory equip the method with an ability to sample from the posterior distribution of all possible gene network models without pre-defining the gene network structure, i.e. the number of gene states. The author verifies the method's robustness through the use of synthetic snapshot data, designed to closely represent experimental smFISH data sets, across a range of gene network model structures, parameters and experimental settings (number of probed cells and timepoints).