Biographical Sketch (Template)

Name: Matthias Chung	Title: Assistant Professor
Email: mcchung@vt.edu	Department: Mathematics

Education/Training:

Institution/Location	Degree/Postdoc	Year(s)	Field of Study
University of Hamburg, Germany	Dipl. Math. (MS equiv.)	2001	Applied Mathematics
University of Lübeck, Germany	Dr. rer. Nat. (PhD equiv.)	2006	Applied Mathematics

Personal Statement:

My research interests concern various forms of **inverse problems**. Driven by its application, I develop and analyze efficient numerical methods for inverse problems. Applications of interest are, but not limited to, **systems biology**, **medical** and **geophysical imaging**, and **dynamical systems**.

Challenges for solving such problems include the high dimensionality of the problem, potential ill-posedness, and constraints enforced by its application. For instance, ill-posedness of inverse problems require prior knowledge and is usually integrated as **regularization**. I investigate such regularization methods to obtain meaningful solutions. With respect to the inverse problem, I develop and investigate efficient **optimization methods** to overcome challenges such as constraints and discontinuity. Methods for **large scale** inverse problems, such as problems from imaging applications, require special considerations methods. For instance, structure or low rank approximation are investigated to solve nearby problems efficiently. To **quantify uncertainty** in model and estimates, I utilize **Bayes** and **empirical Bayes** frameworks. **Estimating parameter** for **dynamical systems** (ODE constraint optimization) can be particular challenging. I investigate robust parameter estimation methods to handle even chaotic systems.

Selected Publications:

- 1. Q. Mu, V. Tavella, J. Kirby, T. Cecere, M. Chung, J. Lee, S. Li, S. Ahmed, C. Reilly, and X. Luo. Antibiotics ameliorate Lupus-like symptoms in mice. Accepted for publication at Scientific Reports, 2017.
- 2. M. Chung, J. Krueger, and M. Pop. Robust parameter estimation for biological systems: A study on the dynamics of microbial communities. Accepted for publication at Mathematical Bioscience, 2017.
- 3. A.C. Rodriguez, M. Chung, and S.M. Ciupe. Understanding the complex patterns observed during hepatitis B Virus therapy. Viruses, 9(117):1–15, 2017.
- 4. Y. Zhao, M. Chung, B.A. Johnson, C.S. Moreno, and Q. Long. Hierarchical feature se- lection incorporating known and novel biological information: Identifying genomic features related to prostate cancer recurrence. Journal of the American Statistical Association, 111(516):1427–1439, 2016.
- 5. B. Göbel, K.M. Oltmanns, and M. Chung. Linking neuronal activity to the glucose metabolism. Theoretical Biology and Medical Modelling, 10(50), 1–19, 2013.
- 6. M. Chung, B.A. Johnson and Q. Long. A tutorial on rank-based coefficient estimation for censored data in small- and large-scale problems. Statistics and Computing, 1–14, 2013.
- 7. M. Chung and E. Haber. Experimental design for biological systems. SIAM Journal on Control and Optimization, 50(1):471–489, 2012.
- 8. M. Chung and B. Göbel. Chapter: Mathematical modeling of the energy metabolism based on the Selfish Brain Theory. Advances in Systems Biology, pages 425–440, Springer, 2012.
- 9. B. Göbel, M. Chung, K.M. Oltmanns, A. Peters, and D. Langemann. Robust modeling of appetite regulation. Journal of Theoretical Biology, 291:65–75, 2011.
- 10. M. Chung, B. Göbel, A. Peters, K. M. Oltmanns, and A. Moser. Mathematical model of the biphasic dopaminergic response to glucose. Journal of Biomedical Science and Engineering, 4:136–145, 2011.

USDA NIFA: 2016-08687 Ogejo, Mukhopadhyay, M. Chung 08/01/2017 - 07/31/2020

Quantifying Nitrogen Transformations and Loses Associated with Manure Storage to Improve Accuracy of Whole Farm Process Based Nitrogen Accounting Models

Nitrogen (N) and phosphorus (P) management is essential in animal production systems if sustainable and healthy agroecosystems are to be maintained. Our proposal focuses on manure storage aspect of N cycling on the farm with a long term goal of increasing the knowledge and understanding of the fundamental processes, including microbial, chemical, and physical processes that impact the transformation and loss of N from stored dairy manure. Our study will attempt to uncover common and distinctive microbial community features in manure storage (concrete tanks and earthen pits) during storage at different times of the year to identify critical bacterial groups involved in degradation of manure and link them to associated aerial pollutants by utilizing mathematical modeling and uncertainty quantification.

NSF DMS 1723005 J. Chung, M. Chung 09/01/2017–08/31/2020

Stochastic Approximations for the Solution and Uncertainty Analysis of Data-Intensive Inverse Problems

In scientific fields ranging from geophysics and atmospheric science to medical imaging and network communication, data are being generated at remarkable rates. Such data are typically indirectly related to quantities of interest and the data sets are in many cases dynamically growing. Extracting desired information from these data then requires the solution of very large data-intensive inverse problems, perhaps repeatedly and in real time. The computational challenges of obtaining such a solution are compounded by the demands of validation and uncertainty analysis, which can easily become computationally prohibitive. This project will develop mathematical/statistical methods and computational tools for the solution of data-intensive inverse problems. The core of this approach is a stochastic reformulation of such problems that aims to significantly reduce the computational costs while adapting to modern hardware architectures.

NSF I/UCRC 1650463 Chung, Hole, Westman 02/01/2017–01/31/2018

Virginia Tech Planning Grant: I/UCRC for Advanced Subsurface Earth Resource Models

This grant is for establishing a center for subsurface modeling.

 NIH
 R21 GM107683-01
 M. Chung, Pop
 09/15/2013-08/31/2016

Identifying the dynamics of small and large microbial communities

The goal of this project is to develop a computational framework that can learn microbe-microbe and host-microbe interactions from time series of small and large microbial communities. Molecular analyses of human-associated microbial communities have already started to reveal associations between community structure and human health and disease. Novel analytical methods will be developed that can robustly learn the parameters of dynamic models from time-series data. Furthermore, several approaches will be explored for reducing the complexity of the systems derived from large microbial communities comprising hundreds to thousands of microbes.