THE UNIVERSITY OF CHICAGO

MONTE CARLO METHODS AND DEEP VARIATIONAL INFERENCE FOR FAST BAYESIAN ANALYSIS OF HIGH DIMENSIONAL BIOLOGICAL SYSTEMS

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ABSTRACT

CHAPTER 1

PRIMER ON EXACT BAYESIAN METHODS AND VARIATIONAL INFERENCE

1.1 Markov Chain Monte Carlo

The invention of fast digital computers gives us the ability to simulate random processes and perform inference

1.1.1 Metropolis-Hastings and Gibbs sampling

1.1.2 Langevin Monte Carlo

The metropolis adjusted Langevin algorithm (MALA) aka Langevin Monte Carlo

1.1.3 Hamiltonian Monte Carlo

1.1.4 Stochastic Gradient Langevin Dynamics

1.2 Variational Inference

1.2.1 Neural networks represent probability distributions

1.2.2 Training criteria for neural networks

1.2.3 The evidence lower bound

CHAPTER 2

DECONVOLVING IMMUOGENIC TUMOR SUBSTRUCTURE WITH VARIATIONAL INFERENCE

Single cell variational inference. Using deep generative modeling to discover latent structure in the data, establish how that latent structure relates to immunogenicity. This latent structure can be used to design fluorescent probes, which will be added to T-cell markers to measure degree of inflammation for different modes of the data. Malignant cells are isolated first using standard methods e.g, filtering, normalization, and UMAP clustering

CHAPTER 3

A BAYESIAN APPROACH FOR INFERRING NEURONAL CONNECTIVITY FROM CA2+ IMAGING DATA AND MONTE CARLO SIMULATIONS

CHAPTER 4

BAYESIAN INFERENCE OF THE KINETIC PARAMETERS OF INTERFERON-GAMMA INDUCED TRANSCRIPTION