In the field of Monte Carlo (MC) methods, problems related to continuous time Markov chains are among the most promising research directions. Monte Carlo methods are indispensable tools for analysis of real world processes modelled as continuous time Markov chains. Design of more efficient algorithms for such models and analysis of their properties present difficult problems, which are very important for applications.

Among the challenging applications of MC are those to Hidden Markov Models (HMM). A HMM is a Markov process which is not directly observed. Only some partial and noisy observations on this process are available. The objective is to ``reconstruct'' the path of the hidden process
and/or to estimate its parameters. These problems are usually formulated as Bayesian statistical inference problems. The goal is to computete/approximate/explore the posterior (probability distribution on a multidimensional or infinite-dimensional space). As a rule, the analytical form of the posterior is intractable and even deterministic numerical methods are inefficient. This explains the crucial role of Monte Carlo algorithms for HMMs. Monte Carlo methods have been successfully applied to HMMs in such various fields as speech recognition, climatology, image processing, econometrics, finance, epidemiology, biology and chemistry. In recent years much work has been devoted
to HMMs with continuous time, modelling kinetics of chemical reactions and biochemical networks. The dynamics of biochemical networks at the level of single cells exhibit stochastic behaviour. When small numbers of molecules react in a stochastic
manner, macroscopic concepts do not provide an adequate description. Discreteness of molecular processes and their stochastic nature are best modelled by jump, continuous time Markov processes. Since these processes are usually observed at discrete times and with random errors; this is a typical setup for HMMs. Due to the complicated nature of the hidden processes, inference problems become especially difficult.

In our project we focus on continouos time HMMs. We intend to analyse and modify algorithms for sampling from the conditional distribution of the complete continuous time path of the hidden states and the posterior distribution of the parameters.

The mathematical analysis of algorithms, which we intend in this project, is crucial for understanding the limitations of Monte Carlo methods; in the case of continuous time HMM processes, this does not have adequate treatment in the literature.