Stochastic differential equations and a biological system

The purpose of this Ph.D. study is to explore the property of a growth process. The study includes solving and simulating of the growth process which is described in terms of stochastic differential equations. The identification of the growth and variability parameters of the process based on experimental data is considered. As an example, the growth of bacteria Pseudomonas fluorescens is taken. Due to the specific features of stochastic differential equations, namely that their solutions do not exist in the general sense, two new integrals - the Ito integral and the Stratonovich integral - have been developed. Their properties and the relationship between them are discussed. The evolution of a dynamic system or process is usually of great practical interest. In order to simulate the evolution of the process, alternative methods are used to get numerical solutions. In this study, Euler, Milstein and Runge-Kutta methods are used. Because of the specific feature of the model for the growth process, that its solution does not exist in the general sense, we combine these numerical integration methods with a transformation technique, and the solutions are derived in the Ito sense. The simulated results are compared with the experimental data, and it is found that the Euler method is the most simple and efficient method for the stochastic growth model considered. Estimation of the parameters of the growth model is based on the stochastic Kalman filter and a continuous Markov process description. In order to identify the parameters, a Maximum likelihood estimation method is used together with a simplified truncated second order filter. Because of the continuity feature of the predictor equation, two numerical integration methods, called the Odeint and the Discretization method, are developed. By the simulation and identification of the parameters in the theoretical model, a satisfactory match is found.
Project: PhD