Meeting: 1003, Atlanta, Georgia, MAA CP X1, MAA General Contributed Paper Session, I

1003-X1-534 **Gretchen A Koch*** (kochg@rpi.edu), Rensselaer Polytechnic Institute, Department of Math Sciences, AE 301, 110 Eighth Street, Troy, NY 12180-3590, and **Donald A Drew**. *Modeling the MinCDE System in Escherichia coli.* Preliminary report.

In order to survive, all species must reproduce. In the case of *Escherichia coli*, this involves dividing into two equal daughter cells via the MinCDE system. This system relies on the combined effort of three proteins, MinC, MinD, and MinE, as well as the oscillatory behavior that they exhibit when working together. MinC and MinD combine to form chains in two polar zones that grow out towards the center of the cell, while MinE caps and disassembles these chains before they reach the center of the cell. Thus, the division apparatus can form in center of the cell. We model the system using several continuous time Markov processes. Each process represents the different states of the system: chain growth, capping, and decay. If we consider the addition or removal of a protein to a chain as an event, we can use the idea of waiting times. The Monte Carlo simulation generates an exponentially distributed random time for each protein chain; these times are dependent upon the state of each individual chain as well as its neighboring chains so that the growth and decay of a chain is affected by its neighbors. This leads to a situation where we have piecewise homogeneous transition probabilities, and thus creates a unique Monte Carlo simulation. (Received September 20, 2004)