999-15-41 **Yan Zhao***, yanzhao@math.vanderbilt.edu. *The model for strep throat infection.*

An ordinary differential euqations model for strep throat infection is developed. This model is used to compute the population of bacteria which causes strep throat in an infected host. The bacteria population is divided into genotype classes based on contingency genes. These genes are turned off or on according to a selection process within the host. A combination of turned-on genes is necessary for the bacteria population to adapt to the host. Random mutation provides the background source of the contingency gene combinations. Both a theoretical analysis and numerical analysis of this model are performed. In the theoretical analysis, the steady state of the system is determined. Also, it is proved that the solutions converge exponentially asymptotically to the steady state. In the numerical analysis, the dominant genotype class of bacteria is investigated. To enhance the efficiency of the computation, a new ODE model is then constructed by reducing the number of equations in the old model. It has been proved that the solutions of the old model can be obtained by the solutions of the new one under a certain assumption, and the asymptotic behaviors of these two models are equivalent by the given condition of the mutation frequency. (Received July 20, 2004)