1080-92-188 **Assieh Saadatpour*** (saadat@math.psu.edu), 109 McAllister Building, University Park, PA 16802, and **Reka Albert**. *Boolean and hybrid dynamic modeling of the T-LGL leukemia signaling network.*

T cell large granular lymphocyte (T-LGL) leukemia is a blood cancer characterized by an abnormal increase in the abundance of a type of white blood cell called T cell. As there is no known curative therapy for this disease, identification of potential therapeutic targets is of utmost importance. In the first part of this talk, I will highlight the results of our recent work on how Boolean dynamic modeling with the aid of a network reduction technique is capable of identifying the disease states of the components of the system as well as potential therapeutic targets. In particular, we identified the T-LGL (disease) states of 54 components of the system, 67% of which are corroborated by previous experimental evidence and the rest are novel predictions. In addition, by the dynamic analysis of the underlying network, we identified 19 component perturbations that lead to programmed cell death, thereby suggesting several novel candidate therapeutic targets for future experiments. In the second part of my talk, I will present preliminary results on the comparison of the state space of the Boolean model of this system with that of the piecewise-linear differential equation (hybrid) model to determine which additional properties can be captured by the hybrid model. (Received January 26, 2012)