

development of graph models that more accurately represent social networks. [61, 12, 89, 83, 8, 85, 87]. Development of accurate random graph models as primarily focused on replicating the degree distribution of vertices, [14, 27, 75, 89]. Barabási and Albert [13, 12] proposed a model for graphs with a power-law degree distribution in order to capture the structure of the web graph. Considerable focus has been paid to random graphs with an explicit degree sequence based on a model by Bender and Canfield [14]. Molloy and Reed [75, 76] showed that there exists edge density threshold for the emergence of a giant component. This work was extended by Newman [84] and Meyers [69] who provide calculations for expected disease outbreak size. Chung and Lu [27] propose a model for graphs with an expected degree distribution which was extended by Eubank et al. [38] to model people and the locations they visit for the city of Portland, OR. More recently, Newman [82] has proposed new graph models for graphs with given degree sequence and neighbor correlations. Bansal and Meyers [8] and Newman [87] have both introduced graph models that capture degree sequence and vertex clustering.

In Chapter 3 we consider a number of candidate random graph models to describe our HCW contact networks. Our results show that simple random graph models that only pay attention to local structure (i.e., mean degree and degree distribution) fail to capture epidemiologically relevant aspects of the HCW contact networks, and thus may be poor models for real world social networks in general. Moreover we show compelling evidence that, for HCW contact networks, the correlation between degrees of adjacent (neighboring) vertices plays an important role in disease diffu-