In mathematical epidemiology, the standard compartmental models assume homogeneous mixing in the host population, in contrast to the disease spread process over a real host contact network. One approach to incorporating heterogeneous mixing is to consider the population to be a network of individuals whose contacts follow a given probability distribution. Here we investigate in analogy both homogeneous mixing and contact network models for infectious diseases that admit latency periods, such as dengue fever, Ebola, and HIV. We consider the mathematics of the compartmental model as well as the network model, including the dynamics of their equations from the beginning of disease outbreak until the disease dies out. After considering the mathematical models we perform software simulations of the disease models. We consider epidemic simulations of the network model for three different values of \( R_0 \) and compare the peak infection numbers and times as well as disease outbreak sizes and durations. We examine averages of these numbers for one thousand simulation runs for three values of \( R_0 \). Finally we summarize results and consider avenues for further investigation. (Received August 01, 2017)