connections between latent variables, since these networks are typically sparse, and the incorporation of structure resulting from network-specific prior knowledge in $H$ can also often be leveraged. For example, as in the epidemics model, $H$ can become a simple function of a few parameters and sufficient statistics of connected states.

4 GCHMMS FOR MODELING INFECTION DYNAMICS

In this section, we show that the GCHMM can be used as a discrete-time multi-agent epidemic model, where the spread of infection is modeled on an individual level as opposed to the standard population-level models commonly used in epidemiology. In section 6, we show that the GCHMM can be applied to real-world data based on individual proximity and symptom reporting.

In particular, the GCHMM that we apply to epidemics can be seen as an individual-level version of the classic susceptible-infectious-susceptible (SIS) epidemiology model. The SIS model describes infection dynamics in which the infection does not confer long-lasting immunity, and so an individual becomes susceptible again once recovered (e.g., the common cold).

Using the GCHMM to model SIS dynamics identifies paths of infection based on individual-level interactions that are captured in our data. The classical differential equation and stochastic models of SIS dynamics work at the population level, and their variables are density and size of susceptible and infectious populations, respectively. The differential equation model $\dot{S} = -\beta \cdot SI + \gamma \cdot I$ and $\dot{I} = \beta \cdot SI - \gamma \cdot I$ for SIS specifies that the rate of change of infectious-population density is bilinear for both infectious-population density and susceptible-population density. In this system, any two individuals from the infectious population are treated as the same, as are any two individuals from the susceptible population, and therefore any two individuals from different populations have an equal chance of causing infection. The stochastic model $S + I \rightarrow 2I$, rate $= \beta' \cdot |S| \cdot |I|$ and $I \rightarrow S$, rate $= \gamma' \cdot |I|$ specifies that infection happens at a bilinear rate for both the infectious-population density and the susceptible-population density. This model enables us to reason about the randomness in the SIS system when the population size is small and randomness cannot be ignored.

The above models focus on the statistics of the spread of infection over a homogeneous population. However, we are instead interested in predicting the spread of infection on an individual level, given relevant information about each specific individual. Our goal is to explain symptom observations in a community with susceptible-infectious-susceptible dynamics at any given point in time. How likely is a person to be infectious at time $t$, given that his friends are reporting symptoms, reporting no symptoms, or not answering surveys, and given the infectious person’s own survey responses and his recent proximity to his friends? Which nodes and links are critical in spreading infection in the community? How can we control infection in this community?

We use the GCHMM to address these questions, following the generative model given in section 3 and the details (state space, $H$, $F$, and so on) specified here.

$G_t = (N, E_t)$ is a dynamic network, where each node $n \in N$ represents a person in the network, and $E_t = \{(n_i, n_j)\}$ is a set of edges in $G_t$ representing the fact that person $n_i$ and person $n_j$ have interacted or come into contact at time $t$. There are two possible latent states for each person $n$ at each time $t$, $X_{n,t} \in \{0, 1\}$, where 0 represents the susceptible state and 1 the infectious state. There are six possible symptoms that can be displayed by a person at any given time, $Y_{n,t,i}$, which are runny nose, coughing, fever, feeling stressed, sadness, and diarrhea, and each symptom $Y_{n,t,i} \in \{0, 1\}$ represents the presence or absence of symptom $i$.

Our generative model is therefore as follows:

$$X_{n,t} \sim \text{Bernoulli}(\phi_{n,X_{n-t}} \in G_{t-1})$$  \hspace{1cm} (9) 
$$Y_{n,t,i} \sim \text{Bernoulli}(\theta_{X_{n,t}})$$  \hspace{1cm} (10)