attention to a single person looking up, but we would look up if a group of people look up.

5 INFERENCE

In this section, we present an efficient inference algorithm for our GCHMM in order to describe and predict the spread of infection. We start by describing inference in the most general, worst case for GCHMMs, and progress from there to much more efficient inference for the epidemics model. The worst case inference algorithm for GCHMMs will be the same as for CHMMs (the case where the graph is complete).

A Gibbs sampling algorithm for a particular CHMM with two chains is given in [Rezek et al., 2000], which we extend here to an unconstrained number of chains. The two sampling steps relevant to the extension to multiple chains become:

\[ X_{n,t+1} \sim \text{Categorical}(\frac{p(X_{n,t+1} = j, Y|\gamma, \phi)}{\sum_k p(X_{n,t+1} = k, Y|\gamma, \phi)}) \]

\[ \phi_{n,i} \sim \text{Dirichlet}(\alpha_j + \sum_{\tau=1}^T 1(X_{n,\tau+1} = j \land X_{s,\tau} = i)) \]

Here \( j \) and \( k \) are states of \( n \), and \( i \) is the transition matrix row number corresponding to a combination of states for all nodes. We can see that this sampling procedure is not very efficient, particularly for a reasonably large number of chains.

Fortunately, in practice most social networks are sparse - far from complete. The number of parameters needed to be inferred will decrease dramatically for sparse networks (from \( O(N^2) \) to \( O(n_{\text{max}}) \) where \( n_{\text{max}} \) is the maximum number of connections for node \( n \)). The parameters of the transition matrix can now be sampled conditioned on the network structure:

\[ \phi_{n,i} \sim \text{Dirichlet}(\alpha_j + \sum_{\tau=1}^T 1(X_{n,\tau+1} = j \land X_{s,\tau} = i)) \]

Here \( i \) now corresponds to a combination of the states of nodes connected to \( n \) only. While significantly better than the full CHMM, this may still be intractable for large \( N \) or \( T \). However, the interaction structure that we are interested in is also not typically governed by unrestricted transition matrices, \( \phi \). There is structure to interactions or behavior that we can leverage to drastically increase efficiency. One common example is that all agents may be subject to the same \( \phi \). Another is that interactions themselves have a structure which can be captured by an \( H(\mu, g(X)) \), where \( H \) is now a function parameterized by a reasonably small set of parameters \( \mu \) and sufficient statistics of the current state space \( g(X) \). This allows us to sample \( p(\mu|g(X)) \), and then compute \( \phi \), unlike in the algorithms above. This form of \( H \) applies to many multi-agent network models including the emergence of collaboration, the spread of rumors and the formation of culture. It similarly applies to our epidemics model, as described in section 4, where \( g(X) \) can be efficiently computed at each node, at each time step. We now describe the resulting inference method for the epidemics model, and then briefly discuss applying the same inference scheme to some more general, \( g(X) \).

The epidemics inference algorithm learns the parameters of infection dynamics, including the rate of infection and rate of recovery. It then estimates the likelihood that an individual becomes infectious from the contact with other students based on the reported symptoms of others, and even when the individual’s own symptom report is not available. Finally, the algorithm enables us to make useful predictions about the spread of infections within the community in general.

We employ a Gibbs sampler to iteratively sample the infectious/susceptible latent state sequences, to sample infection and recovery events conditioned on these state sequences, and to sample model parameters.

The Gibbs sampler for the GCHMM for epidemics is given in detail below.

The Gibbs sampler takes the following as its input:

\( G = (N, E) \): a dynamic network where nodes \( n \in N \) represent a person in the network, and \( E_t = \{(n_i, n_j)\} \) is a set of edges in \( G_t \) representing that person \( n_i \) and person \( n_j \) have interacted or come into contact at time \( t \).

\( Y \): an observation matrix of symptoms indexed by time and node.

The Gibbs sampler gives the following output:

\( \{X, \alpha, \beta, \gamma, \theta\}_s \): samples \( s \). This includes several parameters: \( \alpha \), the base rate of infection; \( \beta \), the rate of infection by each infectious neighbor in \( G_t \); and \( \gamma \), the rate of recovery. It includes the emission matrix \( \theta \), which expresses the probability of seeing each of the six symptoms given the infectious/susceptible latent state. It also includes the state matrix \( X \) of the epidemics GCHMM, which shows sequences of states 0 (susceptible) and 1 (infectious) for each individual over time.

We randomly initialize the model parameters and set the state matrix so that every individual in the network is in the susceptible state. The Gibbs sampler