

TODO

TODO

March 21, 2020

### Abstract

## 1 Algorithm notes

- Graph convolution:

$$h_{v_i}^{(l+1)} = \text{softmax}(\sum_{j \in \hat{A}(i)} h_{v_j}^{(l)}) \quad (1)$$

with  $\hat{A}(i)$  the infection-weighted neighbours of node  $v_i$  as derived from the infection-weighted neighbours adjacency matrix  $\hat{A}$ .

- $\hat{A}$  is constructed from  $A$  and  $I$  which are the regular adjacency matrix and the infection matrix, respectively.
  - The adjacency matrix  $A$  is time dependent,  $A(t)$ , and inferred from data. In our use case,  $A_{ij} = 1$  if nodes  $v_i$  and  $v_j$ , hence persons  $i$  and  $j$ , have been in contact. This corresponds to  $\text{dist}(v_i, v_j) \leq \epsilon$  with  $\epsilon = 0$  in the discrete case that we consider here.
  - The infection matrix is constructed as

$$I = \begin{pmatrix} 0 & 0 & p_a & 0 \\ 0 & 0 & p_a & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \quad (2)$$

with  $I_{ij}$  and  $i$  is the index of the host state and  $j$  is the index of the contact person state. The states that we consider here are ordered as follows: unknown, susceptible, infected, recovered.  $p_a$  denotes the probability of infection after contact (also known as attack rate).

- $\hat{A}$ , with  $\hat{A}_{ij} \in \{0, 1\}$ , is the adjacency matrix that takes the infection interactions into account and is computed as follows

$$\hat{A}_{ij} = A_{ij} \cdot \frac{I_{\text{indexOfState}(i), \text{indexOfState}(j)} + I_{\text{indexOfState}(j), \text{indexOfState}(i)}}{p_a} \quad (3)$$

with `indOfState( $k$ )` as index of the state of agent  $k$  in order to access the elements from  $I$ . The sum comes from the fact that both, agent  $i$  and  $j$ , can act as host during a contact. The division by  $p_a$  normalises the factor to one to ensure  $\hat{A}_{ij} \in \{0, 1\}$ . Since  $I$  is not symmetric,  $p_a$  is a proper normalisation because the sum is in  $\{0, p_a\}$ .

- The feature matrix,  $H$ , consists of all agents' features and is thereby of dimension  $N \times D$  where there are  $N$  agents in the population and each agent is described by  $D$  features. A four dimensional feature space is used,  $D = 4$ . The unit vectors of this space are interpreted as following:
  - $\vec{e}_1$ : unknown state
  - $\vec{e}_2$ : susceptible state
  - $\vec{e}_3$ : infected state
  - $\vec{e}_4$ : recovered state
- Open modeling aspects:
  - Incorporate that an infected person recovers over time.