

Propensities

April 22, 2020

1 Prerequisites

Input is a graph G_{multi} that allows more edges between nodes. Each edge is identified by its weight (intensity) $w_{i,j,t,s}$, type t and subtype s .

From this graph we create the graph G with single edges only, where edge aggregates information over sublayers. Edges in G have weights $w_{i,j}$.

The weights are computed as follows:

$$w_{i,j,t} = \sum_s w_{i,j,t,s} \text{ (sum over intensities of sublayers)}$$

Final weight:

$$w_{i,j} = 1 - \prod_t (1 - l_t * w_{i,j,t})$$

- (weights on layers t are taking as probabilities of contact on that layer and are the final weight is probability of contact on any layer)
- l_t is coefficient of layer t

2 Probabilites of state transitions

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| x | — | — | n | — | — | — | — | — | — | — | — |
| S | — | s | | | | | | | | | |

3 Probability of being infected

$$P_{infection} = p \frac{\beta N_I + q \beta_D N_{I_d}}{N} + (1 - p) \frac{\beta \sum_{j \in C_{G(i)}} w_{ij} \delta_{X_j=I} + \beta_{I_d} \sum_{j \in C_{G(i)}} w_{ij} \delta_{X_j=I_d}}{|C_{G(i)}|}$$

- N_I the total number of I -states, i.e. sum of I_n, I_a, I_s
- N_{I_d} number of nodes in I_d
- N current size of population
- $\delta_{X=I} = 1$ if and only if $X \in \{I_n, I_a, I_s\}$
- $\delta_{X=I_d} = 1$ if and only if $X = I_d$

- $|C_{G(i)}| = \sum_{j \in C_{G(i)}} w_{ij}$

4 State S_s

bud se nakazím nebo zůstanu Skova, pokud zůstanu Skova tak bud odezni falešné příznaky a jdu do S , nebo zustavam, kde jsem

possible transtitions: $S_s \rightarrow E, S_s \rightarrow S, S_s \rightarrow S_s$

$$P[S_s \rightarrow E] = P_{infection}$$

$$P[S_s \rightarrow S] = (1 - P[S_s \rightarrow E]) * false_symptoms_recovery_rate$$

$$P[S_s \rightarrow S_s] = (1 - P[S_s \rightarrow E]) * (1 - false_symptoms_recovery_rate)$$

5 State S

bud se nakazím nebo zůstanu Skova, pokud zůstanu Skova tak bud prijde chripka (falesne priznaky) a jdu do S_s , nebo zustavam, kde jsem

possible transtitions: $S \rightarrow E, S \rightarrow S_s, S \rightarrow S$

$$P[S \rightarrow E] = P_{infection}$$

$$P[S \rightarrow S_s] = (1 - P[S \rightarrow E]) * false_symptoms_rate$$

$$P[S \rightarrow S] = (1 - P[S \rightarrow E]) * (1 - false_symptoms_rate)$$

6 State E

může se stát, že mě pozitivne otestují a přejdu do I_d , jinak čeká až začnu být infekční, pokud začnu být infekční, jdu bud do I_n nebo do I_a

possible transitions: $E \rightarrow I_d, E \rightarrow I_n, E \rightarrow I_a, E \rightarrow E$

$P[E \rightarrow I_d] = \theta_E * \psi_E$ (puvodne tam jeste maji clen, který zavisi na poctu I_d kontaktu, ala contact traicing, to mame vypnuto)

$$P[E \rightarrow I_n] = (1 - P[E \rightarrow I_d]) * \sigma * asymptomatic_rate$$

$$P[E \rightarrow I_a] = (1 - P[E \rightarrow I_d]) * \sigma * (1 - asymptomatic_rate)$$

$$P[E \rightarrow E] = (1 - P[E \rightarrow I_d]) * (1 - \sigma)$$

7 State I_n

ve stavu I_n setrvavam, dokud se neuzdravim, mohu byt ale otestovana a prejit do I_d (tady je trosku zanedbano, ze pokud by v tom jednom dni doslo k memu otestovani i uzdraveni, tak bych sla do R_d)

possible transitions: $I_n \rightarrow I_d, I_n \rightarrow R_u, I_n \rightarrow I_n$

$$P[I_n \rightarrow R_u] = \gamma_{i_n}$$

$$P[I_n \rightarrow I_d] = (1 - P[I_n \rightarrow R_u]) * \theta_{I_n} * \psi_{I_n}$$

$$P[I_n \rightarrow I_n] = 1 - P[I_n \rightarrow R_u] - P[I_n \rightarrow I_d]$$

8 State I_a

čekám na projevení symptomů, v mezičase mohu být testovaná

possible transition: $I_a \rightarrow I_d, I_a \rightarrow I_s, I_a \rightarrow I_a$

$$P[I_a \rightarrow I_d] = \theta_{I_a} * \psi_{I_a}$$

$$P[I_a \rightarrow I_s] = (1 - P[I_a \rightarrow I_d]) * \text{symptom_manifest_rate}$$

$$P[I_a \rightarrow I_a] = (1 - P[I_a \rightarrow I_d]) * (1 - \text{symptom_manifest_rate})$$

9 State I_s

mohu se uzdravit, umřít nebo zůstat, kde sem. taky můžu být otestovaná

possible transitions: $I_s \rightarrow R_u, I_s \rightarrow R_u, I_s \rightarrow I_d, I_s \rightarrow I_s$

$$P[I_s \rightarrow R_u] = \gamma_{I_s}$$

$$P[I_s \rightarrow D_u] = \mu \quad \$ (\text{predpokladam, ze gamma + mu} < 1)$$

$$P[I_s \rightarrow I_d] = (1 - P[I_s \rightarrow R_u] - P[I_s \rightarrow D_u]) * \theta_{I_s} * \psi_{I_s}$$

$$P[I_s \rightarrow I_s] = (1 - P[I_s \rightarrow R_u] - P[I_s \rightarrow D_u]) * (1 - \theta_{I_s} * \psi_{I_s})$$

10 State I_d

mohu jen do R_d a D_d

possible transitions: $I_d- > R_d, I_d- > D_d, I_d- > I_d$

$$P[I_d- > R_d] = \gamma_{I_d}$$

$$P[I_d- > D_d] = \mu$$

$$P[I_d- > I_d] = 1 - P[I_d- > R_d] - P[I_d- > D_d]$$

11 States R_u, R_d, D_u, D_d are final

(pro kazdy stav se radek secte na 1! to je to, co jsme opravovali dnes)

12 Parameters

Scalars: (but last four can be also made to be vectors)

| parameter | desription |
|------------------------------|--|
| p | probability of interaction outside adjacent nodes |
| q | probability of detected individuals interaction outside adjacent nodes |
| false_symptoms_rate | $S \rightarrow S_s$ |
| false_symptoms_recovery_rate | of $S_s \rightarrow S$ |
| asymptomatic_rate | rate of going to I_n instead of I_a from E |
| symptoms_manifest_rate | $I_a \rightarrow I_s$ |

Vectors: (each node has its own value, if only a single float is given than all nodes share the same value)

| parameter | desription |
|-----------|--|
| beta | rate of transmission (exposure) |
| beta_D | rate of transmission (exposure) for detected inds |
| sigma | rate of infection (upon exposure) |
| gamma_In | rate of recovery (upon infection) |
| gamma_Is | |
| gamma_Id | |
| mu | rate of infection-related death |
| theta_E | rate of testing for exposed individuals |
| theta_Ia | rate of testing for Ia individuals |
| theta_Is | rate of testing for Is individuals |
| theta_In | rate of testing for In individuals |
| psi_E | probability of positive test results for exposed individuals |
| psi_Ia | probability of positive test results for Ia individuals |
| psi_Is | probability of positive test results for Is individuals) |
| psi_Is | probability of positive test results for Is individuals) |

(psi mame vsude jedna)

[]:

[]: