model

April 18, 2020

1 Extended Network Model

1.0.1 States

$S_s, S, E, I_n, I_a, I_s, I_d, R_d, R_u, D_d, D_u$

1.0.2 Transitions

$$S \rightarrow S_s$$

$$S \rightarrow E$$

$$S_s \rightarrow S$$

$$S_s \rightarrow E$$

$$E \rightarrow I_n$$

$$E \rightarrow I_a$$

$$I_n \rightarrow R_u$$

$$I_a \rightarrow I_s$$

$$I_s \rightarrow R_u$$

$$I_s \rightarrow D_u$$

$$I_s \to I_d$$

$$I_d \to R_d$$

$$I_d \to D_d$$

$$I_a \to I_d$$

$$E \to I_d$$

1.0.3 Seirsplus propensity

$$P[X_i = S \to E] = \left[p\frac{\beta I}{N} + (1-p)\frac{\beta \sum_{j \in C_{G(i)}} \delta_{X_j = I}}{|C_{G(i)}|} \right] \delta_{X_t = S}$$

where I is a number of infected, N total number of living individuals, β rate of transmission (may be individual for each node), $\delta_{X_j=I}$ is 1 if $X_j = I$, 0 otherwise, X_i state of individual i, $C_{G(i)}$ is a set of close contacts (nodes j, that edge (i,j) is in the given graph G).

1.0.4 Extended propensity

We use the same formula for $P[X_i = S- > E]$ with these modifications:

- I is the total number of I-states, i.e. sum of I_n, I_a, I_s, I_d
- $\delta_{X=I} = 1$ if and only if $X \in \{I_n, I_a, I_s, I_d\}$
- edges has weights
- $|C_{G(i)}|$ is not the number of edges from i, but the sum of their weights (!there is only one edge between (i,j) in G)
- $\sum_{j \in C_{G(i)}} \delta_{X_j=I}$ is replaced by $\sum_{j \in C_{G(i)}} w_{(i,j)} \delta_{X_j=I}$

1.0.5 Constraction G from G_multi

Graph G_{multi} may contain more edges between i, j. Each edge has type t and subtype s and weight $w_{i,j,t,s}$ (intensity).

Graph G has max one edge (i,j) between nodes i, j. Edge as weight $w_{i,j}$.

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

Weight $w_{i,j} = 1 - \prod_t (1 - w_{i,j,t})$ (weights on layers t are taking as probabilities of contact on that layer and are the final weight is probabily of contact on any layer) !!!! **this is probably the problem, that this is not correct**

1.0.6 SEIRS + testing

in fact, we use the variant with testing, where I_d states has their own probs, TODO rewrite formulas

```
propensities[("S", "S_s")] = model.false_symptoms_rate*(model.X == "S")

#  "S" -> "E"
numI = model.current_state_count(
    "I_n") + model.current_state_count("I_a") + model.current_state_count("I_s")

S_to_E_koef = (
    model.p * (
        model.beta * numI +
        model.q * model.beta_D * model.current_state_count("I_d")
    ) / model.current_N()
    +
    (1 - model.p) * np.divide(
        model.beta * numContacts_I +
        model.beta_D * numContacts_Id, model.degree, out=np.zeros_like(model.degree), wher
    )
)
propensities[("S", "E")] = S_to_E_koef * (model.X == "S")

propensities[("S_s", "S")
             ] = model.false_symptoms_recovery_rate*(model.X == "S_s")

# becoming exposed does not depend on unrelated symptoms
propensities[("S_s", "E")] = S_to_E_koef * (model.X == "S_s")

exposed = model.X == "E"
propensities[("E", "I_n")] = model.asymptomatic_rate * \
    model.sigma * exposed
propensities[("E", "I_a")] = (
    1-model.asymptomatic_rate) * model.sigma * exposed

propensities[("I_n", "R_u")] = model.gamma * (model.X == "I_n")

asymptomatic = model.X == "I_a"
propensities[("I_a", "I_s")
             ] = model.symptoms_manifest_rate * asymptomatic

symptomatic = model.X == "I_s"
propensities[("I_s", "R_u")] = model.gamma * symptomatic
propensities[("I_s", "D_u")] = model.mu_I * symptomatic

detected = model.X == "I_d"
propensities[("I_d", "R_d")] = model.gamma_D * detected
propensities[("I_d", "D_d")] = model.mu_D * detected
```

```
    # testing  TODO
    propensities[("I_a", "I_d")] = (
        model.theta_Ia + model.phi_Ia * numContacts_Id) * model.psi_Ia * asymptomatic

    propensities[("I_s", "I_d")] = (
        model.theta_Is + model.phi_Is * numContacts_Id) * model.psi_Is * symptomatic

    propensities[("E", "I_d")] = (
        model.theta_E + model.phi_E * numContacts_Id) * model.psi_E * exposed
```

2 Engine

2.1 Seirsplus implementation

```
t = 0
while True:
    propensities = calculate_propensties()
    alpha = propensities.sum()
    r = rand()
    # Compute the time until the next event takes place
    tau = (1/alpha) * log(float(1/r))
    t += tau
    # Compute which event takes place
    transition_node, transition_type = select(propensities)
    # Update node states and data series
    update_states(transition_node, transition_type)
```

On Hodonin there are 4500 events per day on average. So propensities are recalculated 4500 times every day.

2.2 Experimental *"daily"* implementation

```
t = 0
todo_list = []
while True:
    propensities = calculate_propensties()
    alpha = propensities.sum()
    r = rand()

    # Compute the time until the next event takes place
    tau = (1/alpha) * log(float(1/r))
    t += tau

    # Compute which event takes place
    transition_node, transition_type = select(propensities)
    todo_list.append((transition_node, transition_type))

    if day_changed:
        # Update node states and data series
        for transition_node, transition_type in todo_list:
            update_states(transition_node, transition_type)
```

The second implementation is much faster, now waiting for results on Hodonin to be able to compare the two implementations.

Implementation hack: Append to todo_list is done only if node is not yet in todo list (node can change state only once per day). I.e. if (node_5, (S->E)) and (node_5, (S->S_s)) are selected during the day, only the first one is considered. It is not possible to do both, because node_5 is no more in state S, the second transition is not applicable.

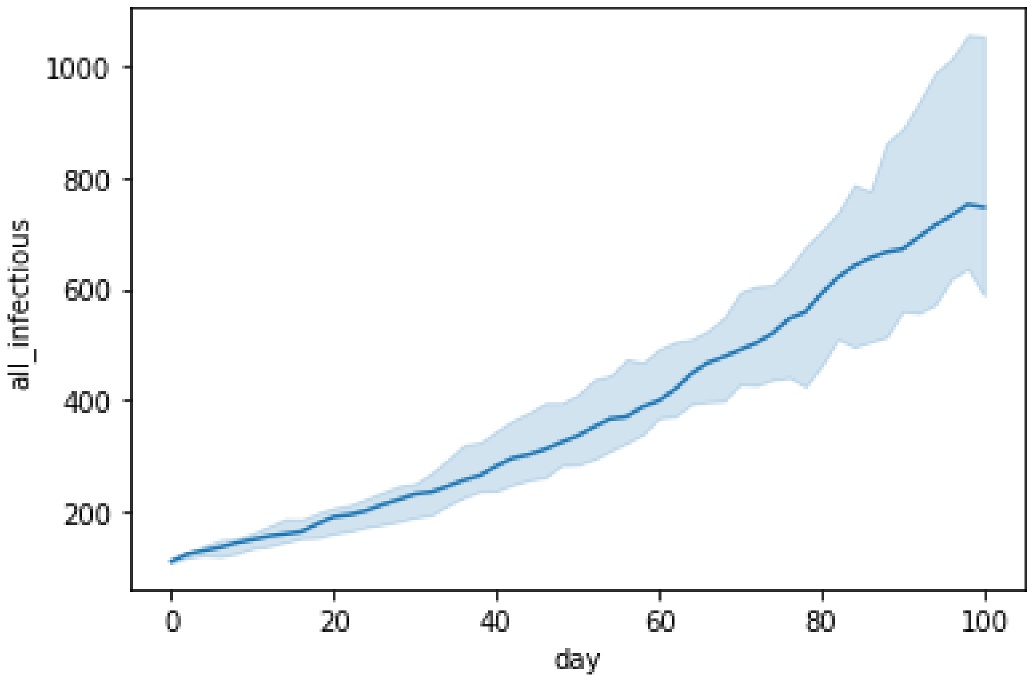
2.3 Final sequential implementation

Iterates in days, and each day for each node decides to which state it moves (including current state).

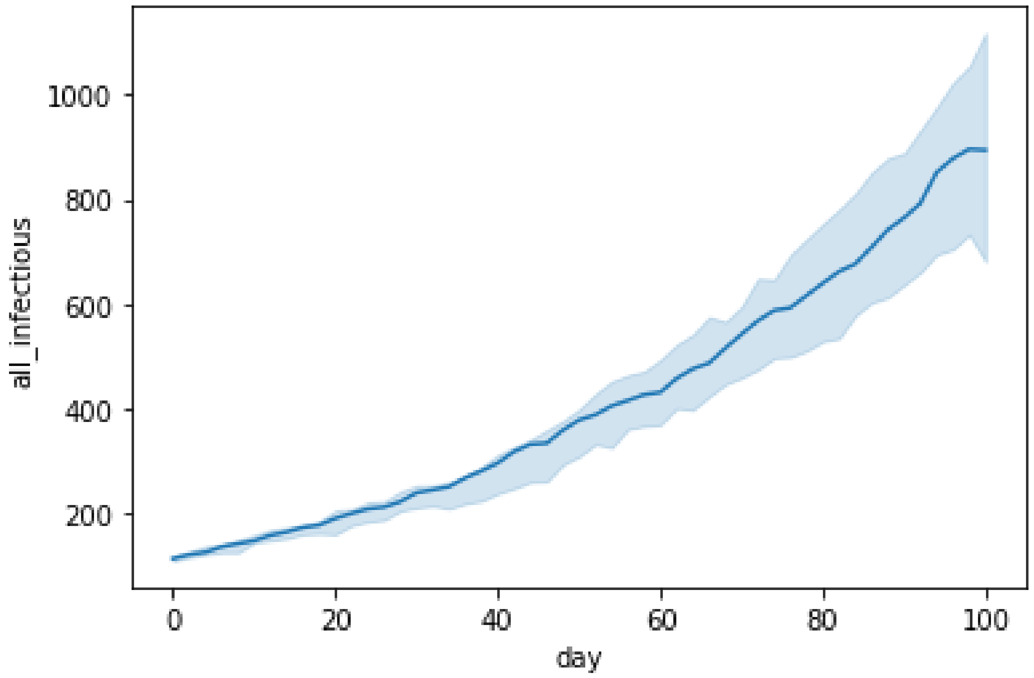
```
for t in 1, ... , T:
    propensities = calculate_propensities()
    # for each node select one action (including X->X) based on propensities[node_id]
    trainsitions = select_transitions(propensities)
    # update node states according selected transitions
    update_states(transitions)
```

2.3.1 Difference between original implementation and daily implementation

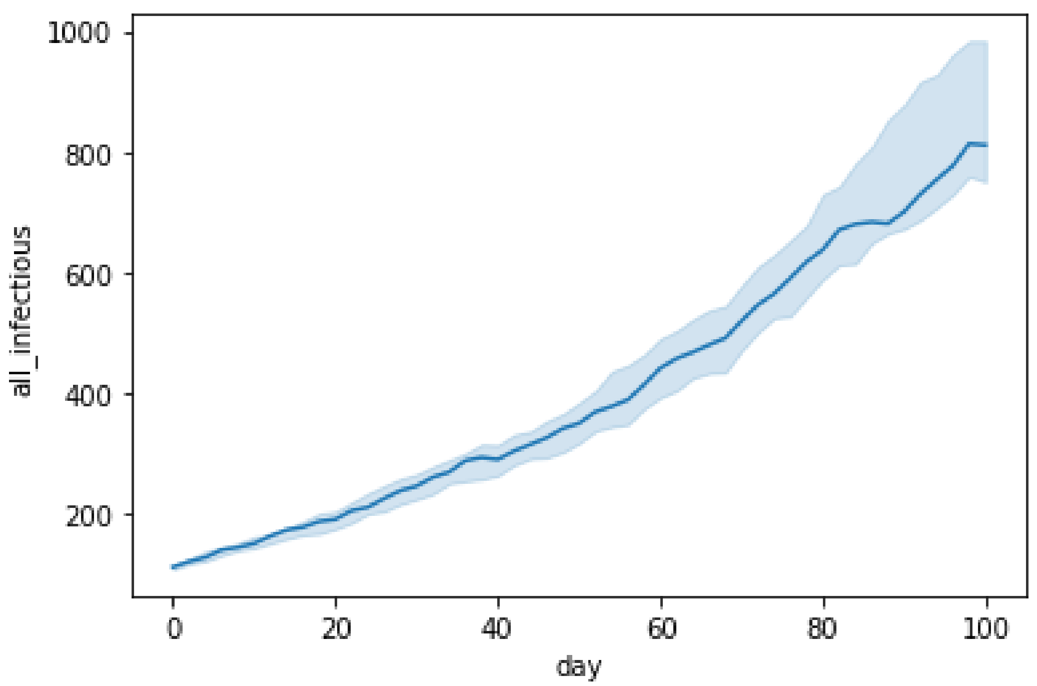
With policy function (detected nodes go to quarrantine): (top original, bottom



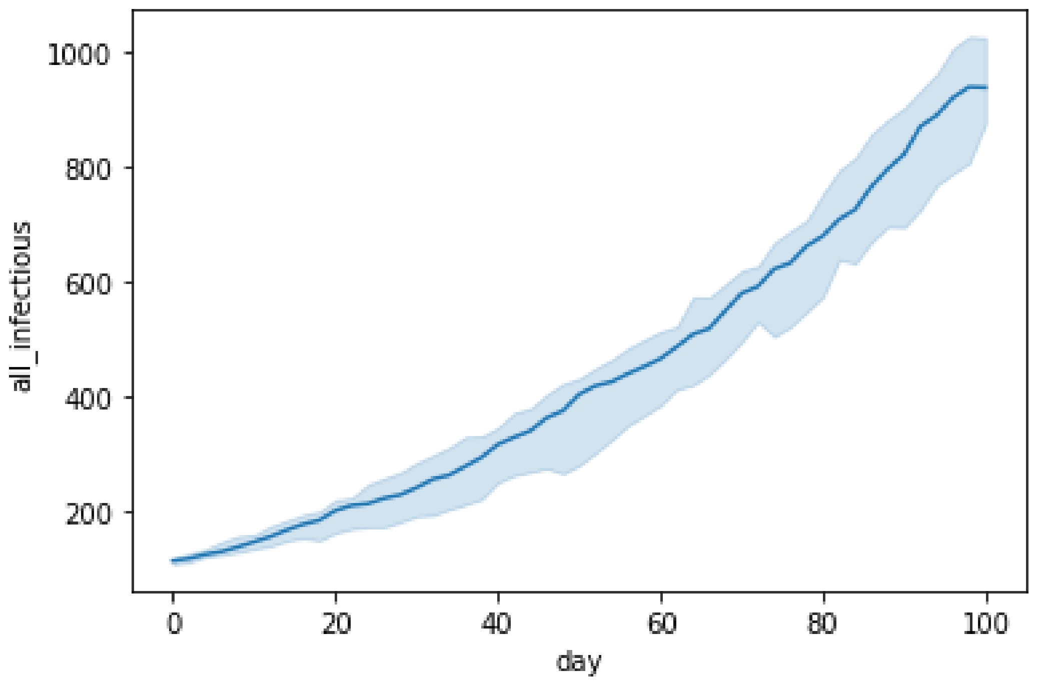
daily)



With no policy function (no quarrantine): (top original, bottom daily)



all_infectious
day



all_infectious
day

```
[ ]:
```