LIFE DATA EPIDEMIOLOGY

Study of the influence of the time structure in a network for sexually transmitted diseases spreading and vaccination

Agostini Federico, Bottaro Federico, Pompeo Gianmarco

University of Padua

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Contents

Introduction

- Data from growing Brazilian online community of sex buyers and sellers (studied by Rocha in 2010)
- We have at disposal node identification numbers and times of their activations: 16500 nodes in about 2200 days

GOAL

Study of the influence of the time structure in a network for sexually transmitted diseases spreading and vaccination

Activation

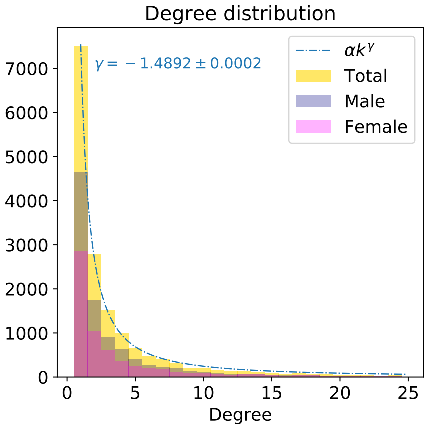
By **activation** we take the time a feedback post is uploaded in the forum by either the seller or the buyer $\rightarrow$ inevitable lack of resolution!

Analysis outline

Initial hypotheses: (1) bipartite network but no distinction between males and females; (2) no costraint to specific diseases

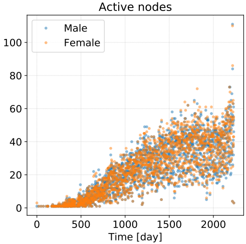
We consider our network from two complementary standpoints:

- **static network**, also known as *aggregated*, in which the time dimension is compressed: all nodes and links are present at once (418 connected components)

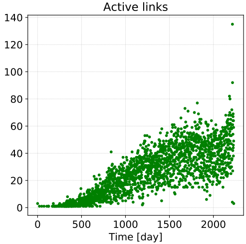


Analysis outline

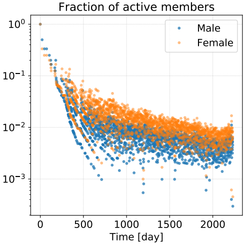
- **temporal network**, made of a sequence of networks organized according to a predefined order



Active nodes

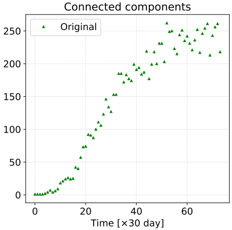


Active links



Fraction of active nodes

It is possible to follow the time evolution of the community, which remains greatly sparse: intrinsic effect of pair interaction?



We briefly present the main analysis tools employed

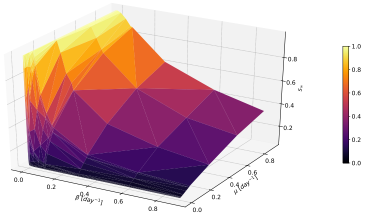
- `networkX` package used to characterize the properties of and to manipulate the networks we are working with
- `EoN` package for dynamics studies on networks: efficient epidemiological simulations
- `fast_SIR` at each iteration the script creates a priority queue of transmission or recovery events; the earliest event is performed and if it is a transmission one the queue is updated. Similarly for SIS

We fix $x_0 = 0.005$, so fraction of initial infected is 0.5% of the total population

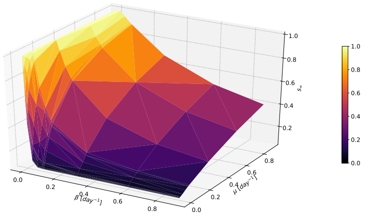
Grid search on β and μ

Study of the behaviour of s_∞ as function of β and μ for the values $[1, 3, 6, 9]$ at orders of magnitude $10^{-4}, 10^{-3}, 10^{-2}, 10^{-1}$. For greater β, we have less susceptibles, for greater μ we have more: the behaviour of the network is more or less the same for both models.

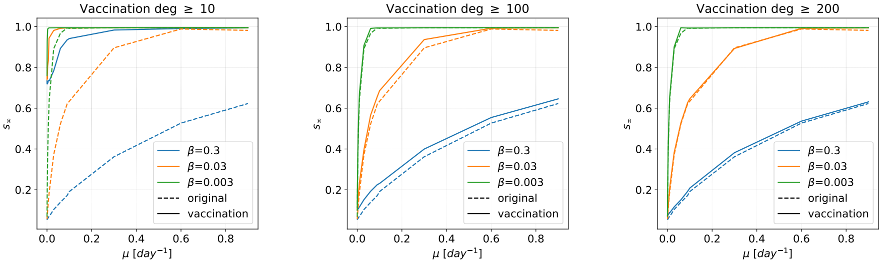
SIR



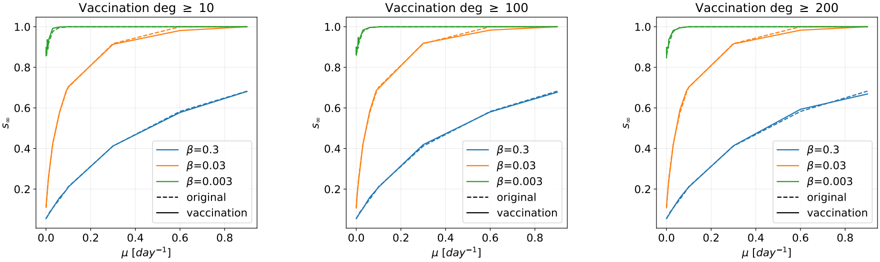
SIS



For SIR, straightforward vaccination of nodes with degree greater than 100 and 200 does not produce a noticeable effect → related to the huge number of connected components wrt total number of nodes



In the case of SIS, little effect in any case.
This could be explained by the fragmentation of the network and the absence of a recovered state.



Temporal Network

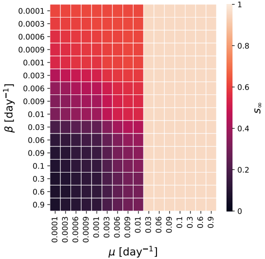
Simulations

- Aggregated in time windows of 30 days, with periodic boundary conditions (restarting at regime)
- Code written in pure Python, without using any specific library other than `networkX`
- Syncronous update + probabilistic simulation
- SIR and SIS models, studying the $\beta - \mu$ plane with a grid search (as before)

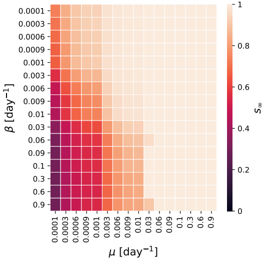
Temporal Network

Grid search in SIR/SIS

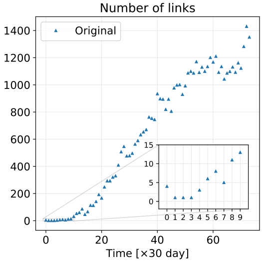
SIR



SIS



Number of links

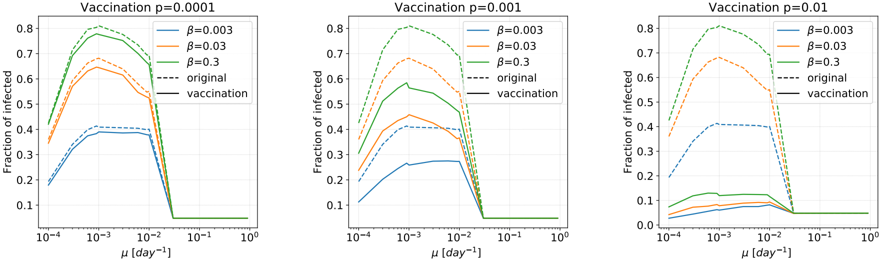


Results of the simulations

For both the models, we have that there is a clear change in the behaviour around $\mu \approx 0.03$ (more visible for SIR): limited number of links present in the early stages

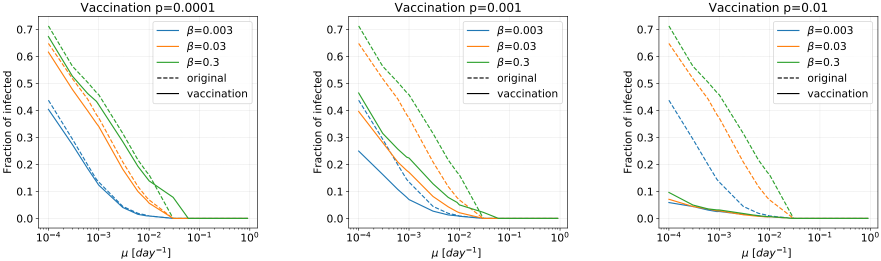
Temporal Network
Vaccination – SIR

Vaccination strategy: whenever a node activates, it has a probability to be removed from the network → information about time flow is preserved



Plots represent the number of people that got the disease. We notice that applying a vaccination technique based on the number of activations of a node can help to reduce the spreading.

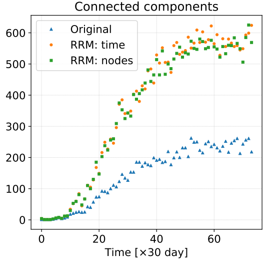
Temporal Network
Vaccination – SIS

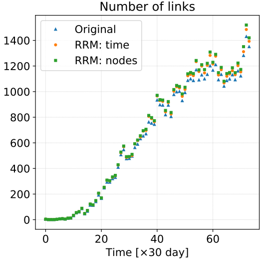


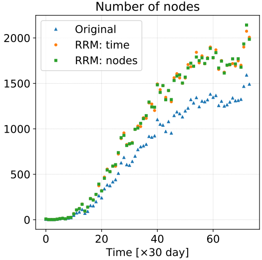
Plots now represent the number of infected at equilibrium.
Also in this situation, this vaccination approach appears to be more efficient

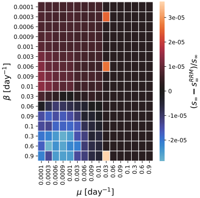
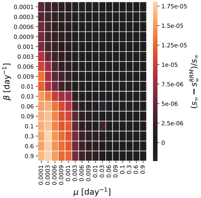
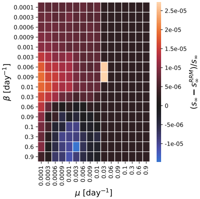
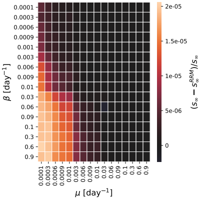
Two RRMs are tested in order to compare the spreading of the epidemic with the original one

- RRM_1: time sequence is shuffled
- RRM_2: node lists are randomized



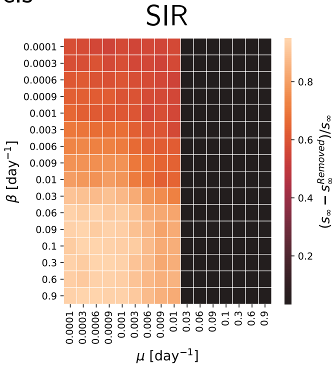


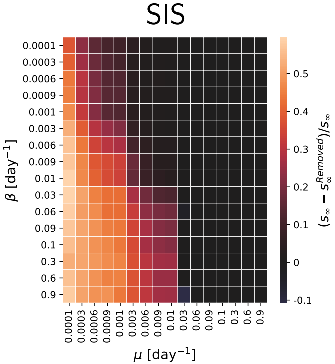


	SIR	SIS
RRM time		
RRM nodes		

From the heatmap it emerges that the RRM models do not change the behaviour of the network in disease transmission $\rightarrow$ it happens basically "at random"

Removal of nodes with less than 5 activations: more spreading for both models





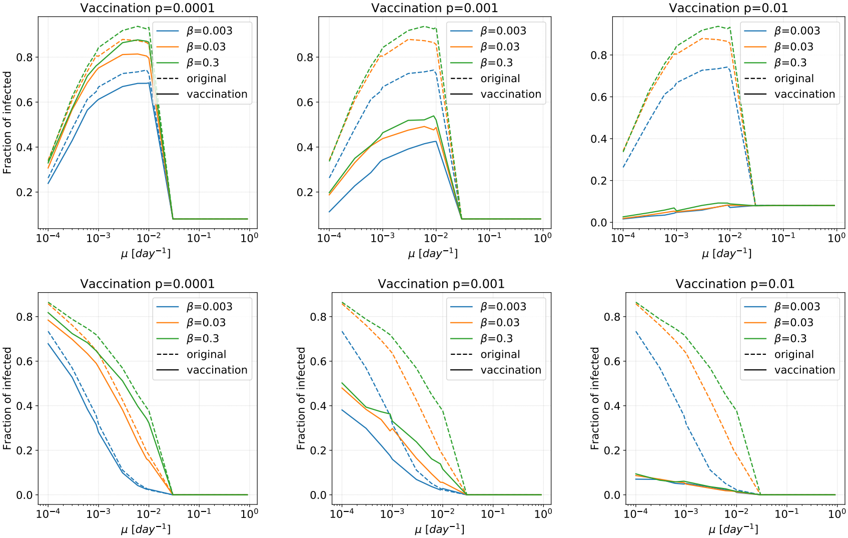
$\Rightarrow$ in general, lower s_∞, so broader spreading

Manipulative Analyses

Removal of bystanders - Vaccination

SIR

SIS

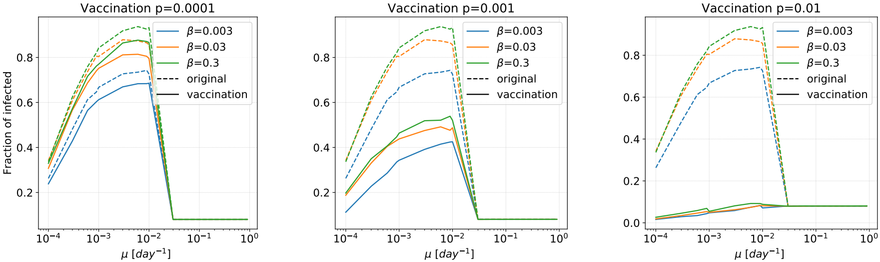


Conclusions

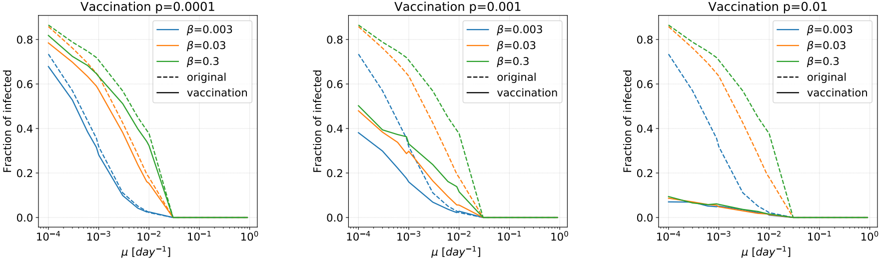
- The time dimension increases complexity and it allows for richer descriptive tools
- The presence of a critical recovery time emerged in a SIR model with time dimension; vaccinations appeared to be more effective by several % points
- Extreme sparsity of our network was a limitation in the analysis: few significant results: need to try different social structures?

Thank you for your attention

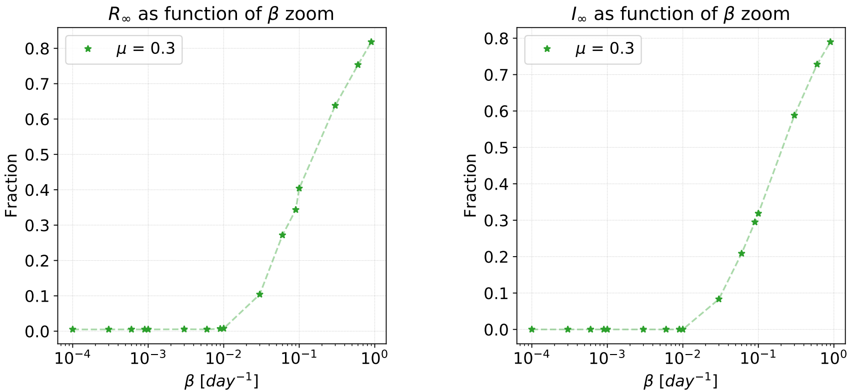
Vaccination on network without bystanders
SIR



Vaccination on network without bystanders
SIS



Critical values for β in aggregate network



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