

# 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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- 4 Manipulative analysis

- 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 activation: 16000 nodes in about 2200 days

## GOAL

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

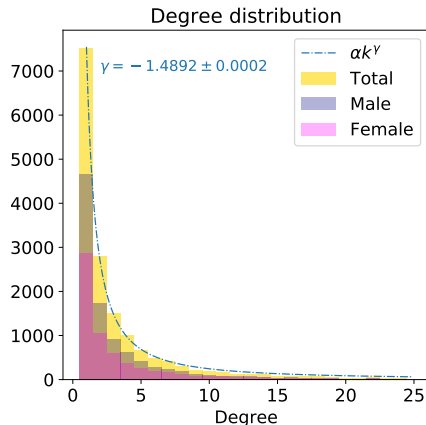
### Activation

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

# Context and hypothesis

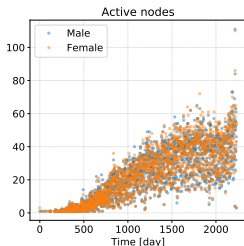
We consider our network from two complementary standpoints:

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

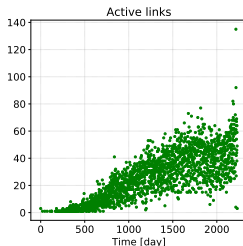


# Context and hypothesis

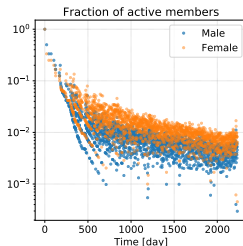
- **temporal network**, made of a sequence of networks organized according to a predefined order



Active nodes

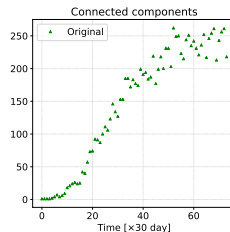


Active links



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 throughout.

`networkX` package for network manip is a package for the creation, manipulation and study of the structure, dynamics, and functions of complex networks

`EoN` package for epidemiological simulation on network (Joel Miller and Tony Ting)

`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. Similar for SIS

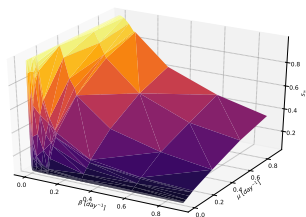
# Static Network

## SIR/SIS grid search

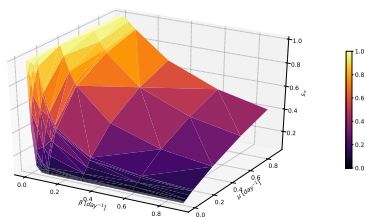
### Grid search on $\beta$ and $\mu$

We study the behaviour of  $s_\infty$  as function of  $\beta$  and  $\mu$  for the values  $[1, 3, 6, 9]$  at the power  $10^{-4}, 10^{-3}, 10^{-2}, 10^{-1}$ . As expected for a greater  $\beta$  we have less susceptible and on the other hand for greater values of  $\mu$  we have more susceptible. In all the simulation we fix the fraction of initial infected to 0.5% of the total population. The behaviour of the network is more or less the same for both the model.

SIR

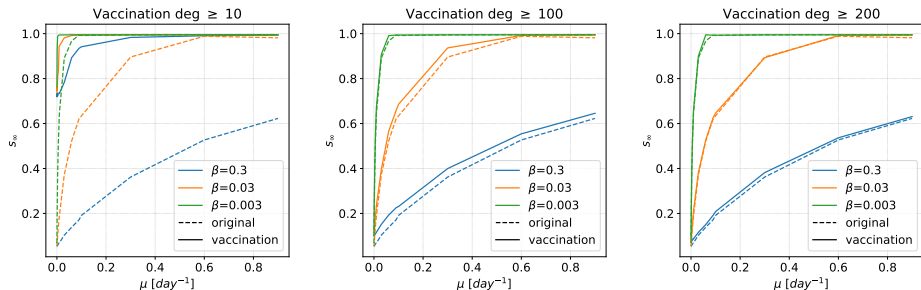


SIS



# Static Network

## Vaccination SIR

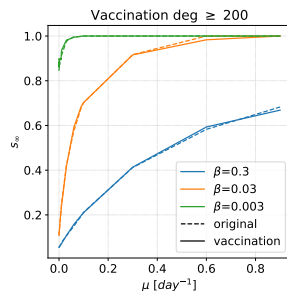
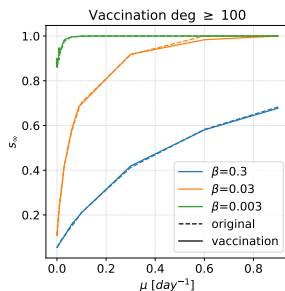
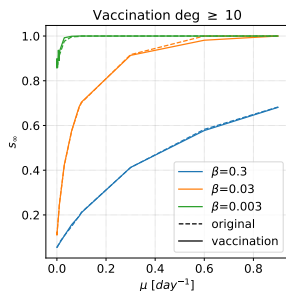


From the plot we get that the vaccination excluding all the nodes with degree greater than 100 and 200 does not produce a noticeable effect. This could be related to the huge number of connected component of the network with respect to the total number of nodes.



# Static Network

## Vaccination SIS



In this case we have that also with the removal of nodes with degree greater than 10 we cannot see any effect of the vaccination. This could be explained due to the fragmentation of the network and the absence of a recovered state.

# Temporal Network

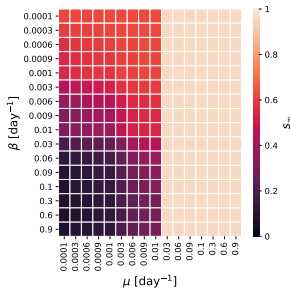
## Simulations

- 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
- Synchronous update, probabilistic simulation
- SIR and SIS models, studying  $\beta/\mu$  space with a grid search (as before)
- Vaccination strategy: whenever a node activates, it has a probability to be removed from the network

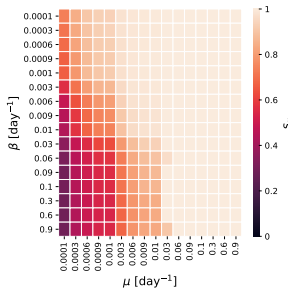
# Temporal Network

## SIR/SIS grid search

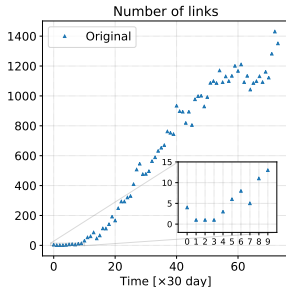
SIR



SIS



Number of links

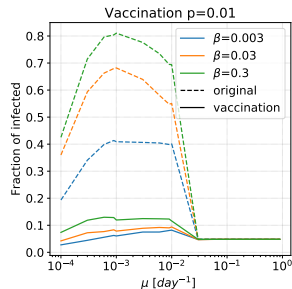
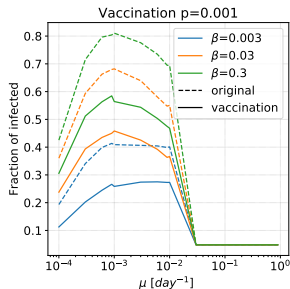
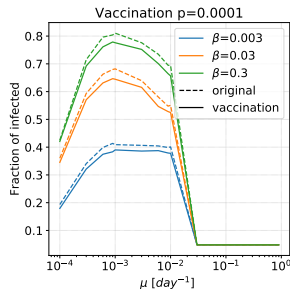


## Results of the simulations

For both the models, we have that there is a clear change in the behaviour around  $\mu = 0.03$  (more visible for SIR): it could be explained due to the limited number of links present in the early stages.

# Temporal Network

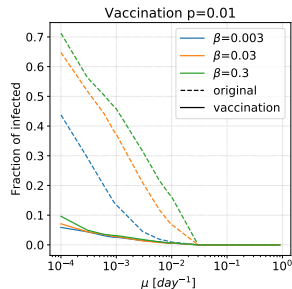
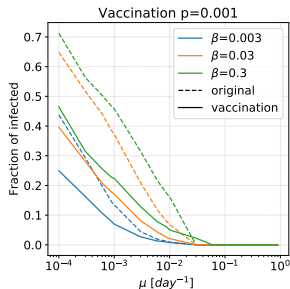
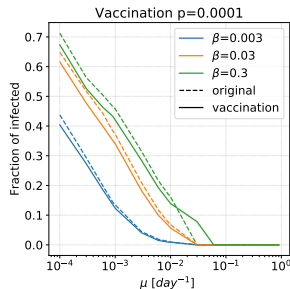
## Vaccination SIR



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



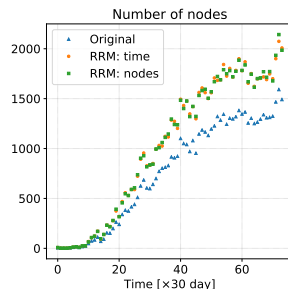
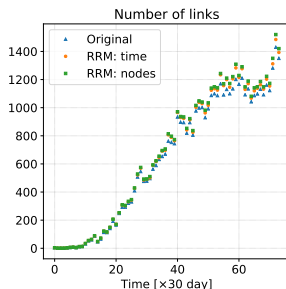
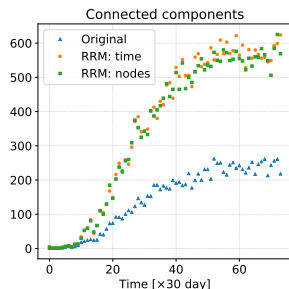
Plots represent the number of infected at equilibrium.

Also in this situation we have that the same vaccination technique results in a efficient method to reduce of the spreading.

# Manipulative Analyses

## Random Reference Models

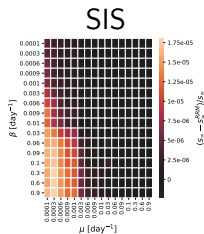
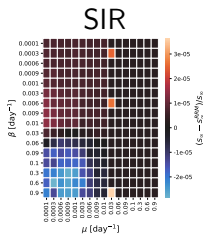
Two RRM are tested in order to compare the spreading of the epidemic against the original one. In the first one the time sequence is shuffled, while in the latter the nodes are randomized.



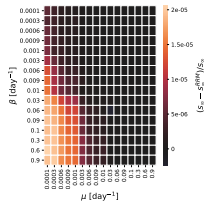
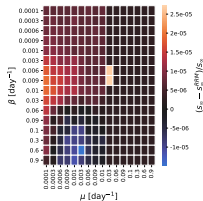
# Manipulative Analyses

## Random Reference Models

RRM:  
time



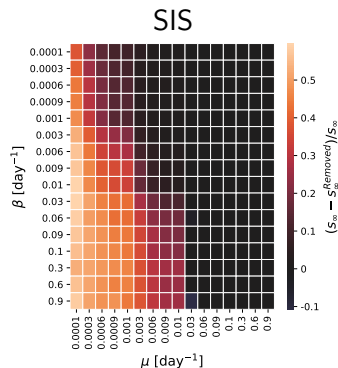
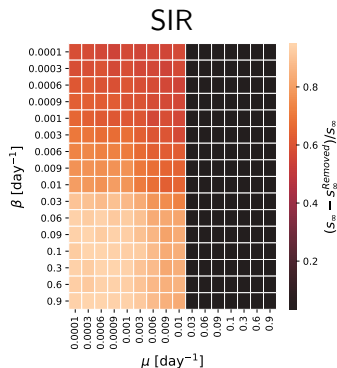
RRM:  
nodes



From the heatmap it emerges that the RRM models do not change the behaviour of the network in the field of the transmission of disease.

# Manipulative Analyses

## Removal of bystanders



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

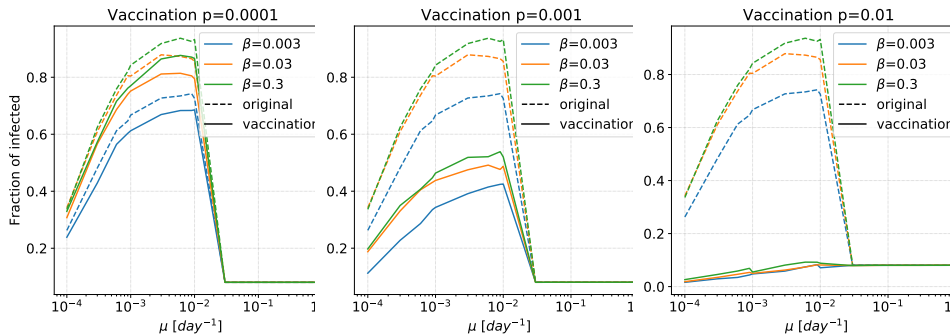
→ in general, lower  $\infty$



- 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 %
- Extreme sparsity of our network was a limitation in the analysis: few significant results: need to try different social structures?

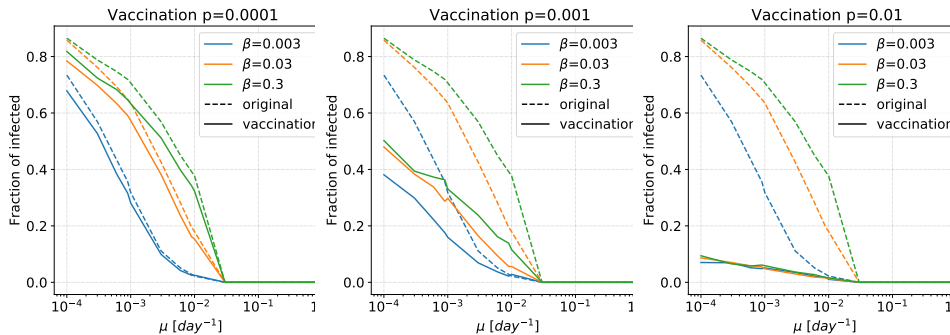
Thank you for your attention

# Vaccination on network without bystanders




# Vaccination on network without bystanders


## SIS





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