**INTERESTING STUFF**

Usually, to model a disease like covid-19, a SEIR model is used. This is done because it is a class of illness where there is a certain delay between when a person is exposed to the virus and when it becomes infectious.

In the model developed in the present work it is preferred a simpler compartmental class. It is in fact considered a SIRS. The population can be only in one of three categories, instead of the four that there are in the SEIR model. This is due to the choice of have less compartments in the epidemiological layer because it can make more significant the combination with the effects deriving from the behavioural epidemics. The work of \cite{ Dehning\_2020} shows how a SIR model can be used effectively to model the first phases of covid-19.

In the first phases of development of a new epidemic, so when there are small quantities of data available, a large statical and systematic error affect a dynamic model. According to this initial statant they use a simpler model. Because with this it is possible to evaluate better, effectively constraint, each of the chosen parameters. A modification to the standard SIR that they done is the introduction of a delay value D. It is a time between the new infection and the newly reported cases. With this parameter they include the incubation period and a delay between when a person become and when is tested positive to the disease.

In the absence of external control or behaviour modification in the population, the evolution of a disease using a SIR or SIRS model is done assuming that the number of infected individuals change due to a constant spreading rate.

**MODELS INTRODUCTION**  
   
~~In order to develop a multi-layer network, with a epidemiological substrate joined to a behavioural one, a first study of the dynamics of both layer separately is performed and now presented.   
In this section we describe the developed SIRS epidemiological model and then a Careless, Complaint, Against behavioural model. A sensitivity analysis is also implemented. A good comprehension of the underlying dynamics of each graph is crucial. With this is possible to better understand the dynamic deriving from the multi-layer structure.~~

**DESCRIPTION OF THE SIRS EPIDEMIOLOGICAL MODEL**

%% Primo spezzone, sotto c’è il secondo li unisci, correggi integri e hai fatto.

The choice of a SIRS model is done because it is suitable with the characteristics of the hypothesized disease. It is considered interesting the possibility of reinfection. After a certain amount of time, the immunity gains with having recovered from infection fades away. It is the case with influenza cases or virus like covid. Another possibility causing reinfection is the development of virus variants. Viruses are formed by genetic materials and can change their genetic structure with several mechanism. When a new variant developed can elude the immune system of the attacked host, generating a new infection.   
Using this reinfection mechanism, it is possible to observe cycles of reinfection in the population. It is a documented phenomenon, initially studied for influenza CITA. Here, every two years there is a new peak of infected in the population.

The other parameters considered in the definition of SIRS+D model are:

* $\beta$ coefficient, the infectivity rate;
* $\gamma$ coefficient, the rate of infection duration in $d^{-1}$;
* $\omega$ coefficient, the rate of becoming again Susceptible;
* $\delta$ coefficient, the rate of excess in mortality caused by the infection.

The last coefficient, $\delta$ is initially neglected. It is preferred to study the network without, using the assumption that there is a natural balance between newborn and death. Therefore, the population number is considered constant.

The initial simulations are performed varying the coefficients value. It is done to observe how the combination of the various rate can condition the SIRS model. The observed properties are:

* Composition at infinite time of each compartment, S, I or R. This is the equilibrium state of the system.
* Number of peaks in the infection.
* Time between each infection peak.
* Rise-time of infection

FARE la simulazione e descrivere qualcosa.

*Simulation with a variable $\beta$ coefficient*

In the simulation performed with fixed coefficient value for $\beta$ there are several peaks, but with a decreasing magnitude. Trying to simulate a scenario in which the $\beta$ coefficients can create a different situation. A first experiment is done simulating a simple central government controller. The number of infected is the parameter observed, and if a certain threshold is reached, a lockdown measure is implemented. The consequences of this are a modification in the infectivity ratio, reducing it. When the number of $I$ returns lower of the alarm value, the lockdown can be removed. An additional condition imposed is that the $\beta$ can be modified only after a certain period.   
With this scenario, it is observed a periodicity in the peaks for the epidemics.

QUA SIMULARE con dei dati interessanti per magari ottenere una situazione simil influenza con picchi ogni due anni.

%%%%%%%% SECONDO SPEZZONE DA UNIRE E INTEGRARE AL PRIMO

$\beta$ is the transmission rate parameter for person-to-person

contact, $\gamma$ is the recovery rate, $\delta$ is the rate at which

immunity recedes following recovery, and $R(t)$ is the recovered

fraction of the population

To describe the epidemic evolution a SIRS model is implemented. It is an extension of the most famous SIR. Its main addition is the possibility for individuals to become again susceptible after a certain period of time beyond the end of the infection. The choice of a SIR-like model is done because they are well-known as capable to describe disease like the COVID-19 CITA. From an epidemiological point of view, an "Exposed" compartment will be very suitable, to describe better the evolution of the disease. In fact, in this class of infections, after the contact with an infectious there is a certain period of incubation before the development of symptoms and contagiousness. Nevertheless this compartment was not insert in the model, because it was demonstred CITA, that also a more simple SIR can be able to model correctly the disease. In this case for realise a better fit of the real data a delay in the time scale of the system can be added in the model. This delay can be considered as an extra time to ... CITA E VEDI ARTICOLO.

The possibility of become again susceptibles is added in the model, because it is considered an interesting feature in the study of a long range time scenario.

Considering the effect of people behaviour on the evolution of a disease, it is hypothesized that two keys moment of this influence can be the initial stages and after the first peak of epidimic.

All'inizio il sirs si comporterà come un modello sir normal, perchè non ci saranno abbbastanza tempo trascorso perchè le persone possano reinfettarsi. Però dopo le persone posso no reinfettarsi e la loro opinione e comportamento diventerà importante. da spiegare meglio

**DESCRIPTION OF BEHAVIOURAL MODEL**

The implemented behavioural model is composed of three compartments: Careless individuals, Complaint and Against.

At the start time of the simulation most of the population is in the Careless compartment. The hypothesis is that if a new infection developed, it is not well known and so there are little information about it. The Careless compartment is composed by people that do not know about the risk associated with becoming infected, or that have not sufficient fear of the infection to modify their normal behaviour.

As an example of this possible initial configuration consider the covid-19 in Italy. At the early stage of its development, when the disease was spreading in China it was not considered a menace for most of the population of western countries. It is seen as a disease involving a different and far country. So, when the epidemic arrives in Europe and Italy, both the population and the government did not expect it and there is an initial time delay before the countermeasures were activated.

There are then two opposite behavioural standings: Compliant and Against.

In the Compliant set there are population worried about the disease and that want to reduce their possibilities of becoming infected. Conversely, the Against is formed by a group of individuals that have anti-scientific ideas about the disease. Here are summarised phenomena like:

* Vaccine denialism;
* Misinformation diffusion;
* Refusal about existence of the disease;
* Lack of trust on doctors and government policies.

CITA LE FONTI CHE PARLANO DI QUESTE COSE

The idea of having the Against compartment is born, because specially in the early phase of a new disease diffusion, there is a lack of reliable knowledge. This documented CITA event can cause the spread of wrong beliefs in the population. It has also been demonstrated CITA that the effect of false information can eradicate, if associated with fears. The most famous example is the conviction about the possibility that vaccine against rosolioa eccettera can generate autism in child. Even if the original publication describing this effect has been scientifically disproved, this idea is still today the most popular and had caused a reduction in the percentage of vaccine population, the so-called “free rider problem”. CITA

Also, for this model a study of the evolution with different coefficient values has been performed. The rates considered in the models are the following:

* $k\_1$ influence rate between Ca and Co;
* $k\_2$ influence rate between Ca and Co;
* $\lambda\_1$ rate of leave compliant behaviour due to fatigue;
* $\lambda\_2$ rate of leave against behaviour due to fatigue.

The behaviour of the model is a lot influenced by the value of each of this parameter.  
For example if the compliant have strong influence, the equilibrium of the model will be composed by most of the population with Compliant behaviour and an Against groups that tend to zero. On contrary, the opposite group composition will be the result. However, if the fatigue due to being Against is less than the one related with being Compliant the final equilibrium can be favourable w.r.t the Against group, even if the rate of $k\_1 \ge k\_2$.   
In the end, the equilibrium at time that goes to infinite depends on comparison between the ratios that can be calculated with the formula:

\[ R\_i =\frac{ k\_i }{ \lambda\_i}

\subsubsection{Behavioural model experiment}

To better comprehend all the possible scenarios that can emerge with the behavioural model a simulation is performed. Four vectors are defined, one for each parameter of the model. A different simulation for each combination of the coefficient is then roll out. In this case the value of the parameters is kept constant.

The range of variation of each parameter is the following:

\begin{itemize}

\item $k\_1$ between $0.1$ and $0.99$  
\item $k\_2$ between $0.1$ and $0.99$  
\item $\lamda\_1$ between $1/5$ and $1/30$ $d^{-1}$  
\item $k\_1$ between $1/5$ and $1/30$ $d^{-1}$

\end{itemize}

We observe the evolution of the dynamics of all the states, and to present a summary of the effects we collect for each simulation data such as the final value of the compartment.

**DESCRIPTION OF THE BEHAVIURAL EPIDEMIOLOGICAL MODEL**

The development of an original model was an interesting travel. In the first instance an analysis of the state-of-the-art academic literature existing is performed. The main topics analysed was four:

* Opinion models;
* Behavioural models;
* Epidemic models;
* Multi-layer networks.

After having understood the focal point of each of these works the model here presented is the result of a tentative to include behavioural effect into the evolution dynamics of a disease.

A mean field structure is used. Using a model based on differential equations permits to directly implement the future evolution of each state analysed. With this approach we don’t observe the single agent situation, but an average development of both behaviour and disease.

Previously it has been described the compartments and dynamic of each of the layer involved in the network separately. By joining them, the objective is to study how they mutually interact. As an example, it is expected that a more Compliant behaviour can help in avoiding severe condition w.r.t the percentage of deaths or sick. Another interesting property too verify is the influence of Against people on the evolution of the system. How can misinformation worsen the epidemic?

From an opposite perspective, the prevalence of disease can change people behaviour. For example, the fear of becoming infected can amplify the effect of dissuasion. This can be modelled with a large rate Co-Ca rate, causing am increment in the population that is Compliant to safety rules.   
A last aspect of interest that is supposed to be observed is how strong the interaction and prevalence of the disease can influence the behaviour. To modify the conduct of a significative percentage of the population, are government’s policies necessary?

The multilayer network developed wants to be an instrument to comprehend all these possible relations. It is designed starting from two no too-complex networks to permits a clearer correlation between the combined effects of all the coefficients and groups considered.

ON MULTILAYER NETWORKS

The complex dynamic of interactions existing in the real world, develops in multiple patterns, with complicated relationships. This connection can change over time, and using the theory of multilayer systems it can improve the comprehension of such complexity. This is a more recent development of the research, the traditional network theory was revisited, to create a framework that can include multiple networks, that evolve and influence each other \cite{DeDomenico2016}.

One possible way to develop models with this structure is to imagine that each layer represents a different type of interaction. An epidemiological example is a layer in which the physical contact between people is simulated and another represents social structure, the network of relations that every person has. This case has been presented in multiple works in the last year, for example in CITA.

The dynamic realized in multiple system can be single or coupled. In the first, there is a top layer with its own dynamic evolution influencing another one. The coupled structure instead is the one in which the phenomena described in each layer evolve with the influence of what is happening in the other. There is a coupled connection with the presence of intra-layer connections.