

# Flu epidemic and Graph Network

## Project Proposal

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### ABSTRACT

To complete,

### KEYWORDS

Epidemic modelling, Model prediction, Pandemic influenza, SIR, Graph Network

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## 1 INTRODUCTION

The project aims at modelling an epidemic with graph network and verify some theoretical results from well know papers in epidemiology. To model an epidemic, we will focus on the well known SIR model from Kermack and McKendrick [2], implemementing on a graph network and generating Monte Carlo simulation to check theoretical results built on SIR model. To check the different theoretical model from literature, we will use data from Flu epidemic in the United State during 2016-2017 season.

Flu can be model only on one season because this epidemy occurs mainly during winter (Figure 1).

## 2 SIR MODEL

The SIR model is a comportmental model in epidemiology and serve as a base mathematical framework of the main paper in this area. It's help understanding complex dynamics of the spread of desease.

The model splits the population into three categories :

- (1) Susceptible: (denoted by S). The number of people from the population susceptible to be ill. Then vaccinated people are not susceptible.

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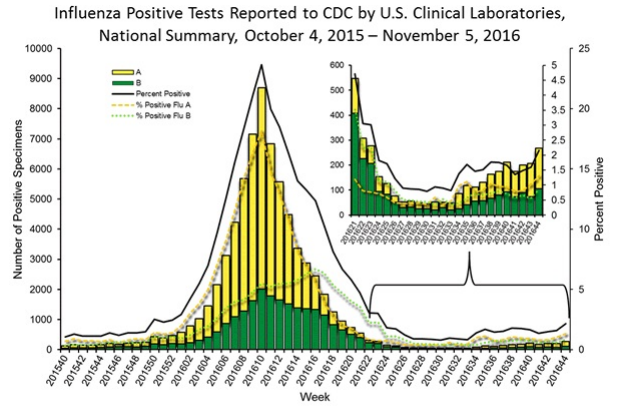


Figure 1: Flu positive test over 2016-2017 in the U.S

- (2) Infected: (denoted by I). The number of people from the population infected.
- (3) Recovered (denoted by R) the number of people from the population recovered and immune.

The dynamic of these tree variables over time can be expressed by the following differential equations:

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta IS}{N} \\ \frac{dI}{dt} &= \frac{\beta IS}{N} - \frac{I}{\lambda} \\ \frac{dR}{dt} &= \frac{I}{\lambda}\end{aligned}$$

$N$  is the number of people in population. We assume that the population is constant over time because the dynamic of death and birth is often slower than the dynamics of Flu. Then :

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

$\beta$  is the incidence ratio. Then  $\beta IS$  is the number of people from susceptible to infected during  $dt$ . We can expressed  $\beta$  as the product between the number of people met during  $dt$  time the probability than a infected person transmits the virus to someone else.

$\lambda$  is the average number of days a person is ill. Then  $\frac{I}{\lambda}$  is the flow from infected people to recovered people.

### 3 MODEL OF FLU EPIDEMY WITH GRAPH NETWORK

Our goal is to test three models from literature and check if they are fitted to model flu

#### 3.1 Pastor-Satorras and Vespignani (2001) [3]

First, the model has exponential distribution. The first result from this paper is when  $\beta_0 k \lambda s_0 > 1$  then the network will reach steady state in which  $I(t) > 0$ . Then we want to check if this result can be apply with flu epidemic.

Second, the edge distribution follows a Power-law degree.  $(P(k) k^{-\nu}$

In the same way, we want to test if flu epidemic can be modeled by Power-law degree distribution. Then, we want to apply the result from this paper to flu epidemic in the U.S. Here, the authors show that:

- for  $2 < \nu < 3$  the network will reach a steady state in which  $I(t) > 0$  for every set of parameter values.
- for  $3 < \nu$  the infection will be endemic in the network if and only if

$$\beta_0 \lambda > \frac{\nu - 1}{m\nu}$$

#### 3.2 Wang et al. and Ganesh et al., (2005) [1, 4]

Here, the authors models the network as a arbitrary network. The result from the paper is that  $\beta \lambda < \frac{1}{\lambda_A}$ , where  $\lambda_A$  is the largest eigenvalue.

#### 3.3 Watts et al., 2005 [5]

The authors use stochastic approach to model epidemic. we want to check if these approach is suited to model flu in the U.S

## 4 DATA

Our project data is focus in flu epidemic in 2016-2017 in the U.S over all states. We have gathered data from the Centers for Disease Control and Prevention<sup>1</sup> which get weekly data from flu epidemic. These data are aggregated by state and by week. A dynamic data visualisation<sup>2</sup> is also provided by the website.

The more accurate data representing flu epidemic and how many people are infected, is the number of respiratory specimens tested (the entire population) and the number positive for influenza types A and B from this population. This data are collected by American laboratories<sup>3</sup>

Besides, we need the vaccinated ratio among population. The Centers for Disease Control and Prevention gives this ratio over week, by state and by age group.

Finally, we have determined some parameters:

- $\lambda$  the number of days a people is ill is set at 2 weeks.
- $\beta$  is the product between the number of people met during  $dt$  time the probability than a infected person transmits the virus to someone else. Then the number of people met during

<sup>1</sup><https://www.cdc.gov/flu/>

<sup>2</sup><https://gis.cdc.gov/grasp/fluview/fluportaldashboard.html>

<sup>3</sup>Exclusively WHO and NREVSS collaborating laboratories

**Table 1: Frequency of Special Characters**

Non-English or Math	Frequency	Comments
$\emptyset$	1 in 1,000	For Swedish names
$\pi$	1 in 5	Common in math
\$	4 in 5	Used in business
$\Psi_1^2$	1 in 40,000	Unexplained usage

$dt$  is  $k$ , the number of edges for one nodes in the graph. We set  $p_i n f$  at 0.6<sup>4</sup>.

The last parameters to set is  $\lambda$

## 4.1 Tables

Because tables cannot be split across pages, the best placement for them is typically the top of the page nearest their initial cite. To ensure this proper “floating” placement of tables, use the environment **table** to enclose the table’s contents and the table caption. The contents of the table itself must go in the **tabular** environment, to be aligned properly in rows and columns, with the desired horizontal and vertical rules. Again, detailed instructions on **tabular** material are found in the *L<sup>A</sup>T<sub>E</sub>X User’s Guide*.

Immediately following this sentence is the point at which Table 1 is included in the input file; compare the placement of the table here with the table in the printed output of this document.

To set a wider table, which takes up the whole width of the page’s live area, use the environment **table\*** to enclose the table’s contents and the table caption. As with a single-column table, this wide table will “float” to a location deemed more desirable. Immediately following this sentence is the point at which Table 2 is included in the input file; again, it is instructive to compare the placement of the table here with the table in the printed output of this document.

It is strongly recommended to use the package booktabs [?] and follow its main principles of typography with respect to tables:

- (1) Never, ever use vertical rules.
- (2) Never use double rules.

It is also a good idea not to overuse horizontal rules.

## 5 CONCLUSIONS

This paragraph will end the body of this sample document. Remember that you might still have Acknowledgments or Appendices; brief samples of these follow. There is still the Bibliography to deal with; and we will make a disclaimer about that here: with the exception of the reference to the L<sup>A</sup>T<sub>E</sub>X book, the citations in this paper are to articles which have nothing to do with the present subject and are used as examples only.

## REFERENCES

- [1] A. Ganesh, L. Massoulié, and D. Towsley. The effect of network topology on the spread of epidemics. In *INFOCOM 2005. 24th Annual Joint Conference of the IEEE Computer and Communications Societies. Proceedings IEEE*, volume 2, pages 1455–1466. IEEE, 2005.
- [2] Kermack and McKendrick. A contribution to the mathematical theory of epidemics. *Proceedings of the Royal Society of London A: Mathematical, Physical and Engineering Sciences*, 115(772):700–721, 1927.

<sup>4</sup>explication

**Table 2: Some Typical Commands**

Command	A Number	Comments
<code>\author</code>	100	Author
<code>\table</code>	300	For tables
<code>\table*</code>	400	For wider tables

- [3] R. Pastor-Satorras and A. Vespignani. Epidemic spreading in scale-free networks. *Phys. Rev. Lett.*, 86:3200–3203, Apr 2001.
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- [5] D. J. Watts, R. Muhamad, D. C. Medina, and P. S. Dodds. Multiscale, resurgent epidemics in a hierarchical metapopulation model. *Proceedings of the National Academy of Sciences of the United States of America*, 102(32):11157–11162, 2005.