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## **Individual-Based Modeling of COVID-19 Vaccine Strategies**

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# 1 Introduction

## 1.1 What is COVID-19?

SARS-CoV-2, better known as COVID-19, is an infectious respiratory disease with influenza-like symptoms. Per April 13th, 2021, the disease has more than 136 000 000 confirmed cases and almost 3 000 000 confirmed deaths worldwide [1]. The number of infected is expected to be much higher since most countries only test people in risk groups or people who have been in contact with someone with the virus. It originated in Wuhan, China, in November or December 2019 and has spread globally, with massive outbreaks, especially in Italy and Spain in early 2020, later in the United States, and most recently in India. Most countries introduced some measures to limit spread and importation. In Norway, schools, kindergartens and universities closed on March 13th, 2020. With kindergartens reopening up April 20th, schools up to the 4th grade reopening on April 27th, 2020, and the rest of schools opening again May 11th, 2020. Other measures have been closing borders for tourists, quarantine for travelers from other countries, closing bars and restaurants, limits on the size of events, among other things.

Four different vaccines are accepted by the European Medicine Agency(EMA) and the Norwegian medicine agency. Those are the RNA-vaccines Vaccine Moderna and Comirnaty (from BioNTech/Pfizer), the virus vector vaccines Vaxzevria from AstraZeneca, and Janssen-Cilag vaccine. None of the virus vector vaccines are in use in Norway as of May 12th because of links to rare blood-clot complications, low amounts of platelets, and bleedings. The vaccines also have some less serious side effects like fever, headaches, tiredness, and pain in muscles and joints [15]. Some countries have gotten further than others in their vaccination efforts; large countries with a high degree of vaccination per May 20th, 2021 are Israel (58.1% fully vaccinated), Chile (39.5%), USA (37.3%), and the UK (30.7%). Some poorer countries are lagging in vaccine coverage, most notably India (10.4% at least one dose 2.9% fully vaccinated) and many African countries risking significant outbreaks in the near future.

Currently, there is a massive outbreak in India, Peaking at more than 400 000 new cases per day and a total of almost 4 700 000 registered cases in the last 14 days (May 6th - May 19th, 2021).

The first vaccine in Norway was administered on December 27th, 2020. By May 20th, 2021, 12.63% of the Norwegian population have received both vaccine doses, while 29.50% have received at least one of the two doses. In Norway, we have prioritized older adults and Health Care/Elderly care Workers to get the vaccine first. Estimates for when every person aged 18+ in Norway is offered at least the first dose of the vaccine varies from late July to early August for the most optimistic scenarios. More realistic scenarios point to early September.

A CDC study [2] of vaccine efficacy in health care professionals, first responders, and other essential workers shows that the mRNA vaccines reduce the risk of getting infected by COVID-19 by 80% two weeks after the first dose. The efficacy increases to 90% two weeks after the second dose, which is higher than estimates from similar studies in the UK and Israel, which show about 70 and 60 % lowered chance of getting infected after the first dose.

Vaccines make this pandemic much easier to handle if we compare it to the 1918 H1N1 pandemic (the Spanish flu) [3], where 500 million people were infected (1/3 of the world's population), and around 50 million people died. With a successful vaccination effort, it seems likely that the total COVID-19 cases will be much lower despite the world population increasing five-fold.

## 1.2 What do we investigate in this thesis?

In this thesis, we investigate vaccination strategies for COVID-19. The two strategies we are testing are (i) prioritizing old, vulnerable people and (ii) prioritizing younger people with the most contacts. We measure success by looking at the number of deaths and years of life lost (YLL) for each scenario. Other interesting aspects we could have taken into consideration are the number of infections, the length of the pandemic, and hospitalizations. Other than that, investigating the consequences of lock-downs, economic burden, and the population's physical and mental health burden could be interesting things to study.

## 1.3 Summary of methods

We use an Individual-based model (IBM), which models each individual with age and their contacts, creating a network in a community. Some individuals start with being infected and infectious, while the rest are susceptible to the disease. As time passes, each infectious individual has a chance of infecting its contacts with a probability  $p$ , and everyone that gets infected has an incubation time of three days before becoming infectious for five days. Adding a vaccine into this model makes it so the vaccinated people can not be infected or infectious and are practically taken out of the network together with the people that are recovered or dead.

## 1.4 Short summary of results

The safest and most consistently optimal vaccine strategy for COVID-19 is vaccinating the oldest and most vulnerable people first. However, there are some scenarios where vaccinating the people with the most contacts could be optimal.



## 2 Basic mathematical theory of vaccination

There are two main types of models used to model the spread of infectious diseases, Individual-based models (IBMs) and compartmental models (typically SIR or SEIR models).

IBMs are used in this thesis. These modes have become more popular recently as computers with more processing power have become available.

Compartmental models [4] were developed by Daniel Bernoulli when modelling smallpox in the 18th century, and refined by Kermack and McKendrick in the 20th century. In these models one partitions the population into compartments of susceptible, infected and recovered (SIR). In the simplest SIR-models, infected individuals infect susceptible people at a rate  $\beta$  that depends on the number of infected/infectious individuals and susceptible individuals. After infection, individuals recover at a rate  $\lambda$ . The result is a simple non-linear system of differential equations

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \lambda I \tag{2}$$

$$\frac{dR}{dt} = \lambda I \tag{3}$$

The equations describe the evolution of the infectious disease over time. There are several options for expanding the model. For instance, by introducing a new compartment, the exposed. Individuals exposed to the disease will either go back to being susceptible or become infected (This is called an SEIR model.) One can also include death rates (both from disease and natural deaths) and birth rates to the society, vaccines (taking people from the susceptible compartment to the recovered compartment). Another option is to split the compartment by age groups and to introduce social contact matrices to describe the level of social contact between different age groups.



### 3 Other studies of vaccination

Vaccination strategies for transmissible diseases are extensively studied using mathematical models. Moore et al. [5] use an SEIR (susceptible, exposed, infected, recovered) of COVID-19 model and social contact matrices to test different vaccine strategies. They considered the UK population and vaccines with varying effects. They measure both deaths and Quality Adjusted Life Years (QALYs) losses. The different vaccines they have tested are reduction in susceptibility (type 1), reduction in becoming symptomatic (type 2), and reduction in experiencing severe symptoms (type 3). They also introduce comorbidities, individuals with pre-existing conditions that make them more likely to die from COVID-19, and healthcare workers, who are much more likely to get exposed to COVID-19 than the average in the age group. For each vaccine, Moore et al. test three different vaccine strategies. The first strategy is vaccinating by age group (80+,60+,40+,20+, and the rest).

The second strategy is vaccinating by age group and including comorbidities as a separate group (comorbidities,80+,60+,40+,20+, and rest). The third strategy is vaccinating evenly across all age groups. In all scenarios, the evenly distributed vaccine leads to significantly more deaths than the other strategies. In all the scenarios, the best strategy is to vaccinate by age; when introducing comorbidities, they find that for a low level of social distancing measures, comorbidities should be put after the 80+ group for vaccines 1 and 2. For vaccine 3, they should be put after 60+, and with no social-distancing measures, comorbidities should come after the 60+ group. For all scenarios, the optimal strategy is very similar, both when considering deaths and QALYs lost. This result is expected considering the morbidity in the older age groups is much higher compared to younger age groups. When adding healthcare workers for vaccine 1, they should be prioritized after the 80+ group. At the same time, they argue that they might have lower priority for vaccines 2 and 3 because those do not significantly lower the transmission rate for the average healthcare worker. They check vaccines with different efficacies (50%,70+%, and 90%) and find that with a vaccine with 50% efficacy, they need to vaccinate 70% (all 20+) of the population in their scenario to avoid a significant second wave. In contrast, with a 70-90% efficacy, they can avoid a second outbreak with only 40%(40+) coverage.

MacIntyre et al. [6] use an SEIR model to study vaccine strategies in New South Wales, Australia. They consider both a limited supply of 1 million vaccines, and an unlimited supply of vaccines, with the capacity of vaccinating 50 000 - 300 000 people per day. For most of this study, it is assumed a vaccine efficacy of 90%. The strategies they test are: giving 1 million doses to targeted age groups (65+, 10-29 and Healthcare workers + 10-29), giving 1 million doses through ring vaccination, which requires contact tracing, and vaccination of contacts, and mass vaccination with a supply big enough for the whole population of New South Wales, with different priorities (oldest first, young people first and healthcare workers, then young people). Their findings are that vaccinating the young will significantly limit the spread of the virus compared to vaccinating older adults, but vaccinating older adults would still lead to fewer deaths since they have a much higher risk of dying from COVID-19. For ring vaccination, they tested varying success in contact tracing, 70%, 80%, and 90%, with a reduction in efficacy from 90% to 45%. They found that with a limited supply, successful ring vaccination leads to way fewer cases and deaths. With an unlimited supply of vaccines, the interesting part of the study is the speed of vaccination and vaccine efficacy. They tested 50 000, 75 000, 100 000, 125 000, and 300 000 doses per day, where 125 000 is the estimated maximum of what the health care system in New South Wales could realistically do. They find that 50 000 doses per day would lead to a significantly larger outbreak than 75 000 doses per day, and 100 000 would lead to about half the outbreak size compared to 75 000 doses per day. Varying

vaccine efficacy, with 125 000 doses per day, showed led to significant differences in results. For herd immunity they use the formula  $V_c = \frac{1}{V_e} * (1 - \frac{1}{R_0})$  with  $R_0 = 2.5$   $V_e$  is vaccine efficacy and  $V_c$  is vaccine coverage. They find that herd immunity with a vaccine efficacy of 60% they need 100% vaccine coverage, while 90% one would only need vaccine coverage of 66%.

Dubé et al. [11] use a Personal Contact Network (PCN) to study the spread of an epidemic, looking at both size and length of an outbreak and the effects of different vaccine strategies. They are looking at static networks, networks that do not change after the vaccine is deployed, and evolving networks that change as the vaccine is deployed. The vaccine strategies they looked at are random vaccination, high degree vaccination (vaccinating individuals with the most contacts), ring vaccination, and no vaccination. They tested for many different networks and found the 30 networks that give the most prolonged epidemic outbreak and the 30 that gave the most infections. The results show that for static networks, ring vaccination and high degree vaccination performs similarly in most scenarios, both significantly better than random vaccination when it comes to the length of the epidemic. At the same time, the results are somewhat inconclusive when it comes to the size of the epidemic, with ring vaccination either performing poorly or with high variance. For evolving graphs, high degree vaccination slightly outperforms random vaccination, while ring vaccination performs poorly. This result is not necessarily intuitive but can be interpreted as vaccinating too much in an area that leaves large parts of the network unvaccinated and vulnerable to outbreaks due to an evolving network.

Bubar et al. [7] use an age-stratified SEIR-model with an age-based social contact matrix to model different vaccination strategies, looking at a number of incidents, mortality, and YLL. For vaccination strategies, they tested prioritizing children and teenagers, 20-49 year-olds, 20+, 60+ and everyone evenly. For most of the study, they considered a vaccine efficacy of 90% vaccination speed of 0.2% of the population per day and the reproduction number  $R$  varying between 1.1 and 2.0. They also have a vaccine hesitancy factor making it such that a maximum of 70% from any age group is eligible to take the vaccine. With  $R > 1.2$  and vaccine speed of 0.1% and 0.2% of the population, they find that one should always prioritize older adults, while if  $R_0 < 1.2$  we could consider either the 20-49 or 20+ strategy. They also tested for different population and social contact networks in 9 different countries, with  $R_0 = 1.5$  again the 60+ strategy is optimal, while there were different optimal strategies for the different countries with  $R_0 = 1.15$ . Introducing age-dependent vaccine efficacy with decreasing efficacy at older ages reduced the effect of vaccinating older adults first. However, they still found that prioritizing 60+ still was the optimal strategy with  $R_0 = 1.5$ .

Folkehelseinstituttet (FHI, the Norwegian Institute of Public Health) has been tasked with investigating the effects of geographical prioritization of vaccines to areas in Norway with a high spread of infection like Oslo county and some municipalities in Viken county [9]. They use both individual-based models and SEIR models to check if such a strategy would be efficient compared to even geographical distribution based on population. They have considered both geographical prioritizations until everyone above 65 and healthcare workers have been offered a vaccine in the prioritized areas. Everyone above age 45 and healthcare workers have been offered a vaccine.  $R$  varies from 0.8-1.3. They also try scenarios with a new 50% more contagious disease mutation from April 1st, 2021. The results in both models with geographical prioritization to Oslo give considerably less burden of disease for large  $R$  or a more contagious virus from April 1st. The effect on hospitalization is smaller but still noticeable. The new, more contagious virus always leads to more disease, not surprisingly, as there are no new measures taken for the mutated virus. When prioritizing Oslo and Viken county, the reduction in disease and deaths is less than when

only prioritizing Oslo county, which could be attributed to it not considering the prioritization of municipalities in Viken with high infection over municipalities with low infection. When prioritizing until individuals older than 45 years and healthcare workers have been offered a vaccine, the number of deaths sometimes increases nationally, which could be attributed to at-risk groups in other places of the country having their vaccine postponed for too long.

Di Ruscio et al. [10] used an IBM to look at the spread of Methicillin-resistant *Staphylococcus aureus* (MRSA) in a low prevalence country such as Norway. They have 5 million nodes in the network; each node has an associated age, ethnic background, occupation, hospitalization status, and epidemiological status. A network of contacts is built based on the Norwegian national registry (2008-2015) and household prevalence data. Each node has a chance to get infected at time  $t$  based on whether someone infectious is nearby and based on data of chance of infection in the current setting (work, school, home, hospital, nursing home). Running the model, they found a reproduction number  $R_e = 0.68$  (95% CI 0.47 – 0.90), which means that the virus would be eradicated in Norway without importing MRSA from abroad. There will still be some outbreaks with imports, while 60% of imported cases will not spread to a single person, 2% of importations spreads to at least 50 people.



## 4 Description of the model

### 4.1 The transmission model

Our model uses a population of size  $n$  with assigned ages consistent with the age distribution in Norway. Each individual has a number of contacts determined by a random graph distribution. The random graphs are generated using a built-in routine in the Mathematica software. Our age-assignment algorithm ensures that the most contacts are in the age range 16-44 years. We start the model experiments with two infected and infectious individuals with a probability  $p$  of infecting each contact each day. Every individual that gets infected has an incubation time of 3 days where they are not infectious. After three days, they are infectious for five days, where they, for each day, have a probability  $p$  of infecting each contact for the next five days if their contacts are not yet infected or vaccinated. For each day, we calculate newly infected people; for each susceptible person  $i$ , the chance of getting infected is  $p_i = 1 - (1 - p)^n$  where  $n$  is the number of infectious contacts.

### 4.2 Modelling vaccination

A vaccine is given to a random (Poisson distributed integer) number of individuals each day. In our experiments, we vary the vaccination rate from 0.01 to 10.01 per day. We explore two different vaccination strategies. The first strategy is to vaccinate the people with the most contacts first to try to limit the outbreak as much as possible. The second strategy is to vaccinate the oldest people first to protect the most vulnerable people. We compare the number of expected deaths and the YLL. Comparing these numbers could tell us if we should prioritize vaccinating older adults first or people with lots of contacts.

### 4.3 Modelling deaths and years-of-life lost

For estimating deaths, we use the Center for Disease Controls (CDCs) data on relative probability for dying from COVID-19 [12]. These data are presented in table 1. The raw data is interpolated using a built-in interpolation function in Mathematica using the center value of each age group. We also added extra numbers at age 0 (we used 1/9 relative to the age group 18-29 years) and at age 100 (we used 1000 relative to 18-29 years). The result is the graph in figure 1. This function gives the probability for each age to die from COVID-19 compared to an 18-29-year-old, which we set this to be 0.1%. Our results are insensitive to this choice since it only scales the number of deaths by a factor and relative numbers. We run the model and record who gets infected with COVID-19 and then sum the chances of every infected person at the end of the run dying. This analysis gives the expected number of deaths. The formula for the number of deaths then becomes

$$\text{Deaths} = \sum_{i=1}^N I_i \cdot D(\text{age}_i), \quad (4)$$

where  $I_i$  is 1 if person  $i$  was ever infected and 0 if not,  $D(\text{age}_i)$  is chance of dying for a person of the age  $\text{age}_i$ , and  $\text{age}_i$  is the age of person  $i$ .

To get the expected number of years of life lost, we need the expected years of life remaining. To do this, we use the expected years of life remaining in Sweden [13], which should be similar to Norway, and the life expectancy at birth in Norway, found in table 2. We again take the center value for each age range and fit a 4th-degree polynomial to get the expected years of life left for

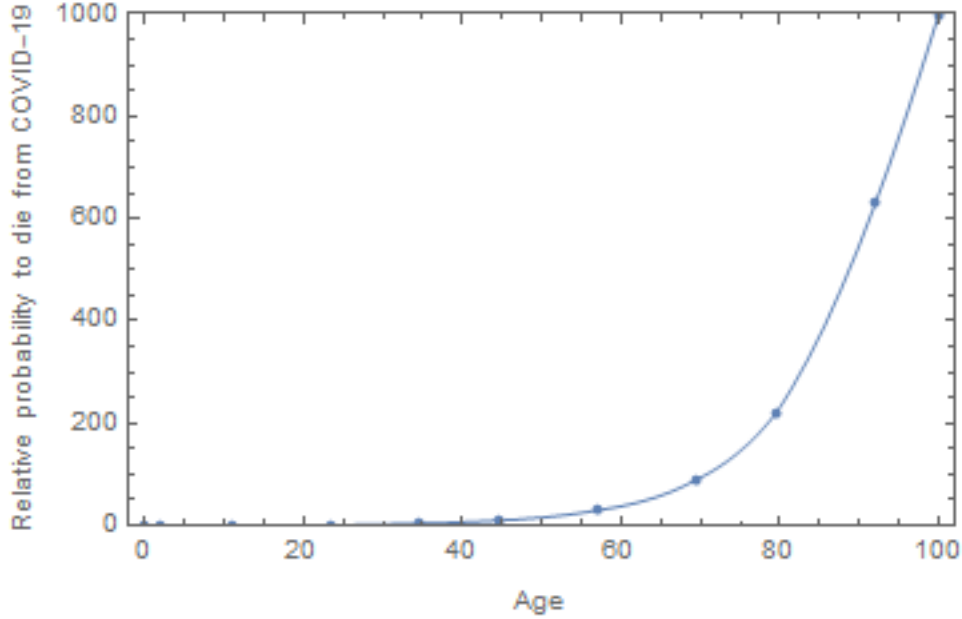


Figure 1: The relative chance of dying from COVID-19 based on age compared to an 18-29 year-old based on interpolated data from the CDC

each age, resulting in the graph in figure 2. The reason for using a 4th-degree polynomial is that we expect the life expectancy to increase the most towards the later ages; someone going from 2 to 7 years old is not going to increase their expected age drastically, but someone going from 95 to 99 years old they already exceeded their expected age at 95. Then the years of life lost for each person that gets COVID-19 is Chance of death times expected Years of life left, giving us the formula

$$YLL = \sum_{i=1}^N I_i \cdot D(\text{age}_i) \cdot LE(\text{age}_i) \quad (5)$$

where  $LE(\text{age}_i)$  is the remaining life expectancy of a person at  $\text{age}_i$ .

#### 4.4 The basic reproduction number

The basic reproduction number  $R_0$  describes how many people one infectious person is expected to infect at the start of an outbreak. We use  $R_0$  derived for IBMs in Britton [14]:

$$R_0 = p \left( E(D) + \frac{V(D) - E(D)}{E(D)} \right), \quad (6)$$

where  $p$  is the probability for an infectious person to infect a contact in a day,  $E(D)$  is the expected value of number of contacts for a person in the IBM, and  $V(D)$  is the variance in number of contacts in the IBM. This gives us a formula for  $p$  given  $R_0$ :

$$p = \frac{R_0}{E(D) + \frac{V(D) - E(D)}{E(D)}}. \quad (7)$$



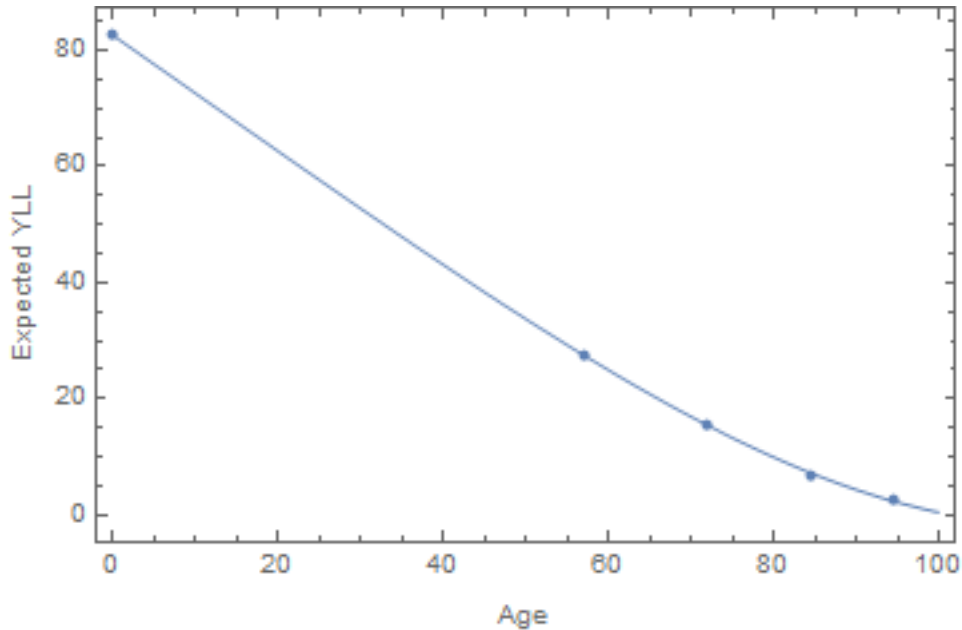


Figure 2: The expected years of life remaining based on age fitted to a 4th degree polynomial based on data from SCB

#### 4.5 Model runs

We run our model 5 times for each initial condition and find the number of deaths and YLL for each starting condition. We then find the 95% confidence intervals for different vaccine paces for each starting condition. We run it with populations of  $n = 300$  and  $n = 1000$  and  $R_0 = 1.5$  and  $R_0 = 1.15$ , vaccine pace varying from 0.01 per day to 10.01 per day, using Watts-Strogatz Graph Distribution, Barabasi-Albert Graph Distribution, Uniform Graph Distribution, and Spatial Graph Distribution.

#### 4.6 Description of network models

Our models use four different types of random graphs to generate synthetic contact networks: Spatial Graph Distributions, Barabasi-Albert Graphs, Uniform Graph Distributions, and Watts-Strogatz Graphs.

In the Spatial Graph Distribution, we have  $n$  nodes uniformly distributed on a unit square and a maximum distance  $r$  for how far two connected nodes can be apart. This set-up is well-suited for simulating families. Disease spread through these networks is slow for small values of  $r$ .

The Barabasi-Albert Graphs start with a number  $m_0$  of nodes. Nodes are added one by one, assigning new node links to the already existing nodes, with a higher probability of linking to nodes with many contacts. This set-up is well-suited for simulating highly social people in a community since they are more likely to have lots of contacts but might not describe typical family structures in the network.

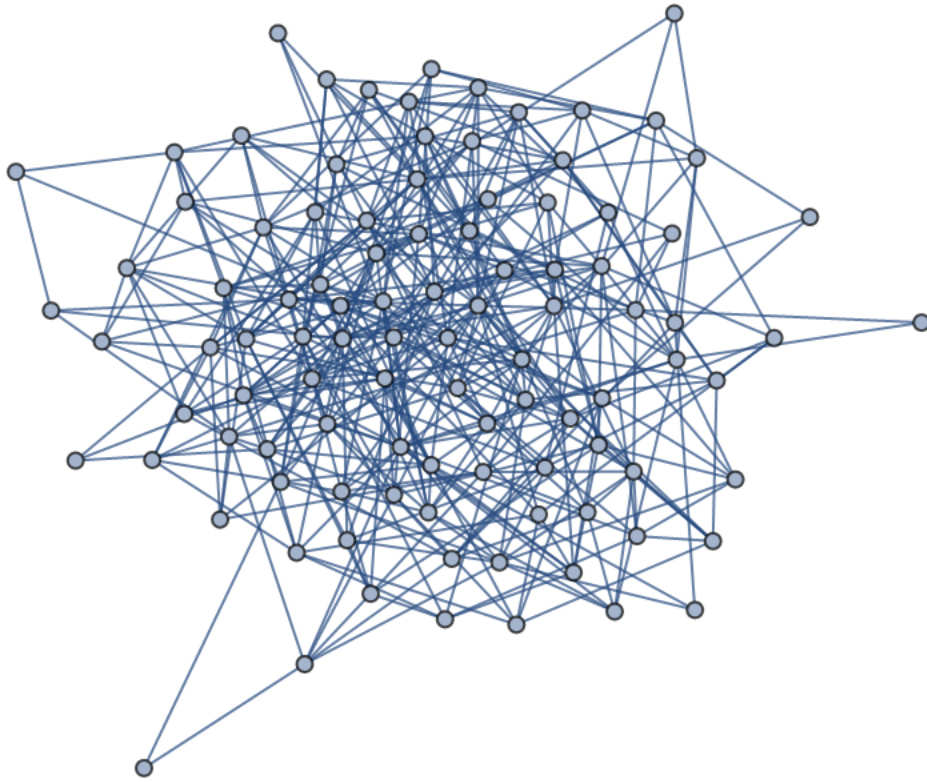


Figure 3: A population with the Uniform Graph Distribution, with  $n = 100$



Figure 4: A population with the Spatial Graph Distribution, with  $n = 100$

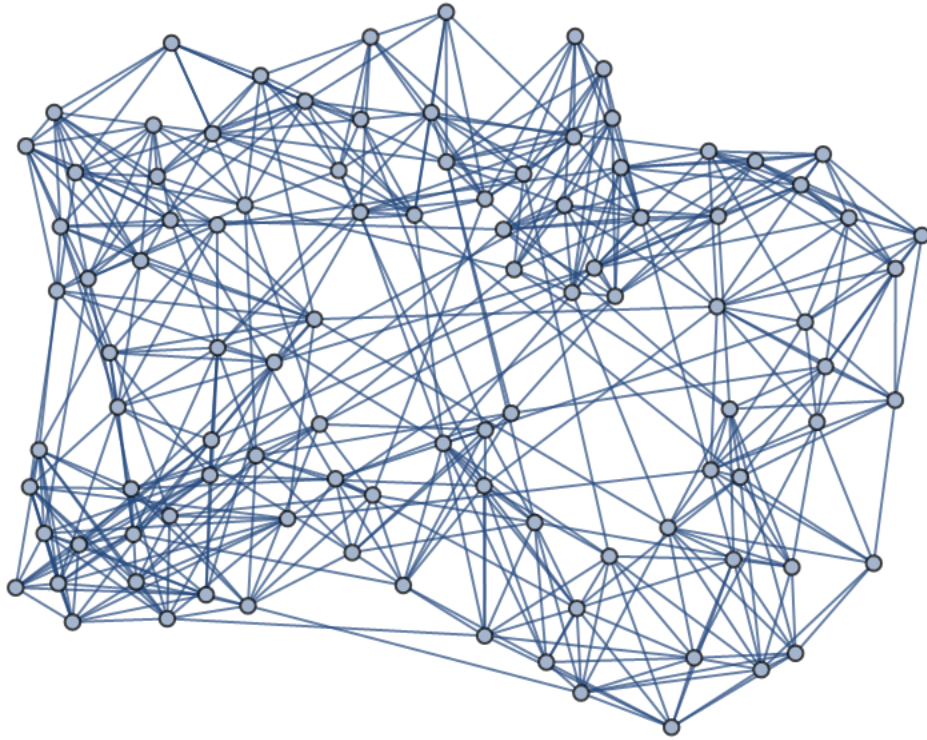


Figure 5: A population with the Watts-Strogatz Graph Distribution, with  $n = 100$

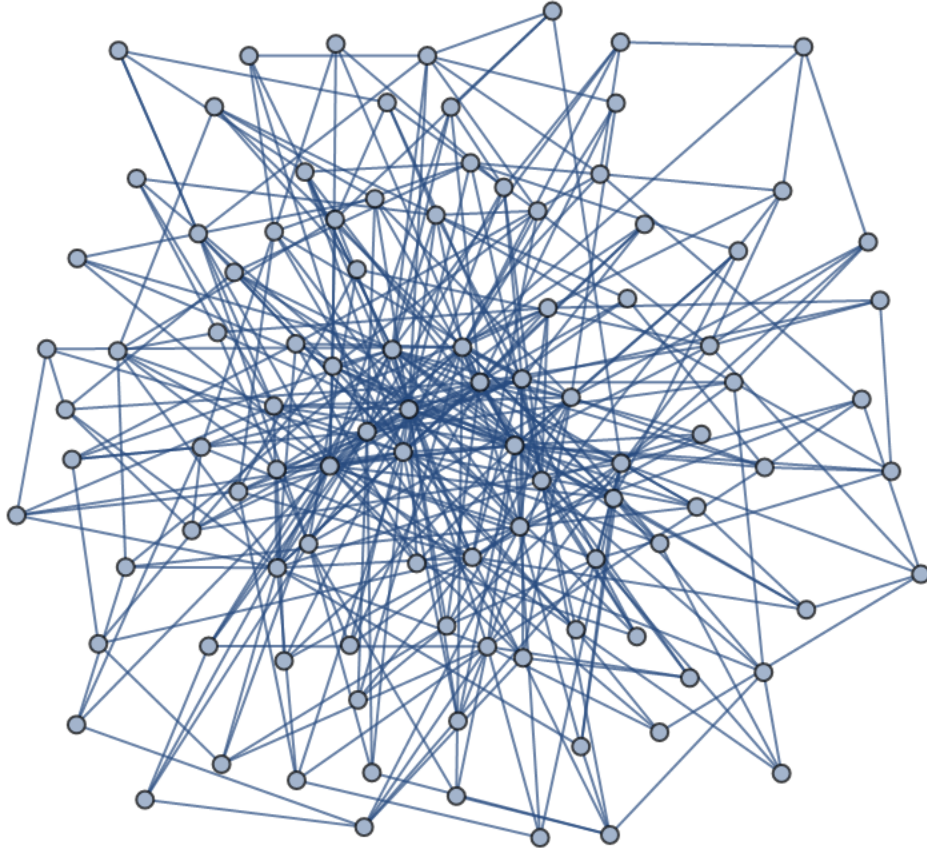


Figure 6: A population with the Barabasi-Albert Graph Distribution, with  $n = 100$

Age	Relative chance of death
0-4	1/9
5-17	1/16
18-29	1
30-39	4
40-49	10
50-64	30
65-74	90
75-84	220
85-99	630

Table 1: The chance of dying from COVID-19 relative to a 18-29 year old according to data from the CDC

Age	expected Years of life remaining
0	82.5
50-64	27.5
65-79	15.6
80-89	7.0
90-99	2.5

Table 2: Life expectancy used in this work, at age 0 is life expectancy in Norway, while the rest of the data is years of expected life left for Sweden

In a Uniform Graph Distribution, we give some  $n$  nodes and  $m$  number of total connections for the network. Every connection has an equal chance of existing.

In the Watts-Strogatz model, we start with  $n$  nodes where every node initially is connected to  $m$  nodes to the left of itself and  $m$  nodes to the right. Then we give a probability  $p$  that any connection between two nodes is broken and replaced with another random connection. This network is well-suited for simulating families if  $p$  is not too high since many groups of three or four nodes connected, with some random nodes are connected, representing schools or workplaces.

Illustrations of the different types of graphs are shown in figures 3, 4, 5 and 6.

## 5 Results

Looking at deaths and YLL for the Uniform, Spatial or Watts-Strogatz Graph Distributions with a population  $n = 300$  and basic reproduction number  $R_0 = 1.5$  (figures 7, 8 and 9) we see significant differences between the different vaccination strategies. Vaccinating older adults first is far superior to vaccinating the ones with most contacts first.

Generally, there are slightly fewer cases when vaccinating the ones with the most contacts (figures 23, 24 and 26), but not enough to compensate for the increased risk of severe disease and death in the most vulnerable groups.

Increasing the population to  $n = 1000$  and/or lowering the basic reproduction number to  $R_0 = 1.15$  does not change the results significantly (figures 11, 12, 13, 15, 16, 17, 19, 20 and 21). We can see in figures 27, 28, 30, 31, 32, 34, 35, 36, and 38 that there are generally fewer cases when vaccinating the ones with the most contacts, but again, it is not enough to compensate for the increased risk of dying from COVID-19 in the older parts of the population.

For the Barabasi-Albert Graph Distribution with a population of  $n = 300$  and basic reproduction number  $R_0 = 1.5$  (figure 10) the number of deaths is slightly higher for vaccinating the ones with the most contacts. However, the YLL is very similar for both vaccination strategies. The number of cases in figure 25 shows a significant difference for higher vaccination numbers. This difference is enough to compensate for the increased mortality of the older population.

Increasing the population to  $n = 1000$  and/or lowering the basic reproduction number to  $R_0 = 1.15$  (figures 14, 18, and 22) gives similar number of deaths. In contrast, YLL is noticeably lower in all 3 scenarios when vaccinating the ones with the most contacts. Looking at the number of cases in figures 29, 33, and 37, we see a huge drop in number of cases for higher vaccination rates, almost ending the outbreak entirely.

For the 95% confidence intervals, we see across all figures that the uncertainty is consistently smaller when vaccinating older adults first compared to vaccinating the ones with the most contacts first. This result is likely because vaccinating older adults first is aimed at protecting them, and since they have few contacts, it does not do much to stop or limit the outbreak. While vaccinating young people first aims to stop or limit the outbreak as much as possible. If it is successful in one run and unsuccessful in another, it makes the uncertainty of the strategy higher.

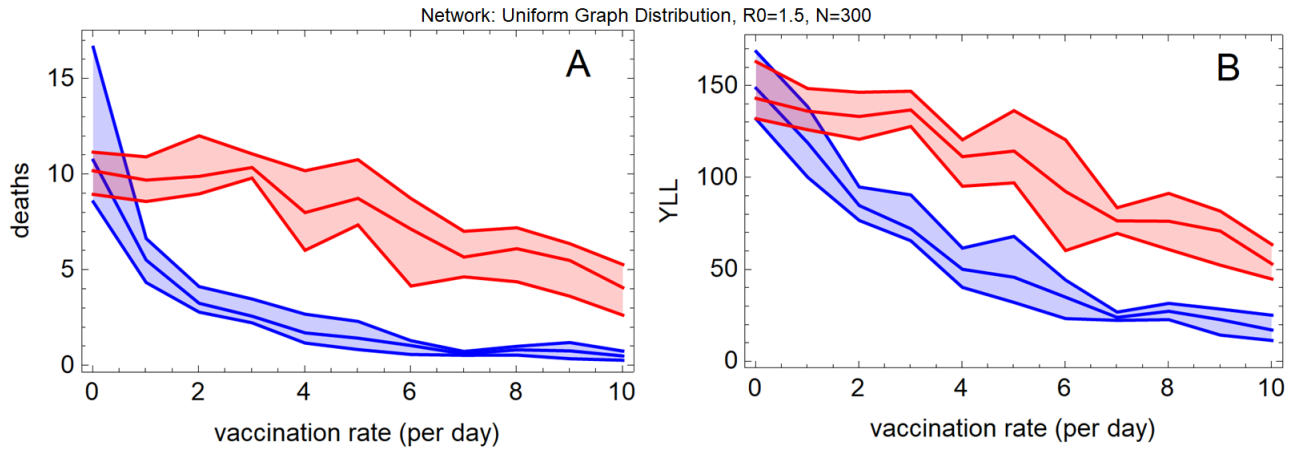


Figure 7: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Uniform Graph Distribution with  $R_0 = 1.5$  and a population  $n = 300$ .



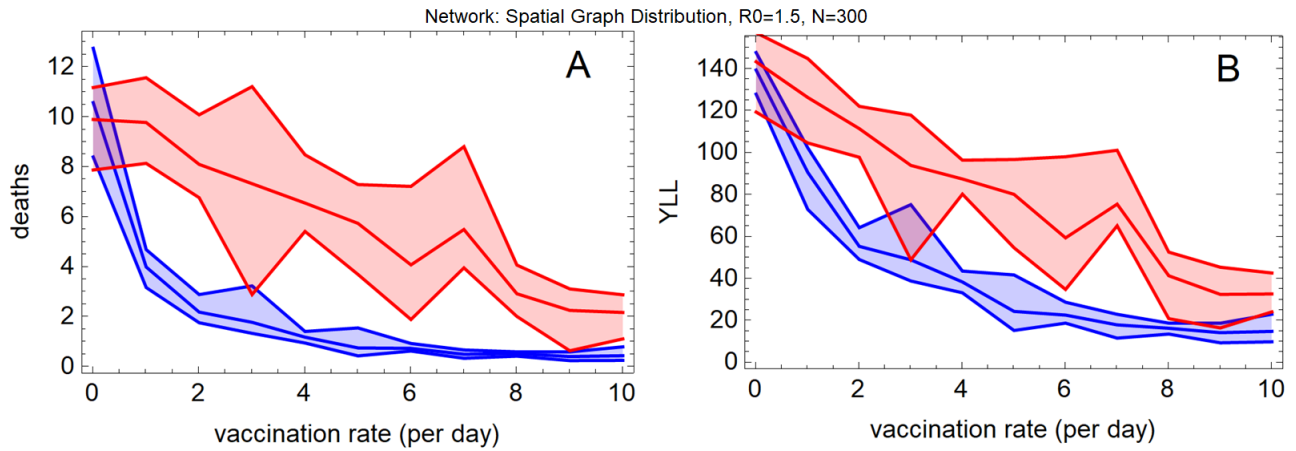


Figure 8: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Spatial Graph Distribution with  $R_0 = 1.5$  and a population  $n = 300$ .

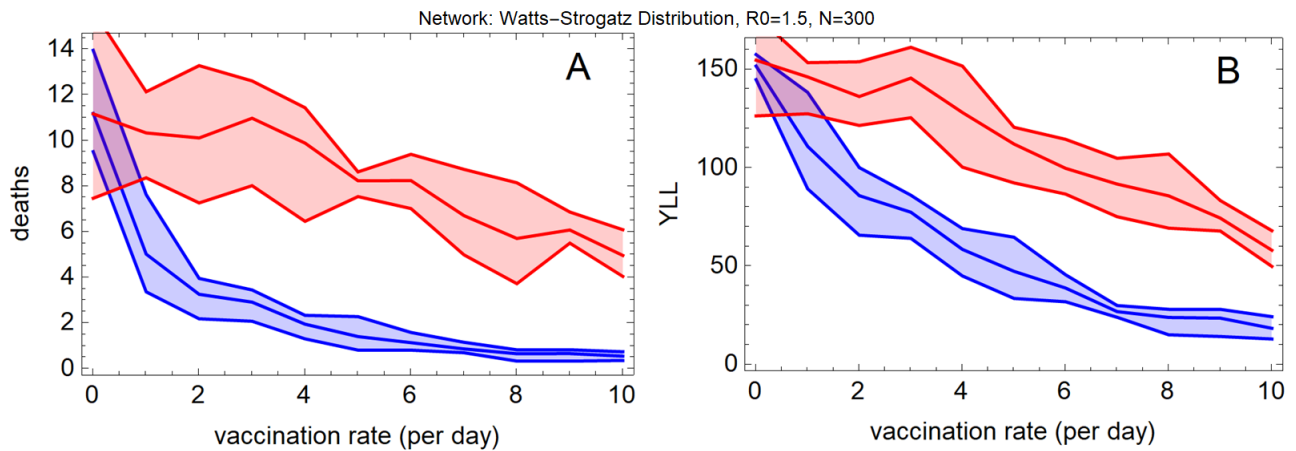


Figure 9: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Watts-Strogatz Graph Distribution with  $R_0 = 1.5$  and a population  $n = 300$ .

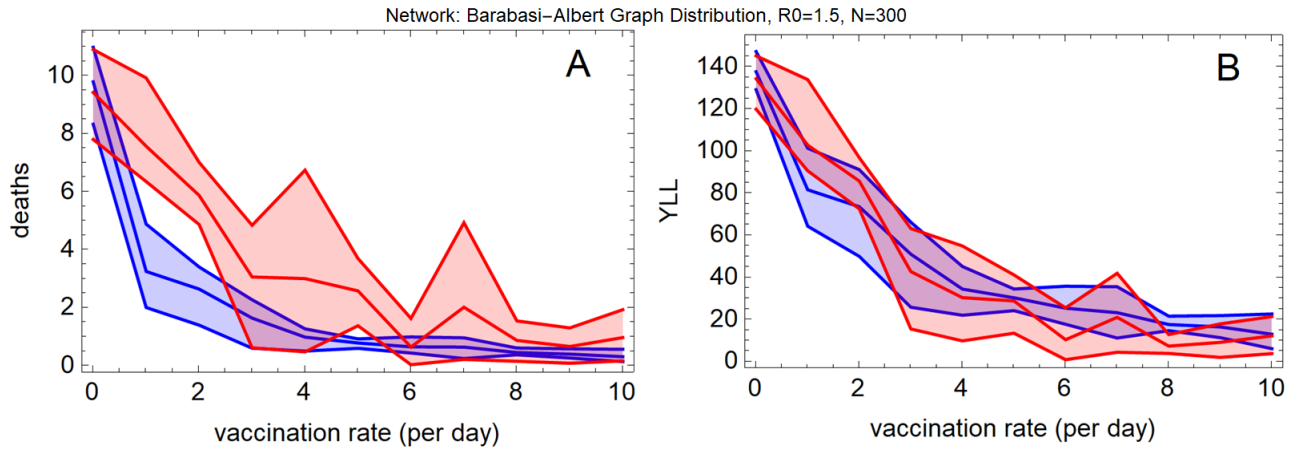


Figure 10: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Barabasi-Albert Graph Distribution with  $R_0 = 1.5$  and a population  $n = 300$ .

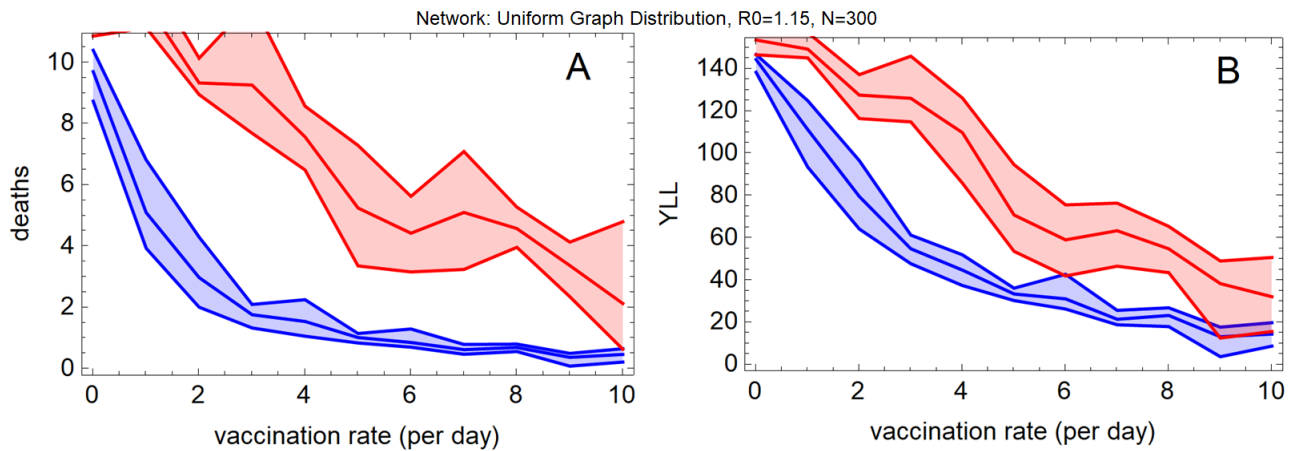


Figure 11: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Uniform Graph Distribution with  $R_0 = 1.15$  and a population  $n = 300$ .

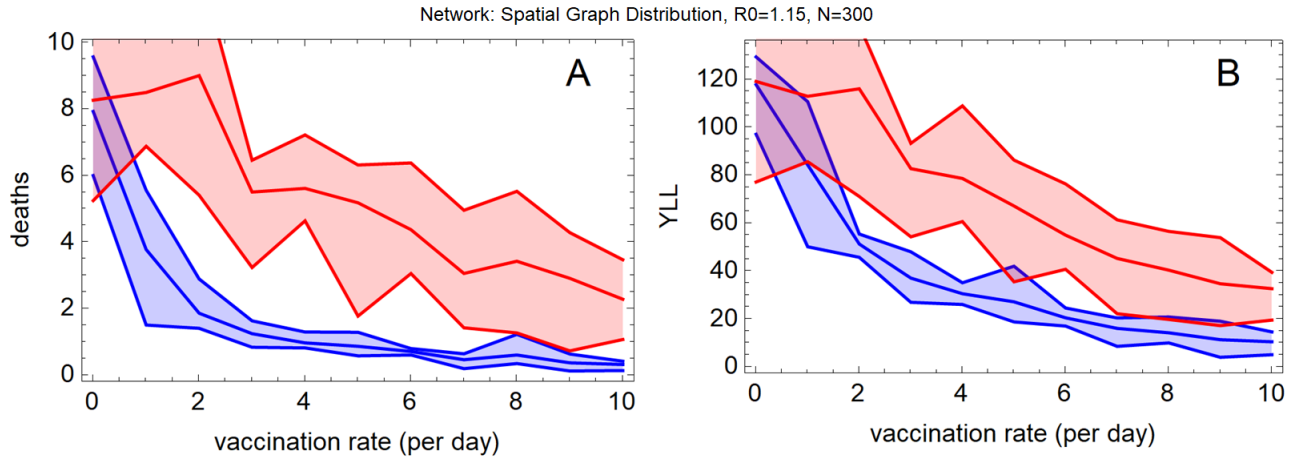


Figure 12: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Spatial Graph Distribution with  $R_0 = 1.15$  and a population  $n = 300$ .

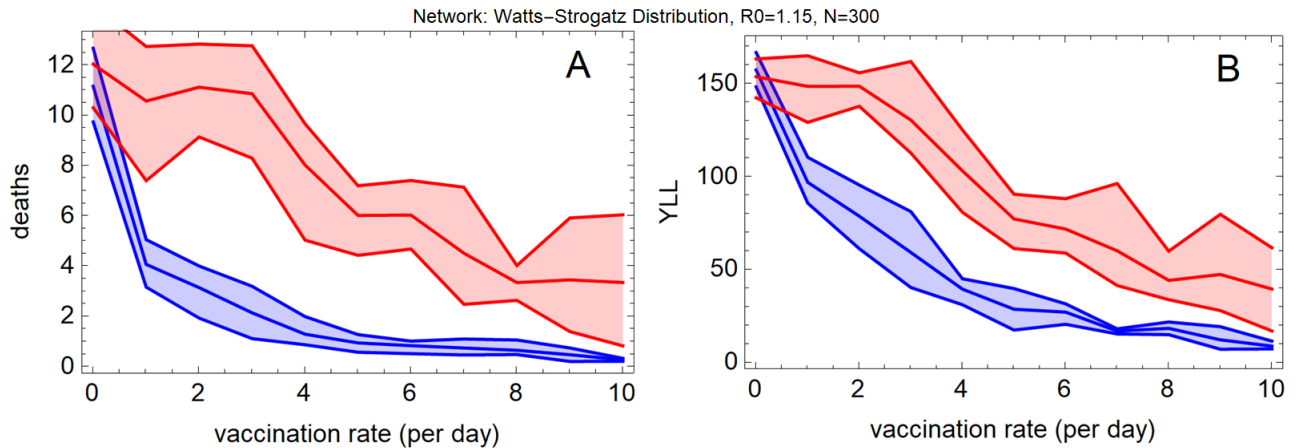


Figure 13: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Watts-Strogatz Graph Distribution with  $R_0 = 1.15$  and a population  $n = 300$ .

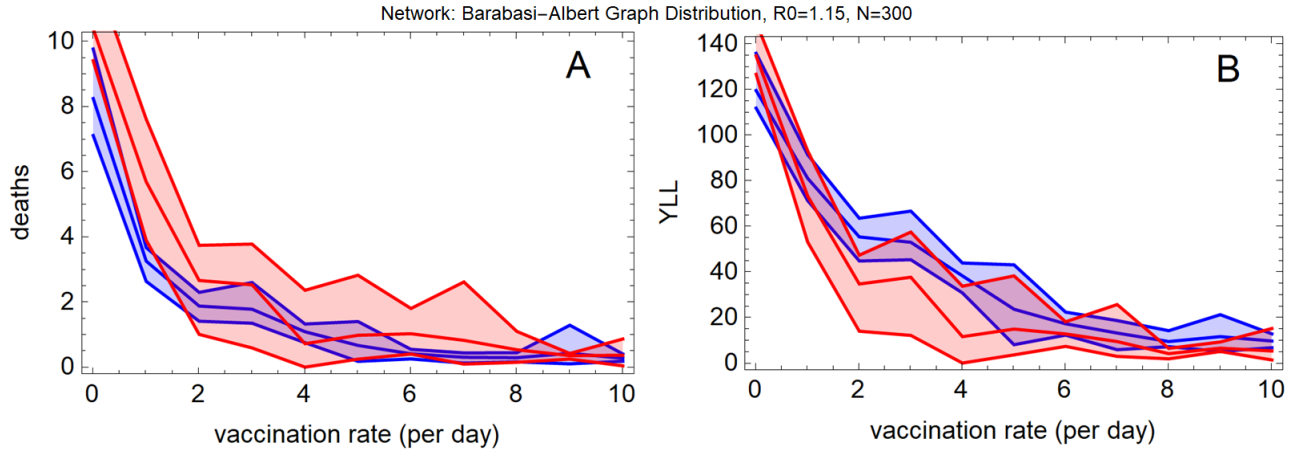


Figure 14: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Barabasi-Albert Graph Distribution with  $R_0 = 1.15$  and a population  $n = 300$ .

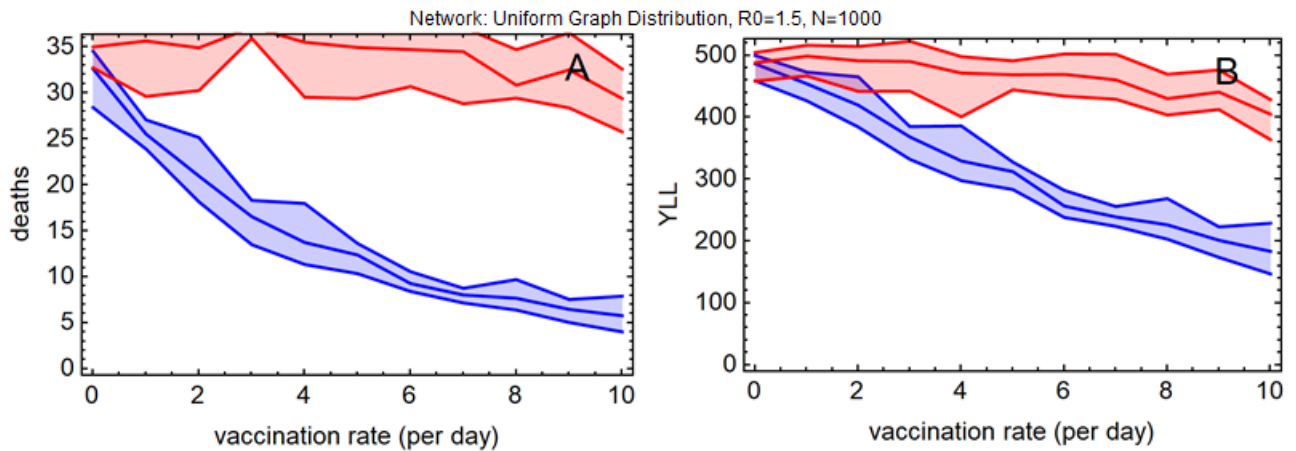


Figure 15: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Uniform Graph Distribution with  $R_0 = 1.5$  and a population  $n = 1000$ .

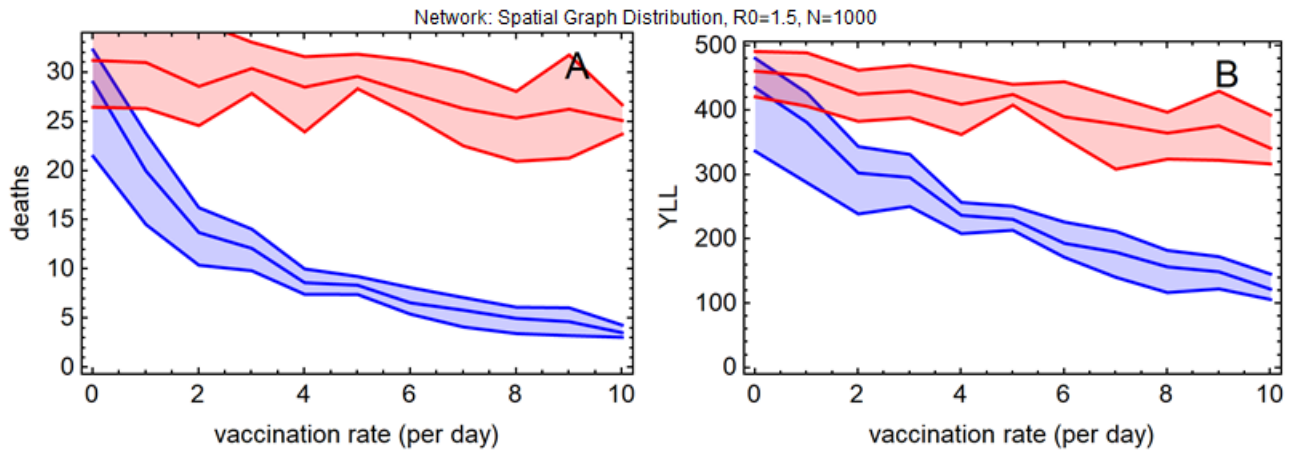


Figure 16: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Spatial Graph Distribution with  $R_0 = 1.5$  and a population  $n = 1000$ .

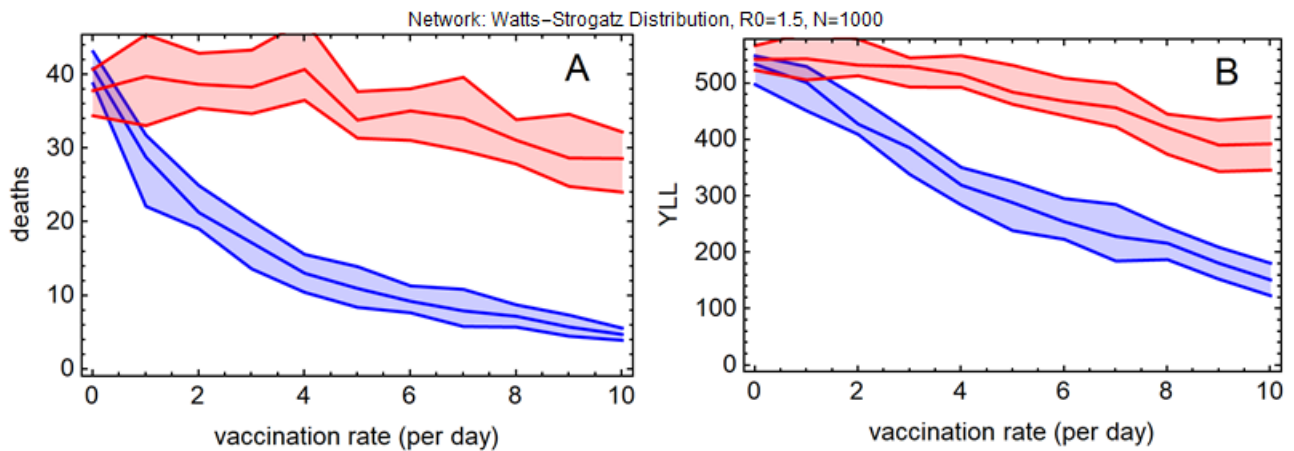


Figure 17: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Watts-Strogatz Graph Distribution with  $R_0 = 1.5$  and a population  $n = 1000$ .

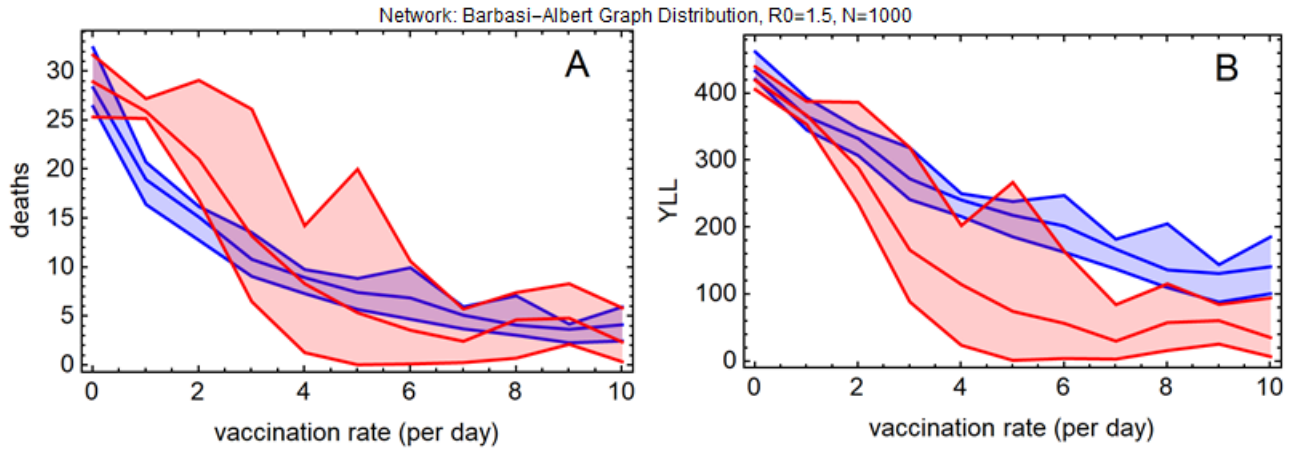


Figure 18: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Barabasi-Albert Graph Distribution with  $R_0 = 1.5$  and a population  $n = 1000$ .

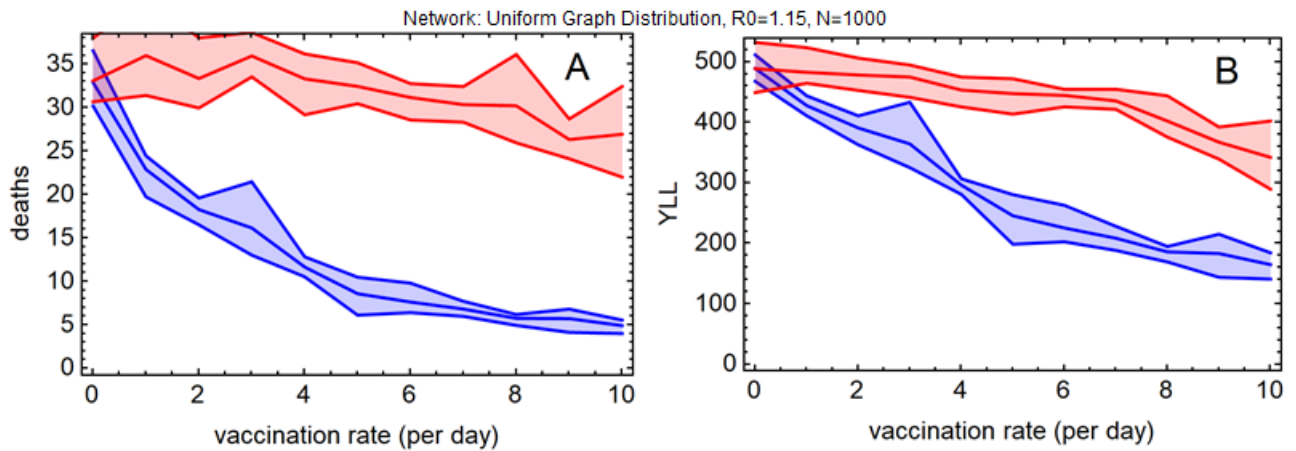


Figure 19: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Uniform Graph Distribution with  $R_0 = 1.15$  and a population  $n = 1000$ .

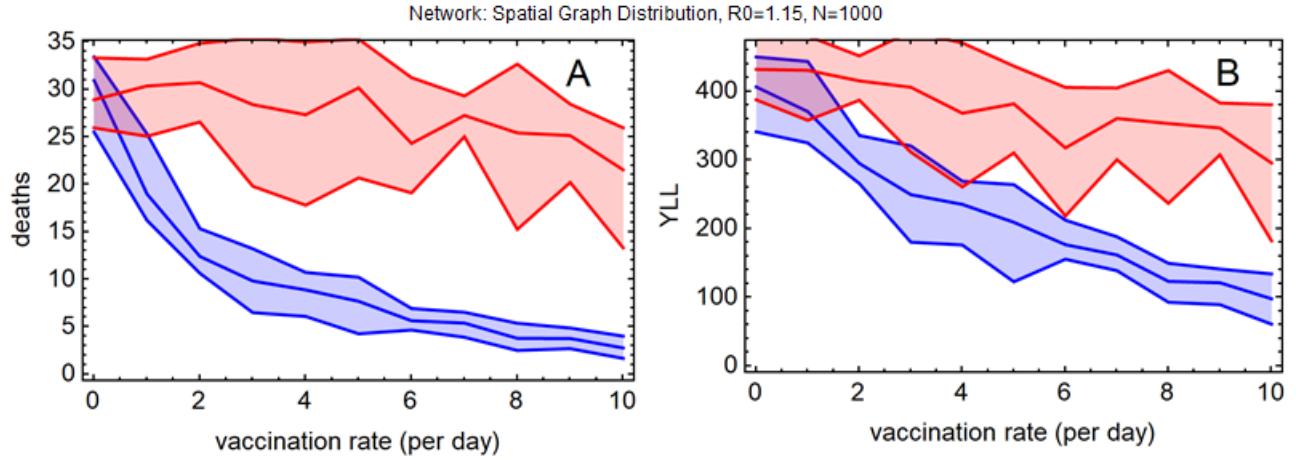


Figure 20: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Spatial Graph Distribution with  $R_0 = 1.15$  and a population  $n = 1000$ .

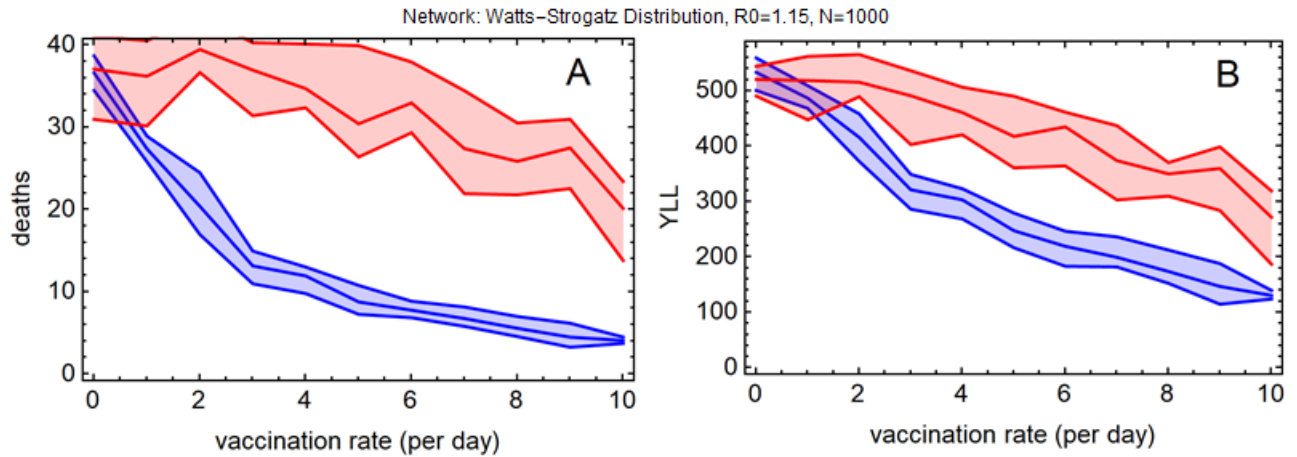


Figure 21: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Watts-Strogatz Graph Distribution with  $R_0 = 1.15$  and a population  $n = 1000$ .

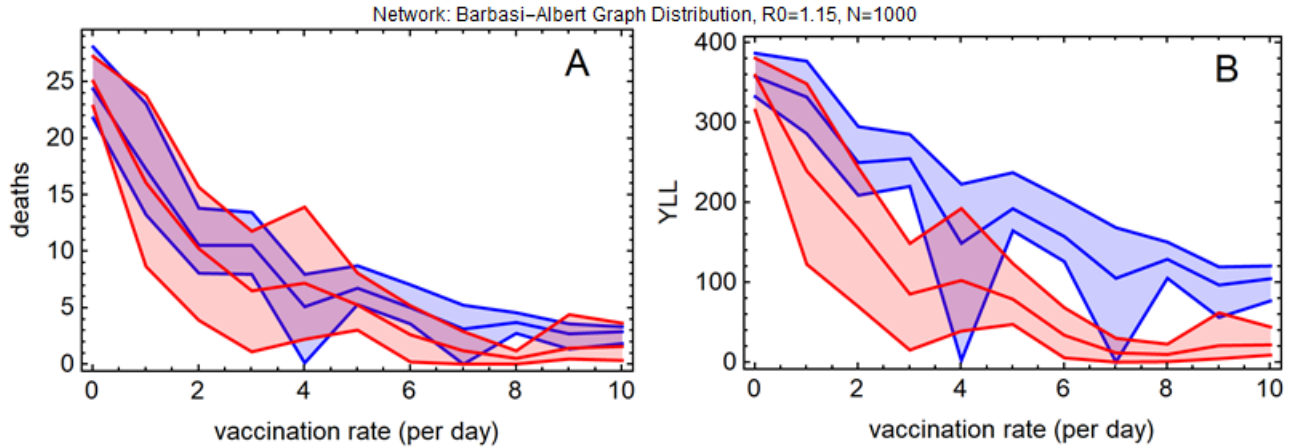


Figure 22: The red lines are when we vaccinate the people with the most contacts while blue are when we vaccinate old people first. The middle line for each color is the mean value, while the upper and lower line shows the 95% confidence interval. In figure A we see the number of deaths and in B we see the number of YLL with the Barabasi-Albert Graph Distribution with  $R_0 = 1.15$  and a population  $n = 1000$ .

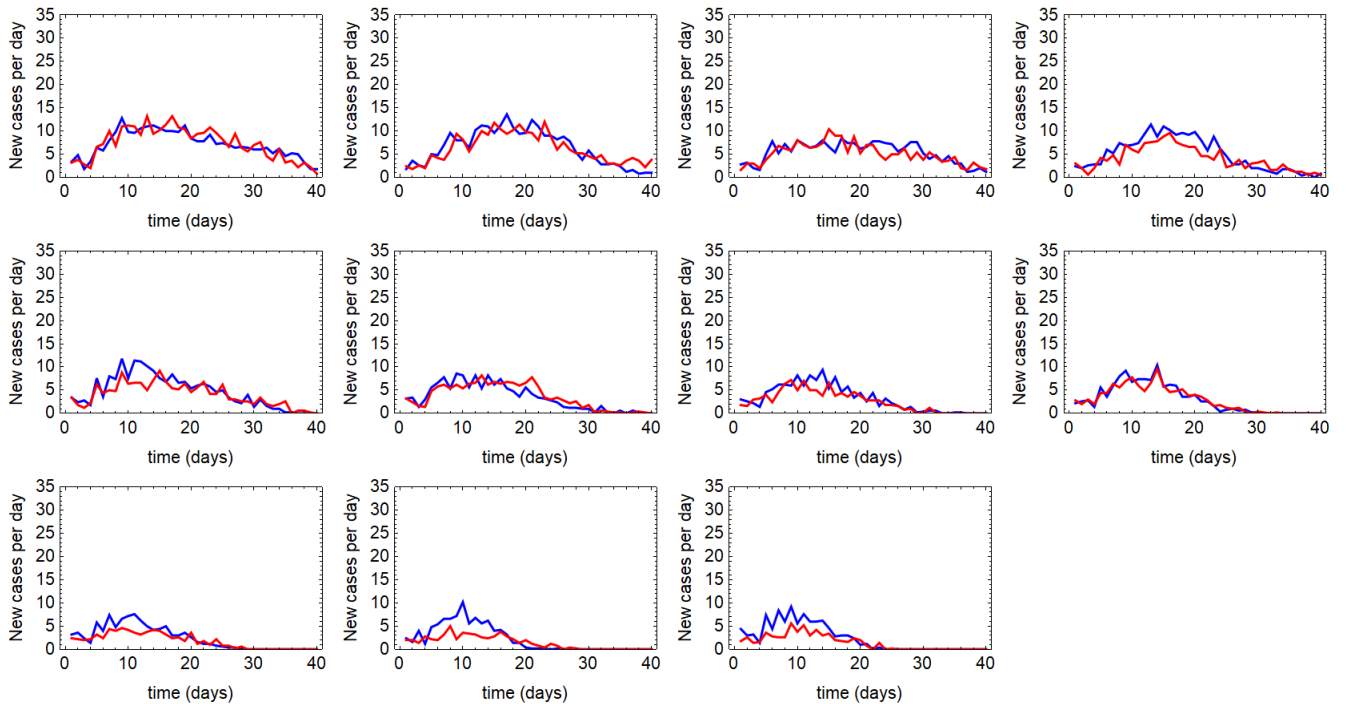


Figure 23: The average number of new cases each day with Spatial Graph Distribution with  $n = 300$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.



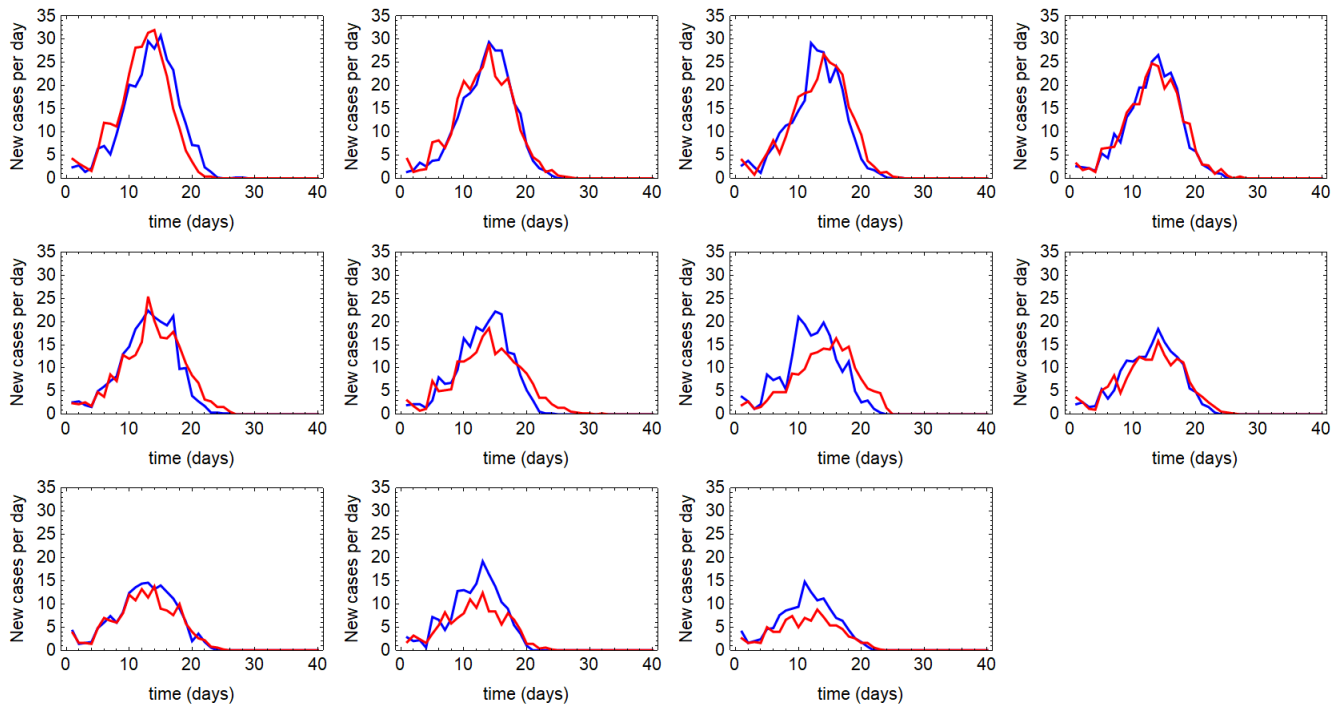


Figure 24: The average number of new cases each day with Watts-Strogatz Graph Distribution with  $n = 300$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

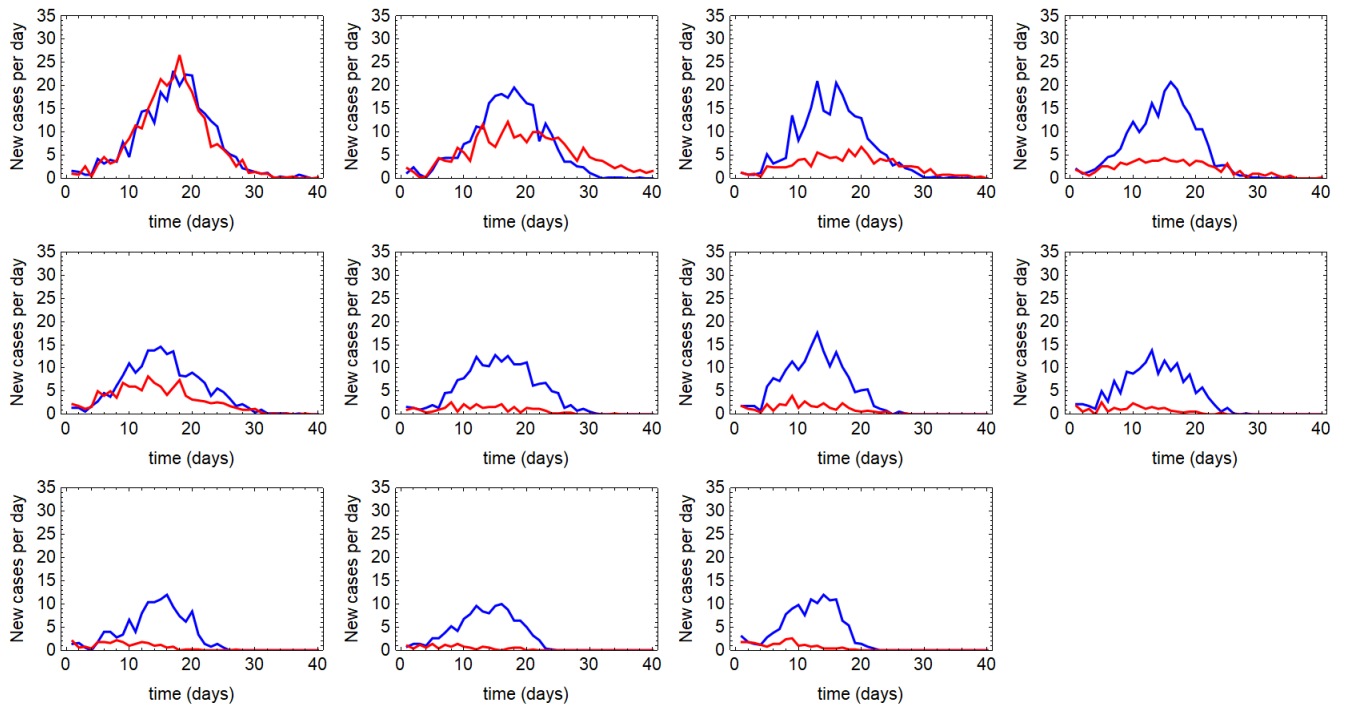


Figure 25: The average number of new cases each day with Barabasi-Albert Graph Distribution with  $n = 300$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

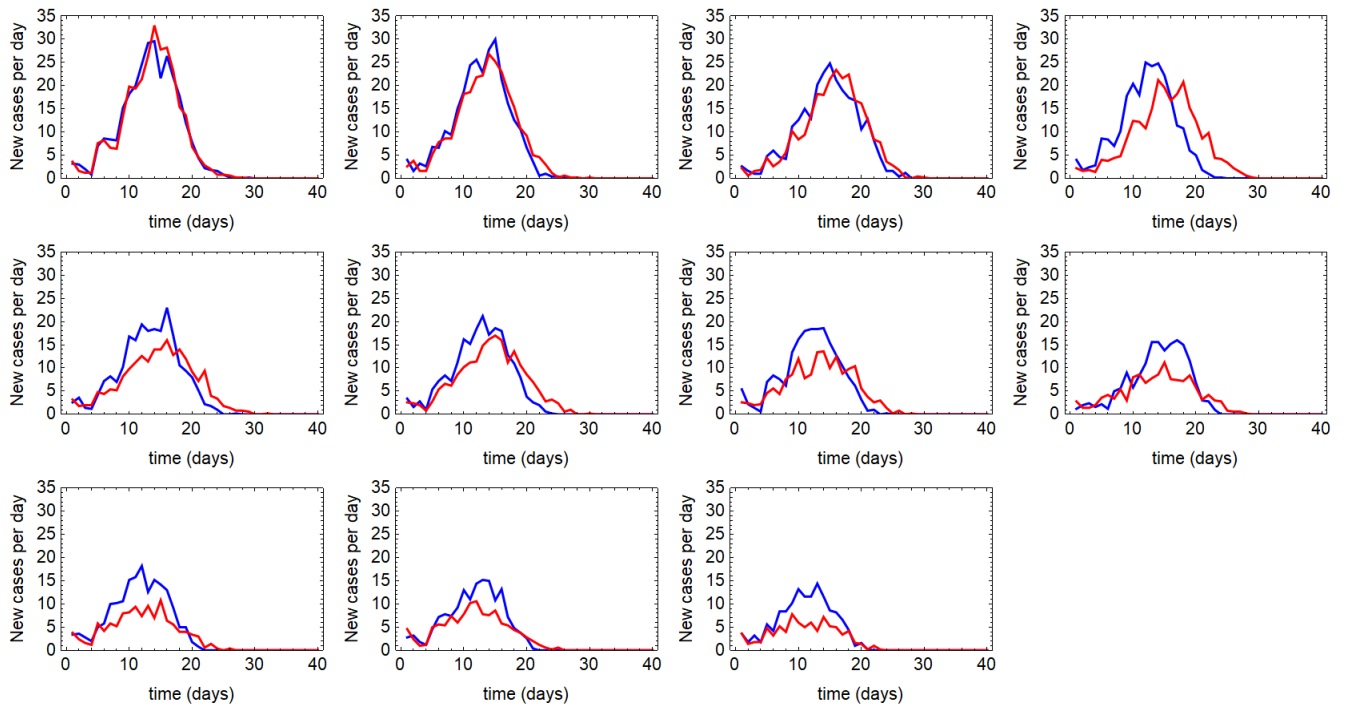


Figure 26: The average number of new cases each day with Uniform Graph Distribution with  $n = 300$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

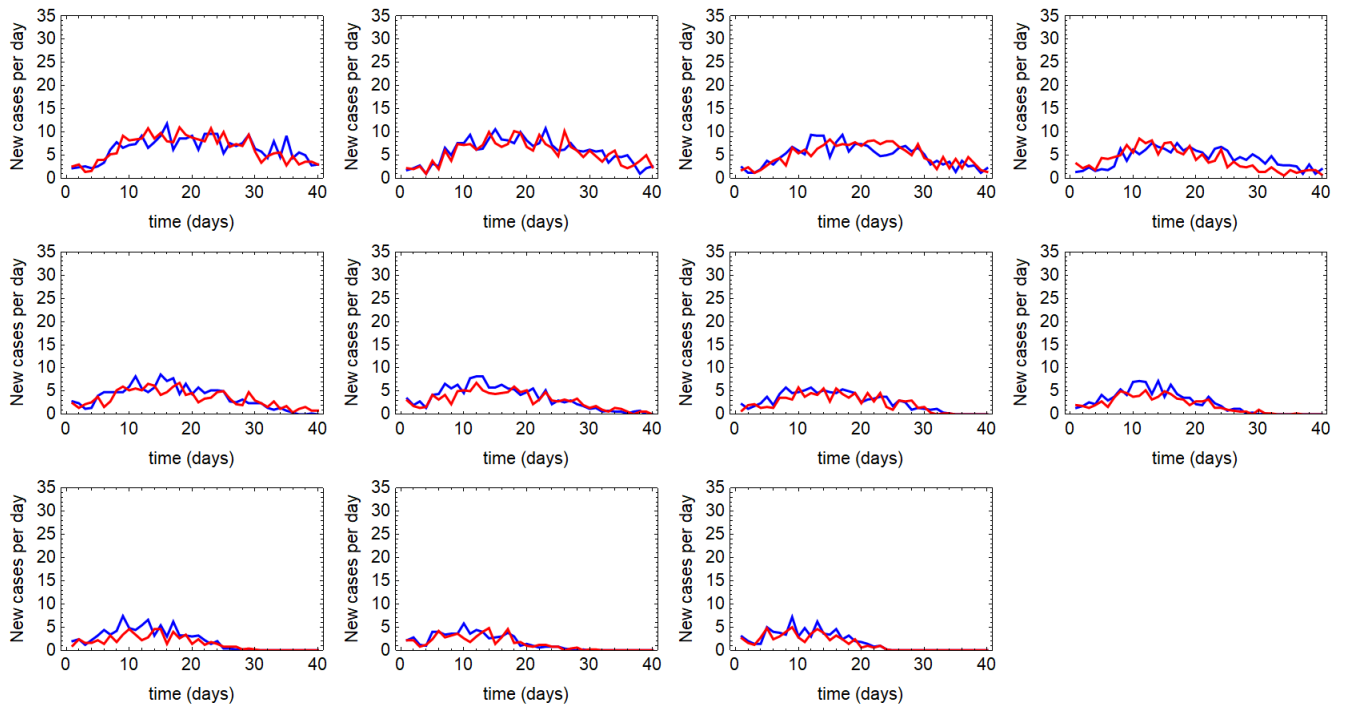


Figure 27: The average number of new cases each day with Spatial Graph Distribution with  $n = 300$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

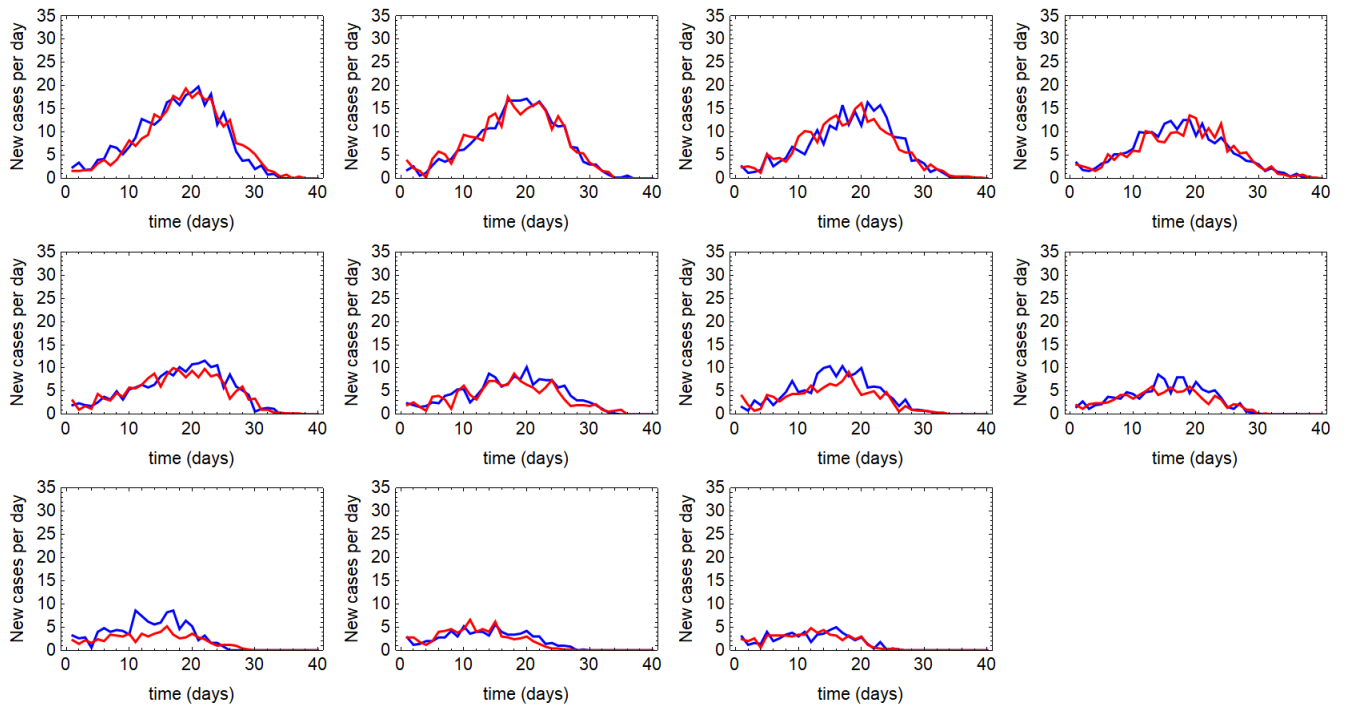


Figure 28: The average number of new cases each day with Watts-Strogatz Graph Distribution with  $n = 300$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

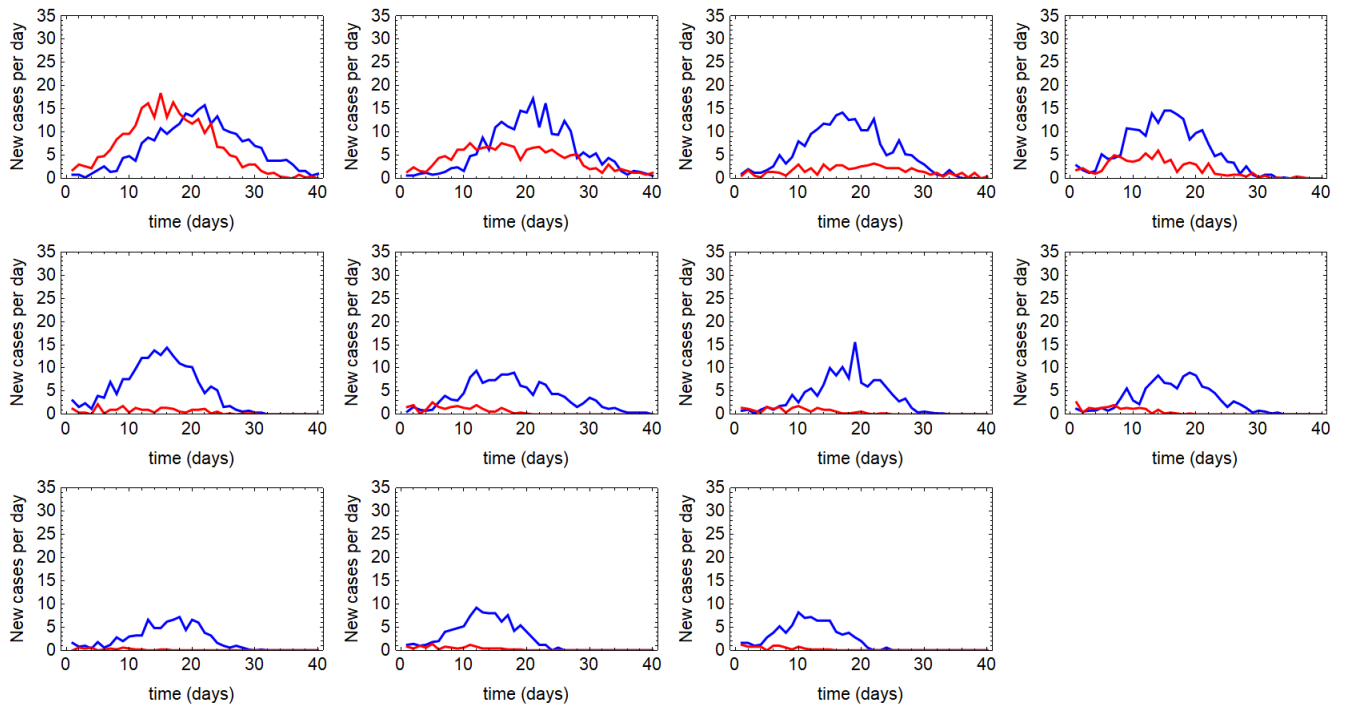


Figure 29: The average number of new cases each day with Barabasi-Albert Graph Distribution with  $n = 300$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

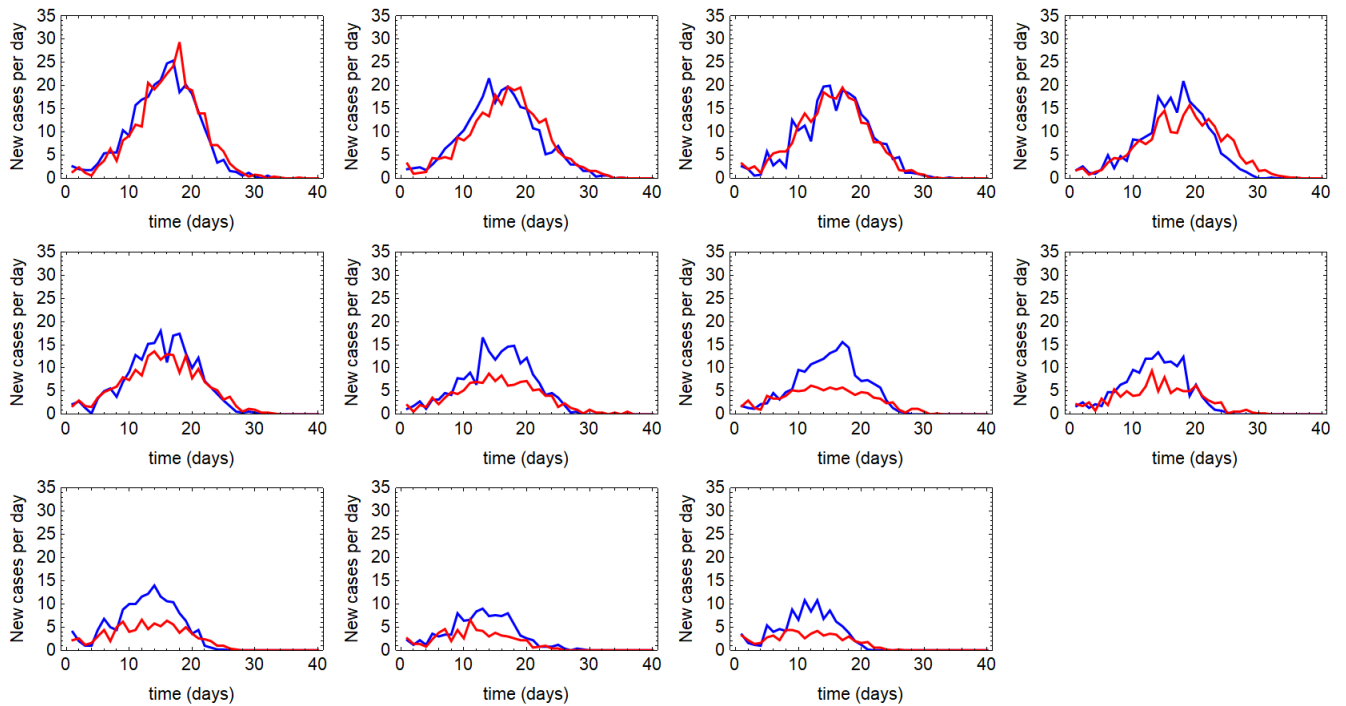


Figure 30: The average number of new cases each day with Uniform Graph Distribution with  $n = 300$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

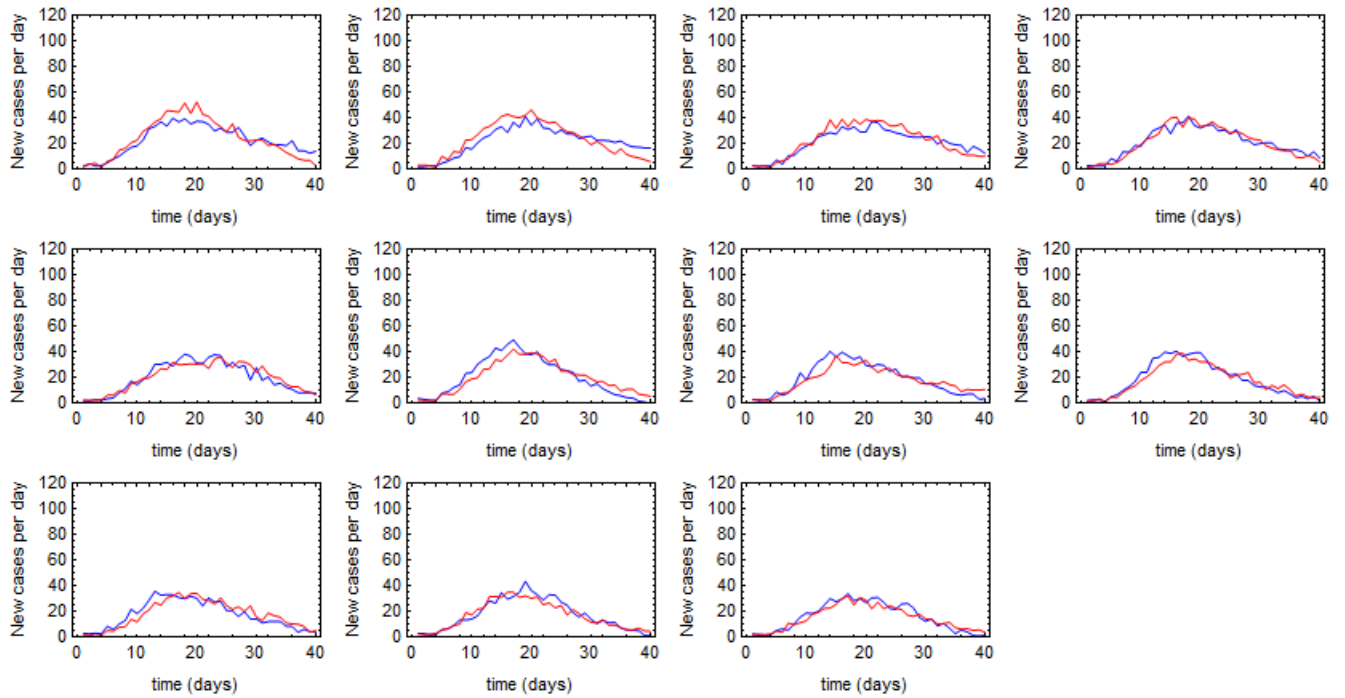


Figure 31: The average number of new cases each day with Spatial Graph Distribution with  $n = 1000$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.



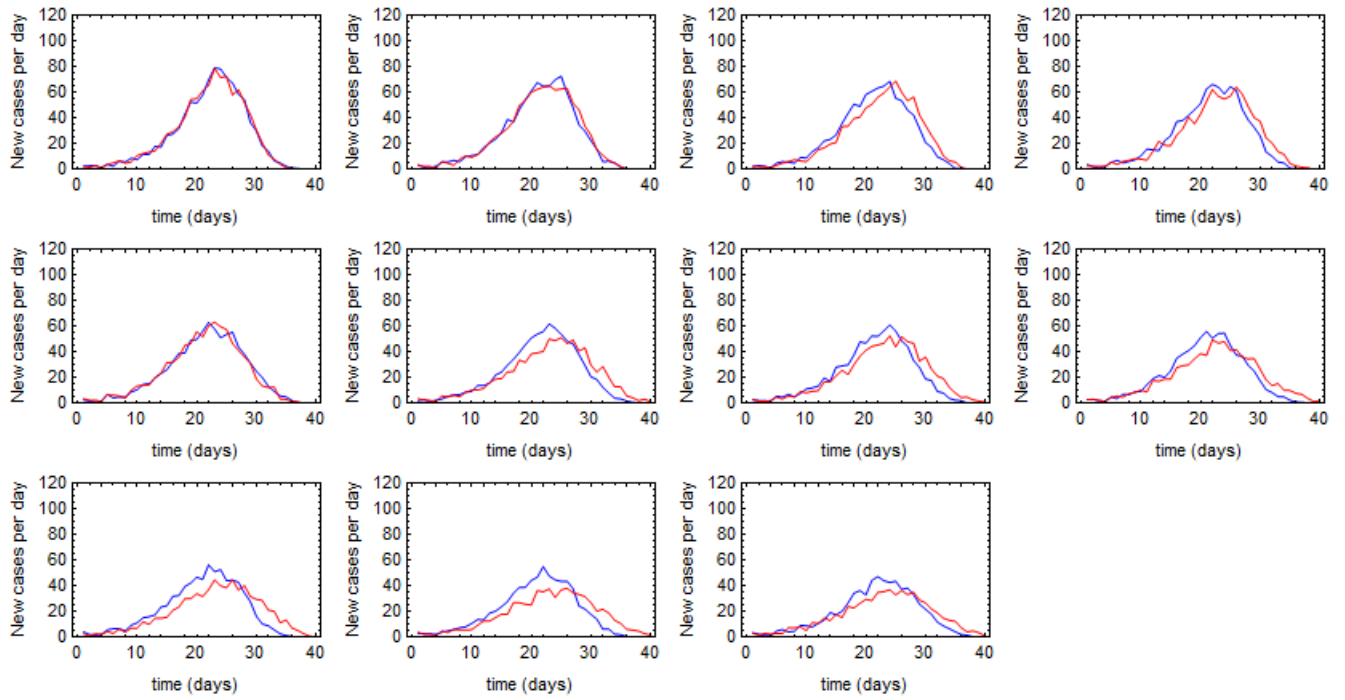


Figure 32: The average number of new cases each day with Watts-Strogatz Graph Distribution with  $n = 1000$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

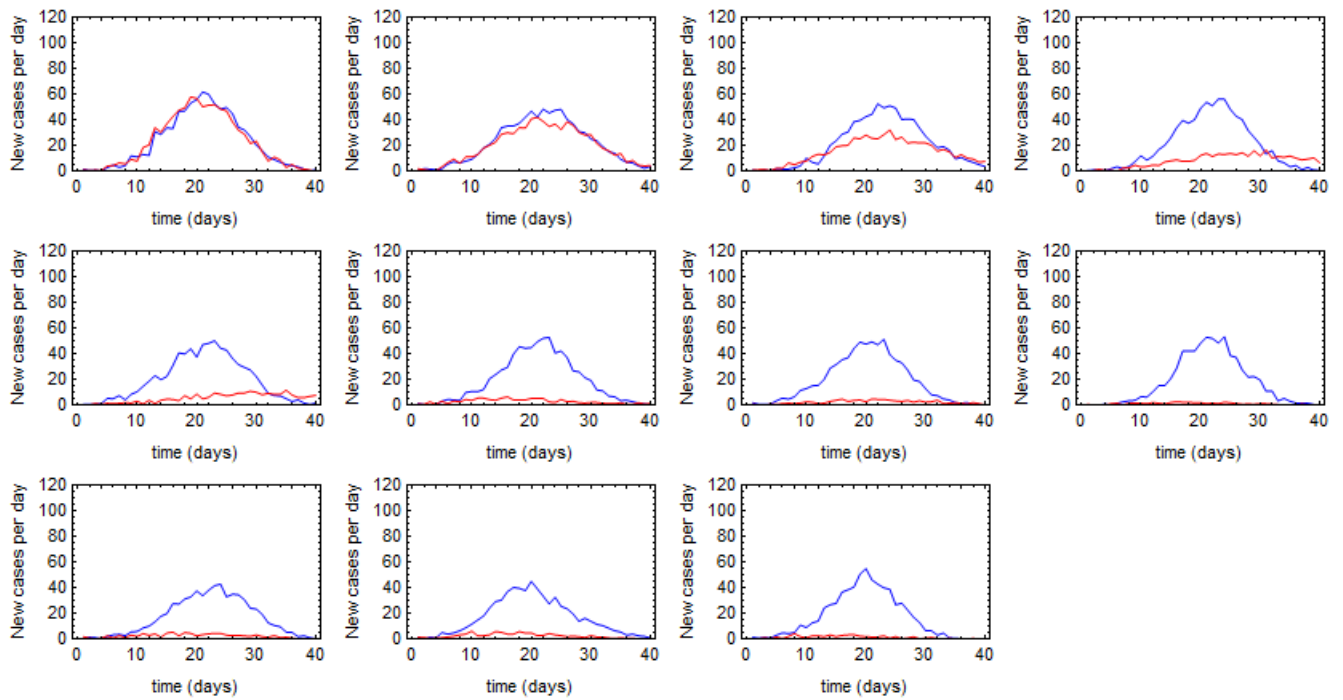


Figure 33: The average number of new cases each day with Barabasi-Albert Graph Distribution with  $n = 1000$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

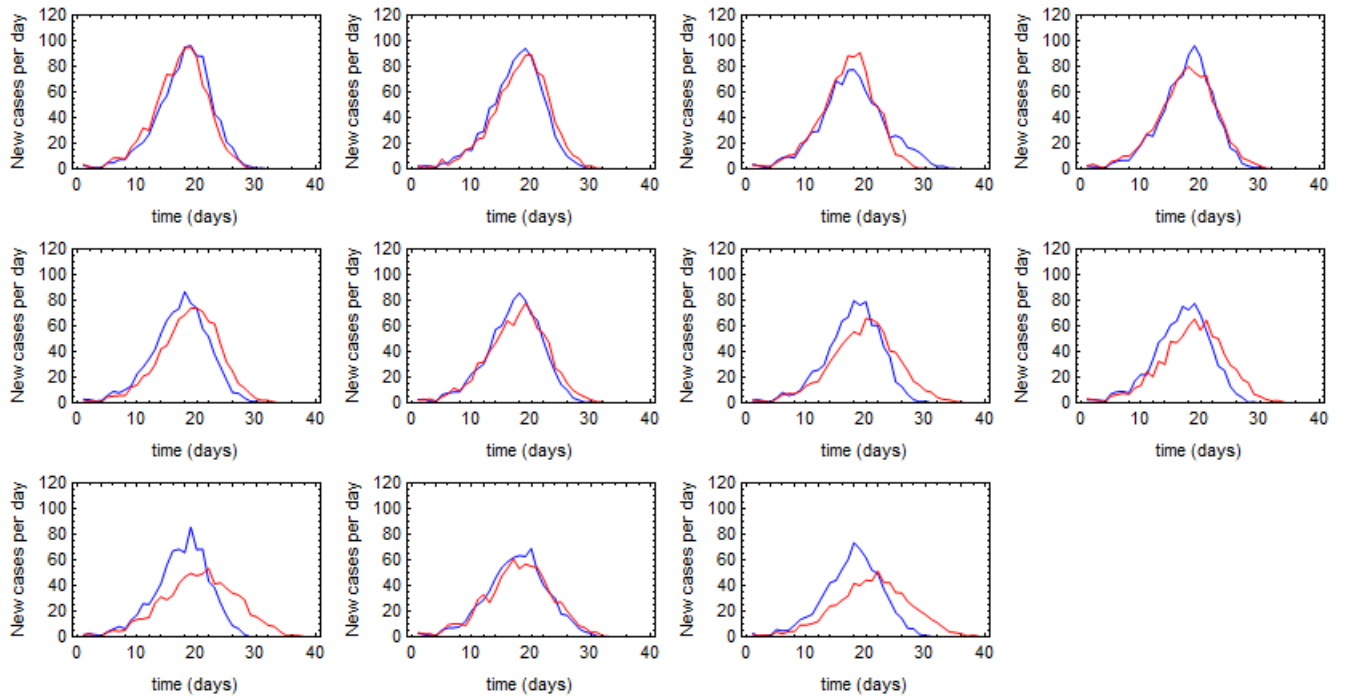


Figure 34: The average number of new cases each day with Uniform Graph Distribution with  $n = 1000$  and  $R_0 = 1.5$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

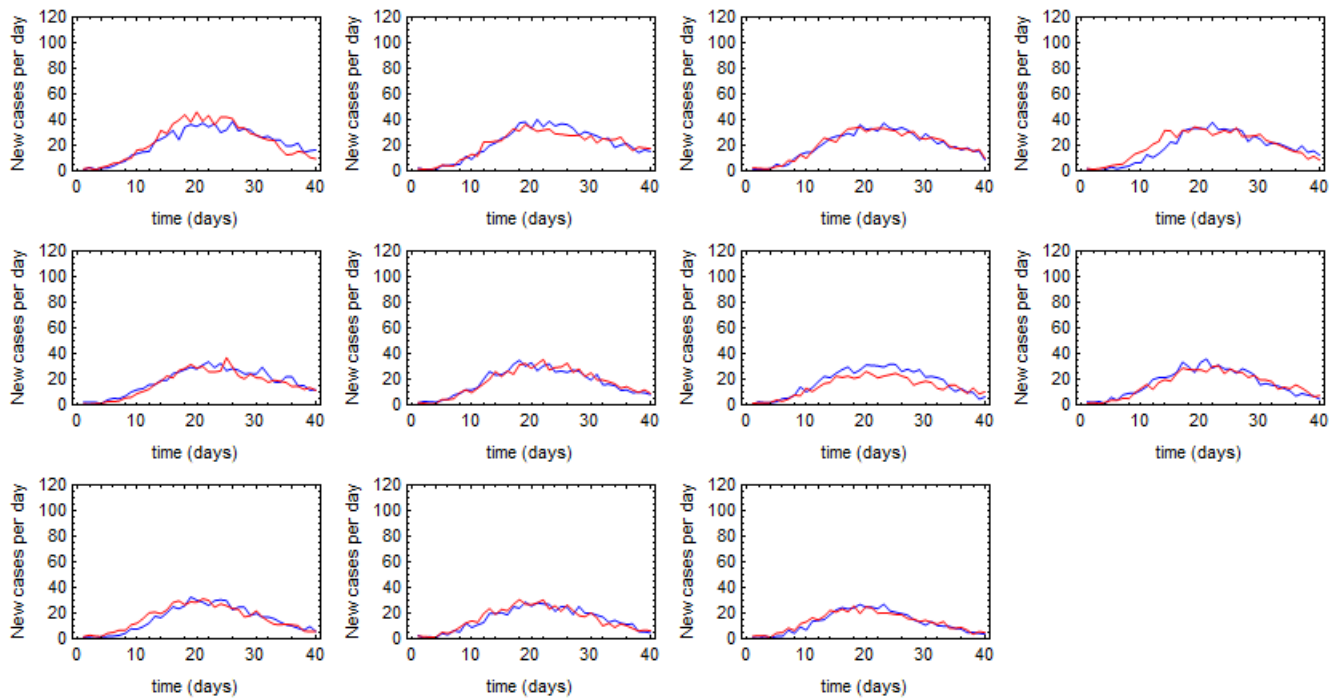


Figure 35: The average number of new cases each day with Spatial Graph Distribution with  $n = 1000$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

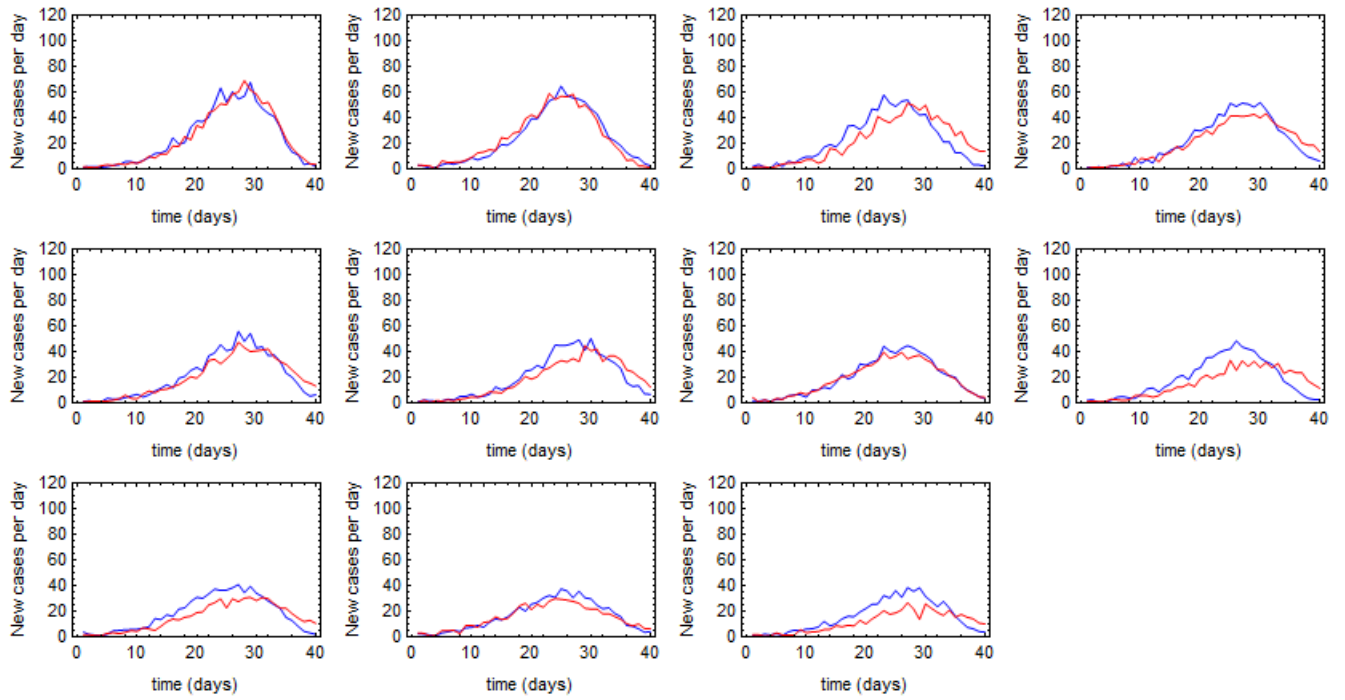


Figure 36: The average number of new cases each day with Watts-Strogatz Graph Distribution with  $n = 1000$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

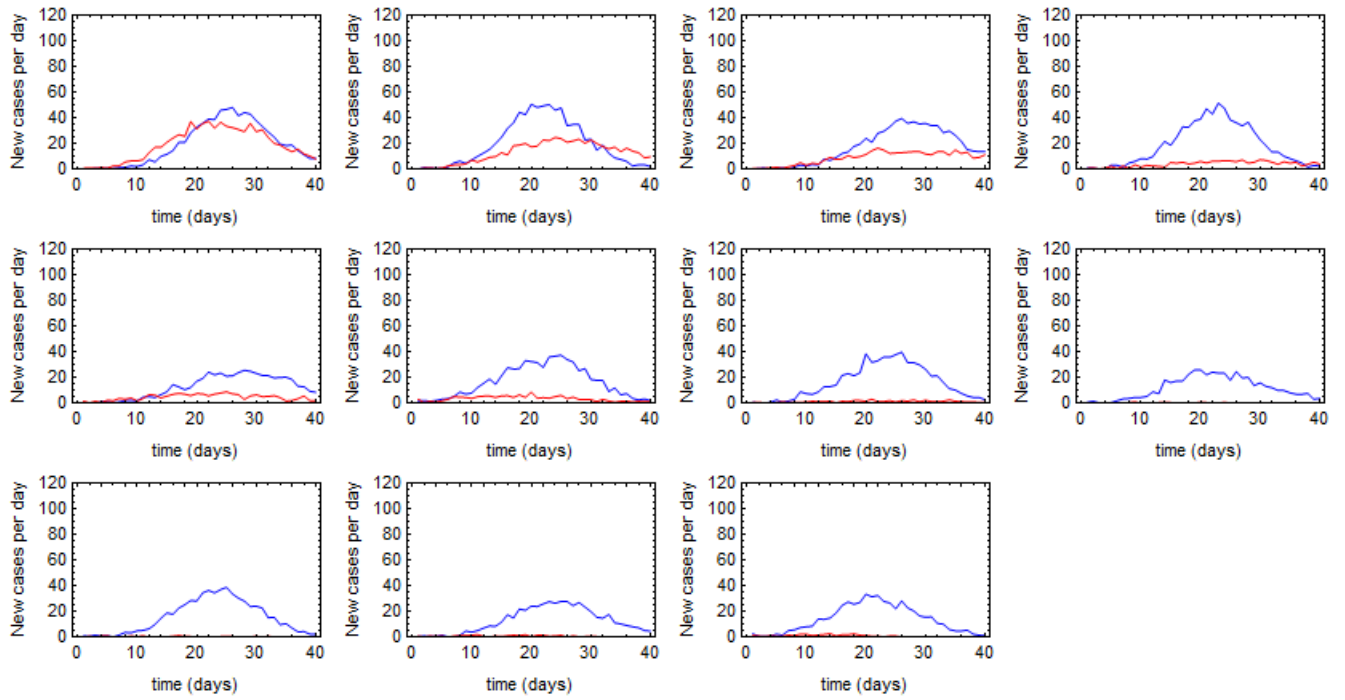


Figure 37: The average number of new cases each day with Barabasi-Albert Graph Distribution with  $n = 1000$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.

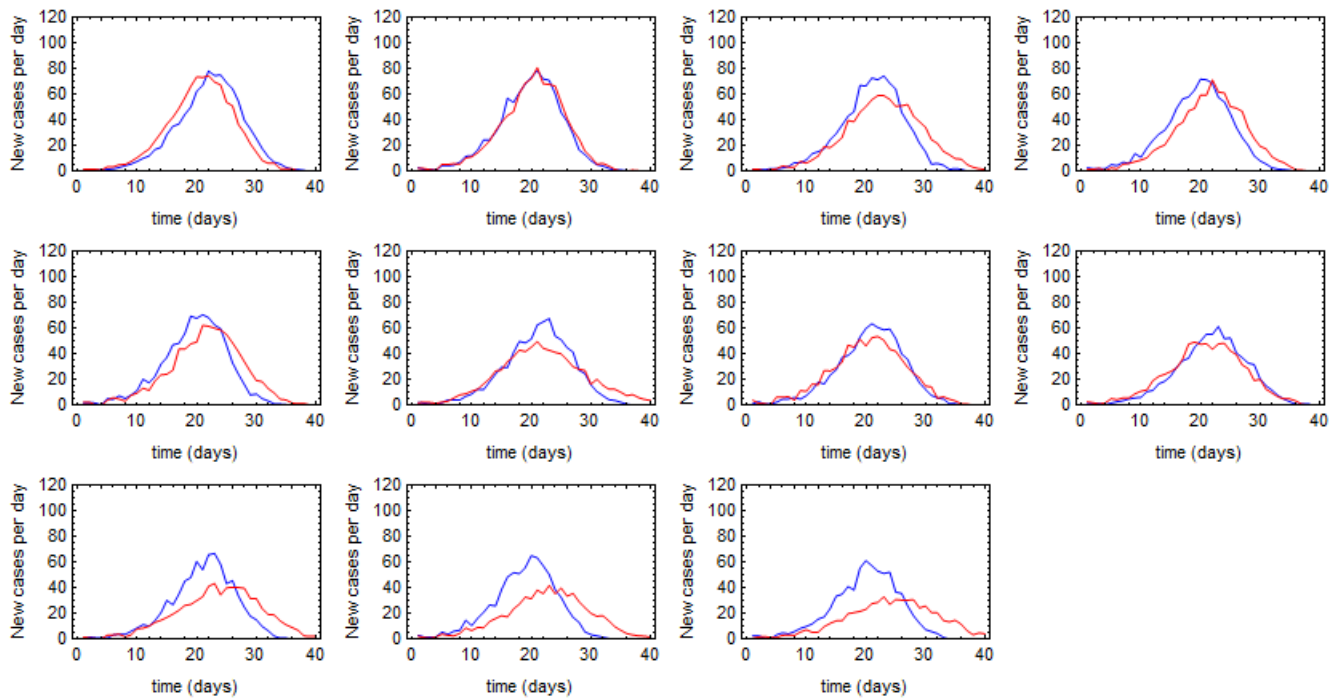


Figure 38: The average number of new cases each day with Uniform Graph Distribution with  $n = 1000$  and  $R_0 = 1.15$ . The red line shows new cases when vaccinating the ones with the most contacts, while the blue line is when vaccinating old people first. Each graph is for one vaccine-pace from 0.01 per day in the top left to 10.01 in the bottom right.





## 6 Discussion and conclusions

The strategy of prioritizing older adults outperforms the alternative strategy across experiments using the Spatial, Uniform, and Watts-Strogatz Graph Distributions regardless of whether  $R_0 = 1.5$  or  $R_0 = 1.15$ , and whether  $n = 300$  or  $n = 1000$ . It can be viewed as the safest solution based on this model.

For the Barabasi-Albert Graph Distribution, we see potential situations where vaccinating those with the most contacts first is the better strategy. The Barabasi-Albert Graph Distribution is also the graph distribution that creates the network with super-spreaders. Hence, it is reasonable that vaccinating the people with the most contacts performs better for this graph. Whether it is realistic or not is another question.

The results from this model show that the safest strategy is to vaccinate the most vulnerable first. Vaccinating the people with the most contacts is a potentially high-risk, high-reward strategy. It has the potential to stop the outbreak, but the costs if it fails are potentially high.

The strengths of this study are that we have tested this model for many different networks. We have tested it for many different vaccination rates for each network, running it multiple times for each scenario.

Potential weaknesses of this study are that we have only tried this for relatively small populations. The networks are not based on any real-life data and could be unrealistic.

We have also assumed perfect information; we know who has the most contacts, which would require detailed surveillance data in a real-world scenario. We also make the unrealistic assumption that as soon as an individual is infected, he/she is removed from the vaccine queue. We also assume that the vaccine has 100% efficacy, and there is no vaccine hesitancy in our populations.

Possible future work with this model includes making networks based on real-life data and looking at other measurements for success, like Quality-adjusted YLL. We can also study hospitalizations. High hospitalization numbers can make the pandemic more deadly due to limits in the health care system's capacity.

It is also possible to add different settings, with different contacts at different times of the day, adding smaller time-steps, and adding variables like school, work, and household contacts. We can also fix weaknesses mentioned previously, like defect vaccines, either in all or nothing vaccine efficacy, efficacy decaying over time, age-dependent efficacy, and adding vaccine hesitancy to the population.



## 7 Computer code

Everything is coded using Wolfram Mathematica version 12.1 and 12.2

Valg av graf og R0 og n

```
R0 = 1.5;
n = 300;
(*H=SpatialGraphDistribution[n,0.15];*)
(*H=BarabasiAlbertGraphDistribution[n,4];*)
H = UniformGraphDistribution[n, 4*n];
(*H = WattsStrogatzGraphDistribution[300,0.15,5];*)
(*H=DegreeGraphDistribution[Table[3,n]];*)

dødelighet = {{0, 1/9.}, {Mean[Range[0, 4]], 1/9.}, {Mean[Range[5, 17]],
  1/16.}, {Mean[Range[18, 29]], 1.}, {Mean[Range[30, 39]],
  4.}, {Mean[Range[40, 49]], 10.}, {Mean[Range[50, 64]],
  30.}, {Mean[Range[65, 74]], 90.}, {Mean[Range[75, 84]],
  220.}, {Mean[Range[85, 99]], 630.}, {100, 1000.}};
d = Interpolation[dødelighet];
aldersfordeling =
  Round[n*{54827, 296332, 451246, 191130, 255214, 1789814, 1501597, 596710,
    185480, 45230}/5367580.];
gruppe1 = {0};
gruppe2 = Range[1, 5];
gruppe3 = Range[6, 12];
gruppe4 = Range[13, 15];
gruppe5 = Range[16, 19];
gruppe6 = Range[20, 44];
gruppe7 = Range[45, 66];
gruppe8 = Range[67, 79];
gruppe9 = Range[80, 89];
gruppe10 = Range[90, 100];
grupper = {gruppe1, gruppe2, gruppe3, gruppe4, gruppe5, gruppe6, gruppe7,
  gruppe8, gruppe9, gruppe10};
levedata = {{0, 82.5}, {(50 + 64)/2, 27.5}, {(65 + 79)/2, 15.6}, {(80 + 89)/2,
  7.0}, {(90 + 99)/2, 2.5}};
gg = Fit[levedata, {zz^4, zz, 1}, zz];
pl1 = ListPlot[levedata];
pl2 = Plot[gg, {zz, 0, 100}];
Show[pl2, pl1]

Oldest First

Monitor[
```

```

dødsliste = {};
levearliste = {};
nyetilfellerliste = {};
Do[
  vaksinerate = v;
  dliste = {};
  lliste = {};
  Do[
    g = RandomGraph[H];
    A = AdjacencyMatrix[g];
    links = Drop[ArrayRules[A][[All, 1]], -1];
    L[i_] :=
      Map[{-#} &,
        Extract[links, Position[links[[All, 1]], _?(# == i &)][[All, 2]]];
    antallkontakter = Table[Length[L[i]], {i, 1, n}];
    G = (Mean[
      antallkontakter] + (Variance[antallkontakter] -
        Mean[antallkontakter])/Mean[antallkontakter]);
    \[Beta] = R0/G;
    alder0 =
      Flatten[Table[
        RandomChoice[grupper[[k]], aldersfordeling[[k]], {k, 1, 10}]];
    alder = {};
    terskel = Quantile[antallkontakter, 0.75];
    Do[
      If[
        antallkontakter[[k]] > terskel,
        alder = Append[alder, RandomChoice[Join[gruppe5, gruppe6]]];
        ,
        alder = Append[alder, RandomChoice[alder0]];
      ];
      , {k, 1, Length[alder0]};
    forventetlevetid = gg /. zz -> alder;
    alderwp = Table[{alder[[i]], i}, {i, 1, n}];
    tmax = 40;
    inkubasjonstid = 3;
    smittsomtid = 5;
    plotliste = {};
    nyetilfeller = {};
    pimune = {};
    vaksinert = {};
    smittende = Table[0, {n}];
    k = RandomInteger[{1, n}];
    smittende[[k]] = 1;
    k = RandomInteger[{1, n}];

```

```

smittende[[k]] = 1;
smittetever = smittende;
psmittende = Position[smittende, _?(# == 1 &)];
farge = Map[# -> Red &, Flatten[psmittende]];
plotliste = Append[plotliste, GraphPlot[g, VertexStyle -> farge]];
imune = Table[0, {n}];
nysmittedeliste = Table[
  Table[0, {n}], {inkubasjonstid};
smittendeliste =
  Prepend[Table[Table[0, {n}], {smittsomid - 1}], smittende];
Do[
  vaksinerperdag = RandomInteger[PoissonDistribution[vaksinerate]];
  ksmitte = Flatten[Position[smittende, _?(# == 1 &)]];
  nyimune = smittende;
  vaksineliste = Reverse[SortBy[Delete[alderwp, pimune], First]];

  If[Length[vaksineliste] >= vaksinerperdag,
    Do[
      nyimune[[vaksineliste[[kk, 2]]]] = 1;
      vaksinert = Append[vaksinert, vaksineliste[[kk, 2]]];
      , {kk, 1, vaksinerperdag}];
    ,
  nyimune = Table[1, {n}];
  ];
imune = UnitStep[imune + nyimune - 1];
mulige =
  Plus @@ Table[
    MapAt[# + 1 &, Table[0, {n}], L[ksmitte[[j]]]], {j, 1,
      Length[ksmitte]};
probsmitte = 1 - (1 - \[Beta])^mulige;
probsmitte = probsmitte*(1 - imune);
If[Length[ksmitte] > 0 ,
  nysmittede =
    UnitStep[Sign[probsmitte - Table[RandomReal[], {Length[mulige]}]]];
  nysmittede = UnitStep[nysmittede - smittetever - 1];
  smittetever = UnitStep[smittetever + nysmittede - 1];
  smittende =
    smittende + UnitStep[Last[nysmittedeliste] - 1] - Last[smittendeliste];
  smittendeliste = Drop[smittendeliste, -1];
  smittendeliste = Prepend[smittendeliste, Last[nysmittedeliste]];
  nysmittedeliste = Drop[nysmittedeliste, -1];
  nysmittedeliste = Prepend[nysmittedeliste, nysmittede];
  pnysmittende = Position[nysmittede, _?(# == 1 &)];
  psmittende = Position[smittende, _?(# == 1 &)];
  pimune = Position[imune, _?(# == 1 &)];

```

```

nyetilfeller = Append[nyetilfeller, Plus @@ nysmittede];
,

smittende =
  smittende + UnitStep[Last[nysmittedeliste] - 1] - Last[smittendeliste];
smittendeliste = Drop[smittendeliste, -1];
smittendeliste = Prepend[smittendeliste, Last[nysmittedeliste]];
nysmittede = Table[0, {n}];
nyetilfeller = Append[nyetilfeller, 0];
nysmittedeliste = Drop[nysmittedeliste, -1];
nysmittedeliste = Prepend[nysmittedeliste, nysmittede];
];
(*farge1=Map[#\[Rule]Orange&,Flatten[psmittende]];
farge2=Map[#\[Rule]Green&,Flatten[pimune]];
farge3=Map[#\[Rule]Red&,Flatten[pnysmittende]];
farge=Join[farge2,farge1, farge3];
plotliste=Append[plotliste,GraphPlot[g,VertexStyle\[Rule]farge]];*)
, {t, 1, tmax}];
referanse = 0.001;
døde = Plus @@ (referanse*d[alder]*smitteteveer);
tapteveear = Plus @@ (referanse*d[alder]*smitteteveer*forventetlevetid);
dliste = Append[dliste, døde];
lliste = Append[lliste, tapteveear];
nyetilfellerliste = Append[nyetilfellerliste, nyetilfeller];
, {teller, 1, 5}];
dødsliste = Append[dødsliste, {v, dliste}];
leveearliste = Append[leveearliste, {v, lliste}];
, {v, 0.01, 10.01, 1.0}
];
, {teller, v}];

utbrudd1 =
  Table[Map[Mean[# + 0.] &,
    Transpose[Partition[nyetilfellerliste, 5][[i]]], {i, 1, 11}];
Grid[Partition[
  Table[ListPlot[utbrudd1[[i]], Joined -> True, PlotRange -> {0, 35},
    ImageSize -> 200], {i, 1, 11}], UpTo[4]]

mean = Transpose[{dødsliste[[All, 1]], Map[Mean[#] &, dødsliste[[All, 2]]]};
lower = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.25] &, dødsliste[[All, 2]]]};
upper = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.75] &, dødsliste[[All, 2]]]};
plot1 = ListPlot[{mean, upper, lower}, PlotStyle -> {Blue, Blue, Blue},
  Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,

```

```

GridLinesStyle -> Black, Axes -> False, Frame -> True,
FrameLabel -> {"vaccination rate (per day)", "deaths"},
FrameStyle -> Directive[12, Black]]
mean = Transpose[{levarliste[[All, 1]],
  Map[Mean[#] &, levarliste[[All, 2]]]}];
lower = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.25] &, levarliste[[All, 2]]]}];
upper = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.75] &, levarliste[[All, 2]]]}];
plot1b = ListPlot[{mean, upper, lower}, PlotStyle -> {Blue, Blue, Blue},
  Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,
  GridLinesStyle -> Black, Axes -> False, Frame -> True,
  FrameLabel -> {"vaccination rate (per day)", "YLL"},
  FrameStyle -> Directive[12, Black]]

mean = Transpose[{dødsliste[[All, 1]], Map[Mean[#] &, dødsliste[[All, 2]]]}];
lower = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.025] &, dødsliste[[All, 2]]]}];
upper = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.975] &, dødsliste[[All, 2]]]}];
plot1c = ListPlot[{mean, upper, lower}, PlotStyle -> {Blue, Blue, Blue},
  Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,
  GridLinesStyle -> Black, Axes -> False, Frame -> True,
  FrameLabel -> {"vaccination rate (per day)", "deaths"},
  FrameStyle -> Directive[12, Black]]
mean = Transpose[{levarliste[[All, 1]],
  Map[Mean[#] &, levarliste[[All, 2]]]}];
lower = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.025] &, levarliste[[All, 2]]]}];
upper = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.975] &, levarliste[[All, 2]]]}];
plot1d = ListPlot[{mean, upper, lower}, PlotStyle -> {Blue, Blue, Blue},
  Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,
  GridLinesStyle -> Black, Axes -> False, Frame -> True,
  FrameLabel -> {"vaccination rate (per day)", "YLL"},
  FrameStyle -> Directive[12, Black]]

```

Many Contacts First

```

Monitor[
  dødsliste = {};
  levarliste = {};
  nyetilfellerliste = {};
  Do[
    vaksinerate = v;

```

```

dliste = {};
lliste = {};
Do[
  (* lager nettverk *)
  g = RandomGraph[H];
  A = AdjacencyMatrix[g];
  links = Drop[ArrayRules[A][[All, 1]], -1];
  L[i_] :=
    Map[{-#} &,
      Extract[links, Position[links[[All, 1]], _?(# == i &)][[All, 2]]];
  antallkontakter = Table[Length[L[i]], {i, 1, n}];
  G = (Mean[
    antallkontakter] + (Variance[antallkontakter] -
      Mean[antallkontakter])/Mean[antallkontakter]);
  \[Beta] = R0/G;
  alder0 =
    Flatten[Table[
      RandomChoice[grupper[[k]], aldersfordeling[[k]], {k, 1, 10}]];
  alder = {};
  terskel = Quantile[antallkontakter, 0.75];
  Do[
    If[
      antallkontakter[[k]] > terskel,
      alder = Append[alder, RandomChoice[Join[gruppe5, gruppe6]]];
      ,
      alder = Append[alder, RandomChoice[alder0]];
    ];
    , {k, 1, Length[alder0]};
  forventetlevetid = gg /. zz -> alder;

  antallkontakterwp = Table[{antallkontakter[[i]], i}, {i, 1, n}];
  tmax = 40;
  inkubasjonstid = 3;
  smittsomtid = 5;
  plotliste = {};
  nyetilfeller = {};
  pimune = {};
  vaksinerter = {};
  smittende = Table[0, {n}];
  k = RandomInteger[{1, n}];
  smittende[[k]] = 1;
  k = RandomInteger[{1, n}];
  smittende[[k]] = 1;
  smittetever = smittende;

```



```

psmittende = Position[smittende, _?(# == 1 &)];
farge = Map[# -> Red &, Flatten[psmittende]];
plotliste = Append[plotliste, GraphPlot[g, VertexStyle -> farge]];
imune = Table[0, {n}];
nysmittedeliste = Table[
  Table[0, {n}], {inkubasjonstid}];
smittendeliste =
  Prepend[Table[Table[0, {n}], {smittsometid - 1}], smittende];
Do[
  vaksinerperdag = RandomInteger[PoissonDistribution[vaksinerate]];
  ksmitte = Flatten[Position[smittende, _?(# == 1 &)]];
  nyimune = smittende;
  vaksineliste = Reverse[SortBy[Delete[antallkontakterwp, pimune], First]];

  If[Length[vaksineliste] >= vaksinerperdag,
    Do[
      nyimune[[vaksineliste[[kk, 2]]]] = 1;
      vaksinert = Append[vaksinert, vaksineliste[[kk, 2]]];
      , {kk, 1, vaksinerperdag}];
    ,
  nyimune = Table[1, {n}];
  ];
imune = UnitStep[imune + nyimune - 1];
mulige =
  Plus @@ Table[
    MapAt[# + 1 &, Table[0, {n}], L[ksmitte[[j]]]], {j, 1,
      Length[ksmitte]};
  ];
probsmitte = 1 - (1 - \[Beta])^mulige;
probsmitte = probsmitte*(1 - imune);
If[Length[ksmitte] > 0 ,
  nysmittede =
    UnitStep[Sign[probsmitte - Table[RandomReal[], {Length[mulige]}]]];
  nysmittede = UnitStep[nysmittede - smittetever - 1];
  smittetever = UnitStep[smittetever + nysmittede - 1];
  smittende =
    smittende + UnitStep[Last[nysmittedeliste] - 1] - Last[smittendeliste];
  smittendeliste = Drop[smittendeliste, -1];
  smittendeliste = Prepend[smittendeliste, Last[nysmittedeliste]];
  nysmittedeliste = Drop[nysmittedeliste, -1];
  nysmittedeliste = Prepend[nysmittedeliste, nysmittede];
  pnysmittende = Position[nysmittede, _?(# == 1 &)];
  psmittende = Position[smittende, _?(# == 1 &)];
  pimune = Position[imune, _?(# == 1 &)];
  nyetilfeller = Append[nyetilfeller, Plus @@ nysmittede];
  ,

```

```

smittende =
  smittende + UnitStep[Last[nysmittedeliste] - 1] - Last[smittendeliste];
smittendeliste = Drop[smittendeliste, -1];
smittendeliste = Prepend[smittendeliste, Last[nysmittedeliste]];
nysmittede = Table[0, {n}];
nyetilfeller = Append[nyetilfeller, 0];
nysmittedeliste = Drop[nysmittedeliste, -1];
nysmittedeliste = Prepend[nysmittedeliste, nysmittede];
];
(*farge1=Map[#\[Rule]Orange&,Flatten[psmittende]];
farge2=Map[#\[Rule]Green&,Flatten[pimune]];
farge3=Map[#\[Rule]Red&,Flatten[pnysmittende]];
farge=Join[farge2,farge1, farge3];
plotliste=Append[plotliste,GraphPlot[g,VertexStyle\[Rule]farge]];*)
, {t, 1, tmax}];
referanse = 0.001;
døde = Plus @@ (referanse*d[alder]*smitteteveer);
taptelevear = Plus @@ (referanse*d[alder]*smitteteveer*forventetlevetid);
dliste = Append[dliste, døde];
lliste = Append[lliste, taptelevear];
nyetilfellerliste = Append[nyetilfellerliste, nyetilfeller];
, {teller, 1, 5}];
dødsliste = Append[dødsliste, {v, dliste}];
levearliste = Append[levearliste, {v, lliste}];
, {v, 0.01, 10.01, 1.}
];
, {teller, v}];

utbrudd2 =
  Table[Map[Mean[# + 0.] &,
    Transpose[Partition[nyetilfellerliste, 5][[i]]], {i, 1, 11}];
Grid[Partition[
  Table[ListPlot[{utbrudd1[[i]], utbrudd2[[i]]}, PlotStyle -> {{Blue}, {Red}},
    Axes -> False, Frame -> True,
    FrameLabel -> {"time (days)", "New cases per day"},
    FrameStyle -> Directive[Black, 11], Joined -> True, PlotRange -> {0, 35},
    ImageSize -> 200], {i, 1, 11}], UpTo[4]]

mean = Transpose[{dødsliste[[All, 1]], Map[Mean[#] &, dødsliste[[All, 2]]]}];
lower = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.25] &, dødsliste[[All, 2]]]}];
upper = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.75] &, dødsliste[[All, 2]]]}];
plot2 = ListPlot[{mean, upper, lower}, PlotStyle -> {Red, Red, Red},

```

```

    Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,
    GridLinesStyle -> Black, Axes -> False, Frame -> True,
    FrameLabel -> {"vaccination rate (per day)", "deaths"},
    FrameStyle -> Directive[16, Black]];
mean = Transpose[{levarliste[[All, 1]],
  Map[Mean[#] &, levarliste[[All, 2]]]}];
lower = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.25] &, levarliste[[All, 2]]]}];
upper = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.75] &, levarliste[[All, 2]]]}];
plot2b = ListPlot[{mean, upper, lower}, PlotStyle -> {Red, Red, Red},
  Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,
  GridLinesStyle -> Black, Axes -> False, Frame -> True,
  FrameLabel -> {"vaccination rate (per day)", "YLL"},
  FrameStyle -> Directive[16, Black]];
figa = Show[plot1, plot2, ImageSize -> 300,
  Epilog -> Inset[Style["A", 18], Scaled[{0.9, 0.9}]]];
figb = Show[plot1b, plot2b, ImageSize -> 300,
  Epilog -> Inset[Style["B", 18], Scaled[{0.9, 0.9}]]];
FIG1 = Show[Rasterize[Grid[{figa, figb}], RasterSize -> 2000],
  PlotLabel ->
  Style["Network: Uniform Graph Distribution, R0=1.5, N=300", Black, 12],
  ImageSize -> 800]

mean = Transpose[{dødsliste[[All, 1]], Map[Mean[#] &, dødsliste[[All, 2]]]}];
lower = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.025] &, dødsliste[[All, 2]]]}];
upper = Transpose[{dødsliste[[All, 1]],
  Map[Quantile[#, 0.975] &, dødsliste[[All, 2]]]}];
plot2c = ListPlot[{mean, upper, lower}, PlotStyle -> {Red, Red, Red},
  Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,
  GridLinesStyle -> Black, Axes -> False, Frame -> True,
  FrameLabel -> {"vaccination rate (per day)", "deaths"},
  FrameStyle -> Directive[16, Black]];
mean = Transpose[{levarliste[[All, 1]],
  Map[Mean[#] &, levarliste[[All, 2]]]}];
lower = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.025] &, levarliste[[All, 2]]]}];
upper = Transpose[{levarliste[[All, 1]],
  Map[Quantile[#, 0.975] &, levarliste[[All, 2]]]}];
plot2d = ListPlot[{mean, upper, lower}, PlotStyle -> {Red, Red, Red},
  Filling -> {2 -> {3}}, Joined -> True, PlotRange -> All,
  GridLinesStyle -> Black, Axes -> False, Frame -> True,
  FrameLabel -> {"vaccination rate (per day)", "YLL"},
  FrameStyle -> Directive[16, Black]];

```

```
figc = Show[plot1c, plot2c, ImageSize -> 300,  
  Epilog -> Inset[Style["A", 18], Scaled[{0.9, 0.9}]]];  
figd = Show[plot1d, plot2d, ImageSize -> 300,  
  Epilog -> Inset[Style["B", 18], Scaled[{0.9, 0.9}]]];  
FIG2 = Show[Rasterize[Grid[{{figc, figd}}], RasterSize -> 2000],  
  PlotLabel ->  
  Style["Network: Uniform Graph Distribution, R0=1.5, N=300", Black, 12],  
  ImageSize -> 800]
```

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