University of Camerino

PAS Project Report:
comparing the effectiveness of vaccination strategies through augmented SIRD models.

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1. Project Description

The project aim at creating a variant of the SIRD model in which vaccination is added. Furthermore, the population must be divided in 6 age groups: from 0 to 50 years old; from 50 to 60 years old; from 60 to 70 years old; from 70 to 80 years old; from 80 to 90 years old; over 90 years old.

We want to keep track of the impact of the disease among the different age groups and also test the efficacy of several vaccination strategies:

- No Vaccination: no one will be vaccinated. This is also used as a baseline to show the disease behaviour;

- Random Vaccination: anyone can be vaccinated at any time;

- Older First: the priority is given to the older and most vulnerable individuals. The vaccination starts from them and then continues towards the lower groups in terms of age;

- Younger First: the priority is given to the younger individuals. The vaccination starts from them and then continues towards the greater groups in terms of age;

For the *older first* and *younger first* strategies the vaccinations start from a group and when only a certain percentage of susceptible individuals remains we pass to the next group, we keep doing this until we finish.

1.1 Adapting the SIRD Model

The SIRD model, is a well known model used to make distinction between Recovered and Deceased.

Figure 1.1 represent the aforementioned model where β, γ and μ are respectively the rates of infection, recovery, and mortality.
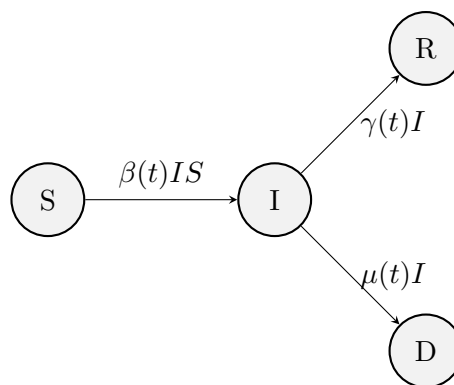

Figure 1.1: Representation of a SIRD model.

However this is not enough to represent our case. As a matter of fact, we need to introduce the vaccination and the distinction of the different rates between the age groups.
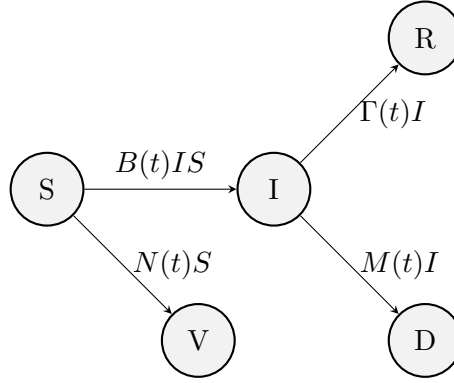
Figure 1.2: Representation of a SIRD model.

Figure 1.2 shows a different representation that consider the aforementioned concepts. Indeed if we consider $\beta(t, ag)$, $\gamma(t, ag)$, $\mu(t, ag)$, $\nu(t, ag)$ respectively as the rates of infection, recovery, mortality and vaccination at time t for a particular age group (ag) belonging to the set of all the age groups (AG), we will have that:

$$
\begin{aligned}
B(t) &= \sum_{ag \in AG} \beta(t, ag) \\
\Gamma(t) &= \sum_{ag \in AG} \gamma(t, ag) \\
M(t) &= \sum_{ag \in AG} \mu(t, ag) \\
N(t) &= \sum_{ag \in AG} \nu(t, ag)
\end{aligned}
\tag{1.1}
$$

where $B(t)$, $\Gamma(t)$, $M(t)$, $N(t)$ are respectively the total rates of infection, recovery, mortality and vaccination at time t considering all the age groups.

The extended model now is suitable to handle our case. As a matter of fact this model uses the following system of differential equations:

$$\frac{dS}{dt} = -\frac{B(t)IS}{P} - N(t)S,$$

$$\frac{dI}{dt} = \frac{B(t)IS}{P} - \Gamma(t)I - M(t)I,$$

$$\frac{dR}{dt} = \Gamma(t)I, \tag{1.2}$$

$$\frac{dD}{dt} = M(t)I,$$

$$\frac{dV}{dt} = N(t)S$$

where $P = S(t) + I(t) + R(t) + V(t)$, which is the alive population at time t.

1.2 Data gathering

Since I wanted to add a little bit of reality to the model, I decided to use real data related to COVID-19 pandemic. Data have been collected from different institutional sources and are focused on Italy.

These information have been collected in the early October 2021, thus some values will be outdated for sure.

All the statistics related to the COVID-19 disease have been extracted and processed from the *Istituto Superiore della Sanità*, which is an Italian public institution that leads the technical-scientific body of the Italian National Health Service.

Italian population age distribution: These information represents the distribution of Italian population by age. These data have been collected from [4] and have been aggregated into the 6 age groups. They will be useful to calculate the infection rate, which will be higher for an age group if it is easier to meet an individual of that group.

Basic reproduction number: One of the most sneaky parameters that can totally change the outcomes of simulations is the Basic reproduction number, or R_0. This number is associated to an infection and it is the expected number of cases directly generated by one case in a population where all individuals are susceptible to infection [5].

This number can be also used to represents the spread of an infection when no restriction is given to the susceptibles or the infected, which is the case of our simulation.

In order to approximate this parameter as better as possible I gathered data related to the R_t index also called, effective reproduction number. The latter represents the number of cases generated by an infected individual in the current state of a population (at time t).
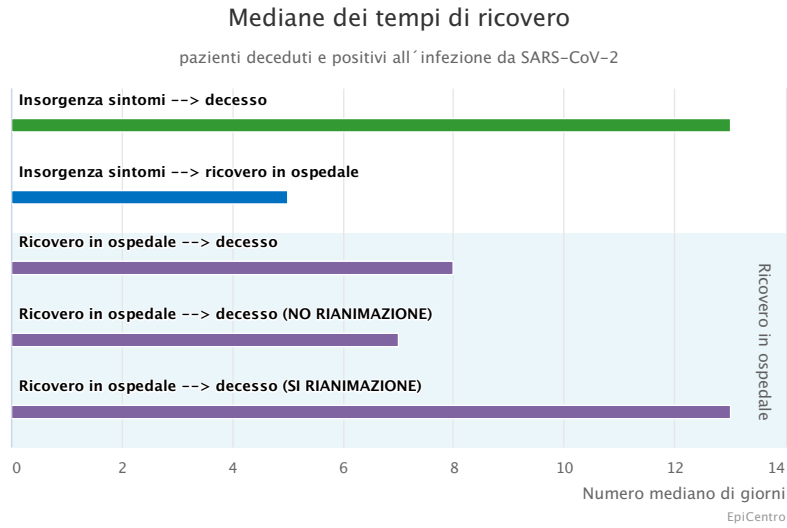
Figure 1.3: Medians of recovery times.

These data contains the trend of the R_t index from the start of the pandemic to October 2021, date of the data gathering. By performing the mean of such indexes I found a value of *2.28*, this will be the value used as R_0 in the model.

Positives By Age Groups: These data show the age distribution of positives aggregated by age groups. They represent the fraction of individuals of a certain age group that had been infected, in other words it is the incidence of infections per age group. The fraction has been calculated on the Italian population age distribution given by ISTAT [3]. They have been used to calculate the lethalities and, in the model, to dynamically instantiate the species during the simulation, more insights will be given in the next chapter.

Lethality by age group: Lethality is the proportion of people diagnosed with a certain disease, who end up dying of it [6]. Since we are modelling different age groups we need to know the lethality associated to each of them. Unfortunately the *Istituto Superiore della Sanità* did not provide these information so I had to calculate it by myself.

To do so I extracted data related to the age distribution of deaths and I combined them with the data regarding the age distribution of positives, discussed in the previous paragraph. For each age, knowing the number of deaths and positives individual, I calculated the lethality of the disease and then aggregated the values into the 6 age groups.

These information will be used as rates to simulate the death of infected individuals.

Average death time: Another sneaky parameter that I needed during the modelling was the recovery rate of infected.

Since there are not so many data about recoveries I decided to approximate that by looking at how many days pass (on average) before a COVID-19 infected dies.

Figure 1.3, retrieved from [2], shows some medians of days that passes from the onset of symptoms to death, including also medians for hospitalizations. The green bar show

that, on average, 13 days pass between the onset of symptoms to death. The blue bar shows a median of 5 days from the onset of symptoms to hospitalization, while the last 3 purple bars shows the median times from hospitalization to death, which span from 7 to 13 days depending on whether patients were transferred to the intensive care.

This data will be used to calculate the rate of recovery, indeed as a simplification an infected will recover after being 13 days infected, if he does not die before.

The next chapter shows an in-depth overview of the models.

2. Models Description

In this Chapter the 4 models are presented: No Vaccine Strategy, Older First Vaccine Strategy, Random Vaccine Strategy and Younger First Strategy.

Since the models differ only in the rules, the Sections 2.1 and 2.2 introduce all the common elements.

2.1 Parameters, Constants, Labels and Species

This section contains some common elements of the implemented models, which are the parameters, the constants, the labels and the species.

Parameters: are all the values that can also be set from outside, when launching the model. There are three parameters: *r0*, *A* and *vaccination_threshold*.

r0 is the basic reproduction number (see section 1.2) that has a default value of 2.28, which has been computed during the data gathering.

The parameter *A* represents the total population size which will then be split into infected and susceptibles for each age group. Its default value is 1000.

The *vaccination_threshold* is included only in the *younger first* and *older first* models. It represents the percentage of remaining susceptible of an age group that we must reach in order to start the vaccination of the next age group.

```
1  param r0 = 2.28;
2  param A = 1000;
3  param vaccination_threshold = 0.1;
```

Code 2.1: The models parameters.

Constants: are all the values that can't be set from outside (when launching the model). Most of them represent values that have been computed during the data gathering.

N represents the number of age groups, which is 6. They are: from 0 to 49; from 50 to 59; from 60 to 69; from 70 to 79; from 80 to 89; over 90.

```
1  const N = 6;
```

Code 2.2: The number of age groups.

Then, a probability of meeting an individual belonging to a certain age group is defined in code 2.3. This probability has been extracted during the data gathering from the distribution of Italians inhabitants by age groups (see Section 1.2).

As a matter of fact, 54% of the Italian population is under 50, thus the probability of meeting an under 50 individual will be 54%. These information have been also used to

calculate the initial population.

```
1  const probIU50meet = 0.5445;
2  const probIO50U60meet = 0.1578;
3  const probIO60U70meet = 0.1235;
4  const probIO70U80meet = 0.10;
5  const probIO80U90meet = 0.061;
6  const probIO90meet = 0.0133;
```

Code 2.3: The percentage of individuals for each age group, which is also the probability to meet an individual of that age group.

Other fundamental constants based on real values previously extracted are the percentage of positives for each age group (see Section 1.2).

For example, based on real values, among the under 50 Italian individuals the 8% had been positive.

See code 2.4 for all the percentages.

```
1  const positives0 = 0.0795;
2  const positives1 = 0.0823;
3  const positives2 = 0.0661;
4  const positives3 = 0.0596;
5  const positives4 = 0.0746;
6  const positives5 = 0.1218;
```

Code 2.4: The percentage of positives for each age group.

To initialize the model two values are needed: the initial number of susceptible, and the initial number of infected. In this case since there are 6 age groups, we need those values for each group, which means 12 constants are needed to initialize the model.

I wanted to make sure that these constants are based on real values too.

```
1  const n_I0_init = A*probIU50meet*positives0;
2  const n_I1_init = A*probIO50U60meet*positives1;
3  const n_I2_init = A*probIO60U70meet*positives2;
4  const n_I3_init = A*probIO70U80meet*positives3;
5  const n_I4_init = A*probIO80U90meet*positives4;
6  const n_I5_init = A*probIO90meet*positives5;
```

Code 2.5: The initial number of infected for each age group.

The code 2.5 shows that the initial number of infected for a certain age group is given by multiplying the total size of the population by the percentage of individuals of that age group and the percentage of individuals of the same group that had been positives.

For instance, if $A = 1000$ then the initial number of infected under 50 will be 43, which is the 8% of the 54% of 1000.

Then, the number of susceptible for each age group is given by the number of individuals of that age group minus the ones that are infected.

```
1  const n_S0_init = (A*probIU50meet)-n_I0_init;
2  const n_S1_init = (A*probIO50U60meet)-n_I1_init;
3  const n_S2_init = (A*probIO60U70meet)-n_I2_init;
4  const n_S3_init = (A*probIO70U80meet)-n_I3_init;
5  const n_S4_init = (A*probIO80U90meet)-n_I4_init;
6  const n_S5_init = (A*probIO90meet)-n_I5_init;
```

Code 2.6: The initial number of susceptible for each age group.

For example, looking at code 2.6, the initial number of susceptible under 50 for $A = 1000$ will be $n\_S0\_init = 1000 * 0,5445 - 43 = 502$.

Doing so it is possible to maintain the distributions of the age groups as they are for the Italian population (code 2.3), indeed $tot\_under\_50 = n\_S0\_init + n\_I0\_init = 544$.

Furthermore the lethalities extracted from the data (section 1.2) are declared as constants, see code 2.7.

```
1  const lethality0 = 0.0006;
2  const lethality1 = 0.0061;
3  const lethality2 = 0.0277;
4  const lethality3 = 0.0929;
5  const lethality4 = 0.1996;
6  const lethality5 = 0.2801;
```

Code 2.7: The lethalities for each age group.

Last but not least, code 2.8 shows the constant that is used to store the number of days that an infected needs to recover.

The value used for this constant is the average death time for an infected individual, extracted during the data gathering phase. This is a simplification since when the data gathering were performed, as stated in the previous chapter, data regarding recoveries were not available.

However, if an infected in average dies after 13 days from the infection, this means that if he is not dead after the same amount of time then I can consider him recovered.

```
1  const recovery_time = 13; /* days */
```

Code 2.8: The time needed for an infected to recover.

Species   Each model has 5 ”kind” of species: (S)usceptible, (I)nfected, (R)ecovered, (D)ead, (V)accinated. The only exception is the *no vaccine model* that does not have the vaccinated specie since it does not model the vaccination.

The Susceptible, Infected, Recovered and Dead species are arrays of N species where N is the number of age groups. Since we have 6 age groups each array goes from 0 to 6.

Each specie is associated to an age group by its index from the youngest to the oldest, which means that: the specie at index 0 is the one for the ”under 50 y.o.” age group; the index 1 is for the ”over 50 under 60 y.o.”; the index 2 is for the ”over 60 under 70 y.o.”; the index 3 is for the ”over 70 under 80 y.o.”; the index 4 is for the ”over 80 under 90 y.o.”; the index 5 is for the ”over 90 y.o.”;

For instance S[0] is the specie of susceptible under 50 years old.

The Vaccinated (V) specie is the only non-array specie, this because once an individual is vaccinated it is not necessary anymore to keep track of which age group he belongs to.

```
1  species S of [0, N]; /* susceptible */
2  species I of [0, N]; /* infected */
3  species R of [0, N]; /* recovered */
4  species D of [0, N]; /* dead */
5  species V;            /* vaccinated */
```

Code 2.9: The species (S)usceptible, (I)nfected, (R)ecovered, (D)ead, (V)accinated.

Labels The labels are used to group the arrays in order to get metrics on them, for example the total number (or fraction) of infected.

They are used later in the measures.

Regarding the *alive* label all the models except for the *no vaccine* one have the specie V.

```
1  label susceptibles = {S[i for i in [0, N]]}
2  label infected = {I[i for i in [0, N]]}
3  label dead = {D[i for i in [0, N]]}
4  label recovered = {R[i for i in [0, N]]}
5  label alive = {S[i for i in [0, N]], I[i for i in [0, N]], R[i for i
       in [0, N]], V}
```

Code 2.10: The labels of the models.

2.2 Common SIRD Rules

This section contains all the common rules to all the implemented model. As a matter of fact the SIRD rules are the same for all of them, they only differ in the rules that regulate the vaccination.

There are 4 kind of rules:

- **Susceptible to Infected:** 1 rule that models the behaviour of the susceptible individuals for each age group when they meet an infected.

- **Infected to Dead:** 6 rules, one for each age group, that model the death of an infected individual.

- **Infected to Recovered:** 1 rule that models the recovery of an infected individual for each age group.

Susceptible to Infected The rule in Code 2.11 models the behaviour of the susceptible individuals for each age group when they meet an infected.

```
1  rule s_to_i for i in [0, N] and k in [0, N] {
2      S[i]|I[k] -[ r0 * #I[k] / #alive ]-> I[i]|I[k]
3  }
```

Code 2.11: Rule code which models the behaviour of a susceptible that meets an infected.

These rules basically state that whenever a susceptible ($S[x]$) meets an infected, then he is infected ($I[x]$) with a rate given by the basic reproduction number multiplied by the total probability to meet an infected individual. The latter is given by the percentage of infected among the alive population.

Infected to Dead The 6 rules in Code 2.12 model the death of an infected individual. An infected dies with rate given by the lethality associated to its age group.

```
1   rule i_to_d_U50 {
2       I[0] -[ lethality0 ]-> D[0]
3   }
4
5   rule i_to_d_O50U60 {
6       I[1] -[ lethality1 ]-> D[1]
7   }
8
9   rule i_to_d_O60U70 {
10      I[2] -[ lethality2 ]-> D[2]
11  }
12
13  rule i_to_d_O70U80 {
14      I[3] -[ lethality3 ]-> D[3]
15  }
16
17  rule i_to_d_O80U90 {
18      I[4] -[ lethality4 ]-> D[4]
19  }
20
21  rule i_to_d_O90 {
22      I[5] -[ lethality5 ]-> D[5]
23  }
```

Code 2.12: Rules to model the death of infected individuals.

Infected to Recovered The rule in Code 2.13 models the recovery of an infected individual.

The recovery rate of an infected is given by the average death time, which is 13 days. Indeed this means that if 13 days passed and the individual is not dead, then he can be considered as recovered.

```
1  rule i_to_r for i in [0, N] {
2      I[i] -[ 1/avg_death_time ]-> R[i]
3  }
```

Code 2.13: Rule to model the recovery of infected individuals.

2.3   No Vaccine Model Rules

This model does not implement any vaccination strategy, thus it neither contains the *V* specie and the rules associated with it. It has been implemented in order to have a sort of baseline to perform benchmarks on the other models, hence it contains only the common elements of a general SIRD model.

Indeed the resulting model approximates well the behaviour of a general SIRD model in an epidemic scenario ($R_0 > 1$).

Figure 2.1 shows a comparison between the behaviour of the *novaccine* model (left image) and the behaviour of a general SIRD model (right image). Although the parameters are different, indeed the *novaccine* model takes more time unit to replicate the same behaviour (2190 days, 6 years), the result is pretty similar.
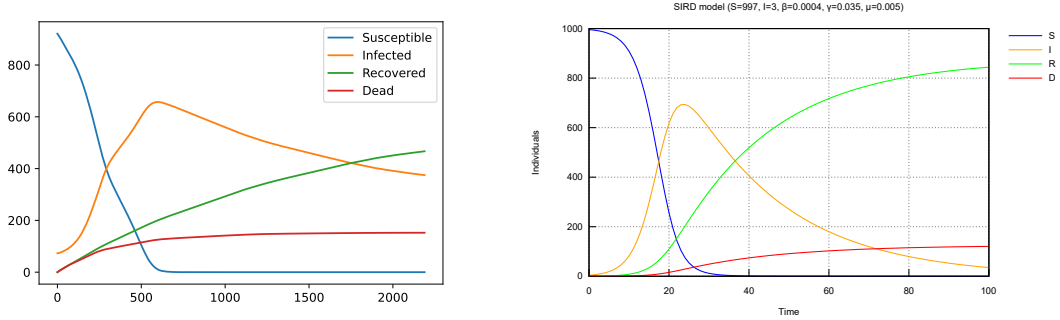

Figure 2.1: Diagram of the *no vaccine* model compared to the diagram of a general SIRD model. Right figure taken from [1]

2.4   Random Model Rules

The rule to model the random vaccination strategy in which anyone can be vaccinated, regardless of the age group he belongs to, is straightforward.

```
1  rule s_to_v for i in [0, N] {
2      S[i] -[ 1.0 ]-> V
3  }
```

Code 2.14: Rule to model the random vaccination of susceptible individuals.

As shown in code 2.14 every age group of susceptible individuals has the same probability to be vaccinated, hence they are vaccinated randomly.

2.5   Older First Model Rules

In this model a new parameter, the *vaccination_threshold* introduced in Section 2.1, is used. The latter is set as 0.1 by default, but it can be changed when the model is run too.

In this model the vaccination strategy requires that the older individuals are vaccinated first. Then, when the higher group in terms of age reaches the percentage of remaining

susceptible individuals, the next group starts the vaccination. The procedure continues from age group to age group down to the younger individuals.

```
1  rule s_to_v_O90 {
2      S[5] -[ 1.0 ]-> V
3  }
4
5  rule s_to_v_O80U90 {
6      [#S[5] <= (vaccination_threshold * n_S5_init)] S[4] -[ 1.0 ]-> V
7  }
8
9  rule s_to_v_O70U80 {
10     [#S[4] <= (vaccination_threshold * n_S4_init)] S[3] -[ 1.0 ]-> V
11 }
12
13 rule s_to_v_O60U70 {
14     [#S[3] <= (vaccination_threshold * n_S3_init)] S[2] -[ 1.0 ]-> V
15 }
16
17 rule s_to_v_O50U60 {
18     [#S[2] <= (vaccination_threshold * n_S2_init)] S[1] -[ 1.0 ]-> V
19 }
20
21 rule s_to_v_U50 {
22     [#S[1] <= (vaccination_threshold * n_S1_init)] S[0] -[ 1.0 ]-> V
23 }
```

Code 2.15: Rules to model the vaccination of susceptible individuals starting by the older ones toward the youngest ones.

As shown in code 2.15 the guard expressions are applied to each rule in order to simulate a sort of waterfall approach. Indeed by default the vaccination of the next age group can't start until the previous group reaches the 10% of remaining susceptible individuals. However, when the next group starts the vaccination, the previous continue to do it too so that at the end all the susceptible will be vaccinated, dead or recovered.

2.6   Younger First Model Rules

The rules that model the behaviour of the younger first vaccination strategy are analogous to the ones that model the older first vaccination strategy.

Codes 2.16 and 2.17 together contains all the aforementioned rules, but they are split for sake of readability.

```
1  rule s_to_v_U50 {
2      S[0] -[ 1.0 ]-> V
3  }
4
5  rule s_to_v_O50U60 {
6      [#S[0] <= (vaccination_threshold * n_S0_init)] S[1] -[ 1.0 ]-> V
7  }
```

Code 2.16: Rules to model the vaccination of susceptible individuals starting by the younger ones toward the oldest ones.

```
1  rule s_to_v_O60U70 {
2      [#S[1] <= (vaccination_threshold * n_S1_init)] S[2] -[ 1.0 ]-> V
3  }
4
5  rule s_to_v_O70U80 {
6      [#S[2] <= (vaccination_threshold * n_S2_init)] S[3] -[ 1.0 ]-> V
7  }
8
9  rule s_to_v_O80U90 {
10     [#S[3] <= (vaccination_threshold * n_S3_init)] S[4] -[ 1.0 ]-> V
11 }
12
13 rule s_to_v_O90 {
14     [#S[4] <= (vaccination_threshold * n_S4_init)] S[5] -[ 1.0 ]-> V
15 }
```

Code 2.17: Rules to model the vaccination of susceptible individuals starting by the younger ones toward the oldest ones.

The difference is given by the fact that the vaccination starts from the susceptible individuals under 50 years old. Moreover the order in which the rules are written is reversed but the mechanism is the same. As a matter of fact, the next age group still starts the vaccination when the previous one reaches a certain percentage of remaining susceptible individuals.

While on the older first strategy the next age group is younger than the previous one, here it is older.

2.7   Measures

Code 2.18 shows the measures used. By mean of the labels I keep track of the total infections, deaths, susceptible individuals and recoveries.

The *.csv* files generated from the execution are then processed through several Python notebooks.

```
1  measure n_infected = #infected;
2
3  measure n_dead = #dead;
4
5  measure n_susceptible = #susceptibles;
6
7  measure n_recovered = #recovered;
```

Code 2.18: Measures used in every model.

2.8   System Initialization

Last but not least the system named *corona* is initialized as shown in code 2.19. Indeed the susceptible and infected of each age group have a different initial number which is given by the related constants.

```
1  system corona = S[0]<n_S0_init>|S[1]<n_S1_init>|S[2]<n_S2_init>|S
       [3]<n_S3_init>|S[4]<n_S4_init>|S[5]<n_S5_init>|I[0]<n_I0_init>|I
       [1]<n_I1_init>|I[2]<n_I2_init>|I[3]<n_I3_init>|I[4]<n_I4_init>|I
       [5]<n_I5_init>;
```

Code 2.19: Initialization of susceptible and infected.

3. Results

This Chapter contains the result obtain through the execution of the four models.

Regarding the *younger first* and the *older first* strategies all the results have been performed with a vaccination threshold set to 0.1, except for those parts in which it is stated differently.

3.1   General Trend

Figures 3.1 shows the general trend of the disease when following different vaccination strategies.

Indeed when no vaccination is put in place then the number of infected and dead individuals is maximum. On the other hand, by vaccinating the younger individual first, the infected decreases even though it takes some time to do so, but the deaths does not improve. This is due to the fact that the younger individuals are less prone to die by the disease, hence by starting the vaccination from them does not prevent the older ones to die.
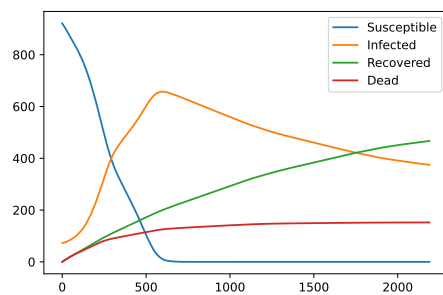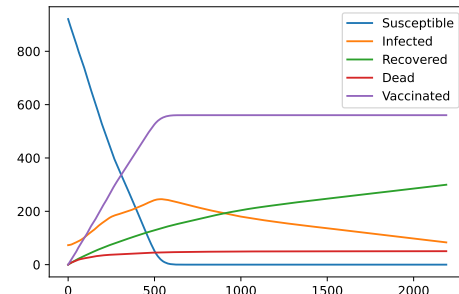

No vaccination strategy.
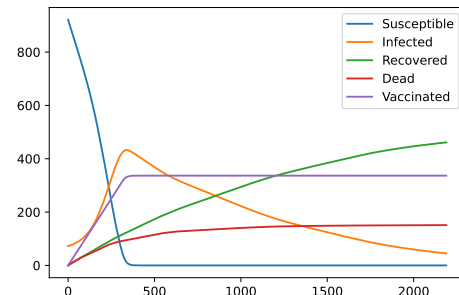
Younger first strategy.
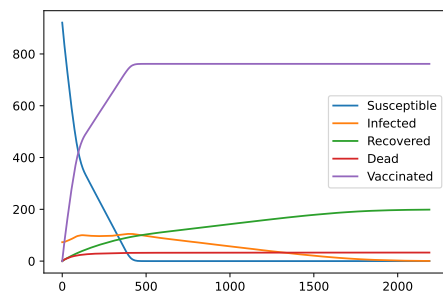
Random vaccination strategy.

Older first strategy.

Figure 3.1: General disease trend for each strategy.

The random vaccination strategy seems to be the best one to minimize the infections and the deaths. However, this strategy is impossible to adopt in a real scenario due to the limitations on the number of vaccines available on a daily basis.

The strategy in which the older individuals are vaccinated first is a good compromise that allows a substantial reduction on infections and deaths by prioritizing the vulnerable individuals.

Table 3.1 compares the different techniques under different perspectives. The *Peak of Infections* reports the number of individuals that are infected in a certain time unit, in particular it shows the mean, standard deviation and the time unit when this number reached its maximum peak.

	Peak of Infections	Infections	Vaccinations	Recoveries	Deaths
No Vacc.	657.62 ± 1.58 @ 598	921	N.A.	466.91 ± 0.71	152.31 ± 0.39
Younger First Vacc.	432.61 ± 1.91 @ 338	584.34 ± 1.18	336.66 ± 1.18	461.38 ± 0.78	151.07 ± 0.41
Older First Vacc.	245.49 ± 2.13 @ 538	360.52 ± 1.95	560.48 ± 1.95	299.64 ± 0.92	50.45 ± 0.32
Random Vacc.	105.24 ± 1.08 @ 404	159.26 ± 1.18	761.74 ± 1.18	198.77 ± 1.06	32.98 ± 0.24

Table 3.1: Comparison of the different techniques by reporting the mean and standard deviation values.

3.2 Deaths

Figure 3.2 compares the total number of deaths for each vaccination strategy.

It is pretty clear that by focusing on the younger individuals first we do not have an actual improvement, indeed at the end there is a total of 151.06 ± 0.41 deaths against the 152.31 ± 0.39 deaths coming from the no vaccination strategy.

The figures also confirms the random vaccination as the ideally best one with 32.98 ± 0.24 deaths. However, the older first vaccination strategy is close to it with 50.45 ± 0.32 deaths, which make it an equally good strategy, but more feasible.

This result is what we expected because the older individuals have a higher chance to die from the infection, hence by vaccinating them first we reduce the overall mortality. Instead, by starting from the younger individuals there is not an improvement in this perspective.
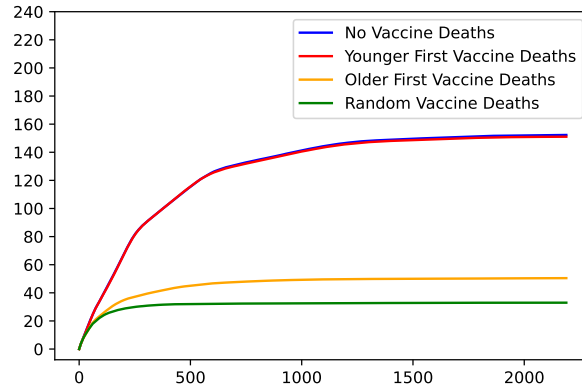

Figure 3.2: Deaths trend for each vaccination strategy.

Worth to notice is the importance of the vaccination threshold explained in Section 2.1. As a matter of fact, the lower is the age group the greater the number of individuals it is made up of, hence it takes more time to vaccinate a certain amount of them by reaching the threshold. This implies that by starting from the lower age groups it takes more time to reach the older and most vulnerable ones, so they will continue to die even though the vaccination is in progress.
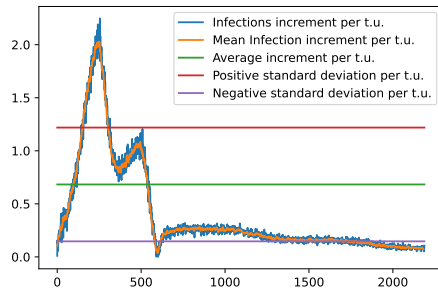
3.3 Infections

By looking at the trend and the total number of infections we wouldn't extract further information on the situation. For this reason it could be useful to look at this data with a different perspective.
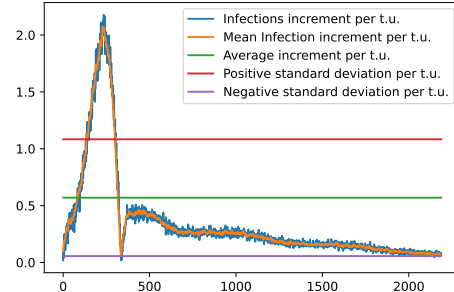
Figure 3.3 shows the increment of positives for each time unit. While the blue line shows the actual increment, the orange one shows the average increment on a window of 7 days. Along with these two lines also the mean increment and the standard deviation are plotted.

What is worth to notice is that even though the *younger first* strategy is the worst one regarding the general trend of infections and deaths, in this perspective of increment, it does a decent job with respect to the *no vaccination* strategy by decreasing the second peak of infections that comes around the 500th time unit.
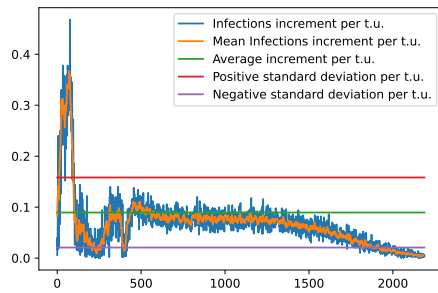
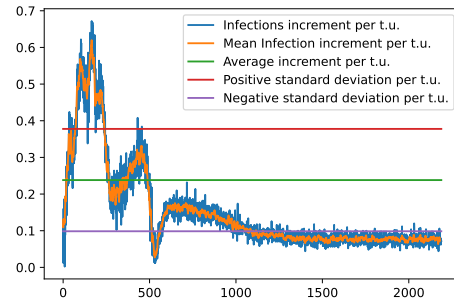This is due to the fact that the lower age groups form the majority of the population,

No vaccination strategy.

Younger first vaccination.

Random vaccination.

Older first vaccination.

Figure 3.3: Increment of positive individuals for each strategy.

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so it is easier to be infected by one of them. By starting the vaccination from them we will reach a certain point in which the majority of the population can't infect others, hence we avoid the occurrence of an impacting second peak of infections.

However, even though we reduce the occurrence of a second peak, there still are a lot of infections and deaths going on.

On the other hand, by looking at the infection increment of the *older first* strategy we can see that there is still the second peak, but there are a lot less infections in general.

Also in this case the vaccination threshold is a key factor. If we still look at the distribution of individuals among the different age groups we can clearly see that the lower is the age group the greater is the number of individuals, hence the greater the time needed to vaccinate them. By starting from the higher age group we will reach the lower age groups in a short time, since there are less individuals to vaccinate for each age group. On the other hand, by starting from the lower age groups the process will be stuck on their vaccination for much longer, allowing the disease to spread.

This can also be viewed in Figure 3.4 in which it is clear that the *younger first* strategy reduces significantly the infections among the individuals under the age of 50, leaving the trend of the other age groups untouched with respect to the *no vaccination* strategy.

On the other hand the *older first* strategy improves the trends of all the age groups, and the *random* strategy outperforms all of others.
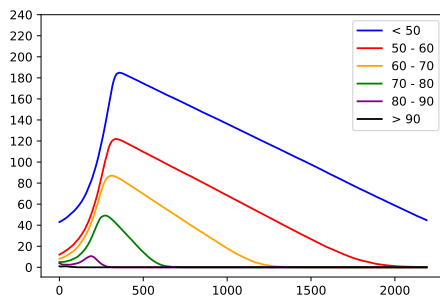
Figure 3.5 confirms the results by putting in relation the peaks in infections and the time units when they are reached. Indeed the *younger first* strategy reach its peak
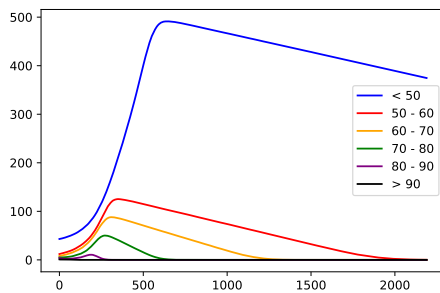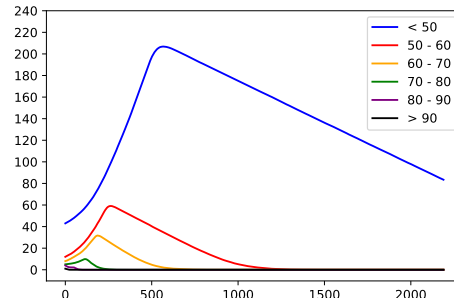

No vaccination strategy.   Random vaccination.
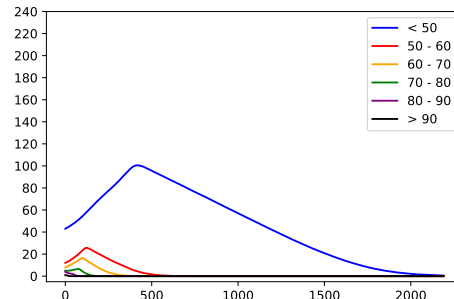
Younger first vaccination.   Older first vaccination.

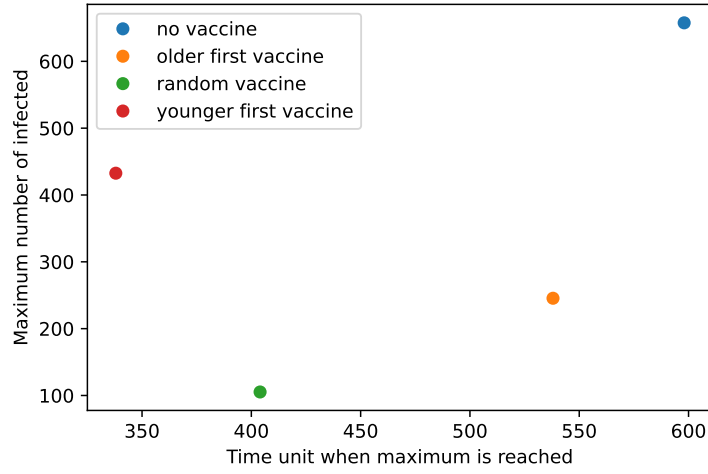Figure 3.4: Trend of infections per age group for each strategy.

Figure 3.5: Peaks on the number of infected individuals reached and the time unit when that happened, for each strategy.

earlier than the other approaches, but the value is higher. It would be interesting to find a way to lower this value leaving intact the time unit when it is reached and compare it to the *older first* approach.

Indeed by increasing the threshold we should not have a significant improvement for the *older first* strategy, but maybe we could significantly improve the *younger first* strategy. Some experiments with the threshold are shown in the next Section.

3.4   Optimal vaccination threshold value

Table 3.2 compares the *younger first* and *older first* vaccination strategies as the threshold changes.

		Peak of Infections	Infections	Vaccinations	Recoveries	Deaths
0.1	Y.F.	432.61 ± 1.91 @ **338**	584.34 ± 1.18	336.66 ± 1.18	461.38 ± 0.78	151.07 ± 0.41
	O.F.	**245.49 ± 2.13** @ 538	**360.52 ± 1.95**	**560.48 ± 1.95**	**299.64 ± 0.92**	**50.45 ± 0.32**
0.3	Y.F.	394 ± 1.87 @ **337**	543.15 ± 1.45	377.85 ± 1.45	430.35 ± 0.92	143 ± 0.41
	O.F.	**206.46 ± 1.95** @ 518	**310.41 ± 1.91**	**610.59 ± 1.91**	**283.99 ± 0.92**	**45.86 ± 0.34**
0.5	Y.F.	316.28 ± 2 @ **338**	460 ± 1.61	460.82 ± 1.61	377.1 ± 0.97	121.18 ± 0.41
	O.F.	**175.06 ± 1.8** @ 489	**265.54 ± 1.79**	**655.46 ± 1.79**	**265.9 ± 0.94**	**41.98 ± 0.30**
0.7	Y.F.	221.37 ± 2.01 @ **350**	350.4 ± 1.78	570.6 ± 1.78	314.64 ± 1.1	89.95 ± 0.41
	O.F.	**143.38 ± 1.47** @ 457	**219.3 ± 1.51**	**701.7 ± 1.51**	**243.87 ± 1.01**	**37.88 ± 0.3**
0.9	Y.F.	131.97 ± 1.31 @ **387**	218.07 ± 1.35	702.92 ± 1.35	236.79 ± 1.06	51.36 ± 0.32
	O.F.	**116.52 ± 1.24** @ 424	**178.78 ± 1.30**	**742.22 ± 1.31**	**215.06 ± 1.07**	**34.05 ± 0.25**

Table 3.2: Comparison of *younger first* and *older first* vaccination strategies as the vaccination threshold increases.

Of course as the threshold increases all the values improve because the next group will always start earlier and earlier.

It is also clear that by increasing it both the two strategies tend to approximate the *random vaccine* strategy, which obviously still outperform them.

Anyway, the *younger first* strategy always reaches the peak of infections before the

other strategy. This behaviour could be a double edged sword due to the fact that, in the real world, the faster we reach the peak the higher will be the difficulty to manage the pressure on the healthcare system. On the other hand, it is also true that the faster we reach the peak the faster we will overcome the issues. For instance, when the threshold is 0.1 the *younger first* reaches the peak at the 338*th* day, while the *older first* at the 538*th* day, which means a difference of 200 days, almost 7 months. This means that the pressure on the healthcare system would last much less and the economy, but more in general the society, may return faster to normality. Unfortunately this would happen at the cost of 3 times the deaths that there would be with the *older first* strategy, 151 deaths against 50.

All things considered, the *older first* strategy outperforms the *younger first* strategy in every measure.

4. Conclusions

After having thoroughly described the work done so far I want to conclude by summing up the main ideas.

The project specification requires to model a variant of a SIRD model in which the population is divided in age groups and the vaccination is added. We want then to keep track of the evolution of the disease and test different vaccination strategies: Random Vaccination, Younger first vaccination, Older first vaccination.

In the first Chapter I attempted the formalization of a variant of the SIRD model in which all the aforementioned concepts have been included. Furthermore, since I wanted to add a little bit of reality to the model I also explained how I gathered data regarding COVID-19, which are then used within the models.

The second Chapter describe the 4 implemented models, starting from the common elements to the specific vaccination rules that distinguish all of them. Furthermore the *younger first* and the *older first* strategy are provided with the vaccination threshold parameter which let us decide when to extend the vaccination further to the next age group.

Last but not least, the third Chapter shows the results under different perspectives: the general trend of the disease when the vaccination threshold is set to 0.1; the increment trend of positives individuals; the comparison of the *younger first* and *older first* strategies as the vaccination threshold increases.

The results show that the *random vaccine* strategy outperforms the others under every aspect. However, if this strategy where to be adopted in a real scenario, then it would not produce the same outcomes due to the fact that in reality there are limitations in the number of vaccines that are available to the centers on a daily basis. Still it can be considered as the "ideal" strategy to face the disease.

The other two strategies are limited by the vaccination threshold, indeed by increasing it they tend to approximate the *random vaccination* strategy. This suggest that we should try to keep the threshold as high as possible. Still the *older first* strategy seems to be best one when we want to reduce at minimum the casualties and the infections, furthermore this strategy is also more applicable in the reality since we can tune the vaccination threshold to respect the vaccines availability in the centers. However, if we focus only on eradicating the disease as earlier as possible, then the *younger first* strategy is a good choice since we aim at reaching the immunity among the majority of the population as soon as possible. The downside of this strategy is that we will have to pay the prize with an increased number of deaths with respect to the other strategy, indeed the casualties in the *younger first* are 3 times those of the *older first*.

To conclude the report I am satisfied with the entire project and the PAS course. Indeed it let me dive into the area of simulation which is quite interesting, especially when applied in a real scenario as a pandemic that all of us actually lived through.

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