Analysis of the extension of SEIR models by analyzing COVID-19 on Turkey

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Abstract

In this paper, we looked at the extensions of the SEIR model, SEI^3RD and SEI^3Q^3RD model. Then we checked the graphs of the SEI^3Q^3RD model with different tracing app user populations and with the parameters we collected from Turkey's data. We figured that the effect of the infection on the people is negligible if nearly 75% of the population use tracing apps. Besides that, we made an R_0 calculation of the extended models and used them on Turkey's 15 April data. Then we argued that quarantined populations also have some chance to infect people, but lower than non-quarantined infected people. So we suggested adding the Q compartments into the S compartment's differential equation as an infector parameter.

Introduction

COVID-19 started spreading in December 2019 and became a pandemic disease swiftly. Some governments take cautions like closing the borders, isolating the people from each other, and others do nothing against spreading because they do not take COVID-19 seriously. To determine whether we should take COVID-19 seriously or not, we have some models to predict the infection's effect on the population. This paper used model extensions of the SEIR model given by Grimm et al.(2021) [1] on COVID-19 to analyze how these models behave. These models extend the SEIR model by dividing the population into risk groups, dividing the infection's severity, or giving the people a

chance to use tracing apps to trace the infection. For our example government, we aimed to examine Turkey's COVID-19 prediction and get the parameters from the data provided by the Government of Turkey.

Turkey's report on COVID-19 has low infectious rates, even though the people of Turkey do not obey the regulations. There was a strict lockdown in Turkey, in which no one was allowed to leave their house on weekends, a long period of shut down of schools, cafes, and pubs, and wearing a face mask outside of the house and inside of cars. Even with these restrictions stated by the government, many people did not obey these strict rules. Even in government congress, people disobeyed face masks and did not keep their distance at the start of the infection. Still, one can see that Turkey showed low infection and death rates in some periods of the COVID-19 pandemic. Low infection and death rates with broken pandemic rules are related to Turkey's false infection reports. Many countries have warned Turkey of giving incorrect information. We did our models with reported numbers provided by Government of Turkey, so we should bear in mind the false reports while doing our model.

Firstly, we explained the SIR and SEIR models, which are ODE problems to solve the rate of the given population's states regarding time. Secondly, we found our models' parameters and then look at the models. These models are the SIR, SEIR, and extension of the SEIR models, named SEI^3RD and SEI^3Q^3RD models. We used the SEI^3RD model to examine the given population by their risk groups and severity of their infections. With the SEI^3Q^3RD, we introduced a function to the population, which tracks the infectious people and isolates them into quarantine. After that, we found the next generation matrix of all our models and find their R_0 values. Then, we saw how important it is to use a tracing app to fight against the endemic and then discuss the optimal point for the number of tracing app users. After that, we looked at the problems of our extended models and tried to come up with some solutions. After that, we checked the graphs of Turkey with our extended models by taking 15 April as the initial phase. Finally, we concluded everything.

Materials and methods

Parameters

Table 1. Notation of the parameters

symbols	explanation
N	Number of individuals
K	Number of groups
η	Fraction of asymptomatic infectious individuals
ν	Fraction of severely symptomatic infectious individuals to symptomatic individuals
β	Infection rate
β^{asym}	Infection rate of asymptomatic infectors
β^{sym}	Infection rate of symptomatic infectors
β^{sev}	Infection rate of severely infected infectors
γ	Multiplicative inverse of average infectious period
γ^{asym}	Multiplicative inverse of average infectious period of asymptomatic infected individuals
γ^{sym}	Multiplicative inverse of average infectious period of symptomatic infected individuals
γ^{sev-r}	Multiplicative inverse of average infectious period of severe but recovered infected individuals
γ^{sev-d}	Multiplicative inverse of average infectious period of severe but died infected individuals
ε	Multiplicative inverse of average latent period
σ	Lethality rates
B	Number of ICU beds
ψ	Percentage of tracing app users

Notations are taken from Grimm et al.(2021) [1]

To discuss our models, we choose our parameters depending on Turkey's COVID-19 data because, in the end, we want to find a prediction of Turkey's COVID-19. So we can find how the real COVID-19 was established compare to the given reports of Turkey.

N — It is the population parameter. Turkey's population is roundly 85 million people in 2020 [2]. According to WHO's report on COVID-19 [3], some of the high-risk groups of corona disease are cancer patients, people with diabetes, and people with cardiovascular disease. Getting cancer before age 75 is 23% [4], getting diabetes is 11% [5], and overall cardiovascular disease is at 5.4% [6] in Turkey. Some people belong to several groups of risky diseases. At least 23% percent and at most 39.4% of the population is at high risk. We estimate the number of people with at least one risky disease as 30% by taking a point in the middle of the least and most percentage of

people.

$\boldsymbol{K}$ — It is the number of groups we are using in the extended models. We used two groups to analyze COVID-19, which are the low-risk group and the high-risk group.

$\boldsymbol{\eta}$ — It is the fraction of asymptomatic cases that occur among the infected population. Based on the meta-analysis made by Buitrago-Garcia et al. (2020) [7], the η is 20%. So we take the low-risk group as 0.2 and the high-risk group as 0.002. We take the high-risk group as 0.002 because we wait for most of them to end up in a non-asymptomatic group (more precisely in a severe group).

$\boldsymbol{\nu}$ — ν is the percentage of severe cases among non-asymptomatic cases. Wu and McGoogan found that [8] , there is 19% severely infected among non-asymptomatic cases. So we assume 5% for the low-risk group to be in a severe case. Since we claimed that 30% of the population is in the high-risk group, we need to choose the parameter of ν for the high-risk group as 51.6%, if we want the average ν to be 19%.

Since we claimed that 20% of cases are asymptomatic, we can find the percentage of symptomatic and severe cases in the infected population. We also claimed, among all non-asymptomatic cases, 19% of them are severe cases. So we are left with 81% of non-asymptomatic cases are mild cases (we named them symptomatic). Since 80% is non-asymptomatic and 81% is symptomatic, we deduce that 64.8% is symptomatic, rounding it to 65%. Then we are left with 15%, which is the percentage of someone to be a severe case if they are infected.

$\boldsymbol{\beta}$ — β is the infection rate of the virus. The infection rate is calculated by a constant times number of infections over the population at risk. On 17 September 2021, The infection per 100,000 people reported last seven days in Turkey was 211 [9] on 17 September 2021. We take the constant 100, so the infection rate represents a percentage. Then the average corona infection rate for 17 September 2021 is 0.211(1).

$$\begin{aligned} \beta &= \frac{\#\text{ of infections}}{\text{infectiable population size}} \times 100 \\ \Rightarrow \beta &= \frac{211}{10^5} \times 100 = 0.211 \end{aligned} \tag{1}$$

For SEI^3RD and SEI^3Q^3RD models, we need to divide this infection rate into groups. We earlier claimed that 20% of cases are asymptomatic, 65% of cases are

symptomatic, and 15% are severe. Also, stated by Johansson et al. (2021) [10], we know 24% of all infections spread by asymptomatic infected people. We wait for low infection where the infector is a severe case. We take it low because severe cases show symptoms quickly and are isolated in a hospital. So we claim they have a low infection rate. That is why we take infections coming from severe cases to be 5%. Then 71% left for the infections coming from symptomatic cases. For every infection type (asymptomatic, symptomatic, severe), since we know how much of the infection spreads from each type of infection and overall infection rate, we can find all of the individual groups' infection rates taking their factor on the infection. We calculate the factor of any infectious group type by taking their infection spread percentage and dividing it by population percentage. Then we calculate the share of infection rate coming from an infection type by multiplying the overall infection rate with this factor. We calculated this way because individual infection rate is positively correlated with infection spread percentage. We get the overall infection rate when we take the average of the individual infection rates with their given population percentage sizes. So with this calculation, we can deduce that the average β for asymptomatic cases is 0.253 (2.1), for symptomatic cases is 0.230 (2.2), for severe cases is 0.070 (2.3).

$$\beta_{avg}^{xx} = \beta \times \frac{\text{infection spread perc.}}{\text{pop. rate}}$$

$$\Rightarrow \beta_{avg}^{asym} = 0.211 \times \frac{24}{20} \approx 0.253 \tag{2.1}$$

$$\Rightarrow \beta_{avg}^{sym} = 0.211 \times \frac{71}{65} \approx 0.230 \tag{2.2}$$

$$\Rightarrow \beta_{avg}^{sev} = 0.211 \times \frac{5}{15} \approx 0.070 \tag{2.3}$$

Then we need to distribute these average numbers to group-specific cases. By Government of Turkey regulations, people older than 65 are banned from going outside for a long time during the COVID-19 outbreak [11]. So we wait for the corona infection rate for elderly citizens a little lower than others. We claim that most of the high-risk group population comes from older people since one can wait for them to get cancer in their lifetime at least once or have a cardiovascular disease because they have lived more than others. So we take the regulation for the elders as regulation for the high-risk

population. Therefore, we take a slightly lower infection rate towards high-risk people and slightly higher towards low-risk people while remaining both numbers near their group average. We take 0.005 higher for the low-risk group to the low-risk group infection while we 0.005 lower for the high-risk group to the high-risk group infection.

$\boldsymbol{\gamma}$ — It is the multiplicative inverse of the infectious period. We assume the infectious period is ended when there is no symptom appearing on the patient. However, we make this assumption for non-asymptomatic cases. We need to guess a number for asymptomatic cases since there is no easy way to track their infectious period. So we just take asymptomatic cases' infectious period same as the symptomatic cases. According to The Centers for Disease Control and Prevention [12], symptoms ended between 10 and 15 days in most cases, and for severe cases, it can go up beyond 20 days. Since there is no distinction of infection type in SIR and SEIR models, we take our γ value for SIR and SEIR as $\frac{1}{12}$. For SEI^3RD and SEI^3Q^3RD models, we start our infectious period for asymptomatic cases as low as ten days while increasing the number for severe cases up to 25 days and giving more infectious time for the high-risk group than the low-risk group. However, we take severe cases who are ended up dying, a little lower than severe cases with recovery, since the dying group can leave the infectious period early by deceasing. So we take the infectious period for severe cases with death as 20 days.

$\boldsymbol{\varepsilon}$ — ε is the multiplicative inverse of the incubation period, which is the time period when someone is exposed to infection but not infectious yet. The incubation period varies from different sources from 2 days to 14 days, with an outlier of 27 days, but the mean of the incubation period is accepted as 5.2 days stated by Li et al. [13].

$\boldsymbol{\sigma}$ — σ is the lethality rate of the infection. Data provided by Worldometer.info [14], we know the lethality of corona among people with no pre-existing condition is 0.9%. With a pre-existing condition, the confirmed lethality rate varies from 7.6% with cancer to 13.2% with cardiovascular disease. In Turkey, the cancer is higher, among other pre-existing conditions, while cardiovascular disease is lower than others. So we take our lethality rate for the high-risk group closer to the lethality rate of COVID-19 for cancer patients. That is why we take the lethality rate of COVID-19 for the high-risk group as 9%.

$\boldsymbol{B}$ — ICU beds are the special beds for those who are severely ill. In our models, we

use ICU beds as a parameter to decrease the lethality of the infection by the availability of the ICU beds. There are approximately 46 ICU beds per 100,000 people, according to TRTWorld [15]. Since there are 85 million people, there are approximately 39,100 ICU beds in Turkey.

$\boldsymbol{\psi}$ — It is the percentage of tracing app users by group. We only use this parameter on the SEI^3Q^3RD model, and we tested different ψ values on the following pages.

Initial case — For our initial case, if we have no exposed compartment(only applicable for SIR model), we take the number of infected people as one in a million. If we have an exposed compartment, we still take the number of infected people as one in a million, and for the exposed compartment, we take one in 1.6 million. We take the exposed initial phase 1.6 times more than the initial infected phase since exposed people are pre-state of infected people. We assume, with the given parameters for the infection to multiply by 1.6 (we will see this result from the R_0 section of the SEIR model, which we will see on further pages.). For the SEI^3Q^3RD model, we divide the initial phase of the exposed compartment by given average ψ (tracing app user percentage) by the weight of the groups. Then with the same logic, we divide the infected compartment into infection groups by the percentage of infected group percentages in the whole infected population, which we discussed earlier. At last, we take the recovered and death compartments as 0, and the rest of the population goes to susceptible compartment since there is no logic to take initial death and recovered numbers non-zero, and all the population can be infected.

Table 2. SIR and SEIR models' parameters

Parameters	Value
N	85,000,000
β	0.211
γ	$\frac{1}{12}$
ε	$\frac{1}{5.2}$

Notations are taken from Grimm et al.(2021) [1]

Table 3. SEI^{3}RD and SEI^{3}Q^{3}RD models' parameters

Parameters	Low Risk		High Risk	
	LL	**LH**	**HL**	**HH**
N	59,500,000		25,500,000	
β^{asym}	0.258	0.250	0.250	0.242
β^{sym}	0.238	0.230	0.230	0.222
β^{sev}	0.078	0.070	0.070	0.062
γ^{asym}	$\frac{1}{10}$			
γ^{sym}	$\frac{1}{10}$		$\frac{1}{15}$	
γ^{sev-r}	$\frac{1}{25}$		$\frac{1}{25}$	
γ^{sev-d}	$\frac{1}{20}$		$\frac{1}{20}$	
ε	$\frac{1}{5.2}$		$\frac{1}{5.2}$	
η	0.200		0.002	
ν	0.050		0.516	
σ	0.009		0.090	
B	39,100			

LL: low-risk group to low-risk group infection rate, **LH**: low-risk group to high-risk group infection rate, **HL**: high-risk group to low-risk group infection rate, **HH**: high-risk group to hig- risk group infection rate

Table 3 is based on Grimm et al.(2021) [1]

Model analysis

Table 4. Notation of the models

symbols	explanation
S	Susceptible individuals
E	Exposed individuals in the latent period
E^{nt}	Exposed and non-tracing app user individuals in latent period
E^{tr}	Exposed and tracing app user individuals in latent period
I	Infectious individuals
I^{asym}	Asymptomatic infectious individuals
I^{sym}	Mildy symptomatic infectious individuals
I^{sev}	Severely symptomatic infectious individuals
Q^{asym}	Quarantined asymptomatic infectious individuals
Q^{sym}	Quarantined symptomatic infectious individuals
Q^{sev}	Quarantined severely infectious individuals
R	Recovered individuals with immunity
D	Died individuals because of the infection

Table 4 is based on Grimm et al.(2021) [1]

SIR model has three compartments, S, I, and R. At every time step, we mark the number of susceptible people times the infection rate as infected and carrying the I

compartment. Since every infected individual has an infected period, we hold them in the I compartment for the infectious period. After then, when they finish their infectious period, we carry them to the R compartment.

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

SEIR model is similar to the SIR model. Still, it also has another compartment E, an intermediate compartment between the S and I compartments, where a person is infected but not infectious yet. First, we take all of our infected individuals to the E compartment. After some latent period, we carry them to the I compartment. The I compartment in the SEIR is the same as SIR's I compartment.

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dE}{dt} &= \beta SI - \varepsilon E \\ \frac{dI}{dt} &= \varepsilon E - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

SEIR equations are taken from Grimm et al. [1]

Unlike SIR and SEIR models, our extended model, SEI^{3}RD, has a D compartment and three different I compartments with divided population into risk groups. So with the SEI^{3}RD model, firstly, we accept that infection has a lethality rate. Since we expanded our I compartments, we take all of them to infect the S compartment. As all risk groups interact, we take the infection rates of all groups and multiply them with all of the I compartments individually. Then we transfer the S compartment to the E compartment. Then after the latent period, we divide the E compartment into three I compartments by the infectious severity types' chances of emerging to their groups.

After that, we carry a part of the I^{sev} compartment to D compartment by the lethality of the infection since we claim only severe cases can die because of the infection. After their infectious periods, we put them into the R compartment for every other I compartment and the rest of the I^{sev} compartment.

$$
\begin{aligned}
\frac{dS_k}{dt} &= -\sum_{l=1}^{K}(\beta_{lk}^{asym} I_l^{asym} + \beta_{lk}^{sym} I_l^{sym} + \beta_{lk}^{sev} I_l^{sev}) S_k \\
\frac{dE_k}{dt} &= \sum_{l=1}^{K}(\beta_{lk}^{asym} I_l^{asym} + \beta_{lk}^{sym} I_l^{sym} + \beta_{lk}^{sev} I_l^{sev}) S_k - \varepsilon_k E_k \\
\frac{dI_k^{asym}}{dt} &= \eta_k \varepsilon_k E_k - \gamma^{asym} I_k^{asym} \\
\frac{dI_k^{sym}}{dt} &= (1-\eta_k)1 - (\nu_k)\varepsilon_k E_k - \gamma_k^{sym} I_k^{sym} \\
\frac{dI_k^{sev}}{dt} &= (1-\eta_k)\nu_k \varepsilon_k E_k - ((1-\sigma_k(t))\gamma_k^{sev-r} + \sigma_k(t)\gamma_k^{sev-d}) I_k^{sev} \\
\frac{dR_k}{dt} &= \gamma^{asym} I_k^{asym} + \gamma_k^{sym} I_k^{sym} + (1-\sigma_k(t))\gamma_k^{sev-r} I_k^{sev} \\
\frac{dD_k}{dt} &= \sigma_k(t)\gamma_k^{sev-d} I_k^{sev} \\
\forall k \in \{1, \ldots, K\}
\end{aligned}
$$

where $\sigma(t)$ is changing on SEI^{3}RD:

$$
\sigma_k(t) = \begin{cases} \hat{\sigma_k}, & \text{if} \quad I_k^{sev} N_k \leq B_k \\ \frac{\hat{\sigma_k} Bk + I_k^{sev} N_k - B_k}{I_k^{sev} N_k}, & \text{if} \quad I_k^{sev} N_k > B_k \end{cases}
$$

with $B_k = (\frac{N_k}{N})B$

SEI^{3}RD equations are taken from Grimm et al. [1]

Like the SEI^{3}RD model SEI^{3}Q^{3}RD model also have a D compartment and three different I compartments. Also, we divide a E^{tr} compartment from the E compartment, and add three Q compartments to carry infectious people from the E^{tr} compartment. Firstly we carry all exposed but asymptomatic cases into the E^{nt} compartment. Even tracing app users would not get any notification from their tracing app since their infections are asymptomatic. That is why they should end up in the asymptomatic I compartment. To obtain the E^{tr} compartment, We first need to find the tracing app users' interaction rate. For that, we take every combination of tracing app user group rates and multiplying them two by two. These are the user interaction rates between the each group. Then we carry the exposed people infected by a symptomatic or severe

case since the tracing app only responds if the infector shows symptoms and a tracing app user. To find the part of exposed tracing app users in a time step for any group, we take the group's interaction rate and multiply them with infection rates and the population of I compartments. We sum them up to find the population exposed by a non-asymptomatic tracing app user in a given time step.

Then we left all of the other exposed cases in the E^{nt} compartment. As in earlier models, the E compartment start to infect compartments after the incubation period, but we carry the E^{tr} compartment to Q compartments. We carry E^{tr} to Q compartments by the same rates we used to divide the severity of infection cases. Because these cases are still infected, we take them to pseudo-infection compartments, which are the Q compartments. In the Q compartments, we claim they cannot infect the S compartment. Then we distribute the I and Q compartments the same way since we claim infection is not working differently if you are in quarantine or not. So after their infectious period, we deliver part of the severely infected and severely quarantined individuals to the D compartment by the lethality rate of the infection on severe cases and put the rest to the R compartment.

$$
\begin{aligned}
\frac{dS_k}{dt} &= -\sum_{l=1}^{K}(\beta_{lk}^{asym} I_l^{asym} + \beta_{lk}^{sym} I_l^{sym} + \beta_{lk}^{sev} I_l^{sev}) S_k \\
\frac{dE_k^{nt}}{dt} &= \sum_{l=1}^{K}(\beta_{lk}^{asym} I_l^{asym}) S_k \\
&\quad + \sum_{l=1}^{K}(\beta_{lk}^{sym}(1-\psi_l\psi_k) I_l^{sym} + \beta_{lk}^{sev}(1-\psi_l\psi_k) I_l^{sev}) S_k) - \varepsilon_k E_k^{nt} \\
\frac{dE_k^{tr}}{dt} &= \sum_{l=1}^{K}(\beta_{lk}^{sym}(\psi_l\psi_k) I_l^{sym} + \beta_{lk}^{sev}(\psi_l\psi_k) I_l^{sev}) S_k - \varepsilon_k E_k^{tr} \\
\frac{dI_k^{asym}}{dt} &= \eta_k \varepsilon_k E_k^{nt} - \gamma^{asym} I_k^{asym} \\
\frac{dI_k^{sym}}{dt} &= (1-\eta_k)(1-\nu_k)\varepsilon_k E_k^{nt} - \gamma_k^{sym} I_k^{sym} \\
\frac{dI_k^{sev}}{dt} &= (1-\eta_k)\nu_k \varepsilon_k E_k^{nt} - ((1-\sigma_k(t))\gamma_k^{sev-r} + \sigma_k(t)\gamma_k^{sev-d}) I_k^{sev}
\end{aligned}
$$

$$
\begin{aligned}
\frac{dQ_k^{asym}}{dt} &= \eta_k \varepsilon_k E_k^{tr} - \gamma^{asym} Q_k^{asym} \\
\frac{dQ_k^{sym}}{dt} &= (1-\eta_k)(1-\nu_k)\varepsilon_k E_k^{tr} - \gamma^{sym} Q_k^{sym} \\
\frac{dQ_k^{sev}}{dt} &= (1-\eta_k)\nu_k \varepsilon_k E_k^{tr} - ((1-\sigma_k(t))\gamma_k^{sev-r} + \sigma_k(t)\gamma_k^{sev-d}) Q_k^{sev} \\
\frac{dR_k}{dt} &= \gamma^{asym} I_k^{asym} + \gamma_k^{sym} I_k^{sym} + (1-\sigma_k(t))\gamma_k^{sev-r} I_k^{sev} \\
&\quad + \gamma^{asym} Q_k^{asym} + \gamma_k^{sym} Q_k^{sym} + (1-\sigma_k(t))\gamma_k^{sev-r} Q_k^{sev} \\
\frac{dD_k}{dt} &= \sigma_k(t)\gamma_k^{sev-d} I_k^{sev} + \sigma_k(t)\gamma_k^{sev-d} Q_k^{sev}
\end{aligned}
$$

$\forall k \in \{1, \ldots, K\}$

where $\sigma(t)$ is changing on SEI^{3}Q^{3}RD:

$$
\sigma_k(t) = \begin{cases} \hat{\sigma_k}, & \text{if} \quad (I_k^{sev} + Q_k^{sev})N_k \leq B_k \\ \frac{\hat{\sigma_k} Bk + (I_k^{sev} + Q_k^{sev})N_k - B_k}{(I_k^{sev} + Q_k^{sev})N_k} & \text{if} \quad (I_k^{sev} + Q_k^{sev})N_k > B_k \end{cases}
$$

with $B_k = (\frac{N_k}{N})B$

SEI^{3}Q^{3}RD equations are taken from Grimm et al. [1]

Our models' graphs' y-axis represents the rate of the number of people to the whole population, where 1.00 is the entire population and 0.00 is 0 people. The x-axis represents time in days. We take 750 days for the x-axis since we want the x-axis to be the same in all of our graphs, and some of our graphs give late results, but all end before 750 days.

In all of our models, the S compartment decreases until some time, then after it stops moving. The S compartment is a continuously decreasing compartment since there is no positive component that feeding the S compartment. It stops at some time t when there are no infectious people left, and the endemic ends since we are losing the population of the S compartment with relation to the number of people in the I compartment. On the other hand, in all of our graphs, R and D in our SEI^{3}RD and SEI^{3}Q^{3}RD models always increase until some time t. R and D continuously increase with the same reason the S compartment decrease since they are cumulative compartments because there are no negative components to make them decrease. R and D are also stopped moving when the endemic ends. Our other compartments E, I, and Q start increasing from some time t, and they end up being 0 when the endemic ends. Compartments E and I are the ones indicating if the endemic ended or not since the E

compartment feeds the I compartment, and the I compartment cuts from the S compartment and feeds R and D compartments. While Q compartment just plays a role in the SEI^{3}Q^{3}RD model of the middle step from E^{tr} compartment to R or D compartment. Since E compartment feeds the I compartment, and I compartment spreads infection, we can deduce that the endemic ends when both of E and I compartments hits 0. Then we achieve Fig 1, 2, 3, and 4 with our parameters summarized in Table 3.

Fig 1. SIR model with our chosen parameters

Fig 2. SEIR model with our chosen parameters

Fig 3. SEI^{3}RD model with our chosen parameters

Fig 4. SEI^{3}Q^{3}RD model with our chosen parameters
ψ is taken as (.25, .25).

R_0 calculation

R_0 is a value of any infection that shows if the infection is spreading or ending. To find the R_0 of our given models, first, we need to distinguish which of the compartments we should use to generate our matrices F and V, where F is the matrix of derivatives of compartments that rate of appearance of new infections by compartments and V is the matrix of derivatives of compartments that rate of individuals out of those compartments.

It would be just I compartment for the SIR model since it is the only compartment related to infection. For the SEIR model, it would be I and E compartments. For the SEI^{3}RD model, our compartments come from E and all groups of I compartments. Since we also investigate our model with several groups (in our case, it is two), we need to expand our matrices dimensions accordingly. So a SEI^{3}RD model with only two groups has matrices F and V with 8×8 dimensions since we take all of E, I^{asym}, I^{sym}, and I^{sev} twice. If we look at the SEI^{3}Q^{3}RD, we achieve the same matrices with the SEI^{3}RD since there would be no infection with compartment E^{tr} because they would be quarantined immediately.

We divide our compartments to F and V by their positive and negative terms. All positive terms of our compartments go to F, while negative terms go to V. We take all of these terms derivative by all infection compartments [16]. Eventually, we achieve our F and V values for all of our models given in Table 5 and 6, respectively.

Table 5. F values respect to models

Models	$\boldsymbol{F}$
SIR	βS
SEIR	$\begin{bmatrix} 0 & \beta S \\ \varepsilon & 0 \end{bmatrix}$
SEI^{3}RD and SEI^{3}Q^{3}RD	$\begin{bmatrix} 0 & 0 & \beta_{LL}^{asym} S_L & \beta_{HL}^{asym} S_L & \beta_{LL}^{sym} S_L & \beta_{HL}^{sym} S_L & \beta_{LL}^{sev} S_L & \beta_{HL}^{sev} S_L \\ 0 & 0 & \beta_{LH}^{asym} S_H & \beta_{HH}^{asym} S_H & \beta_{LH}^{sym} S_H & \beta_{HH}^{sym} S_H & \beta_{LH}^{sev} S_H & \beta_{HH}^{sev} S_H \\ \eta_L \varepsilon_L & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \eta_H \varepsilon_H & 0 & 0 & 0 & 0 & 0 & 0 \\ \eta_L \nu_L \varepsilon_L + \varepsilon_L & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \eta_H \nu_H \varepsilon_H + \varepsilon_H & 0 & 0 & 0 & 0 & 0 & 0 \\ \nu_L \varepsilon_L & 0 & 0 & 0 & 0 & 0 & \sigma_L \gamma_L^{sev-r} & 0 \\ 0 & \nu_H \varepsilon_H & 0 & 0 & 0 & 0 & 0 & \sigma_H \gamma_H^{sev-r} \end{bmatrix}$

Table 6. V values respect to models

Models	$\boldsymbol{V}$
SIR	γ
SEIR	$\begin{bmatrix} \varepsilon & 0 \\ 0 & \gamma \end{bmatrix}$
SEI^{3}RD and SEI^{3}Q^{3}RD	$\begin{bmatrix} \varepsilon_L & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \varepsilon_H & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma^{asym} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma^{asym} & 0 & 0 & 0 & 0 \\ \eta_L \varepsilon_L + \nu_L \varepsilon_L & 0 & 0 & 0 & \gamma_L^{sym} & 0 & 0 & 0 \\ 0 & \eta_H \varepsilon_H + \nu_H \varepsilon_H & 0 & 0 & 0 & \gamma_L^{sym} & 0 & 0 \\ \eta_L \nu L \varepsilon L & 0 & 0 & 0 & 0 & 0 & \gamma_L^{sev-r} + \sigma_L \gamma_L^{sev-d} & 0 \\ 0 & \eta_H \nu H \varepsilon H & 0 & 0 & 0 & 0 & 0 & \gamma_H^{sev-r} + \sigma_H \gamma_H^{sev-d} \end{bmatrix}$

After that, to find out R_0, we need to find the spectrum of FV^{-1}. It is easy for the SIR model since there is only one infection compartment to work with, so the dimension is just 1. For other models, the spectrum calculation is done in Julia with respective models coding. If one wants to find the R_0 values of the SIR and SEIR models by hand, they can take the initial S value as 1 and other compartments as 0 because the population except the S compartment is negligible. On the other hand, this would not be correct for extended models if we take S compartment as 1 since we divide the compartments into groups. However, with S1 code SIR, code SEIR, code SEI^{3}RD, and code SEI^{3}Q^{3}RD are calculating the R_0 values of the models in a given state without taking other compartments as 0, but with their initial rates. One can reach the codes; S1 code SIR, code SEIR, code SEI^{3}RD, and code SEI^{3}Q^{3}RD, which are Julia files to analyze the models, on GitHub.

Results

Stability analysis

We cannot change the infectious period of the virus since it is fixed for the given infection, then the only parameter left that can change the R_0 is β in the SIR and ε in the SEIR model. Lethality rate (σ) of the virus depends on available ICU beds (variable of σ) in SEI^3RD and SEI^3Q^3RD model. We took the infectious period of COVID-19 as 12. So γ is $\frac{1}{12}$.

We calculate R_0 of the SIR model with $\frac{\beta}{\gamma}$. So to make R_0 bigger than 1, we need to take β bigger than $\frac{1}{12}$, and to make R_0 less than 1, we need to take β less than $\frac{1}{12}$.

$$R_0 = \frac{F}{V} = \frac{\beta}{\gamma}$$

For the SEIR model, our R_0 is the spectral radius of a matrix multiplication, where the matrices parameters are β, γ, and ε. However, the calculation of FV^{-1} depends only on β, the S compartment, and γ (3.1), and if we do the calculation, we find out that radius can only be $\sqrt{\frac{\beta}{\gamma}S}$ (3.2). Since we took γ constant, we can only change β to adjust R_0 to bigger or smaller than 1. Same as before, we took γ $\frac{1}{12}$. So similar to the SIR model, if we take β bigger than $\frac{1}{12}$, we make R_0 bigger than 1 and taking β less than $\frac{1}{12}$ make R_0 less than 1.

$$F = \begin{bmatrix} 0 & \beta S \\ \varepsilon & 0 \end{bmatrix}$$

$$V^{-1} = \begin{bmatrix} \frac{1}{\varepsilon} & 0 \\ 0 & \frac{1}{\gamma} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} 0 & \frac{\beta}{\gamma}S \\ 1 & 0 \end{bmatrix} \tag{3.1}$$

$$\Rightarrow \lambda = \pm\sqrt{\frac{\beta}{\gamma}S} \tag{3.2}$$

If we take β as $\frac{1}{15}$ and $\frac{1}{8}$ in both SIR and SEIR models, the R_0 of the models would

be 0.8 and 1.5 as given on Fig 5 and 6 respectively for the SIR model and 0.9 and 1.2 for the SEIR model as given on Fig 7 and 8, respectively. If we look at graphs with these R_0 values, we see that the low R_0 valued model will not create any endemic, while R_0 with higher than 1 creates an endemic. Still, the endemics starting point postpones and gets less infectious if we decrease the R_0 value towards 1.

Fig 5. SIR model with low R_0

Fig 6. SIR model with high R_0

Fig 7. SEIR model with low R_0

Fig 8. SEIR model with high R_0

For SEI^3RD and SEI^3Q^3RD, we have the same calculation for R_0 since traced people exposed to the virus do not infect anyone by going to quarantine. So we do not include them in our R_0 calculation. However, the matrices' dimension is 8×8 for a population with only two groups. To make the calculation more manageable, we take ICU beds as a constant at 39,100. We take the ψ value for SEI^3Q^3RD model (.3, .3), percentage of tracing app users to the population 30% and distributed uniformly among groups. Note that we are looking at initial R_0 values of these models. Since σ value changes over time, the R_0 value changes with it. Besides that, we have several types of β to work with. So we estimate the point where R_0 equals 1 by trial and error on S1 code SEI^3RD. If we take all entries of β as $\frac{1}{21}$, we achieve R_0 equals 1.01. Any positive change in the entries of β gives us a higher R_0. However, these selected numbers for parameters of β are just one point which makes R_0 near to 1.

If we take any β matrix groups lower than the above estimation for SEI^3RD and SEI^3Q^3RD model, we will achieve a lower R_0, and the graph would be flat. For example, if we take all β matrices $\frac{1}{30}$, our R_0 for both the SEI^3RD and the SEI^3Q^3RD model be 0.83 and our graphs will be Fig 9 for SEI^3RD model and Fig 10 for SEI^3Q^3RD. The graph would be flat, which means there would be no endemic if we took our β matrices higher than our threshold. For example, if we take $\frac{1}{10}$ for all β values, then our R_0

would be 1.54 for both graphs as one can see on Fig 11 and 12, and we would see an endemic curve for both of our models. We took t value from 0 to 1200 for Fig 11 and 12 since with our given parameters, the endemic starts later than other graphs.

Fig 9. SEI^{3}RD model with low R_0

Fig 10. SEI^{3}RQ^{3}D model with low R_0
ψ value is taken as (.25, .25).

Fig 11. SEI^{3}RD model with high R_0
Time variable (t) is between 0 and 1200.

Fig 12. SEI^{3}RQ^{3}D model with high R_0
ψ value is taken as (.25, .25). Time variable (t) is between 0 and 1200.

As one can see, when we get R_0 lower than 1, the infection does not spread with initial conditions.

Now let's examine what happens if we take the initial exposed and infected population high with low R_0 on the SEIR model. We take initial exposed and infected populations as 1 in a 100 with β equals $\frac{1}{15}$. With Fig 13, we can see there is still an infection observed even the R_0 is lower than 1. Still, there is no strong endemic going on. The endemic's duration and the number of infected people are fairly low. So depending on Fig 13, we can still observe an endemic even the R_0 is low if we have a high infected initial phase.

Fig 13. SEIR model with low R_0 and high initial infection

Parameter change

We have ψ value only in the SEI^{3}Q^{3}RD model where it indicates the proportion of the population that uses a corona tracing app by groups. According to model, users immediately go to quarantine, and by doing that, they stop the infection by their part. So they are actually slow down the infection to spread by going to quarantine. Since we used two groups in our model (low-risk group, high-risk group), we examine this parameter for both groups.

First, we divide tracing app users uniformly among both groups. We examine them by 10%, 30%, 40%, 60%, and 75% tracing app users. The first thing to notice here is the similarity between Fig 3 and 14, where Fig 14 is the 10% tracing app users with uniformly distributed among groups. That means our models SEI^3RD and SEI^3Q^3RD coincide with each other. Another analysis of graphs Fig 14, 15, 16, 17, and 18, is that increasing uniform tracing app users delay the infection's breaking point and spreads less infection to the population. The result of the increase in the uniform tracing app users is that we get fewer deaths, mainly in the high-risk group since we took their death risk is higher than the low-risk group. That is why we see a more significant impact when we increase the tracing app users. As we hit the 75% of uniform tracing app users with our given parameters like we did on Fig 18, the graph starts to flatten, which means if 75% of the population uses the tracing app, we can eliminate the death rate of the infection near 0.

Fig 14. SEI^3Q^3RD model with uniformly distributed tracing app users to risk groups with ψ=(.1, .1)

Fig 15. SEI^3Q^3RD model with uniformly distributed tracing app users to risk groups with ψ=(.3, .3)

Fig 16. SEI^3Q^3RD model with uniformly distributed tracing app users to risk groups with ψ=(.4, .4)

Fig 17. SEI^3Q^3RD model with uniformly distributed tracing app users to risk groups with ψ=(.6, .6)

Fig 18. SEI^3Q^3RD model with uniformly distributed tracing app users to risk groups with ψ=(.75, .75)

Now we investigate ψ not by population percentage but by population size. 30% of the low-risk population has the same size as 70% of the high-risk population due to our choice of population division in the first place. So we compare values of ψ (.3, .0) and (.0, .7). With our given parameters, there is not such a big difference between Fig 19 and 20. There is a slight decrease in the low-risk group's R compartment from changing ψ values (.0, .7) to (.3, .0), but there are no visible changes for other compartments for

both high and low-risk groups. So we can deduce that the importance of the tracing app is the overall number of users, but not which group is using the tracing app more.

Fig 19. SEI^{3}Q^{3}RD model with ψ=(.3, .0)

Fig 20. SEI^{3}Q^{3}RD model with ψ=(.0, .7)

Then we look at the tracing app users distributed by 10% for low-risk group and 90% for high-risk group (ψ value (.1, .9)) and 90% for low-risk group, 10% for high-risk group (ψ value (.9, .1)). The first observation is how these Fig 21 and 22 are similar to the uniformly distributed tracing app user graphs. Fig 21 is similar with Fig 15. Both groups have nearly similar tracing app user population sizes. While ψ with (.1, .9) has 34% of tracing app users, (.3, .3) has 30% of tracing app users. Besides this, ψ value (.9, .1), which has 69% of tracing app users, has a similar graph with (.6, .6), which has 60% of app users in its population as we can see with Fig 22 and 17. With these observations, we can deduce, uniformly distributed tracing app users among the population have better survivability than an uneven distribution of tracing app users with the same population size as uniform distribution.

At last, we check the impact of increasing tracing app users in one risk group while remaining the other unchanged. We compare 10% for the low-risk group with 30% for the low-risk group while for both taking high-risk group's users as 90%. With only increasing one group's tracing app user population and letting the remaining unchanged as we did with Fig 21 and 23, we see that it positively impacts both groups' infection graphs. We have this result because we earlier indicated that the infection could travel between groups by selecting non-diagonal elements of our β matrix non-zero. So increasing the number of tracing app users in one group does not only decrease infection in that given group, but it also decreases infection in other connected groups.

Fig 21. SEI^{3}Q^{3}RD model with ψ=(.1, .9)

Fig 22. SEI^{3}Q^{3}RD model with ψ=(.9, .1)

Fig 23. SEI^{3}Q^{3}RD model with ψ=(.3, .9)

Model discussion

In this paper, we used two extended SEIR models: the SEI^3RD and SEI^3Q^3RD models. Grimm et al. [1] extended the SEIR model by adding different types of infection with the SEI^3RD and SEI^3Q^3RD models and tracing and quarantine options with the SEI^3Q^3RD model. These compartments coincide with COVID-19's infection types and current regulations used by governments, but these models do not perfectly describe the current COVID-19 pandemic.

The biggest mistake of these models is, there is no feedback to the S compartment. Highlighted by Ripperger et al. [17], COVID-19 immunity only lasts 5 to 7 months on average. Since our models do not have any feedback from R to the S compartment, we do not consider the second infection after immunity. We could change this by adding a six-month immunity period parameter and reintroduce the R compartment to the S compartment with this given new immunity parameter.

Also, it is emphasized by Kitagawa et al. [18] that UV-C kills the COVID-19 virus, which means that the virus is weak in the summer season. So our models do not work accurately if we change seasons because we need to change the infection rate during the seasonal change. Although, we can find an overall infection rate to use on extended periods. This overall infection rate works better on the periods with multiples of the period we took in the first place to calculate the overall infection rate.

So by both of these assumptions, using these models for more than 200 days to predict COVID-19 will not be accurate. This is not only true for our extended models but also true for SIR and SEIR models. Since the 200-day time limit is valid for all models, including SIR and SEIR, we will not discuss it deeper to find a solution because we are discussing shortcomings of the SEI^3RD and SEI^3Q^3RD, not the SIR and SEIR models.

SEI^3RD model divides the population into groups to help us examine the infection on different groups and add more infection compartments to distinguish the infection severity. Besides that, it creates a compartment that we can carry the dead population. Earlier, we assumed all of the infected population recovers because there was no D compartment in SIR and SEIR models. Though, with the SEI^3RD extension, we added the infection a lethality function, which is more accurate with the actual situation of

COVID-19. Since the SEI^{3}RD model does nothing different from the SEIR model except taking different types of infection, dividing the population into groups, and dividing the R compartment into two, there is nothing much to discuss. On the other hand, the SEI^{3}Q^{3}RD model creates a new function and compartments compared to former models, which these function and compartments are the tracing app users and Q compartments. So our discussion is on the SEI^{3}Q^{3}RD model.

The traced group in the SEI^{3}Q^{3}RD model is assumed to go into quarantine once exposed to infection. The assumption here is that if one is in quarantine, they cannot infect anyone. However, it is not true in real COVID-19 situations. These people are still in contact with the people they stay in the same apartment at least. So there is still a slight chance that they can infect somebody, but it is claimed that the people in quarantine are not contagious in the SEI^{3}Q^{3}RD model. The only way to achieve entirely non-contagious quarantine would be to isolate quarantined individuals from everyone in the S compartment, but that would be nearly impossible and cruel.

Another problem with the SEI^{3}Q^{3}RD model is that we cannot know when the first exposure started for tracing app users in the real world. A person in a tracing group may be in the infectious period even though the tracing app has not marked them as exposed. In the SEI^{3}Q^{3}RD model, we claim users are aware of the infection only if a non-asymptomatic tracing app user infects them. However, our tracing app users can be infected by an asymptomatic or non-tracing app user. In that case, there would be an infection that is not trackable in the tracing app user community. It would take some time for the tracing app to find the unreported infection in the tracing app community's system because we need to wait for someone in the tracing app user community to show infection symptoms and report it. That is why it is not easy to identify the tracing app users as infected or not immediately. Still, the SEI^{3}Q^{3}RD model takes exposed tracing app users immediately into the quarantine compartment after their latent period, where they cannot spread the infection.

To extend the model of SEI^{3}Q^{3}RD, we could first add E^{tr} to I compartments with a positive constant. Since we want infection to spread while people are in quarantine, E^{tr} compartment has to go some compartment where the compartment has η, ν, and ε as a multiplier, like I compartments. However, we want people coming out of E^{tr} to infect people at a different rate than the non-quarantined infected population. Therefore, the

exposed population with tracing app users should not go to the I compartments but create a different compartment for symptomatic and severe cases. We should not create a new asymptomatic compartment for the E^{tr} since no asymptomatic case ends up in E^{tr} in the first place. Instead of writing a new compartment, we can also use Q compartments. For that to work, we need to add Q compartments to the S compartment as an infector, with a factor different from β. Hence we need to create another infection rate parameter, presumably lower than β, for people in quarantine.

15 April, Turkey R_0 value

Now, we make the graph of Turkey with the initial conditions given on 15 April 2021. Since the parameters we earlier found are constant for any given time of Turkey except β parameter, we only need to find β parameter of Turkey on 15 April to find predictions of our model.

First, we need to remove the vaccinated and recovered population from our test population since our model claims one cannot get infected twice. We take fully vaccinated populations from high-risk populations and carry them to initial recovered populations since Turkey vaccinated firstly high-risk groups. Then we carry the recovered population from the low-risk group to the recovered initial phase since the Government of Turkey used strict rules on the high-risk group. We claim most of the recovered population comes from the low-risk group. We do not assume there is a second infection chance since our models do not imply such. So we assume all recovered people are safe from the infection.

On 15 April, 9.1% of the population was fully vaccinated in Turkey [19]. That makes overall 7,735,000 people in the population of turkey vaccinated, which is also nearly 30% of the high-risk group population. So we carry 7,735,000 people from the S compartment of the high-risk group to the R compartment of the high-risk group. Also, cumulative confirmed cases are 4.09 million [20], and there are near 500,000 patients who were infected on 15 April [21]. That makes nearly 3.6 million people recovered from COVID-19, and that is nearly the same number as the 6% of the low-risk population. So as we mentioned earlier, we carry 3.6 million people from the low-risk group of the S compartment to the low-risk group of the R compartment.

We need the rate of S compartment's value for the whole population since the rate is needed for the R_0 calculation. So we have to find all other rates of compartments by groups and subtract them from the whole population to find the rate of S compartment by groups. We mentioned earlier that we carried 30% of the susceptible high-risk group to the high-risk R compartment and 6% of the susceptible low-risk group to the low-risk R compartment. Besides that, we earlier accepted that 30% of the population is in the high-risk group. That makes 9% of the population in R compartments for the high-risk group and 4.2% of the population are in the R compartment for the low-risk group. Now we need to find the rate of E, I, and D compartments in the system. Cumulative death because of the COVID-19 is 35,000 [20], and number of infected people is 500,000 on April 15 [21]. However, we divide the I and D compartments into groups; even it is not needed to calculate R_0, we need initial states of the compartments to sketch the graph. We divide the death numbers into D compartment groups uniformly by groups' population sizes. We indicated 70% for the low-risk, 30% for the high-risk group since we do not have any hint to find the percentages.

Then 24,500 people come from low and 10,500 people come from the high-risk group to the D compartment. We have already taken the percentages of asymptomatic, symptomatic, and severe infection as 20%, 65%, and 15%, respectively. So we take infected people as 100,000 of them are asymptomatic, 325,000 of them are symptomatic, and 75,000 of them are severely infected. Then we divide these I compartments into their risk groups uniformly, the same as we did on the D compartment. For the E compartment, we take twice the I compartment since the logarithmic graph of daily infection on OurWorldData sourced by GitHub [20] seems to be diagonal on 15 April, which means the infection is doubling up. Then we divide the compartment into groups uniformly. So in the E compartment, there is 700,000 people in the low-risk group and 300,000 people in the high-risk group. So overall, 0.0004% of the population goes to the D compartment, 0.005% of the population goes to the I compartment, and 0.01% goes to the E compartment. However, the numbers of E, I, and D are low on a scale of 100, and they will get lower on a scale of 1. It would be nice to take these compartments as 0 since they have little significance in the R_0 calculation. Though, we do not need to calculate the percentages of the compartments at all. We would need to calculate them if we would calculate the R_0 value by hand. After all, S1 code SEI^3RD and code

SEI^3Q^3RD automatically calculates the compartments' rates, so we only need to find the number of people in those compartments. We have already calculated the number of populations in the compartments regarding their risk groups except for the S compartment. For that, we only need to subtract our findings from the total population, which is easy. We can see the compartments' population on Table 7.

Table 7. Turkey's initial states of the SEI^3RD compartments on 15 April

Compartments	Low Risk Group	High Risk Group
S	54,825,500	17,304,500
E	700,000	300,000
I^{asym}	70,000	30,000
I^{sym}	227,500	97,500
I^{sev}	52,500	22,500
R	3,600,000	7,735,000
D	24,500	10,500

Now we need to find β value of the given date. For this, we use the 7-day average of daily infection value on 15 April [20]. The value is near 57,000 people for one day, but we take one week of infection. So we take 11 April's infection number, which is near 52,000, as the average of that week and multiply it by 7. That calculation gives us the average infection number on that given week is near 364,000. The uninfected population is the whole population except the sum of the previously infected or vaccinated population. We claimed the previously infected population is 7,735,000, and the vaccinated population is near 500,000. So our susceptible group size is near 76,765,000. We calculate β with our earlier discussed method in the parameters section. So our average β is roundly 0.470. To divide our average β into groups, we do the same calculation as earlier. We take the group factors of infection and multiply them with the average β value. Since the population is similar (we only took out the vaccinated and recovered population), we took the same factors as before. We earlier claimed asymptomatic, symptomatic and severe infection types' spread percentages are 24%, 71%, and 5%, and population percentages are 20%, 65%, and 15%, respectively. So our average β values for each type of infection are 0.564 for asymptomatic infection, 0.513 for symptomatic infection, and 0.156 for severe infection. Then as same as before, we take 0.005 more infection rate for the low-risk group to low-risk group infection, while we take 0.005 less infection rate for the high-risk group to high-risk group infection. Then our β values are as Table 8 and we are generating Fig 24 with our selected

parameters and initial phases.

Table 8. Predicted β values of Turkey on 15 April

β types	LL	LH	HL	HH
β^{asym}	0.569	0.564	0.564	0.559
β^{sym}	0.518	0.513	0.513	0.508
β^{sev}	0.161	0.156	0.156	0.151

Fig 24. Turkey's SEI^{3}RD graph on 15 April with predicted β values and initial population

Now we will sketch Turkey's COVID-19 graph from 15 April with given parameters by the SEI^{3}Q^{3}RD model. We claim a uniform distribution of tracing app users on the groups, and we take the rate of weekly test results made for the COVID-19 virus to the whole population as tracing group percentage. 3.4 tests were performed per 1000 people on 11 April [22]. Since we take 11 April as the average day of the week as earlier we did on calculating the infection number, the average COVID-19 tests performed is near 23.8 per 1000 people or 2.38%. So our ψ value for our 15 April graph is (.024, .024).

As earlier, we mentioned that if we would calculate the R_0 value by hand, we need to find the percentage of the Q compartments. However, we earlier indicated that the exposed and infected groups are insignificantly low on the population; it is lower for the quarantined population since it is part of the infected population. So as earlier we did on the E compartment, we would take the value for Q as 0. Further, we do not need to calculate the population size of Q to calculate R_0 since the only compartment needed to calculate R_0 is the S compartment. However, if we want to sketch our graph correctly, we need to find the initial people in quarantine. Since only 2.38% of people use the tracing app, we assume that 2.38% of infected people are tracing app users in quarantine. So we transfer 2.38% of the infected population to the quarantined population regarding their risk groups and compartment groups. That makes overall 11,900 people transferring from I compartments to quarantine compartments. We also need to divide the E compartment into two compartments since we now have tracing and non-tracing exposed groups. We divide exposed groups into these two by taking 2.38% of the exposed group to the tracing group and leaving the rest to the non-tracing group. Then the population in each compartment is as Table 9 and our selected parameter and initial phases make Fig 25.

Table 9. Turkey's initial states of the SEI^{3}Q^{3}RD compartments on 15 April

Compartment	Low Risk Group	High Risk Group
S	54,825,500	17,304,500
E^{nt}	683,340	292,860
E^{tr}	16,660	7,140
I^{asym}	68,334	29,286
I^{sym}	222,085	95,180
I^{sev}	51,250	21,965
Q^{asym}	1,666	714
Q^{sym}	5,415	2,320
Q^{sev}	1,250	535
R	3,600,000	7,735,000
D	24,500	10,500

Fig 25. Turkey's SEI^{3}Q^{3}RD graph on 15 April with predicted β values and initial population with ψ=(.024, .024)

Using our new parameters and initial phases on S1 code SEI^{3}RD and code SEI^{3}Q^{3}RD, we found the R_0 values for 15 April as 3.98 for both of SEI^{3}RD and SEI^{3}Q^{3}RD models with Fig 24 and 25, respectively.

Conclusion

Our new models SEI^{3}RD and SEI^{3}Q^{3}RD, which are extended versions of the SEIR model, helped us understand the infection by giving the SEIR model more functionality. With the SEI^{3}RD model, we divided the infection types and divided the population into risk groups. This extension allowed us to specialize our model. With this specialization, we can find the infection graph more accurately since we added more detail to the SEIR model. Also, it added a D compartment to give our infection lethality function. The SEI^{3}Q^{3}RD model, based on the SEI^{3}RD model, also has the same functionality as the SEI^{3}RD model. Besides that, we have seen SEI^{3}Q^{3}RD model has another functionality than the SEI^{3}RD model, creating a tracing app user population. Using tracing apps to detect infection emerged with the COVID-19 pandemic, and tracing app users give the population an option to fight the virus actively by creating trust groups to report their infection swiftly. SEI^{3}Q^{3}RD model modelized the effect of tracing apps not perfectly but effectively. We have discussed what is missing in the SEI^{3}Q^{3}RD model to mimic real-life tracing apps better. Then with our visualization of the SEI^{3}Q^{3}RD model with

different tracing app user percentages, we learned how important are tracing apps to fight against infection. We also saw an optimal point for the percentage of app users to eliminate the virus. Also, one can find an optimal point of distribution of app users into risk groups.

Furthermore, these extended models can be used on modeling the COVID-19, but they are not at their full capability. One can use these models to model not only for COVID-19 infection but also for many other infectious diseases with lethality. Since we can use these models with more risk groups, the tracing app is a general mechanism, not specific for COVID-19. One can even change these models slightly by adding the infection function on the D compartment to simulate Bubonic plague in earlier times, which has an infectious period even if the person dies.

Supporting information

S1 code Codes that are used to analyze the Models and generate the figs that we used in our document. Available from: https://github.com/mertsaru/Extensions-of-SEIR-model-SEI3RD-and-SEI3Q3RD-.git.

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