SIR Model

$S(t)$ = % of susceptible people at time t
$I(t)$ = % of infected people at time t
$R(t)$ = % of recovered people at time t

$t \geq 0$ time is continuous

$$S(t) + I(t) + R(t) = 1 \quad \forall \; t \geq 0$$

$$\vec{x} = \vec{x}(t) = \begin{bmatrix} S(t) \\ I(t) \\ R(t) \end{bmatrix}$$

$$D_t \vec{x} = \vec{f}(\vec{x}) = \begin{bmatrix} -\tau S(t) I(t) \\ \tau S(t) I(t) - \frac{I(t)}{\kappa} \\ \frac{I(t)}{\kappa} \end{bmatrix}$$

$\tau \geq 0$ measures disease spread
$\kappa > 0$ measures recovery time

Fixed Point Analysis

$$D_t \vec{x} = \vec{f}(\vec{x}) = \begin{bmatrix} -\tau S(t) I(t) \\ \tau S(t) I(t) - \frac{I(t)}{\kappa} \\ \frac{I(t)}{\kappa} \end{bmatrix} = \vec{0} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

$-\tau S(t) I(t) = 0 \rightarrow 0 = 0$
$\tau S(t) I(t) - \frac{I(t)}{\kappa} = 0 \rightarrow 0 = 0$
$\frac{I(t)}{\kappa} = 0 \rightarrow I(t) = 0$

Fixed points are all the points along the line

$I_* = 0 \qquad S_* \in [0, 1] \qquad R_* = 1 - S_* \rightarrow \vec{x}_* = \begin{bmatrix} S_* \\ 0 \\ 1 - S_* \end{bmatrix} \quad \forall \quad S_* \in [0, 1]$

$$J_f(x) = \begin{bmatrix} \partial f_1/\partial S & \partial f_1/\partial I & \partial f_1/\partial R \\ \partial f_2/\partial S & \partial f_2/\partial I & \partial f_3/\partial R \\ \partial f_3/\partial S & \partial f_3/\partial I & \partial f_3/\partial R \end{bmatrix} = \begin{bmatrix} -\tau I(t) & -\tau S(t) & 0 \\ \tau I(t) & \tau S(t) - \frac{1}{\kappa} & 0 \\ 0 & \frac{1}{\kappa} & 0 \end{bmatrix}$$

Using Taylor Approximation,

$\vec{x}(t) = \vec{x}_* + \vec{s}(t)$ where $\|\vec{s}(t)\|$ is small $\qquad J_* = J(x_*)$

$$D_t \vec{x} = D_t(\vec{x}_* + \vec{s}) = D_t \vec{x}_* + D_t \vec{s} = D\vec{s} \approx f(\vec{x}_*) + J_* \vec{s} = J_* \vec{s}$$

Thus, $D_t\vec{s} \approx J_*\vec{s}$ when $\|\vec{s}\|$ is small

Let's guess solution $\vec{s} = \vec{v}e^{\lambda t}$

$\lambda e^{\lambda t}\vec{v} = J_*\vec{v}e^{\lambda t} \rightarrow J_*\vec{v} = \lambda\vec{v}$ → eigenvalue equation

Let's calculate J_*

$$J_* = J(x_*) = \begin{bmatrix} 0 & -\tau S_* & 0 \\ 0 & \tau S_* - 1/\kappa & 0 \\ 0 & 1/\kappa & 0 \end{bmatrix}$$

Find eigenpairs of J_*

$\det(J_* - \lambda I) = 0$

$$\begin{vmatrix} -\lambda & -\tau S_* & 0 \\ 0 & \tau S_* - 1/\kappa - \lambda & 0 \\ 0 & 1/\kappa & -\lambda \end{vmatrix} = 0$$

$$-\lambda \begin{vmatrix} \tau S_* - 1/\kappa - \lambda & 0 \\ 1/\kappa & -\lambda \end{vmatrix} + \tau S_* \begin{vmatrix} 0 & 0 \\ 0 & -\lambda \end{vmatrix} + 0 \begin{vmatrix} 0 & \tau S_* - 1/\kappa - \lambda \\ 0 & 1/\kappa \end{vmatrix}$$

$-\lambda(\tau S_* - 1/\kappa - \lambda)(-\lambda) = \tau S_* \lambda^2 - \lambda^2/\kappa - \lambda^3 = 0 \rightarrow \lambda = 0$

When $\lambda \neq 0$

$\tau S_* - \frac{1}{\kappa} - \lambda = 0 \rightarrow \lambda = \tau S_* - 1/\kappa$

So, the eigen values are

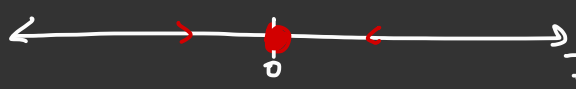
$\lambda_1, \lambda_2 = 0 \qquad \lambda_3 = \tau S_* - 1/\kappa$

Case 1: $\lambda_3 > 0 = \lambda_1 = \lambda_2$; $S_* > \frac{1}{\kappa\tau}$

Since the largest eigenvalue is greater than 0, all of these critical points $x_* \; \forall \; S_* > \frac{1}{\kappa\tau}$ are unstable.

Case 2: $\lambda_3 < 0 = \lambda_1 = \lambda_2$; $S_* < \frac{1}{\kappa\tau}$

The largest eigenvalue is now $\lambda_1 = \lambda_2 = 0$, thus linear stability analysis does not give much information. To analyze stability at these points, lets consider the 1D line of $I(t)$ under the condition that $S_* < 1/\kappa\tau$



$$\frac{dI}{dt} = I(t)\underbrace{(\tau S_* - 1/\kappa)}_{<0}$$

when $I(t) > 0$, $\frac{dI}{dt} < 0$

when $I(t) < 0$, $\frac{dI}{dt} > 0$ → never happens

Thus, these critical points $x_* \; \forall \; S_* < \frac{1}{\kappa\tau}$ are stable

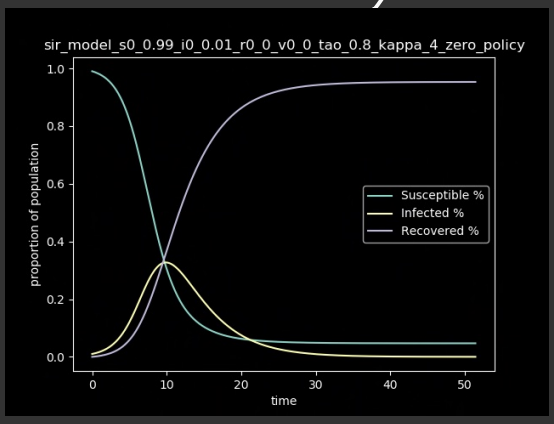
Case 3: $\lambda_3 = \lambda_1 > \lambda_2 = 0$. In this case, even when $I(t) > 0$ (near 0), $\frac{dI}{dt} = 0$ since the recovery rate is equal to the infection rate. However, note $\frac{dS}{dt} < 0$. So, we will immediatly fall into Case 2.

Thus, $x_* \; \forall \; S_* = \frac{1}{\kappa\tau}$ are also stable

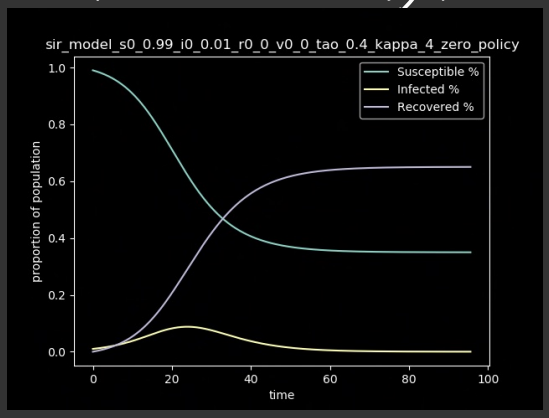
Note that when talking about stability, we are talking about the family of critical points. A small perturbation to a "stable" fixed point $x_*^1 = [S_*^1 \ 0 \ 1-S_*^1]^T$ s.t. $S_*^1 < \frac{1}{K\tau}$, will not necessarily end up back to x_*, but will end at another $x_*^2 = [S_*^2 \ 0 \ 1-S_*^2]^T$ s.t. $S_*^2 < \frac{1}{K\tau}$.

Simulation Results:

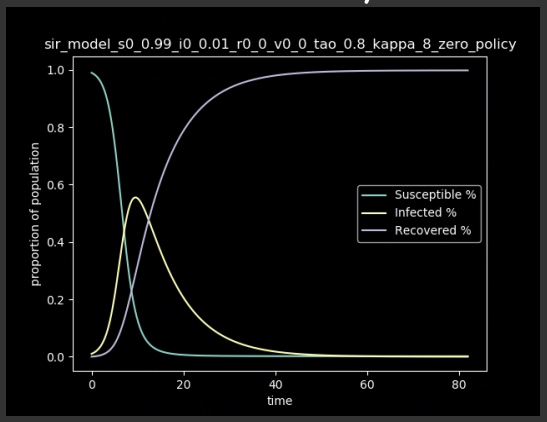
Sim #1: $\tau = 0.8$; $K = 4$



Sim #2: $\tau = 0.4$; $K = 4$



Sim #3: $\tau = 0.8$; $K = 8$



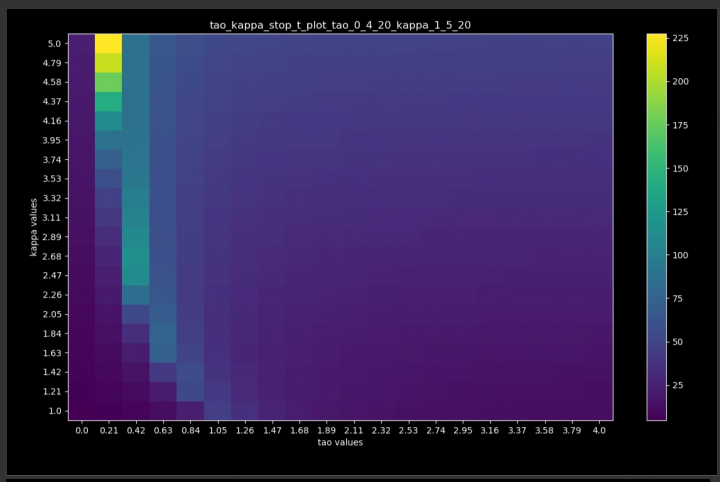
Analysis:

In the three graphs, the stop times were different each time based on the values we set for Tao and Kappa. In Sim 1, the stop time was t=51.43. In Sim 2, the stop time was t=95.64. In Sim 3, the stop time was t=81.92. The stop time depended on both Tao and Kappa, as holding either one constant and changing the other yielded different changes to the stop time. From these results, we can guess that as Tao decreases the stop time increases and as Kappa increases the stop time also increases. However, this guess may not be accurate as we do not have enough data on this yet (see below).

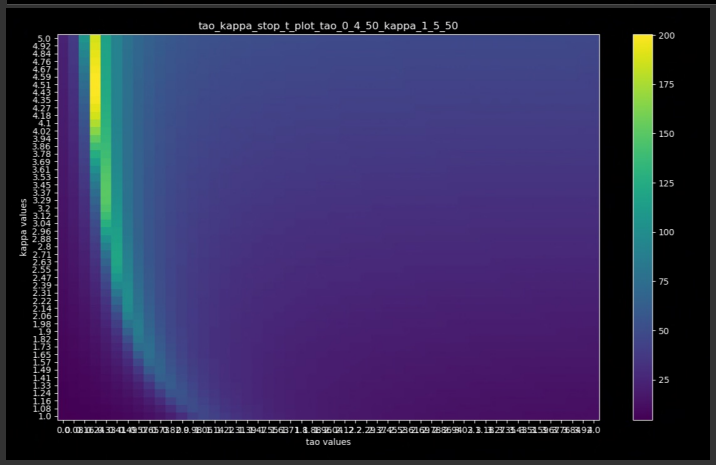
In terms of the peak of the infection curve, Sim 3 had the highest peak at around 0.6, which makes sense since there was a high infection rate and low recovery rate. Sim 1 had the next highest peak and lastly, Sim 2 had the lowest peak by a wide margin. Sim 2 likely had such a low peak due to the infection rate not being able to keep up with the recovery rate. It seems like the faster infection rates cause the peak to occur earlier (see the graphs for Sim 1 and 3), which intuitively makes sense. After that it seems like the magnitude of the peak is effected by the recovery rate: a higher recovery rate (or lower Kappa) results in a lower peak in infection.

Stop T Heatmaps:

τ-range: [0, 4]
τ-resolution: 20
K-range: [1, 5]
K-resolution: 20



τ-range: [0, 4]
τ-resolution: 50
K-range: [1, 5]
K-resolution: 50



The maximums for the stop ts ended up being at values with a high kappa (low recovery rate) and and low tao (low infection rate). These systems just generally move slower that the systems with higher rates in both values. Within our range of tao, there are some low values that seem to converge very quickly (low stop t) even with the high values of kappa. This is likely because the tao value is too low so the infection rate cannot seem to kick off and the infected people basically immediately recover, stopping the spread of the infection. Besides that, our guesses from earlier ended up being correct as the heat map shows.

Vaccinations

Suppose now we add vaccinations to our model. Now,

$V(t)$ = % of population that is vaccinated

$$S(t) + I(t) + R(t) + V(t) = 1$$

$$\vec{x} = \vec{x}(t) = \begin{bmatrix} S(t) \\ I(t) \\ R(t) \\ V(t) \end{bmatrix}$$

$$D_t\vec{x} = \vec{f}(\vec{x}) = \begin{bmatrix} -\tau S(t)I(t) - \frac{dV(t)}{dt} \\ \tau S(t)I(t) - \frac{I(t)}{\kappa} \\ \frac{I(t)}{\kappa} \\ dV(t)/dt \end{bmatrix}$$

$\tau \geq 0$ measures disease spread
$\kappa > 0$ measures recovery time

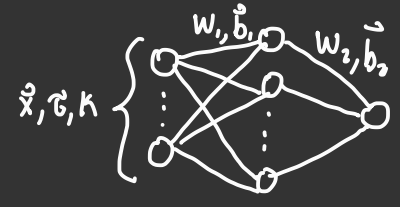
Now, we would like to desin a $dV(t)/dt$ that minimizes $V(x_*)$ and the total number of people ever infected. Similar fixed point analysis yields the following results:

$$x_* = \begin{bmatrix} S_* \\ 0 \\ R_* \\ V_* \end{bmatrix} \quad \text{where} \quad S_* + R_* + V_* = 1$$

where x_* is stable iff $S_* \leq \frac{1}{\kappa\tau}$.

Note that the total number of people infected is $\int_0^{t_*} I(x(t)) = R_* + I_* = R_*$ since $I_* = 0$. Since $S_* + R_* + V_* = 1$ and we want to minimize R_* and V_*, this effectively the same as maximizing S_*. Thus, we will evaluate vaccination policies by using S_* as the "score". Further, it is useful to make $\frac{dV}{dt} \propto S$ since it forces $\frac{dV}{dt} \to 0$ when $S \to 0$, which is required to keep s from becoming negative.

Since we have a score we can use to evaluate different policies and we would like to find a function $\frac{dV}{dt}(S, i, r, v, \tau, \kappa)$ to do so, we can use an algorithm called Neuro-Evolution of Augmenting Topologies (NEAT). In short, this algorithm simulates evolution where the DNA of each "creature" are the parameters of a neural network. First, we define the shape of the network as follows:



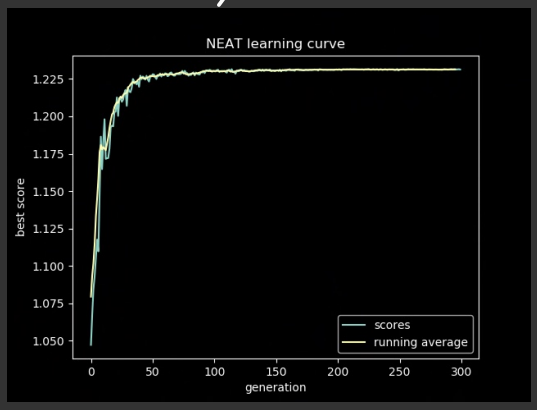
$$\frac{dV}{dt} = y \cdot S$$

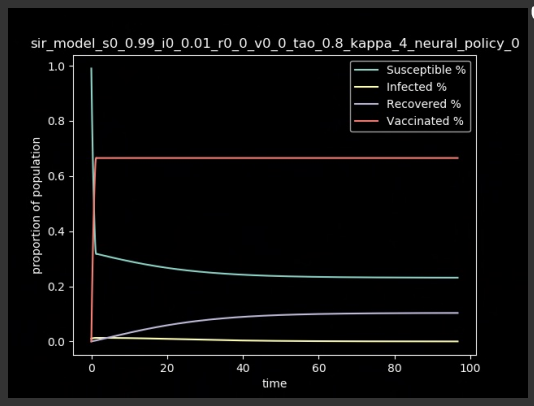
So, each network has $W_1, \vec{b}_1, W_2, \vec{b}_2$

We define mutation as random gaussian noise on the parameters. We define "birth" as averaging the parameters of the two parents. Finally, the fitness of a neural network is S_* using the $\frac{dV}{dt}$ produced by the network.

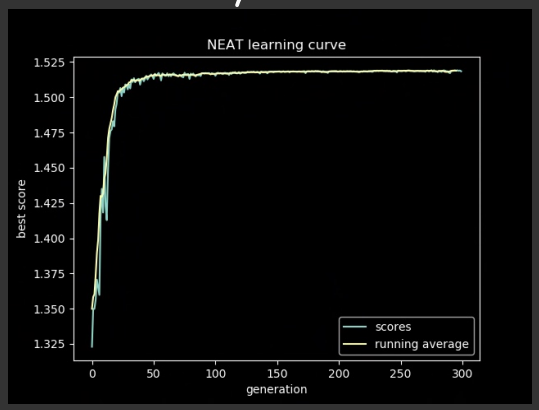
NEAT Results:

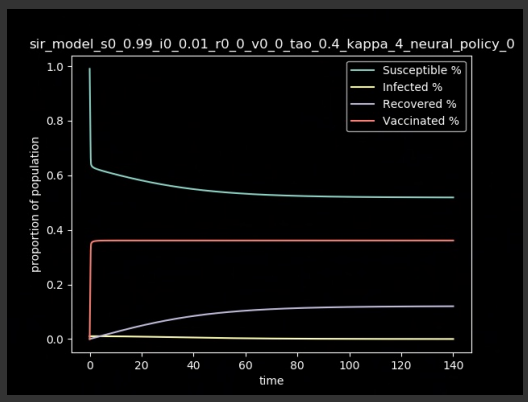
Sim 1: $\tau = 0.8$; $\kappa = 4$



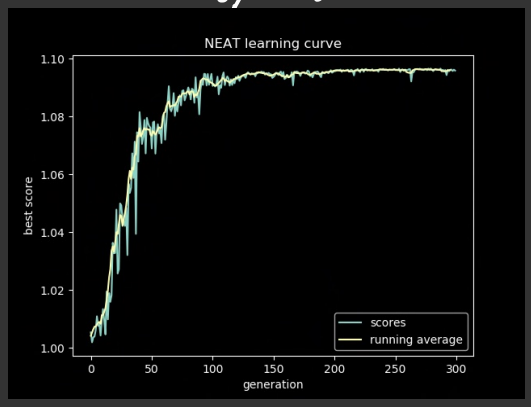


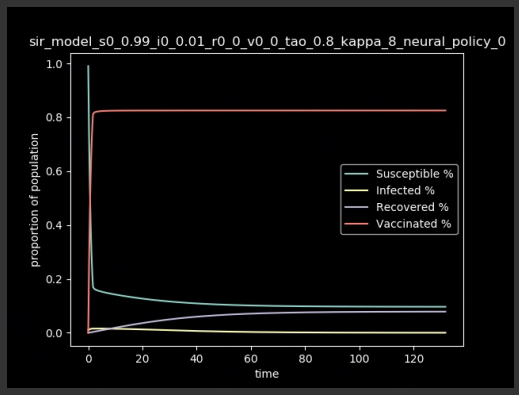
Sim 2: $\tau = 0.4$; $\kappa = 4$





Sim 3: $\tau = 0.8$; $\kappa = 8$





Analysis

These results show that it is likely best to just vaccinate a good number of people as early as possible to stop the infection from being able to spread quickly. Vaccinating people as early as possible stopped the infection early by cutting off the susceptible population, causing the infection population to also be limited. This means dI(t)/dt would be low since both S(t) and indirectly I(t) are being limited by these early vaccinations.

The amount needed to vaccinate is what changed depending on the simulation parameters. The higher the infection rate (high tao) and the lower the recovery rate (high kappa), the more people needed to be vaccinated earlier.

We can use the results gained from the neural vaccination policy model to devise an equation of our own to emulate something similar. Clearly, we want the vaccination to very quickly approach some number (lets call it C). Thus, when v(t) is below C the derivative should be positive and high. Then, once v(t) is nearing C and is essentially at C, the derivative should taper off to 0. The following equation should emulate this well:

$$\frac{dV}{dt} = \alpha(C - V)s$$

where alpha is some large parameter we set to control the speed at which V approaches C. We still include the factor of s(t) for the desired properties mentioned above. Now, this value C is unknown, but we know that it should increase as tao or kappa increases. Further, we notice that when we doubled tao, the final vaccination value almost doubled (~1.9 times the amount) and when we doubled kappa, the final vaccination value was only about 20% more. Thus, we can set the exponents of these values as follows

$\log_2 1.2 \approx 0.25$

$\log_2 1.9 \approx 0.9$

$C = \beta \tau^{0.9} \kappa^{0.25}$

$$\frac{dV}{dt} = \alpha(\beta \tau^{0.9} \kappa^{0.25} - V)s$$

When $\tau = 0.8$, $\kappa = 4$, $C \approx 0.68$

$$\beta = \frac{C}{\tau^{0.9}\kappa^{0.25}} = \frac{0.68}{0.8^{0.9} 4^{0.25}} = 0.588$$

When $\tau = 0.4$, $\kappa = 4$, $C \approx 0.38$

$$\beta = \frac{C}{\tau^{0.9}\kappa^{0.25}} = \frac{0.38}{0.4^{0.9} 4^{0.25}} = 0.613$$

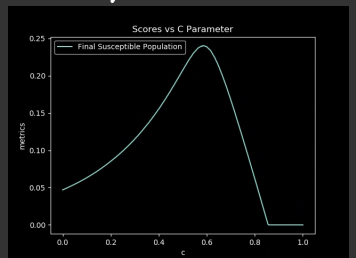
When $\tau = 0.8$, $\kappa = 8$, $C \approx 0.82$

$$\beta = \frac{C}{\tau^{0.9}\kappa^{0.25}} \approx \frac{0.82}{0.4^{0.9} 4^{0.25}} = 0.59$$

Thus, we set $\beta := 0.6$

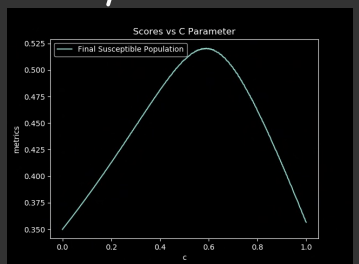
The math done on the right is also supported by the following graphs (here c := beta). These graphs are generated by running the simulation with many different values for Beta within the range 0 to 1 with a fixed alpha = 100 (since alpha does not effect Beta much) and 100 is sufficiently large. Further, these graphs are completely independent form the NEAT runs, so this is a way to find an appropriate value of Beta without using the NEAT runs.

$\tau = 0.8$; $\kappa = 4$



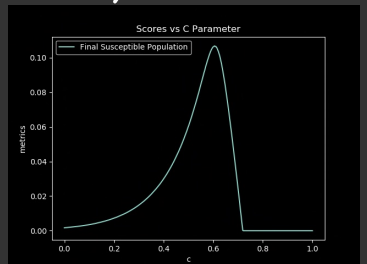
$\beta_{max} = 0.585$

$\tau = 0.4$; $\kappa = 4$



$\beta_{max} = 0.589$

$\tau = 0.8$; $\kappa = 8$



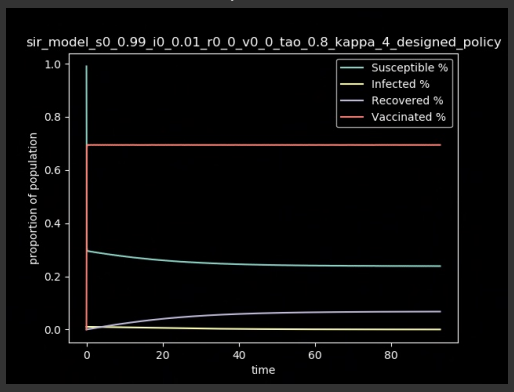
$\beta_{max} = 0.605$

Our final model is:

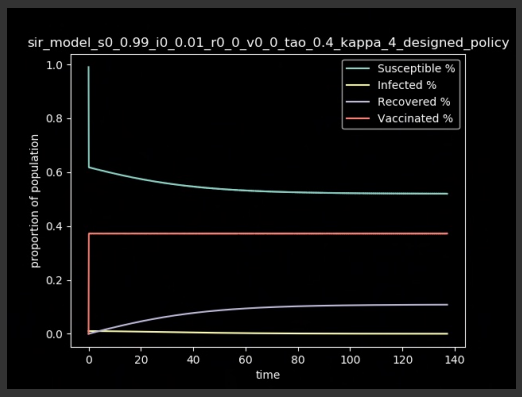
$$\frac{dV}{dt} = 100(0.6\tau^{0.9}\kappa^{0.25} - V)s$$

Designed Policy Results!

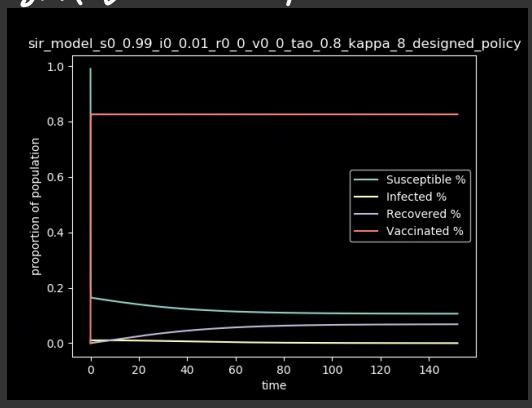
Sim 1: $\tau = 0.8$; $\kappa = 4$



Sim 2: $\tau = 0.4$; $\kappa = 4$



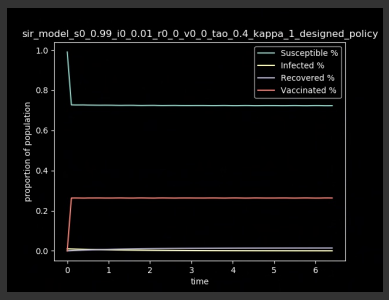
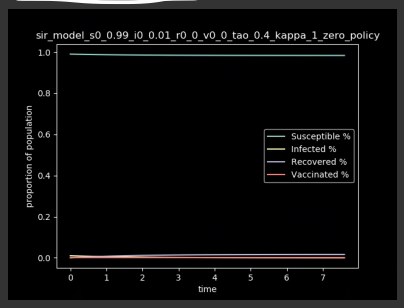
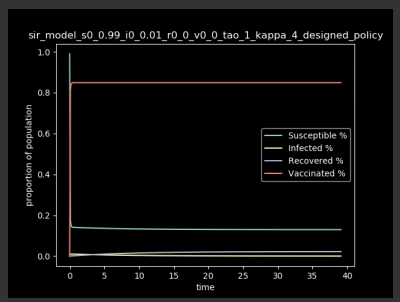
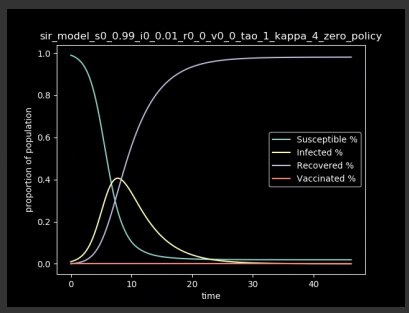
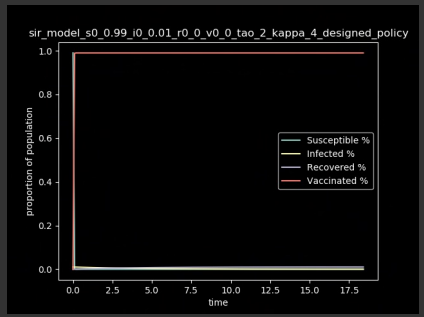
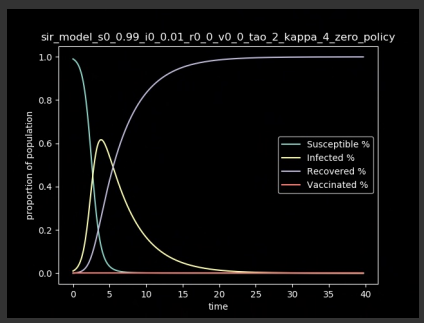
Sim 3: $\tau = 0.8$; $\kappa = 8$



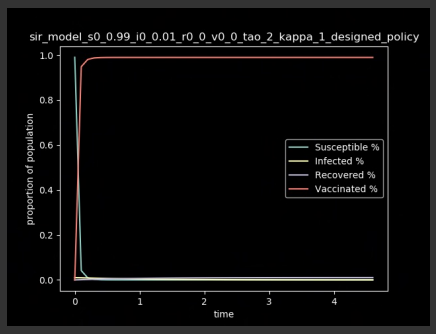
These results are very similar to those generated by the neural policy, which is expected since we based everything off of it. It should be noted that if we would like to optimize for something a little different, or if we want vaccinations to be lower, we can design a new score function and then retrain using the NEAT algorithm. Then, we can perform similar analysis that we did above to design our own equation again optimizing for the new score function.

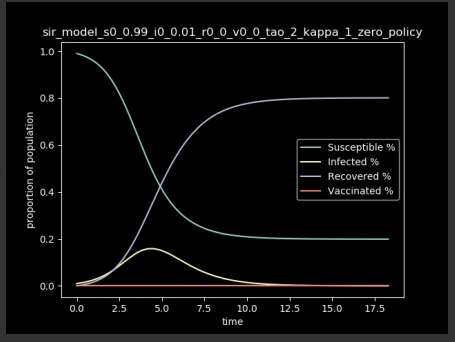
The main differences between these results and the unvaccinated scenarios are the fact that with this vaccination policy we immediately try to vaccination a certain threshold of the population (essentially getting us “herd immunity”). Then the infection is not able to thrive and dies out without infecting too many people. We do note that these solutions are converging slower than the solutions without a vaccine (that is the stop t is higher). This is likely because of the way we modeled recovery. In reality, I will not recover slower because less total people have the infection, but this behavior is modeled by our system. Thus, the small number of infections is slowing down recovery in our model, causing the convergence criteria to be met later.

Now, let’s do some more runs and compare the results with the unvaccinated scenario:

	Vaccinated	Unvaccinated	Analysis
$\tau = 0.4$; $\kappa = 1$			In this simulation, there was no need for a vaccination, but our policy vaccinated people anyways. This is not the ideal solution, showing that there can still be work done for the policy. The susceptible proportion was actually higher in the unvaccinated scenario since there were no vaccinations.
$\tau = 1$; $\kappa = 4$			In this case, we see exactly what is normally expected. We vaccinate a large population initially to get herd immunity and then just allow the simulation to run normally. This is much different from the unvaccinated scenario in which pretty much everyone gets infected and then recovers.
$\tau = 2$; $\kappa = 4$			This is case in which our value of C > 1. This causes our vaccination policy to essentially just try to vaccinate everyone, immediately shutting down the infection. Again, this is not ideal since the final susceptible population is essentially 0, but it might be the best solution.

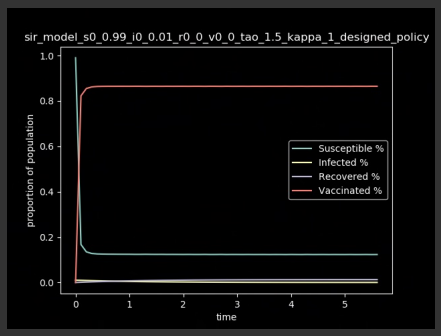
$\tau = 2; k = 1$

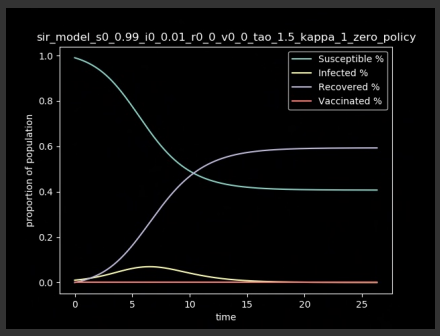




This case is very similar to the one above. Even with the faster recovery rate, C > 1, causing similar behavior. With these two cases, we can extrapolate that any further increases to tao will just result in the policy vaccinating the whole population.

$\tau = 1.5; k = 1$





In this case, we were able to drop the infection rate a little and we see the regular behavior again. Additionally, the solution converged in very little time, likely because of the high proportion of people vaccinated so early, only allowing a really small amount of people to ever get infected.