Modelling Drug Use in Communities

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Introduction

For years, policymakers have been wondering why and how do drugs travel through the community and what they can do to minimise the harm they potentially cause. In this paper, we aim to understand how drug use and addiction develops in a community and what factors can be tweaked to alter the long long term distributions of drug use, abuse and addiction in the community.

The wide variety of past articles and research papers on the topic indicate the importance of the issue. One article in particular by Mushanyu, J, Nyabadza, F, Muchatibaya, G, & Stewart, A G. R. touches on the importance of an adequate health care system since a limited rehabilitation capacity can increase the chances of a drug abuse epidemic. The methods used in this paper are discussed further along our own.

Also, another interesting article is

Method

Initial Model: SIR

It's common to liken drug use to disease, treating drug addiction as an infection that can be recovered from. Using this analogy, we began looking into how diseases are modeled and how we can adapt this model to fit drug usage. One of the simplest drug models is the SIR model, a compartment model based on the concept of mass action that sees infections as caused by interactions between infected people and susceptible people. There are a few reasons that this model is a good fit to begin modeling drug use: Firstly, this model is very simple and easily adaptable to extra compartments or conditions on transfer. Secondly, since we are looking at drug use in a population, relying on mass action rather than discrete modeling allows us to simplify the model. Thirdly, the idea that addiction is caused by individuals interacting seems to be a good assumption for drug use as you would expect people to become addicted by being around other people with the drug.

One divergence we made from the most basic SIR model is allowing for relapse from the recovered group back into the infected group. This represents how recovering addicts will become addicted again at a different rate to people who have never used the drug before. However, we never move people back into the suseptible group as addiction is said to be 'lifelong'.

The SIR model can be defined with the following equations:

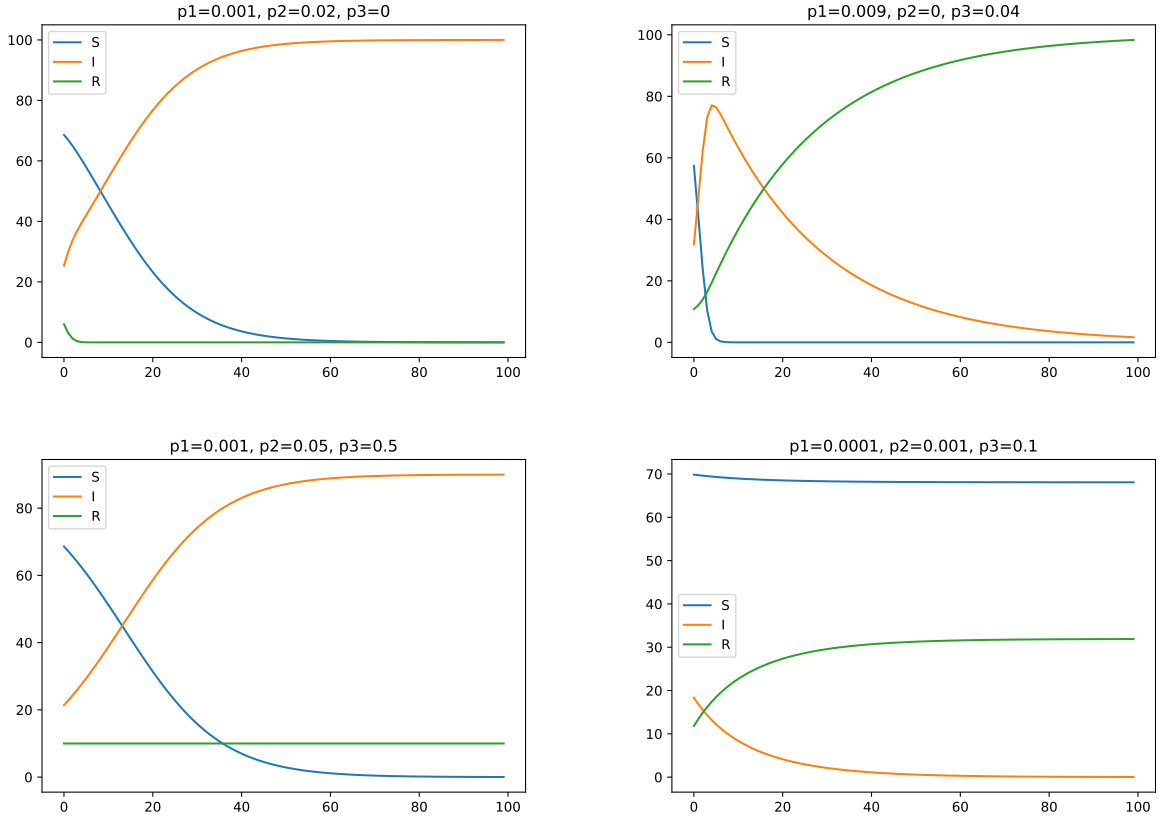
$$\frac{dS}{dt} = -\pi_1 * S * I$$

$$\frac{dI}{dt} = \pi_1 * S * I + \pi_2 * R * I - \pi_3 * I$$

$$\frac{dR}{dt} = -\pi_2 * R * I + \pi_3 * I$$

With the parameters π_1,π_2 and π_3 representing the 'infectiousness' of the drug for susceptible people, the infectiousness for recovering people and the rate of recovery for the drug respecivley.

We can now look at some plots to see how this model plays out for various combinations of parameters:



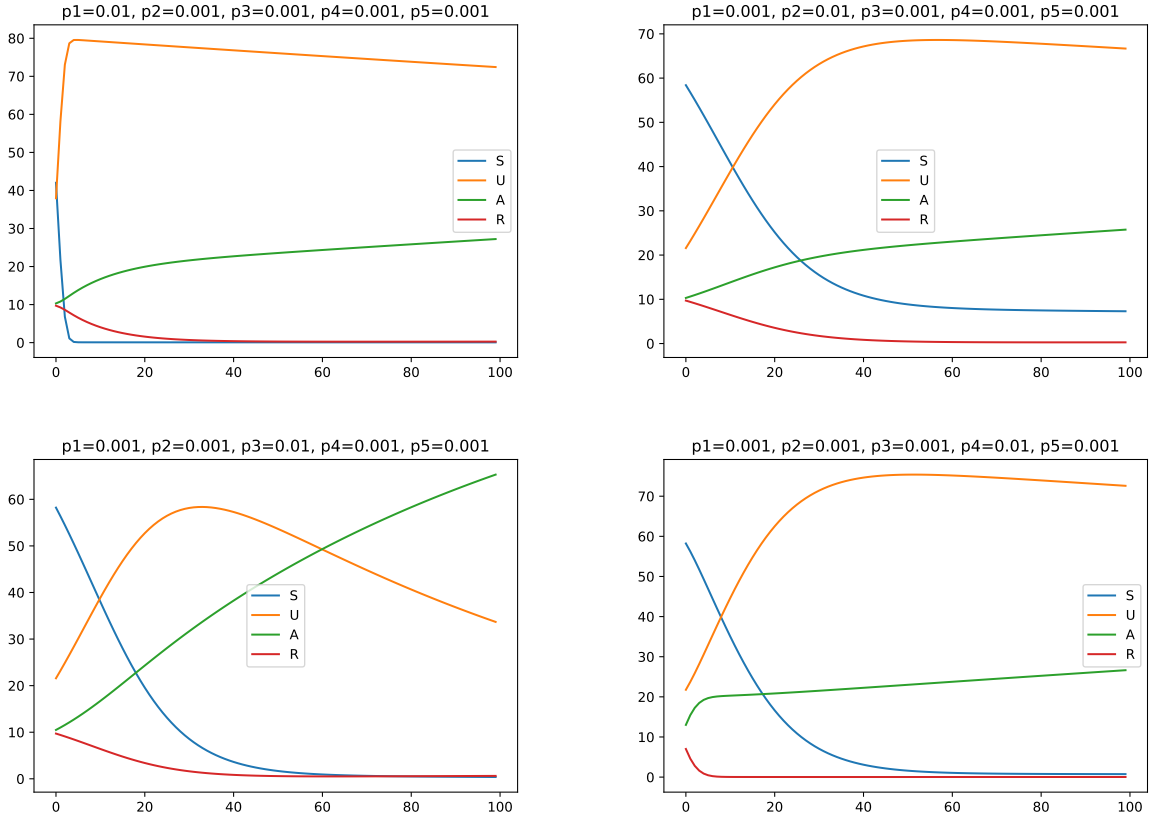
SUAR Model

The SIR model fails to distingush between different severities of addiction. By grouping anyone who is trying the drug once to people who are addicteed in the same group we are failing to capture the behaviour of people trying the drug without becoming reliant on the drug. Because of this, we adapted the SIR model, renaming the infected group to addicted and adding in a new group for users of the drug who are not addicted, labeled as the 'Using' group. Susceptible people will now move into the Using group before moving into the addicted group. Since there are now two groups who are using the drug and interacting with the community, the I terms in the ODEs desribing the SIR now have to be replaced with $U + A$

The new model can now be described with the folowing equations:

$$\frac{dS}{dt} = -\pi_1 * S * (A + U) + \pi_2 * U$$
$$\frac{dU}{dt} = \pi_1 * S * (A + U) - \pi_2 * U - \pi_3 * U$$
$$\frac{dA}{dt} = \pi_3 * U + \pi_4 * (A + U) * R - \pi_5 * A$$
$$\frac{dR}{dt} = \pi_5 * A - \pi_4 * (A + U) * R$$

With parameters π_1, π_2, π_3, π_4, and π_5 being the 'infectiveness' of the drug for susceptible people, the rate that people stop trying the drug, the rate that people become addicted, the 'infectiveness' for recovered people and the recovery rate for addicted people respectivley.



SUAR Model with age

Looking at the stationary points of the previous two models (see appendix for derivation), the only long term behaviour is to either kill off the drug and have no users or addicted people or have eveyone in the addicted or recovered group. However, this behaviour is not consistent with what we see in the real world, where we have a consistent number of people using and addicted to the drug, and a consistently high number of people who are susceptible to the drug. To fix we add age groups into the model, grouping them as children, teens, young adults, adults and seniors. Each of these groups have a distinct rate of death and births are porportioal to the number of young adults and adults. Seperating these groups also allows us to set different parameters according to each age group, capturing more nuanced beahviours such as more experiementation in young people.

Another feture we wanted to tackle is how people recover. In the same way that people start using drugs based on interactions with others who are using the drug, we expect people to recover based on interactions with people who aren't using the drug. This can be represented by support groups, concered parents or friends. Furthermore, we can expect people in one agegroup to be influence by different ammoint from each agregreoup. We can store this information with a matrix I, where I_{ij} is the magnitude of the influence that group j has on group i. We can now go in to further simplify this by defining two new terms, the positive and negitive influence on a age group i, to be:

$$P_i = \sum k = 15 I_{ik} * (S_k + R_K)$$

$$N_i = \sum k = 15 I_{ik} * (U_k + A_K)$$

The model now has 20 compartments with both sideways movment within age groups and downwards movement as people age.

Looking across age group 'i', the model can be described as:

$$\frac{dS_i}{dt} = aS_{i-1} + aU_{i-1}\pi_{i-1,2}P_{i-1} - S_i\pi_{i,1}N_i + (1-a)U_i\pi_{i,2}P_i - aSi - d_{i,s}S_i + (b\sum_{k=2}^{3} S_k + U_k + A_k + R_K | i = 0)$$

$$\frac{dU_i}{dt} = aS_{i-1}\pi_{i-1,1}N_{i-1} + aU_{i-1} - U_i * \pi_{i,3} - aU_i - U_i\pi_{i,2}P_i + (1-a)S_i\pi_{i,1}N_i - d_{i,U}U_i$$

$$\frac{dA_i}{dt} = aU_{i-1}\pi_{i-1,3} + aA_{i-1} + aR_{i-1}\pi_{i-1,4}N_{i-1} - A_i\pi_{i.5}P_i + (1-a)R_i\pi_{i,4}N_i - aA_i + (1-a)U_i\pi_{i,3} - d_{i,A}A_i$$

$$\frac{dR_i}{dt} = aA_{i-1}\pi_{i-1,5}P_{i-1} + aR_{i-1} - aR_i - R_i\pi_{i,4}N_i + (1-a)A_i\pi_{i,5}P_i - d_{i,R}R_I$$

With the paramers being sroted in matrices π, {d} and {i}, containing row-wise versions of the parameters for the SUAR model, the death rate for each comaprtment, and the influecne each age group has on the other, and scalars a and b, which define the aging rate and the birth rate of the population.

Simplified SUAR Model with age

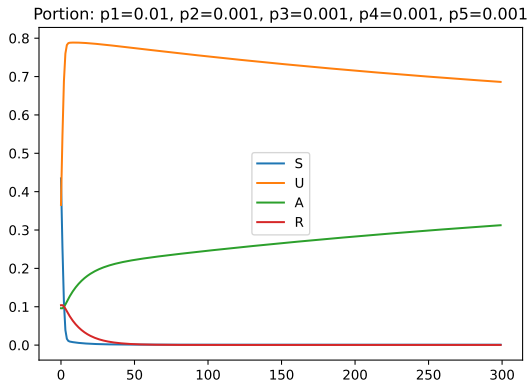
After building the SUAR model with different age groups, we toyed arroung with various combinations of paramenters to see how the model reacted. However, we found that with 20 compartments and 73 parameters, it is realy hard to go through all the combinations to find meaningfull results from the model. We could see that there were stationary points for the population portions, but finding them analyticaly was near impossible. Because of this, we sought to find a way to simplify the model to produce results that are easier to understand. We did this by removing the different age groups all together, while keeping the equations describing the model the same. By removing the age groups, the equations dramaticaly simplify into this form;

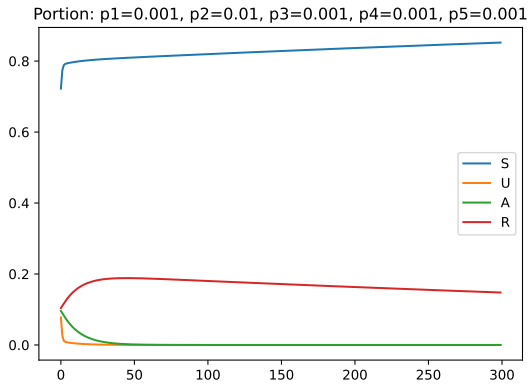
$$\frac{dS}{dt} = -S\pi_1 N + U\pi_2 P - d_S S + b(S+U+A+R)$$

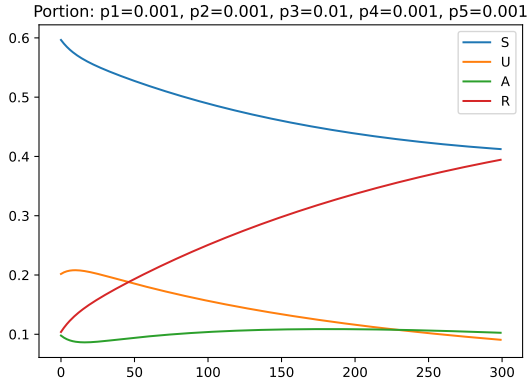
$$\frac{dU}{dt} = S\pi_1 N - U\pi_2 P - U\pi_3 - d_U U$$

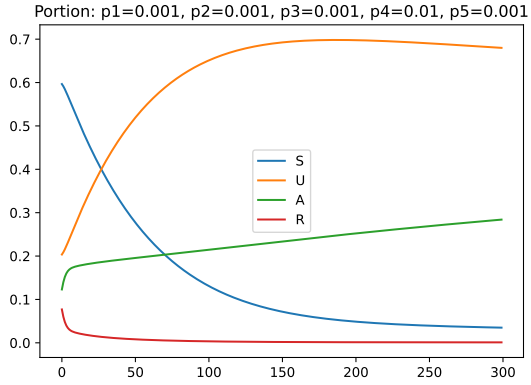
$$\frac{dA}{dt} = U\pi_3 - A\pi_4 P + R\pi_5 N - d_A A$$

$$\frac{dR}{dt} = A\pi_4 P - R\pi_5 N - d_R R$$









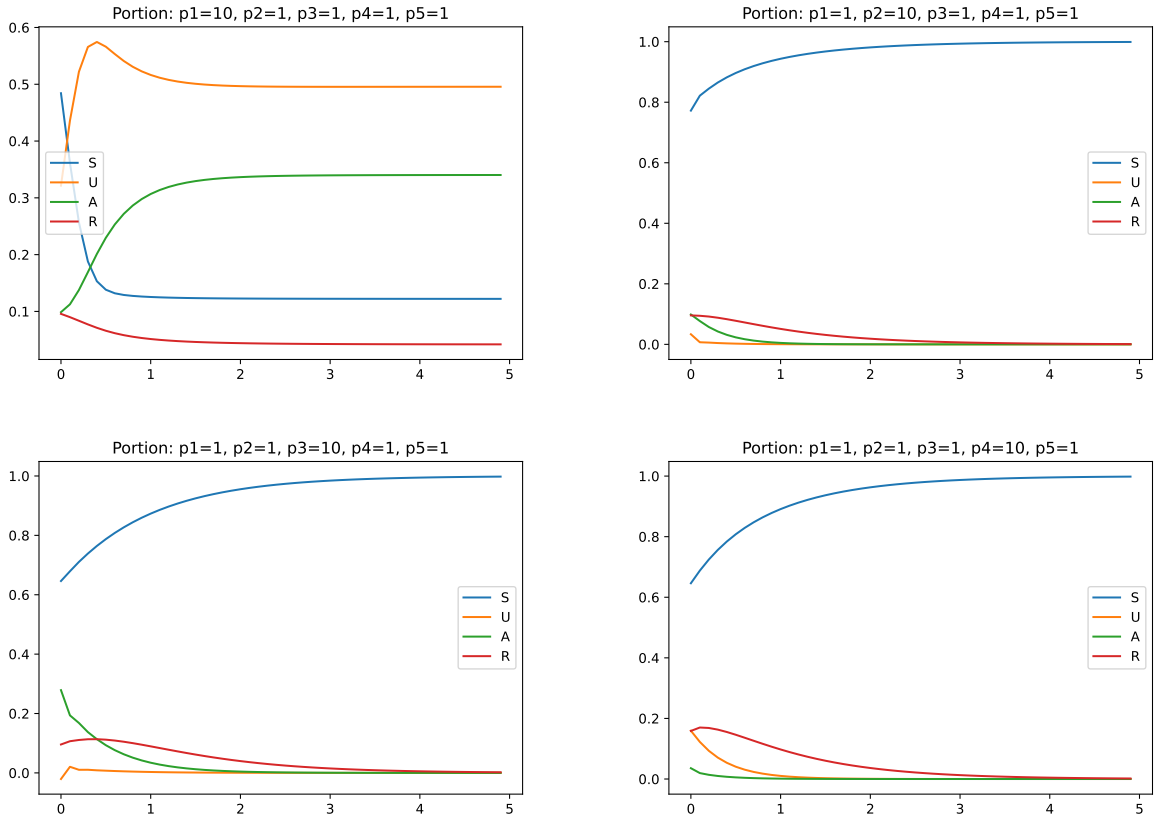
Looking at this model, it is clear to see that we will only find stationary points when births and deaths are equal. However we also want to see long term trends in growing and shrinking populations. To do this, we look at this model through populaton portions, redefinig the system as:

$$T = S + U + A + R$$
$$T' = b(S + U + A + R) - d_S S - d_U U - d_A A - d_R R$$

$$\frac{d\frac{S}{N}}{dt} = \frac{(-S\pi_1 N + U\pi_2 P - d_S S + b(S + U + A + R))T - T'S}{T^2}$$
$$\frac{d\frac{U}{N}}{dt} = \frac{(S\pi_1 N - U\pi_2 P - U\pi_3 - d_U U)T - T'U}{T^2}$$
$$\frac{d\frac{A}{N}}{dt} = \frac{(U\pi_3 - A\pi_4 P + R\pi_5 N - d_A A)T - T'A}{T^2}$$
$$\frac{d\frac{R}{N}}{dt} = \frac{(A\pi_4 P - R\pi_5 N - d_R R)T - T'R}{T^2}$$

Denoting these fractions as s,u,a,r and reformatting the equation using T as a characteristic for population and $\frac{1}{b}$ as a characteristic for time;

$$s + u + a + r = 1$$
$$\frac{ds}{dt} = (-s\pi_1(u + a) + u\pi_2(s + r) - d_S s + 1) - s(1 - d_S s - d_U u - d_A a - d_R r)$$
$$\frac{du}{dt} = (s\pi_1(u + a) - u\pi_2(s + r) - u\pi_3 - d_U u) - u(1 - d_S s - d_U u - d_A a - d_R r)$$
$$\frac{da}{dt} = (u\pi_3 - a\pi_4(s + r) + r\pi_5(u + a) - d_A a) - a(1 - d_S s - d_U u - d_A a - d_R r)$$
$$\frac{dr}{dt} = (a\pi_4(s + r) - r\pi_5(u + a) - d_R r) - r(1 - d_S s - d_U u - d_A a - d_R r)$$

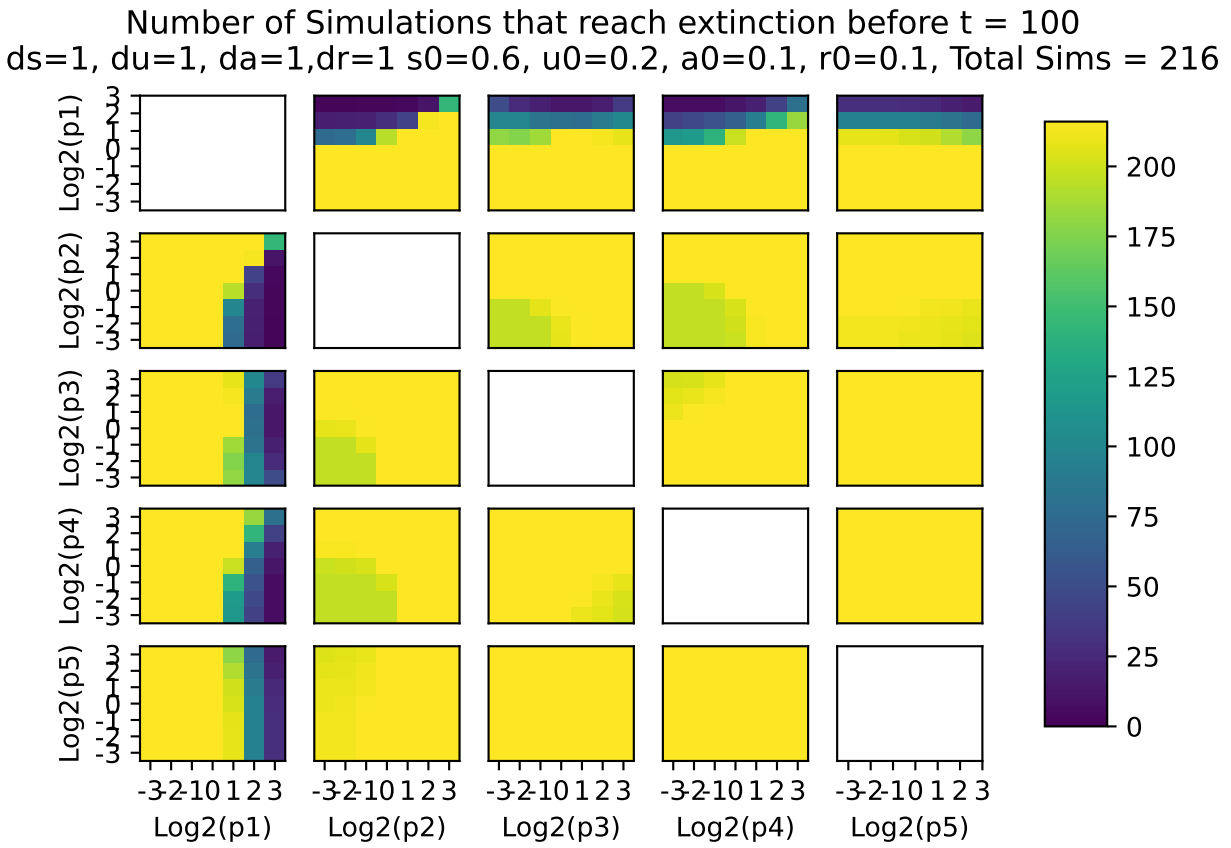


Results

Looking at the above equations, it may not be obvious as to what the stationary points are. However, since we are now looking at population portion, we can think of deaths as a movement from all compartments to the susceptible compartments. This makes it clear the only stationary point is when all the people are in the susceptible compartment, meaning the drug is 'extinct'. Similar, the drug is also extinct when everyone is either in the recovered or susceptible group, as one just has to wait for the recovered people to die for the portion of S to reach 1. These two facts can be seen in appendix 3. This result was confirmed using matlab in appendix 4.

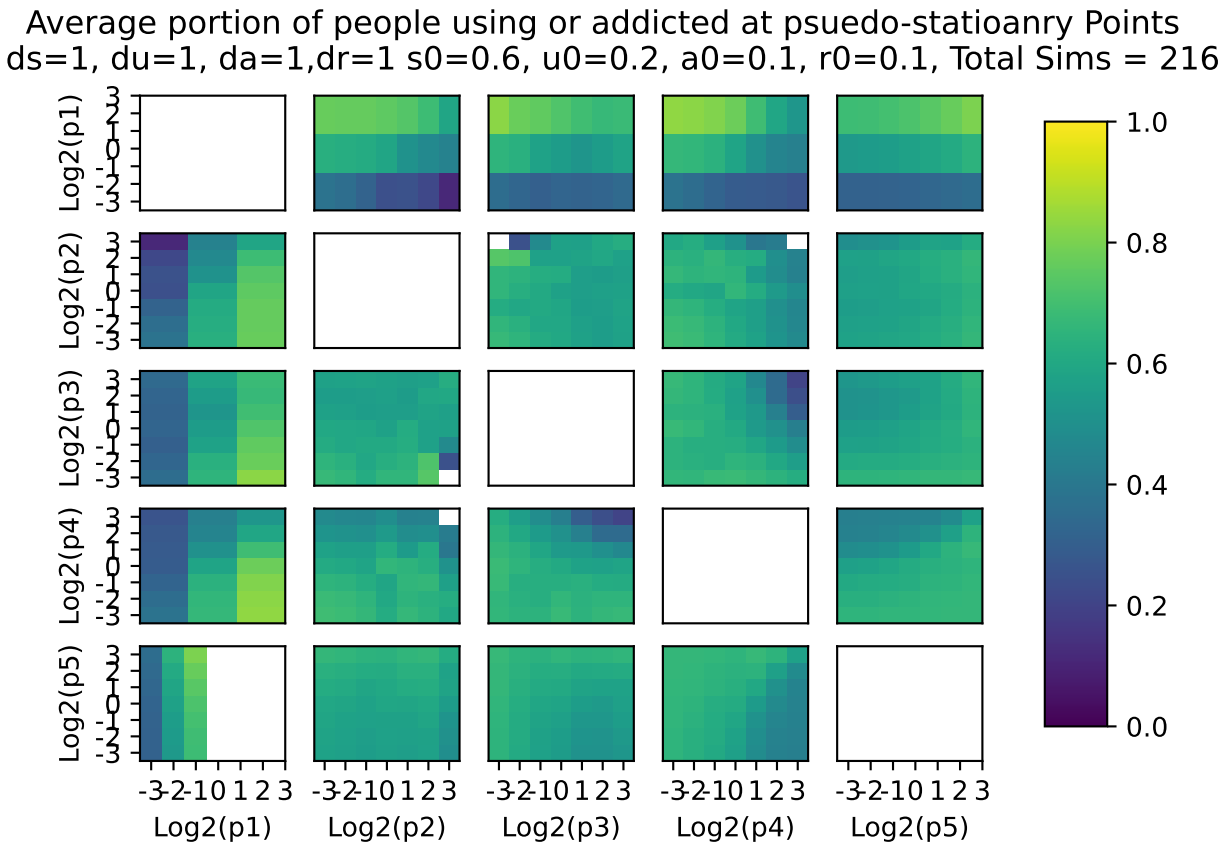
Another point of interest is the conditional stationary points, that occur when the parameters are at specific values. One such case is when the π parameters are much greater than the death rate, indicating transition between the groups occur rapidly in comparison to a lifespan. In this case pseudo-stationary points exist similar to those described in appendix 2.

While simulating various combinations of parameters, we found points that caused underflow errors when calculating the rate of change, since it was so low. Although not a true stationary point, as confirmed by the code in appendix 4, these points represents areas where the model will change extremely slowly, creating another pseudo-stationary point. Looking at some initial population and death parameters, we can plot the number of simulations that end in extinction as a function of their π parameters as shown below.



From this plot, one can see a big factor that influences the creation of these pseudo stationary points is the magnitude of π_1, an in a lesser extent the ratio of π_1 and π_2. In this case, any births will rapidly transition to the using category, meaning that they then have the potential to become addicted. This slows the transition to a state where $r + s = 1$, creating the pseudo stationary point.

Another result one can take from the data is the number of people who are using or addicted to the drug at the pseudo-stationary points, as shown in these plots below.



Looking at these plots we can see the following behaviours:

- Bigger π_1 -> Higher Mean
- Bigger π_2 -> Lower Mean
- Bigger π_3 -> Lower Mean
- Bigger π_4 -> Lower Mean
- Bigger π_5 -> Higher Mean

Therefore, in terms of tweaking the long term state of drug use in communities, the best way to minimise drug use is to minimise π_1 such that a pseudo stationary point wont be reached and the drug will die out. If this cant be done, the number of people using or addicted to drugs can be minimised by lowering the values of π_2, π_3, π_4 or maximising the value of π_5 to make the pseudo-stationay point have a maxal number of people not using the drug.

Discussion

// Compare our model // Inspirations // Limitations // Future Tweaks

In this part of the discussion, we aim to compare our model with the one presented by Mushanyu, J, Nyabadza, F, Muchatibaya, G, & Stewart, A G. R. (2016) and decide what future tweaks and changes can be made to further improve our own model. The use of protein and ligand bonding as well as the Hill function is quite interesting since the authors have effectively linked Biological Modelling and altered it to their own advantage. Firstly, protein and a ligand bonding forming a new product has equivalently been transformed into addicts connecting and creating a bond with a recovery center and as a result being transformed themselves. They have also used the term 'Cooperativity' as a parameter which is how other rehabilitants affect other users either negatively or positively. In our case we have used positive and negative influence of age groups and/or compartment models on each other based on interactions instead of cooperativity. Cooperativity is a way more specific and detailed parameter whilst our own is more general. Applying both the protein-ligand equivalent

and the subdivision of a Recovered Cooperation parameter could help our model in the future. Secondly, the Hill Function was adjusted to suit their drug model. They split Rehabilitation in two sections. Outpatient rehabilitation allows the user to stay productive and around their family while inpatient rehabilitation involves rehabilitation centers and more strict rules. Of course, limited resources and capacities affect users' choices. The rehabilitation capacities are limited in their own way as well since in a lot of countries the health care department is not adequate to help all users which makes the model realistic and pragmatic. We on the other hand have sub compartments in the Infected Area which we have split into Using and Addicted compartments while we have not done the same in the Susceptible and Recovered compartments. Integrating those in the future as well as saturation effects can make our model more effective.

Conclusion

// Conclusion

Appendix

Appendix 1 : Stationary points of SIR model

$$0 = -\pi_1 * S * I$$
$$0 = \pi_1 * S * I + \pi_2 * R * I - \pi_3 * I$$
$$0 = -\pi_2 * R * I + \pi_3 * I$$

Therefore either π_1, S or I must be 0

If $I = 0$:

$$0 = -\pi_1 * S * 0$$
$$0 = \pi_1 * S * 0 + \pi_2 * R * 0 - \pi_3 * 0$$
$$0 = -\pi_2 * R * 0 + \pi_3 * 0$$

Therefore any point $[S,0,R]$ is stationary.

If $\pi_1 = 0$ or $S = 0$:

$$0 = 0 * I$$
$$0 = 0 * I + \pi_2 * R * I - \pi_3 * I$$
$$0 = -\pi_2 * R * I + \pi_3 * I$$

Therefore:

$$\pi_2 * R * I - \pi_3 * I = -\pi_2 * R * I + \pi_3 * I$$
$$\pi_2 * R * I = \pi_3 * I$$

:q

$$R : I = \pi_3 : \pi_2$$

Therefore any point $[0, \frac{P_{total} * \pi_2}{\pi_2 + \pi_3}, \frac{P_{total} * \pi_3}{\pi_2 + \pi_3}]$

Appendix 2 : Stationary points of SUAR

$$0 = -\pi_1 * S * (A + U) + \pi_2 * U$$
$$0 = \pi_1 * S * (A + U) - \pi_2 * U - \pi_3 * U$$
$$0 = \pi_3 * U + \pi_4 * (A + U) * R - \pi_5 * A$$
$$0 = \pi_5 * A - \pi_4 * (A + U) * R$$

By combing the first two and last two equations, one can see that if the parameters are non 0, $U = 0$. Therefore:

$$0 = \pi_1 * S * A$$
$$0 = \pi_4 * A * R - \pi_5 * A$$
$$0 = \pi_5 * A - \pi_4 * A * R$$

Therefore $S = 0$ or $A = 0$ In the case $A = 0$, any point [S,0,0,R] will be stationary

In the case $S = 0$

$$\pi_4 * A * R = \pi_5 * A$$
$$R : A = \pi_5 : \pi_4$$

Therefore any point [0,0, $\frac{P_{total} * \pi_4}{\pi_4 + \pi_5}$, $\frac{P_{total} * \pi_5}{\pi_4 + \pi_5}$]

Apendix 3: Critical Points of Simplified SUAR model

When s = 1:

$$s = 1$$
$$\frac{ds}{dt} = (-d_S s + 1) - s(1 - d_S s) = (1 - S)(1 - d_S s) = 0$$
$$\frac{du}{dt} = 0$$
$$\frac{da}{dt} = 0$$
$$\frac{dr}{dt} = 0$$

When s+r = 1:

$$s + r = 1$$
$$s = 1 - r$$

$$\frac{ds}{dt} = (-d_S s + b) - s(1 - d_S s - d_R r) = (1 - s) * (1 + d_r * s - d_s * s)$$
$$\frac{du}{dt} = 0$$
$$\frac{da}{dt} = 0$$
$$\frac{dr}{dt} = (-d_R r) - r(1 - d_S s - d_R r) = (s - 1) * (1 + d_r * s - d_s * s)$$

References

1) Mushanyu, J, Nyabadza, F, Muchatibaya, G, & Stewart, A G. R. (2016). Modelling Drug Abuse Epidemics in the Presence of Limited Rehabilitation Capacity. Bulletin of Mathematical Biology, 78(12), 2364–2389. https://doi.org/10.1007/s11538-016-0218-5

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