Components of Modeling Part 2

Different Kinds of Mathematical Models of Dynamic Processes

There are many different kinds of mathematical models. Here is a partial list.

1. Discrete Time Versus Continuous Time Models.

Our experience of time is that it evolves continuously. So, typically time is a continuous variable that takes on any real number.

However, there are many models where time is discretized and evolves in steps. These models *can* be easier to formulate and *can* be easier to analyze and simulate (but not necessarily!).

When should we use a discrete time model?

- When variables are evolving one step at a time.

  Example: Many plants and animals have well-defined generations that are seasonally dependent; in such cases it is appropriate to discretize time.

- To simplify the situation.

  Example: The model for the spread of an epidemic in Homework 2.

  However, be aware that in these cases, there is a hidden parameter Δt which measures the amount of time that passes between two discrete points of time.

What do discrete and continuous time models look like?

- Discrete time models often present themselves as
  - difference equations (deterministic with no spatial component) or
  - cellular automata models (deterministic or stochastic with a spatial component) or as
  - discrete time Markov process (stochastic).

- Continuous time models often present themselves as some kind of differential equation. They can be
  - first order differential equations (usually when you understand how fast the quantities will change),
  - second order differential equations (often arising when you apply a physical law such as $F = ma$),
  - partial differential equations (when the variables have a spatial component), or
  - continuous time Markov processes (when the variables evolve stochastically).

2. Stochastic versus Deterministic Models.

In stochastic models the values of the variables evolve *randomly*; in deterministic models they evolve deterministically.

- If you set the values of the parameters and the initial conditions, then in a deterministic model the variables will evolve in exactly one way.
- In contrast, in a stochastic model there are many different ways that the variables can evolve, some of which are more likely than others. In stochastic models you will probably be interested in the *distribution* of the different behaviors that are possible.

When should we model things as stochastic and when as deterministic?

It is appropriate to model a variable as evolving stochastically when

a) the things that are causing it to change its value are variables that are not included in the model and,

b) the cumulative effect of these external variables is likely to vary significantly.

Example: An epidemic evolving over time. We are interested in the number of infected people.

What causes the number of infected people to change?

- The number of infected people will increase when a susceptible person meets an infected person and the interaction is such that the disease is passed.
- We cannot hope to include all the people and their individual behaviors in our model, so the mechanism causing this change depends on variables that are not included in our model.
- What is the cumulative effect of these variables and is it likely to vary significantly?

- In a small population, these individual interactions can make a big difference; for example, if only one person has the disease and that person stays at home and doesn't meet anyone, then the disease will die out. In this case you should use a stochastic model.
- In a larger population, the individual differences in interactions are likely to average each other out, so the total number of people will grow essentially deterministically. In this case it would be appropriate to use a deterministic model.

- Deterministic models are often some kind of average of stochastic models.

  If you have both a stochastic and deterministic model, it can be useful to explore in what sense the deterministic model is an average of the stochastic model.

- Stochastic models are often harder to analyze and understand than deterministic models.

3. Models in which the variables do or do not have a spatial component

In some models the quantities being measured vary only in time. In others, they vary both in time and in space.

Example: In the model of an epidemic on homework 2, the variables have no spatial component; we are simply counting the total number of infected, susceptible, and recovered individuals.

A more detailed model would track these individuals *spatially*. When we do that, we may find that the simple model without a spatial component is not very accurate.

- Models without a spatial component are often some kind of average of a more detailed model in which the variables have a spatial component.
- Models with a spatial component can be considerably harder to understand and analyze.
- Models with a spatial component can present themselves as
  - partial differential equations,
  - stochastic partial differential equations,
  - cellular automata models.

4. Models of Complex Systems

We often want to model complex systems, composed of many individuals, that interact with each other. Examples of this include:

- traffic flow that consists of the behavior of many individual cars,
- the progress of an epidemic that is passed from one individual to another,
- the progression of cancer that consists of many individual cells.

Agent-based Models

One way to model these kinds of systems is to track all the individuals of which the system is composed. These kinds of models are called *agent-based models*.

- Agent-based models are often cellular automata models and are often stochastic.
- They are usually relatively easy to simulate but very difficult to analyze.
- Guiding idea is that patterns can emerge from simple, local rules about how individuals interact.

Compartment Models

Another way to build a model of a complex system is to divide it up into compartments. The compartments are usually determined spatially.

- You assume that each compartment is well-mixed so that you don't need to consider the spatial distribution of the different types of individuals in each compartment. This means that the variables are the total number or concentration of each type of individual in each compartment.
- You model the relationship between the variables in each compartment and the variables between the different compartments.

Example: A simple epidemic

Consider a simple disease like chicken pox. The disease is passed from person to person through physical contact between a person that is infected and a person that is susceptible. Once a person has had the disease, they then recover (or, in rare cases, die) and become immune.

We will develop a number of different models of this disease.

One way to model the spread of the disease would be to model each individual in the population. In theory we could track the movements of each person, their status as susceptible, infected, or recovered, their level of physical contact with other people they meet, and their level of susceptibility when susceptible.

- A ridiculously complex model.
- It would have a ton of parameters whose values we could never hope to determine.
- It would also be unwieldy and not shed much light on the main mechanisms by which the disease is spread and not help us determine, say, what effective measures might be to prevent the spread of the disease.

So, we will look at a number of ways in which we can simplify the situation to understand the spread of the disease.

Reed-Frost Model

We will first consider the spread of the disease in a family. (Imagine that one person becomes infected and the family remains quarantined, so that the disease can pass from person to person in the family but will not spread outside of the family.)

Notice that the spread of the disease is described by the graph

$$S \to I \to R$$

indicating that the susceptible people can become infected, and infected people can recover (or die) but there is no new supply of new susceptible people to the process.

We shall not attempt to track every single individual with their individual behaviors. Instead, we will simply keep track of the following quantities:

$$S = \text{number of susceptible people}$$

$$I = \text{number of infected people}$$

$$R = \text{number of recovered people}$$

We need to describe how S, I and R will change as time goes on. Notice the following:

a) As time goes on, S can only decrease, I can increase or decrease and R can only increase.

b) $S + I + R = N$ is constant. It is the total number of people in the family. This means that if we know the values of S and I then we can determine the value of R; in other words, we really only have two variables instead of three.

We'll make the following assumptions. Some of these are forced on us by the simple act of compartmentalizing the people into three groups.

a) Every susceptible person is as likely as every other susceptible person to acquire the disease. (In other words, people don't differ in their tendency to acquire the disease.)

b) The family is *well-mixed*; every infected person is as likely as every other infected person to pass the disease on to a susceptible person.

c) When different people acquire the disease they all remain infected for the same amount of time.

We understand exactly how I morphs into R; people remain in the I group for a fixed amount of time and then pass into the R group.

However, even this becomes complex; the time at which a person leaves the I group depends on when they entered the I group. This is difficult because we'd like to treat the I-group as a single entity and not as a bunch of individuals.

So, let's discretize time, choosing one time step to be the length of time that an individual remains infected. This means that in every time step the whole of the I group passes to the R group and we have

$$R_{n+1} = R_n + I_n.$$

The factors that determine how many people will pass from the I group to the S group are hopelessly complex and not being tracked in our model. However, they are likely to play a significant role in a small family; in some situations everyone may end up acquiring the disease whereas in other situations maybe only one or two members of the family will acquire the disease.

For these reasons it is appropriate to model this as *random*:

$$S_{n+1} = S_n - X_n$$
$$I_{n+1} = X_n$$

but we need to think carefully about the *distribution* of X_n. In other words, we need to determine $P(X_n = k)$ where $k = 0, 1, 2, \ldots$.

Notice first that $X_n \leq S_n$. This tells us immediately that the distribution of X_n depends on S_n.

In fact, further thought tells us that the distribution depends on both S_n and I_n; for example if one or the other is equal to 0 then X_n must also be equal to 0, since there is no way for the disease to spread. Indeed, for a person to pass from the S group to the I group, they must meet someone in the I group and the disease must be passed.

The meeting of an infected person and a susceptible person is symmetric in S_n and I_n (i.e. if the values of S_n and I_n were swapped the same number of meetings would take place).

However, the disease is passed *from* an infected person *to* a susceptible person, so the distribution of X_n will not be symmetric in S_n and I_n. Indeed, the *possible* values of X_n only depend on S_n; as we noticed above, X_n can range from 0 to S_n.

Let p denote the probability that a particular individual from the S group meets a particular individual from the I group and the meeting results in the disease being passed along. Notice that p is a parameter that doesn't depend on S_n, I_n, R_n or on n. However, it *does* depend on the time step.

Assuming these meetings are independent (this is a result of the well-mixing assumption), then the probability that a particular susceptible person avoids contact with all of the infected people is:

$$q_n = (1-p)^{I_n}.$$

Now we don't have to consider the infected people any more; we have the following situation:

- An event that may or may not happen to each susceptible person (namely, that that person becomes infected). This event occurs with probability $1 - q_n$.
- Whether or not the event occurs to one individual is *independent* of whether it occurs to another individual (this is the well-mixing assumption).
- Our variable X_n counts the *number* of individuals to which the event occurs.

Those of you that have taken probability will hopefully realize that this means that X_n has a binomial distribution with parameters $1 - q_n$ and S_n. For those of you that haven't, let's reason through this.

Let's label the people in the infected group 1, 2, 3, up to S_n.

Let's start by considering $k = 0$. The only way we can have $k = 0$ is for the event to not happen to any of the individuals. The probability of this is:

$$P(X_n = 0) = q_n^{S_n}$$

Now let's consider $k = 1$. There are S_n different ways that we could have $k = 1$; the first could become infected and the rest not, the second could become infected and the rest not, etc. Each of these are disjoint events; if one happens the other does not. This means that the total probability is the sum of these probabilities. In other words,

$$P(X_n = 1) = S_n(1 - q_n)q_n^{S_n - 1}$$

Now let's consider $k = 2$. For X_n to be equal to 2, two people become infected and the rest do not. The number of ways that this can occur is the number of ways that 2 people can be chosen from a group of S_n people. This number is

$$\binom{S_n}{2}$$

and the probability of each of these is $(1 - q_n)^2 q_n^{S_n - 2}$. Thus,

$$P(X_n = 2) = \binom{S_n}{2} (1 - q_n)^2 q_n^{S_n - 2}.$$

In general, we have,

$$P(X_n = k) = \binom{S_n}{k} (1 - q_n)^k q_n^{S_n - k}.$$

for $k = 0, 1, 2, \ldots, n$. This is called a binomial distribution.

We now have a model for how S, I and R change as time evolves.

$$S_{n+1} = S_n - X_n$$
$$I_{n+1} = X_n$$
$$R_{n+1} = R_n + I_n$$

where X_n has a binomial distribution with parameters $1 - q_n = 1 - (1-p)^{I_n}$ and S_n. Given initial conditions (presumably $S_0 = N - 1$, $I_0 = 1$ and $R_0 = 0$) we have a *rule* by which the variables S, I and R evolve.

This is a 3-parameter model;

- N is the total population,
- p is the probability of one specific infected individual meeting a specific susceptible individual and passing the disease, and there is
- the time-step.

However, the probability p is related to both N and the time step; if N increases, p would probably decrease and if the time step increases then p would also increase.

The model is stochastic, so different things can happen. The different things that can happen are called *sample paths*. Our model allows us to calculate the *probabilities* of the different sample paths.

Notice that the first time that X_n is equal to 0, the disease dies out and the system stops evolving.

Moreover, if X_n is not equal to 0 then S_n will decrease by at least 1. This means that after N steps we must have $S_n = 0$, so $X_n = 0$ and the system stops evolving.

One interesting thing to explore is the distribution of the total number of people that get infected before the system stops evolving. (Homework 3)

Kermack - McKendrick Model

Now let's consider a larger population than a family; maybe a small isolated village with, say, a few hundred people.

If you run the Reed-Frost model with $N = 200$ or so, you'll see that the different sample paths all look pretty similar.

This is the averaging effect that is frequently observed in stochastic models. We'll derive a deterministic model that depicts this typical average behavior.

Recall that X_n in the Reed-Frost model is the number of susceptible people that acquire the disease in one time step and that each susceptible person had a probability of $1-(1-p)^{I_n}$ of acquiring the disease.

Thus, the average or *expected* number of people that acquire the disease is $S_n(1-(1-p)^{I_n})$.

In the Kermack-McKendrick model we replace the random variable X_n with this value.

This gives us

$$S_{n+1} = S_n - S_n(1 - (1-p)^{I_n}) = S_n(1-p)^{I_n}$$
$$I_{n+1} = S_n(1 - (1-p)^{I_n})$$
$$R_{n+1} = R_n + I_n$$

Notice: $S_n((1-1-p)^{I_n})$ isn't necessarily an integer.

Since N is largish this isn't so important; the model is only an approximation of reality, so when we need to interpret the values of the variables as numbers of people we'll just round to the nearest integer appropriately.

To simplify the notation

- let $a = -\ln(1-p)$ so that $(1-p)^{I_n} = e^{-aI_n}$ and
- since S_n, I_n, and R_n may not be integers and are also not random let's call them x_n, y_n and z_n respectively.

We have:

$$x_{n+1} = x_n e^{-ay_n}$$

$$y_{n+1} = x_n(1 - e^{-ay_n})$$

$$z_{n+1} = z_n + y_n$$

This isn't quite the Kermack-McKendrick model.

They also weakened the assumption that the time step is exactly equal to the length of time that a person remains infected.

In this case we run back into the problem that different people become infected at different times, so it seems like we won't be able to treat the infected group as a single entity.

To deal with this, let's make a different assumption about the disease.

If the time-step isn't too small, we would expect the distribution of the number of time-steps a person has the disease to be decreasing and concave up. This is what a geometric distribution looks like.

In other words, we will assume that once a person is infected, they have a fixed chance $1 - b$ of recovering every time step after that until they recover.

In this case, the fraction of the whole population that moves from the infected group to the recovered group at time n will be (on average) $(1-b)y_n$.

This gives us the following model.

$$x_{n+1} = x_n e^{-ay_n}$$

$$y_{n+1} = y_n + x_n(1 - e^{-ay_n}) - (1-b)y_n = x_n(1 - e^{-ay_n}) + by_n$$

$$z_{n+1} = z_n + (1-b)y_n$$

This is the Kermack-McKendrick model of the disease.

This is a 4-parameter model:

- N is the total population,
- $a = -\ln(1-p)$ is determined by the probability that a particular infected individual meets a particular susceptible individual in the length of one time-step and passes the disease,
- b is the fraction of infected individuals that remain infected each time step, and there is
- the time step.

These parameters are related to each other however. The value of a probably depends on both N and the time step; if N increases a would decrease and if the time step increases then a increases. The value of b depends on the time step; if the time step is increased then b will also increase.

This model is *deterministic*; given initial conditions (and fixed values of the parameters) the values of the variables x_n, y_n and z_n evolve in one way and only one way.

Unlike the Reed-Frost model, the orbit of the Kermack-McKendrick model never stops evolving. This is because the values of x_n, y_n and z_n aren't integers, so x_n can get small (much less than 1) but it will never become 0.

This means that to answer the question of how many people total become infected you need to look at $\lim_{n\to\infty} z_n$.

It would be interesting to explore the exact nature of the connection between the Reed-Frost model and the Kermack-McKendrick model.

It's not the case that the values of x_n, y_n and z_n are the average or expected values of S_n, I_n and R_n respectively.

However, simulations reveal that they do seem to be *typical* values.

Another Discrete Time Deterministic Model

The Kermack-McKendrick model was derived from the Reed-Frost model.

However, if you started by wanting to model the spread of the epidemic in an isolated village, you might not develop the Reed-Frost model first.

What kind of model might you get if you went straight to this case?

Because we are dealing with a largish population, we might try to develop a deterministic model from the outset.

Also, since we probably don't want to be specific about the size of the population, we should model the *fractions* of the population that are susceptible, infected and recovered.

For simplicity we'll start with a discrete time model.

We will assume as in the Kermack-McKendrick model that

a) Every susceptible person is as likely as every other susceptible person to acquire the disease. (In other words, people don't differ in their tendency to acquire the disease.)

b) The population is *well-mixed*; every infected person is as likely as every other infected person to pass the disease on to a susceptible person.

c) Once a person has acquired the disease, they have a fixed probability each time step of recovering from the disease.

Let s_n, i_n and r_n denote the fractions of susceptible, infected, and recovered individuals respectively.

As in the Kermack-McKendrick model, a fixed fraction of the individuals pass from the infected group to the recovered group each time step. Thus

$$r_{n+1} = r_n + \beta i_n$$

How should we model the changes in s_n and i_n due to people passing from the susceptible group to the infected group?

- For a person to pass between these two groups, a person in the susceptible group must *meet* a person in the infected group and the disease must be passed.
- The number of such possible meetings is proportional to the *product* of s_n and i_n. (e.g. if there are 5 people in the infected group and 7 people in the susceptible group then the number of possible meetings is 35).
- In other words, we might expect that the number of people that pass from the one group to the other to be proportional to $s_n i_n$. Call this constant of proportionality α.

We get the following model:

$$
\begin{aligned}
s_{n+1} &= s_n - \alpha s_n i_n \\
i_{n+1} &= (1-\beta) i_n + \alpha s_n i_n \\
r_{n+1} &= r_n + \beta i_n
\end{aligned}
$$

This is the model on homework 2.

This is a 3-parameter model:

- α is the proportion of all possible meetings that occur and result in the disease being passed
- β is the fraction of people that leave the infected group each time step and there is
- the time step.

However, the parameters α and β both depend on the time step:

- If the time step is increased both α and β would increase.
- When the time step is small we'd expect α and β to depend linearly on its size but when it gets large there will be multiple meetings between people in one time-step, so we'll no longer have linear dependence.

Notice that β is unit less but α has units of 'per person,' so we might expect α to depend on N. Indeed as N increases we might expect α to decrease but the exact relation isn't clear (to me).

A Continuous Time Deterministic Model

Since time in this model will be a *continuous* variable, the *numbers* of people in each group are actually piecewise constant functions that jump by $+1$ or -1.

This is a little cumbersome.

So instead of using the *numbers* of people in each group as our variables, let's use the *fractions* of people as we did in the model above; that way we can allow the variables to take on any number between 0 and 1.

We will develop our model by starting with the deterministic models above and letting the time step go to 0.

This means that we are making the same assumptions that we had in the two discrete time models above.

We're doing this but it may not be reasonable - the models above relied on the fact that the time step had a specific value or, at least, wasn't too small.

Let $s(t)$, $i(t)$, and $r(t)$ be the fractions of the population that are susceptible, infected and recovered respectively at time t.

From the model above we have in time Δt,

$$\begin{aligned} s(t+\Delta t) &= s(t) - \alpha s(t) i(t) \\ i(t+\Delta t) &= i(t) + \alpha s(t) i(t) - \beta i(t) \\ r(t+\Delta t) &= r(t) + \beta i(t). \end{aligned}$$

However, remember that α and β both depend on the time step Δt; if the time step increases we expect both α and β to increase. Indeed, when Δt is small and we double its size we might expect α and β to roughly double.

Thus we have:

$$\alpha = r\Delta t$$
$$\beta = \sigma\Delta t$$

Another way to think about these equations is that they are the local linearizations of α and β as functions of Δt about $\Delta t = 0$.

The model becomes:

$$\begin{aligned} s(t+\Delta t) &= s(t) - r(\Delta t)s(t)i(t) \\ i(t+\Delta t) &= i(t) + r(\Delta t)s(t)i(t) - \sigma(\Delta t)i(t) \\ r(t+\Delta t) &= r(t) + \sigma(\Delta t)i(t). \end{aligned}$$

We want to understand what happens as $\Delta t \to 0$. If we simply take a limit of each side of the equation as $\Delta t \to 0$ we will get the uninteresting equations

$$s(t) = s(t)$$
$$i(t) = i(t)$$
$$r(t) = r(t)$$

The point is to rewrite the equations so that we can see the *derivatives* of $s(t)$, $i(t)$ and $r(t)$. We can do that as follows:

$$\frac{s(t+\Delta t) - s(t)}{\Delta t} = -rs(t)i(t)$$
$$\frac{i(t+\Delta t) - i(t)}{\Delta t} = rs(t)i(t) - \sigma i(t)$$
$$\frac{r(t+\Delta t) - r(t)}{\Delta t} = \sigma i(t)$$

Taking the limit as $\Delta t \to 0$ we get:

$$s' = -rsi$$

$$i' = rsi - \sigma i$$

$$r' = \sigma i$$

This is a system of three first order differential equations. However, $s + i + r = 1$ for all t, so really there are only two independent differential equations.

There are two parameters r and σ. Balancing units on both sides of the equation we can see that the units of both of them are time^{-1}. This tells us that if we measure time in different units, the values of r and s will change.

It's interesting to do a similar derivation starting with the Kermack-McKendrick model.

From the Kermack-McKendrick model we have in time Δt,

$$\begin{aligned} s(t+\Delta t) &= e^{-ai(t)}s(t) \\ i(t+\Delta t) &= \left(1-e^{-ai(t)}\right)s(t) + bi(t) \\ r(t+\Delta t) &= r(t) + (1-b)i(t). \end{aligned}$$

However, recall that a and b depend on the time step Δt; if Δt increases then a should increase and b should decrease. We are going to let $\Delta t \to 0$ so we are interested in how a and b depend on Δt when Δt is very small.

When $\Delta t = 0$ we should have $a = 0$ and $b = 1$. Thus, linearizing a and b as functions of Δt about $\Delta t = 0$ we get $a = r\Delta t$ and $b = 1 - \sigma\Delta t$. Thus, we have:

$$\begin{aligned} s(t + \Delta t) &= e^{-r(\Delta t)i(t)} s(t) \\ i(t + \Delta t) &= \left(1 - e^{-ai(t)}\right) s(t) + (1 - \sigma\Delta t) i(t) \\ r(t + \Delta t) &= r(t) + \sigma(\Delta t) i(t) \end{aligned}$$

We want to take the limit as $\Delta t \to 0$, so before doing that we want to rewrite our equations so that we can see the derivatives of s, i and r. The last equation is the easiest one to deal with. We can rewrite it as:

$$\frac{r(t + \Delta t) - r(t)}{\Delta t} = \sigma i(t)$$

Taking the limit as $\Delta t \to 0$ yields

$$r' = \sigma i.$$

To deal with the first and second equations, we expand $e^{-r(\Delta t)i(t)}$ about $\Delta = 0$ to get

$$e^{-r(\Delta t)i(t)} = 1 - r(\Delta t)i(t) + O((\Delta t)^2)$$

Now the two equations become:

$$s(t + \Delta t) = s(t) - r(\Delta t)i(t)s(t) + O((\Delta t)^2)$$
$$i(t + \Delta t) = r(\Delta t)i(t)s(t) + (1 - \sigma\Delta t)i(t) + O((\Delta t)^2)$$

Rewriting these we get:

$$\frac{s(t + \Delta t) - s(t)}{\Delta t} = ri(t)s(t) + O(\Delta t)$$
$$\frac{i(t + \Delta t) - i(t)}{\Delta t} = ri(t)s(t) - \sigma i(t) + O(\Delta t)$$

Taking a limit as $\Delta t \to 0$ we have the three equations

$$s' = -rsi$$

$$i' = rsi - \sigma i$$

$$r' = \sigma i$$

which is the same equations we got using the other model as a starting point! This is very reassuring!

A Compartment Model for the Spread of the Disease Between two Isolated Villages

Now suppose we want to model the spread of the disease among two isolated villages.

- The villages are isolated, so we will ignore encounters from the outside.
- There is some contact between the residents of each village but not at the same rate as the contact between the residents of a single village.
- We assume that the behavior of the people in the two villages is similar.

For this model we will have six variables.

Let

- s_1, i_1 and r_1, be the fractions of the total populations of both villages that live in the first village and are susceptible, infected, and recovered respectively and
- s_2, i_2 and r_2, be the fractions of the total populations of both villages that live in the second village and are susceptible, infected, and recovered respectively.

We will adapt the deterministic continuous time model above, so if there were no contact between the two villages, s_k, i_k and r_k would evolve just like s, i and r in the model above.

We need to think about how to model contact between the two villages.

For the disease to pass from the first village to the second village, an infected person in the first village must come into contact with a susceptible person in the second village. This will happen at a rate that is proportional to $i_1 s_2$.

Similarly, the disease will pass from the second village to the first village at a rate that is proportional to $i_2 s_1$.

The constant of proportionality will be the same in both cases, since it is based on the frequency with which residents of the first village come into contact with residents of the second village.

We get the following system of six differential equations.

$$
\begin{aligned}
s_1' &= -rs_1i_1 - \rho s_1 i_2 \\
i_1' &= rs_1i_1 + \rho s_1 i_2 - \sigma i_1 \\
r_1' &= \sigma i_1 \\
s_2' &= -rs_2i_2 - \rho s_2 i_1 \\
i_2' &= rs_2i_2 + \rho s_2 i_1 - \sigma i_2 \\
r_2' &= \sigma i_2
\end{aligned}
$$

An Agent-Based Model for the Spread of the Disease Through a City

It is not reasonable to assume that the population in this case is well-mixed.

Instead we wiil model each individual in the city.

Our model will be a stochastic, discrete time model.

Each individual is in one of three possible states at any point in time; susceptible, infected, or recovered. Let $x_i(n)$ denote the state of the i'th individual at time n. We'll let:

- $x_i(n) = 0$ if the individual is susceptible,
- $x_i(n) = 1$ if the individual is infected, and
- $x_i(n) = 2$ if the individual has recovered.

The state of each individual moves from having value 0 to having value 1 to having value 2.

Passing from state 1 to 2:

We assume that at each time step there is a fixed probability β of an infected individual passing to the recovered state. This probability is the same for all individuals.

Passing from state 0 to state 1:

Let $p_{ij}(n)$ denote the probability that the i'th individual meets the j'th individual in the next time step and the nature of their contact is such that the disease could pass from one to the other.

Assume the event that the i'th individual meets one individual and the disease is passed is independent of the event that they meet any other individual and the disease is passed.

Suppose the i'th individual is in the susceptible group (i.e. $s_i = 0$).

Then the probability he/she does not acquire the disease in one time step is:

$$\prod_{\text{infected individuals } j} (1 - p_{ij}(n))$$

So, the probability he/she passes from state 0 to state 1 in the next time step is:

$$p_i(n) = 1 - \prod_{\text{infected individuals } j} (1 - p_{ij}(n))$$

Thus, at each time step n we do the following:

- Consider each susceptible individual i and compute $p_i(n)$. With this probability have this individual move from state 0 to state 1.
- Consider each infected individual i and allow them to recover with probability β.

This is our model. It is very quick to simulate. I haven't run it myself, but I imagine that on a laptop computer it is feasible to have tens of thousands of individuals and run it for hundreds of hours.

Notice the huge number of parameters in this model! If N is the size of the population we have $N(N-1)+1$ parameters at each point in time n!

How could we possibly hope to estimate all these parameters?

E. Frias-Martinez, V. Frias-Martinez, and Williamson estimated these parameters for a city in Mexico to study the 2009 H1N1 outbreak.

(Paper that appeared in the proceedings of the 2011 International Conference on Social Computing)

They used cell-phone data to determine each individual's social network and to determine their geographic location up to the region covered by the cell phone towers over a certain time period (one month?).

Most people's behavior is very repetitive especially on weekdays.

From the data and tendency of the disease to be passed from one person to another they obtained estimates of $p_{ij}(n)$; the estimates changed every hour of the day but were the same for the same hour on different weekdays and were the same for the same hour on the two weekend days.

Other kinds of agent-based models have the individual agents be families or small communities rather than individual people.

In this case you would need to have variables s_j, i_j, and r_j for each agent representing the *numbers* of susceptible, infected, and recovered individuals in each agent.

Then, at each time step, you'd have a *within-agent* progression of the disease as well as a *between-agent* progression of the disease.

Parameter estimation is a huge undertaking.

It has been done based on census and other government data giving information about schools etc.

These models are also used as *phenomenological* models without estimating parameters.