Mathematical and computational modeling in ecology

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Steps to modeling a biological problem:
1. Formulate the problem (what do you want to know?)
2. Determine the basic ingredients (define the state variables, describe constraints on those variables (population density can't be 0, etc.), describe interactions among the variables, choose discrete or continuous time, and a time scale, units, define parameters and constraints on them)
3. Qualitatively describe the biological system (use a life cycle diagram, flow diagram, or a table for more complicated stuff)
4. Quantitatively describe the biological system (translate #3 to equations, perform checks to catch errors e.g., are units consistent, are constraints satisfied)
5. Analyze the equations (use the equations to simulate and graph the dynamics, perform appropriate analyses, (rarely) solve for general solution). Graphing: state variables vs. time, look for dependence on initial conditions, study dependence on parameter values (aka sensitivity analysis)
6. Checks and balances (check your model results against data or older analyses, determine how general your results are (based on parameter values and assumptions/constraints on variables), consider alternatives to the simplest model, extend or simplify (people usually add too much at the beginning; easier to extra stuff later and easier to understand role of new stuff you add because now you understand the base case) the model as needed and repeat 2-5)
7. Relate the results back to the question (do the results address your original question, are the results obvious or counter-intuitive, do you trust this, interpret the model verbally, describe potential experiments or observations that would test the model)

Formulating a model: population growth in discrete time, using the example of a sheep population on an island (closed population) with births in the spring and mortality during the winter. First question is how will the population change when they are first introduced, second question is how will it change when it gets crowded?

Model 1

1. Let's specify females since they are often rate-limiting. How will the population size of females change when sheep are first introduced to the island? Assume resources are not limiting.

2. Basic ingredients:

- Time is in discrete intervals of one year.

- State variable: n_t = number of females in year t

- Parameters: b = per capita birth rate (expected # of female offspring per mother per year); d = fraction of the population that dies each year (when you multiply it by the population size), or the probability of dying for any individual (which sounds more stochastic and not determinisitic, but this is a deterministic model so it's really more of an expectation of how many will die–if everyone has the same probability, that will manifest a a fraction of the population that will die).

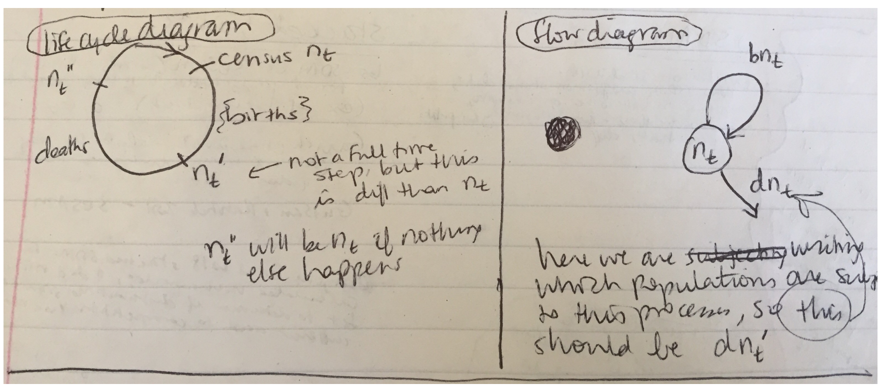
- Constraints: state variable must be ≥ 0, $b \geq 0$ although $b = 0$ is a trivial case, $0 < d \leq 1$ (but if $d = 1$ then everyone will die in the next year, as if they are annual plants). Another way to write this is:

$d \in (0, 1]$.

- Units: Units of b is written as $[b]$. $[b]$ = # baby sheep/# mother sheep and therefore is unitless. Similarly, d is a fraction or probability, which is also unitless. We don't have the "per year" as part of the units because this is discrete time, so time isn't flowing while you're in a particular time step.

3. Qualitative description:

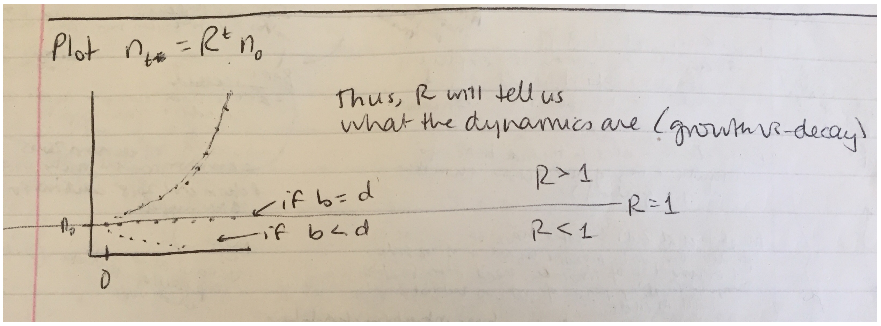
- we'll count sheep just before breeding season.
- We can depict this in several ways (but these terms aren't used the same way by different authors).
- One is a "life cycle diagram". Another is the "flow diagram" (be careful whether you are writing per capita parameters or not)
- See notes for drawing of two diagrams.



4. Quantitative description:

- for this, probably easiest to build from the life cycle diagram
- goal is to write down an equation for n_{t+1} in terms of n_t:
  $n_{t+1} = n_t + bn_t - dn_{t'}$ and $n_{t'} = n_t + bn_t$ so we have: $n_{t+1} = (n_t + bn_t)(1 - d) = n_t(1 + b)(1 - d)$
- In discrete time, we like to write that $R = (1 + b)(1 - d)$, which is sort of a discrete time growth rate, but let's avoid "rate" in discrete time and say it's a growth factor or growth multiplier. Thus, $n_{t+1} = Rn_t$. We also see this as: $n_{t+1} = (1 + r_d)n_t$, and we can call r_d is the per capita change in the number of sheep ("growth rate").
- Now let's perform some checks, starting with units.
- LHS: n_{t+1} is number of sheep. RHS: $[R]$ is the number of future sheep divided by the number of present sheep, no units because b and d are unitless too. $[n_t]$ = number of sheep. So [LHS] = [RHS], yay.
- Sign check: check the state variables using constrained parameter values. We need $n_t \geq 0, \forall t$ (aka for all time). R is always positive, because (1-d) and (1+b) will always be positive, so n_{t+1} will always be 0.

5. Analyze equations:
   $n_{t+1} = Rn_t$ Call $n_{t=0} = n_0$. If we keep plugging in values for n_0 and the next time step, we realize that there is a general solution: $n_t = R^t n_0$
   Then plot it! See image.



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(continuing with exercise from last class)
Usually you don't have a general solution. Most often you analyze the model qualitatively. This means that you consider the equilibrium points and their stability.

Definitions:
System is at equilibrium if the state variables don't change over time. In a dicrete time model, this means you're looking for when $n_{t+1} = n_t$. Satbility of an equilibrium describes whether is is attracting or repelling. Think about response to a perturbation from equilibrium (analogy–ball sitting on top of a hill or at the bottom of a valley, and you push it, how does it roll)

Equilibrium point n^* is locally stable if the system near n^* approaches it, and is globally stable if the system will approach it from anywhere. It is unstable if the system near n^* moves away from it.
Stability is a property of an equilibrium point in a model, and it will depend on parameter values!

For geometric growth model, $n_{t+1} = Rn_t$.
Equilibrium point: Find values of n^* that satisfy $n^* = Rn^*$.
For R = 1, then any n^* works; this is the trivial case.
For $R \neq 1$, then $n^* = 0$, which is the only equilibrium.

Stability of n^*=0 (based on the plot):
$n^* = 0$ is unstable when $R > 1$
$n^* = 0$ is stable when $0 < R < 1$ (when it's less than one, but remembering that it can't be negative). Looking at the model we know that it's globally stable, because the population density will always decrease when R is less than 1.
(trivial solution: when R = 1, that's neutral stability)

6. Checks and balances: Check our model against data. In this case, we can take advantage of the fact that we have a general solution, and transform our data to see if it matches our model:
   $n_t = R^t n_0$ so let's log transform it: $log(n_t) = t * log(R) + log(n_0)$. So we can log our data and plot it against time, and then we expect that the slope of the line should be equal to R. Ultimately, though, we'd expect that the model will break down; unconstrained growth can't go on forever on the island. If you can get away with avoiding some nonlinearities, then do so, such as when there is early growth and things look exponential (or geometric if discrete time) at first. You don't have to bit off every possible complexity.

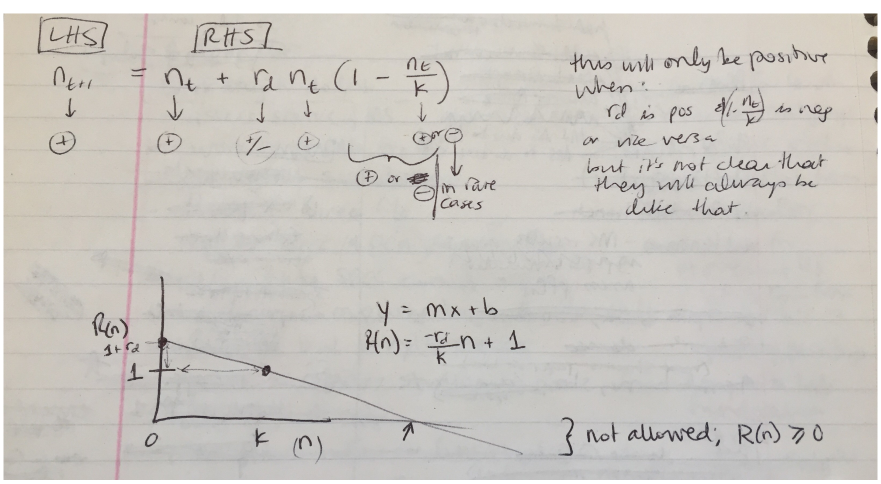
7. Relate back to biological question: what happens after introduction? Geometric growth or decay; it depends (on the values of the parameters, which represent the biology we're thinking about–here,

depends on demographic parameters–remember that R involves the birth and death rate). Note that right now we're talking about a deterministic world, but in the real world there's chance so there will be stochasticity, and there are models that deal with that (both environmental stochasticity, and the stochasticity that comes from being a discrete world where you can't have half of an individual).

Okay, now let's move to question 2, what happens when it gets crowded?

Model 2

1. How does the population size change as resource become limiting?
2. Ingredients: as before, but now let's say that R depends on the population size. We need an additional parameter, aka a carrying capacity (a quantity to level off, what is "crowded"). We'll call it k. This is the population size where each individual replaces itself each year. What values can k take? It must be larger than 0.
3. Qualitative description: R depends on n, or mathematically we say $R(n)$. That's why we call this density dependence. $R(n) \geq 0$. Okay, now let's determine particular values:
Assume (i) $R(n = 0)$, this is the same R as in Model 1. We'll write it as follows: $R(n = 0) = 1 + r_d$. At low population density, we know those dynamics. (ii) $R(n = k) = 1$ by definition. How is $R(n)$ changing between these points? There's no particular answer, but there is a convention: assume that R declines linearly with increasing values of n.
4. Quantitative description: $n_{t+1} = R(n_t)n_t$. So, let's work with the rules to transform this into an equation. Think about it like an equation of a line between points (0, 1+r_d) and (k, 1) where R(n) is the y-axis and n is the x-axis, and slope is (1 - 1 - rd)/(k - 0) = -rd/k. So, $R(n) = (\frac{-rd}{k})n + (1 + r_d) = 1 + r_d(1 - \frac{n}{k})$. Let's plug this back in to our equation: $n_{t+1} = (1 + r_d(1 - \frac{n}{k}))n_t$ or in more classical form: $n_{t+1} = n_t + r_d n_t(1 - \frac{n}{k})$.
Let's check the units to make sure it's behaving: LHS: $[n_{t+1}]$ =sheep; RHS: $[n_t]$ =sheep, $[r_d]$ is unitless (future sheep/current sheep), $[1 - \frac{n}{k}]$ is also unitless (1- sheep/sheep). So yes, [LHS] = [RHS].
Sign: what range of values can r_d take? If $R(n)$ must be greater than or equal to 0, and is equal to $1 + r_d$, then the lowest value r_d can take is -1. $n_t + r_d n_t(1 - \frac{n}{k})$ has the following signs: (see notes). In this case, it is not clear that the RHS will always be positive. Model pathology: red flag, because you need to make sure that you're working in the realm where you're not getting negative population sizes. It's the linear relationship between R(n=0) and R(n=k) that is suspect–if it gets extrapolated beyond k, then you get negative values or R(n). see notes



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continuing. . .

5. Analyze: Find equilibrium points by solving for values of n^* that satisfy $n_{t+1} = n_t$. From $n_{t+1} = n_t + r_d n_t(1 - \frac{n}{k})$, we have $n^* = n^* + r_d n^*(1 - \frac{n^*}{k})$, then $0 = r_d n^*(1 - \frac{n^*}{K})$. Solutions are therefore: $n^* = 0$ and $n^* = K$ ($r_d = 0$ is trivial solution).

Next, look at stability: there are ways of doing this analytically (and he can help with that if we want to do this), but we can also look at model outputs to see what happens. He showed us two plots, one with positive values of r_d and one with negative values, and you can see that $n^* = 0$ is unstable and $n^* = K$ is stable when r_d is positive, and vice versa. Can look at sensitivity to initial conditions, for example by plotting population at time = 25 for different simulations with different initial population sizes against initial population size. Can look at sensitivity to r_d to see how stability of equilbrium points by plotting population at time = 5 against r_d. As you push r_d, you can get to the equilibrium point faster, or you can overshoot a little, and push the system into stable cycles, or into chaos.

7. Relate back to the question: how does the population grow as the island gets crowded? Answer: If r_d is not too high, population will approach K. If it is positive and large, you can get oscillations or even chaos.

Continuous time models

Discrete time models make sense when your system has a kind of rhythmic clock to follow, but in some systems, the events can occur at any time and there isn't a seasonality to them. If your state variables can change at any time with no strong rhythm, you can let time be a continuous variable (world of calculus– infinitessimally small time steps).

Describe the rate of change of our system (state variable) using a differential equation model. $\frac{dn(t)}{dt}$= "some function of n(t)", where n(t) is the state variable and we are looking at the change in the state variable over time. This is called an ODE (ordinary differential equation, in other words, only looking at the rate of change with respect to one variable, here: time). FYI: This is in contrast to PDEs (partial differential equation), which looks at change with respect to more than one thing. For example: $\frac{dn(t)}{dt} + \frac{dn(t)}{dx}$ where x is space or age.

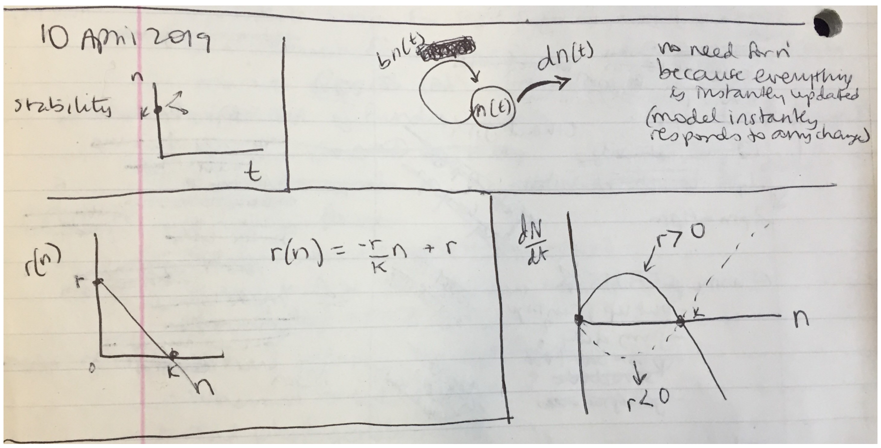
Example: exponential growth model. Consider a closed population with per capita birth rate b per year, and per capita death rate d per year. See notes for flow chart. Note that the model here updates instantly with any change, so need to worry about where the census happens or what the population size is that each b or d is affecting. Thus, we write: $\frac{dn(t)}{dt} = bn(t) - dn(t) = (b - d)n(t) = rn(t)$ where r = b-d (so there is no limits on r) aka the per capita growth rate. You're just looking for changes in the population, so you don't have to add n(t). This is a linear model, which means is it a simple linear function of the state variable (some constant times the state variable). Two consequences of this are that it's easy to model and work with, but it's also not capturing some of the more interesting biological interactions; for that you need nonlinearities. For now let's revel in this simple world and find a solution for this, by taking the integral! $\frac{dn}{dt} = rn$ or $\frac{1}{n}dn = rdt$ and take the integral of both sides, which yields ln(n) = rt + C, which is n = $e^{rt}e^C$ and this can be worked out to be: $n(t) = n_0 e^{rt}$. Usually we won't do this because it's too hard.

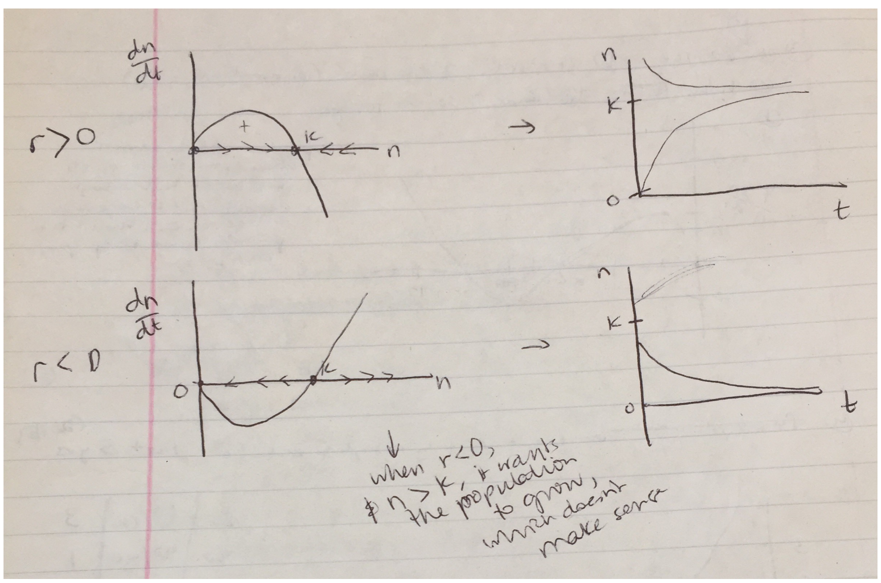
Equilibrium and stability: To find equilibrium points, you're looking for when $\frac{dn}{dt} = 0$. So, we're trying to solve: $rn^* = 0$. This is true when $n^* = 0$ (for $r \neq 0$).

Stability: When will n approach $n^* = 0$ or move away from it? We know that $n(t) \geq 0$, so this depends on r. If r is positive, it is unstable (exponential growth), and if r is negative, it is stable (exponential decay) (and it's globally stable).

Now let's add *density dependence* to this model. As a start, let's follow the same set of logic as in discrete time. We want to capture the influence of crowding. Qualitatively, let r be a function of n: $\frac{dn}{dt} = r(n)n$. Let K be the carrying capacity. Three assumptions, as before, but they look a little different: (i) r(0) = r (aka at low density, we assume it follows exponential growth rules), (ii) r(K) = 0 (continuous time is all about rates of change instead of replacing individuals in discrete time), and (iii) we assume that there is a linear decline between these two rates. See notes for the plot. Slope is $\frac{-r}{K}$ and intercept is r, gives u $r(n) = \frac{-r}{K}n + r = r(1 - \frac{n}{K})$. Let's plug this back in and that gives us the *classic continuous time logistic growth model*: $\frac{dn}{dt} = r(1 - \frac{n}{K})n$.

Equilibrium points: want n^* such that $r(1 - \frac{n}{K})n$ when $n^* = 0$ or $n^* = K$.
Stability: for a given set of parameter values, are the points stable? Let's plot how $\frac{dn}{dt}$ depends on the population size. $\frac{dn}{dt} = r(1 - \frac{n}{K})n = rn - \frac{rn^2}{K}$. We know when $\frac{dn}{dt} = 0$, and let's draw this from knowing this is a parabola. But, it's going to depend on the sign of r: if r is positive, then the coefficient is negative, so it's going to go downward. See image. Can consider those $\frac{dn}{dt}$ plots to determine stability, but can also write them out as a plot of n by t. See image.





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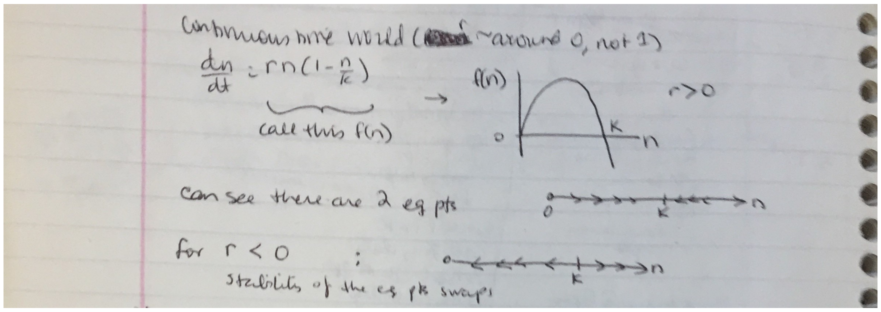
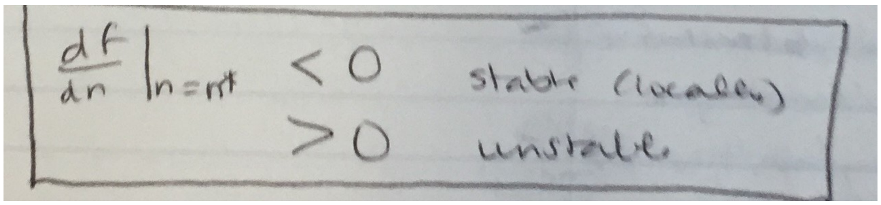
Review
In the continuous time world: (r leads to different dynamics if it is greater than or equal to 0, not 1). If we call $\frac{dn}{dt} = rn\left(1 - \frac{n}{k}\right) = f(n)$ and we plot f(n) by n, you can see that there are two equilibrium points, $n^* = 0$ and $n^* = k$. You can plot the phase line and see the stability of these points (depending on r; stability swaps when r>0 vs. r<0). See image.



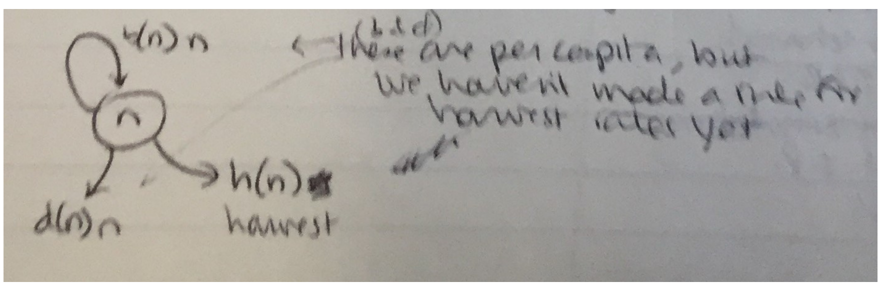
As you can see, knowing whether the slope of the function at the equilibrium point is positive or negative is enough to know the stability of the curve. Thus we can evaluate the derivative of the function at the equilibrium point to see the slope of the line. See image.



Plot of f(n) versus n shows you density dependence, aka how the growth rate changes with density.

Adding complexity: models with "harvesting"

Developing models to know how much to harvest is one of the ways this field developed, especially in fisheries. Let's build off of continuous time logistic and add more stuff, namely that some of the population is lost to harvesting: See image.



Questions: can we define a sustainable harvest rate? Can we maximize yield without risk of collapse? Are some policies better than others for this?

General model:

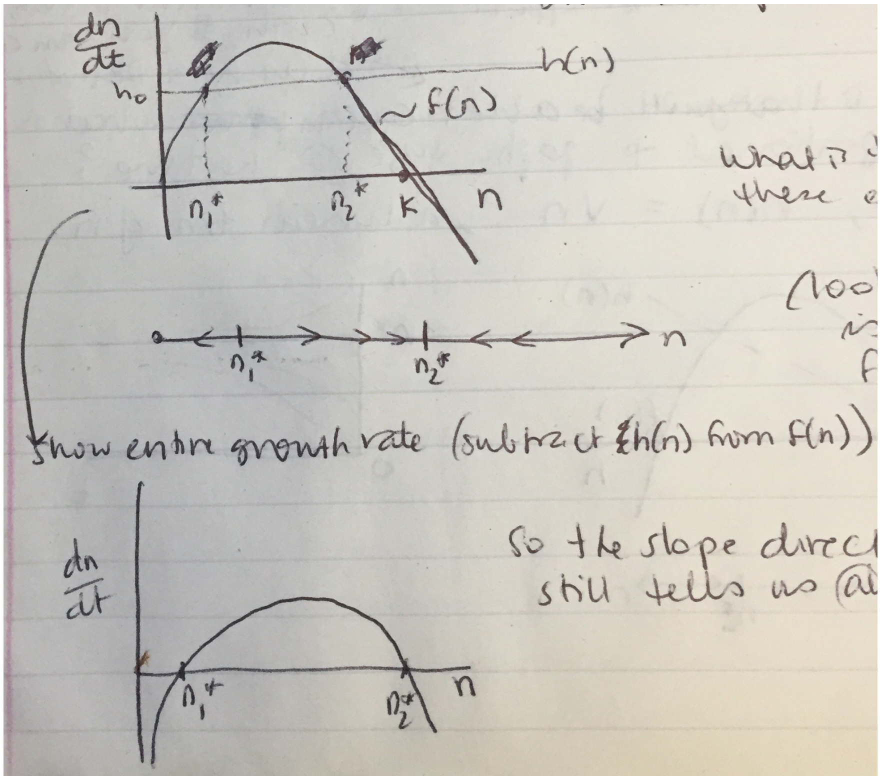
$$\frac{dn}{dt} = f(n) - h(n)$$

where $f(n)$ is the "natural growth dynamics" ($b(n)n - d(n)n$) and $h(n)$ is the harvest rate.

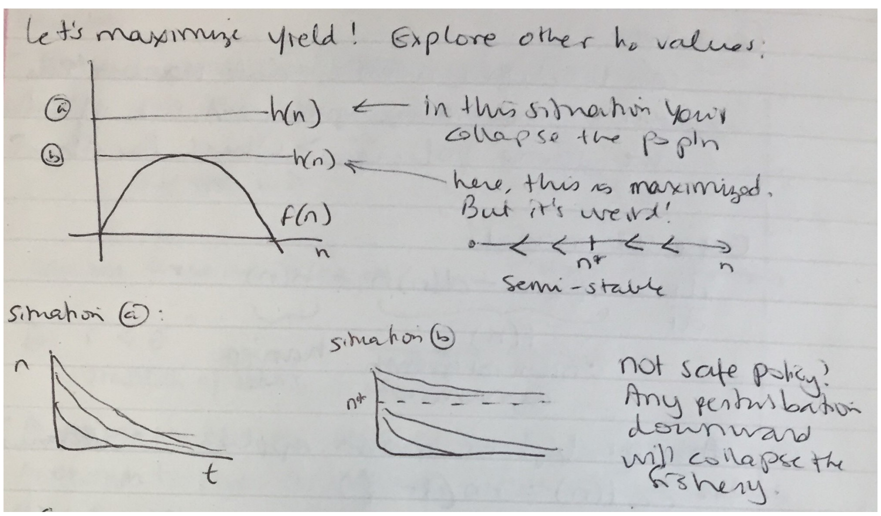
Assume logistic growth applies: (and assume r>0) $f(n) = rn\left(1 - \frac{n}{k}\right)$

Where are the equilibria? Answer where $f(n) = h(n)$, aka at the intersection of the two curves.

Policy 1: constant yield (aka h(n) doesn't depend on n)
$h(n) = h_o$ where h_o is some constant. Draw the two components of $\frac{dn}{dt}$ separately. You can determine the stability by looking at what $\frac{dn}{dt}$ will be by subtracting h(n) from f(n). See image. You can also draw what you would get by subtracting the two (just one function on the plot; see notes), and you can see that the slope of the line rule still applies.

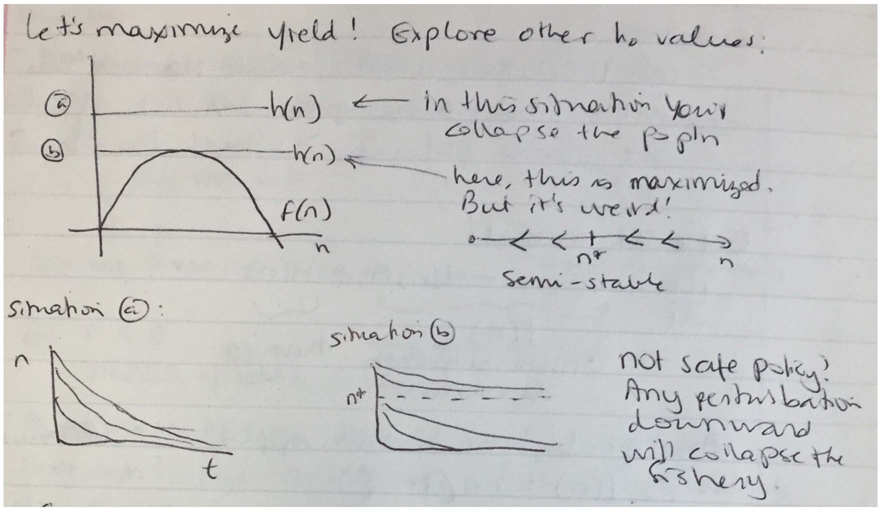


Let's maximize yield! Explore other values of h_o.

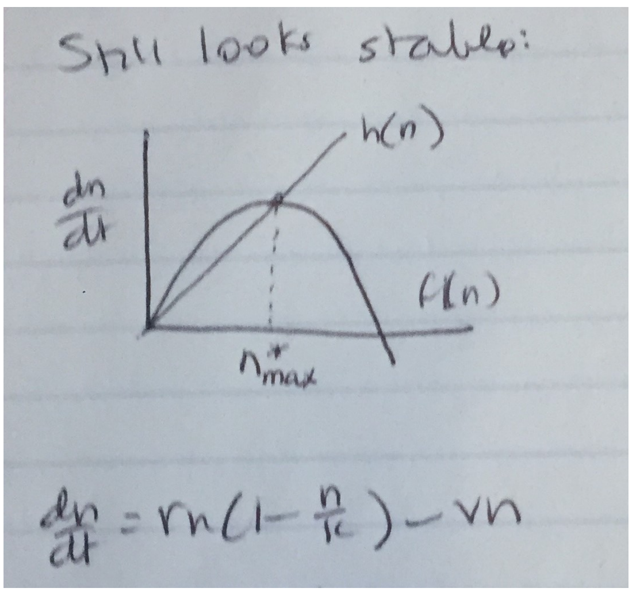


In some cases, you get a semi-stable equilibrium point, but this isn't safe because any perturbation downward will collapse the system. So what do we do? Let's try other policies. Why don't we try to adapt harvest rate based on the current population size.

Policy 2: constant effort (instead of constant number of fish, say catch all you can during a period of time). The ideas is that you will be able to catch what is proportional to population size at the time. So, now $h(n) = vn$, a linear function of n. See image.



How do you maximize the yield here? Choose a v where $h(n)$ intersects $f(n)$ at its peak. See image.



Still looks stable! This is a much better policy because it's self-correcting. But, if vn is too steep (i.e., bigger than r) then you are harvesting too much and the population will crash:
$\frac{dn}{dt} = rn\left(1 - \frac{n}{k}\right) - vn$. When $n << K$, $\frac{n}{k} \approx 0$, so $\frac{dn}{dt} = rn - vn$ (at low densities) and will crash if $v > r$. This happens when humans "cheat" with technology and more effort, but also when other fluctuations lower r.

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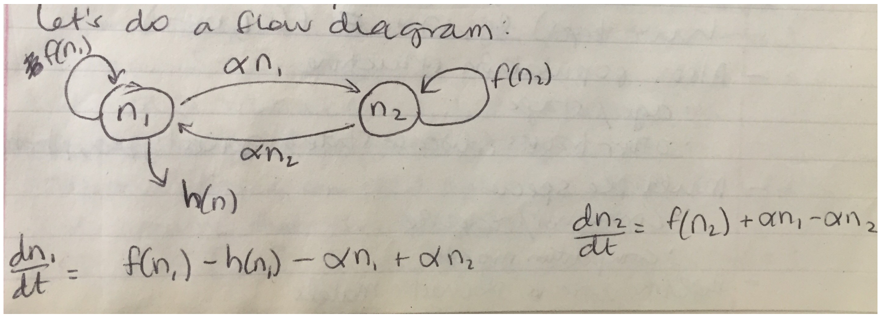
Marine Reserve Model: qualitative description: now assume two habitat patches, one that is harvested and one that is protected. Assume both are subject to logistic rowth, same parameters r and k. Also assume they are connected by migration where each fish can move to the other patch with a constant per capita rate α. Let's do a flow diagram:
See image.



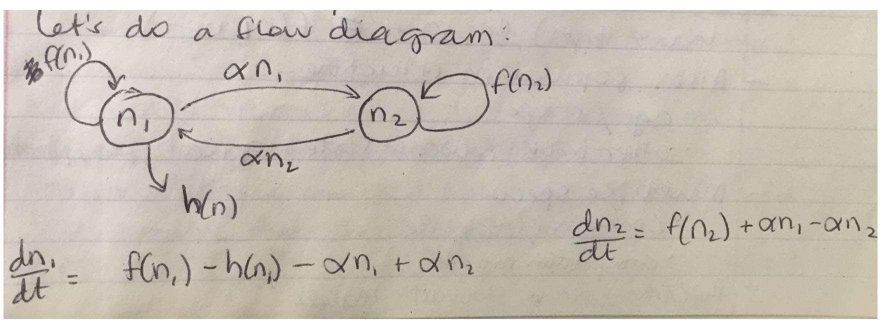
$$\frac{dn_1}{dt} = f(n_1) - h(n_1) - \alpha n_1 + \alpha n_2$$
$$\frac{dn_2}{dt} = f(n_2) - h(n_2) - \alpha n_2 + \alpha n_1$$

With logistic growth:

$$\frac{dn_1}{dt} = rn_1\left(1 - \frac{n_1}{k}\right) - h(n_1) - \alpha n_1 + \alpha n_2$$
$$\frac{dn_2}{dt} = rn_2\left(1 - \frac{n_2}{k}\right) - h(n_2) - \alpha n_2 + \alpha n_1$$

Model elaborations

Models with patches with connections (a "patch model") can be elaborated into a network model. Can also go into a grid system where you divide space into plots and pay attention to which plots are neighboring. Can look at just existence of space –> plane, or take into account landscape detail. See image.



- think about number of dimensions (going down a river is 1 dimension, down and across or down and into different water depths are 2 dimensions)

- can add time delays into the system (responses have lags) (e.g., $n_{t+1} = f(n_t, n_{t-1})$)
- also: population structure (age/stage, other traits such as disease states, genotypes, phenotypes)

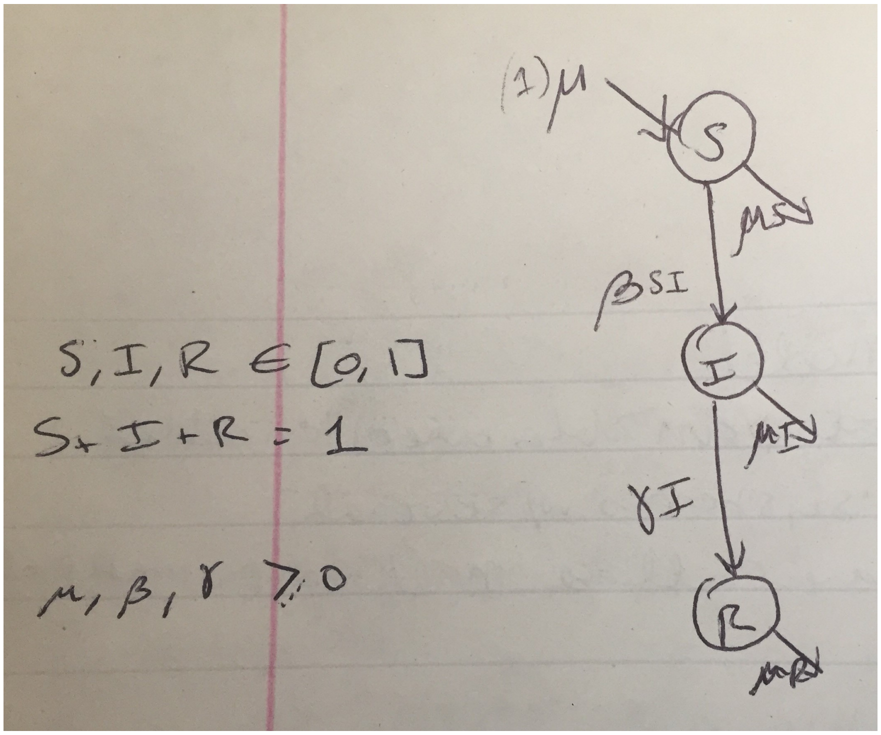
- multiple species (consumer/resource models, competition. . .)

- deterministic vs. stochastic models

We'll talk about a kind of multicompartmental model (the bubbles of state variables are often called compartments; systems with several compartments are called multicompartmental models) called SIR epidemic models. SIR models: consider an infectious disease like measles. It's acute and immunizing (once you've gotten it, you can't get it again), so they're called "childhood diseases", very amenable to vaccination programs.

Questions:
1. When infection is introduced to a population, what determines whether you get an outbreak?
2. How much of the population do you need to vaccinate to prevent an epidemic? "Herd immunity" –> once vaccination level is beyond a certain point, everyone is protected, even those who can't get vaccinated.

Divide the population into groups based on their status with respect to disease: Susceptible (never been infected); Infectious (infected and can infect others); Recovered (previously infected, no longer infectious) (hence S-I-R). Let state variable S, I, and R represent the proportion of the population in each group. Assume closed, constant population size, allow for birth and death but assume they balance out. Since S, I, R are proportions, S, I, R $\in [0, 1]$ and S + I + R = 1.



Births and deaths: μ is the per capita birth rate into S group, and also the per capita death rate from all groups.
New infections: rate of new infections depends on I individuals contacting S individuals, so we assume it depends on abundance of S and I individuals/hosts. Assume random mixing of the population, which gives us a rate of about SI. β is the transmission rate.
Recovery: assume infectious people recover to immune state at some fixed per capita rate γ.

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SIR models continued: μ, β, and γ cannot be negative. They are rates, and if they were negative it'd be as if you could reverse the direction of a state. All must be equal to or greater than 0.

Aside on residence time: residence time refers to how long an individual stays in a given state. In an ODE model, the expected residence time in a state is the reciprocal of the total outflow rate. For example, if you have a state X and individuals leave at a per capita rate a, then the expected residence time is $\frac{1}{a}$. If state Y has outflow cY and bY, then the expected residence time $E(T_Y) = \frac{1}{c+b}$.

The γ term is the recovery rate. We can come up with an estimate of γ from observable biology, but it's hard to estimate the recovery rate. Instead, you can look at how long individuals stay in the infected class and use that to estimate the rate at which they leave the class: estimate parameter values using data/observations of residence times in the real world.

Back to SIR: let's say that the infectious period for measles = 8 days. Therefore, we can estimate $\gamma = \frac{1}{8days} = 0.125days^{-1}$. Similarly, if we say "residence time" of being alive is 80 years, then $\mu = \frac{1}{80years} = 0.0125years^{-1}$. If you want to use these two models, you need to convert these so you're either in days or years. As you can see, these are on very different orders of magnitude, so it allows us to focus on the effect of measles–death by measles is more likely than average death rate).
Adding death from measles: if you wanted to, you could have $\mu' = \mu + \alpha$ where μ is natural death and α is death from measles.

Quantitative model:

$$\frac{dS}{dt} = \mu - \mu S - \beta SI$$
$$\frac{dI}{dt} = \beta SI - \mu I - \gamma I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

First question: what determines whether an introduction of disease leads to an epidemic? Epidemic means that you have transmission of infection and an upswing of infections (and ultimately a downswing when you run out of people to infect).

First, initial conditions: $I > 0$, but small: $I << 1$, naive population $R = 0$, so $S = 1 - I$ but since I is small, $S = 1$. This is essentially asking if, when we add a few I individuals, will I grow?

Two ways to translate this to math. First way ("instantaneous flow"): is $\frac{dI}{dt} > 0$? This is true when $\beta SI - \mu I - \gamma I > 0$. Simplifying this and taking into account initial conditions aka $S(0) = 1$ (and that I is not 0, so we don't have to worry about dividing by 0), we can see that: $\beta > \mu + \gamma$ or $\frac{\beta}{\gamma+\mu} > 1$. Aka, is this equilibrium stable? Does a small perturbation cause I to grow or not?

Second way ("generational approach"): are infected individuals infecting more than just one other person before they recover, aka is the expected number of new infections caused by each case greater than 1. The "expected number of new infections caused by each case" in epidemiology is called R_0 or the basic reproductive number (we call it this when the population is naive and susceptible). The condition we're looking for is $R_0 > 1$. This is the dominant paradigm for how we think about disease spread, borrowed from population demography (are genotypes replacing themselves–absolute fitness).

$R_0 =$ (rate of production of new cases by 1 infectious individual in susceptible population) times (expected duration of infectious period) which is (βS) times $(\frac{1}{\gamma+\mu})$, but S(0) = 1 so:

$R_0 = \beta * \frac{1}{\gamma+\mu}$ and we want $R_0 > 1$.

These two approaches give the same formula, so you can think about it two ways and get the same condition.

Second question: what is the critical vaccination threshold to reach the state of "herd immunity" and prevent an epidemic? Goal is to shift an unstable equilibrium point (where a perturbation would lead to epidemic) to a stable one.

Assumptions: a perfect vaccine (vaccination changes S to R). Let v = proportion of population that is vaccinated when the pathogen is introduced. This means that we are going to deal with vaccination in the initial conditions instead of as a flow in the model: S(0) = 1-v, R(0) = v, I(0) = small but positive. Also assume that $R_0 > 1$. How big does v need to be to prevent epidemic?

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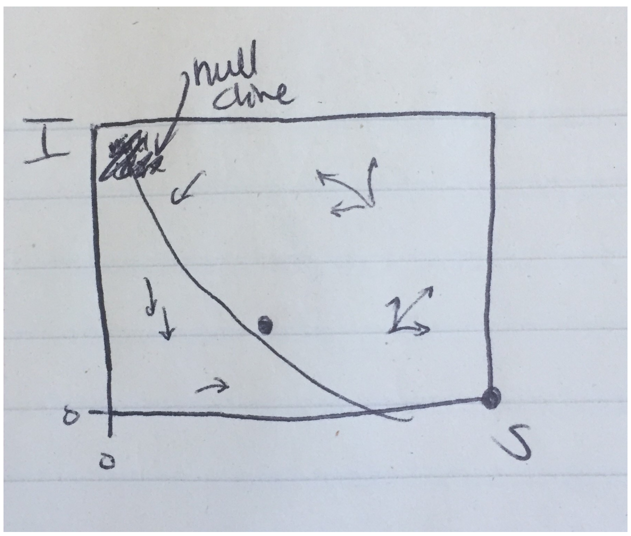
Effective population number: R_{eff} or R is the expected number of cases caused by an infected individual in a partially immune population. The R_0 world is best case scenario for the pathogen (completely susceptible population). Now we're trying to find the conditions that give us $R_{eff} > 0$.

$\frac{dI}{dt} > 0$ when $\frac{dI}{dt} = \beta S - \gamma - \mu > 0$. With initial conditions $S = 1 - v$, then: $\beta - \beta v > \gamma + \mu$ and we need $v_{critical} < 1 - \frac{\gamma+\mu}{\beta} = 1 - \frac{1}{R_0}$, so now we can just plug in R_0. For measles, R_0 is thought to be 20 (very infectious!), so the critical vaccination level is 0.95. You could even plot the critical vaccination level needed for different values of R_0.
From the approach of R_{eff}, you get $R_{eff} = R_0(1 - v)$ aka $R_{eff} = R_0 S$ and since we want $R_{eff} > 1$ then we find the same critical vaccination level.

What is this missing? Assumes random mixing, doesn't take into account heterogeneity in the population.

Qualitative analysis: equilibria and stability. You can find equilibrium points in a multicompartmental model by setting all equations equal to 0 and solving a system of equations. Also, because we are working with proportions, we only need to work with two of the equations, because we can figure out the other state since S + I + R = 1. Do some math to find values of S^*, I^*, and R^* to satisfy equilibrium assumptions.
Disease-free equilibrium: $S^* = 1$, $I^* = 0$, and $R^* = 0$
Endemic equilibrium (disease exists in the population): $S^* = \frac{\gamma+\mu}{\beta}$, $I^* = \frac{\mu}{\beta}(\frac{\beta}{\gamma+\mu} - 1)$, and $R^* = 1 - S* - I*$.
This makes sense because at equilibrium, $R_{eff} = 1 = R_0 S^*$ so it makes sense that $S^* = \frac{1}{R_0}$.

Stability: instead of phase line, we can look at a phase plane. In this case, let's look at S and I. The system has to be in the box somewhere, and if it doesn't add up to 1 then you know the remainder is in the R group. You can basically map out the vector field (what direction will the system go in), or also do null clines (draw boundaries). See image.



Slides on HIV. First question: why does the viral load peak and then drop off? (either immune systems figures it out, or the virus runs out of CD4 cells to infect) Someone tracked infected/uninfected CD4 cells and saw that depletion of CD4 cells leads to that viral load peak pattern without invoking immune response. Second question: why the long stable "set-point" phase before viral load increases? (could be that virus-infected cells live a long time, turnover very slowly) Ho et al 1995 treated HIV patients (as a way of cutting off the births) and looked at viral load response to determine death rate. Found that those cells are actually dying really quickly, so to hold this set-point the virus is constantly rapidly re-generating itself (major conceptual breakthrough, knowing that it can evolve so quickly).
Model 3: how will antiretroviral drugs impact the HIV epidemic? There was a fear of "behavioral disinhibition", that people would go back to risky behavior if drug therapy lowered fears of contracting HIV. Blower et al 2000 model that allowed for change in behavior and for evolution of resistence, used the model to explore uncertainty.
Model 4: estimating the rate of new infections, and who is at risk. Williams (2000) saw that HIV is still happening among the women with the most HIV, and that there was greater risk for younger women that you could tell just by looking at prevelance.
Model 5: impact of male circumcision on HIV risk.