

# Brilliant: Differential Equations II

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Note: Latex reference: <http://tug.ctan.org/info/undergradmath/undergradmath.pdf>

## 1 Chapter 1: Basics

### 1.1 Chapter 1: Nonlinear Equations

The two types of problems in this course are:

- Nonlinear equations (several equations on one independent variable)
- Partial differential equations (single equation with several independent variables)

**Linear** equations have solutions like  $y_1, y_2$  that can be combined using any  $c \in \mathbb{R}$  like  $y_1 + cy_2$ .

**Example:** Bacteria in a dish with a lot of food, no deaths

- $b'(t) = r_b b(t), r_b > 0$  would be the rate of growth.
- This is linear. Reason 1:  $\frac{d}{dt}(y_1 + cy_2) = y_1' + cy_2' = r_b(y_1 + cy_2)$  since  $y' = r_b y(t)$ , and same for  $y_2$ .
- Also, this works because the solution is  $b(t) = b(0)e^{r_b t}$ , so  $b_1(t) + cb_2(t) = b_1(0)e^{r_b t} + cb_2(0)e^{r_b t} = (b_1(0) + cb_2(0))e^{r_b t}$

**Example: Logistic** equation: Bacteria in a dish with a lot of food, limited by carrying capacity  $M$ .

- $b'(t) = r_b b(t)[M - b(t)]$ .
- This is nonlinear. Reason:  $\frac{d}{dt}(y_1' + cy_2') = y_1' + cy_2' = r_b[y_1 + cy_2][M - y_1 - cy_2] = My_1 + Mcy_2 - y_1^2 - 2cy_1y_2 - cy_1^2y_2^2$
- $\neq My_1 - y_1^2 + Mcy_2 - c^2y_2^2$  because of the extra  $-2cy_1y_2$  term.

Sidebar: Note that this equation  $b' = r_b b[M - b]$  is *separable*, so it can be solved.

- $\frac{db}{dt} = rb[M - b]$
- $\frac{db}{b(M-b)} = rdt$
- $\frac{1}{M}(\frac{1}{b} + \frac{1}{M-b})db = rdt$  after partial fractions work
- $(\ln(b) - \ln(M - b)) = Mrt + C \Rightarrow \ln(\frac{b}{M-b}) = Mrt + C$
- $\frac{b}{M-b} = e^{Mrt} e^C$
- Initial conditions  $b = b(0), t = 0 \Rightarrow \frac{b}{M-b} = \frac{b(0)}{M-b(0)} e^{Mrt}$
- $b(1 + \frac{b(0)}{M-b(0)} e^{Mrt}) = M \frac{b(0)}{M-b(0)} e^{Mrt}$
- $b(M - b(0) + b(0)e^{Mrt}) = Mb(0)e^{Mrt}$
- $b = \frac{Mb(0)e^{Mrt}}{M+b(0)[e^{Mrt}-1]}$

This logistic solution will taper off to  $M$  at some point. Note that  $\lim_{t \rightarrow \infty} b(t) = M$  since the non-exponential terms stop mattering. Also  $b(t) = M$  sticks as a constant solution or **equilibrium** immediately. *These equilibria tell us what matters - the long-term behavior of solutions!*

Another **Example**: Lotka-Volterra equation pairs: Bacteria ( $b$ ) and bacteria-killing phages ( $p$ ), with kill rate  $k$ .

- The “product”  $kb(t)p(t)$  measures the interactions and kills resulting from this.
- $b'(t) = r_b b(t) - kp(t)b(t)$ , or the normal growth rate minus kill rate
- $p'(t) = kp(t)b(t)$  since its population grows as it kills bacteria.
- Equilibria include  $b = 0, p = 0$  and  $b = 0, p > 0$ , since these are *constant* solutions, or places where  $b'(t) = 0, p'(t) = 0$ .

**Direction fields**, with vector pointing towards  $\langle b'(t), p'(t) \rangle$  (TODO - I think) let us follow the arrows to determine the curve over time. In this case, the bacteria will always go extinct.

However, if we add a new death rate term  $-d_p p(t)$  so  $p'(t) = -d_p p(t) + kp(t)b(t)$ :

- We get an equilibrium at  $b = \frac{d_p}{k}, p = \frac{r_b}{k}$ . (Since  $0 = b'(t) = r_b b - kpb, (\Rightarrow pk = r_b), 0 = p'(t) = -d_p p + kpb, (\Rightarrow bk = d_p)$ )
- But otherwise the solutions swirl around this point. This is called a **cycle**. TODO What is a **limit cycle**?

Note that there are systems where the “solution particle” neither reaches an equilibrium or cycles around one point. The **Lorenz system** famously has this owl-eye shaped double attractor (an example of **strange sets**) where initially close particles diverge unpredictably if the constants  $\rho, \sigma, b$  are chosen right:

- $x'(t) = \sigma(y - x)$
- $y'(t) = x(\rho - z) - y$
- $z'(t) = xy - bz$
- TODO

## 1.2 Chapter 1.2: PDEs

Many methods of attack for PDEs

- Separation of variables
- Power series (Note: did we actually touch on this?)
- Fourier Transform

**Example:** Standing wave, where one end of a rope is fixed.

- Vertical displacement from a line of rope:  $u(x, t)$  depends on where ( $x$ ) and when ( $t$ ).
- Rope’s **wave equation** is  $u_{tt} = v^2 u_{xx}$ , where  $v$  is the “constant wave speed”, and the others are the space, time partials.
- Note that  $u = \cos(vt)\sin(x)$  and  $u = \sin(vt)\cos(x)$  both work.
- If you guess the solution has split variables like  $u = X(x)Y(y)T(t)$ , then, upon substitution and division by  $X(x)Y(y)T(t)$ ,  $\frac{\delta^2 u}{\delta t^2} = v^2[\frac{\delta^2 u}{\delta x^2} + \frac{\delta^2 u}{\delta y^2}]$  yields  $\frac{T''(t)}{T(t)} = v^2[\frac{X''(x)}{X(x)} + \frac{Y''(y)}{Y(y)}]$
- This method may or may not work. But if it does, it means that since  $x, y$ , and  $t$  are independent variables, each individual piece must be constant.
- So, for example, if we know  $\frac{X''(x)}{X(x)} = -4\pi^2$ , we can get to  $X(x) = \sin(2\pi x)$
- The wave equation is similar in 3D:  $u_{tt} = v^2[u_{xx} + u_{yy} + u_{zz}]$ , or using the Laplacian,  $u_{tt} = v^2 \nabla^2 u$ . Here,  $u$  measures not displacement but expansion/compression of air at  $(x, y, z)$ , time  $t$ .

Using Fourier transforms helps turn difficult PDEs into an easier problem like an ODE. *Fourier transforms work best when*

- The domain is all of  $\mathbb{R}^n$
- The function  $u$  vanishes at infinity.

The Fourier transform changes the domain of  $x$  to that of  $\omega$ . It comes with the (highly simplified) rule (see Vector Calculus course):  $F[\frac{\delta f}{\delta x}] = i\omega F[f]$ . **Example:** Drunkard's walk.

- One dimensional: moves left or right in a random way. Starts at  $x = 0, t = 0$ .
- $u(x, t)$  is probability of being at point  $x$  at time  $t$ . Naturally,  $\int_{x=-\infty}^{x=\infty} u(x, t) dx = 1$ .
- Also, it obeys the 1-dD diffusion equation  $\frac{\delta u}{\delta t} = \frac{\delta^2 u}{\delta x^2}$
- The Fourier transform doesn't affect  $t$  at all.
- So by taking Fourier transform of both sides of diffusion equation we get
  - $F(u_t) = \frac{\delta}{\delta t} F(u)$  since  $F$  doesn't care about  $t$ .
  - $\frac{\delta^2 u}{\delta x^2} = i\omega F(\frac{\delta u}{\delta x}) = -\omega^2 F(u)$
  - So  $\frac{\delta}{\delta t} F(u) = -\omega^2 F(u)$
  - This is solvable as  $F(u) = ce^{-\omega^2 t}$ . Take it on faith that  $c = \frac{1}{2\pi}$  for now. TODO
  - Known fact:  $F[Ae^{-\frac{ax^2}{2}}] = \sqrt{\frac{1}{2\pi a}} Ae^{-\frac{\omega^2}{2a}}$
  - This means  $t = \frac{1}{2a}$  and  $a = \frac{1}{2t}$
  - $F(u) = \frac{1}{2\pi} e^{-\omega^2 t}, F[Ae^{-\frac{ax^2}{2}}] = \sqrt{\frac{1}{2\pi a}} Ae^{-\frac{\omega^2}{2a}}$  so  $u = Ae^{-\frac{ax^2}{2}}$
  - Solving, you get  $A = \sqrt{\frac{1}{4\pi t}}, a = \frac{1}{2t}$ , so  $u(x, t) = \sqrt{\frac{1}{4\pi t}} e^{-\frac{x^2}{4t}}$

## 2 Chapter 2: Nonlinear Equations

### 2.1 2.1: Lotka-Volterra I

Major ideas:

- **phase plane:** TODO
- **nullcline:** TODO
- **direction field:** TODO
- **equilibria:** TODO

**Example:** Bacteria vs. phages (again)

- Bacteria unrestrained grow in proportion to their population, so  $\frac{db}{dt} = r_b b(t)$  (solved:  $b(t) = b(0)e^{r_b t}$ )
- Phages unfed decrease in proportion to current size, so  $\frac{dp}{dt} = -d_p p(t)$  (solved:  $p(t) = p(0)e^{-d_p t}$ )
- Bacteria die with likelihood of meeting a phage, and phages increase with likelihood of meeting a bacterium. So the set of equations, for constant  $k$ , becomes:
  - $b'(t) = r_b b(t) - kb(t)p(t)$
  - $p'(t) = -d_p p(t) + kb(t)p(t)$
  - *The product of  $p$  and  $b$  makes our equations nonlinear (WHY?)*
  - I guess, very generally,  $b_1 p_1 = k, b_2 p_2 = k$ , but  $(b_1 + b_2)(p_1 + p_2) = b_1 p_1 + b_2 p_2 + b_1 p_2 + b_2 p_1 = 2k + b_1 p_2 + b_2 p_1 \neq 2k$ , so the last two “mixed” terms mean you can’t just add solutions  $(b_1, p_1)$  and  $(b_2, p_2)$ .

General thoughts on this solution:

- So a solution  $(b(t), p(t))$ , traces out a curve on the bp-phase plane (b is x-axis, p is y-axis) as time (unrepresented in the plane) continues.
- If we add a unit tangent vector at every point  $(B, P)$  aligned with  $(b'(t), p'(t)) = (r_b B - kBP, -d_p P + kBP)$ , we can follow the arrows to see the solution over time.
- The above is called a **direction field**
- This is sometimes hard to sketch analytically, so we can look to the **nullclines**: places where one of the components of the direction field is zero.
- In this case,  $r_b B - kBP = (r_b - kP)B = 0$  when  $P = 0$  or  $P = \frac{r_b}{k}$ , and  $-d_p P + kBP = (kB - d_p)P = 0$  when  $P = 0$  or  $B = \frac{d_p}{k}$ .
- The **upshot of nullclines** (since we don’t care about  $P, B \leq 0$ ): The lines  $B = \frac{d_p}{k}, P = \frac{r_b}{k}$  divide the plane into pieces where the components of this (continuous) function pair can’t change sign.
- For instance,  $B > \frac{d_p}{k}, P < \frac{r_b}{k}$  means  $r_b b - kbp > 0, -d_p p + kdp > 0$ , so both populations are growing here. This helps to sketch the curve.
- The curve looks like a counterclockwise whirlpool around the  $(B, P) = (\frac{d_p}{k}, \frac{r_b}{k})$ . (bacteria grow with low but growing phages; bacteria decrease as phages overwhelm; both decrease as phages starve; bacteria start coming back)
- The center point is a (constant **equilibrium**) solution, and other solutions swirl around it but don’t get attracted or repelled.

There are a few types of equilibria:

- This one is a **center** around which solutions circle.
- A **stable equilibrium** would see small upsets come back to an unchanging state.
- An **unstable equilibrium** would see small upsets create wildly divergent paths.

## 2.2 2.2: Lotka-Volterra II

In the Bacteria-Phage system, we can't yet prove everything rotates around the **center**. Let's do that.

Developing a **conserved quantity** will help to do that. **Example:** Block on a horizontal spring with mass  $m$ , spring constant  $k_s$ :

- $x(t)$ : Displacement from rest position.
- $v(t) = \frac{dx}{dt}$ : Horizontal velocity
- $\frac{dv}{dt} = -\frac{k_s}{m}x(t)$  by Hooke's law, I think.
- Suppose there's some Energy function  $E(x, v)$ . By chain rule  $\frac{d}{dt}E(x(t), v(t)) = \frac{dE}{dx}\frac{dx}{dt} + \frac{dE}{dv}\frac{dv}{dt}$
- $= \frac{dE}{dx}v - \frac{k_s}{m}\frac{dE}{dv}x$ . If we set  $E$  as conserved, as in  $E'(t) = 0$ , then  $\frac{dE}{dx}v = \frac{k_s}{m}\frac{dE}{dv}x$
- We can eyeball and see that  $E = \frac{1}{2}k_s x^2 + \frac{1}{2}mv^2$  solves this equation, or we can assume  $E(x, v) = F(x) + G(v) \Rightarrow 0 = E'(t) = F'(x)v - \frac{k_s}{m}G'(v)x = 0$  from the above equations and guess from there.
- This means in the  $xv$  phase space, that there's a fixed  $E$  such that the particle follows the ellipse  $E = \frac{1}{2}k_s x^2 + \frac{1}{2}mv^2$  in phase space around the solution point  $(0,0)$ .

**Extended Example:** Continuing on finding a conserved quantity for Bacteria / Phage:

- We need to find  $U(b(t), p(t))$  such that  $U'(t) = 0$ , or by chain rule  $\frac{\delta U}{\delta b}\frac{\delta b}{\delta t} + \frac{\delta U}{\delta p}\frac{\delta p}{\delta t} = 0$
- Subbing in,  $\frac{\delta U}{\delta b}[r_b b - kbp] + \frac{\delta U}{\delta p}[-d_p p + kbp] = 0$
- A hint suggests finding  $U$  such that  $\frac{\delta U}{\delta b} = -\frac{d_p}{b} + k$ ,  $\frac{\delta U}{\delta p} = -\frac{r_b}{p} + k$  to make terms cancel.
- Integrating these gives us  $U$  as both  $-d_p \ln(b) + kb + Q(p)$  and  $-r_b \ln(p) + kp + R(b)$  so  $U = -d_p \ln(b) - r_b \ln(p) + kb + kp$ . This weird curve constitutes a level set in  $pb$ -space upon which a solution sits.
- The spring example has an elliptic paraboloid solution. There's an absolute minimum ( $E = 0$  at  $(0,0)$ ) but level sets become closed loops away from it.

- For the Lotka example, there is a critical point ( $\nabla U = \vec{0}$ ) when  $\nabla U(b, p) = (\frac{\delta U}{\delta b}, \frac{\delta U}{\delta p}) = (k - \frac{d_p}{b}, k - \frac{r_b}{p})$ , which is  $(0, 0)$  at our known center  $(\frac{d_p}{k}, \frac{r_b}{k})$
- Showing that we always increase going away from the point  $(\frac{d_p}{k}, \frac{r_b}{k})$  should guarantee us closed level sets.
- One method: Assume we're picking a unit vector  $\vec{v} = \langle \hat{v}_b, \hat{v}_p \rangle$  so that our line from our center is  $\vec{v} = \langle \frac{d_p}{k} + tv_b, \frac{r_b}{k} + tv_p \rangle$ .  $U = F(b) + G(p)$  in this case, so sub the  $b$  part into  $F$  to get  $F(\frac{d_p}{k} + tv_b) = d_p[1 - \ln(\frac{d_p}{k} + tv_b)] + kt\vec{v}$ . Taking derivative of that w.r.t  $t$  shows it is always positive. Same goes for the  $G(p)$  portion of  $U$ .
- Another (DF) method: Note that  $\nabla U = (k - \frac{d_p}{b}, k - \frac{r_b}{p})$ 's grad (second derivative) is always positive. So derivative always has positive curvature (maybe using that term wrong), and we'll always increase around this point.
- Also, we know that the particle travels around the level set (loop) and doesn't reverse course, because then,  $b'(t) = p'(t) = 0$ , and we only have that at the center point (nullcline intersection).

## 2.3 2.3: Linearization

**Extended Example:** Suppose there's a limit to bacterial growth, so we cap our population at  $M_b$ .

- If  $b(t) \ll M_b$ , things should be similar. If  $b(t)$  is nearly  $M_b$ , then growth should approach 0. So, this implies  $\frac{db}{dt} = r_b b(t) \rightarrow \frac{db}{dt} = r_b b(t)(1 - \frac{b(t)}{M_b})$ . Note: This isn't the only possibility but we'll use it.
- This updates our Lotka-Volterra model to something more complicated:
  - $b'(t) = r_b b(t)(1 - \frac{b(t)}{M_b}) - kb(t)p(t)$
  - $p'(t) = -d_p p(t) + kb(t)p(t)$
- Other than  $b = 0, p = 0$ , the meaningful nullclines are solved by setting  $b'(t) = 0$  (yielding  $r_b(1 - \frac{b}{M_b}) - kp = 0$ ) and  $p'(t) = 0$  (yielding  $b = \frac{d_p}{k}$ )
- Note: We'll clean up through some MAGIC non-dimensionalization (how to derive?) to simplify:
  - $x(t) = \frac{1}{M_b} b(\frac{t}{r_b}), y(t) = \frac{k}{r_b} (\frac{t}{r_b}), \alpha = \frac{d_p}{r_b}, \beta = \frac{kM_b}{r_b}$
  - Gives us new equations:  $\frac{dx}{dt} = x(t)[1 - x(t)] - x(t)y(t), \frac{dy}{dt} = -\alpha y(t) + \beta x(t)y(t)$
  - And new nullclines:  $x + y = 1, x = \frac{\alpha}{\beta}$

- So there's an equilibrium point in the positive xy quadrant if:  $y = 1 - x = 1 - \frac{\alpha}{\beta}$  and  $y > 0$  implies  $1 - \frac{\alpha}{\beta} > 0 \Rightarrow \frac{\alpha}{\beta} < 1$
- Looking at the direction field, it appears solutions swirl around and are attracted *into* the center point  $(\frac{\alpha}{\beta}, 1 - \frac{\alpha}{\beta})$ , making it a **stable equilibrium**

This is similar to the block-spring example, if a damping term  $-\frac{\gamma}{m}v$  is added.

- $\frac{dx}{dt} = v, \frac{dv}{dt} = -\frac{k_s}{m}x - \frac{\gamma}{m}v$
- This can be thought of in matrix terms:  $\frac{d}{dt} \begin{pmatrix} x(t) \\ v(t) \end{pmatrix} = \begin{pmatrix} 0 & 1 \\ -\frac{k_s}{m} & -\frac{\gamma}{m} \end{pmatrix} \begin{pmatrix} x(t) \\ v(t) \end{pmatrix}$  Call the matrix  $A$ .
- From Diff Eq I, the solution is  $\exp(tA)$  (matrix exponential), making  $\mathbf{x}(t)$  a linear combination of  $e^{\lambda t}$  or possibly  $te^{\lambda t}$  terms, with the eigenvalues as  $\lambda$ s.
- The eigenvalues in this case, using the quadratic formula, could be:
  - Two real, distinct, negative roots. So, these  $e^{\lambda t}$  terms decay, and  $\mathbf{x}(t)$  levels off.
  - Two distinct complex roots with real part  $-\frac{\gamma}{2m} < 0$ . This ends up being some sines and cosines multiplied by  $e^{-\frac{\gamma t}{2m}}$ , which decays too.
  - Finally, if we have a repeated negative real eigenvalue, we have solution  $x(t) = Ae^{-\frac{\gamma t}{2m}} + Bte^{-\frac{\gamma t}{2m}}$ , also decaying.
  - So any disturbance in the spring will oscillate and come to rest at  $x(t) = v(t) = 0$  quickly.

So with linear systems  $\vec{x}'(t) = A\vec{x}(t)$ , the eigenvalues determine what happens around the equilibrium point. However, the **bacteria-phage model is non-linear**. Here is **how we linearize** for nearby solutions in a nonlinear system:

- Set small disturbance  $\delta x(t) \ll 1, \delta y(t) \ll 1$  so  $x(t) = \frac{\alpha}{\beta} + \delta x(t), y(t) = 1 - \frac{\alpha}{\beta} + \delta y(t)$
- Since they're small, all powers like  $\delta x(t)^2$  and  $\delta x(t)\delta y(t)$  are considered basically zero.
- So substitute  $x(t) \rightarrow \frac{\alpha}{\beta} + \delta x(t), y(t) \rightarrow 1 - \frac{\alpha}{\beta} + \delta y(t)$  into our  $\frac{dx}{dt}$  and  $\frac{dy}{dt}$  equations.
- This gives us the A solving  $\frac{d}{dt} \begin{pmatrix} \delta x(t) \\ \delta y(t) \end{pmatrix} = A \begin{pmatrix} \delta x(t) \\ \delta y(t) \end{pmatrix}$ , which is  $A = \begin{pmatrix} -\frac{\alpha}{\beta} & -\frac{\alpha}{\beta} \\ \beta - \alpha & 0 \end{pmatrix}$  after working through the substitution.



- Finding the eigenvalues here yields the same situation as the block-spring example: decays in all situations.

It turns out through the **Hartman-Grobman Theorem** that  $\vec{x}'(t) = \vec{F}(\vec{x}(t))$ , for some continuously differential vector field  $F$ , if we linearize near equilibrium  $x_0$ , then what falls out of this  $A$  approach works if the eigenvalues *aren't all purely imaginary*.

It turns out the uncapped bacteria system from before looks like  $\frac{d}{dt} \begin{pmatrix} \delta x(t) \\ \delta y(t) \end{pmatrix} = \begin{pmatrix} 0 & -1 \\ \alpha & 0 \end{pmatrix} \begin{pmatrix} \delta x(t) \\ \delta y(t) \end{pmatrix}$ , with characteristic equation  $\lambda^2 + \alpha = 0, \alpha > 0$ . This means both values are imaginary, and we had to use the conserved quantity approach!

### 3 2.4: Hartman-Grobman Theorem

**Extended Example:** Consider a phage that dies off quickly:

- $\frac{db}{dt} = r_b b(t) - k_b b(t)p(t), \frac{dp}{dt} = -r_p p(t) = 0 \cdot b(t)p(t)$ , where  $k_p$  is the zero (phages don't increase), and  $k_b$  is still the kill factor for the bacteria.
- In this base,  $b(t) = p(t) = 0$  is the only equilibrium.
- Non-dimensionalize as  $x(t) = b(\frac{t}{r_b}), y(t) = \frac{k_b}{r_b} p(\frac{t}{r_b}), \alpha = \frac{r_p}{r_b}$
- This makes the equations  $x'(t) = x(t) - x(t)y(t), y'(t) = -\alpha y(t)$ , and the nullclines therefore  $x(t) = 0, y(t) = 1, y(t) = 0$
- Looking at this six-section direction field, we see that solutions exactly on the y-axis are attracted to equilibrium  $(0, 0)$ , and other are repelled.
- This makes sense since if the bacteria is 0, the phage die and approach  $(0, 0)$ , otherwise the bacteria multiply and win (so it's a *saddle point*)
- The way to tell: linearize the equations.  $\frac{d}{dt} \begin{pmatrix} x(t) \\ y(t) \end{pmatrix} \approx \begin{pmatrix} 1 & 0 \\ 0 & -\alpha \end{pmatrix} \begin{pmatrix} x(t) \\ y(t) \end{pmatrix}$  since, if  $x(t), y(t) < 1, x(y)t(t) = 0$ .
- Then the eigenvalues are  $\lambda = 1, -\alpha$  so the solution is  $Ae^t, Be^{-\alpha t}$  for  $x(t), y(t)$  (TODO respectively?) **Hartman-Grobman ensures this is the general solution.**

However, let's solve directly and see if we come to the same result.

- $y'(t) = -\alpha y(t), y(0) = y_0 \Rightarrow y(t) = y_0 e^{-\alpha t}$
- With this in hand,  $\frac{dx}{dt} = x(t) - x(y)y(t) = x(t)[1 - y_0 e^{-\alpha t}], x(0) = x_0$  separates out to

- $\frac{dx}{x} = [1 - y_0 e^{-\alpha t}] dt$
- $\ln(x) = [t + \frac{y_0}{\alpha} e^{-\alpha t}] + C$
- $x = e^C e^t \exp(\frac{y_0}{\alpha} e^{-\alpha t})$
- $x(0) = x_0 \Rightarrow e^C = x_0 e^{-\frac{y_0}{\alpha}}$
- $\Rightarrow x(t) = x_0 e^t \exp(\frac{y_0}{\alpha} (e^{-\alpha t} - 1))$

But how do we deform the phase plane so this looks linear? We need some mapping  $\vec{h}(x, y) = \langle u(x, y), v(x, y) \rangle$  that is continuous and invertible (so we don't "damage" the phase plane). This is called a **homeomorphism**.

- So near the equilibrium  $(0, 0)$ , the equations  $y'(t) = -\alpha y(t), y(0) = y_0 \Rightarrow y(t) = y_0 e^{-\alpha t}$  linearized for  $\delta x, \delta y$  must be similar to those for  $u(x(t), y(t), v(x(t), y(t)))$
- This means we need  $\frac{du}{dt} = u, \frac{dv}{dt} = -\alpha v$
- After doing the substitution, we see that  $v = v_0 e^{-\alpha t}$  exactly mimics  $y(t) = y_0 e^{-\alpha t}$  for the phage solution. So we take  $v = y$ .
- Therefore, we know that since  $u = u_0 e^t$  and  $x(ty) = x_0 \exp(t + \frac{y_0}{\alpha} (e^{-\alpha t} - 1))$ , that we need  $u(x(t), y(t)) = u(x_0, y_0) e^t$
- And this is satisfied if we guess  $u(x, y) = x e^{-y/\alpha}$  and work it out.
- This function  $\vec{h}(x, y) = (u, v) = \langle x e^{-\frac{y}{\alpha}}, y \rangle$  is invertible by  $(x, y) = \langle u e^{\frac{v}{\alpha}}, v \rangle$ , which is continuous.

## 4 2.5: Application - Lasers

Lasers create excited atoms, which then emit photons while transitioning to an unexcited state. This system has a close analogue with the previous phages (like photons) and bacteria (like atoms) model.

- $n(t)$ : number of photons in the laser;  $r_g$ : rate of photons gained (created by excited atoms transitioning to unexcited state);  $r_l$ : rate of photons lost (emitted)
- $\Rightarrow \frac{dn}{dt} = r_g - r_l$  by definition.
- We can assume we're losing a constant  $k$  (kill?) portion of photons per unit time, so  $\frac{dn}{dt} = r_g - kn(t)$
- $e(t)$ : number of excited atoms (that will maybe create photons). Atoms are excited by external energy pump.
- Excited atoms radiate when meeting a photon (which survives the meeting)

- So we can use the same setup from the bacteria: with  $I$  the constant of meeting (intersect?),  $r_g = Ie(t)n(t) \Rightarrow n'(t) = Ie(t)n(t) - kn(t)$

**Mini example: Assume no photons leave** (cap the end of the laser)

- $k = 0$  in this scenario.
- So every meeting creates one more photon ( $n \rightarrow n + 1$ ) while energizing one excited atom ( $e \rightarrow e - 1$ ). This implies, equivalently:
  - $e + n$  is a conserved quantity,
  - $e(t) + n(t) = e(0) + n(0)$ ,
  - $[e(t) + n(t)]' = 0$
  - Then, if  $k = 0$ ,  $n'(t) = Ie(t)n(t)$ , and coupled with  $e'(t) + n'(t) = 0$  above, we have  $e'(t) = -Ie(t)n(t)$

**Extended example: Atoms spontaneously lose energy.** This is actually what happens

- From quantum physics, we have a rate  $s$  of atoms just (s)pontaneously losing energy.
- We also have an energy (p)ump that energizes atoms with quantity  $p$ .
- Then, our change in (e)xcited atoms is  $e'(t) = p - s - Ie(n)(t)$
- If we want to find the smallest  $p$  guaranteeing  $n \geq 1$  (there's at least one photo) at equilibrium ( $e'(t) = n'(t) = 0$ ):
  - $n'(t) = 0 \Rightarrow Ien = kn \Rightarrow n(Ie - k) = 0$ . If  $n \neq 0$ ,  $\Rightarrow e = \frac{k}{I}$
  - $e'(t) = 0 \Rightarrow Ien = p - se$
  - Together,  $p - se = Ien = kn \Rightarrow kn + se = p \Rightarrow kn + s\frac{k}{I} = p$
  - $n \geq 1 \Rightarrow p \leq k + \frac{ks}{I}$
  - **Another tactic:** We could also assume we *start out at equilibrium*, so  $n_0, e_0$  are constant solutions.
  - Solving  $n' = 0 = Ie_0n_0 - kn_0$ ,  $e' = 0 = Ie_0n_0 - se_0 + p$ , we find equilibria  $n_0 = \frac{p}{k} - \frac{s}{I}$ ,  $e_0 = \frac{k}{I}$
  - Then,  $n_0 \geq 1 \Rightarrow \frac{p}{k} - \frac{s}{I} \geq 1 \Rightarrow p \geq k + \frac{ks}{I}$

**Non-dimensionalization time:**

- Scale against  $e_0 (= \frac{k}{I})$ ,  $n_0 (= \frac{p}{k} - \frac{s}{I})$  like this:  $x(t) = \frac{n(\alpha t)}{n_0}$ ,  $y(t) = \frac{e(\alpha t)}{e_0}$

- NOTE: What does this do? This makes (1,1) the equilibrium, as  $x(t) = \frac{n_0}{e_0} = 1, y(t) = \frac{e_0}{e_0} = 1$  !
- What  $\alpha$  lets us take  $n' = Ien - kn, e' = -Ien - se + p$  and write
  - $\frac{dx}{dt} = x(t)y(t) - x(t)$
  - $\frac{dy}{dt} = \frac{1}{k}(\frac{pI}{k} - s)[1 - x(t)y(t)] + \frac{s}{k}[1 - y(t)]$
  - $x' = \frac{\alpha n'(\alpha t)}{n_0} = xy - x = \frac{Ie(\alpha t)n(\alpha t)}{kn_0} - \frac{n(\alpha t)}{n_0}$
  - $\frac{\alpha Ien - \alpha kn(\alpha t)}{n_0} = \frac{Ie(\alpha t)n(\alpha t)}{kn_0} - \frac{n(\alpha t)}{n_0}$
  - $\alpha Ie - \alpha k = \frac{Ie(\alpha t)}{k} - 1 \Rightarrow \alpha(Ie - k) = \frac{Ie - k}{k} \Rightarrow \alpha = \frac{1}{k}$
  - This solves the x equation, and I suppose it can be validated in the y equation (tediously).
  - If we chunk up our (somehow positive?) constants as  $c = \frac{1}{k}(\frac{pI}{k} - s), d = \frac{s}{k}$ , we end up with  $y' = c[1 - xy] + d[1 - y]$
  - We only care about  $x, y > 0$ , so  $x' = 0 = xy - x = x(y - 1)$  implies  $y = 1$  is a nullcline
  - $y' = 0 = c[1 - xy] + d[1 - y] = c - cxy + d - dy \Rightarrow c + d = y(d + cx) \Rightarrow y = \frac{c+d}{d+cx}$ , a scaled and shifted hyperbola.

**Look at the solutions:**

- It appears we have a counterclockwise swirl around (1,1), and nearby solutions tend toward this equilibrium.
- Hartman-Grobman: rewrite our linearized solution in neighborhood of (1,1) as  $x(t) = 1 + \delta x(t), y(t) = 1 + \delta y(t)$
- Using  $x' = xy - x, y' = c[1 - xy] + d[1 - y]$  and  $\frac{d}{dt} \begin{pmatrix} \delta x(t) \\ \delta y(t) \end{pmatrix} = A \begin{pmatrix} \delta x(t) \\ \delta y(t) \end{pmatrix}$ , we can solve and write  $A = \begin{pmatrix} 0 & 1 \\ -c & -c - d \end{pmatrix}$
- Eigenvalues:  $\lambda = \frac{1}{2}(-c - d \pm \sqrt{(c + d)^2 - 4c})$ 
  - \* If square root term is zero, we have repeated eigenvalue, so  $\delta x(t), \delta y(t)$  are combos of  $e^{-\frac{c+d}{2}}, te^{-\frac{c+d}{2}}$ , which decays
  - \* If square root term is greater than zero, we have two distinct real, negative eigenvalues (since c, d are positive), so this decays.

- \* If square root term is less than zero, we have distinct complex eigenvalues, but combos of  $e^{-\frac{c+d}{2}} \cos(\frac{1}{2}\sqrt{-(c+d)^2 + 4c})$ ,  $e^{-\frac{c+d}{2}} \sin(\frac{1}{2}\sqrt{-(c+d)^2 + 4c})$  decay too
- \* Note : I suppose Hartman-Grobman can't work in purely imaginary scenario, because these kinds of functions don't converge or diverge without a term outside the sin or cos (?)
- \* And in any case, since these lambdas aren't strictly imaginary, Hartman-Grobman works.

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