

Brilliant: Differential Equations II

Dave Fetterman

9/2/22

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

- $b'(t) = r_b b(t), r_b > 0$. r_b 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 ρ, σ, 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 ω . 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 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 λ 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 $\vec{h}(x, y) = (u, v) = \langle x e^{-y/\alpha}, y \rangle$ is invertible by $(x, y) = \langle u e^{\frac{y}{\alpha}}, v \rangle$, which is continuous.

- TODO