Mathematical Biology

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0 Miscellaneous

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Moodle page: Handwritten notes by lecture; Matlab/Python programming examples; solved exercises.

This course involves 3 models: Deterministic temporal models (11 lectures), Stochastic temporal models (5 lectures), Deterministic spatio-temporal models (8 lectures).

The focus of this course is biochemical reactions and population processes.

(some introductory speech)

Example. (1, Transient population) If we use n(t) to denote the size of a population, we may want to model $\frac{dn}{dt} = f(n)$ by an ODE, or maybe if we have several components $\mathbf{n}(t)$ then we may want to model $\frac{d\mathbf{n}}{dt} = \mathbf{f}(\mathbf{n})$ which is a system of ODEs.

Note that although n should be an integer (discrete), when n >> 1 we may model it with continuous equations.

Example. (2) $n \to \partial_t P(n,t) = W \cdot P(n,t)$, Markov processes. Here P(n,t) is a probability(?), n being a state, and W being the transition matrix.

Example. (3)

If we include spatial aspect, we may have n(t) becoming n(x,t). Now there might be 'diffusion': $\partial_t n(x,t) = f(n(x,t)) + D\nabla^2(x,t)$ where $\nabla^2 = \frac{\partial^2}{\partial x^2}$; this is the reaction-diffusion equation.

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1 Birth-death models

The general idea is that we have a population of size n(t); per capita per unit time, we have births of rate b and deaths of rate d. Then we can write

$$n(t + \Delta t) = n(t) + bn\Delta t - dn\Delta t$$

So we have an ODE

$$\frac{dn}{dt} = (b - d)n = rn$$

where r = b - d. This has an easy solution $n(t) = n_0 e^{rt}$, assuming r is a constant. We see that if r is positive then the population grows exponentially, and if r is negative then the population decreases to 0 asymptotically.

Now probably b and d are related to n by b(n) = bn and $d(n) = dn^2$ due to competition. Then we have

$$\frac{dn}{dt} = bn - dn^2$$

which we can definitely rewrite as

$$\frac{dn}{dt} = \alpha n(1-n)$$

by some change of variable on n. Now

$$\frac{dn}{n(1-n)} = \alpha dt$$

$$\implies \frac{dn}{n} + \frac{dn}{1-n} = \alpha dt$$

$$\implies \ln n - \ln(1-n) = \alpha t + c$$

$$\implies n = \frac{n_0 e^{\alpha t}}{(1-n_0) + n_0 e^{\alpha t}}$$

where we are given that t = 0, $n = n_0$. If $t \gg \frac{1}{\alpha}$, when $t \to \infty$ we have $n(t) \to 1$. Now we can investigate if the population size is stable, and if it has any fixed points.

Let's now define $\mathbf{n} = (n_1, ..., n_p)$, i.e. p populations, and $\frac{d\mathbf{n}}{dt} = \mathbf{f}(\mathbf{n})$. If $\mathbf{n} = \mathbf{n}^*$ is a fixed point, then $\frac{d\mathbf{n}}{dt} = 0$, i.e. $\mathbf{f}(\mathbf{n}) = 0$. Now if we apply a small perturbation $\mathbf{n} = \delta \mathbf{n}^* + \delta \mathbf{n}$, i.e.

$$\frac{d}{dt}\delta\mathbf{n} = \mathbf{f}(\mathbf{n}^* + \delta\mathbf{n})$$

$$a = \mathbf{f}(\mathbf{n}^*) + \frac{\partial f_i}{\partial n_j}\delta_{nj} + \frac{1}{2}\frac{\partial^2 f_i}{\partial n_j\partial n_k}\delta_{n_j}\delta_{n_k}$$

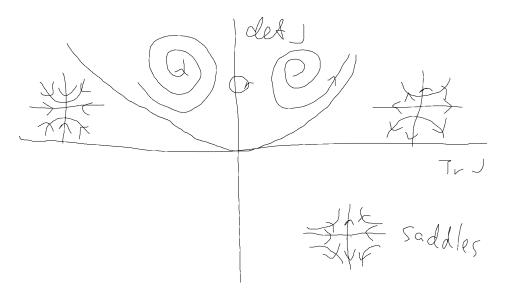
So $\frac{d}{dt}\delta \mathbf{n} = J \cdot \partial \mathbf{n}$, so $\delta n(t) = e^{Jt} \cdot \delta n(0)$. If λ_i 's are the eigenvalues of J, we consider the real part of λ_i : if $Re(\lambda_i) < 0$, then if $p \ge 5$ we only have numerical solutions, if $3 \le p \le 5$ we have analytic solutions, and p = 2 is an easy case (recall p is the number of populations):

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• If p = 2, $\mathbf{n} = (n_1, n_2)$, then

$$\frac{d}{dt}\begin{pmatrix}\delta_{n_1}\\\delta_{n_2}\end{pmatrix} = \begin{pmatrix}\frac{\partial f_1}{\partial n_1} & \frac{\partial f_1}{\partial n_2}\\ \frac{\partial f_2}{\partial n_1} & \frac{\partial f_2}{\partial n_2}\end{pmatrix} \cdot \begin{pmatrix}\delta_{n_1}\\\delta_{n_2}\end{pmatrix}$$

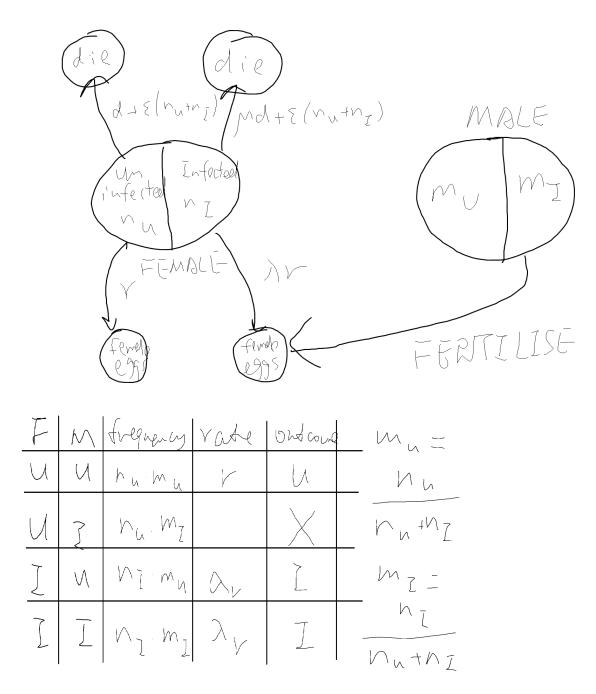
Where the matrix is J. Now we have $\lambda_1\lambda_2 = \det J$ and $\lambda_1 + \lambda_2 = \operatorname{tr} J$. Determined by the signs of those two, we have different possible behaviours:



Now let's consider the spread of Dengue. There are several processes going on at the same time:

- (1) Mosquitos carry dengue;
- (2) Wolbachia infect mosquitos;
- (3) Infected mosquitos do not transmit dengue;
- (4) Wolbachia transmission only across generations.

Question: will an intially infected population of mosquitos eventually spread over the entire population as $t \to \infty$?



We always assume that there are enough males to fertilise the female eggs.

Now consider $\frac{d}{dt}$ of n_U and n_I (uninfected and infected females). From the above tables we should be able to get (hopefully)

$$\frac{d}{dt}n_U = rn_U \frac{n_U}{n_U + n_I} - dn_U - \varepsilon(n_U + n_I)n_U$$

$$\frac{d}{dt}n_I = \lambda rn_I \frac{n_U}{n_U + n_I} + \lambda rn_I \frac{n_I}{n_U + n_I} - \mu dn_I - \varepsilon(n_U + n_I)n_I \ (*)$$

This is our model when p=2. The term with ε is the death rate associated with competition.

We'll try to simplify these equations. By rescaling the time as $t \to rt$, and rescaling the population as $n \to \frac{\varepsilon}{r}n$, we get (?)

$$\frac{d}{dt}n_U = n_U \frac{n_U}{n_U + n_I} - \frac{d}{r}n_U - (n_U + n_I)n_U$$

$$= n_U \left[\frac{n_U}{n_U + n_I} - \frac{d}{r} - (n_U + n_I) \right]$$
(1)

and the second equation becomes (???)

$$\frac{d}{dt}n_I = n_I \left[\lambda - \mu \frac{d}{r} - (n_U + n_I) \right] (2)$$

We'd like to see that the model has at least the fixed points $\mathbf{n}^* = (n_U^*, 0)$ and $(0, n_I^*)$. The lecture then somehow defines

$$n_I^* = \lambda - \mu \frac{d}{r}$$
$$n_U^* = 1 - \frac{d}{r}$$

so that our differential equations become

$$\frac{d}{dt}n_U = n_U \left[n_U^* - \frac{n_I}{n_U + n_I} - (n_U + n_I) \right]$$

$$\frac{d}{dt}n_I = n_I \left[n_-^* (n_U + n_I) \right]$$

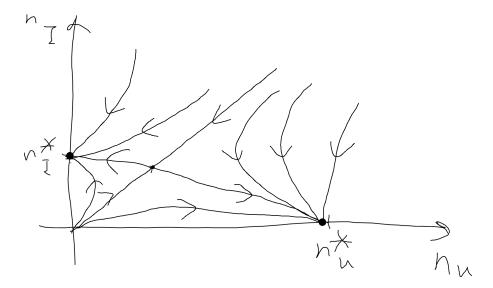
which has fixed points $(0,0), (n_U^*,0), (0,n_I^*), (n_I^*(1-n_I^*-n_U^*), n_I^*(n_U^*-n_I^*))$. The first is unstable, the second two are stable and the last fixed point is a saddle. This is disappointing because we want a small infection to be spread out to the whole population, but in that case the second fixed point needs to be unstable.

1.1 Global analysis

We can plot the flow of the ode system,

$$\frac{d}{dt} \binom{n_U}{n_I} = \binom{f_U(n_U, n_I)}{f_I(n_U, n_I)}$$

This is usually done by programming. We'll try to sketch the flow of this model:



Qualitative behaviour: we need a finite (large) $n_I(0)$.

For quantitative part we can only do numerical integrations.