

### Project 3: Bacteria growth and diffusion

Math 647, Spring 2009

*Due Tuesday, 5/5 (redefined day)*

The population growth models which we looked at at the beginning of the semester were fairly crude in a number of ways, and I'd like to take a more sophisticated approach in this project. When a (solid) piece of food is contaminated by bacteria, to get a decent model one must also take motion of the bacteria into account. I was contacted earlier this semester by Mr. Ezekiel Chimbombi, a graduate student in the department of Biological and Agricultural Engineering (in the College of Agriculture and Life Sciences), requesting help in understanding data from an experiment in bacterial contamination.

The set-up is this: a cylinder is cut out of a melon of some sort. The cylinder is 19.05 mm in diameter, and 50 mm long. One end is "painted" with a solution containing salmonella (specifically *Salmonella enteritica* serovar Typhimurium, whatever that means). After a certain period of time, the cylinder is cut into 10 mm pieces, and the number of bacteria is estimated in each piece. Eventually bacteria spread through the melon, and was observed throughout. This was done many times and the averaged results are presented below. In the experiments, they tried several orientations of the cylinder, but didn't observe any noticeable difference due to gravity. Thus the assumption is that the bacteria diffused independent of gravity. In the tables, the bacteria is introduced at the top. The numbers are the log base 10 of the estimated number of bacteria in each 10 mm piece. The columns are labelled at the top with the number of hours after inoculation, the rows are the number of bacteria observed in the corresponding section. I intend that we set this up with one space variable (distance down the column) and time.

	0.5	5	10	15	20	25	30
10	3.47	3.45	4.00	4.79	5.95	6.38	7.23
20	2.00	2.00	2.84	3.60	4.83	5.01	6.07
30	1.97	1.85	2.38	2.83	4.38	4.81	4.99
40	1.82	1.79	2.22	2.58	3.45	3.59	4.77
50	1.81	1.82	1.84	2.64	3.48	3.37	4.53

I interpret these results as space integrals: if  $u(x, t)$  is the population density at location  $x$  at time  $t$ , for example, then the first entry in the table

says that  $\int_0^{10} u(x, 0.5) dx = 10^{3.47}$ . The lower entries represent background noise that the detector can't resolve: it looks like anything below about 1.9 or 2 is negligible.

Here's one way to include diffusion of bacteria into bacterial growth. With no diffusion, and assuming that the growth at a point is logistic, the PDE is

$$u_t = ru \left( 1 - \frac{u}{u_\infty} \right),$$

where  $u_\infty$  is the carrying capacity. This is not really a PDE: it's just an ODE at each point. Putting diffusion in, we get

$$u_t = cu_{xx} + ru \left( 1 - \frac{u}{u_\infty} \right),$$

where  $c$  is a constant relating to how fast the bacteria move through the melon. Fine and dandy, but unfortunately not what happens in real life. It turns out that when you plunk bacteria into a new environment, there's a lag time before it starts growing (which you can see going from 0.5 hours to 5 hours in the table).

Here are some possible approaches to incorporating lag time. The first is to assume nothing happens until a time  $t_1$  (to be estimated from the data), after which the bacteria starts growing logistically and diffusing. The second is to assume that the bacteria doesn't grow until time  $t_1$ , but starts diffusing immediately. The third is outlined in reference 1, below, which introduces another function representing an internal physiological state. See also reference 2, which, although it refers to two competing populations, can be specialized to one population. I'd like each group to use at least two of the above three approaches in modeling the problem. The purpose is to determine values of parameters which will fit the given data best, probably in some least squares sense.

Your report should be understandable by someone whose biological knowledge is limited (e.g., your instructor), and by someone whose mathematical knowledge is limited (e.g., Mr. Chimbombi).

#### References:

1. Baranyi, J., Roberts, TA, 1994, *A Dynamic Approach in Predicting Bacterial Growth in Food*, Int. J. Food Microbiol. vol. 23, 277-294.

2. Dens, EJ, van Impe, JF, 2001, *On the Need for Another Type of Predictive Model in Structured Foods*, Int. J. Food Microbiol. vol. 64, 247-260.
3. Renshaw, E. **Modelling Biological Populations in Space and Time**, Cambridge University Press, 1991. (I'll put a copy on reserve at Evans Library.)