Biol 398/Math 388:

A simple chemostat model of nutrients and population growth

**Background.** The chemostat is an idealization of a reactor for growing populations of cells like yeast. Nutrients are fed continuously at a fixed flow rate and concentration, and effluent is extracted at a fixed flow rate. A slight subtlety in the extraction part is that what is extracted is at a fixed flow rate, to keep the volume constant, but the effluent has a concentration that depends on the reaction. An illustration of the chemostat is given below.



Figure 1. Chemostat cartoon from Wikipedia.

The basic assumption of the chemostat is that the contents are sufficiently well mixed that the concentration of the mixture is uniform throughout the container. Under this assumption, we do not need to consider spatial effects or non-uniformity of nutrients and cells: all cells have equal access to nutrient.

If the volumetric inflow rate is *Q* (vol/time), then the **dilution rate** is *q= Q/V*  in units of (1/time), where the volume of the mixture in the tank is *V* (and that’s constant: the effluent outflow rate is assumed the same as the inflow dilution rate). The **feed concentration** is *u* (in concentration units, mass or molar). Then the concentration of the nutrient *y(t*) can be determined as follows:

Rate of change of nutrient = inflow rate – outflow rate – rate consumed in the tank.

Now, the inflow rate is *q*\**u* (and this is assumed to be a constant, independent of time). The outflow rate is *q*\**y*(*t*), because the effluent is extracted from the uniform, well-mixed tank contents. Thus, we have

consumption rate

The model of consumption we consider is called Monod, Michaelis-Menten, or Briggs-Haldane, depending on the context, and it adds a third term to the mass balance equation due to cell population consumption of the nutrient.



to capture inflow, outflow, and metabolism of the nutrient. Here we introduce *x*, the concentration of yeast cells in the mixture, and the parameter e denotes a unit conversion rate between biomass (the units of x) and nutrient concentration.

We model the population of cells with its own differential equation, coupled with the nutrient by



so that the net growth rate depends on the nutrient level. This model leads to a coupled pair of differential equations, because the consumption model depends on the size of the population:



Among the interesting things to consider is the equilibrium, or steady state. By equilibrium, we mean a state that would remain constant in time if we reached it. Since constant functions have 0 derivative, steady states can be found by setting the right hand side of the DE system to 0:



Looking at the second equation, we see that x=0 works (but that’s not interesting, as the cell population would be extinct). If x is not 0, then we must have



as part of the equilibrium condition. Plugging the first part of this into the first equation, we get that



Two important things to note are that the steady state nutrient concentration is independent of the federate *u*, while the cell population depends linearly on *u*. That’s not what we observed in the terSchure experiments.

Many organisms require and/or live off multiple nutrients. What happens in such a case? There are at least three possible structures for multiple nutrients, each of which can be written



in which *y* and *z* denote the two nutrients, with *x* again denoting the cell population. All three of these state variable quantities are measured in concentration units. The numbers **and ** denote conversion rates of biomass concentration/nutrient concentration. The choice of the function *f* is the tough bit of modeling, with the following three being popular:



We will start with the last form, working out the steady state and data comparison in detail. More to come on this topic.