HOME WORK PROJET :

SHIFT OF REGULATION SIGNALS BETWEEN MICROORGANISM COMMUNITY MEMBERS

I. GLOBAL DESCRIPTION OF THE PROJECT

This goal of this *in silico* project is to simulate the regulation of a consortium of microorganisms and describe in a word document the molecular and/or biological mechanisms that correspond to your model.

II. MODE DETAILED DESCRIPTION OF THE PROJECT

Students are asked to develop a code that simulate a population-dependent shift that transform a positive interaction to a negative interaction (activation to inhibition) or vice versa. This is equivalent to change the type of arrow in a interacting graph (as if the mother in law decide to change her attitude towards Alice in the family crisis model). In ecology framework, it means that you are able to shift in between any kind of the three basic interactions : mutualism, competition, predation for a consortium of at least two species.

To simulate this shift, I ask you to get inspired from the modeling of the Allee Effect that we see in class. The Allee logistic equation is in fact a way to introduce a delay in the logistic growth (which can mimic a group effect). The Allee effect has apparently nothing to do with our objective of creating an “induced shift”. However, it introduce a very nice ingredient, a factor (Nj-A) or (A-Nj) which can be very useful to model a shift when the population Nj pass the threshold A.

I therefore ask you to use this computational trick to introduce a change of the type of interaction between any pairs of your interaction graph. This is equivalent of changing the sign of the cross terms in the differential equation dN_i/dt for each population N_i interacting with population N_j.

As this class is an initiation to research, you need to discover yourself how to use the term (N-A) or (A-N) in the equation for this shift to append correctly. You can follow the advice of this mathematician Alexander Groethendick, which immediately tried to generalize the problem for finding the most general framework. So here, try to imagine that you have to model the interaction of 10 groups of species. Each of the 10 differential equations dN_i/dt will contain 9 terms involving $(N_j - A_{ij})$ (j=1,10 except j=/=i). In that case, you will have to consider A as a 10x10 matrix with 0 in the diagonal… You also have to decide whether the matrix A should be symmetric or not. In your case of 2 groups of bacteria, you have to model the interaction between species i and j (i.e. 1 and 2).

Show that you can shift in between any one of the three interactions type: mutualism, predation, competition.

You might take various modeling strategies with respect to the following points:

- How to model the internal growth : rN(1-N/K) as for rabbit or bacteria or a positive cross term as for the predator in the prey-predator model.

- Which molecular mechanism of action : through presence / absence of Sugar ? …or Toxin? Or both?
- Introduce molecules (sugar and/or Toxin) explicitly? A explicit negative impact of Toxin on Sugar in that case…?
- But remember… The absence of an inhibitor is equivalent to the presence of an activator. So introducing both a Toxin (through a Threshold A1) and a Sugar (through a threshold A2) might be useful only if you want to model more subtle molecular mechanisms.
- …

You might also decide (it is ok) to model a consortium of three bacteria with three types of interactions : mutualism between pair 1 & 2, competition between pair 2 & 3 and prey-predator between pair 1 & 3 and decide yourself whether you introduce only Toxin, only Sugar or both for each interaction N_i with N_j (i.e. one threshold A_1, or one threshold A_2 or two thresholds A_1 and A_2 for each of the three differential equation dNi/dt).

This generalization may help you to generalize the approach and think of a general “Quorum Sensing” (QS) inhibitor and activator… (type Google : model Quorum sensing activator inhibitor and see the first few item to get inspired) to simplify your system.