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The practical uses a standard chemostat model of bacterial growth. Substrates arrive in the inflow. Substrates and bacteria leave in the outflow. Bacteria metabolise the substrates and grow following Michaelis-Menten kinetics. The resource use of a species is specified by the amount of enzyme it allocates to the metabolism of each substrate. The total amount of enzyme is fixed at 1, but species can either specialise on one substrate or be a generalist on several.

A) The basics of the model.

I've coded versions with multiple species and evolving resource use. In the folder "bacteria.2species", I've provided three files that add in these features successively. Go through each of them in turn and work out what each part is doing.

Code1Species.R presents a single species growing on a single resource, with annotations to explain each line.

Code2sp2subs.R has 2 species growing on 2 resources. In this model, both resources come in via the input. Think about how you would alter this to have substrate 2 produced as a waste by metabolism of substrate 1.

Code2sp2subs.evo.R is the same but now the species can evolve in their resource use. Evolution in enzyme levels is specified by a mutation rate parameter multiplied by the selection gradient: how would the per cell growth rate vary if we vary enzyme allocation by a small amount? Because of the linear trade-off, an increase in growth rate on substrate 1 is associated with a reduced growth rate on substrate 2.

B) A multi-species version.

The above versions are discrete models with looped time-steps so you can see what's going on and change them easily. We can simulate changes in continuous time using the *lsoda()* solver. In the folder "bacteria.multispecies" I've provided a version that does this and also is coded in a more efficient way for exploring different metabolic pathways, parameter values and plotting solutions. Try running this version. Can you work out what metabolic pathway it is simulating? Try changing it to a linear pathway breaking down a single input substrate via 4 intermediates into a final waste product.

Happy? Now your mission, should you choose to accept it, is to add new features into the model and to address new questions.

Task 1: The present version of the model lacks any specification of abiotic conditions. pH especially is a major determinant of bacterial growth and community composition. Try adding in pH as an environmental variable and an optimum pH to each species. Then if you alter the pH, how do species respond to those changes? Do species interactions

(such as competition or facilitation) alter how the bacteria adapt to pH?

Task II: Bacterial phage are ubiquitous and could have a big impact on bacterial growth and potentially on interactions between species. Try adding in a phage population (or 2) that coevolves with the bacteria. Now there are 2 ways for species interactions to evolve – by a change in resource use or a change in phage resistance (which could be specialist on one species or generalist on several). OMG, what happens now?

Task III: The above models consider average trait values for populations. There is no way that populations can diversify into two ecotypes using different resources. But this is known to happen in bacteria, at least when single species are cultured in the lab. Try to make a new version that specifies the genetics of resource use in a way that diversification is possible. Does diversification occur? Does standing diversity inhibit it?

Task IV: The de Mazancourt et al. model found that increasing species richness reduces the amount of evolution. Does this happen in the bacteria-resource model or does species richness increase evolution? Use the multispecies version of the model to run multiple simulations with increasing diversity and record how the amount of evolution per species changes accordingly. You might want to modify the metabolic pathway.

Task V: There is no task V, but if you have an idea you'd like to try instead, go for it!

I've put reading on Blackboard. Do not attempt to make your models as complex as those but they might give you some ideas or useful nuggets.