Summary on 3 state simulations

"Method"

I originally computed the optimal parameters as in the two state case, that is by computing the averate time it would take to consume all the nutrients (T_S). However, to isolate T_S I had to make an assumption that I on closer inspection did not trust. Now I have redone the calculations, and compute the optimal parameters without the previous assumption, but instead by numerically determining T_S. For a given set of antibiotic parameters (p, T_0, T_{ab}) I determine T_S for every set of bacterial parameters (λ_d, λ_r, δ). The optimal combination of (λ_d, λ_r, δ) is the one that minimizes T_S.

The competition average parameters are computed by evolving several species according to the differential equations and using a solver to find T_S for 10 000 consecutive cycles.

The mutation simulations are done like the competition simulations, but with a mutation rate between the different species. Every simulation is started from a single species with a specific set of bacterial parameters (min and max?)

- What about mutation from λ_d=0? Create exception?
- Extinction?

Coupled nutrients and antibiotics, $T_0 = 0$

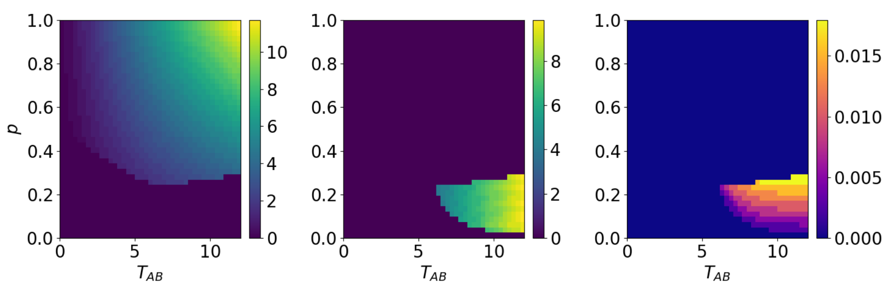


Figure 1: Optimal parameters for $T_0 = 0$

I still get same result as before: optimal strategy is either only triggered persistence, or only spontaneous persistence. The result is confirmed by a competition simulation, with competition between many species with different combinations of parameters. Having very small fraction of spontaneous persistence affects the growth very little, however after very many cycles the loss is significant.

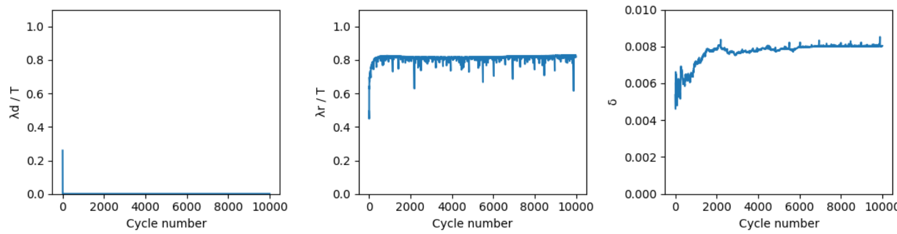
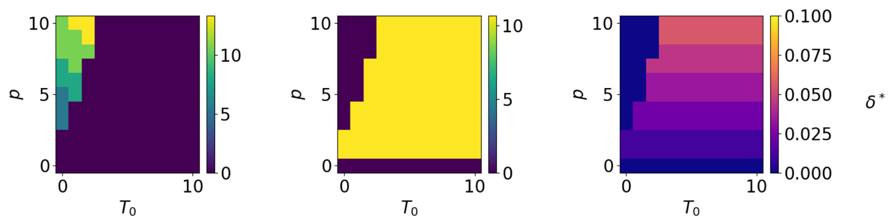


Figure 2: Interspecies competition at $T_0 = 0$, $T_{ab} = 12$

10 example feast-famine cycles

Figure 3: 10 example feast-famine cycles

Decoupled nutrients and antibiotics, $T_0 > 0$



Also when the antibiotics are decoupled from the addition of nutrients the two strategies are separated.

Interspecies competition at $T_0 = 2$, $T_{ab} = 12$

Figure 4: Interspecies competition at $T_0 = 2$, $T_{ab} = 12$

Mutation

Redo competition simulations with mutation.

To do

1) Reorganize folder structure to suit new system. Data is saves as it is, but figs and config file is saved in separate folders
2) Redo heatmaps with correct labels/titles/legends, etc. . .
3) Write script for plotting bacterial parameters from config file
4) Modify code so it saves 10 cycles
5) Write script for plotting feast-famine cycles
6) Run competition
7) Modify to add mutation
8) Run mutation

10 example feast-famine cycles

Figure 5: 10 example feast-famine cycles