The Pheno-Evo model: Evolution of microbial phenotypic diversity in 2D space

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Biologists appreciate microbes for their simplicity and predictability: we assume that a population of genetically identical cells in a uniform environment will all behave the same way. While this assumption is often useful, it is also often wrong. Not only might microbes in a clonal population act differently from one another, the differences may be categorical (growing v. non-growing; toxin-sensitive v. tolerant), and this diversity might be an evolved trait conferring increased fitness on the population. How does such phenotypic heterogeneity evolve? And how does a population find the optimal distribution of phenotypes for a given environment? Efforts at modeling microbial phenotypic heterogeneity often focus on populations with two discrete phenotypic types; phenotypes in continuous distributions remain poorly explored. To address this gap and to explore the role of spatial relationships, we use agent-based modeling to simulate a phenotypically diverse population of microbial cells evolving in the presence of periodic toxic stress. Cells on patches in a 2D grid may degrade toxin, suffer damage from toxin, switch phenotype, and reproduce. An individual's phenotype its toxin degradation rate– for which there is a tradeoff with reproduction– and the genotype encodes the distribution of phenotypic values in the population. The rate of toxin diffusion determines how individuals influence their neighbors' environments. We examine the effects of toxin concentration, diffusion rate, and environmental predictability on the survival success of populations with different phenotype distributions, and populations' evolutionary trajectories when phenotype distribution is allowed to evolve. We conduct all simulations on the platform NetLogo, which provides a friendly interface allowing users of any experience level to tweak parameters and run their own simulations. We have also created custom tools in R for analyzing and

visualizing the results of multiple runs.