Intro:

A population of viruses is trying to infect a population of bacteria, and we want to see how they coevolve. We are planning on implementing the gene for gene model of virus-host interaction (described below, and possibly the other if we have time). A virus attempts to infect the bacteria. If successful, it will create clones for itself and kill the host bacteria. The ultimate fitness is how many clones of an individual exist in either population. There are costs in evolving multiple virulence or resistance genes, both of which result in fewer offspring for either organism. The bacteria have additional viability genes which have the possibility to mutate to be deleterious (which would prematurely kill the host before reproduction of either).

Representation:

Array of genes:

Virus

|  |  |  |  |
| --- | --- | --- | --- |
| Index | Implemented | # bits | Meaning |
| 0 | no | 1 | Interaction model |
| 1 | No | 1 | Mutator |
| 2 |  |  |  |
| 3 |  |  |  |
| 4 |  |  |  |

Other variables:

Cost of virulence

Host

|  |  |  |  |
| --- | --- | --- | --- |
| Index | Implemented | # bits | Meaning |
| 0 | no | 1 | Interaction model |
| 1 | No | 1 | Mutator |
| 2 | No | 1 | Viability |
| 3 | No | 1 | Viability |
| 4 | no | 1 | Viability |
| 5 | no | 1 | Viability |
| 6 | no | 1 | Viability |

Other variables:

Cost of resistance

Mutation rate

* Interaction model: Parasite must exactly match host genotype to avoid detection and successfully infect the host. In other words, if the genes match, the host can’t tell the difference between itself and the virus, and thus can’t defend itself (matching allele model). Possibly implement gene for gene model, the host will have a resistance gene for a virus’ virulence gene. A virulence gene is required for the virus to infect a host, but if the host has resistance to that, the infection will be unsuccessful. Many genes can build up, but there is a tradeoff for a large number of genes.
* Mutator: Rate of mutation. If 1, multiply mutation rate by 100
* Viability: Affect host fitness only, has no effect on virus. Wild type /deleterious (initialize at all wild type)
* Based off of Coevolution with viruses drives the evolution of bacterial mutation rates (Pal et al.) http://www.nature.com/nature/journal/v450/n7172/full/nature06350.html

Plans?

Pairing of viruses and hosts

One to one- each individual virus can infect exactly one host

If there are multiple clones of virus, each can infect its own host

Each host can only have one virus in it at a time

Virulence/resistance genes

How does fitness work in practical terms?

Viability affects how much virus host can hold

Virus replication/mutation

How many offspring/clones end up in main population?

Find host fitness--- how precisely are we coding this?

Host replication/mutation

Crossover—not sure it’s a thing? Probably not going to implement because there’s not really a viral analogue

If we have time- dynamic populations/LV competition model

Other interaction model