21/10/2021

Notes on simulation model Fisherian Gandon:

* Current situation:
  + working code with t and p alleles – t1 and p1 are “wildtype”; t2 is harmful and only present in plasmid; p2 is resistant, only present in chromosome
  + mutation of t only possible in plasmid and mutation of p only possible in chromosome; hence we “lock” p2 and t2 to chromosome and plasmid, respectively
  + a p1t2 plasmid is equivalent to the Bad plasmid in Gandon & Vale, a p1t1 plasmid is equivalent to a Good plasmid
  + so far no co-infection allowed
* Sensitivity analysis should look at following parameters:
  + Strength of resistance
  + Force/coefficient of infection (note that we’re using a model with ecological feedback, so the probability of infection will depend on the number of infected cells)
  + Death rate of t2 plasmids
  + Cost of resistance
  + Fitness effect of having a bad plasmid (additional to the death rate)