A graph of different colored dots

AI-generated content may be incorrect.A graph of different colored dots

AI-generated content may be incorrect.

init\_wd <- 300

init\_wb <- 250

init\_sd <- 300

init\_sb <- 250

m\_rate\_wm <- 0.001

m\_rate\_sm <- 0.001

decay\_rate\_wm <- 0.05

decay\_rate\_sm <- 0.09

max\_gen <- 1000

no\_replicates <- 10

How do 2 deleterious mutations of different strength, which can mutate to beneficial ones, influence the probability of rescue and how does their frequency in the population change?

Answering the question: Set the parameters to certain values (see above) and measuring their frequency in the population after 1000 generations. Proposal: the strong mutation (beneficial) does slightly better with a mean frequency of a little over 0.75 (75%) with a selection coefficient of 0.3🡪which is high but because we are studying exactly that we set it high to see an effect. The weak mutation (beneficial) does less good with a frequency of little below 0.6 (60%) with a selection coefficient of 0.2. That’s why we propose that the trade-off is worth it to persist in the population, meaning that starting with a big disadvantage (higher decay rate and stronger selection coefficient witch has a negative impact) then pays off after mutation to the strong beneficial mutation, rather than starting with a less deleterious mutation but after mutating only being slightly beneficial.   
In this example: rescue is 1🡪this is to show the different frequencies

Anti-microbial-resistance

A graph of different colored dots

AI-generated content may be incorrect.

A graph with different colored dots

AI-generated content may be incorrect.

A graph of different colored lines

AI-generated content may be incorrect.

output <- simulate\_pop(init\_wd=300, init\_wb=300, init\_sd=300, init\_sb=300, decay\_rate\_wm=0.1, decay\_rate\_sm=0.2, s\_wm=0.1, s\_sm=0.2, m\_rate\_wm=0.0005, m\_rate\_sm=0.0005,max\_gen)