

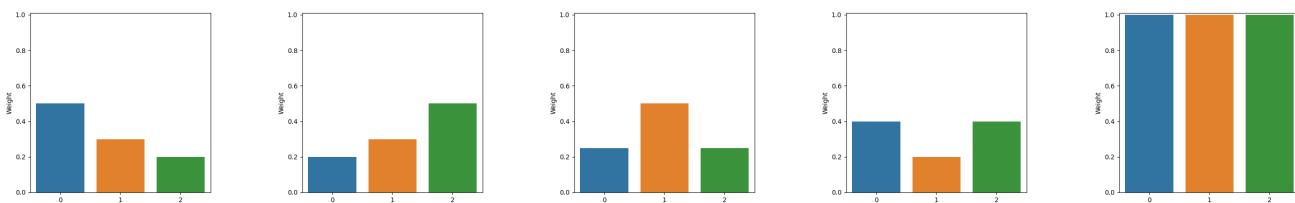
Tests using genome of length 3

Init paramenters:

```
num_hosts = 1000
wt_seq = 'AAA' # wild-type genome sequence
re_seq = 'BBB' # drug resistant mutant genome sequence
len_seq = 3
inf_frac = 0.5 # base infected fraction
# (this ultimately doesn't matter as long as it's high)
```

Weights distributions:

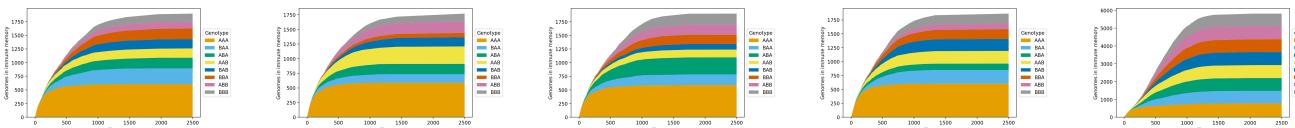
```
w1 = [0.5,0.3,0.2] # decaying weights
w2 = [0.2,0.3,0.5] # increasing weights
w3 = [0.25,0.5,0.25] # bell weights
w4 = [0.4,0.2,0.4] # U weights
pmw1 = [1] # Perfect matching weight
```



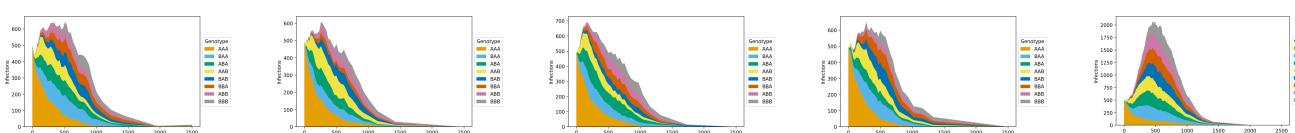
This is the same order for the figures below

First we'll try with **recombination turned off**

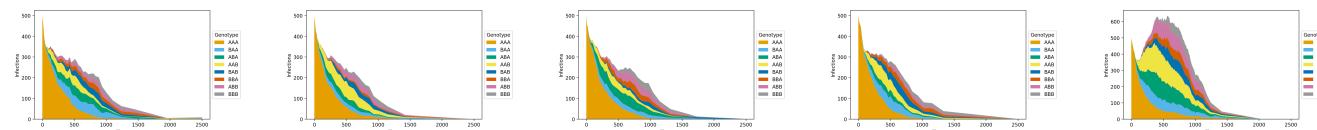
Immune memory



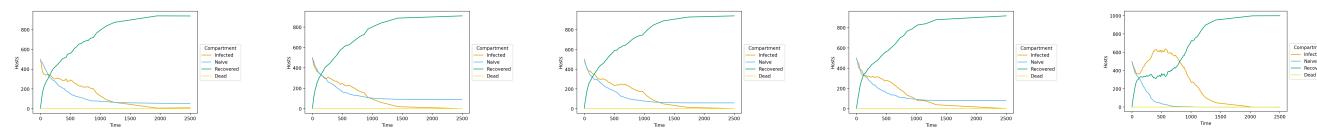
Pathogen composition



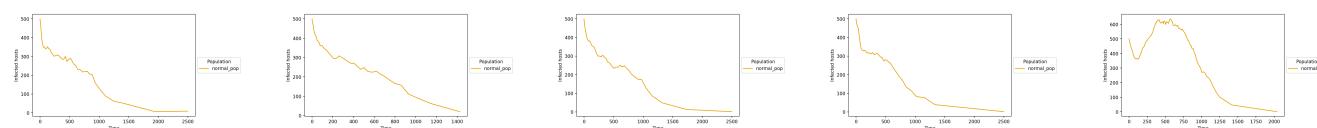
Composition



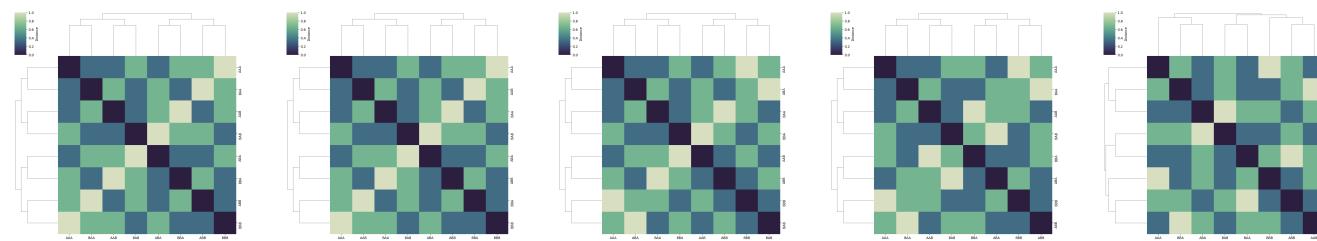
Compartments



Infections

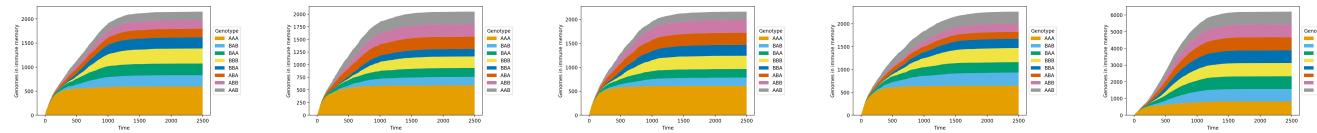


Cluster map

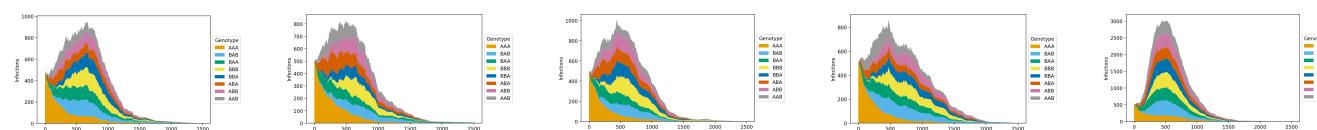


Now with recombination turned ON

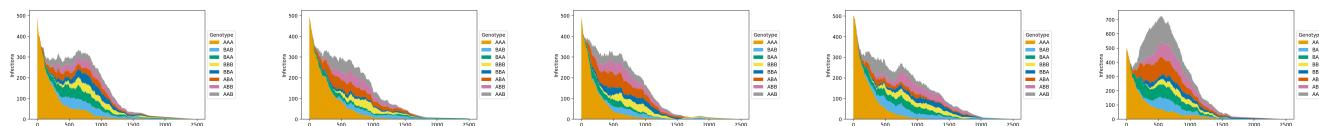
Immune memory



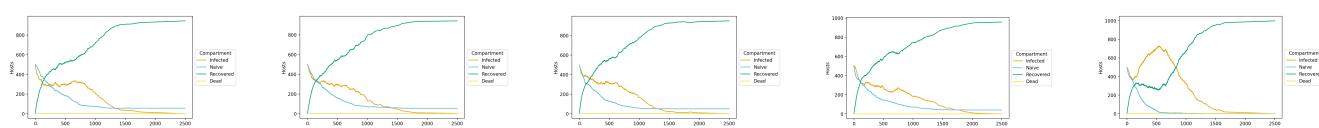
Pathogen composition



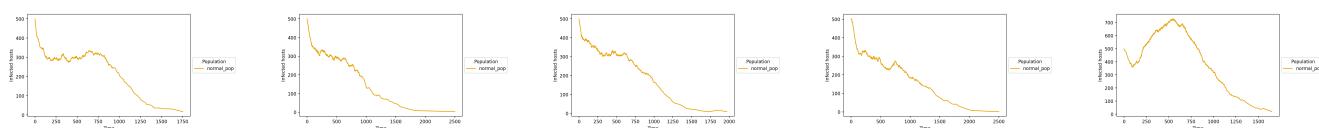
Composition



Compartments



Infections



Cluster map

