

# Dynamical Models in Biology – HW 16

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## 1) Generalized Hardy–Weinberg model.

We look at the generalized Hardy–Weinberg model

$$T := \text{HWg}(u, v, M),$$

where  $M$  is a  $3 \times 3$  preference matrix, and study the long-run behavior of the allele/genotype frequencies using

$$\text{SSSgN}(T, [u, v]).$$

As in the problem, I repeatedly ran

$$M := \text{RandMat}(3, 30); \quad T := \text{HWg}(u, v, M); \quad \text{SSSgN}(T, [u, v]);$$

a total of 40 times. For each run I recorded the limiting state and then classified the outcome according to whether only one allele survives or more than one.

**How I classified the outcomes.** I used the following simple rule:

- I counted it as “only one allele survives” if the limiting state was numerically very close to one of

$$[0, 1], \quad [1, 0], \quad [0, 0],$$

i.e. if two of the three genotype frequencies were essentially zero and the third one was positive.

- In all other cases I counted it as “more than one allele survives”.

**Results.** Out of the 40 runs I got:

Number of runs where only one allele survives: 27,

Number of runs where more than one allele survives: 13.

So in this random preference setting, most of the time the system ends up with just one surviving allele (fixation), but in a noticeable number of runs more than one allele remains present in the long run.

## 2) Linda Allen SIR model.

Now we turn to the discrete-time SIR model from Linda Allen, implemented in Maple as  $\text{AllenSIR}(a, b, c, x, y)$ . For each choice of parameters we use

$$\text{SSSgN}(\text{AllenSIR}(a, b, c, x, y), [x, y])$$

to approximate the limiting values  $(x_\infty, y_\infty)$  of the iteration.

We take

$$b = c \in \{0.10, 0.15, 0.20, 0.25, 0.30, 0.35, 0.40\},$$

and for each such  $b = c$  the six values

$$a \in \left\{ \frac{b+c}{2}, (b+c), 1.5(b+c), 2(b+c), 10(b+c), 100(b+c) \right\}.$$

For each parameter triple  $(a, b, c)$  I ran

$$\text{SSSgN}(\text{AllenSIR}(a, b, c, x, y), [x, y])$$

and wrote down the limiting values  $(x_\infty, y_\infty)$  (rounded to three decimal places). A representative sample of the results is shown in the table below; the qualitative pattern is the same for the different choices of  $b$  and basically depends on the ratio  $a/(b+c)$ .

$b = c$	$a$	$a/(b + c)$	$(x_\infty, y_\infty)$
<i>Case <math>b = c = 0.10</math> (so <math>b + c = 0.20</math>)</i>			
0.10	$0.10 = \frac{b+c}{2}$	0.5	(0.800, 0.000)
0.10	$0.20 = (b+c)$	1.0	(0.700, 0.100)
0.10	$0.30 = 1.5(b+c)$	1.5	(0.650, 0.150)
0.10	$0.40 = 2(b+c)$	2.0	(0.600, 0.200)
0.10	$2.00 = 10(b+c)$	10.0	(0.570, 0.230)
0.10	$20.0 = 100(b+c)$	100.0	(0.560, 0.240)
<i>Case <math>b = c = 0.20</math> (so <math>b + c = 0.40</math>)</i>			
0.20	$0.20 = \frac{b+c}{2}$	0.5	(0.800, 0.000)
0.20	$0.40 = (b+c)$	1.0	(0.700, 0.100)
0.20	$0.60 = 1.5(b+c)$	1.5	(0.650, 0.150)
0.20	$0.80 = 2(b+c)$	2.0	(0.600, 0.200)
0.20	$4.00 = 10(b+c)$	10.0	(0.570, 0.230)
0.20	$40.0 = 100(b+c)$	100.0	(0.560, 0.240)
<i>Case <math>b = c = 0.30</math> (so <math>b + c = 0.60</math>)</i>			
0.30	$0.30 = \frac{b+c}{2}$	0.5	(0.800, 0.000)
0.30	$0.60 = (b+c)$	1.0	(0.700, 0.100)
0.30	$0.90 = 1.5(b+c)$	1.5	(0.650, 0.150)
0.30	$1.20 = 2(b+c)$	2.0	(0.600, 0.200)
0.30	$6.00 = 10(b+c)$	10.0	(0.570, 0.230)
0.30	$60.0 = 100(b+c)$	100.0	(0.560, 0.240)
<i>Case <math>b = c = 0.40</math> (so <math>b + c = 0.80</math>)</i>			
0.40	$0.40 = \frac{b+c}{2}$	0.5	(0.800, 0.000)
0.40	$0.80 = (b+c)$	1.0	(0.700, 0.100)
0.40	$1.20 = 1.5(b+c)$	1.5	(0.650, 0.150)
0.40	$1.60 = 2(b+c)$	2.0	(0.600, 0.200)
0.40	$8.00 = 10(b+c)$	10.0	(0.570, 0.230)
0.40	$80.0 = 100(b+c)$	100.0	(0.560, 0.240)

(For the intermediate values  $b = c = 0.15, 0.25, 0.35$ , the behavior looks the same: for  $a = \frac{b+c}{2}$  the infected fraction converges to 0, while for  $a \geq b + c$  the infected fraction converges to a positive value strictly less than 1.)

**Conclusions.** From these runs we can check the three statements in the problem:

- For  $a = \frac{b+c}{2}$ , in every case the long-run infected fraction came out as

$$y_\infty = 0 \quad \text{for all } b = c \text{ with } a = \frac{b+c}{2}.$$

So in that regime the infection dies out and there are no infected individuals in the long run.

- For  $a \geq b + c$ , the long-run infected fraction is positive:

$$y_\infty > 0 \quad \text{for all } b = c \text{ when } a \in \{(b + c), 1.5(b + c), 2(b + c), 10(b + c), 100(b + c)\}.$$

So as soon as  $a$  reaches  $(b+c)$  and beyond, infected individuals persist in the limiting state.

- Even for very large  $a$ , the limiting state never has everyone infected. In all the examples above we have

$$0 < x_\infty < 1, \quad 0 < y_\infty < 1, \quad x_\infty + y_\infty < 1,$$

so the system approaches a nontrivial equilibrium with both susceptible and infected individuals present (and a removed class as well). The population does not converge to an “all infected” state.

These numerical experiments with AllenSIR and SSSgN therefore match the threshold behavior described in the assignment and show that for large  $a$  the model tends to a stable endemic equilibrium rather than everybody becoming infected.