Homework for Lecture 15 of Dr. Z.'s Dynamical Models in Biology class

Email the answers (as a .pdf file) to

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by 8:00pm Monday, Oct. 27, 2025.

Subject: hw13

with an attachment hw13FirstLast.pdf

1. Read and understand, and be able to reproduce without peeking (e.g. in examination conditions) the derivatin of the Hardy-Weinberg rule.

$$(u, v) \rightarrow \left(u^2 + vu + \frac{1}{4}v^2, -2vu - 2u^2 + 2u - \frac{1}{2}v^2 + v\right)$$

2. If right now, 20 percent of the polpulation have genotupe AA, 30 percent of the polpulation have genotype Aa, what is the percentage of aa genotypes (i) Right now? (ii) In the next generation? (iii) In ten generations?

3. If right now the 50 percents of the polpulation are of aA genotypes, and 30 percents of the polpulation are of aa genotypes, what is the percentage of AA genotypes (i) Right now? (ii) In the next generation? (iii) In ten generations?

4. Read and understand Linda Allen's article:

`http://sites.math.rutgers.edu/~zeilberg/Bio25/AllenSIR.pdf`

Experiment with procedure `AllenSIR(a,b,c,x,y)` for various values of a, b, c and find the ultimate behavior using `ORB`

in our Maple package:

`https://sites.math.rutgers.edu/~zeilberg/Bio25/DMB.txt` .

2. If right now, 20 percent of the polpulation have genotupe AA, 30 percent of the polpulation have genotype Aa, what is the percentage of aa genotypes (i) Right now? (ii) In the next generation? (iii) In ten generations?

i)

$AA := 1/5\ (20\%)$
$Aa := 3/10\ (30\%)$
$aa: = 1/2\ (50\%)$

$$\frac{20}{100} + \frac{30}{100} + aa = 1$$

$$aa = 50\%$$

ii)

$$\left(\frac{1}{5}, \frac{3}{10}\right) \to \left(\frac{1}{25} + \frac{1}{5}\left(\frac{3}{10}\right) + \frac{1}{4}\left(\frac{3}{10}\right)^2, -\cancel{2}\left(\frac{1}{5}\right)\left(\frac{3}{\cancel{10}_{5}}\right) - 2\left(\frac{1}{5}\right)^2 + 2\left(\frac{1}{5}\right) - \frac{1}{2}\left(\frac{3}{10}\right)^2 + \frac{3}{10}\right)$$

$$\left(\frac{1}{25} + \frac{3}{50} + \frac{9}{400}, -\frac{3}{25} - \frac{2}{25} + \frac{2}{5} - \frac{9}{200} + \frac{3}{10}\right)$$

$$\left(\frac{16}{400} + \frac{21}{400} + \frac{9}{400}, \frac{-40}{200} + \frac{80}{200} - \frac{9}{200} + \frac{60}{200}\right)$$

$$\left(\frac{46}{400}, \frac{92}{200}\right)$$

$AA \to \frac{46}{400}$ $\quad aa \to \frac{17}{40}$

$Aa \to \frac{92}{200}$

$$\frac{46}{400} + \frac{92}{200} + W = 1$$

$$\frac{46}{400} + \frac{184}{400} + W = 1$$

$$\frac{230}{400} + W = 1$$

$W = \frac{17}{40}$ } aa genome

iii) After the first iteration of H-W transformation, the generation changes, but after that is stays the same. genotype after 10 generations will be $\frac{17}{40}$.

3. If right now the 50 percents of the polpulation are of aA genotypes, and 30 percents of the polpulation are of aa genotypes, what is the percentage of AA genotypes (i) Right now? (ii) In the next generation? (iii) In ten generations?

i)

$aA - 1/2\ (50\%)$
$aa - 3/10\ (30\%)$
$AA - 1/5\ (20\%)$

$$U + 50\% + 30\% = 1$$

$U = 20\%$ OR $1/5$

ii)

$$\left(\frac{1}{5}, \frac{1}{2}\right) \to \left(\frac{1}{25} + \frac{1}{10} + \frac{1}{4}\left(\frac{1}{4}\right), -2\left(\frac{1}{10}\right) - \frac{2}{25} - \frac{1}{2}\left(\frac{1}{4}\right) + \frac{1}{2}\right)$$

$$\frac{1}{25} + \frac{1}{10} + \frac{1}{16}, \frac{-1}{5} - \frac{2}{25} - \frac{1}{8} + \frac{1}{2}$$

$$\left(\frac{81}{400}, \frac{19}{200}\right)$$

iii) After the first iteration of H-W transformation, the generation changes, but after that is stays the same. genotype after 10 generations will be $\frac{81}{400}$.

Problem 4

read `DMB.txt`

For a list of the Main procedures type: Help(); for help with a specific procedure type: Help(ProcedureName); for example Help(Feig); **(1)**

Help(*AllenSIR*)

AllenSIR(a,b,c,x,y): The Linda Allen discrete SIR model given in https://sites.math.rutgers.edu/~zeilberg/Bio25/AllenSIR.pdf

with parameters a,b,c. satisfying 0<a,b,c and 0<b+c<=1 , with initial conditions x0,y0>0 and 0<x0+y0<=1 .Try:

AllenSIR(0.2,0.3,0.4,x,y); **(2)**

Help(*ORB*)

ORB(F,x,x0,K1,K2): Inputs a transformation F in the list of variables x with initial point pt, outputs the trajectory

of the discrete dynamical system (i.e. solutions of the difference equation): x(n)=F(x(n-1)) with x(0)=x0 from n=K1 to n=K2.

For the full trajectory (from n=0 to n=K2), use K1=0. It gives the answer in floating point. Try:

*ORB([5/2*x*(1-x)],[x], [0.5], 1000,1010);*

ORB([(1+x+y)/(2+x+y),(1+x)/(1+y)],[x,y], [2.,3.], 1000,1010); **(3)**

```
# Case H1: R0 = 0.2/(0.6+0.0) = 0.333 < 1
A := AllenSIR(0.2, 0.6, 0, 0.9, 0.1);
ORB(A, [x, y], [2.0, 3.0], 1000, 1010);
#R0 < 1·(infection dies out)
```

$$A := [0.3764729789, 0.6235270211]$$

[[0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211], [0.3764729789, 0.6235270211]] **(4)**

```
#infection persists at a high level
# Case H2: R0 = 0.5/(0.5+0) = 1.0
A := AllenSIR(0.5, 0.5, 0, 0.9, 0.1);
ORB(A, [x, y], [2.0, 3.0], 1000, 1010);
#R0 ≈ 1(threshold behavior)
```

$$A := [0.4862371848, 0.5137628152]$$

$[[0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152], [0.4862371848, 0.5137628152]]$ **(5)**

#endemic steady state with roughly half the population infected.
 # Case H3: R0 = 0.6/(0.1+0) = 6.0
$A := AllenSIR(0.6, 0.1, 0, 0.9, 0.1);$
$ORB(A, [x, y], [2.0, 3.0], 1000, 1010);$
#R0 > 1 (endemic / possible oscillation)

$$A := [0.8517251748, 0.1482748252]$$

$[[0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252], [0.8517251748, 0.1482748252]]$ **(6)**

#endemic steady state but with a much smaller infected fraction (I≈0.1483)
#Case H4: aggressive contact rate — watch for negatives
$A := AllenSIR(1.2, 0.1, 0, 0.9, 0.1);$
$ORB(A, [x, y], [2.0, 3.0], 1000, 1010);$
#Large a, (may produce discrete overshoot / negatives)

$$A := [0.8760404474, 0.1239595526]$$

$[[0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526], [0.8760404474, 0.1239595526]]$ **(7)**

#endemic steady state, I≈0.124
 # Case H5: small initial infection
$A := AllenSIR(0.6, 0.1, 0, 0.99, 0.01);$
$ORB(A, [x, y], [2.0, 3.0], 1000, 1010);$
#Different initial infection (small seed)

$$A := [0.8954788560, 0.1045211440]$$

$[[0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440], [0.8954788560, 0.1045211440],$ **(8)**

$[0.8954788560, 0.1045211440]]$

#endemic steady state with small persistent infection I≈0.1045.