Names: _____   _____

<u>BIOE 149 Disease Ecology Evolution of Virulence Homework Assignment</u>
<u>The evolution of Myxoma virus in rabbits in Australia</u>
Myxoma virus is transmitted between rabbits by direct contact (and also by fleas, but we'll ignore that for now). Through a series of Dr. Evil experiments, biologists infected rabbits with five different strains of the virus. Some lived and some died. Biologists measured how infectious infected rabbits were to other rabbits (the fraction of other rabbits that got infected after spending a day with the rabbits), how long they lived when infected (some died from infection), and how long rabbits that didn't die were shedding the virus (after which they seemed to be immune to reinfection). Biologists also went out into the field and measured how long rabbits lived in areas without the virus. All durations are in days.

Strain	Lifespan in the field when not infected	Average time until death when infected	Probability of infecting another rabbit given contact	Average time surviving rabbits shed virus	
1	335	11	0.35	20	
2	335	15	0.3	26	
3	335	20	0.29	27	
4	335	40	0.19	28	
5	335	118	0.08	8	

1. The evolutionary fitness of a pathogen is proportional to its value of R_0 since this is a measure of the number of "offspring" in pathogen terms. Which of the 5 strains of this virus is the most fit? If you released one infected rabbit with each strain, which strain would you expect to find in the population (if any) three decades later if the average rabbit density was 1 rabbit/ha, and rabbits roam (and contact other rabbits) about 1 ha each day? Put another way, if you first introduced strain 1 (which is what actually happened), but you knew the virus could evolve along a continuum of traits described by the other strains (which is what the data indicate), which set of traits do you think the virus would have after three decades? Why? Is it the deadliest strain? The most infectious strain? Hint: You will need to draw/build a model that captures the biology of myxoma virus and rabbits, write down the equations, derive an R0 expression and fill in the parameter values using the information given. You will need a calculator or Excel and can/should write on the back and show all work!!!

2. The real data are given in the table below. Do these data match your predictions from (1)? Approximately? Completely? For all strains?

Fraction of viral isolates in each strain

Year	Strain 1	2	3	4	5
1950–1951	100				
1952–1955	13.3	20.0	53.3	13.3	0
1955–1958	0.7	5.3	54.6	24.1	15.5
1959–1963	1.7	11.1	60.6	21.8	4.7
1964–1966	0.7	0.3	63.7	34.0	1.3
1967–1969	0	0	62.4	35.8	1.7
1970–1974	0.6	4.6	74.1	20.7	0
1975–1981	1.9	3.3	67.0	27.8	0