Biomath 202 2019 Exam

SIMON LEE

1 Introduction

a. The SIR model equations represent the rates of change of three population groups:

- - Susceptible (S): $\frac{dS}{dt} = -\beta IS$
- - Infected (I): $\frac{dI}{dt} = \beta IS - \gamma I$
- - Recovered (R): $\frac{dR}{dt} = \gamma I$

The total population $N = S + I + R$. Adding the equations:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = -\beta IS + \beta IS - \gamma I + \gamma I = 0$$

So total population is conserved.
The fixed points are found by setting all derivatives to zero. This gives: 1) $S = N$, $I = R = 0$ (disease-free equilibrium) 2) $S^* = \frac{\gamma}{\beta}$, $I^* = \mu(\beta N - \gamma)/(\beta\gamma)$, $R^* = (\beta - \mu)N/\beta$, where $\mu = \frac{\gamma}{\beta N}$ (endemic equilibrium)
$S^* = \frac{\gamma}{\beta}$ is the herd immunity threshold, below which the disease will spread.

b. To incorporate vaccination at rate v and GBS deaths at rate δ:

$$\frac{dS}{dt} = -\beta IS - vS$$

$$\frac{dI}{dt} = \beta IS - \gamma I - \delta I$$

$$\frac{dR}{dt} = \gamma I + vS$$

$$\frac{dD}{dt} = \delta I$$

(new compartment for GBS deaths)
Now $\frac{dN}{dt} = -\delta I$, so total population is not conserved due to GBS deaths.
As $t \to \infty$, the system will approach an equilibrium with $I = 0$ and $S = \frac{\gamma+\delta}{\beta+v}$.

c. Let p be the frequency of the GBS allele, $q = 1 - p$ the normal allele frequency. Assuming HWE, the mean fitness is:

$$\bar{w} = p^2(1 - s) + 2pq + q^2$$

, where $s = 0.1$ is the selection coefficient.
The variance of p is $V(p) = 2pq$, maximized at $p = 0.5$.
From the equation in part b, $\frac{I^*}{N} = \frac{\delta}{\delta+\gamma} \Rightarrow p = \frac{\delta}{\delta+\gamma}$, and $V(p) = 2p(1 - p)$.
The strength of selection against p is:

$$\frac{\partial \ln(\bar{w})}{\partial p} \approx -2qs = -2(1 - p)s$$

By Wright's equation, the change in p per generation is:

$$\Delta p = -V(p)\frac{\partial \ln(\bar{w})}{\partial p} = -2pq \cdot -2qs = 4pq^2 s$$

Since $q \approx 1$ for a rare allele, $\Delta p \approx 4ps$, driven more by the selection coefficient $s = 0.1$ than the variance term $2pq << 1$. The GBS allele frequency will decrease slowly each generation.

d. If the world population is 7 billion and everyone gets vaccinated, then the number of vaccinations needed is simply 7 billion. The number of generations until the GBS mutation is eliminated depends on the selection pressure against it.

e. To make stochastic predictions, we can use the Wright-Fisher model. The variance in allele frequency p is $V(p) = p(1-p)/(2N_e)$, where N_e is the effective population size. The selection term from part c is

$$\frac{\partial \ln(\bar{w})}{\partial p} \approx -2(1-p)s$$

.
Putting these together, the expected change in p per generation is:

$$\mathbb{E}[\Delta p] = -V(p)\frac{\partial \ln(\bar{w})}{\partial p} = -\frac{p(1-p)}{2N_e} \cdot -2(1-p)s = \frac{p(1-p)^2 s}{N_e}$$

At equilibrium, $\mathbb{E}[\Delta p] = 0$, which occurs when $p = 0$ (mutation eliminated) or $p = 1$ (mutation fixed), assuming $s \neq 0$ and N_e is finite.
The time to elimination depends on the initial p and the population size N_e. In a very large population, drift is weak and selection dominates, so elimination would be faster than in a small population where drift is strong relative to selection.
Other factors that could help the GBS allele persist include:

- - Balancing selection (heterozygote advantage)
- - Linked selection (hitchhiking with a beneficial allele)
- - Population structure/migration
- - Mutation-selection balance

f. If a genetic screen identified carriers, the SIR equations would be:

$$\frac{dS}{dt} = -\beta IS - vS$$
$$\frac{dI}{dt} = \beta IS - \gamma I$$
$$\frac{dR}{dt} = vS + \gamma I$$
$$\frac{dG}{dt} = -vG$$

(screened group)
The total population is N = S + I + R + G, conserved since:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dG}{dt} = 0$$

$$\text{As } t \to \infty, S \to 0, I \to 0, R \to N - G, G \to Ge^{-vt}$$

The fraction getting GBS depends on the initial G and vaccination rate v. It decreases exponentially, but is never driven to zero if v < ∞.
So in summary, while screening and vaccination could greatly reduce GBS incidence, eliminating the allele completely from the population is challenging, especially with a large starting frequency. Let me know if you have any other questions!