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Identification of Human Genetic Locus from Unknown Meat Sample by Restriction Fragment Length Polymorphism

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1 Introduction

This project models the effect of two subgroups within a population. These subgroups are colloquially termed either "normally" susceptible (S_n, default average person) or "highly" susceptible (S_h, a subgroup that differs from the average by some parameters). S_h are modelled as a linear-transform of S_n and may differ in any combination of infection rate, recovery rate, death rate, and/or relapsation rate (loss of immunity) from S_n by a scalar increase or decrease relative to S_n's respective transition rate.

2 The SIR Model

Susceptible Population S

This project assumes the total population S consists of two groups as per:

$$S = S_n + S_h = \alpha_n \cdot S + \alpha_h \cdot S$$

where α_i are the percentages of each sub-group within the population, $\alpha_n + \alpha_h = 1$.

Infectious Population I

As both S_n and S_h are assumed to have different susceptibilities, they are assigned two different rates of infection: β_n and β_h, where we assume for simplicity sake (see Introduction) that $\beta_h = k \cdot \beta_n$ for some $k \in \mathbb{R}$. Given the scalar relation between β_n and β_h we abbreviate $\beta_n \equiv \beta$, as we will do for any transition rate henceforth.

Removed Population R

The removed population R consists of two sub-populations, namely the recovered population R' and the deceased population D. Infectious individuals may transition into either R' or D, given two separate transition rates.

We define the recovery rate γ and death rate θ whose scaled rates for the "highly" susceptibles are $\gamma_h = j \cdot \gamma$ and $\theta_h = q \cdot \theta$ for some $j, q \in \mathbb{R}$, respectively.

We further define a relapsation rate δ that mimics how immunity is lost over time (perhaps due to newly emerging mutant pathogens) and allows individuals from R' to relapse into S. Here as well "highly" susceptibles are linearly scaled as $\delta_h = h \cdot \delta$ for some $h \in \mathbb{R}$.

System of Equations

The outlined model allows transitions between Susceptible S to Infectious I, from I to either Removed population R' or D, and from R' back to S. This allows the following set of first order differential equations to be formulated:

$$\frac{dS(t)}{dt} = -\beta\Phi_k \cdot S(t) \cdot I(t) + \delta\Phi_h \cdot R'(t)$$
$$\frac{dI(t)}{dt} = \beta\Phi_k \cdot S(t) \cdot I(t) - \gamma\Phi_j \cdot I(t) - \theta\Phi_q \cdot I(t)$$
$$\frac{dR'(t)}{dt} = \gamma\Phi_j \cdot I(t) - \delta\Phi_h \cdot R'(t)$$
$$\frac{dD(t)}{dt} = \theta\Phi_q \cdot I(t)$$

Where $\Phi_x = \alpha_n + x \cdot \alpha_h$ describes the impact of "highly" susceptibles within the total population for some scalar factor x of a given transition.

This set of differential equations now has four separate rates of transition: (1) β, the rate of infection, where "highly" susceptibles are distinguished by a k-fold increase/decrease. (2) γ, the rate of recovery, where "highly" susceptibles are distinguished by a j-fold increase/decrease. (3) δ, the relapsation rate, where "highly" susceptibles are distinguished by an h-fold increase/drecrease. And (4) θ, the death rate, where "highly" susceptibles are distinguished by a q-fold increase/decrease compared to "normally" susceptibles. All of these are editable to explore different scenarios of heterogeneous populations.

3 Modelling

To apply the formulated model, a `python` module was developed to numerically solve the outlined system of equation using `scipy` and `numpy`. An interactive web-app was developed using `streamlit` to ease model exploration. THE APP IS AVAILABLE WHERE??....

4 Discussion

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Table 1 HEPES 0.5M, pH7.4 | 500ml

Component	Instruction
HEPES	59.58g
MilliQ	fill-up to 450ml
NaOH 5M	to pH7.4 (~17.5ml)
MilliQ	fill-up to 500ml
Sterile Filter	

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5 Supplementary Data

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