

Competitive Exclusion in Two-Strain Epidemiological Models

INTRODUCTION

- ❖ We analyze competition in a multi-strain Susceptible-Low-High-Recovered (SLHR) model. Previous work [1] considered a two-strain model for COVID-19. We discuss our findings in the context of bacterial infection.
- Compartmental epidemiological models use a system of ordinary differential equations (ODEs) to track the movement of a population between disease states.

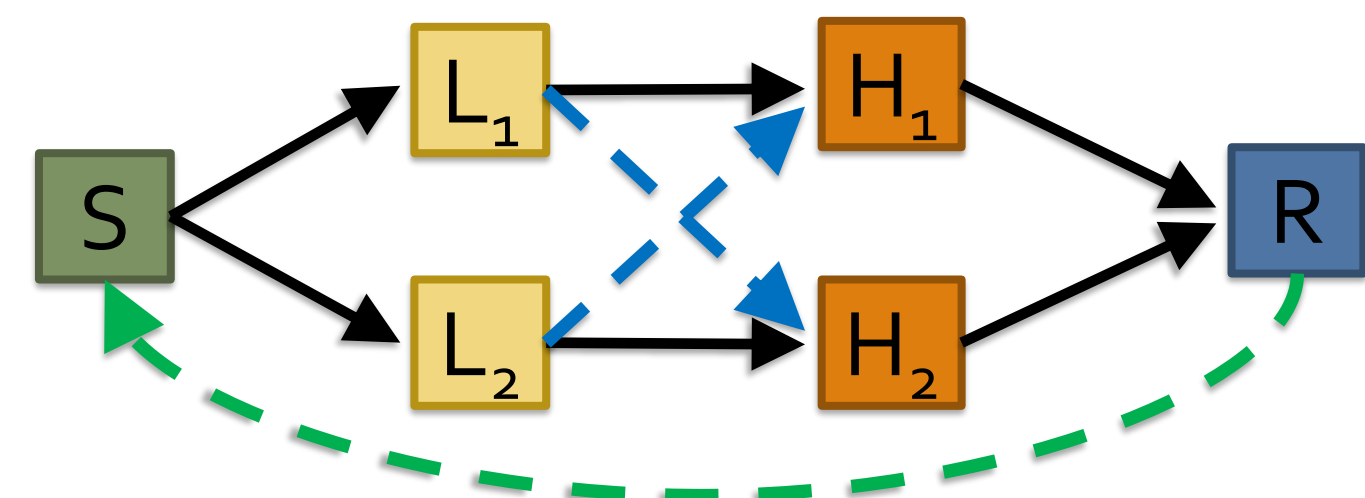


Fig 1: We look at an SLHR model to capture within-host and population-level epidemiological dynamics.

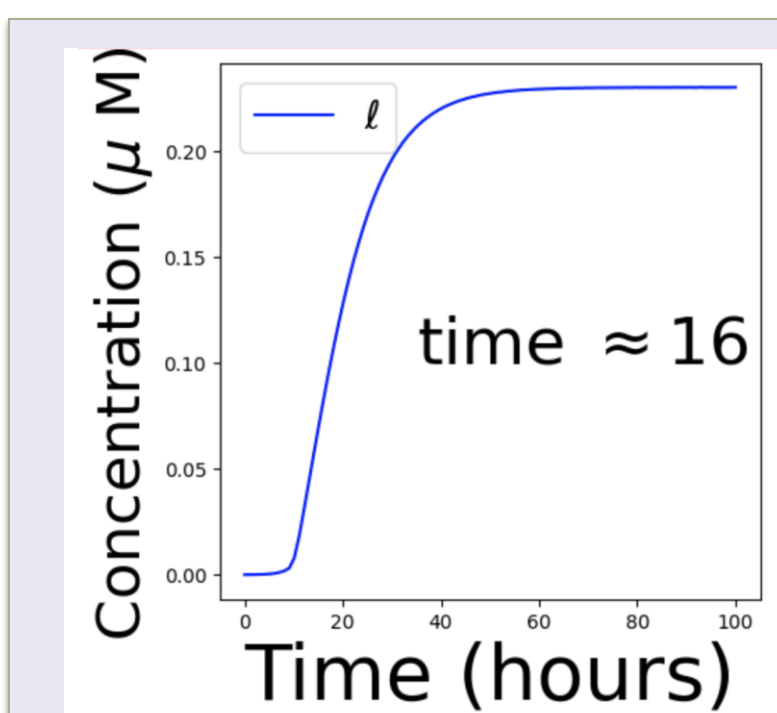


Fig. 2: Progression rate α from strain's signal concentration ℓ , which mediates quorum sensing (QS) — bacterial communication

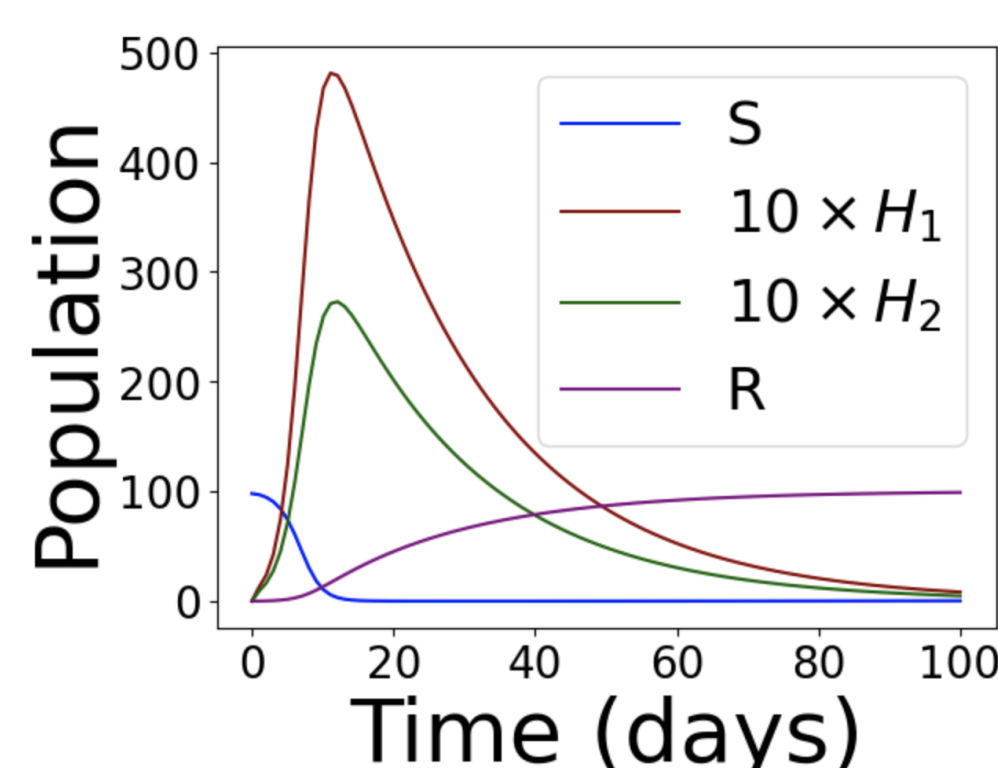


Fig 3: Example of outbreak dynamics for the SLHR model

- A key metric is basic reproduction number, R_0 , which is the average number of cases from one infected person in totally susceptible population.
- For single strain models, if $R_0 > 1$, disease is endemic (persistent). [2]
- Each strain i in our model has its own $R_{0,i}$ derived by linearizing the model at equilibrium points [2].

❖ Is there an endemic equilibrium where both strains coexist if $R_{0,1}, R_{0,2} > 1$?

ANALYTICAL RESULTS

- The basic reproduction numbers for both strains are:

$$R_{0,1} = \frac{\Lambda \alpha_1 \beta_1}{\mu(\alpha_1 + \mu)(\gamma_1 + \mu)} \quad R_{0,2} = \frac{\Lambda \alpha_2 \beta_2}{\mu(\alpha_2 + \mu)(\gamma_2 + \mu)}$$

- ❖ Contrary to [1], there cannot be a biologically feasible ($H_i > 0, R_{0,1} \neq R_{0,2}$) coexistence equilibrium under mass-action incidence βSH .

❖ Our SLHR equations are:

$$\begin{aligned} \dot{S} &= \Lambda - \beta_1 S H_1 - \beta_2 S H_2 - \mu S + \iota R \\ \dot{L}_i &= \beta_i S H_i - \alpha_i L_i - w_j \beta_j L_i H_j - \mu L_i \\ \dot{H}_i &= w_i \beta_i L_j H_i + \alpha_i L_i - \gamma_i H_i - \mu H_i \\ \dot{R} &= \gamma_1 H_1 + \gamma_2 H_2 - \iota R - \mu R \end{aligned}$$

SPECIAL CASE: WANING IMMUNITY ($w = 0, \iota > 0$)

- Waning immunity $\iota > 0$ [3] (green arrow fig 1) replenishes S from R and lessens competitive exclusion.
- ιR term in the SLHR equations.

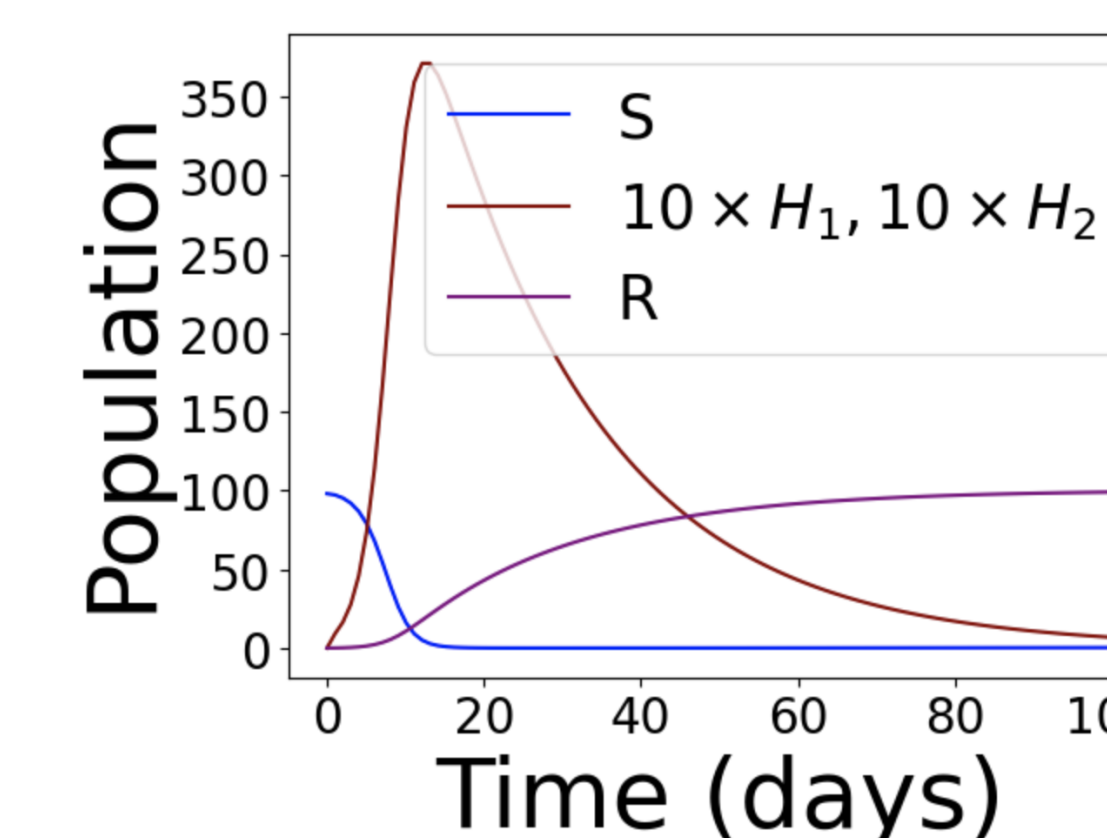
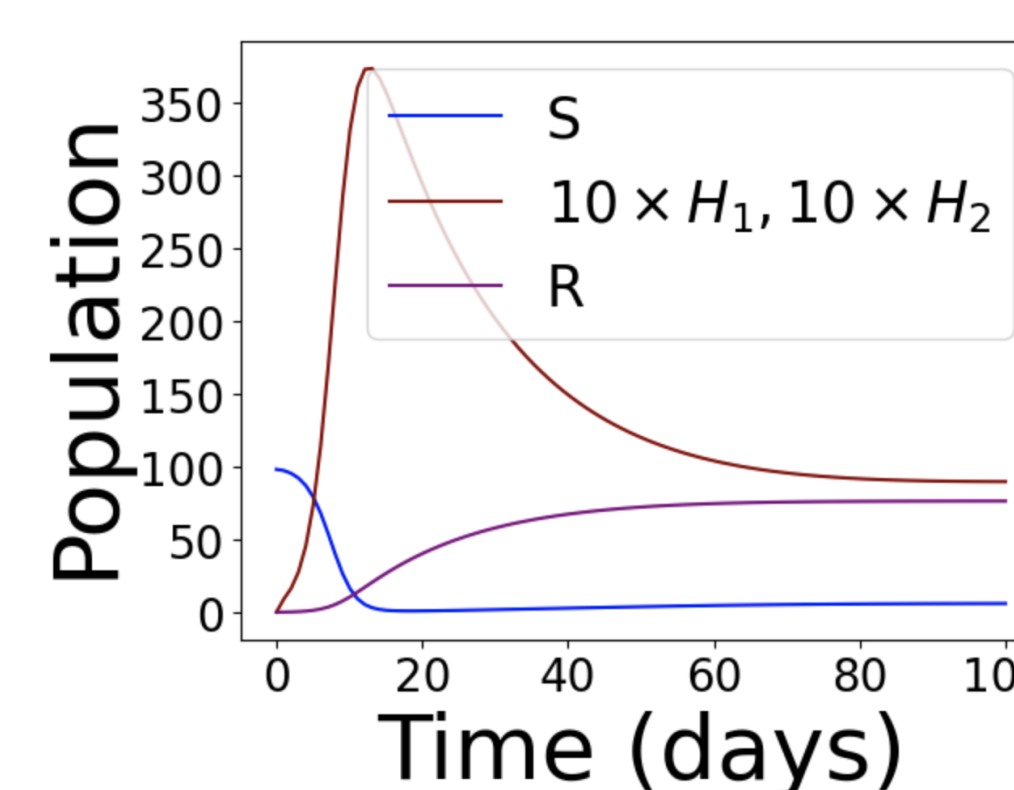


Fig 4: Waning immunity does not add coexistence. Left: ι slows decay. Right: $\iota = 0$. All strain parameters are identical, so the H graphs overlap.

SPECIAL CASE: SUPERINFECTION ($w, \iota > 0$)

- Superinfection: Invader strain outcompetes low density resident (blue arrows fig 1).
- $w_i \beta_i L_j H_i$ term in SLHR equations.

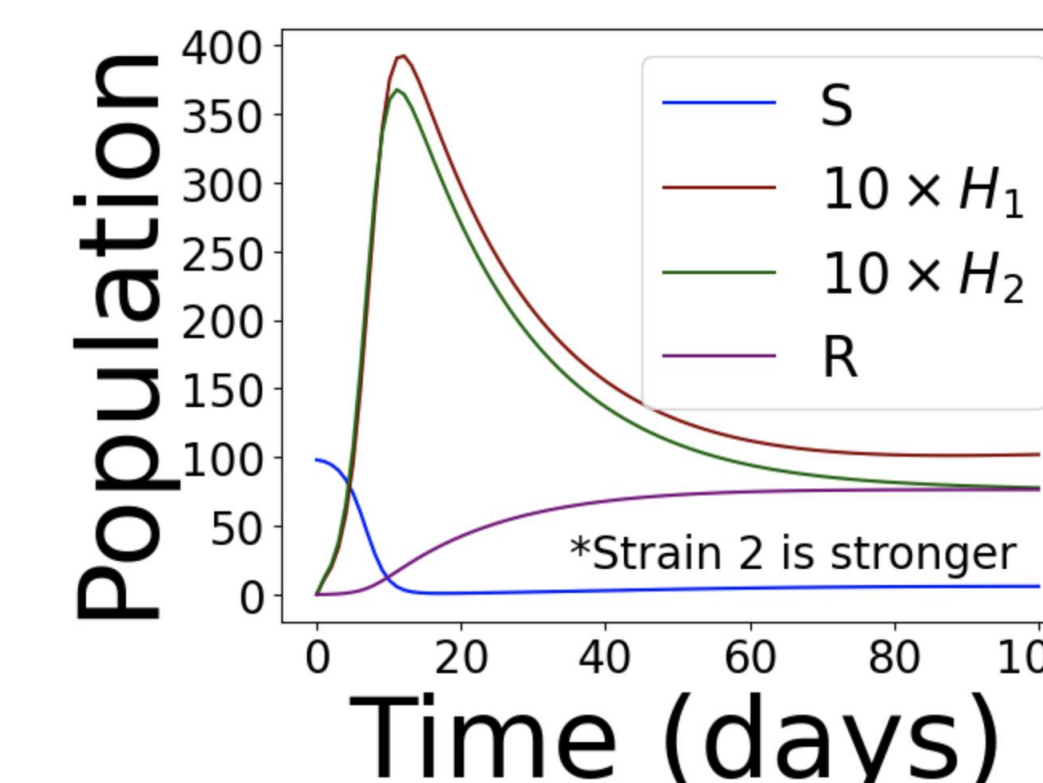
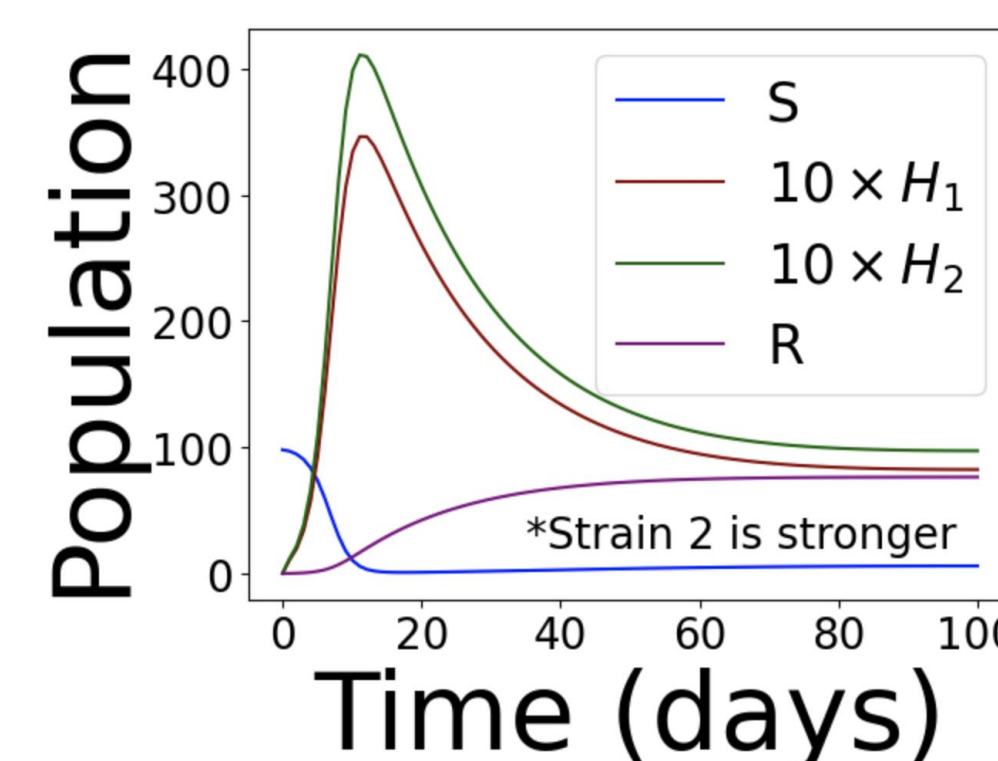


Fig 5: A less fit strain 1 ($R_{0,1} < R_{0,2}$) may take over if $w_1 > w_2$. Left: $w_{1,2} = 0$. Right: $w_1 = 1, w_2 = 0$

ACKNOWLEDGEMENTS

We thank our mentors Dr. Rachel Kuske, Dr. Sam Brown, and Brendan Shrader for their invaluable help on this project. Funding for this REU was provided by NSF grant #2244427 and the Georgia Tech College of Sciences.

Parameter	Meaning
Λ	Population birth rate (population/day)
α	1/incubation time (1/day)
β	Transmission constant (1/day*population)
γ	Recovery rate (1/day)
μ	Death rate (1/day)
ι	Waning immunity rate (1/day)
w	Superinfection proportion

IMPLICATIONS

- The proposed SLHR model can help identify disease prevention and treatment strategies in the case of outbreaks with two serotypes of a pathogen.
- This model also enables deeper analysis of superinfection dynamics.

FUTURE WORK

- Full analysis of superinfection
- Fully incorporate QS dynamics below into SLHR model where:

$$\begin{aligned} \dot{B} &= rB \left(1 - \frac{B}{K} \right) & \text{B bacterial concentration} \\ \dot{\ell} &= cEB - d\ell - m\ell & \ell \text{ QS signal concentration} \\ E &= a + b \left(\frac{\ell}{\ell + q} \right) & E \text{ QS gene expression} \end{aligned}$$

- Consider nonlinear interactions

REFERENCES

- [1] Khyar O, Allali K. Nonlinear Dyn. 2020;102(1):489-509.
- [2] van den Driessche P, Watmough J. Math Biosci. 2002;180:29-48.
- [3] Metcalf BJ, Waldetoft KW, Beall BW, Brown SP. Epidemics. 2023;45:100731.