

# The importance of vaccinated individuals to population-level evolution of pathogens

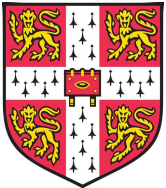
## Alternative title

Population heterogeneity in within-host evolution: consequences for vaccine escape

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Email: [mag84@cam.ac.uk](mailto:mag84@cam.ac.uk) questions very welcomed (even if you aren't here for the talk!)



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# Context: SARS-CoV-2 vaccine escape...

- Cobey et al. Concerns about SARS-CoV-2 **evolution** should not hold back efforts to expand **vaccination**. *Nature Reviews Immunology* (2021)
- Thompson et al. SARS-CoV-2 incidence and **vaccine escape**. *The Lancet Infectious Diseases* (2021)
- Saad-Roy et al. Epidemiological and **evolutionary considerations of SARS-CoV-2 vaccine** dosing regimes. *Science* (2021)
- Gog et al. **Vaccine escape** in a heterogeneous population: insights for SARS-CoV-2 from a simple model. *Royal Society Open Science* (2021)
- Rella et al. Rates of SARS-CoV-2 transmission and vaccination impact the fate of **vaccine-resistant strains**. *Scientific Reports* (2021)
- Gandon et al. Targeted **vaccination** and the speed of SARS-CoV-2 **adaptation**. *PNAS* (2021)
- Day, Gandon et al. Pathogen **evolution** during **vaccination** campaigns. *PLOS Biology*. (2022)
- Lobinska et al. Evolution of **resistance to COVID-19 vaccination** with dynamic social distancing. *Nature Human Behaviour* (2022)
- Zhang et al. A spatial vaccination strategy to reduce the risk of **vaccine-resistant variants**. *PLOS Computational Biology* (2022)

...but hopefully broadly applicable to evo-epi models

# Talk plan

1. Published work
  - a. Evolutionary approach
  - b. Epidemic models
  - c. Escape pressure results
2. Work in progress
  - a. Reinfections
  - b. Immunocompromised
  - c. Multi-wave evolution
3. Discussion
  - a. Conclusions
  - b. Applications
  - c. Further ideas



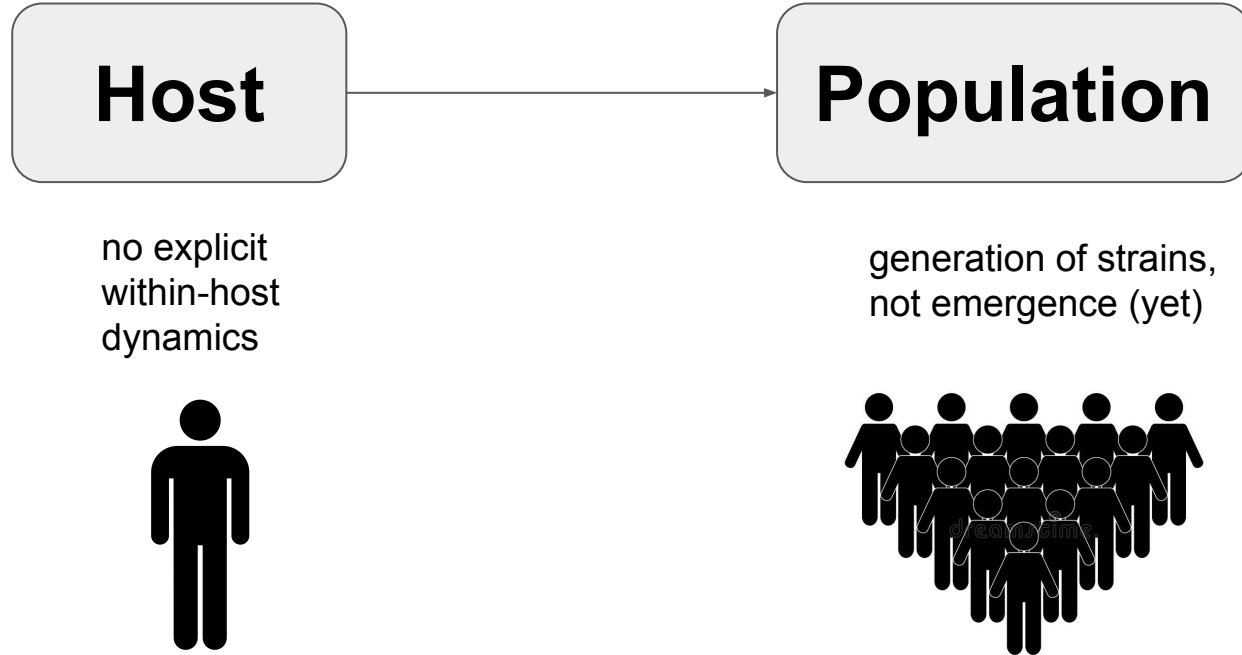
Paper

**Gutierrez, M. A. and Gog, J. R.**  
The importance of vaccinated individuals to  
population-level evolution of pathogens.  
*Journal of Theoretical Biology*  
(21 June 2023)

# Published work

# Evolutionary approach

# Simplified scales of selection



# Population level

[overall constant of proportionality  
unimportant, focus on relative pressure]

Escape pressure (rate)

key parameter!

$$P(t) := I_U(t) + \theta_E I_V(t)$$

infections in unvaccinated hosts      infections in vaccinated hosts

Epidemic wave

Cumulative escape pressure  
(time integral of above)

$$P' = C_U + \theta_E C_V$$

[assumes wave unaffected by new strain(s)]

Endemic equilibrium

Escape pressure rate at equilibrium

$$P^* = I_U^* + \theta_E I_V^*$$

# Within-host level

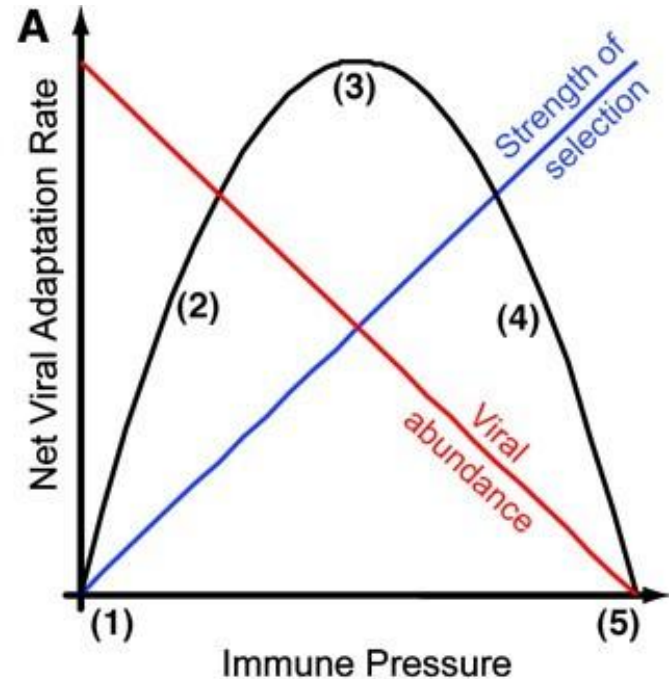
Q: Do infections in vaccinated hosts contribute more or less to the escape pressure than infections in unvaccinated hosts?

$$\theta_E > 1?$$

$$\theta_E < 1?$$

vaccines =>

- more within-host selection for escape
- BUT lower viral load, so less mutations

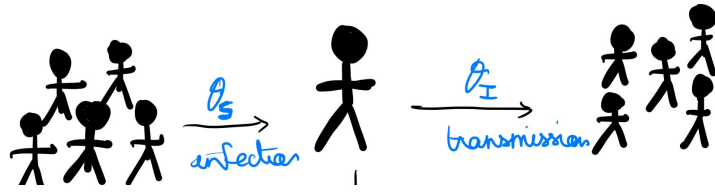


Grenfell et al, Science 2004  
(Phylodynamics)



# Epidemic model

# Transient SIR epidemic wave (endemic also in paper)



- C:** vaccination coverage in population,
- vaccines given before wave
  - no waning of immunity
  - no reinfections

Polarised (“all-or-nothing”) vaccine immunity  
(leaky immunity also in paper)

unvaccinated  
(fraction)  $S_U(0) = 1 - c$

vaccinated  
(fraction)  $S_V(0) = c\theta_S$

Force of infection

$$\lambda = R_0(I_U + \theta_I I_V)$$

^reduced infectivity

$$\begin{aligned}\dot{S}_U &= -S_U \lambda \\ \dot{S}_V &= -S_V \lambda \\ \dot{I}_U &= S_U \lambda - I_U \\ \dot{I}_V &= S_V \lambda - I_V\end{aligned}$$

Assumptions:

well-mixing  
constant  $R_0$ ,  
not time-since-infection,  
same infectious period,  
not SEIR/SIAR,  
no quarantined hosts...

# Analytical final size solution leads to escape pressure

Same ratio of vaccinated to unvaccinated maintained in each stage

$$(S_V, I_V, R_V) = \frac{c\theta_S}{1-c} (S_U, I_U, R_U)$$

$$R_e = R_0 (1 - c(1 - \theta_S\theta_I))$$

Vaccine transmission-blocking factor appears on R number

Can integrate SIR for final sizes  $C_U$ ,  $C_V$  needed in escape pressure

$$P = C_U + \theta_E C_V$$

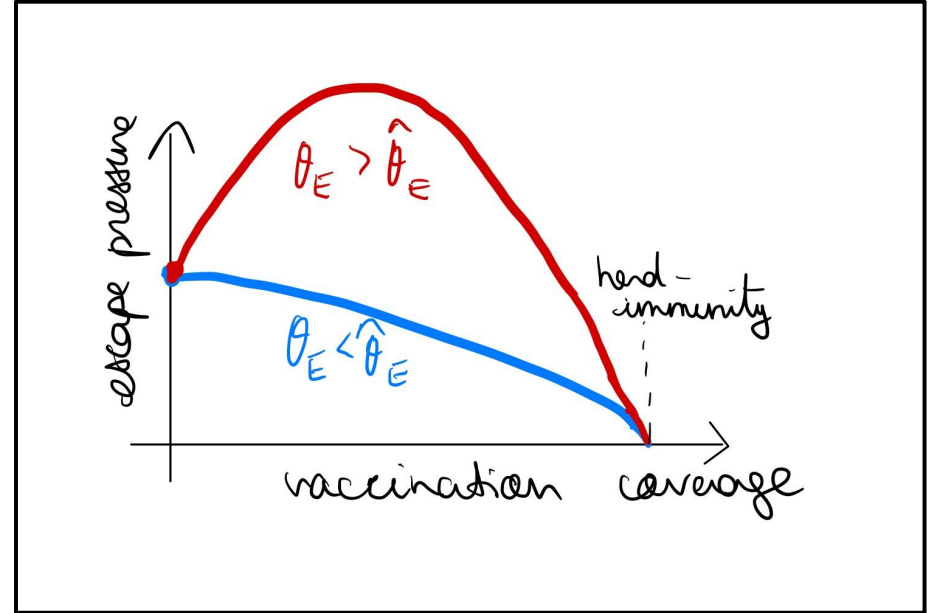
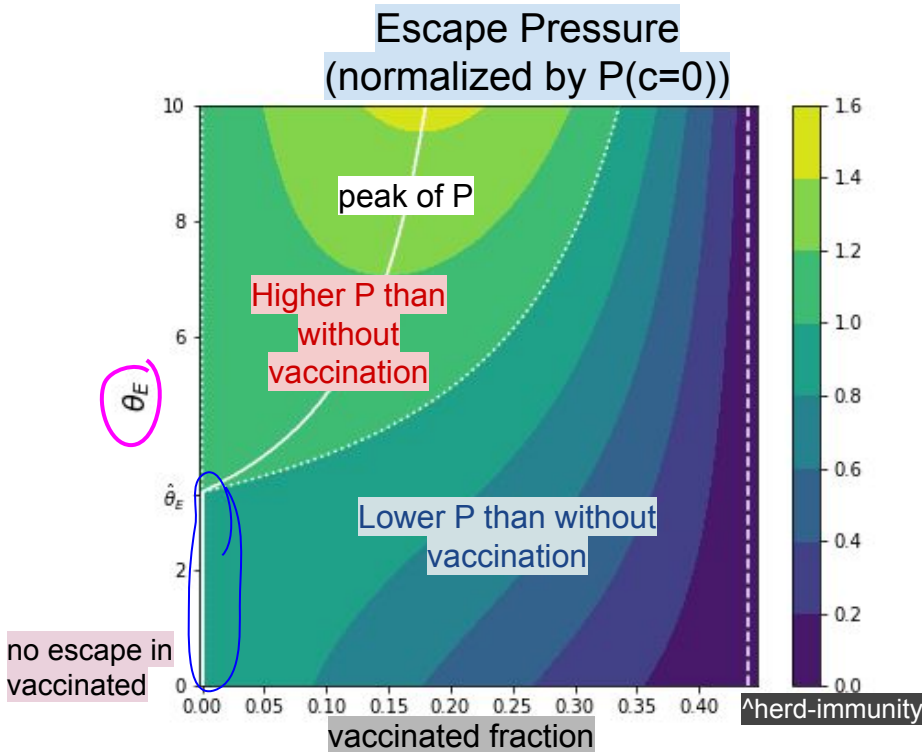
$$P = (1 - c(1 - \theta_S\theta_E))(1 + R_e^{-1} W(-R_e e^{-R_e}))$$

“Escape blocking factor”

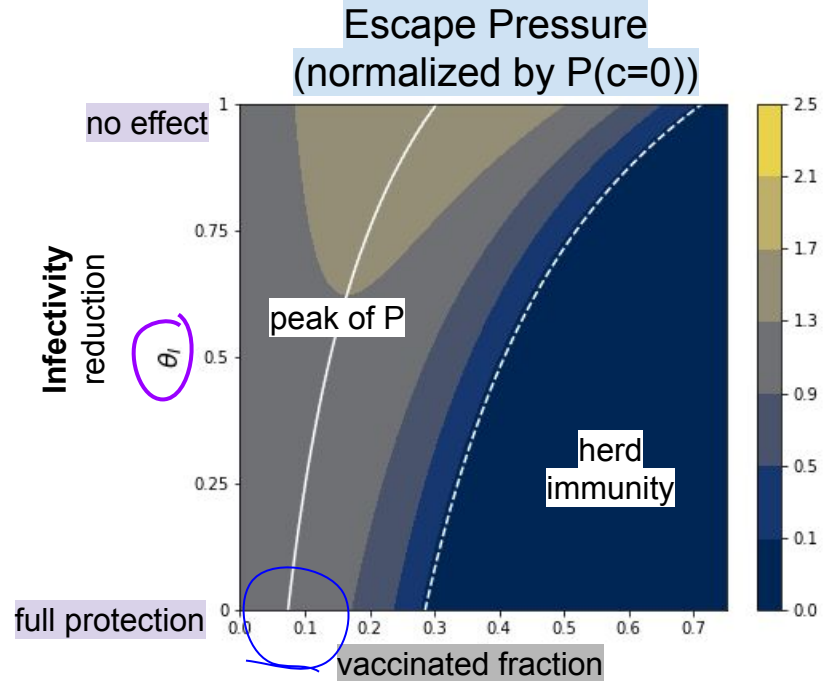
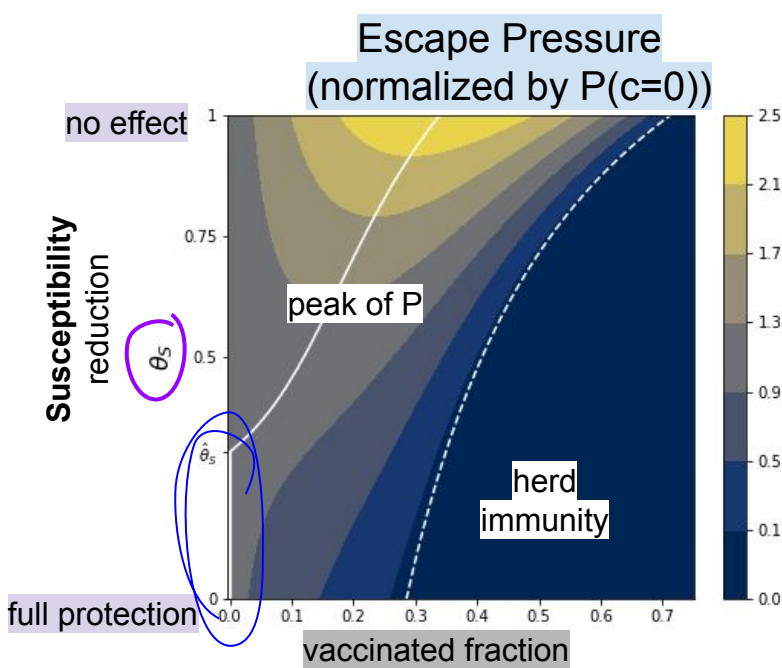
Lambert W function

# Results

# The **relative escape contribution** ( $\theta_E$ ) of vaccinated hosts regulates the shape of the escape pressure



# The vaccine efficacies ( $\theta_S$ , $\theta_I$ ) are also important



# Work in progress

# Reinfections



# What if infections only protect give **partial immunity**?

$$P = \underbrace{(C_U^{(1)} + \theta_E (C_U^{(2)} + C_V^{(1)} + C_V^{(2)}))}_{\text{all infections in hosts with prior immunity}}$$

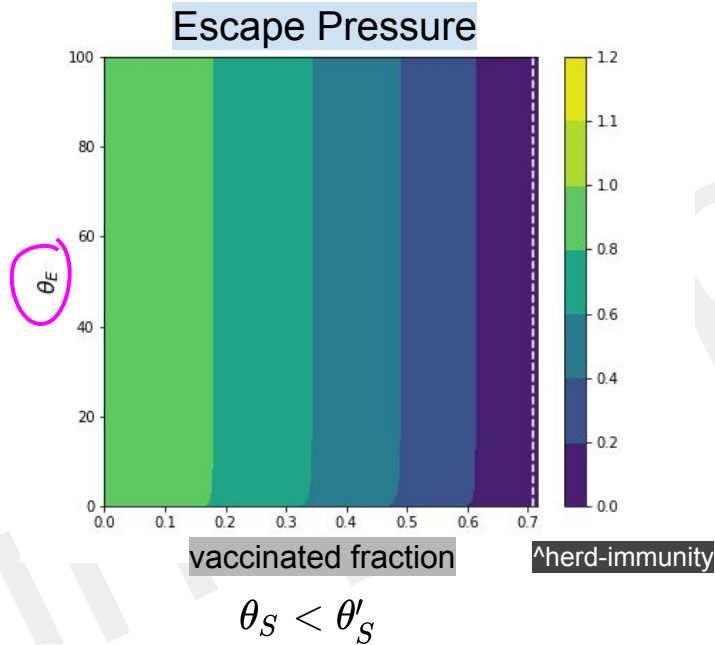
primary cases in unvaccinated      reinfections in unvaccinated      primary cases in vaccinated      reinfections in vaccinated

Modified model to allow for **reinfections**

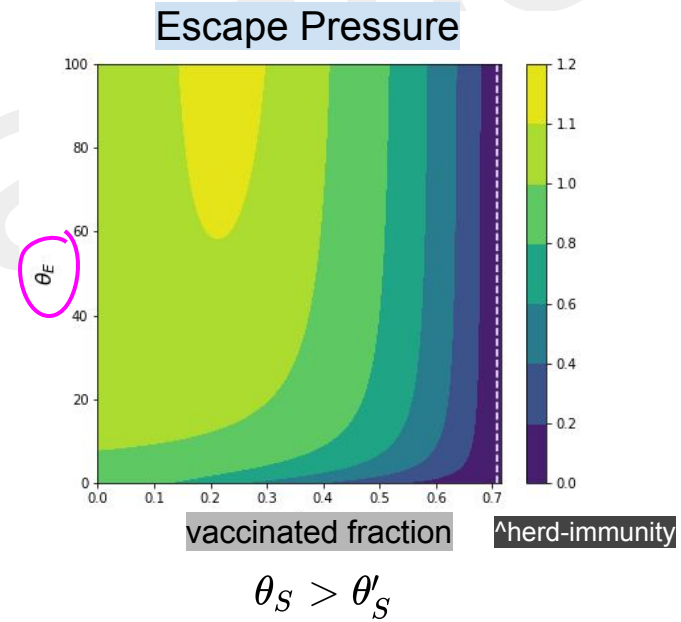
Vaccinated individuals have reduced susceptibility ( $\theta_S$ ) and recovered individuals also have reduced susceptibility ( $\theta'_S$ )

Still can find final size analytically!

**If vaccines give equal or more protection than infection, the escape pressure always decreases with the vaccination coverage**



**If vaccines give less protection than infection, the escape of hosts with prior immunity determines the shape of the escape pressure**



# Population heterogeneity (eg, immunocompromised)

# Population heterogeneity

$$R_e = R_0 \frac{(x - c_1(1 - \theta_S \theta_I)) + \underline{m^2}(1 - x - c_2(1 - \theta_S \theta_I))}{x + \underline{m^2}(1 - x)}$$

Two population groups (as in Gog et al 2021)

#1, size  $x$ : **high escape contribution  $p > 1$**  (“vulnerable”/ immunocompromised),

#2, size  $1-x$ : larger contact rate  $m > 1$  (“mixers”/youth)

$$P = pC_1 + C_2$$

Add vaccination in:

$$P = p(C_{U,1} + \theta_E C_{V,1}) + C_{U,2} + \theta_E C_{V,2}$$

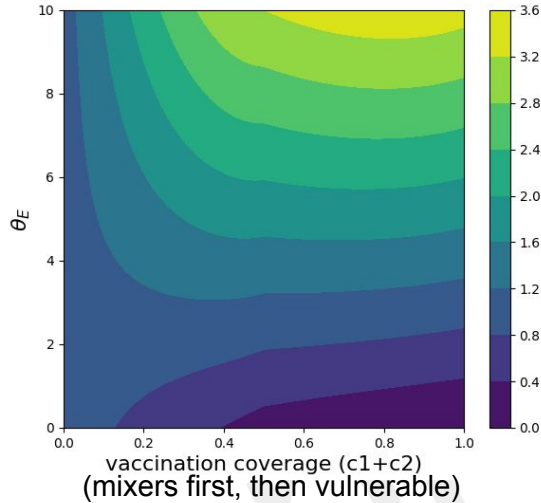
Adapt SIR model from before

Can still solve analytically

$$P = (p(x - c_1(1 - \theta_S \theta_E)) + m(1 - c_2(1 - \theta_S \theta_E))) \left(1 + \frac{W(-R_e e^{-R_e})}{R_e}\right)$$

Best strategy to minimise escape.. (and maybe also severe disease outcomes!) is to **vaccinate first the group with more contacts...** can get **bimodal shape**

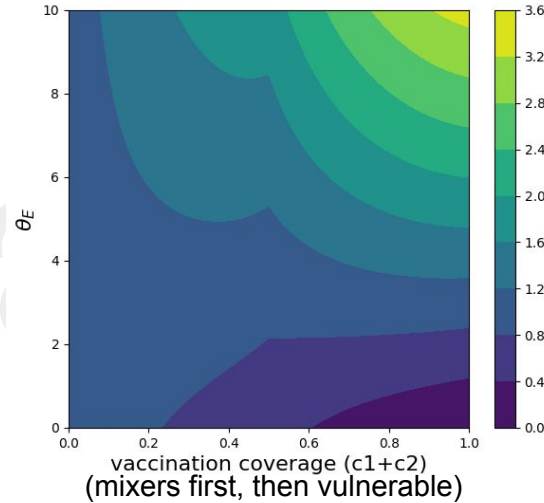
Escape Pressure



$p=1$

$m=2$  in both plots

Escape Pressure



$p=5$

Higher  $p$  (increased escape in immunocompromised) leads to bimodality

# Multi-wave evolution

# Single-strain waves, cross-immunity from escape pressure

Cross-immunity: **exponentially decaying** with antigenic distance (escape pressure here) [Boni, Andreasen et al 2004]

Original transient model for each wave, effective susceptible size changes

**Results 1D map** for effective susceptible size  $S$ , gives effective  $R=S \cdot R_0$

$$S' = S \left( 1 - (1 + W/R) \exp \left[ - \frac{\mu}{1 + \theta_E} \frac{(1 - c(1 - \theta_S \theta_E))}{1 - c(1 - \theta_S)} S(1 + W/R) \right] \right)$$

( $W := W[-R \exp(-R)]$ ) [weight and normalization factors] [final size]

If  $R' = S' \cdot R_0 > 1$ , continue to new wave (can include stochastic extinction)

How to quantify escape over multiple waves? **Total (expected) number of cases**

# New patterns; stochastic extinction matters

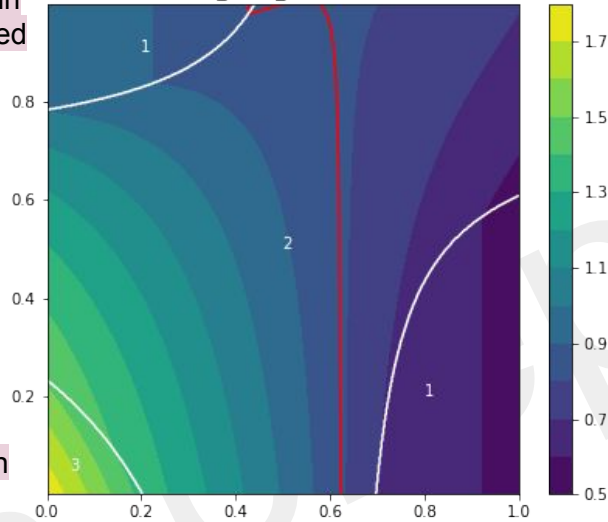
Without stochastic extinction

Total infections (per individual)

no escape in unvaccinated

$$\frac{\theta_E}{1+\theta_E}$$

no escape in vaccinated



vaccinated fraction

white contours: number of waves

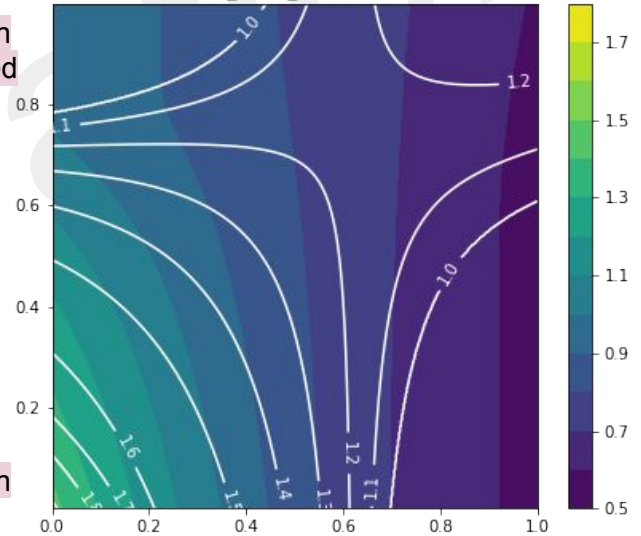
With stochastic extinction

Expected total infections (per individual)

no escape in unvaccinated

$$\frac{\theta_E}{1+\theta_E}$$

no escape in vaccinated



vaccinated fraction

white contours: expected number of waves



# Discussion

# Conclusions

1. Importance of **relative escape from vaccinated individuals**:  
We shouldn't make uninformed assumptions about its value!
2. More generally, importance of **heterogeneous escape**
  - a. immunocompromised
  - b. reinfections
3. **Vaccine efficacies** also matter for escape; especially susceptibility VE
4. More possibilities for escape pressure than “peak at intermediate values of immunity” (described by others)
  - a. monotonically decreasing
  - b. bimodal

# Applications

1. Value in measuring or estimating (or modelling?) the relative escape contribution from each host type?
2. Vaccine design – to minimise escape
3. Vaccination strategies – given a vaccine, to minimise escape (& disease)
4. Target genomic sequencing at populations with highest escape pressure

# Further ideas – suggestions encouraged!

1. **Invasion** dynamics
  - a. Stochastic extinction - changing susceptible size due to original strain
  - b. Replacement or coexistence?
  - c. Fitness cost from escape?
2. **Multiple strains**: mutation rates dependent on immune history
3. **Within-host** dynamics and selection...estimate  $\Theta_E$
4. **Waning** immunity
  - a. from infection and/or vaccination
  - b. within wave or across waves
5. Recombination / multiple infections

A final thought:  $\Theta_E$  depends on “escape strain” of interest and specific vaccine(s)

# Acknowledgements

Many thanks to my supervisor **Julia Gog** and the rest of the group in Cambridge.

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Questions?

Funding:



Paper



**Gutierrez, M. A. and Gog, J. R. (2023).**  
The importance of vaccinated individuals to  
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*Journal of Theoretical Biology*