

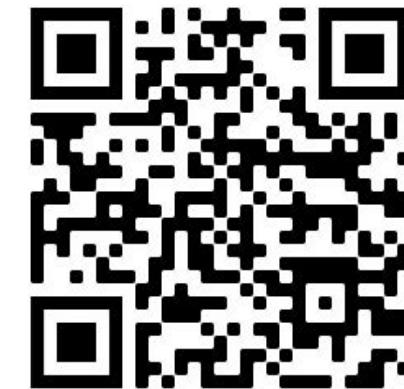
# Epidemiology and the RG

---

Maria A. Gutierrez (she/her)

Informal Soft Matter seminar, DAMTP, 24/02/2022

[www.mariaalegriagutierrez.wordpress.com](http://www.mariaalegriagutierrez.wordpress.com)



## FIELDS ARRANGED BY PURITY

→  
MORE PURE

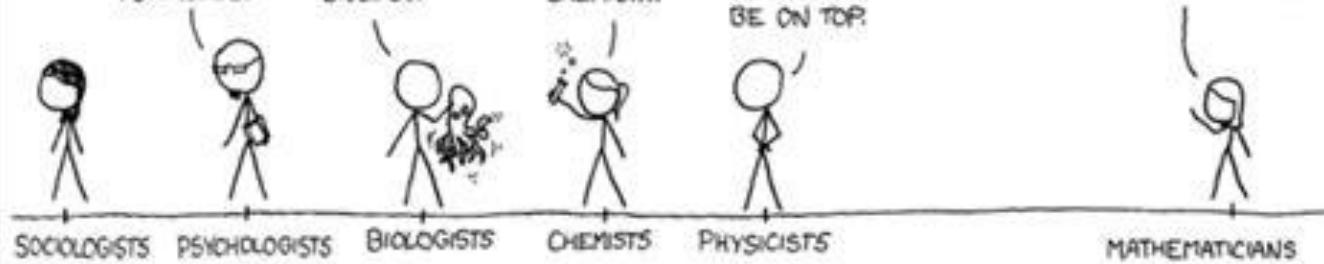
SOCIOLOGY IS  
JUST APPLIED  
PSYCHOLOGY

PSYCHOLOGY IS  
JUST APPLIED  
BIOLOGY.

BIOLOGY IS  
JUST APPLIED  
CHEMISTRY

WHICH IS JUST  
APPLIED PHYSICS.  
IT'S NICE TO  
BE ON TOP.

OH, HEY, I DIDN'T  
SEE YOU GUYS ALL  
THE WAY OVER THERE.



“Biology is the study of the complex things in the Universe.  
Physics is the study of the simple ones.” - Richard Dawkins

# Outline

(Questions welcomed anytime)

1. Evolutionary epidemiology
2. Spatial epidemic RG
3. All together

---

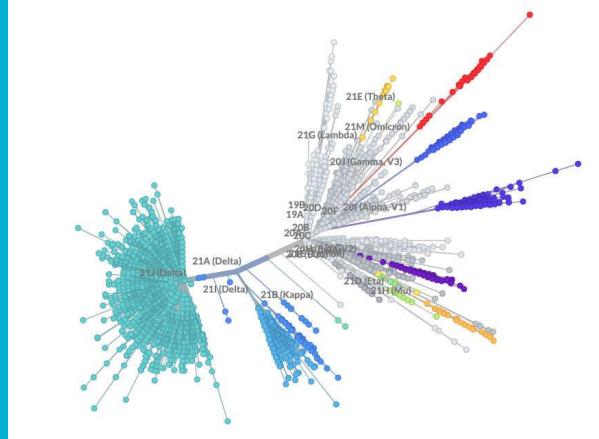
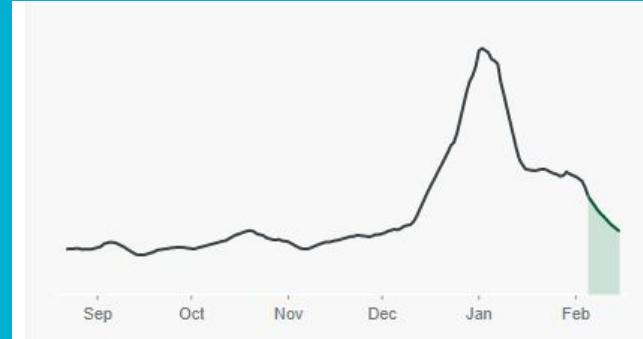
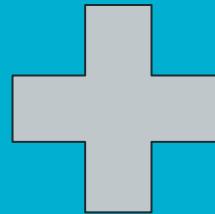
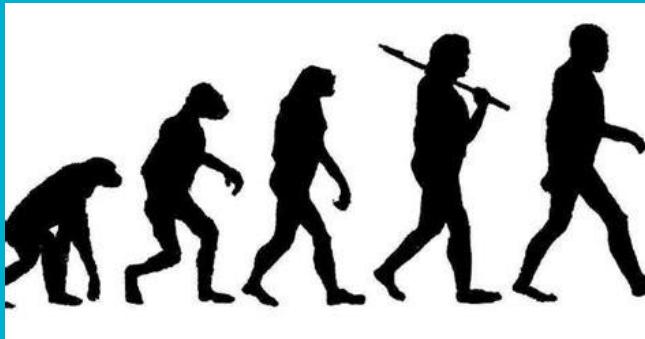
# 1. Evolutionary Epidemiology (my PhD with Julia Gog)



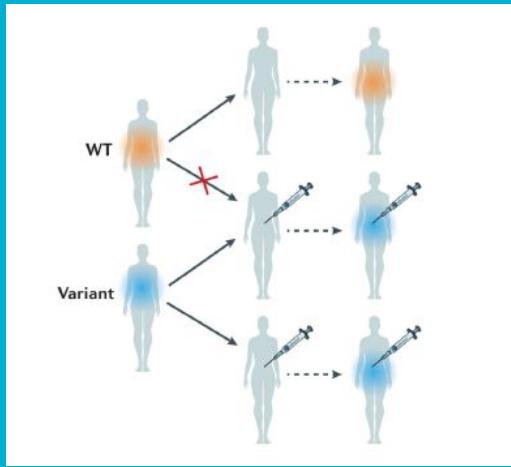
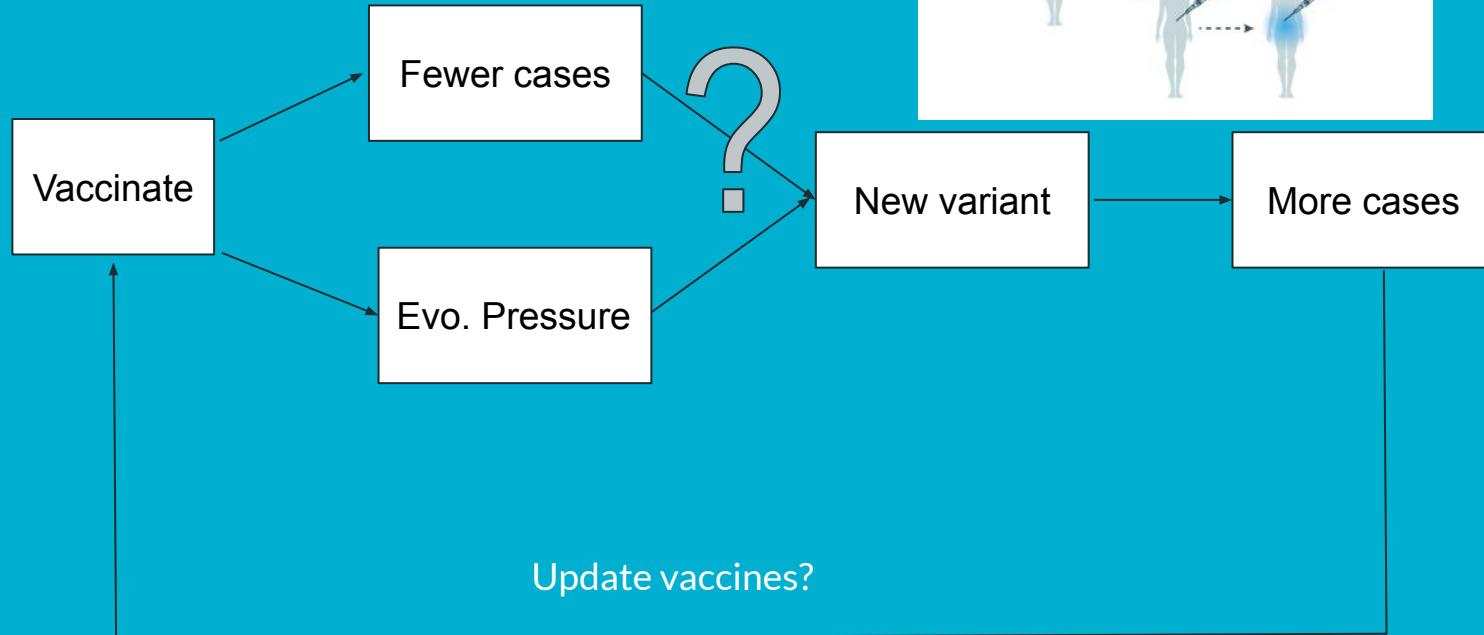
Seen in the light of evolution, biology is, perhaps, intellectually the most satisfying and inspiring science. Without that light it becomes a pile of sundry facts -- some of them interesting or curious but making no meaningful picture as a whole.

(Theodosius Dobzhansky)

# Wait, but what is “evolutionary epidemiology”?



# Add vaccines in...

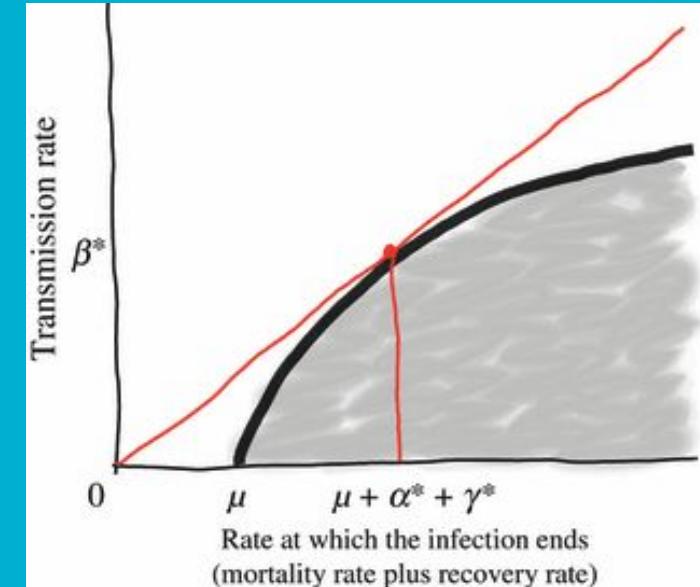


# Viral Evolution 101: the trade-off hypothesis

$$R_0 = \frac{\beta}{\mu + \alpha + \gamma}$$

Diagram illustrating the components of the basic reproduction number  $R_0$ :

- $\beta$  (Transmission)
- $\mu$  (natural deaths)
- $\alpha$  (mortality)
- $\gamma$  (recovery)



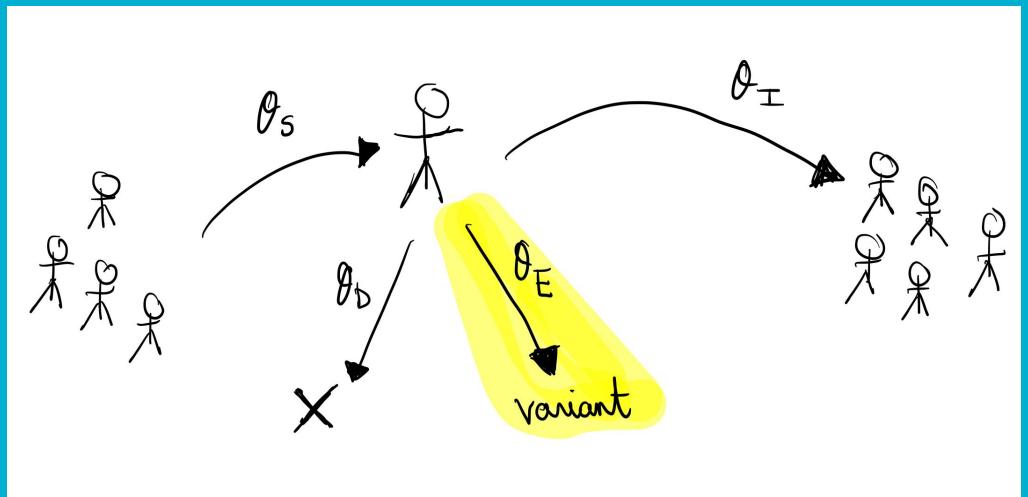
Alizon *et al.* Virulence evolution and the trade-off hypothesis: history, current state of affairs and the future. *J. Evo. Bio.*, 22: 245-259 (2009).

# thetaE

---

Q: Conditional on both getting infected, is a vaccinated host more or less likely to generate a variant that escapes the immunity from vaccines?

$$\theta_E < 1??$$



Vaccine efficacy:

$1 - \theta_S \theta_F$  : transmission blocking

$1 - \theta_S \theta_D$  : disease blocking

$1 - \theta_S$  : case blocking

$1 - \theta_S \theta_E$  : escape blocking

# “Phylogenetics”

$p \propto (\text{viral load}) \times (\text{strength of selection})$

(actually, the time-integral of the above!)

Naively,

$d \propto (\text{viral load})$

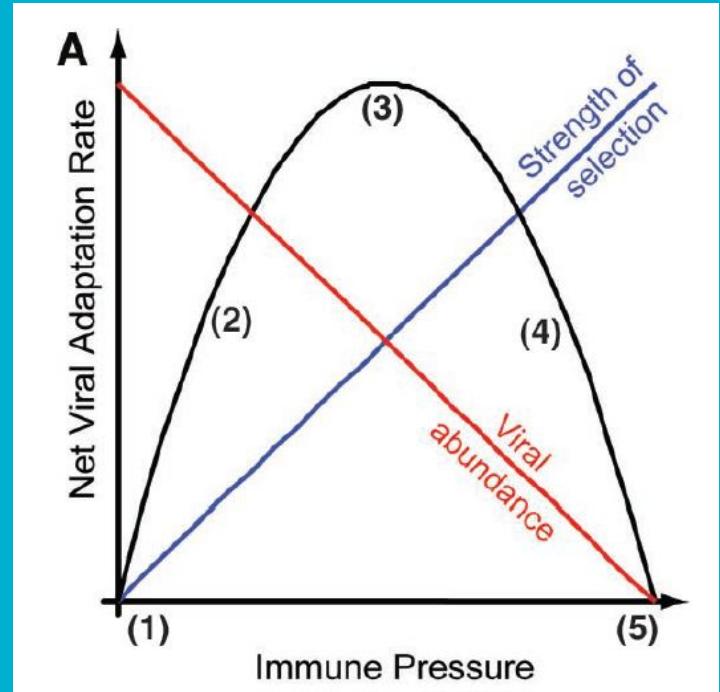
Say  $p_{i,unv} = \gamma d_{i,unv}$

but, due to selection after vaccines,

$$\gamma d_{i,vac} < p_{i,vac} = \gamma \frac{\theta_E}{\theta_D} d_{i,unv}$$

Hence...

$$\theta_E > \theta_D$$

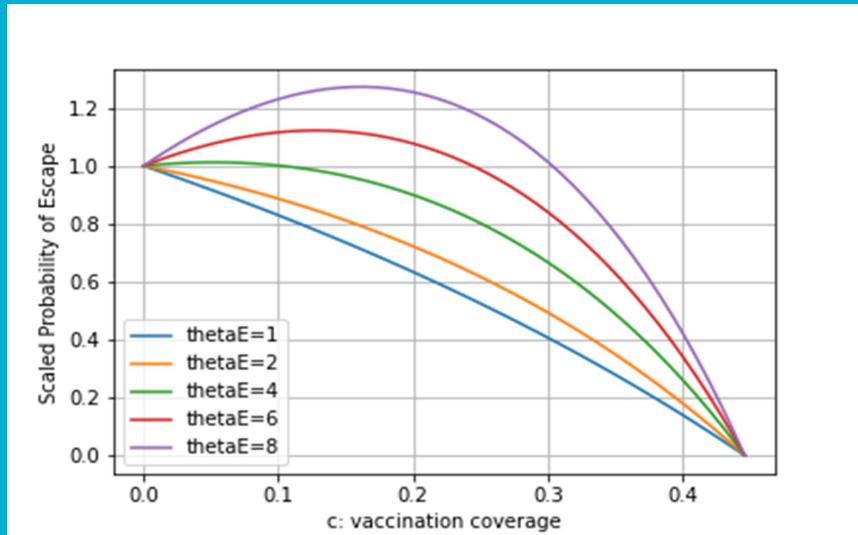
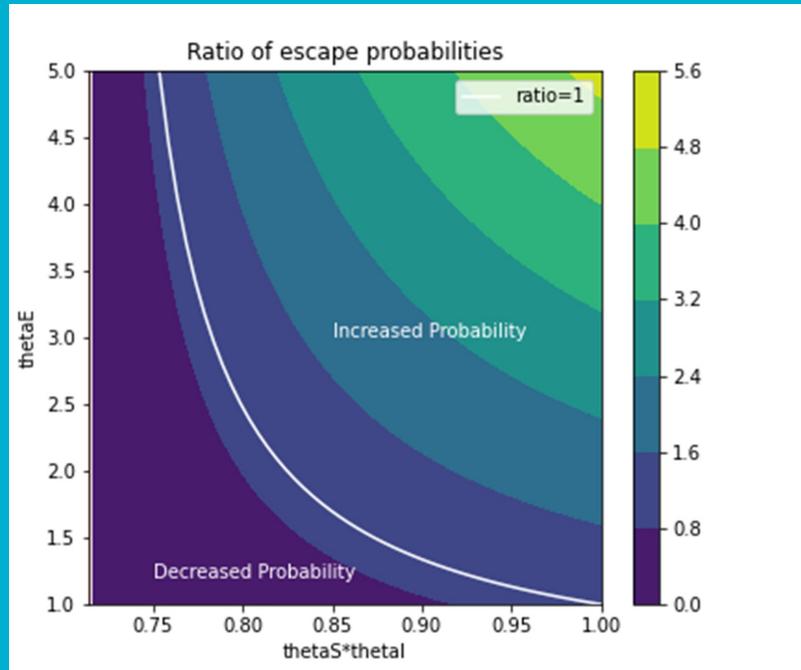


Grenfell et al., *Unifying the Epidemiological and Evolutionary Dynamics of Pathogens*, Science (2004)

# Population level results

---

$$P = p(N_{unvac.} + \theta_E N_{vac})$$



## 2. Spatial Epidemic RG (my Part III essay with Ronojoy Adhikari)

At the start of an  
epidemic, we don't  
know how big it's  
going to be!

# “Relevant” and “Irrelevant” operators

---

- Lots of things to model at different scales
  - eg individual movements,
  - households,
  - regional restrictions,
  - international travels
- Want to understand which matter
- “Relevant” operators: short-scale interactions -> long-range effects
- RG could tell us which bits are irrelevant -> simpler model

# Continuum Spatial Epidemic models

---

SIR model + diffusion

PDE... rescale

Find critical dimension

d=2

$$\dot{S} = -\beta SI + D\nabla^2 S \quad (4.2)$$

$$\dot{I} = +\beta SI - \gamma I + D\nabla^2 I \quad (4.3)$$

$$\dot{R} = \gamma I + D\nabla^2 R \quad (4.4)$$

We assume that the involved variables and terms rescale as

$$\mathbf{x} \rightarrow \zeta \mathbf{x} \quad (4.5)$$

$$t \rightarrow \zeta^z t \quad (4.6)$$

$$\beta \rightarrow \zeta^a \beta \quad (4.7)$$

$$\gamma \rightarrow \zeta^b \gamma \quad (4.8)$$

while keeping  $D$  invariant (as assumed in [15]) and the total number of individuals in each compartment also constant, i.e.  $S(t) \equiv \int S(\mathbf{x}, t) d^d x$  is invariant under the renormalization transformation. Here  $d$  is the dimension of the space we are working at (so usually for epidemics we take  $d = 2$ ). This means that each of the densities  $S, I, R$  scale as  $\zeta^{-d}$ . From the PDE system, we obtain

$$-z - d = a - 2d = b - d = -d - 2 \quad (4.9)$$

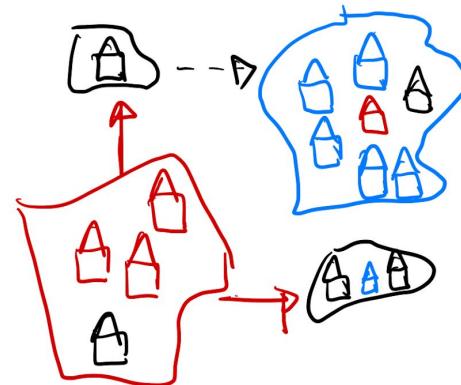
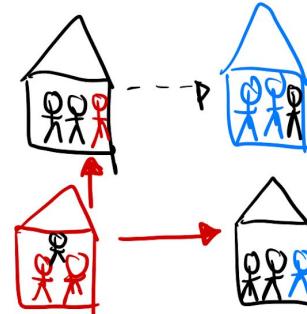
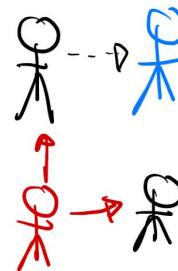
This implies that  $z = 2$ ,  $b = -2$  and  $a = d - 2$ . If this approach is reasonable, we could interpret our results by saying that the recovery term associated with  $\gamma$  is *irrelevant* for all dimensions  $d$  and  $d_c = 2$  is the critical dimension. For  $d = d_c = 2$ ,  $\beta$  is *marginal*, while for  $d < d_c = 2$  it is irrelevant, and for  $d > d_c = 2$  it is *relevant*. One could then perform an  $\epsilon$ -expansion around

# Are epidemics self-similar?

---

Dynamic networks: individuals, households, cities, countries...

RG could tell if they could have a critical point

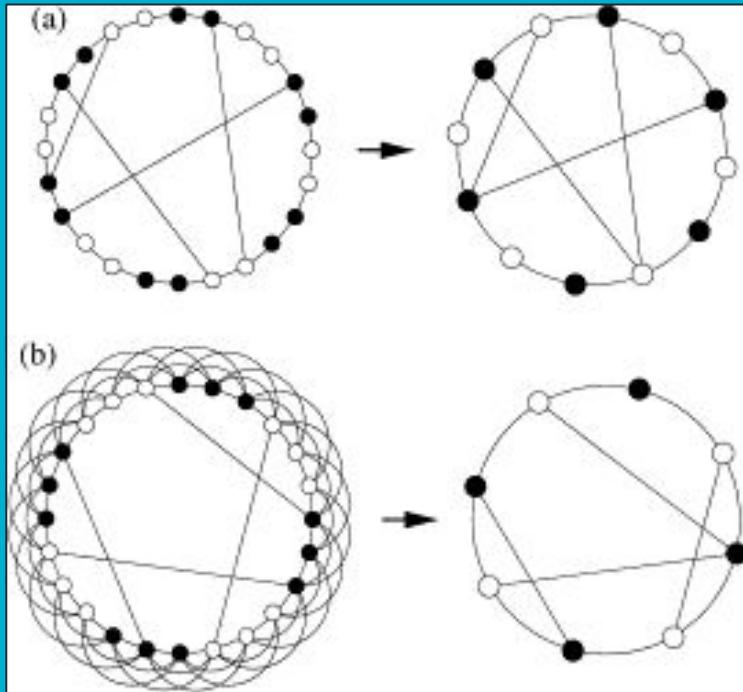


# Metapopulations

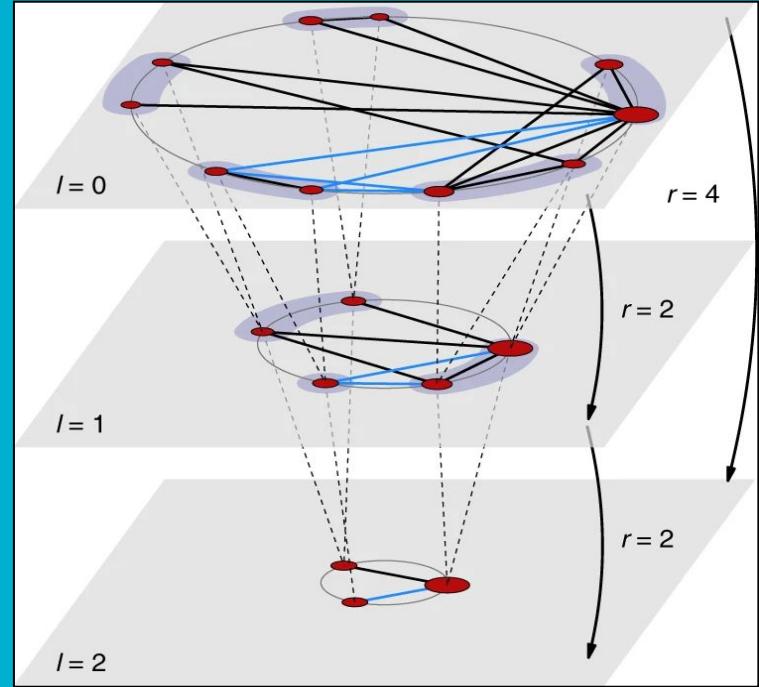
---

- Subdivide population, each “subpopulation” has independent dynamics + minimal cross-metapopulation interaction
- Potential RG flow? Take as continuum the metapopulation size,  $N$ 
  - $N \gg 1 \rightarrow$  Continuum model
  - $N=1 \rightarrow$  individual-based model
- Lattice-based models: forest-fire, cellular-automata, networks...

# RG for (small-world) networks



Newman and Watts, Renormalization group analysis of the small-world network model.  
*Phys. Letters. A*, 263, (4–6) 341–346, (1999).



García-Pérez et al. Multiscale unfolding of real networks by geometric renormalization.  
*Nature Phys* 14, 583–589 (2018).

# Emergence and information

---

“The major thing is to view biology as an information science” - Leroy Hood

*Dynamical independence: discovering emergent macroscopic processes in complex dynamical systems*, Barnett & Seth (arXiv preprint 2021)

- A coarse-grained macroscopic stochastic variable is dynamically independent if its past alone has the same information as the past of the underlying microscopic variables

At which scale does microscopic epidemic past date become redundant/useless for large scale epidemic predictions?

3. All together  
(potentially in the future?)

# Evolution occurs at multiple scales

---

Selection Pressure can be:

- **Within-Host:** viral load vs selection pressure
- **Between-Host:** transmitted shedding vs mucosal antibody protection
- **Population-Level:** number of cases vs existing immunity

Do all of these matter?

How do these interact with each other?

How should we link them?

# Is evolution self-similar?

---



$P(\text{variant from vaccinated host})$

---

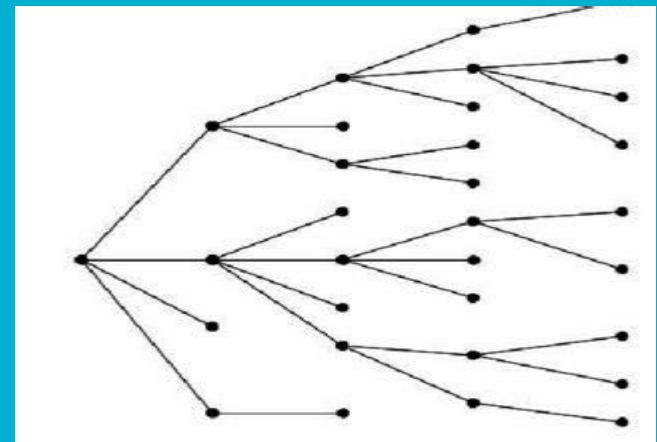
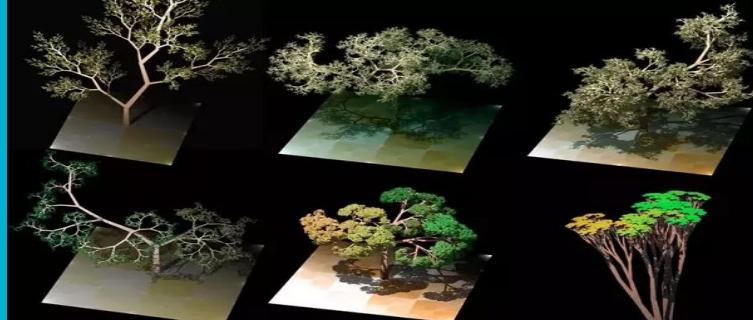
$P(\text{variant from unvaccinated host})$

$P(\text{variant from vaccinated country})$

---

$P(\text{variant from unvaccinated country})$

Could some phylogenetic trees be self-similar?



# Summary:

---

- Evolution during epidemic processes is complicated
  - Within-host uncertainty
  - Vaccines could also help from evo point of view
- Scales in epidemic processes are tricky
  - RG could help, many potential models
  - Don't have a general Lagrangian to work with
- Evolution operates at different scales
  - Understanding better the role of scales would help with evo understanding

# Thank You!

