Title: Percolation theory and exposure-based vaccination strategies

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Series: Mathematical Physics

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Abstract: Human contact patterns are highly heterogeneous in terms of the both the number and nature of interactions. To incorporate these heterogeneities into infectious disease models one naturally represents a population as a weighted network. While there is a large literature on the spread of diseases on networks, most techniques are highly computational in nature. In this talk I will talk about an analytical framework for modeling infectious diseases as a percolation process on weighted networks based on probability generating functions.

In the context of vaccination, human contact heterogeneities become a resource: Vaccinating individuals with greater total exposure leads to a greater reduction in disease spread. We have proposed that exposure notification apps, such as COVID Alert, can be leveraged to improve vaccine uptake among high exposure individuals, thereby optimizing our limited COVID-19 vaccine supply. We demonstrate the efficiency of this proposal using our weighted percolation theory framework.

Percolation theory and exposure-based vaccination strategies

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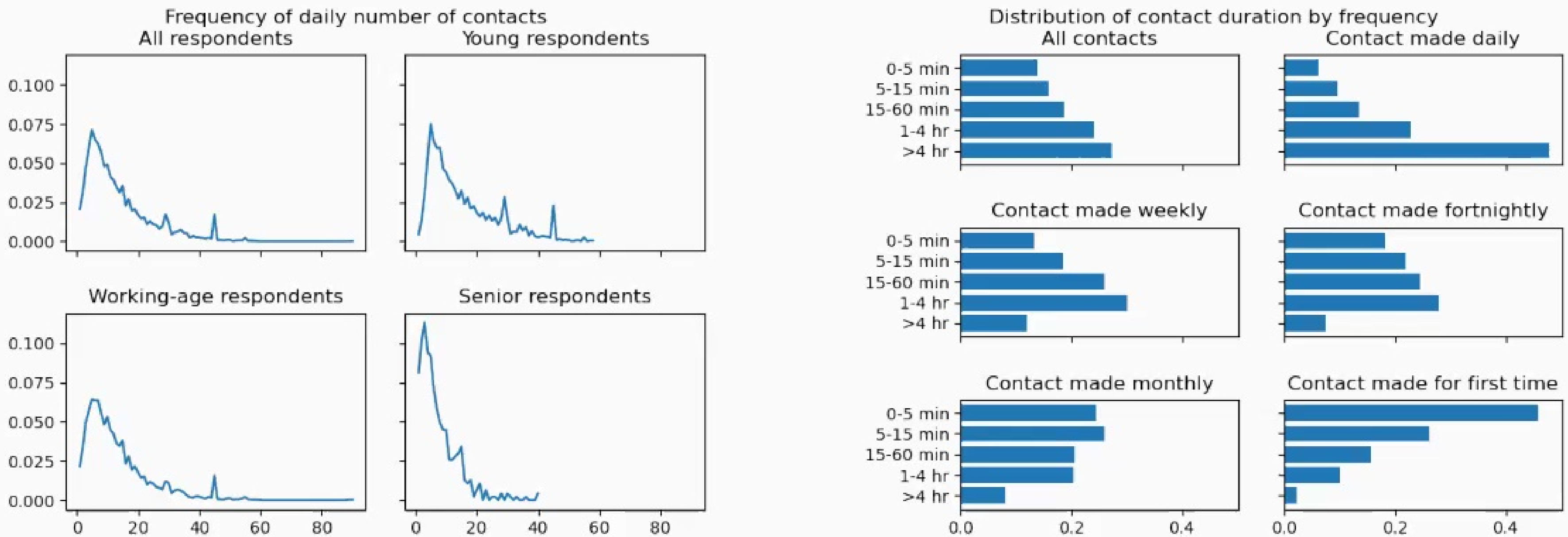
joint with: Y Yargic, L Smolin, E Thommes, M Anand, C Bauch

Contact patterns shape disease spread

Source: POLYMOD survey https://doi.org/10.1371/journal.pmed.0050074



Higher exposure $\Rightarrow$ increased risk of infection and spread to others

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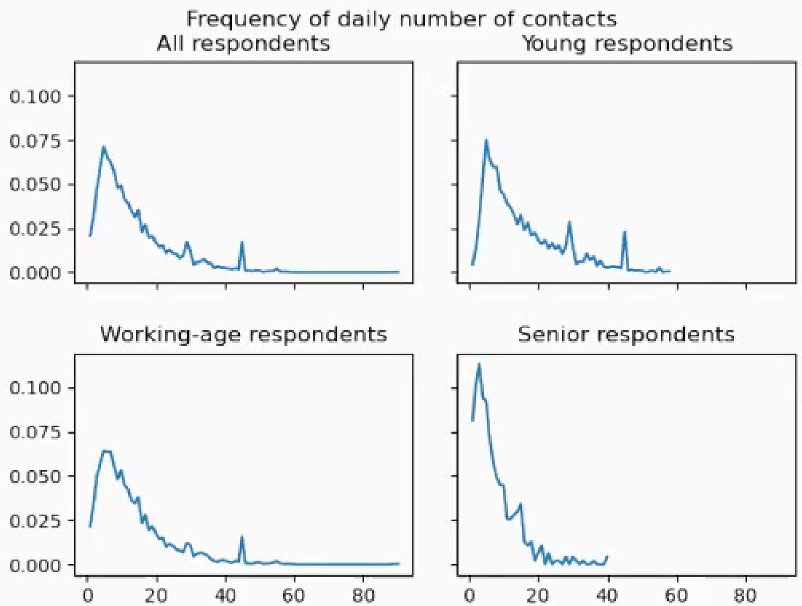

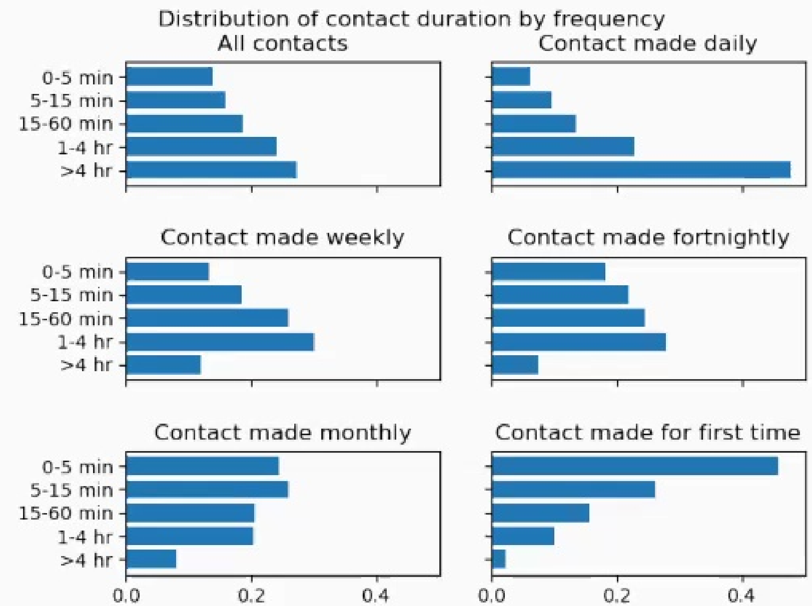

Higher exposure ⇒ increased risk of infection and spread to others

Heterogeneity is a resource:

Prioritise vaccination of high exposure individuals

How can these individuals be identified?

COVID Alert and other exposure notification apps

- Widespread adoption across developed world
- Periodic digital handshakes between nearby users
- Creates local, anonymous encounter log

- Cannot determine number or duration of contacts
- Length of encounter log = total exposure time to app users

“Hot-spotting” vaccine prioritisation strategy

High level idea

- Selection determined by number of entries in encounter log
- Decision made locally on each user’s device
  No personal information shared with public health authorities
- Allows for individualised selection while preserving privacy

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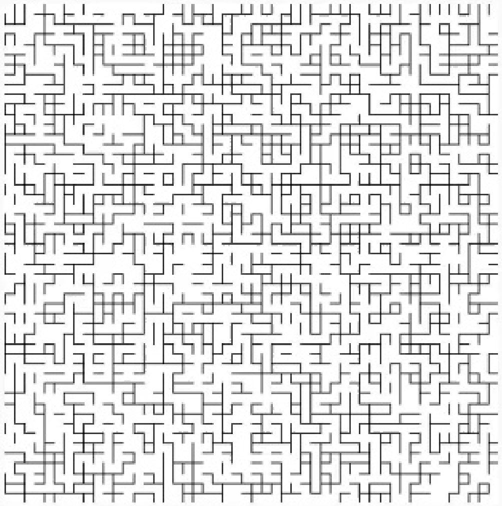
Particular proposal

- β-weighted coin flip for each entry
- Selected if ≥ 1 successes

Percolation on contact networks

Contact network
Vertices are individuals

$i \leftrightarrow j$: i and j in infectious contact



Percolation theory

- Edge occupied with probability T

  Occupied $\leftrightsquigarrow$ successful transmission

  Connected components $\leftrightsquigarrow$ outbreaks

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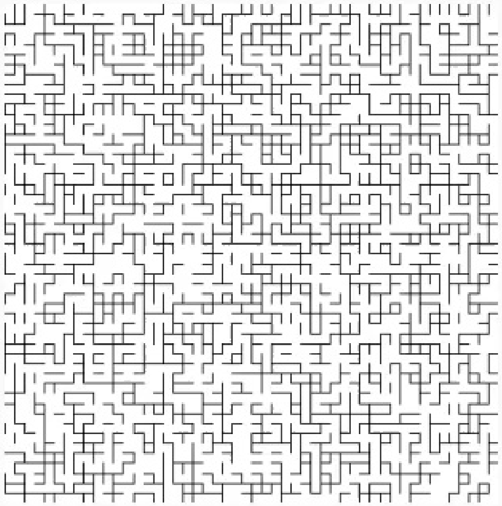

Percolation theory

- Edge occupied with probability T
  Occupied $\leftrightsquigarrow$ successful transmission
  Connected components $\leftrightsquigarrow$ outbreaks
- Phase transition at T_c
  Emergence of ‘giant’ component
  isolated outbreaks $\rightsquigarrow$ epidemic

Newman's formalism

Empirical contact networks

- Small scale: RFID / Bluetooth studies
- Large scale: Contact diary surveys
  Local information, e.g., number and duration of contacts

Contact network assumptions

- Random graph with specified degree distribution $\{p_k\}_{k \in \mathbb{Z}_{\geq 0}}$
  $P_{\mathrm{nbhr}}(k) \propto k p_k$
- Locally tree-like $\Leftrightarrow$ no clustering
- Large vertex limit

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Key object: Generating function for degree distribution

$$G_0(x) = \sum p_k x^k$$

Basic reproduction number

Definition

- $R_0(T) =$ Expected secondary cases from infected individuals
- infected individual $\leftrightsquigarrow$ vertex at end of occupied edge
- Secondary cases $\leftrightsquigarrow$ occupied edges - 1

Theorem (Newman 2002)

$$R_0(T) = T\left[\mu\left(1 + \frac{\sigma^2}{\mu^2}\right) - 1\right]$$

Proof sketch:

- dist. sec. cases $\leftrightsquigarrow$ $G_1(x;T) = \frac{1}{\mu}G_0'(1 + (x-1)T)$
  Why? at $T = 1$: $G_1(x;1) = \sum_k \frac{k\,p_k}{\mu} x^{k-1}$
  Random graph $\Rightarrow \mathrm{Prob}_{\mathrm{nbhr}}(k)\frac{k\,p_k}{\mu}$

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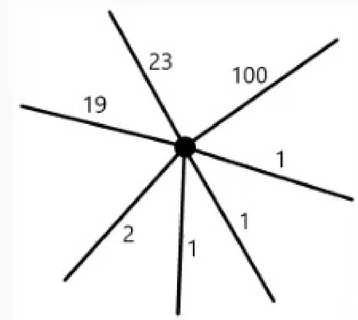
  Random graph $\Rightarrow \mathrm{Prob}_{\mathrm{nbhr}}(k)\frac{k\,p_k}{\mu}$
- $R_0 = \mathbb{E}\,[\mathrm{sec.\,cases}] = G_1'(1;T) = T\,\frac{G_0''(1)}{G_0'(1)}$

Percolation on weighted networks

Weighted contact networks: each edge is equipped with a weight w

Transmissibility T_w for each weight w



Generalized degree of a vertex:

$$\boldsymbol{k} = (k_{w_1}, k_{w_2}, \ldots, k_{w_{\max}})$$

Multi-variable generating function:

$$Q(\boldsymbol{y}) = \sum_{\boldsymbol{k}} q_{\boldsymbol{k}} \boldsymbol{y}^{\boldsymbol{k}} \,, \quad \boldsymbol{y}^{\boldsymbol{k}} = \prod_{w} y_w^{k_w}$$

Basic reproduction number on weighted networks

Theorem (P, Yargic, et al 2020)

$$R_0(\boldsymbol{T}) = \frac{\mathbb{E}\left[\left(\sum_i T_{w(i)}\right)^2 - \sum_i T_{w(i)}^2\right]}{\mathbb{E}\left[\sum_i T_{wi}\right]}$$

where: $\mathbb{E}[\cdot] \leftrightsquigarrow$ *expectation over vertices*

$\sum_i [\cdot] \leftrightsquigarrow$ *sum over adj. edges*

Proof sketch:

- dist. sec. cases $\leftrightsquigarrow \frac{\nabla_{\boldsymbol{T}} Q(x\mathbf{1})}{\nabla_{\boldsymbol{T}} Q(\mathbf{1})}$, where $\nabla_{\boldsymbol{T}} Q(\boldsymbol{y}) = \sum_w T_w \frac{\partial Q(\boldsymbol{y})}{\partial y_w}$
- $R_0(\boldsymbol{T}) = \frac{\nabla_{\boldsymbol{T}}^2 Q(\mathbf{1})}{\nabla_{\boldsymbol{T}} Q(\mathbf{1})}$

  Compare: $R_0(T) = T \frac{G_0''(1)}{G_0'(1)}$

Weights represent contact duration

- Per-unit time transmissibility $T \Rightarrow T_w = 1 - (1 - T)^w$
- Total exposure time = weighted degree = $\sum_i w(i)$

Corollary (P, Yargic, et al 2020)
If $wT << 1$ for all weights w,

$$R_0 \approx T\left[\hat{\mu}\left(1 + \frac{\hat{\sigma}^2}{\hat{\mu}^2}\right) - \delta_2\right] \, ,$$

where $\hat{\mu}$, $\hat{\sigma}$ moments of weighted degree distribution, δ_2 moment of duration distribution

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$\Rightarrow$ COVID Alert measures epidemiologically significant quantity

Modelling vaccination

- Vaccination: Stochastic process which removes vertices
- $v(\boldsymbol{k})$: vaccination probability of a degree-$\boldsymbol{k}$ vertex
- R^v: reproduction number of residual network

Theorem (P, Yargic, et al 2020)

$$\mathbb{E}\left[R^v\right] = \frac{\mathbb{E}\left[(1-v(\boldsymbol{k}))\left\{\left(\sum_i \tilde{T}_{w(i)}\right)^2 - \sum_i \tilde{T}^2_{w(i)}\right\}\right]}{\mathbb{E}\left[(1-v(\boldsymbol{k}))\sum_i \tilde{T}_{w(i)}\right]}$$

where $\tilde{T}_w = T_w \varphi_w$ *and* $\varphi_w = 1 - \mathbb{E}\left[k_w v(\boldsymbol{k})\right] / \mathbb{E}\left[k_w\right]$

Comparing vaccination strategies

Limited vaccine supply

- V : Vaccine coverage $\leftrightsquigarrow$ fraction of vertices removed
- Goal: greatest possible reduction in R^v at fixed V

Definition
Efficiency of vaccine allocation:

$$E^v = \frac{1 - R^v/R_0}{V}$$

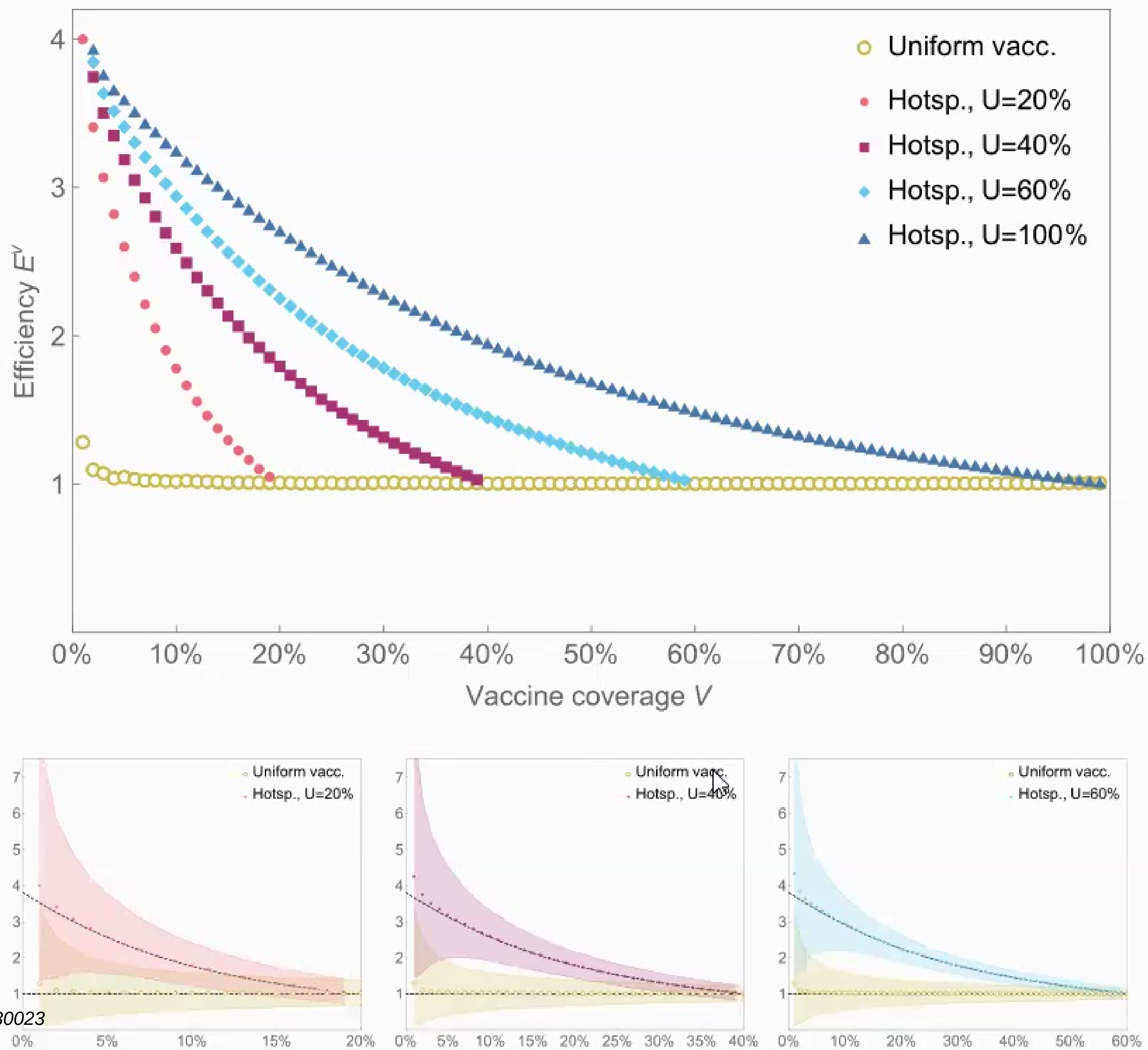
Normalized at $\mathbb{E}\left[E^{\mathrm{uni}}\right] = 1$ for the uniform strategy

Hot-spotting strategy for vaccine allocation

- Implemented on COVID-19 contact tracing apps
- Selection: Success on β-weighted coinflips
  Prob of success on K trials $= 1 - (1-\beta)^K$
- Fraction U of population uses app

$$v(\boldsymbol{k}; \beta, U) = U\left(1 - \prod_w \gamma_w^{k_w}\right), \quad \gamma_w = 1 - U + U(1-\beta)^w$$

Plots: E^v



<u>Features:</u>

$E^v > 1$

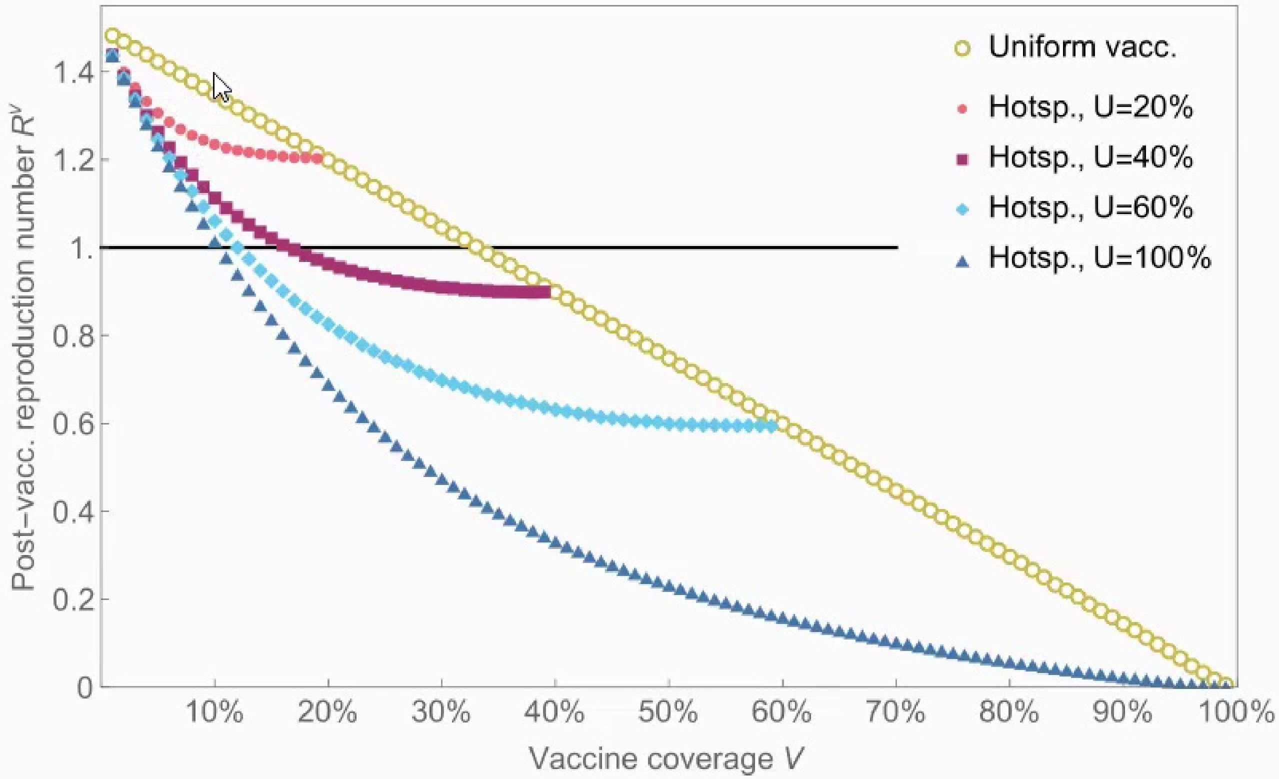
confidence

efficient even at low U

V/U is key

(indep. of T)

Plots: R^v



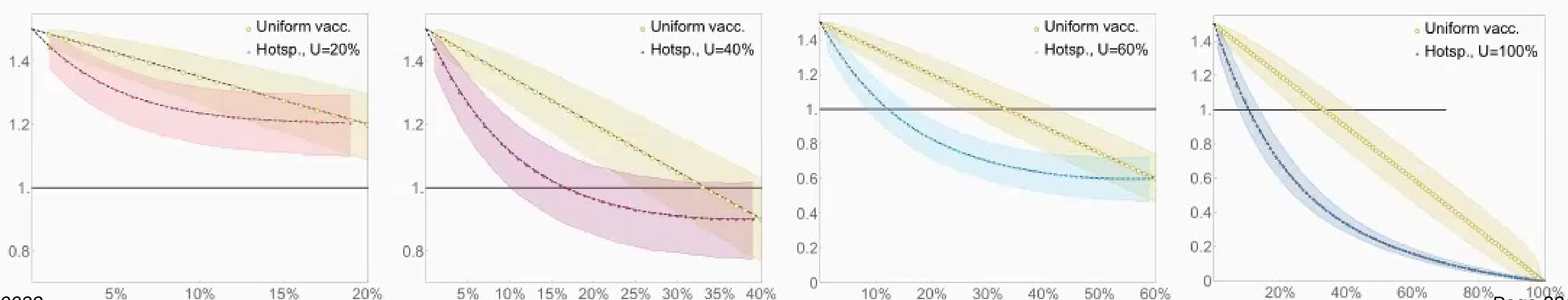
Features:

$R^v < R^{v_{\mathrm{uni}}}$

convex shape

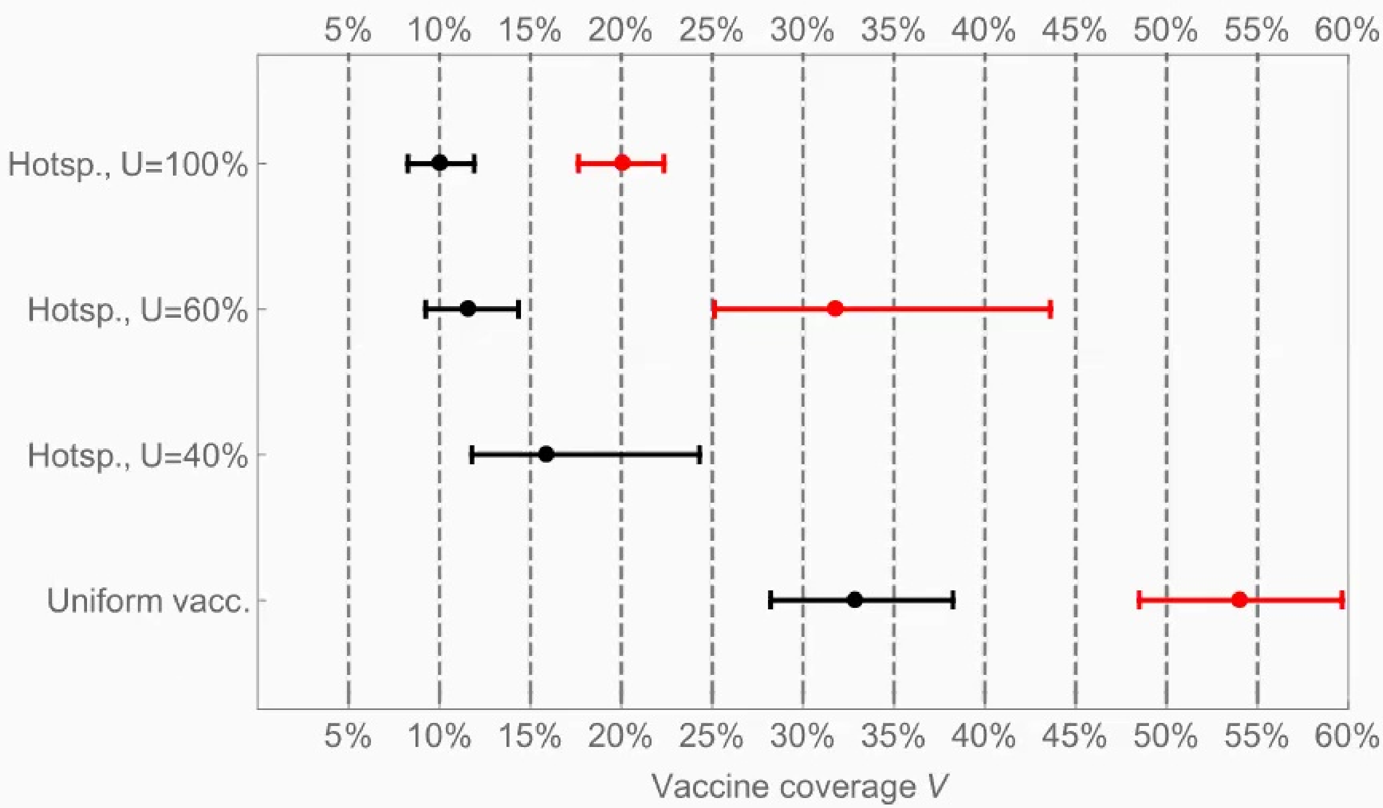
herd imm.
at lower V

greatest diff.
at $V/U \sim 1/3$



Plots: Herd immunity

The necessary vaccine coverage to reach herd immunity (black is for $R_0 = 1.5$, red is for $R_0 = 2.2$)



$$V_H = \frac{1}{E^v(V_H)}\left(1 - \frac{1}{R_0}\right)$$

Future directions

- Temporal dynamics: Degree based mean field
  Agent-based model
- Promotional approach: App promotes uptake
  Behavioural aspects: Vaccine hesitancy, conversion success
  Current results $\Leftrightarrow$ 100% hesitancy, 100% conversion success

Thank you!