Evaluating the predictive power of R_0 in wildlife populations:

dueling timescales of host movement and disease dynamics

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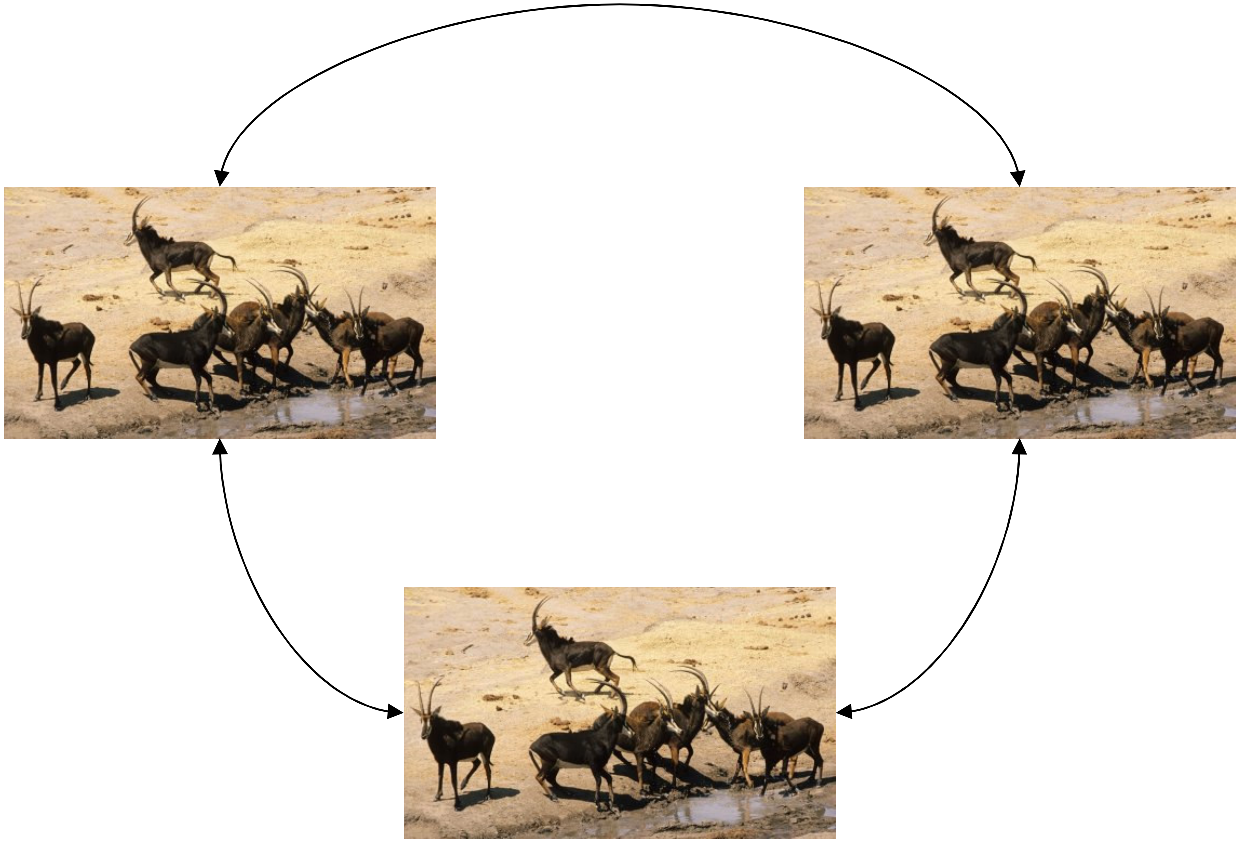
Our question:

- Why does a given disease affect some species much more than other species?

- Potential answers:
  - Immunological differences
  - **Behavioral differences**

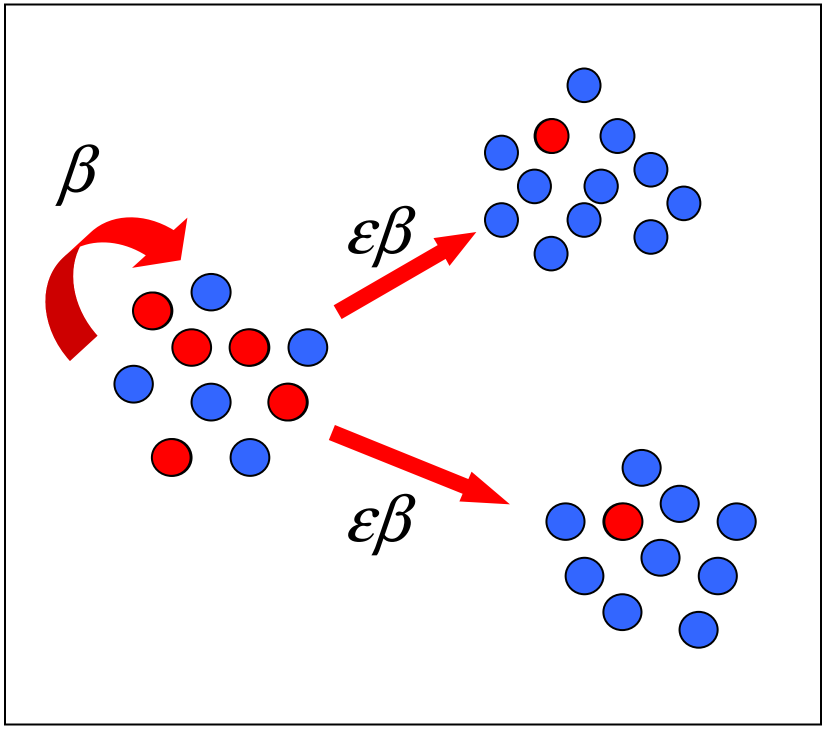
Population structure



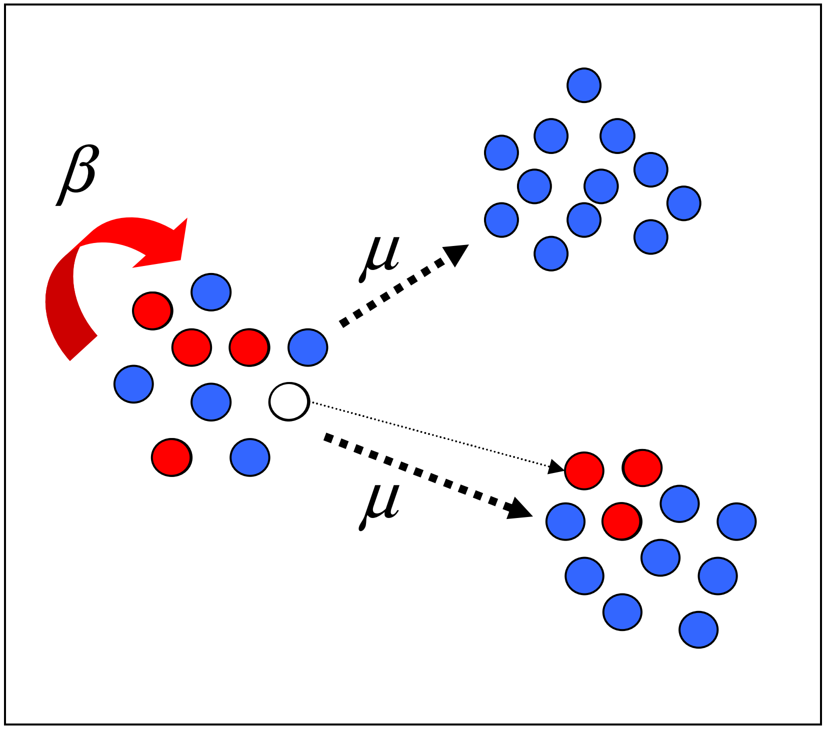
Outline

- Why structure matters
  - Phenomenological coupling
  - Mechanistic coupling
- Our model
- Threshold metrics for disease invasion
  - R_0
  - R_*
- Decision tree prediction of invasion

Why structure matters



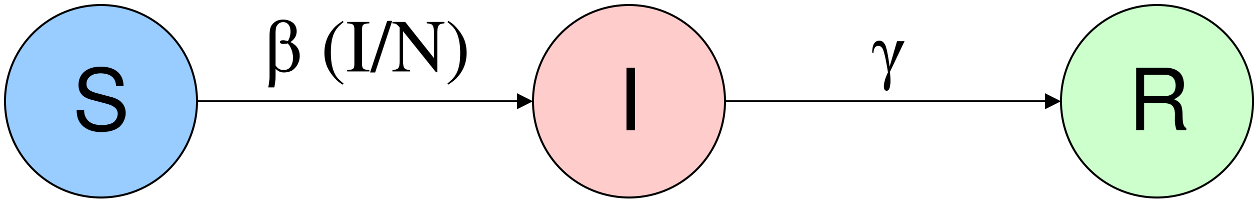
Phenomenological coupling



Mechanistic coupling

Keeling & Rohani (2002): phenomenological coupling is OK when mixing is fast.

Discrete SIR Model

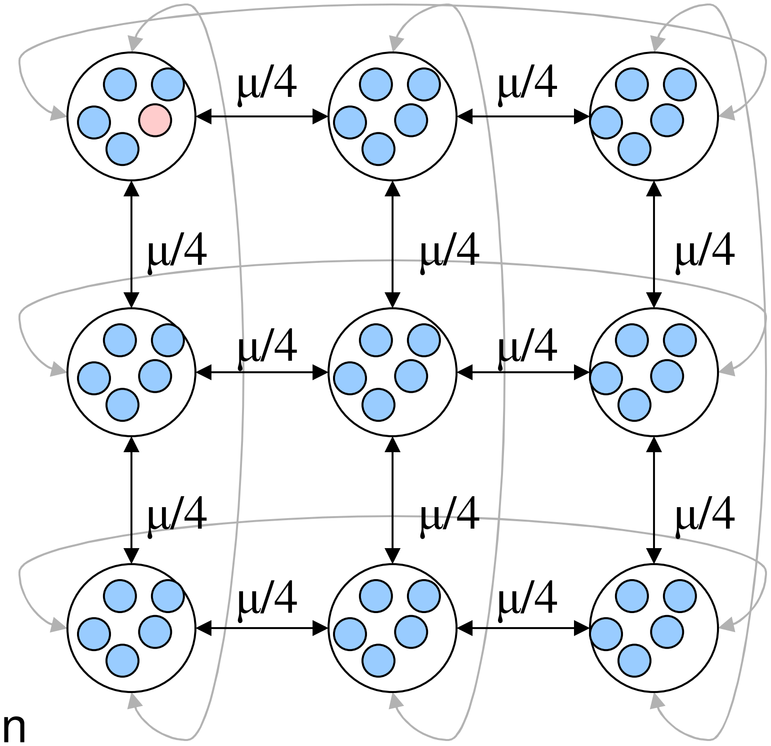


Parameters

β – force of infection

γ – Pr(recovery)

But what about the herds?



Parameters

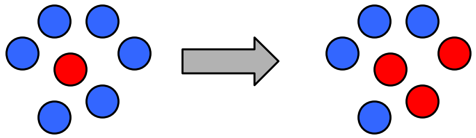
β – force of infection
γ – Pr(recovery)
μ – Pr(movement)
n – group size

Simulation

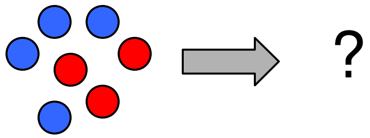
- Discrete-time, nonhomogenous Markov chain
- Initial state: one infected host in one group
- Transition matrices
  - Spatial: 11x11 torus = 1210 groups = 1210x1210 matrix
  - Disease: S,I,R states – 3x3 matrix where S→I transition depends on *I* and *n*

R_0: The basic reproductive

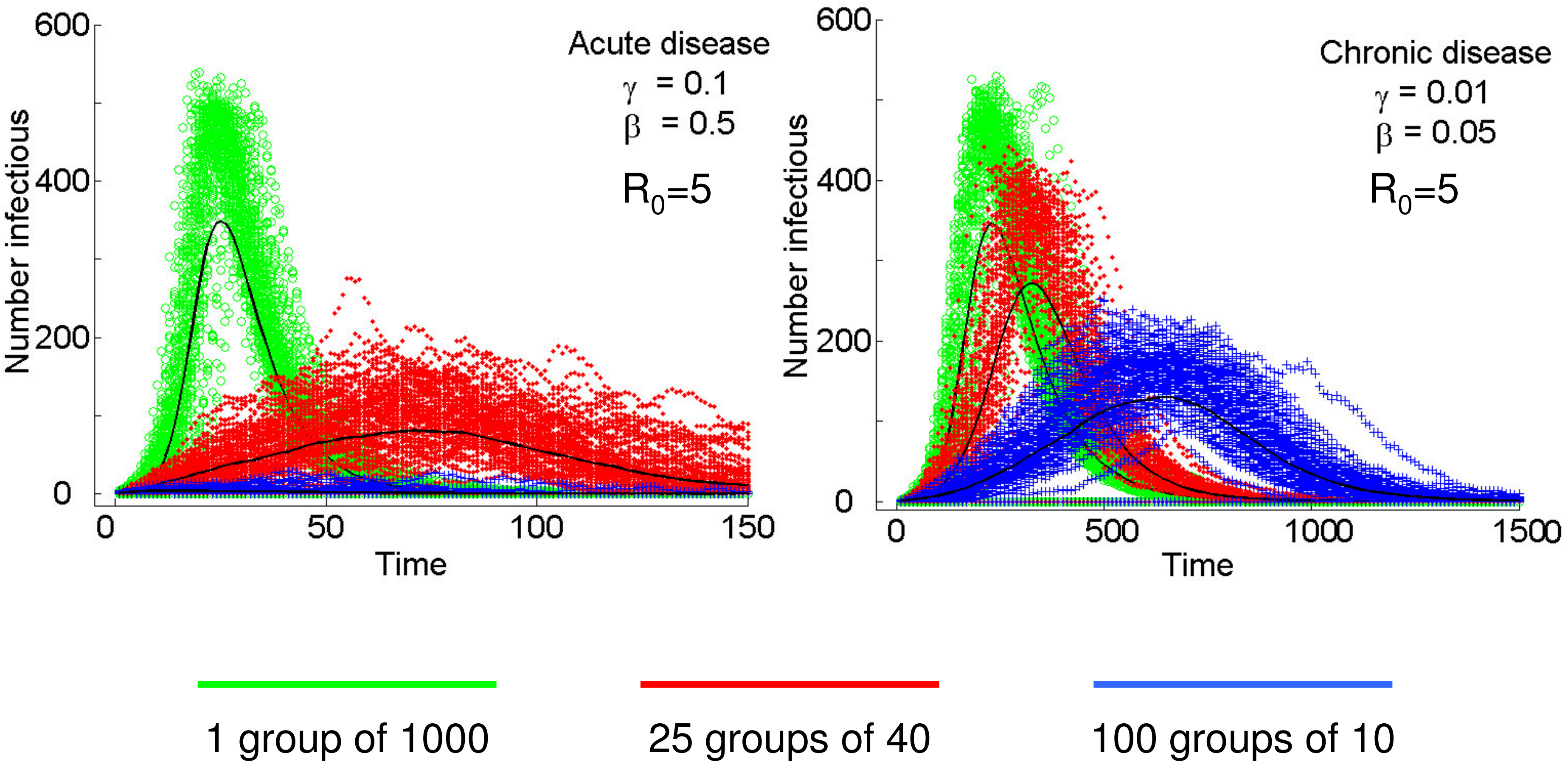
- How the theoreticians see it:
  - **expected** number of new infections caused by a single index case in an **infinite** population where **everyone** is susceptible.



- How it is often interpreted:
  - extrapolation of $R_0 > 1$ threshold to real-life **stochastic** contacts, **finite** population, **depletion** of susceptible pool



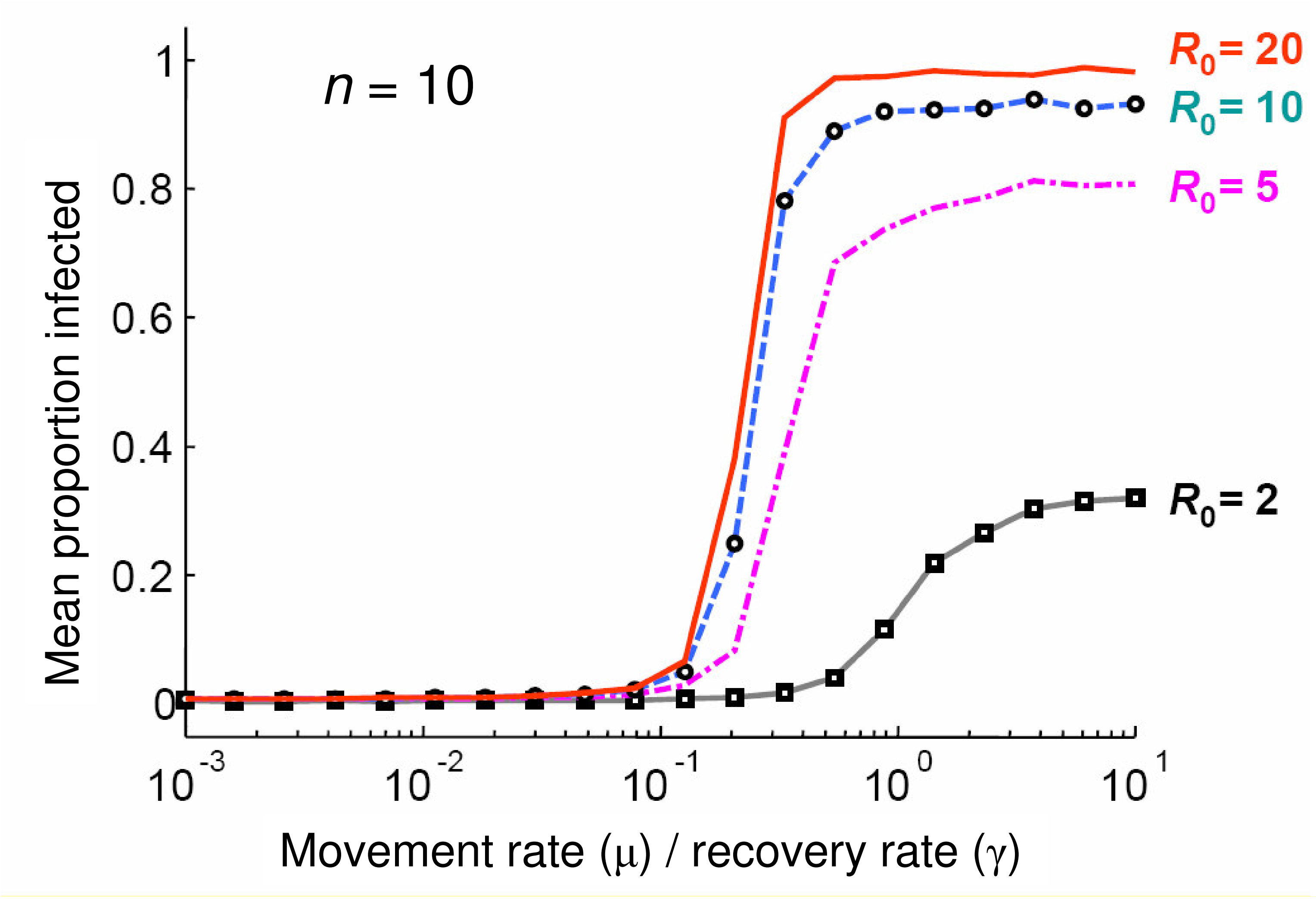
Why structure **really** matters



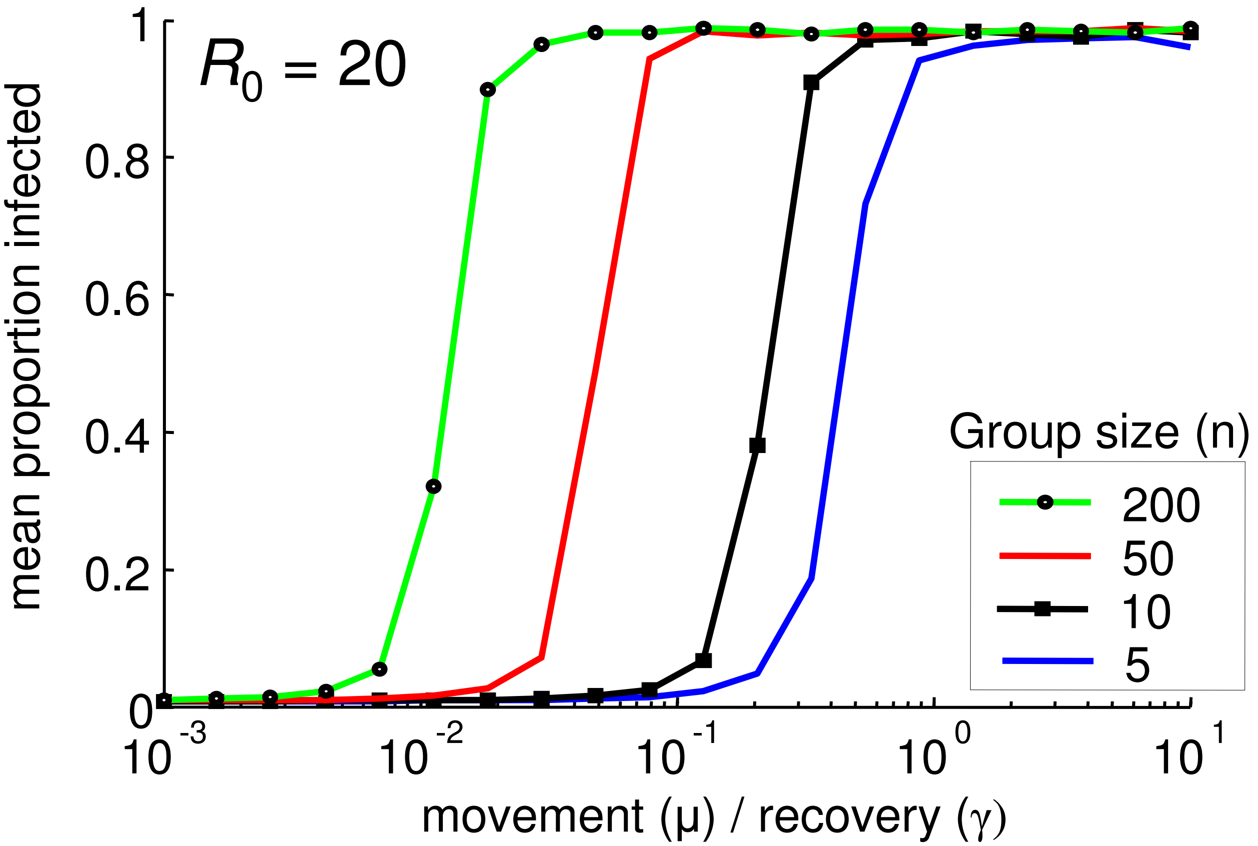
R_*: taking R_0 to the next level

- expected number of new infected **groups** caused by a single initially infected group in a population with infinite susceptible groups
- First coined by Ball *et al.* 1997
- Calculating R_*
  - ☐ analytic
  - ☐ **simulation**

Effect of movement (μ)

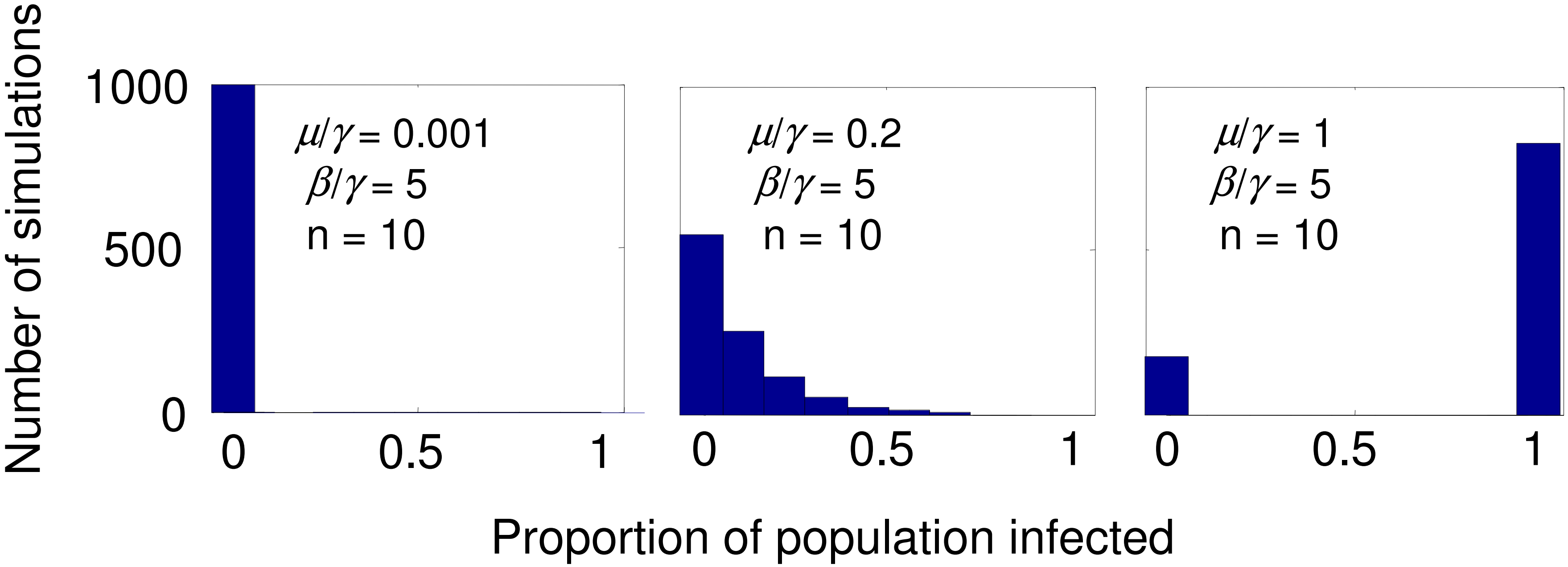


Effect of group size (n)



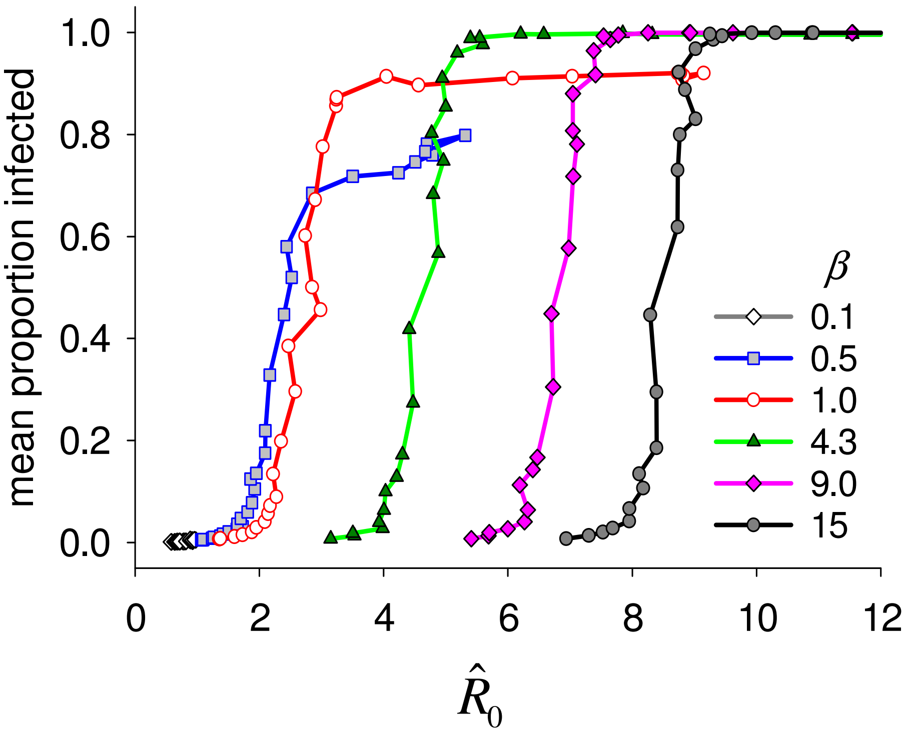
Rule of thumb for high R_0: $n \cdot \mu / \gamma > 1$

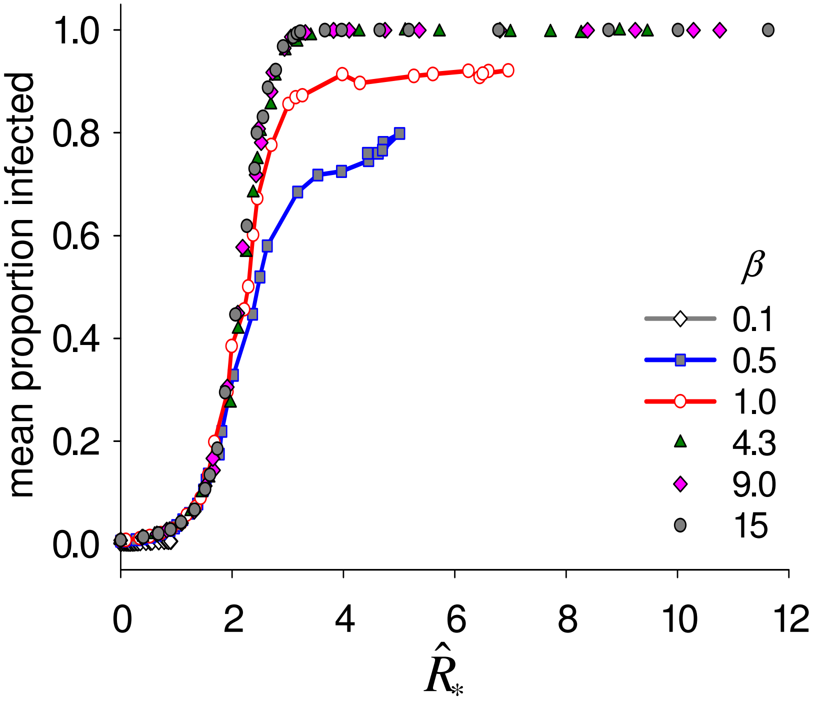
Effect of stochasticity



→ R_0>1 and movement necessary but not sufficient

Empirical R_0 versus R_*





➡ R_* predicts better than R_0

A problem: how to predict?

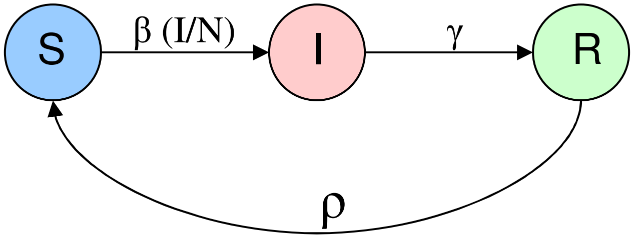
- R_* is great, but cannot be calculated beforehand
- R_0 is easy to calculate, but runs into trouble as a predictor

- What to do, what to do?

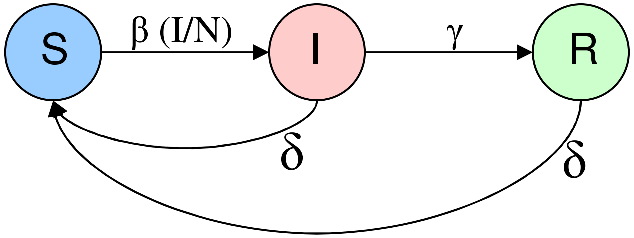
Classification trees to the rescue!

- Past applications:
  - Clinical risk assessments
  - Growing use in ecological literature
- Goal: minimize misclassification rate of response variable (disease invasion) via binary decision tree
- Heuristic penalty used to avoid huge trees

SIRS & SIR-bd

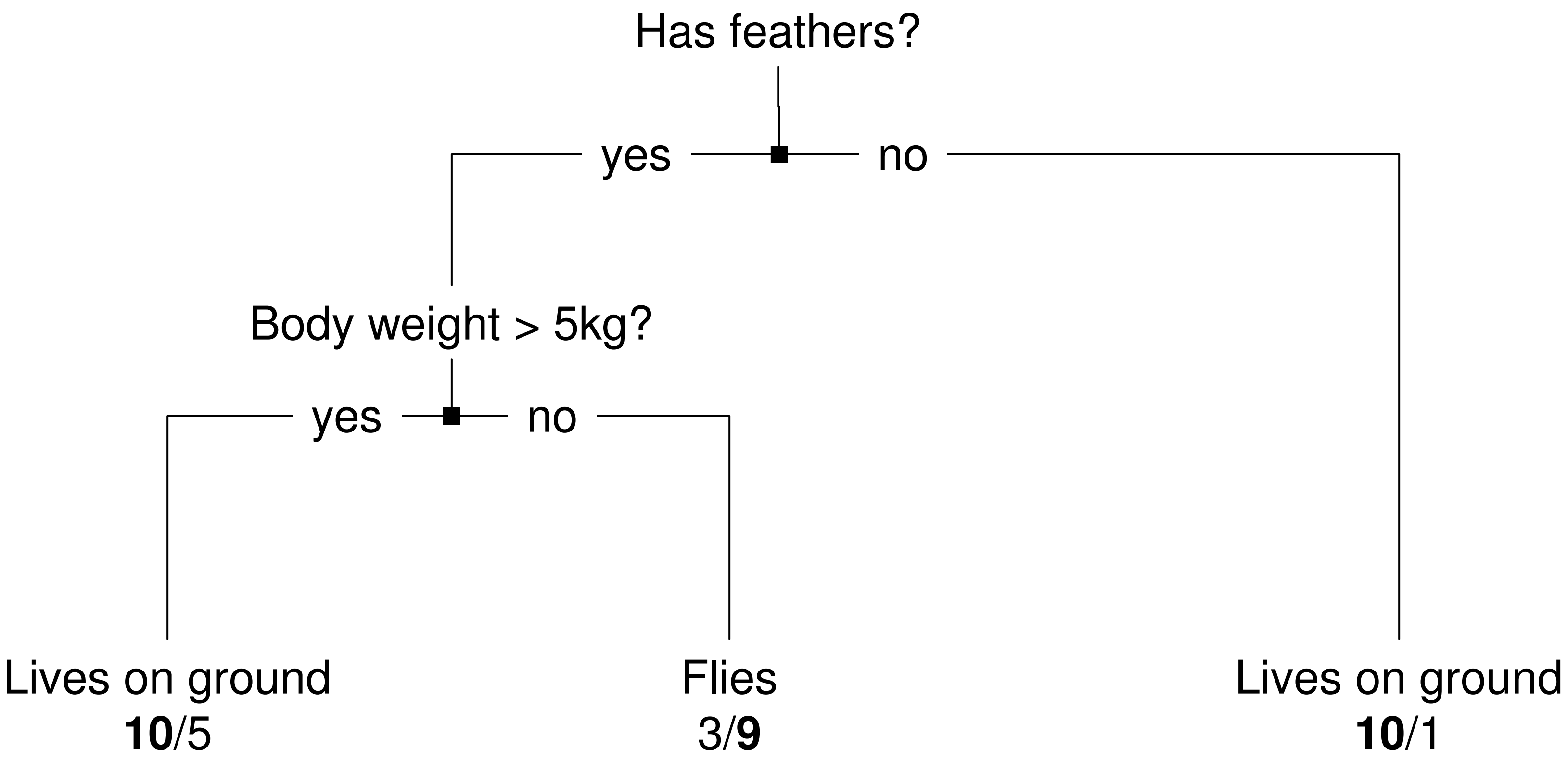


$R_0 \approx \beta/\gamma$



$R_0 \approx \beta/(\gamma+\delta)$

Hypothetical classification tree



Has feathers?

yes

no

Body weight > 5kg?

yes

no

Lives on ground
10/5

Flies
3/**9**

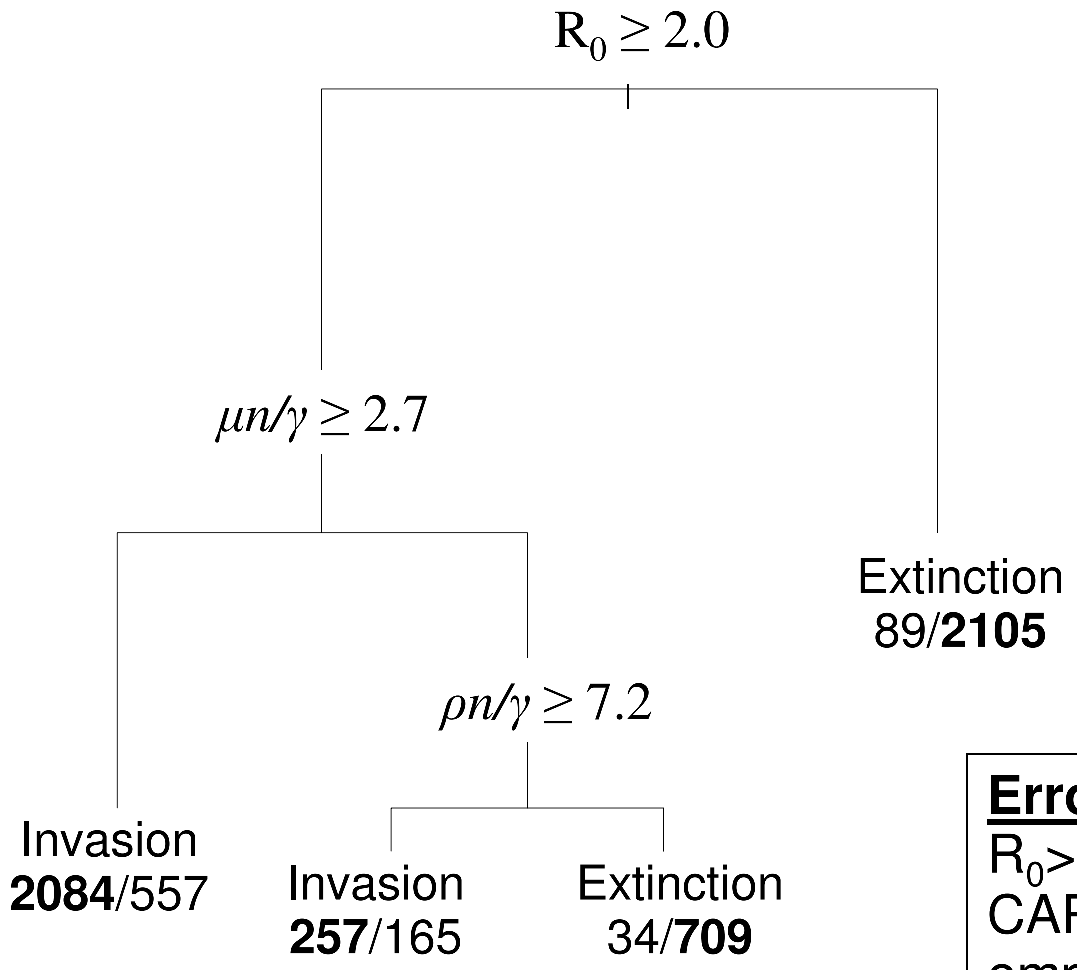
Lives on ground
10/1

Misclassification (error) rate: (5+3+1)/28 = 0.32

CART method

- Aggregate, measurable parameters:
  - β/γ (R_0)
  - $\mu \cdot n/\gamma$ (previous rule of thumb)
  - $\rho \cdot n/\gamma$ or $\delta \cdot n/\gamma$ (influx of new susceptibles)
- Other combinations possible (including raw parameters)

CART results



$R_0 \geq 2.0$

$\mu n/\gamma \geq 2.7$

Extinction
89/**2105**

$\rho n/\gamma \geq 7.2$

Invasion
2084/557

Invasion
257/165

Extinction
34/**709**

Error rates

$R_0>1$: 0.35

CART: 0.14

empirical $R_*>1$: 0.097

Recap

- Model design
  - Population structure critical
  - Mechanistic host movement
- Single predictors
  - R_0 gives high false-positives
  - R_* best, but no way to calculate
- CART's **measurable** parameters
  - R_0, $\mu \cdot n/\gamma$, $\rho \cdot n/\gamma$

Acknowledgements

- Getz Lab

- For more info:
  - Cross, et al. (2005) *Ecology Letters* **8**:587-595
  - Cross, et al. (submitted) *J R Soc Interface*