Eco-evolutionary dynamics of pathogen virulence

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Outline

- 1 Overview
 - The evolution of host-pathogen theory
 - Toy models
- 2 Transient virulence and emerging diseases
 - Overview
 - Toy model
 - Myxomatosis data
- Transient virulence and seasonality
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 - Toy model
 - WNV data
- 4 More on theory vs. data
 - Tradeoff curves
 - Conclusions



Discovery grant

Acknowledgements

People Arjun Nanda and Dharmini Shah; Christophe Fraser; Marm Kilpatrick; Anson Wong Support NSF IRCEB grant 9977063; QSE³ IGERT; NSERC

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Host-pathogen evolutionary biology

Why is it interesting?

- Intellectual merit
 - Coevolutionary loops
 - Cryptic effects
 - Eco-evolutionary dynamics (Luo and Koelle, 2013)
 - Cool stories
 - Lots of data (sometimes)
- Broader applications
 - Medical
 - Conservation and management
 - Outreach

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Virulence: definitions

- General public: badness
- Plant biologists: infectivity
- Evolutionists: loss of host fitness
- Theoreticians: rate of host mortality (mortality rate vs. case mortality vs. clearance)

Classical dogma monotonic trend toward avirulence

Ewald era virulence as an evolved (adaptive) trait. Tradeoff theory, modes of transmission.

post-Ewald more formal tradeoff models, mostly based on R_0 optimization. Adaptive dynamics

Now

- tradeoff backlash
- within-host dynamics/multi-level models
- eco-evolutionary dynamics
- host effects: resistance vs tolerance vs virulence

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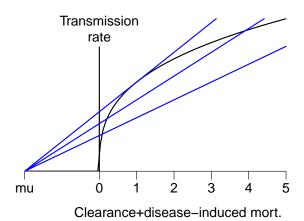
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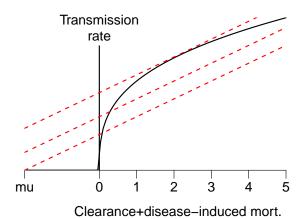
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- host effects: resistance vs tolerance vs virulence

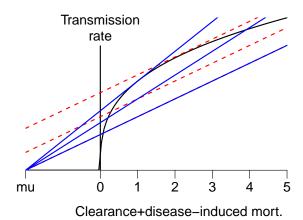
- Homogeneous, non-evolving hosts
- No superinfection/coinfection
- Horizontal, direct transmission
- Tradeoff between rate of transmission and length of infectious period
- Infectious period \propto 1/clearance (= recovery+disease-induced mortality+natural mortality)

Tradeoffs, \mathcal{R}_0 , and r





Tradeoffs, \mathcal{R}_0 , and r



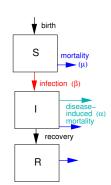
- Overview

 - Toy models
- - Toy model



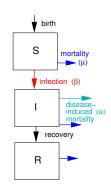
SIR model

- Constant population size
- Ignore recovery
- Rescale: $\mu = 1$, N = 1 (time units of host lifespan

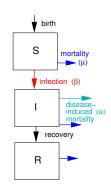


Epidemiological model

- SIR model
- Constant population size (birth=death)
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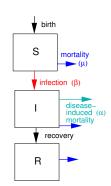


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Incorporate trait dynamics

Standard quantitative genetics model (Abrams, 2001):

- Fitness depends on mean trait value $(\bar{\alpha})$ and ecological context (proportion susceptible)
- ullet Constant additive genetic variance V_g
- Trait evolves toward increased fitness: rate proportional to Δfitness/Δtrait

Alternatives

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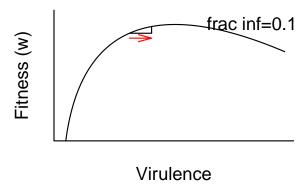
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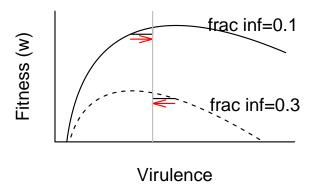
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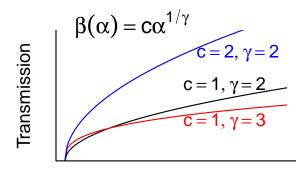
Evolutionary dynamics, cont.



Evolutionary dynamics, cont.



Power-law tradeoff curves



Virulence

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- Pathogens with low virulence go unnoticed
- Hosts less resistant to / tolerant of novel parasites
- High transmission \rightarrow frequent coinfection \rightarrow selection for virulence
- Disease-induced drop in population density decreases selection for virulence (Lenski and May, 1994)

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Transient virulence

Selection differs between the **epidemic** and **endemic** phases of an outbreak (Frank, 1996; Day and Proulx, 2004)

endemic phase selection for per-generation offspring production: maximize R_0 , $\beta N/(\alpha + \mu)$

epidemic phase selection for per-unit-time offspring production: maximize r, $\beta N - (\alpha + \mu)$

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Transient emerging virulence

When a parasite previously in eco-evolutionary equilibrium emerges in a new host population (at low density) it will show a transient peak in virulence as it spreads

How big is the peak? Does it matter?

Outline

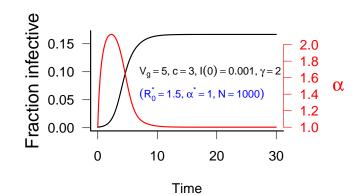
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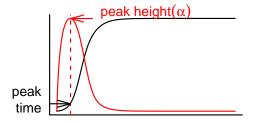
Model parameters

Parameter		Alternative	
С	Transmission	$\overline{\mathcal{R}_0^*}$	Equilibrium \mathcal{R}_0
	scale	-	
γ	Transmission	α^*	Equilibrium
	curvature		virulence
<i>I</i> (0)	Initial	$1/N_0$	Inverse
	epidemic size		population size
	Genetic variance		

Example

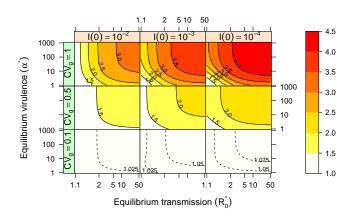


Response variables



Time

Peak height



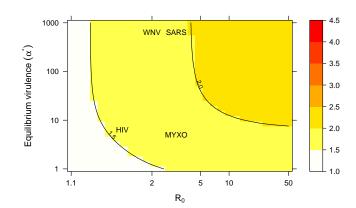
Estimates for emerging pathogens

Order of magnitude estimates for some emerging high-virulence pathogens:

Pathogen	R_0^*	α^*	Reference
SARS	3	640	Anderson et al. (2004)
West Nile	1.61 - 3.24	639	Wonham et al. (2004)
HIV	1.43	6.36	Velasco-Hernandez et al. (2002)
myxomatosis	3	5	Dwyer et al. (1990)

Emerging pathogens: where are we?

$$CV_g = 0.5$$
, $I(0) = 10^{-3}$ (middle panel):



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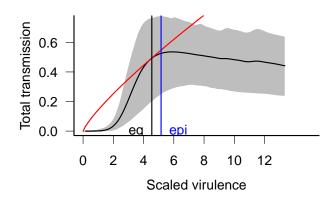
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- - Toy model

Overview

- Mosquito-borne viral disease of rabbits
- Benign in South American rabbits, quickly fatal in European rabbits
- Well characterized (Fenner et al., 1956; Dwyer et al., 1990)

Myxomatosis tradeoff curve



Estimating evolvability (V_g)

- Key parameter: genetic variance in virulence (evolvability)
- Despite case studies of rapid pathogen evolution:
 - myxomatosis (Dwyer et al., 1990)
 - syphilis (Knell, 2004)
 - serial passage experiments (Ebert, 1998)
 - Plasmodium chabaudi (Mackinnon and Read, 1999a)

we rarely have enough information to estimate $V_{\it g}$

 Only (?) for myxomatosis do we know the variation in virulence among circulating strains

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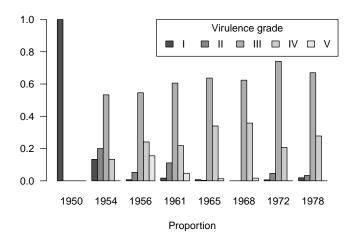
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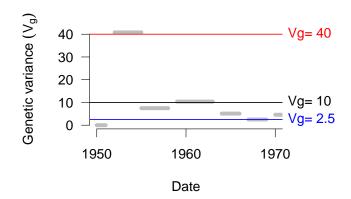
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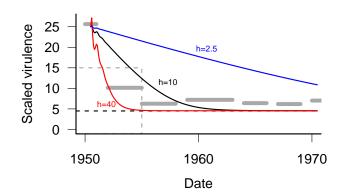
Myxomatosis grades vs. time



Myxomatosis variance vs. time



Myxomatosis virulence dynamics: power-law tradeoff

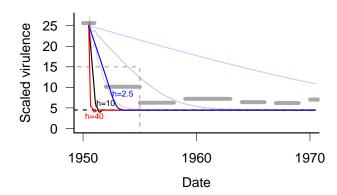


Emerging disease

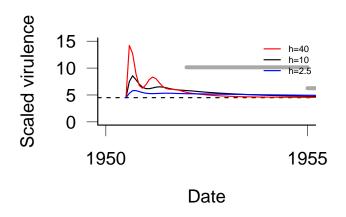
Seasonal disease

Theory vs. data

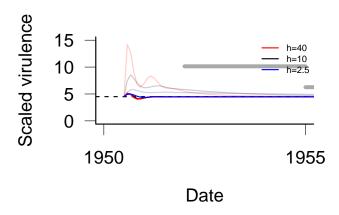
Myxomatosis virulence dynamics: realistic tradeoff



Myxo virulence: equilibrium start, power-law tradeoff



Myxo virulence: equilibrium start, realistic tradeoff



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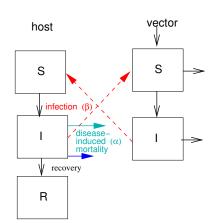
Seasonality

- Many pathogens fluctuate annually
 - Host contact/aggregation patterns
 - Host (or vector) demography
 - Climatic effects on transmissibility
- Fluctuating incidence = fluctuating selection
- Seasonal variation or latitudinal variation?

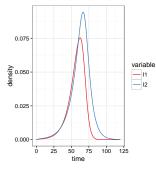
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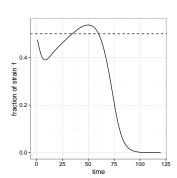
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- Basic Ross-MacDonald vector-host model
- Simple vector (mosquito) demography
- No host demography
- Two pathogen strains

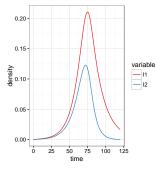


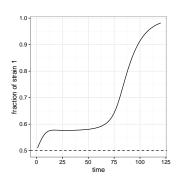
Case I: $r_1 > r_2$, equal \mathcal{R}_0



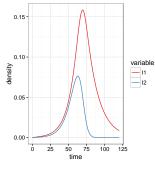


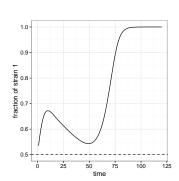
Case II: $\mathcal{R}_{0,1} > \mathcal{R}_{0,2}$, equal r





Case III: $\mathcal{R}_{0,1} > \mathcal{R}_{0,2}$, $\mathit{r}_2 > \mathit{r}_1$

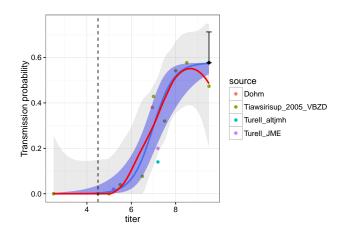




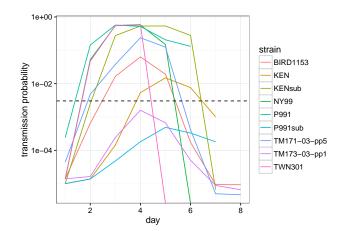
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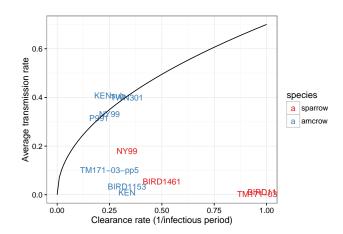
Titer vs infectiousness



Titer curves (American crows)



Transmission vs clearance for WNV



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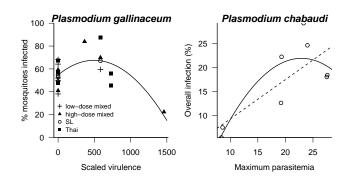
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Estimating tradeoff curves

- Usually assume a tradeoff between virulence and transmission
- Positive correlation virulence and transmissibility (or proxies) known from many systems (Lipsitch and Moxon, 1997)
- shape of tradeoff curves is largely unknown

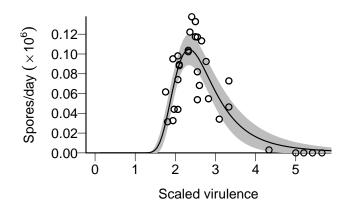
Malaria (Mackinnon and Read, 1999b; Paul et al., 2004)



Emerging disease 0000 000000 000000000 Seasonal disease

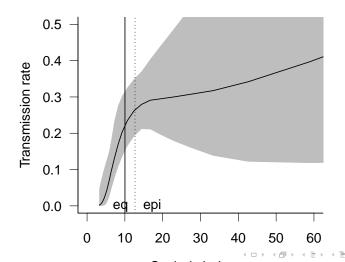
Theory vs. data ○○○●○○○○ References

Pasteuria ramosa (Jensen et al., 2006)



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HIV (Fraser et al., 2007)

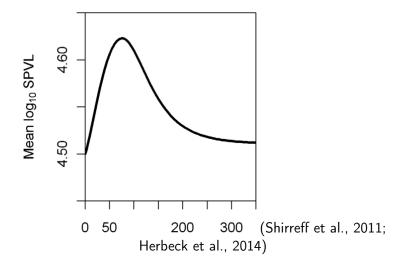


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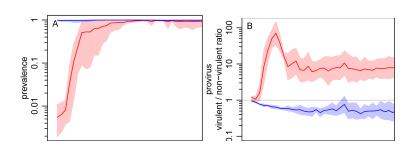
Theory vs. data ○○○○●○○ References

HIV dynamics (Shirreff et al., 2011)



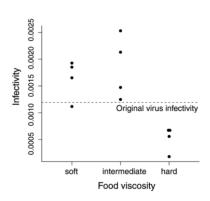
Emerging disease 0000 0000000 000000000 Seasonal disease 00 00000 0000 Theory vs. data ○○○○○●○ ○○○ References

Phage dynamics (Berngruber et al., 2013)



What about space?

- Theory: spatial structure should select for decreased virulence
- Experiment: viscosity decreases infectivity in Plodia (Boots and Mealor, 2007)
- Are we ready for space?



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Conclusions

- Eco-evolutionary dynamics of virulence are still plausible (Alizon et al., 2009; Luo and Koelle, 2013)
- Sensitive to genetic variance and shape of tradeoff curve
- Theory meets molecular biology: mutations of large effect vs. quantitative variability

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Crome (1997) on theory

When we regard theories as tight, real entities and devote ourselves to their analysis, we can limit our horizons and, worse, attempt to make the world fit them. A lot of ecological discussion is not about nature, but about theories, generalizations, or models supposed to represent nature . . .

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References

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