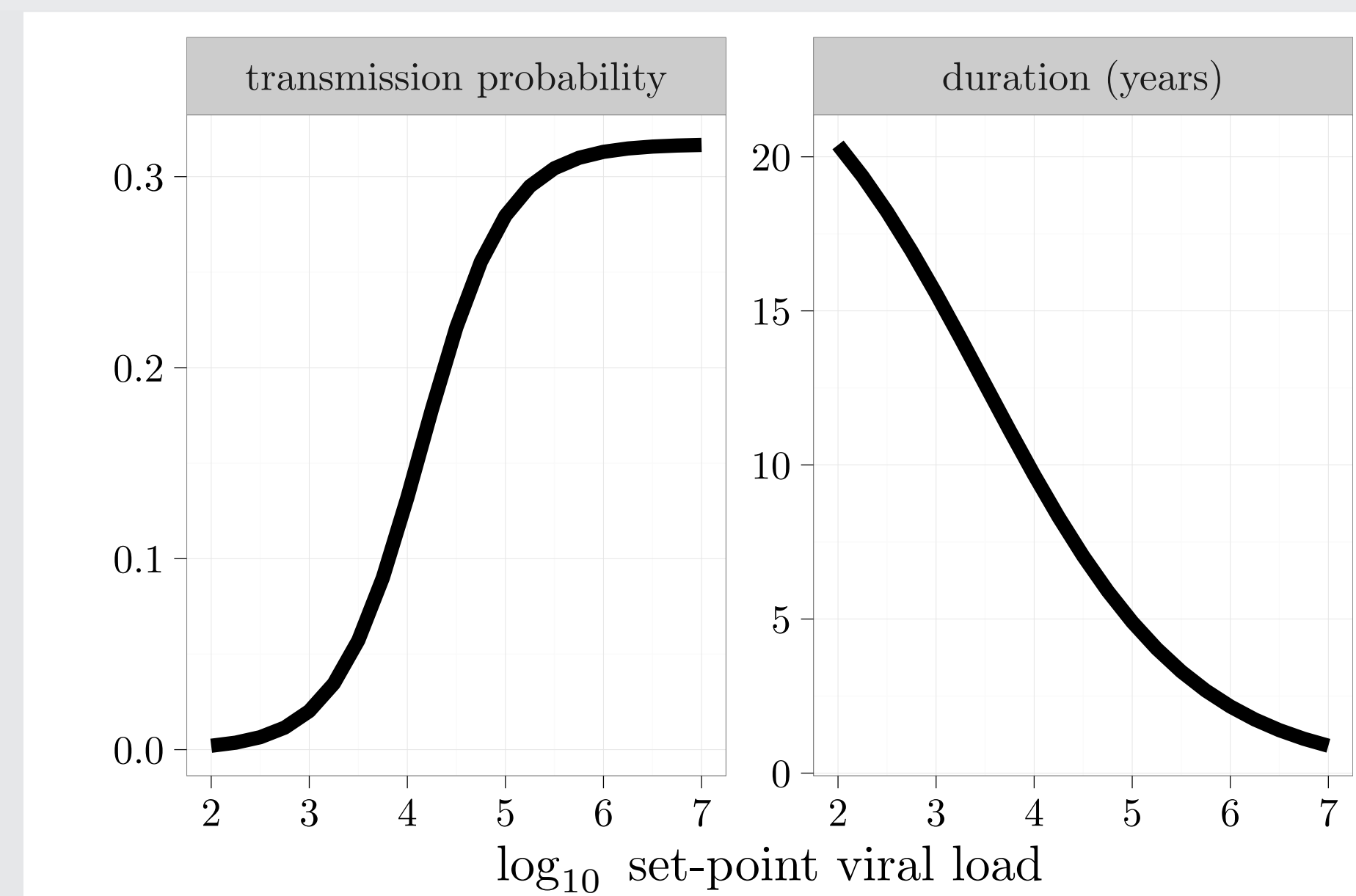


Summary

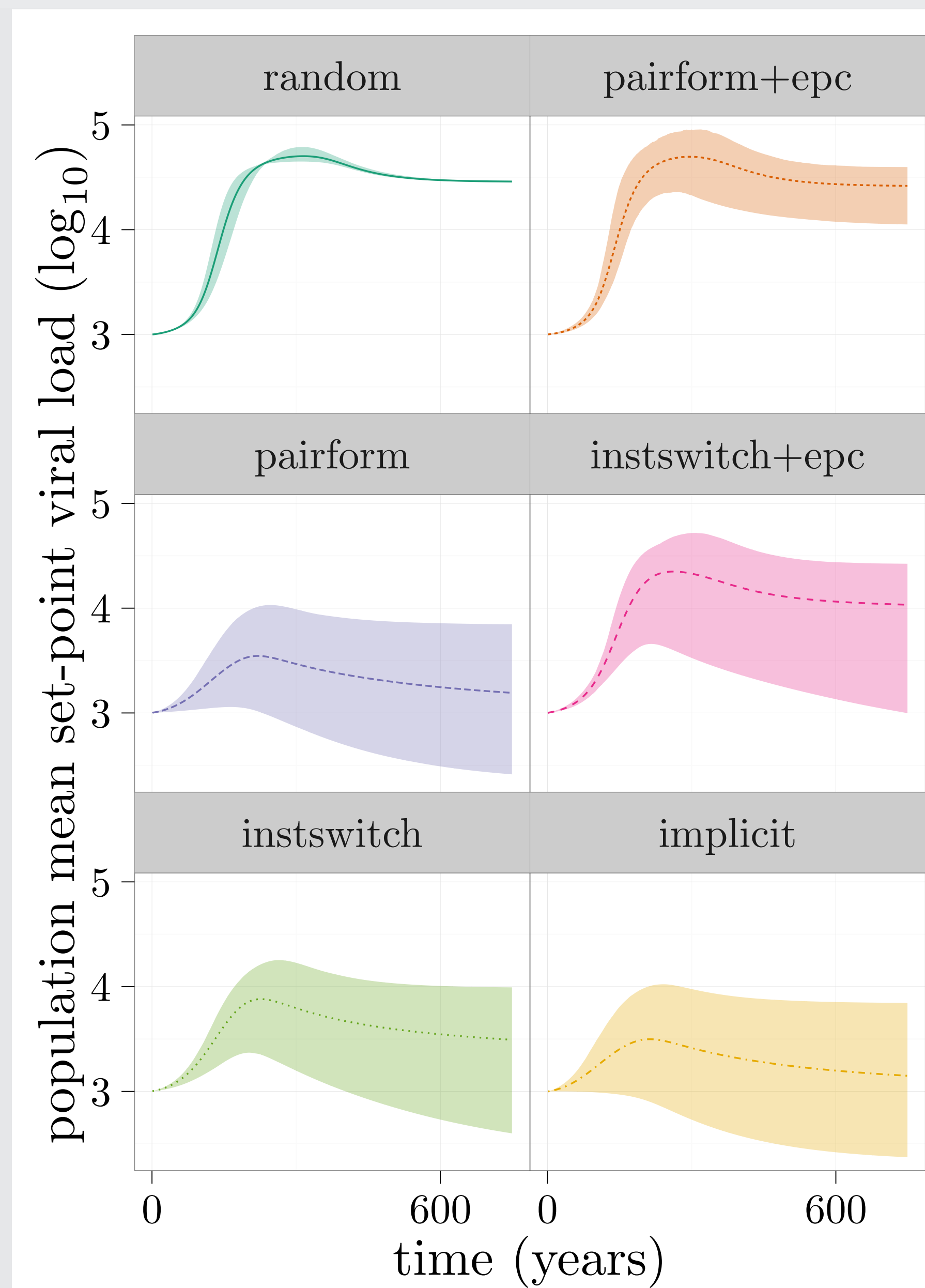
Pathogens can evolve rapidly in response to changing conditions (e.g., epidemic stage or public health interventions). Models of **eco-evolutionary dynamics** often neglect important epidemiological processes, such as the dynamics of sexual partnerships. We compared **models with a range of complexity** of partnership dynamics and extra-partnership contact.

Tradeoff theory



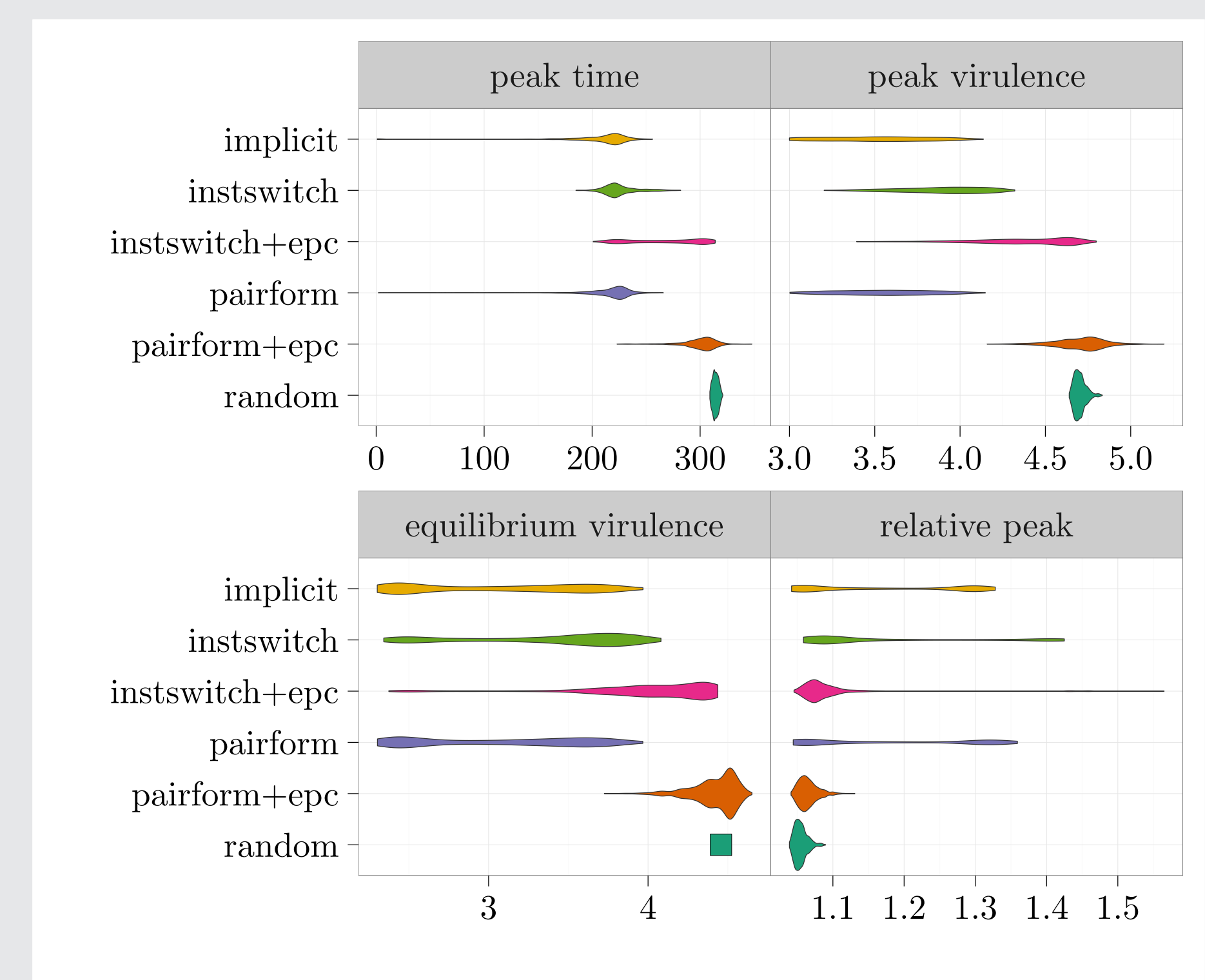
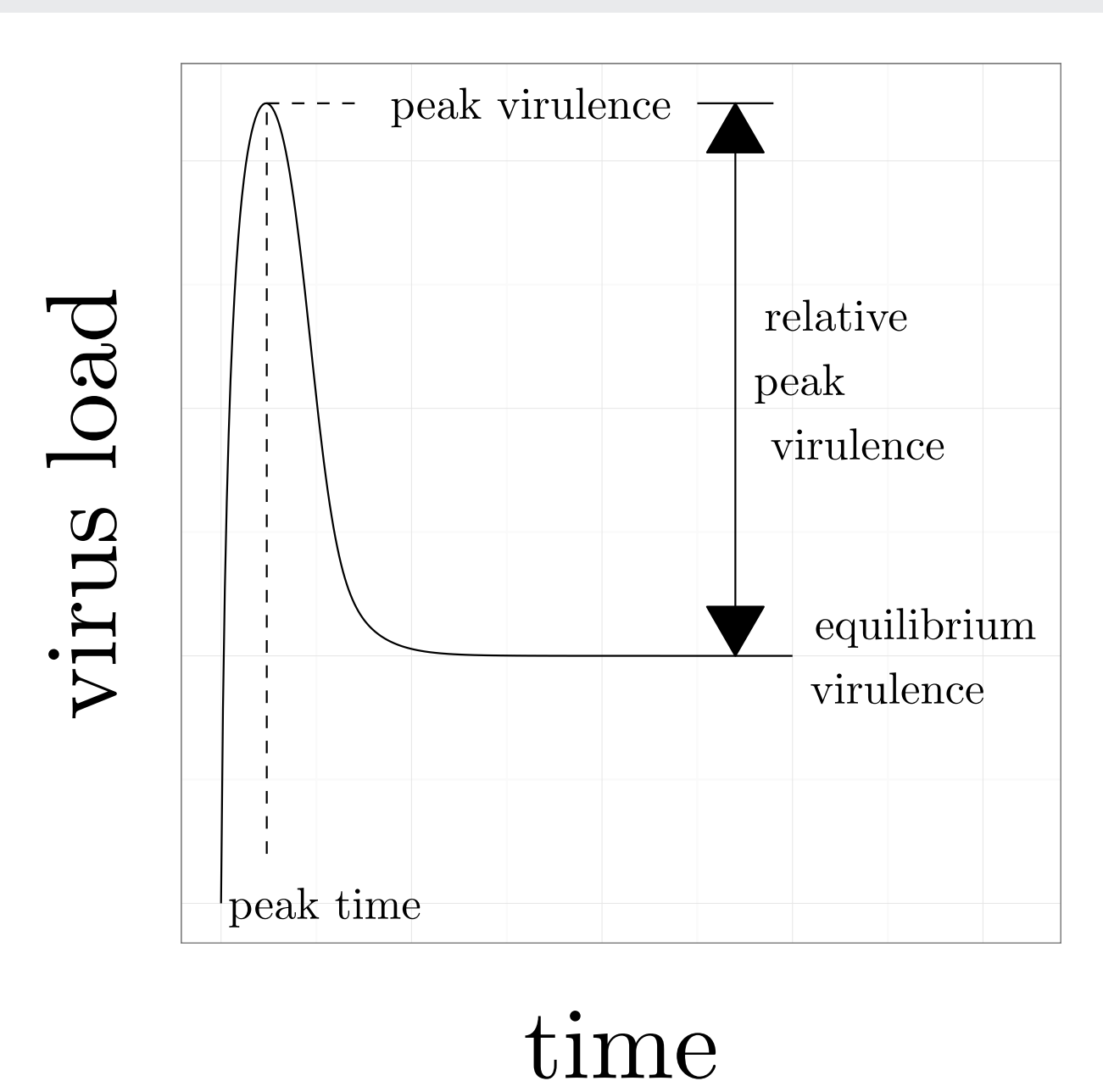
- ▶ virulence evolution mediated by transmission-vs-clearance tradeoff
- ▶ still debated [1, 2]
- ▶ HIV [3]: **set-point viral load** (\approx “virulence”) correlated with transmission probability, rate of progression to AIDS (data from Rakai, Uganda)
- ▶ eco-evolutionary virulence dynamics: [4]

Eco-evolutionary dynamics



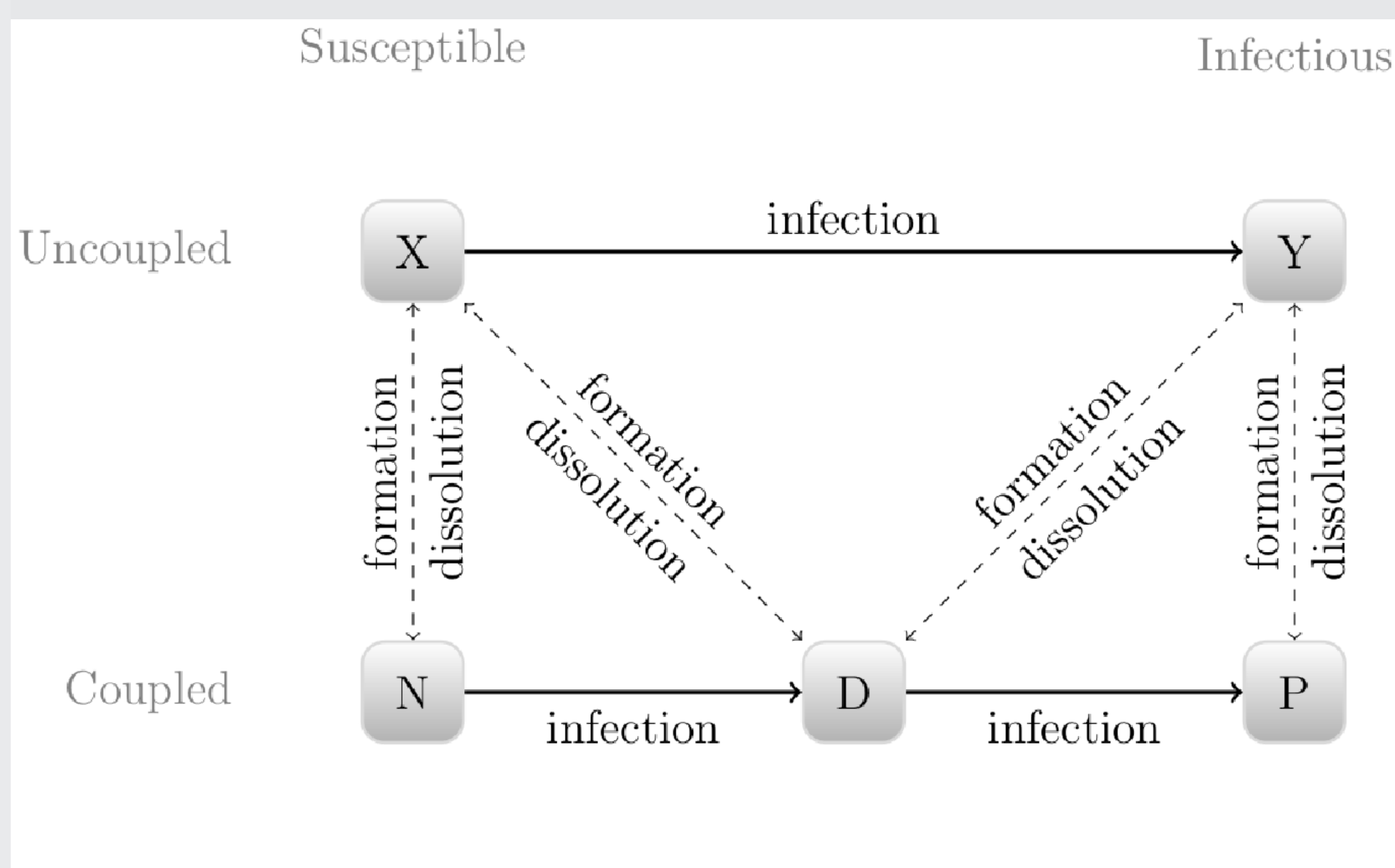
- ▶ least (random) and most (pairform+epc) models **most similar**: single individuals and extra-pair contact wash out effects of structure
- ▶ implicit model is **most different**
- ▶ random-mixing model underestimates variability

Univariate summaries



- ▶ peak timing: $\text{epc} > \text{finite pair-formation effects}$
- ▶ equilibrium virulence: interaction
- ▶ low-equilibrium outcomes for intermediate-complexity models

Epidemiological structure

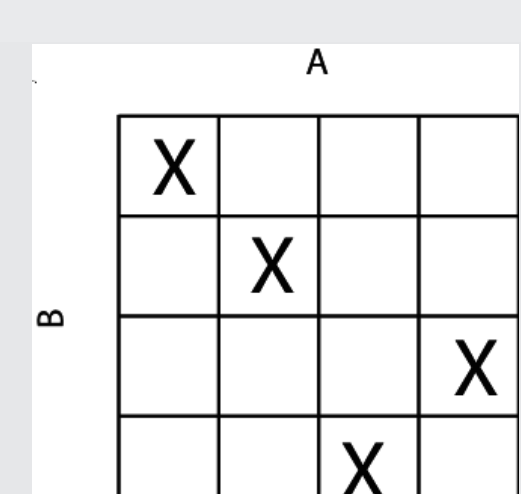


Champreon *et al.* 2013 [5]

infection from (1) infected partner (*SI* couples); (2) other coupled inf.; (3) uncoupled inf.

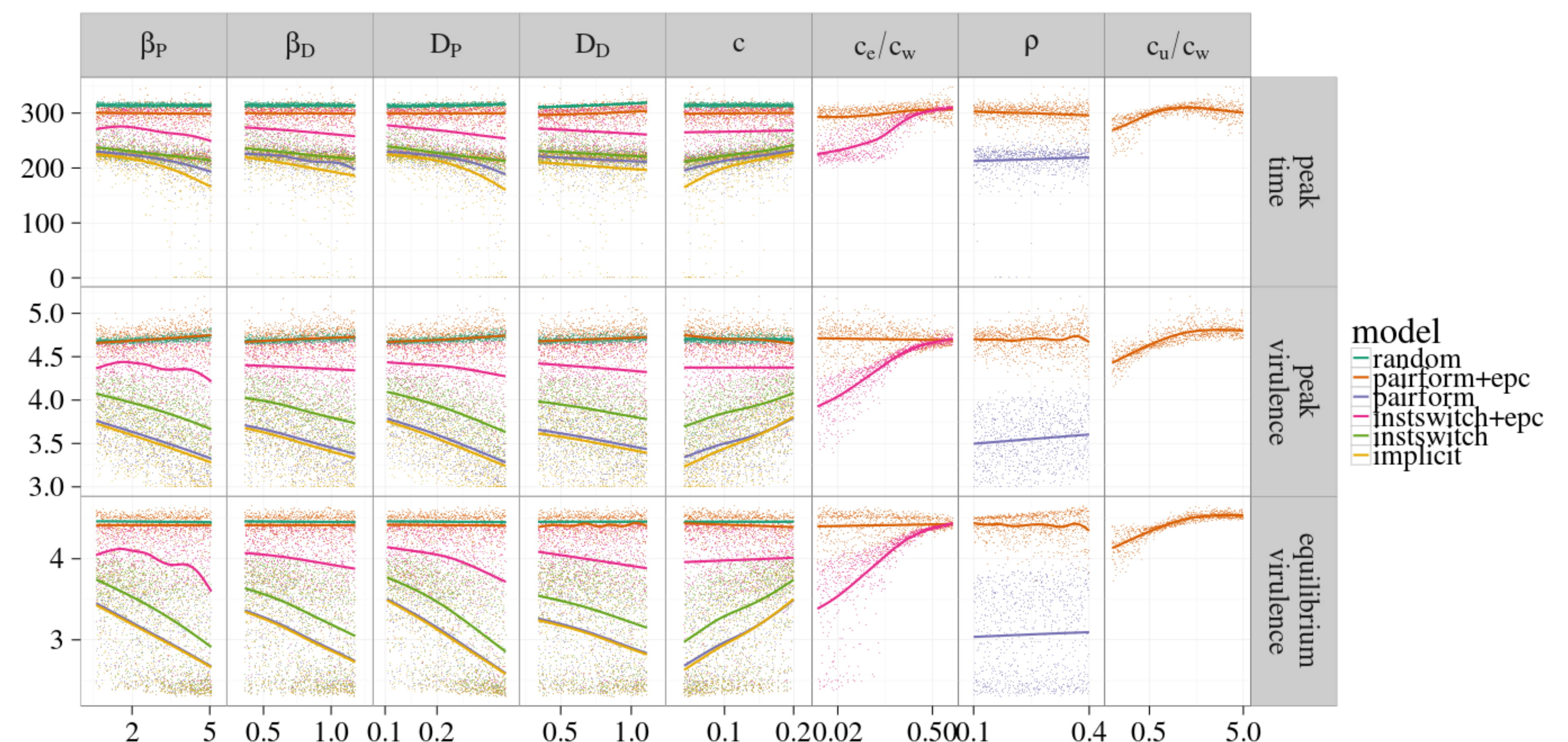
- ▶ **pair formation**: instantaneous or delayed?
- ▶ **extra-pair contact** (epc): present or absent?
- ▶ **implicit model**: no explicit partnerships, force of infection expression derived from \mathcal{R}_0 of pair-formation model (without epc)
- ▶ **random-mixing model**: standard SIR model Simplified disease model (single stage only)

Parameter uncertainty/exploration



- ▶ Latin hypercube sampling: parameters from [5]
- ▶ parameters calibrated across models to the same **initial epidemic growth rate** (r)

Sensitivity



Conclusions and open questions

- ▶ Random-mixing models best matched the most realistic models; extra-pair and uncoupled individuals washed out the effects of epidemiological structure
- ▶ Implicit models did worst
- ▶ Variation among models (model structure) \approx variation within models (parameter uncertainty)
- ▶ Large differences in evolutionary dynamics among different epidemiological models \rightarrow caution in predicting evolutionary responses
- ▶ **neglected**: disease life history details, sex workers, age-structured mixing ... agent-based models?

References

- [1] Ebert D, Bull JJ. Challenging the trade-off model for the evolution of virulence: is virulence management feasible? *Trends Microbiol.* 2003;11(1):15–20.
- [2] Alizon S, Michalakis Y. Adaptive virulence evolution: the good old fitness-based approach. *Trends in Ecology & Evolution.* 2015 Jan;30(5):248–254.
- [3] Fraser C, Lythgoe K, Leventhal GE, Shirreff G, Hollingsworth TD, Alizon S, et al. Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. *Science.* 2014 Mar;343(6177):1243727.
- [4] Shirreff G, Pellis L, Laeyendecker O, Fraser C. Transmission Selects for HIV-1 Strains of Intermediate Virulence: A Modelling Approach. *PLoS Computational Biology.* 2011 Oct;7(10):e1002185. WOS:000297262700019.
- [5] Champreon D, Bellan S, Dushoff J. HIV Sexual Transmission Is Predominantly Driven by Single Individuals Rather than Discordant Couples: A Model-Based Approach. *PLoS ONE.* 2013 12;8(12):e82906.

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