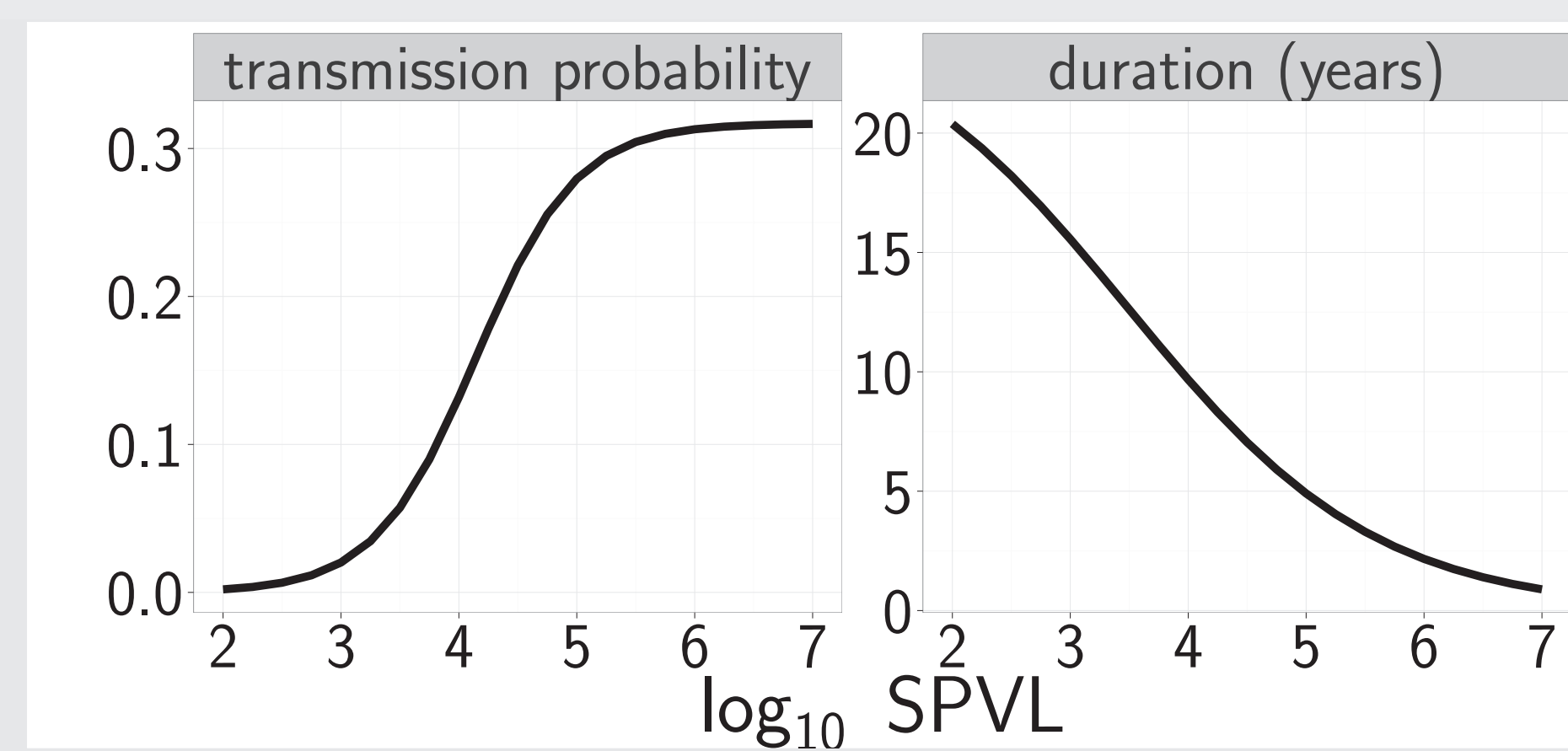


Summary

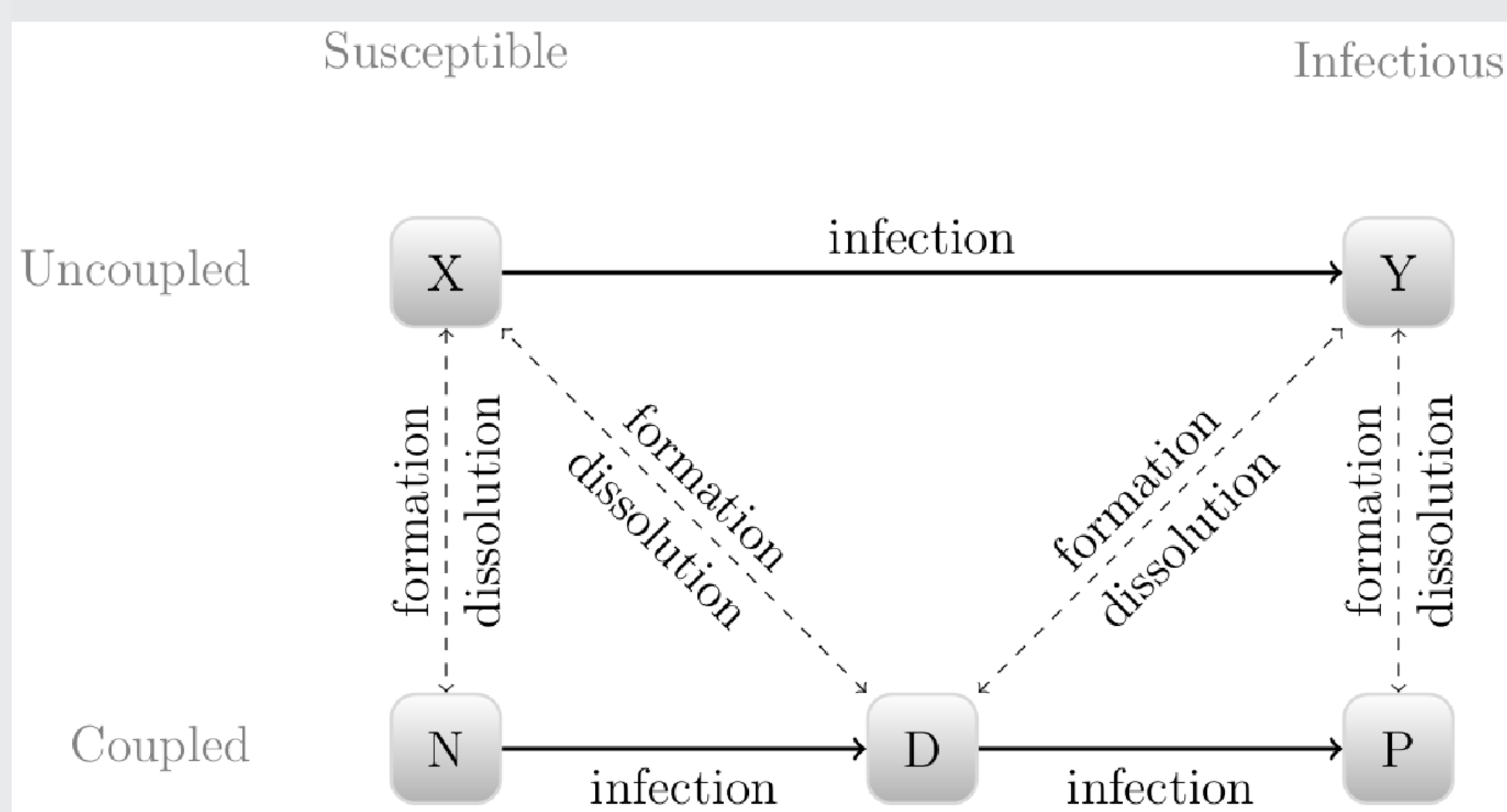
Pathogens can evolve rapidly in response to changing conditions (e.g., epidemic stage or public health interventions). Models of **eco-evolutionary dynamics** often neglect important epidemiological processes, such as the dynamics of sexual partnerships. We compared **models with a range of complexity** 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** correlated with transmission probability, rate of progression to AIDS (data from Rakai, Uganda)
- ▶ eco-evolutionary virulence dynamics: [4]

Epidemiological structure

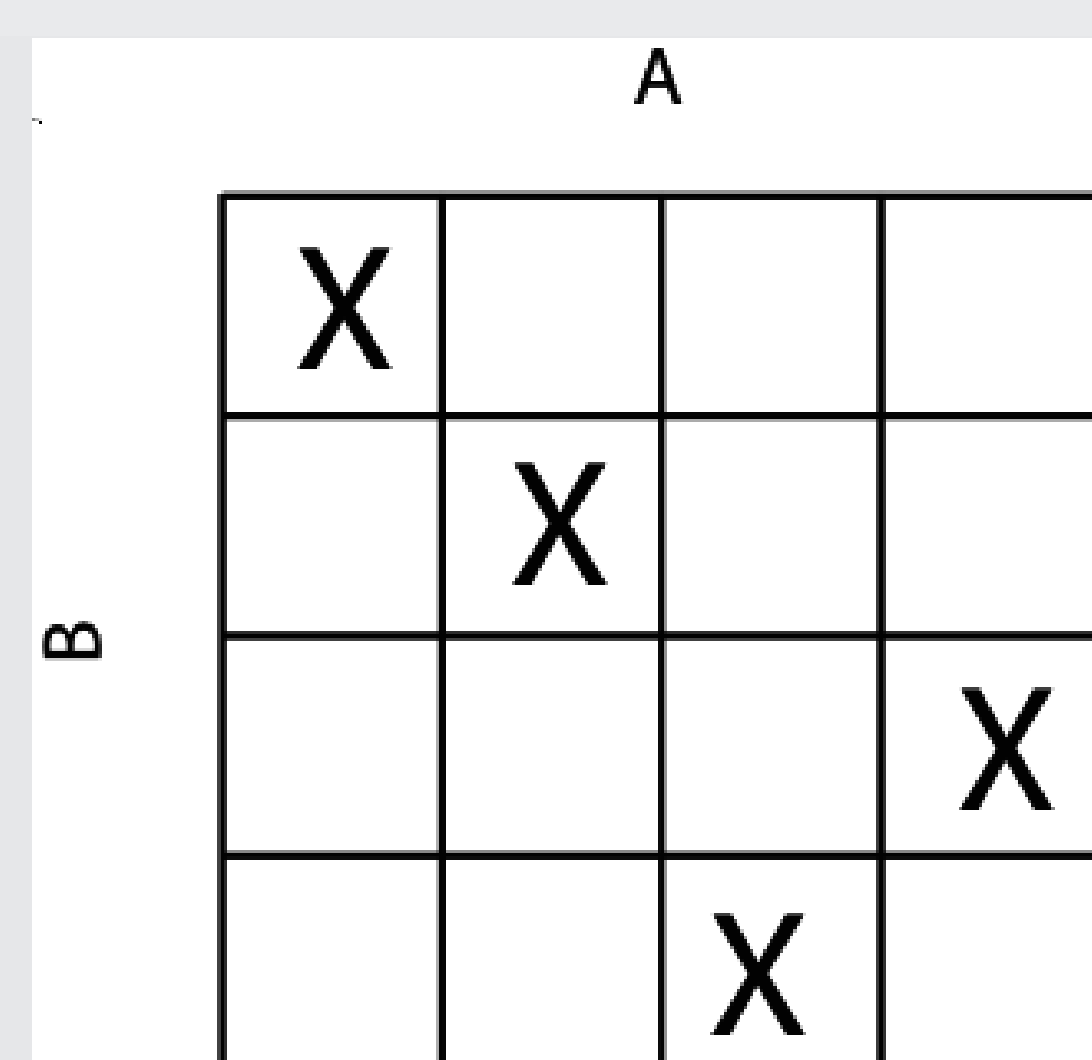


Champredon *et al.* 2013 [5]

Spectrum of model complexity:

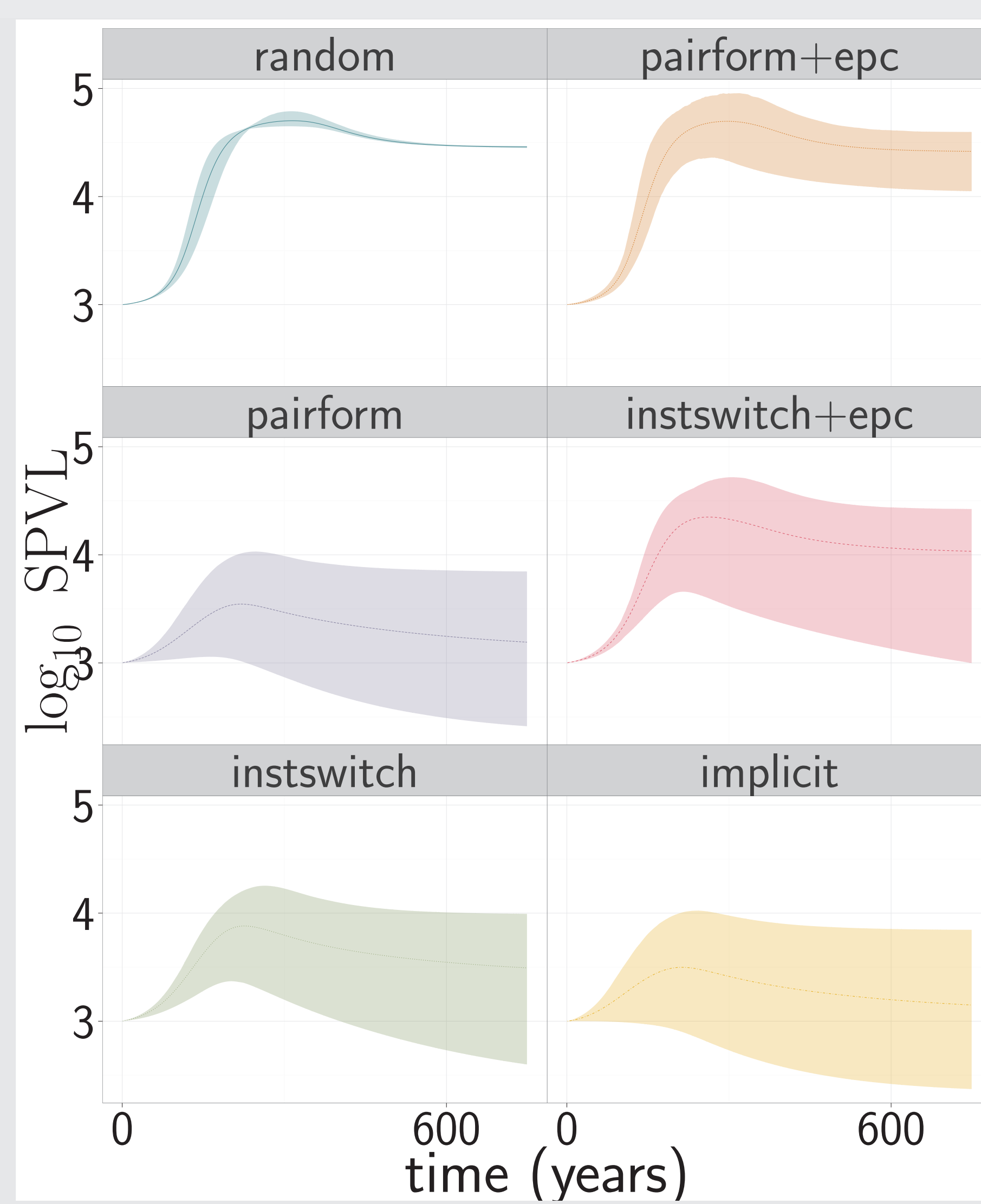
- ▶ **pair formation**: instantaneous or delayed?
- ▶ **extra-pair contact (epc)**: present or absent?
- ▶ **implicit model**: no explicit partnerships, force of infection expression derived from R_0 of pair-formation model (without epc)
- ▶ **random-mixing model**: standard SIR model Simplified disease model (single stage only)

Sampling strategy



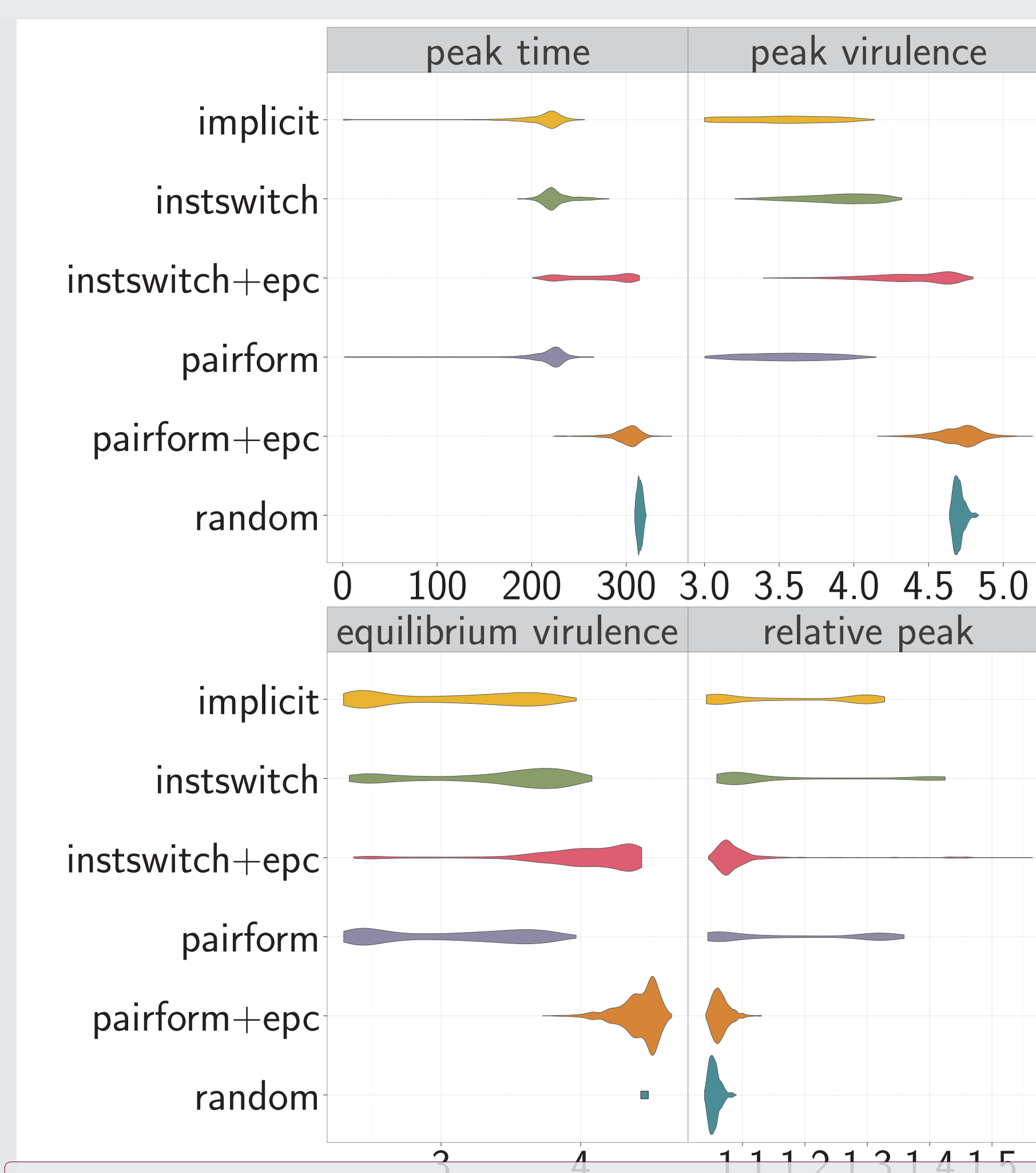
- ▶ Latin hypercube sampling: parameters from [5]
- ▶ parameters calibrated across models to the same **initial epidemic growth rate** (r)

Eco-evolutionary dynamics

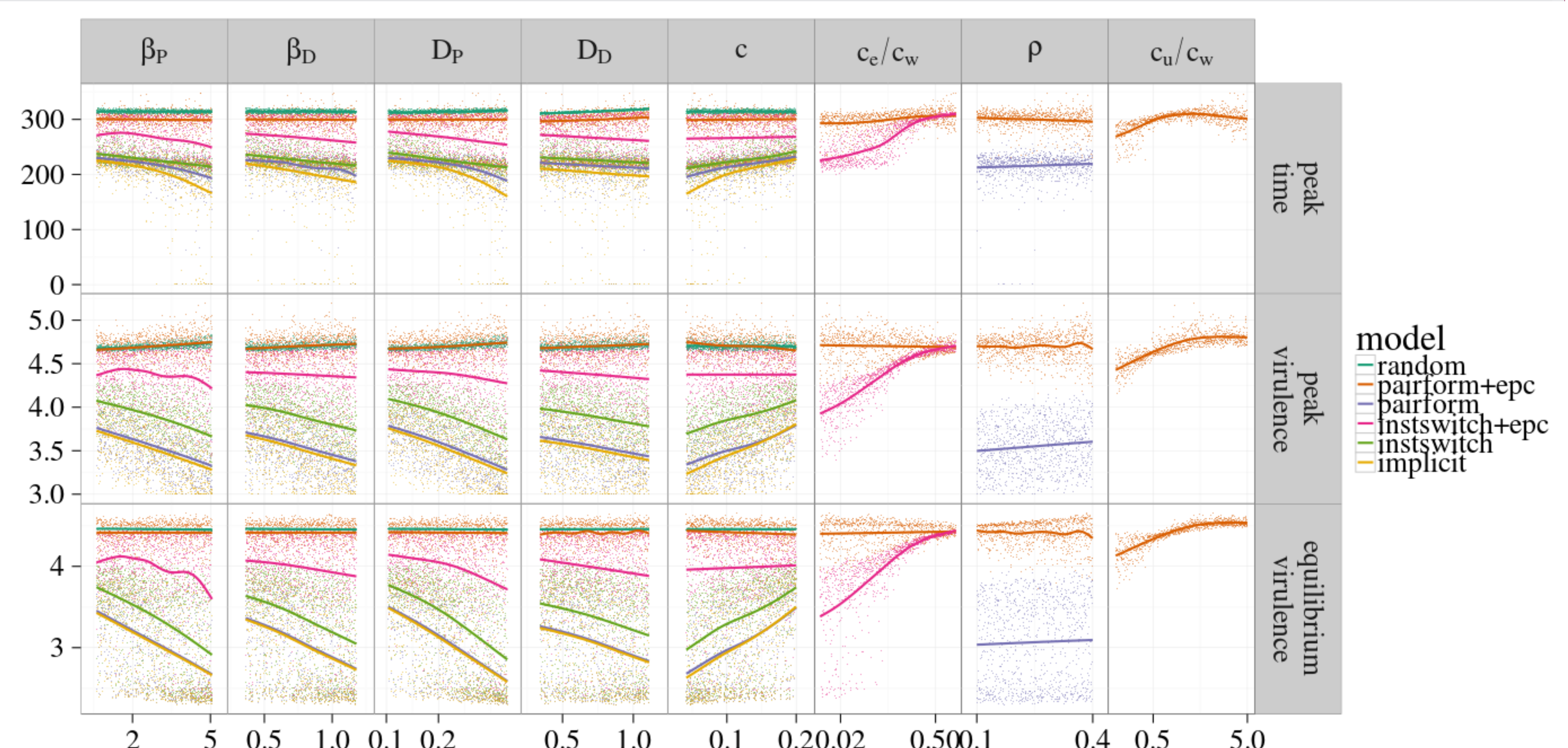


- ▶ significant variation across model structures
- ▶ least (random) and most (pairform+epc) models **most similar**: single individuals and extra-pair contact wash out effects of structure
- ▶ implicit model is **most different**
- ▶ random-mixing model underestimates (?) variability

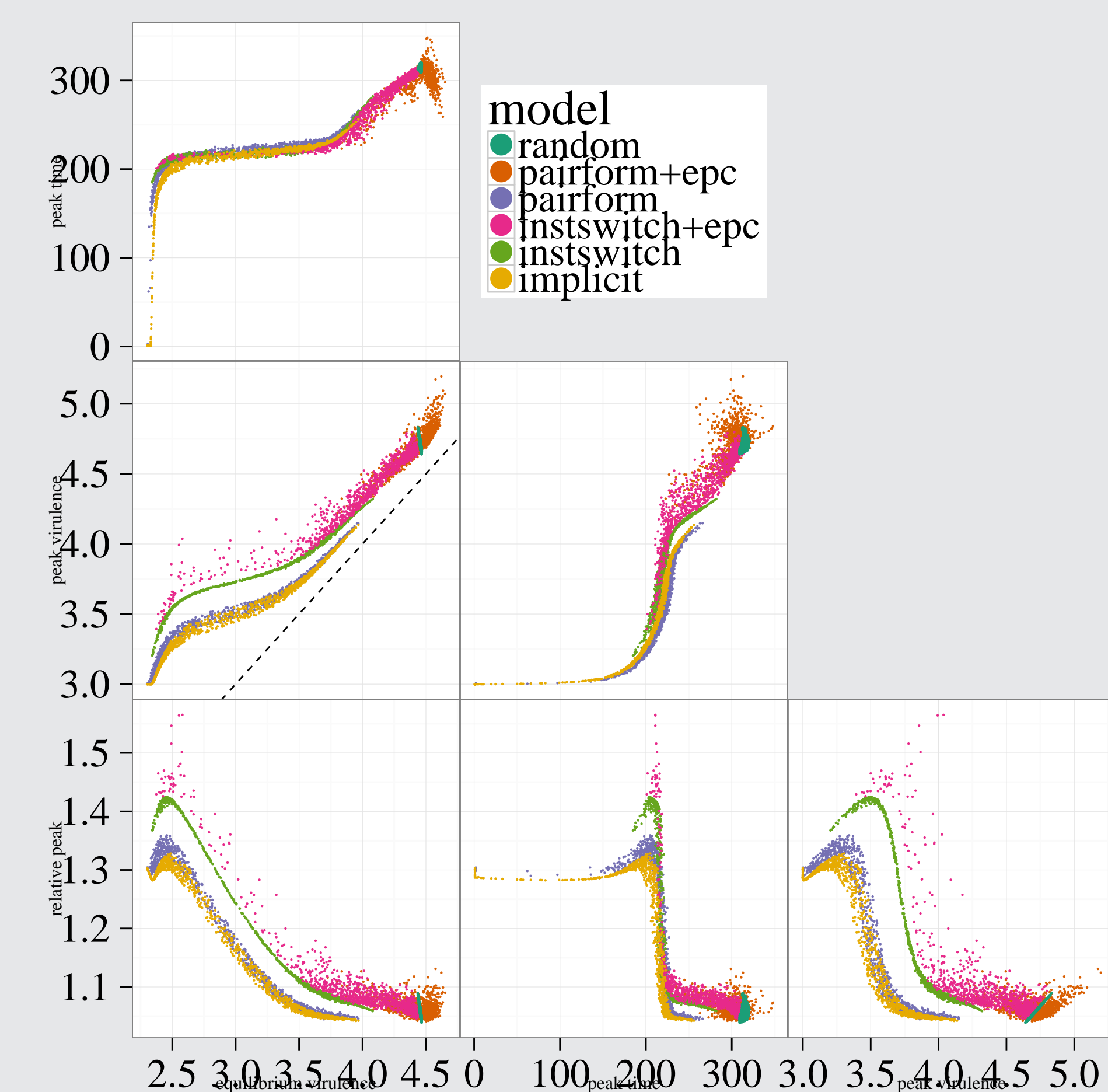
Univariate summary



Sensitivity



Bivariate summary



Conclusions and open questions

- ▶ Random-mixing models gave the closest match to the most realistic models; extra-pair contact washed out the effects of epidemiological structure
- ▶ Variation among models (model structure) \approx variation within models (parameter uncertainty)
- ▶ Large differences in evolutionary dynamics among different epidemiological models suggest caution in predicting evolutionary responses

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