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The structure of infectious disease outbreaks across the animalhuman interface CHRISTOPHER R. MYERS, Cornell University, DAVID J. SCHNEIDER, USDA-ARS and Cornell University, SARABJEET SINGH, Cornell University — Zoonotic infectious diseases that spill over from animal to human populations are responsible for some of the most devastating plagues to haunt humanity throughout its history, including the recent Ebola outbreak. Yet despite considerable efforts by epidemiologists to model specific zoonotic infections, much of the basic underlying structure of cross-species outbreaks has not been well-characterized. Motivated by these gaps and by recent efforts to develop classification schemes for characterizing the spectrum of zoonotic diseases, we have solved – using techniques from multitype branching processes and queuing theory – for the structure and statistics of outbreaks resulting from cross-species spillover, characterizing outbreak sizes, probabilities and first-passage times. In the case of human outbreaks driven by epidemics in animal populations, we find a novel multicritical point at which outbreak size scaling that is different than in a single population. When human outbreaks are driven by an endemic disease in an animal reservoir, we find variable exponents characterizing outbreak size and duration that depend upon the rate of cross-species spillover.

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