A very simple discrete-time SI model leads to sustained multi-generational population cycles

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Many host–pathogen systems are characterized by a temporal order of host reproduction and disease transmission. For example, this can be due to pathogens infecting certain life cycle stages of insect hosts; transmission during the aggregation of migratory birds; or in plant diseases that spread between planting seasons. We develop a very simple discrete-time epidemiological model, based on the Poisson distribution used by Reed and Frost in the 1920s. The separation between the disease transmission and host reproduction phase can lead to sustained multiannual cycles in host abundance and disease prevalence. They emerge as invariant curves in a Neimark–Sacker bifurcation. We will describe a novel causal mechanism of population cycles and disease oscillations, which bears implications for the management of epizootics, zoonoses, and wildlife populations.