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Analytic calculations of finite-population reproductive numbers

The basic reproductive number, \mathcal{R}_0 , provides a foundation for evaluating how various factors affect the incidence of infectious diseases. Recently, it has been suggested that, particularly for vector-transmitted diseases, \mathcal{R}_0 should be modified to account for the effects of finite host population within a single disease-transmission generation. Here, we use a transmission-factor approach to calculate such “finite-population reproductive numbers”, under the assumptions of homogeneous and heterogeneous mixing, for both vector-borne and directly transmitted diseases. In the case of vector-borne diseases, we estimate finite-population reproductive numbers for both host-to-host and vector-to-vector generations, assuming that the vector population is effectively infinite. We find simple, interpretable formulas for these three quantities. In the direct case, we find that finite-population reproductive numbers diverge from \mathcal{R}_0 before \mathcal{R}_0 reaches half of the population size. In the vector-transmitted case, we find that the host-to-host number diverges at even lower values of \mathcal{R}_0 , while the vector-to-vector number diverges very little over realistic parameter ranges.