

EvoSymbiose, a model for the study of zoonoses evolution

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The evolution of zoonoses involves complex interplays between epidemiology and demographic and evolutionary dynamics. EvoSymbiose simulates the co-evolution between hosts and parasitic or mutualistic symbiotes in a multi-host species context while accounting for the stochasticity induced by low population sizes. This allows investigating the evolution of host shifts while accounting for the epidemiology, the co-evolution and the demography. In short, this is a compartmental model, similar to Susceptible Infected Recovered models, where each of these three categories has a large number of compartments that correspond to each combination of host/parasite genotypes. The hosts and parasites genes combination determines i) the probability of infection and ii) the outcome of the infection. This allows modelling the entire continuum of types of host-parasite interactions between the matching allele (MA), gene-for-gene (GfG), inverse matching allele (iMA), and inverse gene-for-gene (iGfG).