

MINISYMPOSIUM

CURRENT DIRECTIONS IN HOST-PARASITE COEVOLUTION

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Understanding the antagonistic coevolution of hosts and their parasites is vitally important given the central role that infectious disease plays in human health, agriculture and natural systems. Alongside experimental and empirical studies, there is a rich history of mathematical modelling of host-parasite coevolution. Early studies of crop diseases gave rise to the ‘gene-for-gene’ models, which have been a basis for understanding coevolutionary disease dynamics in a range of systems ever since. More recently, models that include explicit ecological dynamics have shown how feedbacks between ecology and selection can drive coevolutionary dynamics. Continued advances in experimental methods have led to a plethora of results in need of theoretical attention. Modelling of host-parasite coevolution thus continues to be a major area of inquiry.

This minisymposium will see talks from leading researchers addressing questions at the forefront of host-parasite coevolutionary theory. The talks cover a range of both biological questions and mathematical approaches. In all cases, a guiding principle is for theoretical developments to be developed in close harmony with experimental and empirical results.

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ANTAGONISTIC COEVOLUTION, POPULATION DYNAMICS, AND IMPLICATIONS FOR THE RED QUEEN

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Keywords: Host-parasite, Coevolution, Red Queen, Stochasticity.

Host-parasite coevolution is believed to follow Red Queen dynamics consisting of ongoing oscillations in the frequencies of interacting host and parasite alleles. This belief is founded on previous theoretical work, which assumes infinite or constant population size. To what extent are such sustained oscillations realistic? Besides the coevolutionary dynamics, population sizes of the interactors also change over time. Over a series of studies we have investigated stochastic dynamics acknowledging two critical pieces of realism: (i) population size fluctuations, caused by the antagonism of the interaction in concordance with the Lotka-Volterra relationship; and (ii) stochasticity, acting in any finite population. In deterministic models when including multiple hosts and parasites a similar picture emerges. Together, these two factors cause fast allele fixation. Our results call for a paradigm shift in our understanding of host-parasite coevolution, strongly suggesting that these are driven by recurrent selective sweeps rather than continuous allele oscillations.

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FROM COEVOLUTIONARY DYNAMICS TO GENOMICS AND BACK: INFERRING THE SPEED OF THE RED QUEEN.

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Joint work with Hannah Märkle, Wolfgang Stephan, Aurelien Tellier, Daniel Žikvokić

Keywords: Host-parasite, Coevolution, Polymorphism.

For various fields such as plant breeding it is of interest whether host and parasite species are coevolving and if so to detect loci being involved in this interaction. Two properties that arise from host-parasite coevolution are (i) changes in allele frequencies at associated loci and (ii) changes in the population sizes of both species as driven by the epidemiology. Building our models in a discrete and in a continuous setting we make respective use of these two properties for coevolutionary inference. In the former case (i), we develop an approximate Bayesian computation (ABC) approach tailored for a joint analysis of host and parasite polymorphism data. This joint consideration not only allows us to detect coevolution at candidate loci but also to infer model parameters (cost of disease, resistance and virulence). The ABC is based on site-frequency spectrum (SFS) related summary statistics. In the latter case (ii), we establish a dynamical system that is solved numerically to track the population size changes of hosts and parasites over time. We investigate over which time scales the SFS is indicative of the joint coevolutionary dynamics.

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EVOLUTION OF PARASITE HOST RANGES - GOING BEYOND TRADE-OFFS

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Keywords: Host-parasite, Coevolution, Bacteria-phage, Trade-offs, Host range.

Parasite host ranges are a dynamic ecological trait with the potential for rapid evolution. Nevertheless most parasites show a high degree of host specificity. Host-use trade-offs are a common theoretical explanation for the prevalence of host specialism, but empirical evidence for such host-use trade-offs is rare. I will present an alternative model for limited host-ranges which is based solely on basic features of the parasitic life cycle, namely host selection and subsequent intra-host replication. This theory provides an explanation for the observed host specificity which does not rely on direct costs for extended host ranges.

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HOST-PARASITE COEVOLUTION WITHIN COMMUNITIES

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Keywords: Host-parasite, Coevolution, Predation, Communities.

While host-pathogen co-evolution has been the focus of much experimental and theoretical inquiry, the vast majority of studies assume the host and pathogen interact in isolation. In reality they will form one part of large, complex communities, with feedbacks between co-evolution of hosts and pathogen strategies on the one hand and community dynamics on the other. Understanding the impact of community interactions on host-pathogen coevolution has recently become a key area of focus in the experimental literature, but there is yet to be a fully coevolutionary theoretical study. Here I present results assessing the impact of predation on host-pathogen co-evolution. I show that an array of qualitatively different dynamics may arise, including co-evolutionary cycles, but I find that predation alters the potential for such fluctuations. I demonstrate that while predation may select for low host resistance and high pathogen infectivity, ecological feedbacks mean this in fact results in lower infection rates when predators are present. I also show how host evolution may drive either enemy to extinction. This work emphasises the importance of community interactions and opens up avenues for further investigation.