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Population Biology of Infectious Diseases

The University of Georgia is host to the NSF-funded REU Site program in Population Biology of Infectious Diseases. The goal of the program is to provide students with experiences and opportunities at the intersections of the quantitative sciences (mathematics, computer science, statistics) and empirical disciplines of infectious disease biology (ecology, epidemiology, genetics, immunology). [Population biology of infectious diseases: Part I | Nature](#)

If the host population is taken to be a dynamic variable (rather than constant, as conventionally assumed), a wider understanding of the population biology of infectious diseases emerges.

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Infectious diseases propagate along networks of contacts of infected hosts. Increasingly, epidemiological investigations have used molecular analysis and case investigation to reconstruct these infection paths, which are then quantified as transmission trees.

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If the host population is taken to be a dynamic variable (rather than constant, as conventionally assumed), a wider understanding of the population biology of infectious diseases emerges. In this first part of a two-part article, mathematical models are developed, shown to fit data from laboratory

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In the first part of this two-part article (Nature 280, 361–367), mathematical models of directly transmitted microparasitic infections were developed, taking explicit account of the dynamics of

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The Population Biology of Infectious Diseases REU Site at the University of Georgia is a nine-week NSF-funded program to provide students from across the country with research experiences at the intersections of quantitative and experimental studies in infectious disease biology.

(PDF) Population biology of infectious diseases

One less complex model is the "classic" approach to model the population and disease spread via a dynamical system, where the dynamics of the infected population is described with a system of

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Population biology of infectious diseases: Part II. May RM. Anderson RM. In the first part of this two-part article (Nature 280, 361–367), mathematical models of directly transmitted microparasitic infections were developed, taking explicit account of the dynamics of the host population.

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