962-92-638 **Horst R Thieme*** (h.thieme@asu.edu), Horst R. Thieme, Department of Mathematics, Arizona State University, Tempe, AZ 85287-1804, and **Jinling Yang**. *Disease Persistence in an Evolutionary Influenza Model.* Preliminary report.

The evolutionary influenza model by Pease has the form of an age-structured population model with age representing the number of aminoacid changes in the influenza virus which have occured since an individual recovered from influenza. The model which has no vital dynamics has no obvious disease-free equilibrium and so lacks the usual interplay between the basic replacement ratio being greater than 1 and the disease-free equilibrium being unstable. This makes the concept of persistence very important, for one can show the following: If the basic replacement ratio is greater than one, the disease is uniformly strongly persistent, i.e., the number of infectives is ultimately bounded away from 0 with the bound not depending on the initial data. This is achieved by first proving uniform weak persistence and then considering the solution semiflow. The appropriate state space are the measures on the compactified right real half-line, with the weak * topology. The disease-free equilibrium, in terms of the susceptible individuals, is then represented as a Dirac measure concentrated at infinity. Uniform strong persistence follows from uniform weak persistence because there is a compact (because bounded) attractor due to the Alaoglu-Bourbaki theorem. (Received September 18, 2000)