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PREFACE: TRIBUTE TO HORST R. THIEME ON THE OCCASION OF HIS 60TH BIRTHDAY

It is a great pleasure to congratulate Horst on his 60th birthday and to dedicate this volume to him in honor of his many contributions to the field of mathematical biology.

Horst Thieme has been, over a period of thirty years, one of the most productive scientists in Mathematical Biology, with numerous works on subjects centered on population biology and transmission and control of infectious disease. He has provided a number of rigorous mathematical tools for the study of structured populations, the problem of biological invasion, and the limiting behavior of epidemic and other population models. Horst Thieme's work can be characterized by deep insight into the underlying structure of biological phenomena and mechanisms, great skills in entering these insights into feasible models, and by rigorous mathematics validating or sometimes rejecting modeling approaches.

Horst's earliest contributions, beginning in the late 1970s, centered on Volterra integral equations. These works focused on asymptotic estimates of solutions and, in their application to epidemiology, to the asymptotic speed of spread of an epidemic. These works continue to be cited to this day. He continued this work in the early 1980s, studying renewal theorems for Volterra integral equations in full generality. This is basic work that lies at the foundation of the very general renewal approach to populations structured by age or size and connects this theory to the semigroup approach.

In 1984, a first paper with Odo Diekmann and Henk Heijmans appeared, and this team of population modelers, later joined by Mats Gyllenberg, Philippe Clément, Hans Metz, and others, continued their collaboration until now, with Horst Thieme as a coauthor for at least fifteen years.

Horst's joint paper with H. Bremermann, "A competitive exclusion principle for pathogen virulence," was among the first to rigorously establish the principle that in the absence of multiple infections and the presence of complete cross-immunity, only the parasite strain with the maximal basic replacement ratio survives. It has spawned considerable recent research focusing on relaxing the assumptions such that multi-strain coexistence can occur. A recent Thieme book chapter extends the earlier work on competitive exclusion but also shows that a strain that would become extinct on its own can coexist with a more virulent one if it protects the host against the more virulent strain.

In the 1990s Thieme took on the problem of persistence. His paper on weak persistence (1993) is now a classic in that field. Its main theme is that the strong compactness assumptions on the dynamics typically assumed in order to obtain (uniform) persistence can be substantially relaxed and this allows the theory to be much more broadly used. The paper also contains applications of persistence theory to some well-known models in epidemiology, providing conditions for both host

persistence and disease persistence (endemicity). Following this work, persistence theory began to become a critical tool in the analysis of epidemic models. His subsequent work on persistence extended the theory to non-autonomous dynamical systems.

One of Thieme's most cited works provides mathematically rigorous support for the commonly exploited simplifications that we all use in analyzing problems arising in biomathematics. If one or more components of a dynamical system converge, it is natural to study the reduced system obtained by "freezing" these components at their limiting values. The hope is that limit sets would be the same for the original and reduced systems. This turns out to be false but Thieme shows that key aspects of the Poincaré-Bendixson theory can be applied to the original system if the reduced system is two-dimensional.

Horst's highly cited 2003 monograph "Mathematics in Population Biology" has become a classic reference book on population modeling and mathematical epidemiology but also for the many analytical tools lucidly described there.

Many researchers in mathematical biology may not be aware of Horst's extensive research in non-standard ways of generating dynamical systems in infinite dimensional spaces (integrated semi-groups generated by non-densely defined operators). This work has many applications in mathematical biology and will continue to be useful in the future.

Paul Waltman introduced me to Horst in Bonn in 1978 at the conference "Functional differential equations and approximation of fixed points." I got to know him better in 1986 when he invited me to visit the Center for Stochastic Mathematical Models in the Natural Sciences at the University of Heidelberg where he was doing postdoctoral research. While there, I very much enjoyed the hospitality of Horst and Adelheid and daughters Ruth and Clara. Although my stay was for only a few weeks, I left feeling like part of the family. As a result of the visit, I was greatly impressed with Horst's analytical powers and his research in mathematical biology. The Thieme family left Germany when Horst took a visiting research professorship at Harvey Mudd College in 1987 and the possibility of attracting him to Arizona State University did not take long to germinate in my mind. The ASU research group in mathematical biology began in 1988 with the hiring of Horst, Yang Kuang, and Steve Baer. It has since flourished, due in no small part to Horst's rising stature in the field. My research collaborations with Horst, which began shortly after he arrived at ASU, have produced my most satisfying work. These collaborations focused on monotone dynamical systems and their applications to delay differential equations and to asymptotically autonomous dynamical systems. We continue our collaboration on a forthcoming monograph "Dynamical Systems and Population Persistence."

Many of the contributions to this volume come from participants in the very successful conference on Differential Equations and Applications in Ecology and Epidemiology, organized by Zhilan Feng and Tim Lant, held at Purdue University in December 2008 in honor of Horst's Birthday. Aside from many exciting research reports typical of such a conference, the meeting was distinguished by a wonderful banquet after which many of Horst's former students, colleagues, and mentors provided personal reflections on their experiences with Horst. Without a doubt, the most memorable of these, even beating out Horst's rendition of "The Song of John Matrix," was the masterful power point presentation "Wanderings With Lady M." given by Adelheid Thieme, which appears first in this volume.

Mathematical Biology Conference
December 8-10, 2008

(Left to Right)
First Row: Fred Brauer, Zhilan Feng, Rongsong Liu, Maria Leite, Adelheid Thieme, Horst Thieme, Lih-ing Wu Roeger, Maia Martcheva
Second Row: Fabid Milner, Yiding Yang, Thanate Dhirasakdanon, Willi Jaeger
Third Row: Jia Li, Linda Allen, Xiaohong Wang, Libin Rong, Dashun Xu, Shingo Iwami
Fourth Row: Yuan Lou, Sophia Jang, Azmy Ackleh, Grisele Torres-Garcia, Takafumi Suzuki, Zhipeng Qui
Fifth Row: Ruijnn Zhao, Glenn Web, Xiaoqiang Zhao, Hal Smith
Sixth Row: Daniel Maxin, Wenzhang Huang, Laurentui Sega, Paul Salceanu, K.P. Hadeler
Seventh Row: David Gerberry, A.J. Metz, Mats Gyllenberg, Odo Diekmann

FIGURE 1. Conference participants.

Guest Editor:
HAL L. SMITH