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	Nota di contenuto	Preface -- Searching for superspreaders: Identifying Epidemic Patterns Associated with Superspreading Events in Stochastic Models (Christina Edholm, et al) -- How Disease Risks Can Impact the Evolution of Social Behaviors and Emergent Population Organization (Nakeya Williams, et al) -- Mathematical Analysis of the Impact of Social Structure on Ectoparasite Load in Allogrooming Populations (Heather Z. Brooks, et al) -- Modeling the Argasid Tick (Ornithodoros Moubata) Life Cycle (Sara Clifton, et al) -- A Mathematical Model for Tumor-Immune Dynamics in Multiple Myeloma (Jill Gallaher, et al) -- Fluid Dynamics of Nematocyst Prey Capture (Wanda Strychalski, et al) -- Simulations of the Vascular Network Growth Process for Studying Placenta Structure and Function Associated with Autism (Catalina Anghel, et al) -- Placental Vessel Extraction with Shearlets, Laplacian Eigenmaps, and a Conditional Generative Adversarial Network (Catalina Anghel, et al) -- Author Index.
	Sommario/riassunto	This volume examines a variety of biological and medical problems using mathematical models to understand complex system dynamics. Featured topics include autism spectrum disorder, ectoparasites and allogrooming, argasid ticks dynamics, super-fast nematocyst firing, cancer-immune population dynamics, and the spread of disease through populations. Applications are investigated with mathematical models using a variety of techniques in ordinary and partial differential

equations, difference equations, Markov-chain models, Monte-Carlo simulations, network theory, image analysis, and immersed boundary method. Each article offers a thorough explanation of the methodologies used and numerous tables and color illustrations to explain key results. This volume is suitable for graduate students and researchers interested in current applications of mathematical models in the biosciences. The research featured in this volume began among newly-formed collaborative groups at the 2017 Women Advancing Mathematical Biology Workshop that took place at the Mathematical Biosciences Institute in Columbus, Ohio. The groups spent one intensive week working at MBI and continued their collaborations after the workshop, resulting in the work presented in this volume.