

1. Record Nr.	UNINA9910863190903321
Autore	Wu Jianhong <1964->
Titolo	Transmission Dynamics of Tick-Borne Diseases with Co-Feeding, Developmental and Behavioural Diapause / / by Jianhong Wu, Xue Zhang
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2020
ISBN	9783030540241 3030540243
Edizione	[1st ed. 2020.]
Descrizione fisica	1 online resource (XIII, 160 p. 24 illus., 21 illus. in color.)
Collana	Lecture Notes on Mathematical Modelling in the Life Sciences, , 2193-4797
Disciplina	616.968
Soggetti	Biomathematics Differential equations System theory Medicine, Preventive Health promotion Mathematical and Computational Biology Differential Equations Complex Systems Health Promotion and Disease Prevention
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	1. Ecology, Epidemiology and Global Public Health Burden of Tick-Borne Diseases -- 2. Deterministic Models and Temperature-Driven R0 Maps -- 3. Estimating Infection Risk of Tick-Borne Encephalitis -- 4. Structured Tick Population Dynamics -- 5. Infestation Dynamics and Tick-on-Host Distribution Pattern Formation -- 6. Oscillations Due To Diapause -- 7. Additional Topics for Future Studies.
Sommario/riassunto	This monograph introduces some current developments in the modelling of the spread of tick-borne diseases. Effective modelling requires the integration of multiple frameworks. Here, particular attention is given to the previously neglected issues of tick developmental and behavioral diapause, tick-borne pathogen co-

feeding transmission, and their interactions. An introduction to the required basics of structured population formulations and delay differential equations is given, and topics for future study are suggested. The described techniques will also be useful in the study of other vector-borne diseases. The ultimate aim of this project is to develop a general qualitative framework leading to tick-borne disease risk predictive tools and a decision support system. The target audience is mathematical biologists interested in modelling tick population dynamics and tick-borne disease transmission, and developing computational tools for disease prevention and control.
