

1. Record Nr.	UNINA9910409687103321
Autore	Filippov Alexander E
Titolo	Combined Discrete and Continual Approaches in Biological Modelling / / by Alexander E. Filippov, Stanislav N. Gorb
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2020
ISBN	3-030-41528-7
Edizione	[1st ed. 2020.]
Descrizione fisica	1 online resource (xviii, 317 pages)
Collana	Biologically-Inspired Systems, , 2211-0607 ; ; 16
Disciplina	574.0184
Soggetti	Bioinformatics Surfaces (Physics) System theory Zoology Botany Biology - Technique Computational and Systems Biology Surface and Interface and Thin Film Complex Systems Plant Science Biological Techniques
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Chapter 1. Introduction -- Chapter 2. Various methods of pattern formation -- Chapter 3. Clusterization of biological structures with high aspect ratio -- Chapter 4. Contact between biological attachment devices and rough -- Chapter 5. Anisotropic friction in biological systems -- Chapter 6. Mechanical interlocking of biological fasteners -- Chapter 7. Biomechanics at the microscale -- Chapter 8. Nanoscale pattern formation in biological surfaces -- Chapter 9. Ecology and evolution.
Sommario/riassunto	Basic laws of nature are rather simple, but observed biological structures and their dynamic behaviors are unbelievably complicated. This book is devoted to a study of this "strange" relationship by

applying mathematical modeling to various structures and phenomena in biology, such as surface patterns, bioadhesion, locomotion, predator-prey behavior, seed dispersal, etc. and revealing a kind of self-organization in these phenomena. In spite of diversity of biological systems considered, two main questions are (1) what does self-organization in biology mean mathematically and (2) how one can apply this knowledge to generate new knowledge about behavior of particular biological system? We believe that this kind of “biomimetics” in computer will lead to better understanding of biological phenomena and possibly towards development of technical implications based on our modeling.
