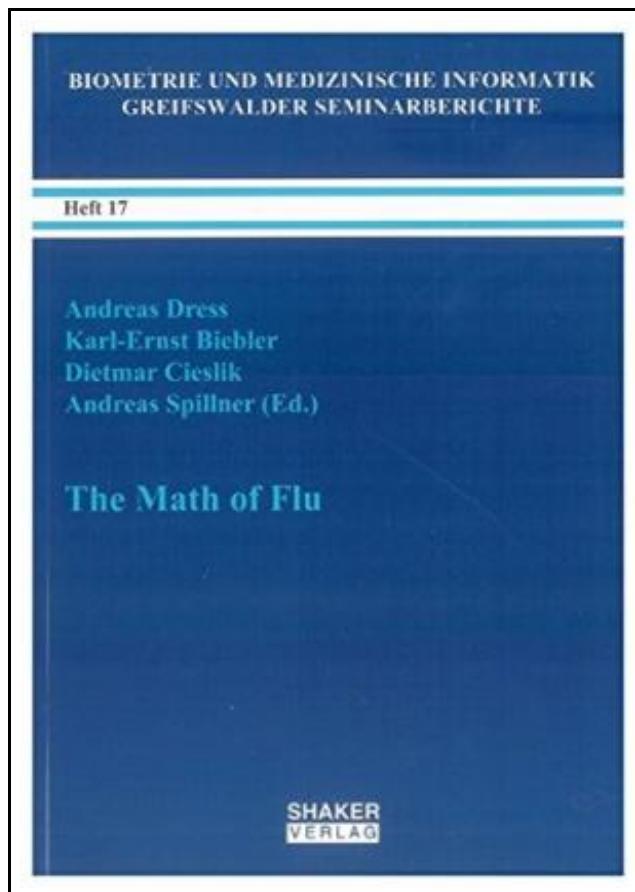


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Shaker Verlag Dez 2010, 2010. Taschenbuch. Book Condition: Neu. Neuware - In this little booklet experts from various fields join forces to discuss such and other tools from mathematics to support the analysis of the evolution of viruses and of epidemics caused by them: . Bulla and M. Stanke present a method that can be used to identify and analyse recombination events in the evolution of HIV and other viruses, . in 'Visualizing Viral Evolution', a short report on Manfred Eigen's theory of selforganization of matter and molecular evolution is given and used to interpret recent diagrams on the webpage of the Shanghai Partner Institute for Computational Biology showing phylogenetic networks presenting the evolution and spreading of the A H1N1 virus during the last 'swine flu pandemic' from 2009 (see picb.ac.cn/picb-dynamic/Desktop/news/shownews.jsp ID=538), . while a rather general approach to 'canonically' relate proper phylogenetic trees to such networks is outlined in 'A Topological Approach to Tree (Re-)Construction'. . J. Haß, S. Matuszewski, D. Cieslik and M. Haase discuss the role of pigs as a 'mixing vessel' for recombining viruses, . C. Spehr, A. Spillner and K.-E. Biebler report on methods that can be used to fit epidemic models and real-world data and . finally M. Ziller, M. Gussmann and A. Karger deal with mathematical challenges posed by mass spectroscopy - one of the most important technologies in the molecular sciences: The classification of mass spectra. We expect that this broad mix of aspects all of which are relevant in the analysis of viral evolution and epidemics will provide the reader with a good introduction into the various tools mathematics can provide to cope with a particular striking phenomenon in human history. 130 pp. Englisch.

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