MATCH Communications in Mathematical and in Computer Chemistry

BOOK REVIEW

Structural Analysis of Complex Networks

edited by

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This book consists a short Preface (written by M. Dehmer), and 19 chapters, written by a total of 30 authors. It seems to be a continuation of the book "Analysis of Complex Networks", edited by M. Dehmer and F. Emmert–Streib (see review in MATCH Commun. Math. Comput. Chem. 65 (2011) 535–536) and reflects the great activity and progress achieved in the theory of complex networks (see also the review in MATCH Commun. Math. Comput. Chem. 66 (2011) 463–464). According to a contemporary definition, a network is a large system consisting of many similar parts that are connected together to allow movement or communication between or along the parts or between the parts and a control center. Complex networks are encountered in numerous, fully unrelated, fields of science and human activity. The curious fact is that certain properties of these networks are identical, which calls for the elaboration of their general mathematical theory. The book "Structural Analysis of Complex Networks" is a immed at surveying various aspects of the emerging mathematical theory of complex networks.

The first chapter (written by Frank Emmert–Streib, pp. 1–26) provides a brief introduction to complex networks and their analysis. The following 18 chapters deal with various topics that – some more, some less – are related to the theory of complex networks. Their titles are self–explanatory: **2.** Partitions of Graphs (pp. 27–47), **3.** Distance in Graphs (pp. 49–72), **4.** Domination in Graphs (pp. 73–104), **5.** Spectrum and Entropy for Infinite Directed Graphs (pp. 105–136), **6.** Application of Infinite Labeled Graphs to Symbolic Dynamical Systems (pp. 137–168), 7. Decompositions and Factorizations of Complete Graphs (pp. 169–196), 8. Geodetic Sets in Graphs (pp. 197–218), 9. Graph Polynomials and Their Applications I: The Tutte Polynomial (pp. 219–255), 10. Graph Polynomials and Their Applications II: Interrelations and Interpretations (pp. 257–292), 11. Reconstruction Problems for Graphs, Krawtchouk Polynomials, and Diophantine Equations (pp. 293–317), 12. Subgraphs as a Measure of Similarity (pp. 319–334), 13. A Chromatic Metric on Graphs (pp. 335–356), 14. Some Applications of Eigenvalues of Graphs (pp. 357– 379), 15. Minimum Spanning Markovian Trees: Introducing Context–Sensitivity into the Generation of Spanning Trees (pp. 381–401), 16. Link–Based Network Mining (pp. 403–419), 17. Graph Representations and Algorithms in Computational Biology of RNA Secondary Structure (pp. 421–437), 18. Inference of Protein Function from the Structure of Interaction Networks (pp. 439–461), 19. Applications of Perfect Matchings in Chemistry (pp. 463–482). Each chapter contains an exhaustive list of references.

Thus, most chapters (2-15) are concerned with different aspects of graph theory, whereas two chapters (17, 18) belong to the area of mathematical biochemistry. In chapter 16 we read on network mining, which is a special kind of data mining, and is also heavily based on graph-theoretical algorithms. The last chapter (19) is an outlier: it outlines a topic of theoretical chemistry that seems to have nothing in common with complex networks and their mathematical apparatus. The book ends with a moderate-sized Index (pp. 483–486).

For readers of *MATCH Communications in Mathematical and in Computer Chemistry* (especially those involved in research in chemical graph theory), the chapters **3**, **14**, and **19**, written, respectively, by Wayne Goddard and Ortruf Oellermann, by Sebastian Cioabă, and by Damir Vukičević, might be most interesting. In particular, in chapter **3** a number of less known results on the Wiener index can be found. Colleagues doing research in mathematical biochemistry will, of course, be most interested in chapters **17** and **18**.

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Anticipating that the mathematical analysis of complex networks is going to become one of the mainstreams of mathematical chemistry, the book is recommended to the readers of *MATCH Communications in Mathematical and in Computer Chemistry*. It should be a must for any decent science library.