**DESCRIPTION**

This handbook and ready reference presents a combination of statistical, information-theoretic, and data analysis methods to meet the challenge of designing empirical models involving molecular descriptors within bioinformatics. The topics range from investigating information processing in chemical and biological networks to studying statistical and information-theoretic techniques for analyzing chemical structures to employing data analysis and machine learning techniques for QSAR/QSPR.

The high-profile international author and editor team ensures excellent coverage of the topic, making this a must-have for everyone working in chemoinformatics and structure-oriented drug design.

**ABOUT THE AUTHOR**

Matthias Dehmer studied mathematics at the University of Siegen (Germany) and received his Ph.D. in computer science from the Technical University of Darmstadt (Germany). Afterwards, he was a research fellow at Vienna Bio Center (Austria) and at Vienna University of Technology. Currently, he is an Associate Professor at UMIT - The Health and Life Sciences University (Austria). His research interests are in bioinformatics, chemical graph theory, systems biology, complex networks, statistics and information theory. In particular, he is also working on machine learning-based methods to design new data analysis methods for solving problems in computational biology and medicinal chemistry.
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