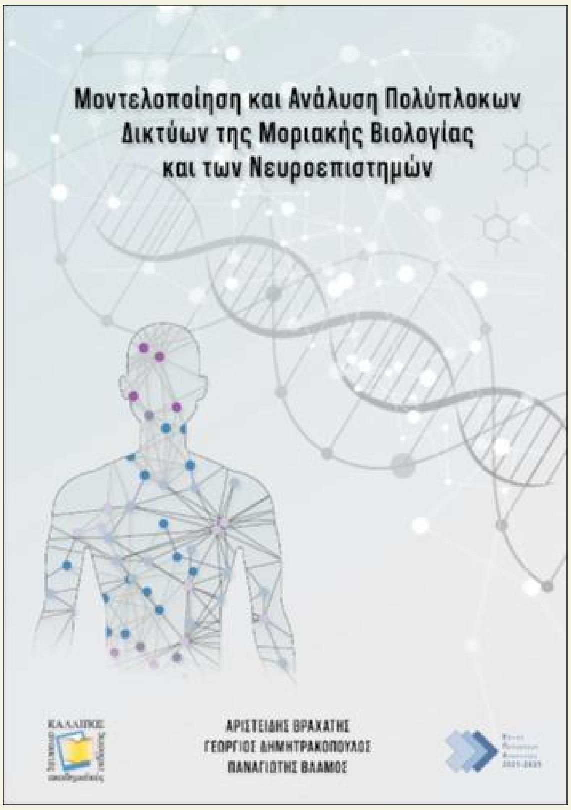

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Abstract

A complex system consists of many components, which may interact with each other in several ways. Graph/Network-based modelling is a suitable approach for understanding such complex systems. Also, machine learning techniques now play an important role in analysing large volumes of data. Two such systems in the wider area of Biology, which are still not fully understood, are the cell and the brain. Bioinformatics is an interdisciplinary scientific field that develops methodologies and software tools for understanding biological data, which can focus on the genomic, transcriptomic, proteomic or metabolomic level. Today, with the recent techniques of Molecular Biology, a huge amount of data is produced; thus, adapted algorithmic techniques are required for their efficient processing. In the field of Computational Neuroscience, we focus on electroencephalography (EEG), which captures signals from multiple areas of the brain. These data require careful pre-processing to be analysed and provide useful information. The most advanced analysis techniques include the generation of networks in time and frequency domains. Therefore, in this book, we present in detail the most recent and widely used methods in the literature for graph analysis of distinct types of data in Molecular Biology and Neurosciences

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