**Péter Antal – Ádám Arany – Bence Bolgár – András Gézsi – Gergely Hajós – Gábor Hullám – Péter Marx – András Millinghoffer – László Poppe – Péter Sárközy**

# BIOINFORMATICS

The Bioinformatics book covers new topics in the rapidly expanding field of bioinformatics, from next-generation sequencing to drug discovery and metagenomics.
The first two chapters overviews genetic measurement methods. The next four chapters discuss topics related to the effect of genetic variants from protein modeling to gene regulatory networks. Standard statistical analysis in association studies are discussed in the next two chapters. The systems biology approach is illustrated by discussing a systems-based biomarker analysis method, the graph-based network science, the dynamical systems based approaches and a Bayesian causal inference method in subsequent chapters. The next chapter discusses text-mining methods in biomedicine, especially their application in interpretation and translation. The decision theoretic approach to study design, especially multi-stage, sequential study design is discussed in the next chapter, introducing the concepts of value of information and the expected value of an experiment. Next, the heterogeneity of biomedical big data sources is overviewed, together with data and knowledge fusion methods, and with the discussion of semantic publishing, which can lead to a new unification of biomedicine. Subsequently, bioinformatic workflow methods are summarized. At last, drug discovery methods are overviewed with an outlook for personalized medicine and the final chapter presents the main steps and workflows in metagenomics.

Keywords: genotyping, next-generation sequencing methods, protein modeling, gene regulatory networks, omic networks, study design, data and knowledge fusion, worklfow systems, association study, biomarker analysis, medical decision support systems, semantic publishing, similarity based drug discovery, metagenomics.

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