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Sommario/riassunto	Recent advances in information technology have brought forth a paradigm shift in science, especially in the biology and medical fields. Statistical methodologies based on high-performance computing and big data analysis are now indispensable for the qualitative and quantitative understanding of experimental results. In fact, the last few decades have witnessed drastic improvements in high-throughput experiments in health science, for example, mass spectrometry, DNA microarray, next generation sequencing, etc. Those methods have been providing massive data involving four major branches of omics (genomics, transcriptomics, proteomics, and metabolomics). Information about amino acid sequences, protein structures, and molecular structures are fundamental data for the prediction of bioactivity of chemical compounds when screening drugs. On the other hand, cell imaging, clinical imaging, and personal healthcare devices are also providing important data concerning the human body and disease. In parallel, various methods of mathematical modelling such as machine learning have developed rapidly. All of these types of data can be utilized in computational approaches to understand disease mechanisms, diagnosis, prognosis, drug discovery, drug repositioning, disease biomarkers, driver mutations, copy number variations, disease pathways, and much more. In this Special Issue, we have published 8 excellent papers dedicated to a variety of computational problems in

the biomedical field from the genomic level to the whole-person physiological level.