Modern Proteomics and the Application of Machine Learning Analyses in Proteomic Studies of Chronic Kidney Disease of Unknown Etiology

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Abstract : Proteomics studies of organisms are considered to be significantly information-rich compared to their genomic counterparts because proteomes of organisms represent the expressed state of all proteins of an organism at a given time. In modern top-down and bottom-up proteomics workflows, the primary analysis methods employed are gel–based methods such as two-dimensional (2D) electrophoresis and mass spectrometry based methods. Machine learning (ML) and artificial intelligence (AI) have been used increasingly in modern biological data analyses. In particular, the fields of genomics, DNA sequencing, and bioinformatics have seen an incremental trend in the usage of ML and AI techniques in recent years. The use of aforesaid techniques in the field of proteomics studies is only beginning to be materialised now. Although there is a wealth of information available in the scientific literature pertaining to proteomics workflows, no comprehensive review addresses various aspects of the combined use of proteomics and machine learning. The objective of this review is to provide a comprehensive outlook on the application of machine learning into the known proteomics workflows in order to extract more meaningful information that could be useful in a plethora of applications such as medicine, agriculture, and biotechnology.

Keywords : proteomics, machine learning, gel-based proteomics, mass spectrometry

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