Computational Proteomics and Genomics

Genomics is the study of the genome, i.e. the whole hereditary information of an organism that is encoded in the DNA (or, for some viruses, RNA). Investigation of single genes, their functions and roles is becoming common practice in today's medical and biological research. Genome-wide sequencing projects have been completed for many organisms, including Homo Sapiens. Currently thousands of genes have been sequenced but still wait for any functional information to be assigned to them: this suggests that current comprehension of most biological and pathological processes is by far incomplete. As a consequence, new technological platforms that exploit the genome sequence information to explore gene function in a systematic way are evolving at an incredibly high pace, e.g. microarray.

Proteomics is a fastly developing area of biochemical investigation and regards the study of the proteins expressed in an organism or a cell. Proteomics studies include: protein identification and quantification, structural genomics, protein-to-protein interaction, post-translational modifications, and so on. In medical studies, the basic aim of proteomic analysis is the identification of specific protein patterns from cells, tissues and biological fluids related to physiological or pathological conditions (biomarker discovery). It provides a different view as compared to gene expression profiling, which does not evaluate post-transcriptional, post-translational modifications as well as protein compartmentalization and half-life changes (for instance ubiquitination and proteasome-driven degradation). All these characteristics make the protein profile much more complex but more informative compared to gene expression profiling.