

	What it is?	Main applications
Genomic	Analyse DNA sequences for studying the structure and function of genomes, gene regulation and genetic alterations	<p>Single nucleotide polymorphisms (SNP), is the most common type of gene polymorphism, are substitutions, deletions, or insertions of a single nucleotide occurring in human genome. SNPs could produce an altered protein, change the expression level of a normal protein, or have no discernible effect on protein function. For example, genetic polymorphisms involved in different cellular function have been linked to sepsis susceptibility. Thus, high risk individuals can be identified and differently treated during infectious conditions</p> <p>Epigenetics modifications in DNA can potentially alter gene expression without modifying the DNA sequence. DNA methylation marks and histone posttranslational modifications are major indicators for the epigenetic regulation of gene expression. For example, epigenetic mechanisms affect an early stage in the progression of sepsis by suppressing proinflammatory gene expression. Thus, epigenetic markers in target genes can serve as biomarkers for the early diagnosis of sepsis</p>
Transcriptomic	Analyse all RNAs synthesized in an organism, including protein coding, non-protein coding, alternatively spliced, alternatively polyadenylated, alternatively initiated, sense, antisense, and RNA-edited transcripts.	<p>Whole gene-expression profiling partially reflects steady-state mRNA abundance and could characterize cell response to different stimuli. For example, the balance between pro- and anti-inflammatory responses is achieved through a tight regulation of gene expression. Thus, it is possible to identify sepsis-specific gene signatures, and its modifications due to specific treatments.</p> <p>MicroRNAs (miRNAs) and small interfering RNA (siRNA) are evolutionarily conserved, non-coding sort-length RNAs with the function of post-transcriptional gene repression. This RNA interference pathways are involved in different aspects of septic response being a promising tool, for example, to phenotyping sepsis. Additionally, due to the ability to knockdown, in theory, any gene they could be an interesting target to new treatment options.</p>
Proteomic	Analyse the set of all proteins that are expressed by an organism, including protein quantification, localization, function and interaction.	<p>The proteome reflects the functional expression of the genome. It reflects the current functioning status of one particular system and helps to understand gene functioning, as it analyses the genome's end product.</p> <p>Plasma profiling can reveal specific proteins implied in sepsis and be used to the early diagnosis and in the follow-up of treatment.</p>
Metabolomic	Analyse molecules focusing on metabolites with molecular weight less than 1000 kDa	<p>Measurement of different metabolites including amino acids, polyols, fatty acids, hydroxy acids, amines, nucleotides and their derivatives. The metabolomic analysis gives accurate snapshot of the patient metabolic status in a given time, reflecting at the same time gene function and enzyme activity. A more timely diagnosis and prognosis of sepsis may be achieved by detecting changes in the concentrations and ratios of metabolites</p>
Machine-learning	Machine learning is the scientific discipline that focuses on how	Supervised learning has the goal of predicting a known output or target and focuses on classification and prediction. In this

	<p>computers learn from data. The major idea under this concept is building statistical models from massive data sets, which can include billions or trillions of data points.</p>	<p>kind of modelling, the computer can find relationships not readily apparent to human beings.</p> <p>Unsupervised learning there are no outputs to predict. The computer tried to find naturally occurring patterns or groupings within the data.</p> <p>Both models allow us to develop robust risk models and redefining patient classes, helping in construct decisions trees. It is possible, for example, determine a subgroup of patients that benefit in a manner unrelated to the mechanism of action of one drug.</p>
<p>Bioinformatic</p>	<p>It is an integrative field in life sciences that combines biology and information technology. The main objective of bioinformatics is to develop methodologies and tools to study large volumes of biological data.</p>	<p>Using machine learning algorithms and several other computational tools such iterative approaches, and molecular modelling /algorithms, bioinformatic can help in integrating genomic, transcriptomic and proteomic data.</p>