
STATISTICAL METHODS AND MODELS FOR INTEGRATING GENOMIC AND FUNCTIONAL DATA

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Abstract:

Thanks to the scientific and technological progress, functional genomics has advanced from the study of a very small number of genes and proteins to the analysis of an entire genome, thereby providing a global vision of the biological mechanisms which dictate how cells work. This groundbreaking opportunity, which allows us to understand the processes by means of which normal cells transform into tumor cells, or stem cells into terminally differentiated cells, must not be disconnected from the development of statistical methods and models for the analysis of the information provided by the latest genome technology. Indeed, despite the significant and rapid technological developments, the severe deficiencies of the methods used to analyze and model biological signals still represent a limiting factor for the real exploitation of genomic data.

The incredible abundance and indescribable variety of gene expression data available in public databases is a resource which has only been partially exploited. In fact, the majority of these data has been analyzed with the purpose of identifying those genes that distinctively characterize a given phenotype; little has been done for using gene expression profiles when studying the regulatory mechanisms of transcription, that is, for the reconstruction of gene networks. We cannot disregard the fact that the effective reconstruction of the circuits that regulate gene expression, expression data must be integrated with functional and structural genomic information. A crucial step is the development of novel probabilistic models and statistical techniques capable of supporting, through the analysis of the large amounts of biological data available, the global study of the mechanisms underlying cell function.

The proposed research programme aims at developing an innovative statistical approach which will integrate functional and structural genomic information into the analysis of the transcriptional and post-transcriptional gene regulatory mechanisms of genomic expression. The results achieved will be applied to the investigation of how hematopoietic stem cells differentiate into myeloid cells.