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Sommario/riassunto	Transcription regulation is a complex process that can be considered and investigated from different perspectives. Traditionally and due to technical reasons (including the evolution of our understanding of the underlying processes) the main focus of the research was made on the regulation of expression through transcription factors (TFs), the proteins directly binding to DNA. On the other hand, intensive research is going on in the field of chromatin structure, remodeling and its involvement in the regulation. Whatever direction we select, we can speak about several levels of regulation. For instance, concentrating on TFs, we should consider multiple regulatory layers, starting with signaling pathways and ending up with the TF binding sites in the promoters and other regulatory regions. However, it is obvious that the TF regulation, also including the upstream processes, represents a modest portion of all processes leading to gene expression. For more comprehensive description of the gene regulation, we need a systematic and holistic view, which brings us to the importance of systems biology approaches. Advances in methodology, especially in high-throughput methods, result in an ever-growing mass of data, which in many cases is still waiting for appropriate consideration. Moreover, the accumulation of data is going faster than the development of algorithms for their systematic evaluation. Data and methods integration is indispensable for the acquiring a systematic as well as a systemic view. In addition to the huge amount of molecular or

genetic components of a biological system, the even larger number of their interactions constitutes the enormous complexity of processes occurring in a living cell (organ, organism). In systems biology, these interactions are represented by networks. Transcriptional or, more generally, gene regulatory networks are being generated from experimental ChIPseq data, by reverse engineering from transcriptomics data, or from computational predictions of transcription factor (TF) - target gene relations. While transcriptional networks are now available for many biological systems, mathematical models to simulate their dynamic behavior have been successfully developed for metabolic and, to some extent, for signaling networks, but relatively rarely for gene regulatory networks. Systems biology approaches provide new perspectives that raise new questions. Some of them address methodological problems, others arise from the newly obtained understanding of the data. These open questions and problems are also a subject of this Research Topic.