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Sommario/riassunto	<p>The recent discovery of small and long non-coding RNAs (ncRNAs) has represented a major breakthrough in the life sciences. These molecules add a new layer of complexity to biological processes and pathways by revealing a sophisticated and dynamic interconnected system whose structure is just beginning to be uncovered. Genetic and epigenetic aberrations affecting ncRNA gene sequences and their expression have been linked to a variety of pathological conditions, including cancer, cardiovascular and neurological diseases. Latest advances in the development of high throughput analysis techniques may help to shed light on the complex regulatory mechanisms in which ncRNA molecules are involved. Bioinformatics tools constitute a unique and essential resource for non-coding RNA studies, providing a powerful technology to organize, integrate and analyze the huge amount of data produced daily by wet biology experiments in order to discover patterns, identify relationships among heterogeneous biological elements and formulate functional hypotheses. This Research Topic reviews current knowledge, introduces novel methods, and discusses open challenges of this exciting and innovative field in connection with the most important biomedical applications. It consists of four reviews and six original research and methods articles, spanning the full scope of the Research Topic.</p>