Software Tools and Algorithms for Biological Systems pp 679-688 | Cite as

Analysis and Clustering of MicroRNA Array: A New Efficient and Reliable Computational Method

Authors Authors and affiliations

Luca Sterpone, Federica Collino, Giovanni Camussi, Claudio Loconsole

Part of the Advances in Experimental Medicine and Biology book series (AEMB, volume 696)

Abstract

MicroRNAs (miRNAs) play determinant roles in gene expression and several cellular processes of mammalian. These processes include differentiation, development, apoptosis, and cancer pathomechanisms. In detail, miRNAs are known to regulate the expression of keys genes relevant to cancer and potentially to other diseases [1–3]. MiRNAs are short noncoding RNAs having a central function in gene expression, since miRNAs are involved in cellular differentiation processes [4, 5], organism developments [6], and apoptosis. Furthermore, recent studies provide growing evidence of the contribution of miRNAs in cancer cellular mechanisms. Therefore, the analysis and the correct identification of miRNAs expression levels play a key role for better understanding and classifying cancer and other diseases. In parallel with the drastic growing of interest into the study of miRNAs, the support of systems and tools that allow an efficient and more robust analysis of miRNA’s expression levels become increasing mandatory to have a better disease identification.