Abstract

Breast cancer is a highly disease which the women's are mostly affected. The main cause of women's death is not only by the tumor cells that affects the Breast Cancer but its metastases at different sites, such as lymph nodes and other organs (i.e. lung, liver and bones). Identifying the circulating tumor cells in the blood that results from tumor cell invasion and intravascular filtration highlights its role which concerns the tumor cells aggressiveness and metastasis. Biological research regarding CTC's monitoring for Breast Cancer is limited due to the cause of indicative genes for their detection and isolation of genes. By using the direct CTC detection, we focus on the identification of factors in peripheral blood that can be indirectly reveals the presence of tumor cells. By selecting the publicly available Breast Cancer tissues and peripheral blood microarray datasets. In this 2 steps are to be followed by eliminating the procedures for the identification of several discriminant factors. The new algorithm CTCBC is proposed to identify the BC in an earlier stage. This procedure provides the facilities of identifying the major genes which involved in the causes of Breast cancer.
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**Index Terms**

Computer Science

Information Sciences

**Keywords**

Breast cancer (BC) signature, Circulating tumor cells (CTC), Peripheral Blood (PB), Biological processes, gene Elimination.