Classification of proteins based on Difference of expression in healthy and cancerous tissue to identify biomarkers of prevalent cancers

Ali. Farid Mohammadzadegan [a], Kazem. Pourbadakhshan*[b]

a- M.S of control engineering, Quchan University of Advanced Technology, Quchan, Iran

b- Assistance Professor, Quchan University of Advanced Technology, Quchan, Iran

*k.poorbadakhshan@qiet.ac.ir

Abstract: Recognition source and stage of cancer has always been one of the issues of interest for scientists. On the other hand, cancer is the second leading cause of death worldwide after cardiovascular disease [1]. Between 2005 and 2015, cancer cases increased by 33%. According to the Global Burden of Disease Cancer(GBDC) report in 2015, there were 17.5 million cancer cases worldwide and over 8.7 million cancer deaths. Based on the same report in 2015, breast cancer, TBL (Tracheal, Bronchus, and Lung) cancer and colorectal cancer were the most common incidents [2]. From another perspective, one of the requirements for the treatment of different cancers is early diagnosis in the initial stages. At the end of the human genome project, molecular medicine moved to a step beyond the genome called "proteomics" [3 ,4]. Its application in biological sciences, especially cancer research and therapeutics, has been unprecedented [5,6]. The promise of proteomics is to perform just as a microarray and to identify all the proteins in human genome [9,8,7,1]. Defective proteins are one of the main causes of cancer. Therefore, they are important indications for cancer diagnosis and treatment. In addition, proteins are the main target for most drugs and are the basis for the design of a variety of drugs. As a result, proteomics studies are highly beneficial for recognizing their role in cancer formation and control [10]. If a specific protein is involved in cancer, by knowing its 3D structure, proteomics can design drug to effectively counteract it and prevents its activity. Proteomics can facilitate discovery of new molecular targets for therapy, biomarkers for early detection, and new endpoints for therapeutic efficacy and toxicity [11]. Identification of specific and sensitive markers of cancer is an important public health concern [12,9]. In recent years, much attention has been paid to the role of biomarkers in the diagnosis of cancer in clinical studies [13]. Biomarkers are important tools for tracking and studying cancer [14]. The development of proteomics and genomics has led to the identification of a wide range of clinically valuable biomarkers. Biomarkers' cognition is helpful in determining the (stage) of the disease and its specific treatment [15]. Biomarkers are really important in timely diagnosis of cancer, the progression of the disease and effective treatment by employing the most effective techniques [16]. To analyze a cancer, identifying only one biomarker does not provide enough information for that cancer, but paying attention to changes in the level of expression of various proteins is valuable [14,17,18]. In this paper, effective proteins for breast, lung and colorectal cancers, have been identified and classified. Biomarkers sparse in different articles are combined using Text Mining and reviewing articles that introduced a cancer biomarker. In fact, a list of identified biomarkers for the three common cancer types is provided. They have been nominated as cancer biomarkers for early diagnosis or even prediction of future illness.

Keywords: Proteomics; biomarkers; breast cancer; lung cancer; colorectal cancer; classification

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