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Research Article

Diagnosis of Lung Cancer by Fractal Analysis of Damaged DNA

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Cancer starts when cells in a part of the body start to grow out of control. In fact cells become cancer cells because of DNA damage. A DNA walk of a genome represents how the frequency of each nucleotide of a pairing nucleotide couple changes locally. In this research in order to study the cancer genes, DNA walk plots of genomes of patients with lung cancer were generated using a program written in MATLAB language. The data so obtained was checked for fractal property by computing the fractal dimension using a program written in MATLAB. Also, the correlation of damaged DNA was studied using the Hurst exponent measure. We have found that the damaged DNA sequences are exhibiting higher degree of fractality and less correlation compared with normal DNA sequences. So we confirmed this method can be used for early detection of lung cancer. The method introduced in this research not only is useful for diagnosis of lung cancer but also can be applied for detection and growth analysis of different types of cancers.

1. Introduction

Cancers are caused by uncontrollable growth of cells which do not die. Normal cells in the body grow, divide, and finally die (apoptosis) in an orderly path. When the death process of cells breaks down, cancer starts. In case of cancer, cells continue to grow and divide instead of having a programmatic death which results in a bunch of abnormal cells growing out of control.

Lungs are spongy organs in the chest which take in oxygen and release carbon when human inhales and exhales, respectively. Lung cancer begins in the lungs. Lung cancer is a dominant type of cancer which kills many people every year compared to other types of cancer.

When the cell's gene cannot correct the DNA damage, the lung cancer appears. Inhaling carcinogenic substances is the main reason of lung cancer.

For years some methods have been investigated in order to diagnose the lung cancer. Most of these methods are based on medical theories. Among these methods, employing computed tomography (CT) image analysis is more dominant. By computed tomography of chest Mets et al. derived and validated a model of lung cancer which studies the coronary and aortic calcium volume in lung [1]. Veronesi et al. analyzed computed tomography images of lung in case of smokers and former smokers in order to detect the lung cancer [2]. In another work Jiménez-Bonilla et al. worked on diagnosis of recurrence and assessment of postrecurrence survival in patients with extra cranial non-small cell lung cancer using 18F-FDG PET/CT [3]. See also [4–6]. On the other hand, some researchers have worked on analysis of patients' DNA for diagnosis lung cancer. An et al. detected tumor-associated aberrant hyper methylation of the *p16* gene in DNA extracted from plasma. Using a modified seminested methylation-specific PCR, they did their experiments on 105 non-small cell lung cancer patients and 92 matched tumor DNA samples [7]. In a recent research, Jelovac et al. detected PIK3CA DNA mutation in plasma of a patient with breast and lung cancers [8]. In another extensive work, Diehn et al. employed deep sequencing for detection of circulating tumor DNA in non-small cell lung cancer [9].

Beside some works done on the prediction and analysis of lung cancer from biological point of view, there are few researches being reported which use mathematical models for diagnosis of lung cancer. McCulloch et al. used mathematical model for developing a model-based CAD algorithm which capture scanner physics and anatomic information. Their model uses multiple segmentation algorithms in order