

## ***Paper name:-***

*Complex Network Characterization Using Graph Theory and Fractal Geometry:  
The Case Study of Lung Cancer DNA Sequences*

## ***Abstract:-***

This paper discusses the evolution of methods of exploiting the elementary motions of evolution to study complex networks by means of co-embedding that lead to common fractal properties. This method is likely to be useful for analyzing lung cancer DNA by different fractal geometries theories. This method is based on a renewed study consideration of network complexity at the level of countries and continents, as many scientists have pointed out to the importance of fractal mathematics, also it's easy to use in lung cancer research, although some researchers and doctors don't realize its value yet. Therefore, this paper aims to examine the assumptions of fractals, analysis of the fractional dimension, and measurements to be applied to the lung cancer network or complex networks as a whole. The results demonstrated the relationship between the fractional dimension and the properties of the lung cancer network, as when the fractional dimension in the lung cancer network decreased, the topological characteristics of the network increased, finally statistical significance between the lung cancer network and the complexity of the network.

## ***Introduction:-***

Theoretical models on complex networks play an important role in many fields such as computer science, engineering, medicine, population biology, and DNA sequence analysis. In the classical conception of DNA geometry, the double helix represents a ribbon constructed from smooth curves describing an idealized structure. How to read and recognize the basic structure of a DNA sequence is a major problem, so in previous years the assembly and sequencing of DNA fragments became important to improve the construction of complete DNA sequences that focus on the pieces of data to be recorded. Incomplete data sets, in this paper reference is made to the concept of graph theory and fractal geometry for analyzing DNA sequences and their properties in different ways. Several papers deal with DNA sequencing analysis, but this paper deals with identifying the advantage of applying graph theory and fractals

in the study of lung cancer DNA sequences. This app shows hidden geometries that help confirm the structure of DNA sequences more clearly and this geometry has fractal structures. To achieve the paper's goal we must observe some basic steps : 1) Converting DNA nucleotides into a new coordinate system; 2) presenting DNA nucleotides as a path in a graph in the new coordinate system; 3) connecting points into a continuous graph; 4) using a method for estimating the Hurst exponent  $H$ ; 5) using fractal geometry to determine the complexity of the graph; 6) constructing visibility graphs; and 7) calculating statistical and topological properties of the DNA network. The concepts of graph theory and fractals are presented for use in calculating the properties of the DNA network and sequence in lung cancer, as this theory continued to develop during the twentieth century in the disciplines of engineering and science.

### ***Related work:-***

*There are several works that are relevant to the topic of this paper like:- Lung cancer—a fractal viewpoint, Fractal Analysis : Methodologies for Biomedical Researchers, Chaos and Fractals: New Frontiers of Science, Design of Additively Manufactured Lattice Structures for Biomedical Applications (A New Method for Biostatistical miRNA Pattern Recognition with Topological Properties of Visibility Graphs in 3D Space), Physica A: Statistical Mechanics and its Applications, Surface roughness evaluation in hardened materials by pattern recognition using network theory, A Ring in Graph Theory, Sequence analysis by iterated maps, fractals and the geometry of nature, New Method for Estimating Fractal Dimension in 3D Space and Its Application to Complex Surfaces, The fractal lung: Universal and species-related scaling patterns, Newly described pattern recognition receptors team up against intracellular pathogens, Effect of Diltiazem Cardioplegia on the Myocardial Protection and Functional Recovery of the Isolated Perfused Rat Heart, HIF1 $\alpha$  and HIF2 $\alpha$ : sibling rivalry in hypoxic tumour growth and progression, Regulation of gene expression by hypoxia, Role of Hypoxia-Inducible Factor 1 $\alpha$  in Gastric Cancer Cell Growth, Angiogenesis, and Vessel Maturation, etc.*

## ***Methodology:-***

The approach used in developing this method focuses on the interaction between assumptions that are relevant to the treatment of lung cancer and theoretical concepts. These concepts are discussed in five sections, namely: 1) We present lung cancer 2) The basic concepts of graph theory and fractal geometry are defined 3) Description of the method Proposed for DNA sequencing 4) Statistical identification of DNA patterns 5) Application and data preparation using DNA data from Homo sapiens HIF1A database.

*It also includes:*

*Carcinoma of the Lung , Graph Theory and Fractal Geometry , A New Method for DNA Sequencing , Statistical DNA Pattern Recognition and Data Preparation—Application.*

## ***Results:-***

*Complexity in biological systems is predicted by describing interactions amongst different DNA structures. Graphs are emerging as indispensable tools in explaining how the DNA structure functions. We calculated topological properties that describe Lung gene networks.*