

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.

