

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.