



RESEARCH ARTICLE

BIOCOMPUTATIONAL ANALYSIS OF GENE EXPRESSION FOR RHEUMATIC ARTHRITIS DISEASE

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Abstract— Rheumatic Arthritis (RA) is a chronic systemic inflammatory disease involving primarily the peripheral synovial joints. The disease is progressive and results in pain, stiffness, and swelling of joints. The genes do contribute for the development of RA. The genes involved may vary among individuals and between populations in different age group.

Bioinformatics have received great attention in recent years, where new effective methods for genomic sequence analysis, such as the detection of Gene coding regions, have been developed. This project presents an overview of the most relevant applications in the analysis of genomic sequences of Rheumatic Arthritis disease. An attempt has been made to develop a tool to investigate the Gene coding regions of RA disease, which provides very useful information about the mutations occurred in the sequence later causing RA. In the developed system the Gene coding regions of both RA gene and a gene of a healthy person is analyzed and compared. The matching and mismatching of the two genes that are being compared are analyzed. The percentage for each nucleotide bases Adenine (A), Guanine (G), Thymine (T) and Cytosine (C) in a gene sequence are to be detected.

Key Terms: - Rheumatic arthritis; Gene sequences; nucleotides; gene sequence

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