

# Abstract

Isochore is one of the most striking features of the DNA sequences of warm-blooded animals. Isochore Human chromosome is believed to be a mosaic structure of different regions of varying nucleotide composition which are otherwise known as isochore. Isochores in human genome are claimed to be classified into five families L1, L2, H1, H2, H3 by their characteristic G+C content <37%, 37%-42%, 42%-47%, 47%-52%, >52%. In this dissertation we have developed a simple bottom up approach for finding isochores of human genome and analyzed distribution of genes among isochores in human genome. We have analyzed all 24 Human chromosomes using our method and found several isochores regions having length up to 16.45 Mbp sizes, which covers almost 93% of human genome. We have mapped 21,799 genes with all the identified isochores and found majority of genes are available in high G+C content isochore.

Keywords : chromosome, isochore, bottom up approach G+C content, genome coverage