Abstract

The genome of each organism is arranged in a unique and mostly undiscovered pattern. Unlike prokaryotic genomes, it has been proposed that the eukaryotic genomes contain isochore regions, mosaics of homogeneous G+C content that abruptly change from one neighbor isochore to the next. Isochores were first identified using CsCl ultracentrifugation (Macaya et al. 1976). These procedures are time consuming and tend to miss the shorter homogeneous regions thus computational tools have been created allowing isochores, now referred to as long homogeneous genomic regions, to be identified by sequence analysis. In genetics, an isochore is a long homogeneous genome region (LHGRs) of DNA with high degree uniformity in guanine and cytosine (GC) content. Isochore theory proposed that isochores composition varied between warm-blooded (homeotherm) vertebrates and cool blooded (poikilotherm) vertebrates. In human genome, it was described as mosaic of alternating low and high GC content isochore belonging to five compositional families, L1, L2, H1, H2, and H3 whose corresponding ranges of GC contents were said to be <37%, 37%-42%, 42%-47%, 47%-52%, >52% respectively. In this dissertation we analyzed Isochores in Human Genome using an existing computational approach developed by Bernaola-Galvan et al. We have analyzed all 24 human chromosomes and found several isochore regions having length up to 17.14Mbp sizes. We observed that the family L2 isochors (G+C% 37.0 to 42.0) are abundantly available in human genome in comparison to other isochors.