

Detection of tandem repeats can be used for phylogenetic studies and disease diagnosis. The numerical representation of genomic signals is very important, as many of the methods for detecting repeated sequences are part of the DSP field. These methods involve the application of a kind of transformation which requires mapping the symbolic domain into the numeric domain in such a way that no additional structure is placed on the symbolic sequence beyond that inherent to it. Here we investigate the application of spectral analysis and spectrograms using a novel numerical representation to isolate position and length of alpha satellite higher order repeats in human chromosome 7.