

# Abstract

Genome is made up of both coding as well as non coding sequences. Relative dinucleotide frequencies (RDFs) in bacterial genomes are similar in different parts of a chromosome while the values are variable among different bacteria. Therefore, this constancy of the RDFs within a genome was termed as “genome signature”. We have tried to understand the possible cause(s) of genome signature in bacterial genomes. To have a better insight towards the functional significance of dinucleotides, we have studied relative dinucleotide frequencies (RDFs) in coding and non-coding regions in bacterial genomes. Analysis of the RDFs in non-coding as well as in coding regions might help in understanding the possible cause(s) of the genome signature.

In this study we observed that the intergenic sequences and the coding sequences within a prokaryotic genome are remarkably different with respect to their dinucleotide usages. Therefore genome signature is not constant throughout the DNA sequence and it varies from regions to regions depending on the usage. Our results suggest that codon usage bias is a major attribute towards dinucleotide constraints in genomes as no constraint was observed when we filtered out biasness in codon usage.