Abstract:

Synonymous codons those encode same amino acid are not used with equal frequencies among genes of an organism. This is known as codon usage bias. Effective number of codons (Nc) is the most widely used method for measuring codon usage bias. First it find out effectively how many codons are used for each amino acid in the gene. Then, summing the 'effective number of codons' used by each of the 20 aa will then yield an Nc, used in a gene. An extremely biased gene would use only 20 codons (i.e., one per aa), whereas an unbiased gene would tend to use all 61 codons equally (after correcting for aa usage). for a gene using the 'universal' code, there are 2 aa with only one codon choice, 9 with two, 1 with three, 5 with four, and 3 with six. These represent five SF types, designated SF types 1, 2, 3, 4, and 6 according to their respective number of synonymous codons. The measure of SCU bias will involve combining contributions to overall bias from each of the five SF types. Effective number of codons(Nc):

$$N_c = 2 + \left(\frac{9}{F_2} \right) + \left(\frac{1}{F_3} \right) + \left(\frac{5}{F_4} \right) + \left(\frac{3}{F_6} \right)$$

Therefore, in this project work it is aimed to develop a web based portal for computing the effective number of codon and few other measures of codon usage bias.