$\boldsymbol{m\widehat{N}_{cFDS}}$

In the genetic code table synonymous codons are arranged systematically as these are usually different from each other at the 3rd position. A set of four codons with degeneracy only at the 3rd position is grouped as a family box in this table. There are eight such family boxes in genetic code table: one for each amino acid having four or more synonymous codons. Third position in these codons is known as four-fold degenerate site (FDS). The FDS in coding sequences is important for studying the effect of any selection pressure on codon usage bias because nucleotide substitution *per se* is not under any such pressure at the site due to the unaltered amino acid sequence in a protein (Satapathy et al 2014).

$m\widehat{N}_{cFDS}$ is a variation of $m\widehat{N}_c$ (Satapathy et al 2017) that calculate effective number of codons only for 32 family box codons.

Reference

Satapathy SS, Sahoo AK, Ray SK and Ghosh TC (2017) Codon degeneracy and amino acid abundance influence the measures of codon usage bias: improved Nc ($\boldsymbol{\widehat{N}_c}$) and ENCprime ($\boldsymbol{\widehat{N}'_c}$) measures. Genes to cells 22:277–283.

Satapathy SS, Powdel BR, Dutta M, Buragohain AK and Ray SK (2014) Selection on GGU and CGU codons in the high expression genes in bacteria. J Mol Evol 78:13–23.