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

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.

$m\widehat{N}_{cFDS}$ is a variation of $m\widehat{N}_{c}$ that calculate effective number of codons only for 32 family box codons. Its value ranges from 8 to 32.