x[n] = [A A T G C A T C A] then,
$u_A[n]$ = [1 1 0 0 0 1 0 0 1],
$u_G[n]$ = [0 0 0 1 0 0 0 0 0],
$u_C[n]$ = [0 0 0 0 1 0 0 1 1] and
$u_T[n]$ = [0 0 1 0 0 0 1 0 0].

Obviously, the sum of all binary indicators at any position n is 1 for all n.

i.e. $u_A[n] + u_G[n] + u_C[n] + u_T[n] = 1$ for n=0, 1, 2,....N-1. (1)

Let $U_A[k]$, $U_G[k]$, $U_C[k]$ and $U_T[k]$ be the Discrete Fourier Transforms (DFT) of the binary sequences $u_A[n]$, $u_G[n]$, $u_C[n]$ & $u_T[n]$ respectively which are given by,

$$U_X[k] = \sum_{n=0}^{N-1} u_X[n] e^{(-j2\pi kn/N)}$$, X=A, G, C, or T and k = 0, 1, 2--- (N-1) (2)

$S[k] = \sum |U_X[k]|^2$ for X=A, G, C or T. & k = 0, 1, 2, ----- (N-1) (3)

S[k] may be used as a preliminary indicator of a coding region as a plot of S[k] against k reveals a peak at k=N/3 for coding region and shows no such peak for noncoding region. **[2]** It has been proved that the pronounced peak actually springs from the nonuniform distribution of the nucleotides in the three coding positions of codons in a coding area. **[3]** And S[k] as a coding measure is model independent as it is not specific to any particular genome.

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