Conflicts resulted in intron evolution Positive FORSD values are widely dispersed throughout genome and greatly exceeds negative FORS-D values [16]. Incapability of a sequence to optimize fold and protein pressures simultaneously resulted in potential conflict between both pressures. The conflict can be bypassed in three ways 1. use of synonymous codons to balance both pressures. 2. broadening of codon choice by use of chemically and functionally similar amino acids 3.Sequence encoding protein can be placed over wide region allowing intervening sequence to optimize fold pressure. When first two options are not sufficient to bypass the conflict only third alternative remains. So introns might correspond to part of genome where constraints of first two ways are most severe. Conflict hypothesis explains the pressures that shape the intron-exon organization found in modern gene [16].

Distribution of Substitution Densities (Fors-D) In Modern Genes

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