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Evolution of gene exon-intron structure by alternative splicing

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Motivation and Aim: At least half of the AS events, manifested by exon skipping/insertion/change of splicing sites 5'-3', are known to result in premature stop codon emergence and are subject to nonsense-mediated decay (NMD) acting as additional means of rapid abolition of expression depending on the dynamics of the local compartment of protein metabolism. It is widely used to maintain homeostasis of multicomponent complex subunits such as ribosomes, spliceosomes, and chromatin remodeling mechanisms, and is especially pronounced in brain cells. However, of greatest interest is the result of splicing encoding a functional protein to assess the increase in diversity of a specific protein in a sample. One approach to filter out NMD-prone splice products is to target ribosome-engaged transcripts, which guarantees the coding ability of the mRNAs used (Furlanis et al., 2020). *Methods and Algorithms*: We arrange a pipeline for examining the exon-skipping events derived from RNA-Seq data.

Results: We observed specific distribution of coding vs non-coding skipping events in the brain tissues. We propose an efficient approach for the selection of coding transcripts beyond non-coding ones by translating the appropriate exon skipping events and validating them against an established protein database. *Conclusion*: We managed to reduce the scan time to a reasonable range, thus proving the possibility of a wide application of the algorithm. We report the frame/phase distribution of alternative exon encoding underlining exon shuffling evolution mode featured the most in animal kingdom [1, 2]. No apparent long range phase compensation observed even in ‘old’ alternative exons. *Acknowledgements*: The work was supported by the Russian Science Foundation project 19-15-00026-П to N.K., V.B.

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