Short Communication

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SRNA (Smart Rapid Nucleotide Analysis) and RMSE (RefSeq Multigene Sequence Extractor) Web Tools for Assessing Nucleotide Composition

Shubh R Nahar[1,3#], Mostafizur Rahman[1#], Syeda Saberin Jahan[2,3], Giulianna Rivero[4], Valeri Drozhenko[3], Walter C Bell[5], Kai Ding[6], Long Ma[1], Bill Zhong[1] and Alexander Kofman[3,7*]

[1]*Department of Computer Science, Troy University, AL, USA*

[2]*Jalalabad Ragib-Rabeya Medical College and Hospital, Bangladesh*

[3]*The Filatov Institute of Eye Diseases and Tissue Therapy, the National Academy of Medical Sciences, Ukraine*

[4]*Department of Biological and Environmental Sciences, Troy University, USA*

[5]*Department of Pathology, Heersink School of Medicine, The University of Alabama at Birmingham, AL, USA*

[6]*John Hopkins University Medical School, AL, USA*

[7]*University of West Alabama, AL, USA*

[#]*Both authors contributed equally to this work*

***Corresponding author:** Alexander Kofman, Human Biology Variations Computational Genomics Research, The Filatov Institute of Eye Diseases and Tissue Therapy, the National Academy of Medical Sciences, Ukraine, University of West Alabama, AL, USA

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ABSTRACT

We present SRNA and RMSE user-friendly web tools for retrieving and analyzing the nucleotide composition of whole and fragmented nucleic acid sequences.

Keywords: Nucleotide; mRNA; Codon

Abbreviations: mRNA: Messenger RNA; UTR: Untranslated Region

Introduction

The growing number of reports indicates that codon usage bias and nucleotide composition are crucial regulatory factors that influence gene expression at various levels. These factors can affect the concentration of nuclear mRNA [1] and its stability [2,3], alter the expression of heterologous genes in bacteria, plants, yeast, mammalian cells, and transgenic animals [4], and impact the formation of Z-DNA and Z-RNA, among other effects [5,6].

SRNA 1.0 (SRNA · Streamlit) and RMSE 1.0 (NCBI RefSeq Multi-Gene Extractor · Streamlit) are user-friendly web tools that enable the retrieval of nucleotide sequences and calculation of their nucleotide composition, including G-C%, A-T%, and Z-DNA propensity by batch analysis (up to 1000 sequences). Furthermore, to assess the variations in nucleotide composition across different parts of the gene, the SRNA tool can split the original sequence into fragments of 50, 100, 200, and 400 bases.

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Alexander Kofman. Biomed J Sci & Tech Res

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