A novel method for determining the non-CDS region by using error-correcting codes

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March 30, 2022

Abstract

Our main motivation question is "Is there any relation between the non-coding region and useless error-correcting codes?". Then we focused CDS and non-CDS areas instead of exon and intron, because CDS involves in process of synthesis a protein and is involved by exons. We get the data of the genes from NCBI (missing citation). In this study, we introduce the method Fi-noncds that is used for determining the non-CDS region by using error-correcting codes. We obtained that the error-correction codes that can't correct any codes named zero error-correcting code, placed in non-CDS areas, densely. This result shows that non-CDS regions (non-coding areas in DNA) match zero error-correcting codes (useless error-correcting code). Frame lengths 7,8,9 and 10,11,12,13 and 14 were tested by the method. Optimal result for selected genes (TRAV1-1, TRAV1-2, TRAV2, TRAV7, WRKY33, HY5, GR-RBP2) is frame length 8, $n=7$, $k=2$, $dnaNo=1$. Moreover, optimal results of the algorithm Fi-noncds matched the best sequence length 8 as in [Lichtenberg, Jens and Yilmaz, Alper and Welch, Joshua D and Kurz, Kyle and Liang, Xiaoyu and Drews, Frank and Ecker, Klaus and Lee, Stephen S. and Geisler, Matt and Grotewold, Erich ve Welch, Lonnie R.,The word landscape of the non-coding segments of the Arabidopsis thaliana genome,Bell Labs Tech. J, Volume 10, no 1].

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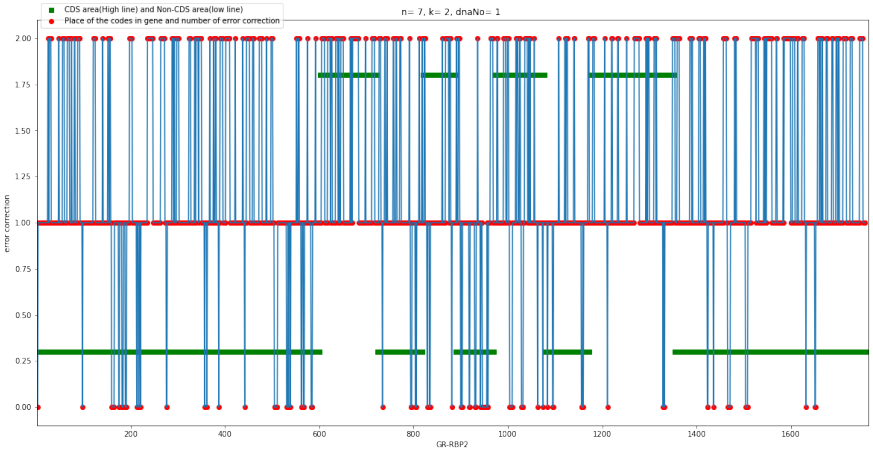

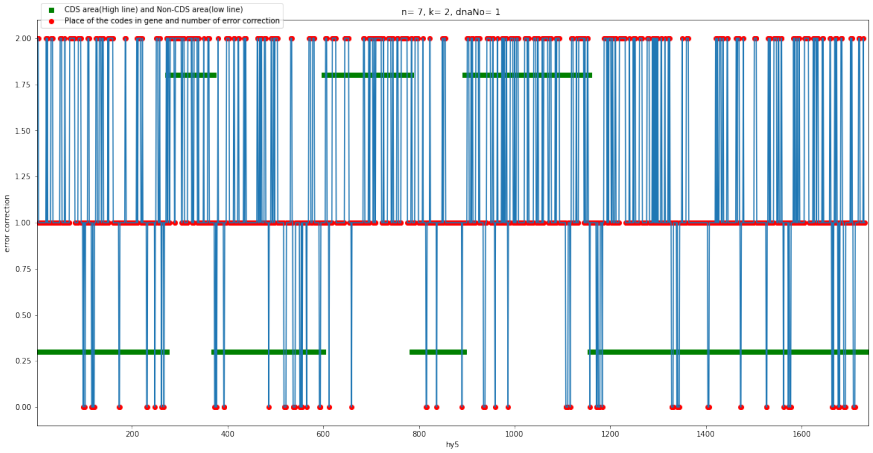

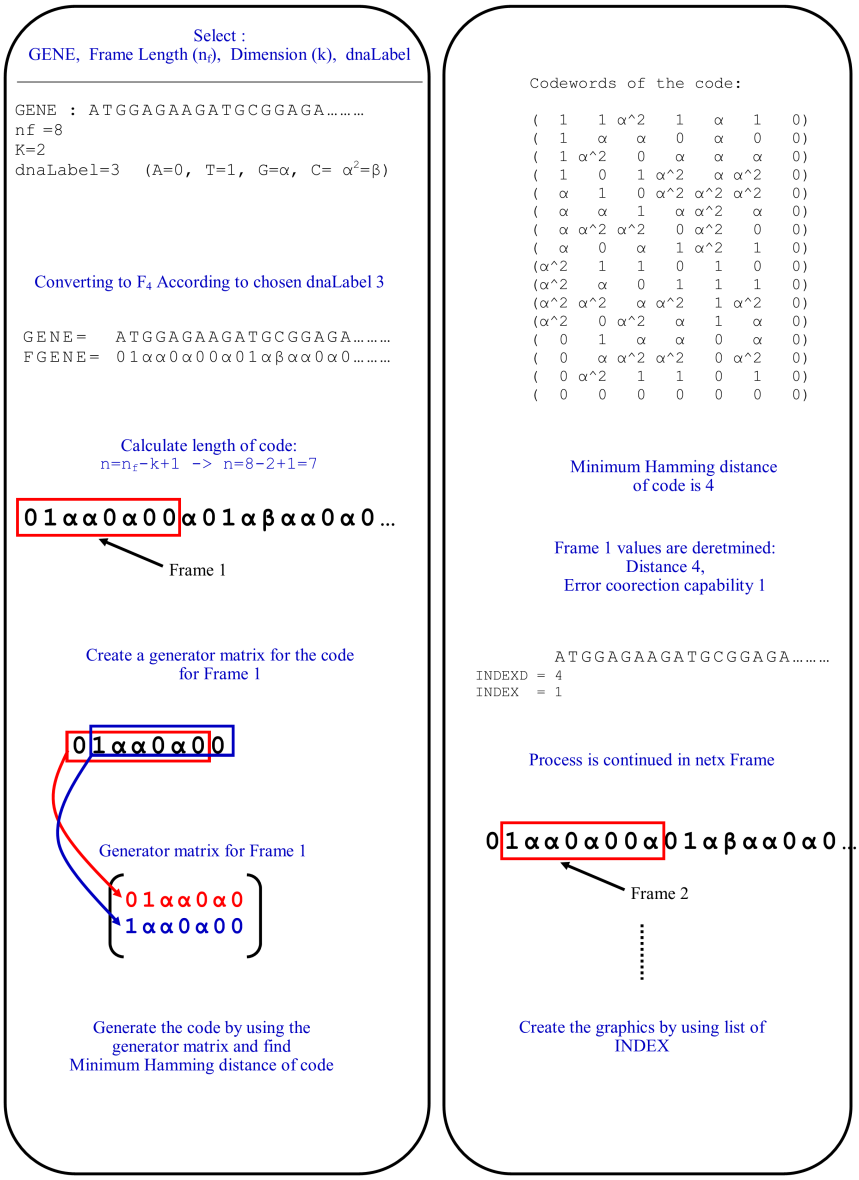

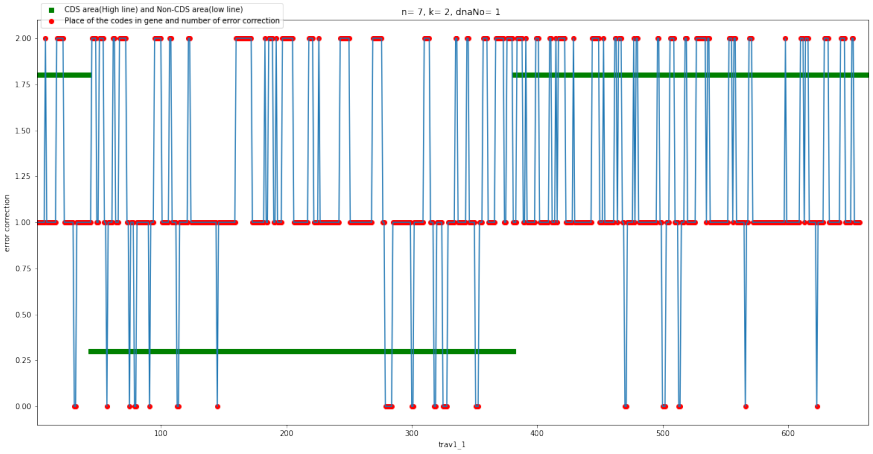

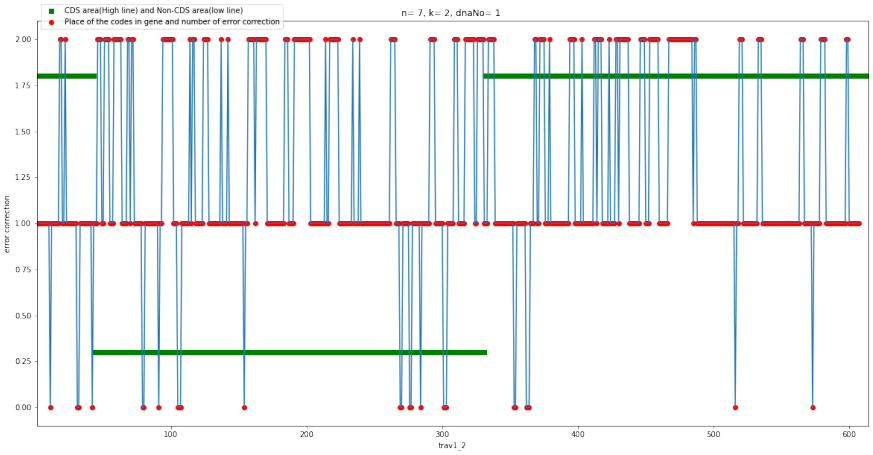

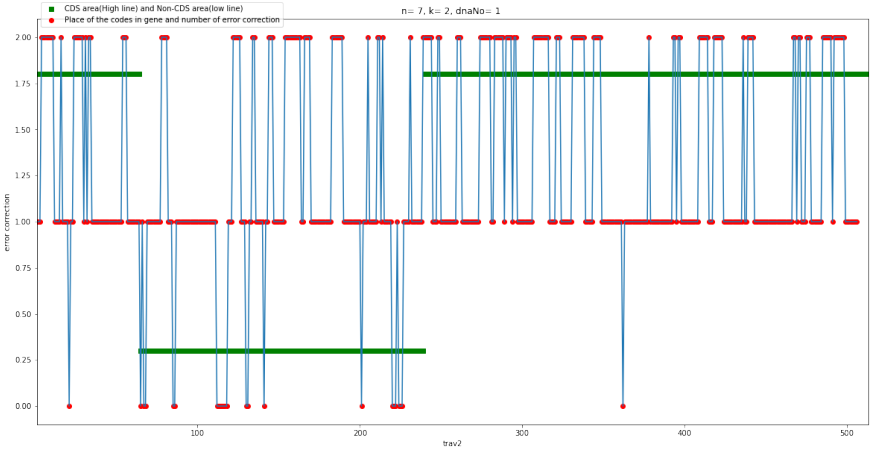

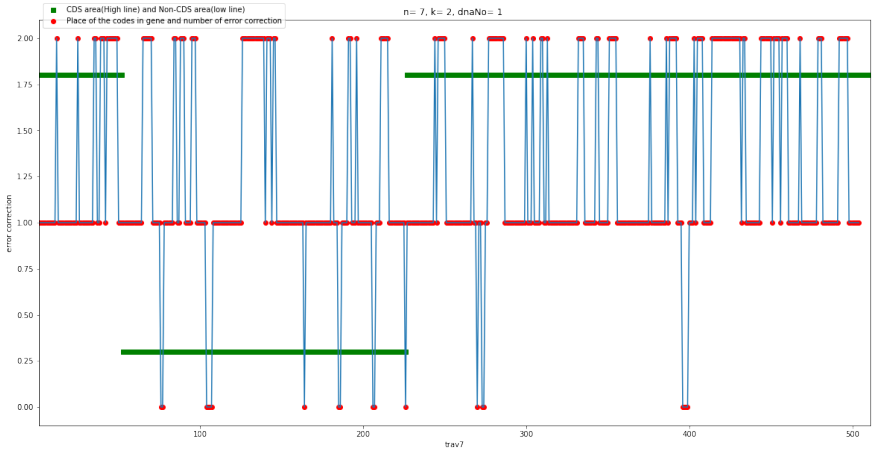

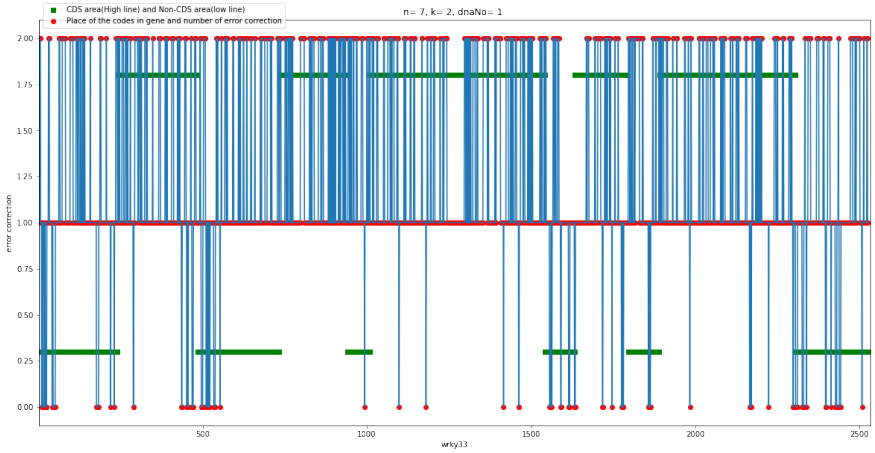

References