

Some theoretical foundation for protein identification through cyclic codes

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In recent work, the possible relationship between protein synthesis processes and digital transmission systems has been successfully investigated. Advances in this area could lead to conclusions about evolution and the connection between species. Based on the Code Theory, biological sequences have been identified as BCH code words to verify the validity of this model. In the article Construction of Cyclic Codes over $\mathbb{Z}_{20}$ for Identifying Proteins¹, three algorithms were designed to identify odd-length biological sequences of amino acids as keywords of cyclic codes. In this talk, we will present some aspects of the mathematical background of the algorithms through which we have been able to detect possible improvements for some steps of the above-mentioned algorithms.

References

- [1] Galíndez Gómez, V., Duarte González, M.E. (2019). Construction of Cyclic Codes over $\mathbb{Z}_{20}$ for Identifying Proteins. In: Figueroa-García, J., Duarte-González, M., Jaramillo-Isaza, S., Orjuela-Cañon, A., Díaz-Gutierrez, Y. (eds) Applied Computer Sciences in Engineering. WEA 2019. Communications in Computer and Information Science, vol 1052. Springer, Cham. https://doi.org/10.1007/978-3-030-31019-6_4

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