

# A Loop Grammar to Understand the roles of miRNAs in the Tumor Cell

Quadrini M.<sup>a</sup>, Merelli E.<sup>a</sup>, Piergallini R.<sup>b</sup>, Pucciarelli S.,<sup>c</sup>

<sup>a</sup>*School of Science and Technology, Computer Science Division, University of Camerino, Via Madonna delle Carceri 9, 62032 Camerino; e-mail: {name.surname}@unicam.it*

<sup>b</sup>*School of Science and Technology, Mathematics Division, University of Camerino, Via Madonna delle Carceri 8, 62032 Camerino; e-mail: riccardo.piergallini@unicam.it*

<sup>c</sup>*School of Biosciences and Veterinary Medicine, Biology Division, University of Camerino, Via Gentile III da Varano 1, 62032 Camerino; e-mail: david.vitali@unicam.it*

A miRNA is a small non-coding RNA molecule that regulates gene expression. Current studies showed that miRNAs may function both as oncogenes and as tumor suppressors, but not revealed the precise conditions that cause miRNAs to alter gene expression of the cancer cells. In this study, we introduce a context-free grammar, *Loop Grammar*, that formalizes the primary and secondary structure as a composition of loops, corresponding to concatenation or nesting of hairpins. We also formalize the *concatenation* and *nesting* on *fatgraphs*, oriented surfaces with boundary, and we define a *Surface Loop Grammar*, whose algebraic expressions uniquely identify such surfaces associated to given RNA structures. The Loop Grammar has been used to model tumor and healthy miRNAs of the mir-515 family, and we observed that the mutations of elements of primary structure involved in loops formation changed the secondary structure of tumor miRNAs. The Surface Loop Grammar is useful to classify RNA structures in terms of loops and relations among them.

## References:

- 1) Peng, Y., Croce, C. M. *The role of MicroRNAs in human cancer. Signal transduction and targeted therapy*, **2016**, 1, 15004.
- 2) Penner, R.C., Knudsen, M., Wiuf, C., Andersen, J.E., *Fatgraph models of proteins. Communications on Pure and Applied Mathematics*, **2010**, 63(10), 1249–1297
- 3) Quadrini, M., Culmone, R., Merelli, E.: *Topological Classification of RNA Structures via Intersection Graph. In: International Conference on Theory and Practice of Natural Computing, Springer*, **2017**, 203–215
- 4) Quadrini, M., Merelli, E.: *Loop-loop interaction metrics on RNA secondary structures with pseudoknots. In: International Conference on Bioinformatics Models, Methods and Algorithms, Proceedings; Part of 11th International Joint Conference on Biomedical Engineering Systems and Technologies, BIOSTEC 2018 3*, **2018**, 29-37.