miRNA-mediated 'tug-of-war' model reveals ceRNA propensity of genes in cancers

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Competing endogenous RNA (ceRNA) are transcripts that cross-regulate each other at the post-transcriptional level by competing for shared microRNA response elements (MREs). These have been implicated in various biological processes impacting cell-fate decisions and diseases including cancer. There are several studies that predict possible ceRNA pairs by adopting various machine-learning and mathematical approaches; however, there is no method that enables us to gauge as well as compare the propensity of the ceRNA of a gene and precisely envisages which among a pair exerts a stronger pull on the shared miRNA pool. In this study, we developed a method that uses the 'tug of war of genes' concept to predict and quantify ceRNA potential of a gene for the shared miRNA pool in cancers based on a score represented by SoCeR (score of competing endogenous RNA). The method was executed on the RNA-Seq transcriptional profiles of genes and miRNA available at TCGA along with CLIP-supported miRNA-target sites to predict ceRNA in 32 cancer types which were validated with already reported cases. The proposed method can be used to determine the sequestering capability of the gene of interest as well as in ranking the probable ceRNA candidates of a gene. Finally, we developed standalone applications (SoCeR tool) to aid researchers in easier implementation of the method in analysing different data sets or diseases. This work was showcased on the **journal cover** of *Molecular Oncology* 12(6): 855-868 (2018); https://doi.org/10.1002/1878-0261.12198