Possible quick alternative for predicting the internal dynamics of RNA molecules

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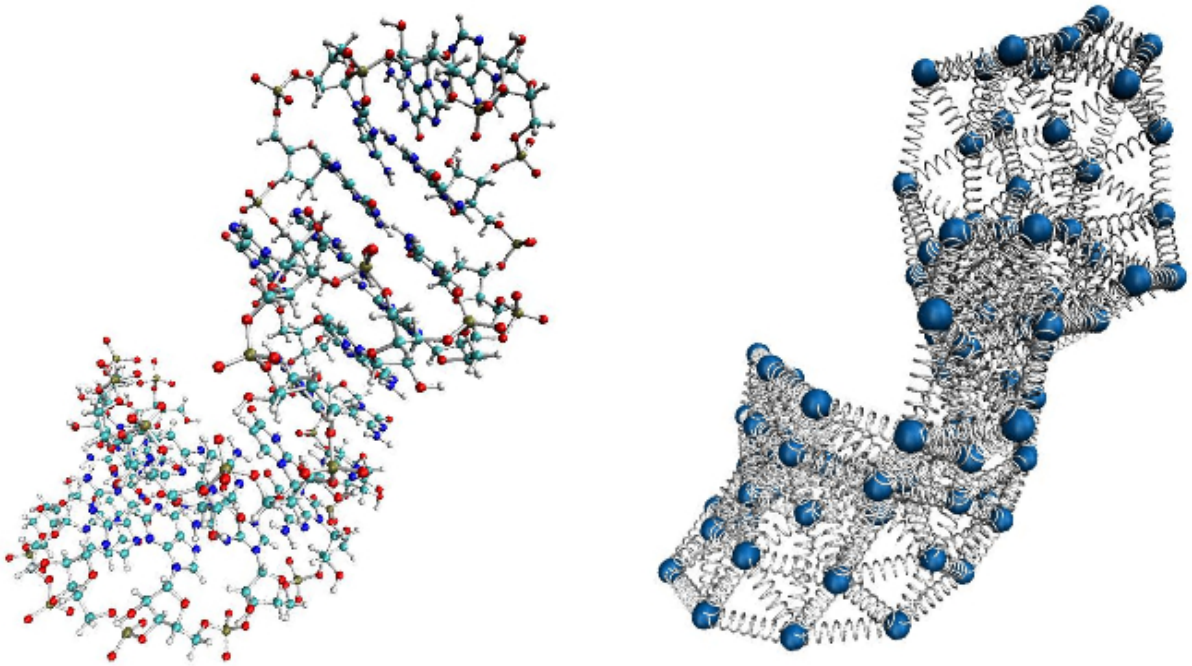

Credit: SISSA

A group of scientists at SISSA proposes a quick alternative for predicting the internal dynamics of RNA molecules (how the different parts move in relation to each other). This simple solution, which uses beads and springs, provides similar results to other, more complex and expensive techniques for analyzing molecules that are currently in use.

The study was published in the journal *Nucleic Acids Research*.

It is called The Elastic Network Model (ENM) and it can predict the internal dynamics of RNA molecules in nearly real time (processing takes just a few seconds). To understand RNA functioning, it is useful to know the composition of the nucleotide sequence and the three-dimensional shape of the molecule as well as its internal dynamics: how the different parts of the molecule move together, which are rigid or more elastic, which are connected or independent, etc. To understand these aspects, Molecular Dynamics, an extremely accurate computer simulation method, is often used but has the drawback of being very expensive. Calculation can take days or weeks.

The group, led by Giovanni Bussi of the International School for Advanced Studies (SISSA) in Trieste, in collaboration with Cristian Micheletti, also from SISSA, built an ENM alternative model based on simple rules. In the SISSA model, tens of atoms are grouped together and represented as beads. These beads are connected by springs, which maintain the structural frame of the molecule.

"In spite of its simplicity, our model is able to predict the structural fluctuations of RNA molecules with the accuracy of more complicated models," explains Bussi. In tests, the ENM gave results that were almost indistinguishable from Molecular Dynamics, and therefore could be a viable alternative to that methodology. Along with Bussi and Micheletti, Giovanni Pinamonti and Sandro Bottaro, both from SISSA, also participated in the research.

In addition to the theoretical part of the work, the team also carried out a comparison with experimental data. SHAPE reactivity experiments use reagents that "attack" the most active nucleotides in the RNA molecule. By sequencing the molecule before and after the reaction, the nucleotides which reacted are identified, or those within the molecule

with the freest mobility. In this way, the experimental technique provides information on the dynamics of the molecule. Bussi and colleagues compared predictions from the Elastic Network Model and found substantial agreement with the experimental data.

More information: "Elastic network models for RNA: a comparative assessment with molecular dynamics and SHAPE experiments." *Nucl. Acids Res*. (2015) DOI: 10.1093/nar/gkv708

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