

Exploring multiple loop motifs in RNA structures

Popular science summary

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Purpose of the project

Bioinformatics is an important field that combines biology with technology to help us better understand biological data. One area of focus in bioinformatics is RNA, which plays a crucial role in genetics. Understanding the 3D structure of RNA is a challenge for researchers. To help overcome this challenge, we use modern computers and algorithms. However, some RNA motifs, such as n-way junctions or multiloops, are rare and poorly understood, making them difficult for these algorithms to process. In this project, we will work on developing advanced computational methods and machine learning (artificial intelligence) to help researchers overcome these challenges. We aim to create valuable tools and resources to help researchers better understand RNA molecules.

Research description

We aim to collect experimental data on RNA 3D structures and select informative ones. Then, we will develop a tool to analyze the data and identify multiloops using artificial intelligence. We will use this to classify RNA structures and learn the rules that govern their 3D arrangements. We will then apply this knowledge to many RNA sequences that still need to be solved. This will help us generate and collect thousands of RNA multiloops. This information will be helpful for other researchers to predict complex RNA 3D structures more effectively.

Why undertake this research topic?

RNA multiloops are a problem for bioinformatics. There is not enough information to study them properly, slowing down progress in biology and biotechnology. However, we have found solutions to this problem that will be available to all scientists. This will help improve research in the field.

Main expected outcomes

Our project aims to solve the problem of RNA multiloop analysis. We plan to achieve this by creating databases and datasets containing proper explanations of RNA structures possessing these motifs. We will also develop a suite of computational tools to analyze and interpret complex RNA structures. All our results will be open for public access, as we support open science.