Docket #: S20-176

Software for Rapid Mapping of RNA Structure

Stanford researchers have developed the first software toolkit for analyzing cutting-edge RNA structure mapping experiments. Experimentally assessing RNA structure remains difficult due to lack of software for analyzing mutate-and-map-sequencing (M2-seq) technology, which combines systematic mutagenesis, chemical mapping, and next-generation sequencing to infer RNA structure. To address this lack of analytical tools, the researchers developed Mutate-and-Map-sequencing Analysis and Data Processing Toolkit (M2-ADaPT) that combines multiple sequencing data processing methods and, in short, helps users interpret M2-seq data. It further provides a set of tools to interface with downstream structural modeling and analysis software such as the RiboKit suite.

This technology is part of a portfolio of innovations aimed at fighting the COVID-19 pandemic.

Stage of Development

The Barna Lab at Stanford is using this software for rapid mapping of many RNA structures essential for developing novel RNA designs used to stabilize and improve antigen expression in mRNA vaccines. Their designs can be extended to any RNA-based therapeutics for optimal expression of candidate genes.

Related technologies for optimizing RNA-based therapeutics and vaccine design:

Stanford docket S20-205 - [Repurposing the SARS-CoV2 5'-UTR for RNA Based Therapeutics](#)
Stanford docket S20-135 - [Translation Enhancer for Gene Regulation](#)
Stanford docket S19-310 - [Rational Design of Ultratight RNA Aptamers against Protein Targets](#)
Stanford docket S19-143 - [Primerize: Software for Designing Primers for Rapid RNA Synthesis](#)

Stanford docket S20-174 - [Optimized Synthesis and Translation of RNA Therapeutics](#)

Applications

- Processing/analyzing mutate-and-map sequencing data
- Rational design of RNA based-therapeutics such as mRNA vaccines (eg. COVID-19 mRNA vaccines)

Advantages

- Only toolkit available for mutate-and-map-sequence structure analysis of long RNAs in vitro and in vivo

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