Docket #: S21-250

EternaFold2: A general method for end-to-end nucleic acid structure inference

Stanford researchers have developed a framework describing an end-to-end approach that infers experimental properties directly from nucleic acid sequence, using a principled statistical mechanical representation of the structure ensemble. Accurate prediction is increasingly important for a range of disciplines, including genome editing, vaccines, and therapeutics. Various algorithms have described and implemented machine learning approaches for either predicting structure from sequence, or predicting properties from structure, but no methods exist that unite both of these steps. EternaFold2 can infer properties directly from sequence and will be fundamental to the next generation of machine-learning-based nucleic acid design.

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

Related technology: S20-164 EternaFold: Accurate RNA Structure Prediction

Stage of Research

- Proof of concept

Applications

- Machine learning approaches for inferring nucleic acid properties
- geneome editing
- mRNA vaccine development
- COVID 19 therapeutics

Advantages

- EternaFold2 builds on EternaFold: fully generalizes the previous approach for predicting structure and properties

Innovators

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