Docket #: S19-143

Primerize: software for designing primers for rapid RNA synthesis

Stanford researchers have developed an algorithm and web server to accelerate the synthesis of DNA and RNA molecules. Many modern medicine applications require 'on-demand' templates for DNA genes. The Primerize software is an archive of Python code that is able to design forward (sense) and backward (anti-sense) primers for PCR assembly of such templates using a novel dynamic programming algorithm. The method keeps each primer under a prescribed length and minimizes their total length, effectively reducing the synthesis cost. Primerize has been optimized to reduce mispriming (a significant issue which can lead to the transcription of undesired products) through the avoidance of primer boundaries that could potentially anneal to incorrect sequences. These resulting primers have been tested through the synthesis and purification of templates for in vitro transcription of RNA sequences of up to 300 nucleotides.

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 S20-176: Software for Rapid Mapping of RNA Structure

Stanford docket S20-135: Translation Enhancer for Gene Regulation
Stanford docket S19-310: Rational Design of Ultratight RNA Aptamers against Protein Targets
Stanford docket S20-174: Optimized Synthesis and Translation of RNA Therapeutics

Applications

- This program allows for the design of primers for genes up to 300 nucleotides with a minimization of mispriming.

Advantages

- The primers designed through this program have been extensively tested to avoid mispriming while reducing cost through the minimization of primer length.

Innovators

- Rhiju Das
- Siqi Tian

Licensing Contact

Sam Rubin

Licensing Associate, Life Science

Email