




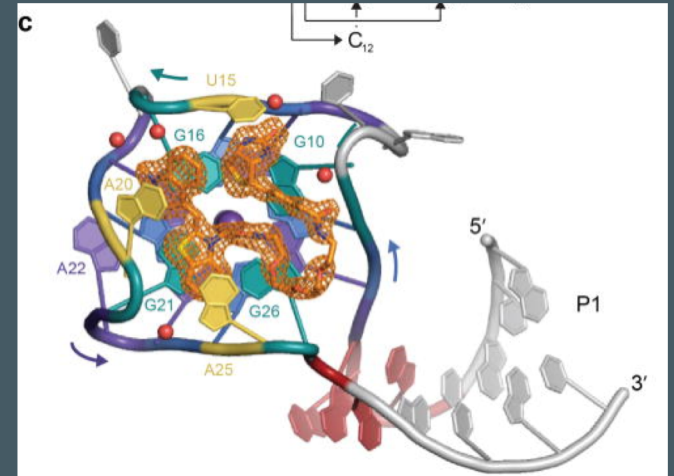
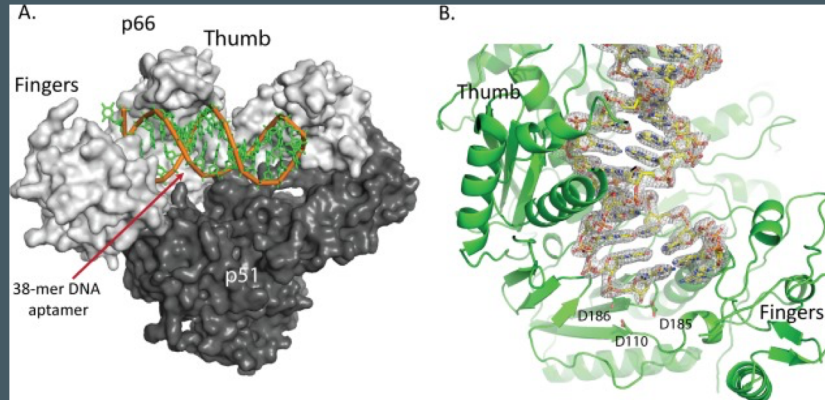
In Silico Tertiary-
Structure-Based
RNA Aptamer
Design

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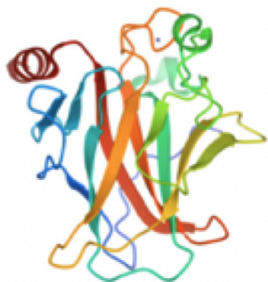


RNA Aptamers

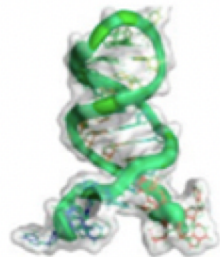
- **Selective and Sensitive Binding**
- Easier chemical synthesis
- Small size
 - Tissue penetrance



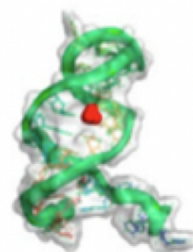
**Novel Target
with Structure**



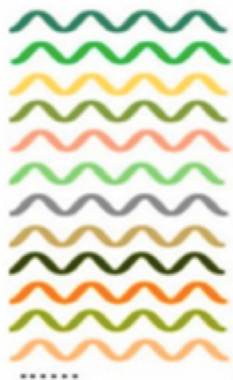
**Binding Pocket
Modeling**



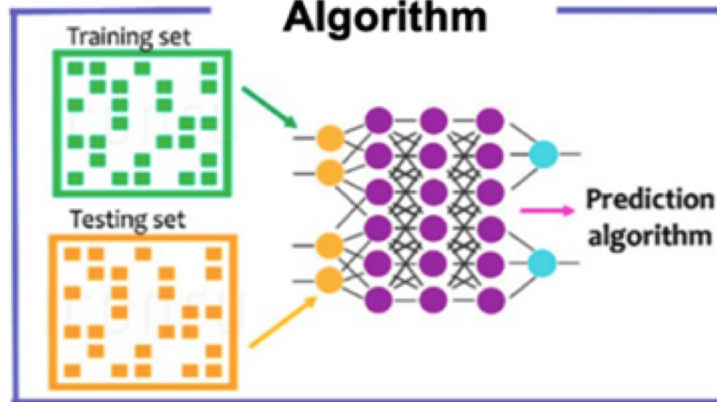
**Desired Aptamer
Tertiary Structure**

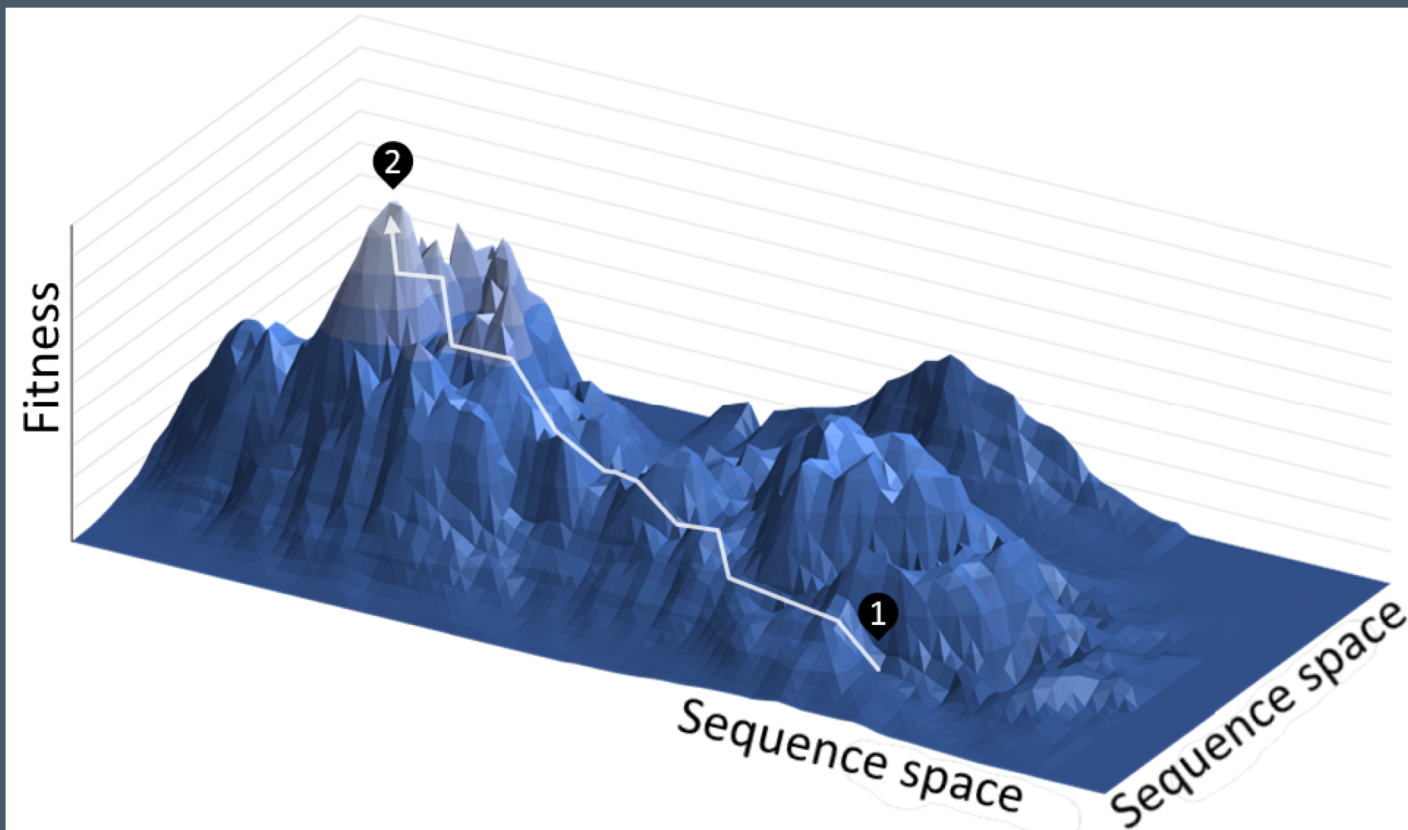


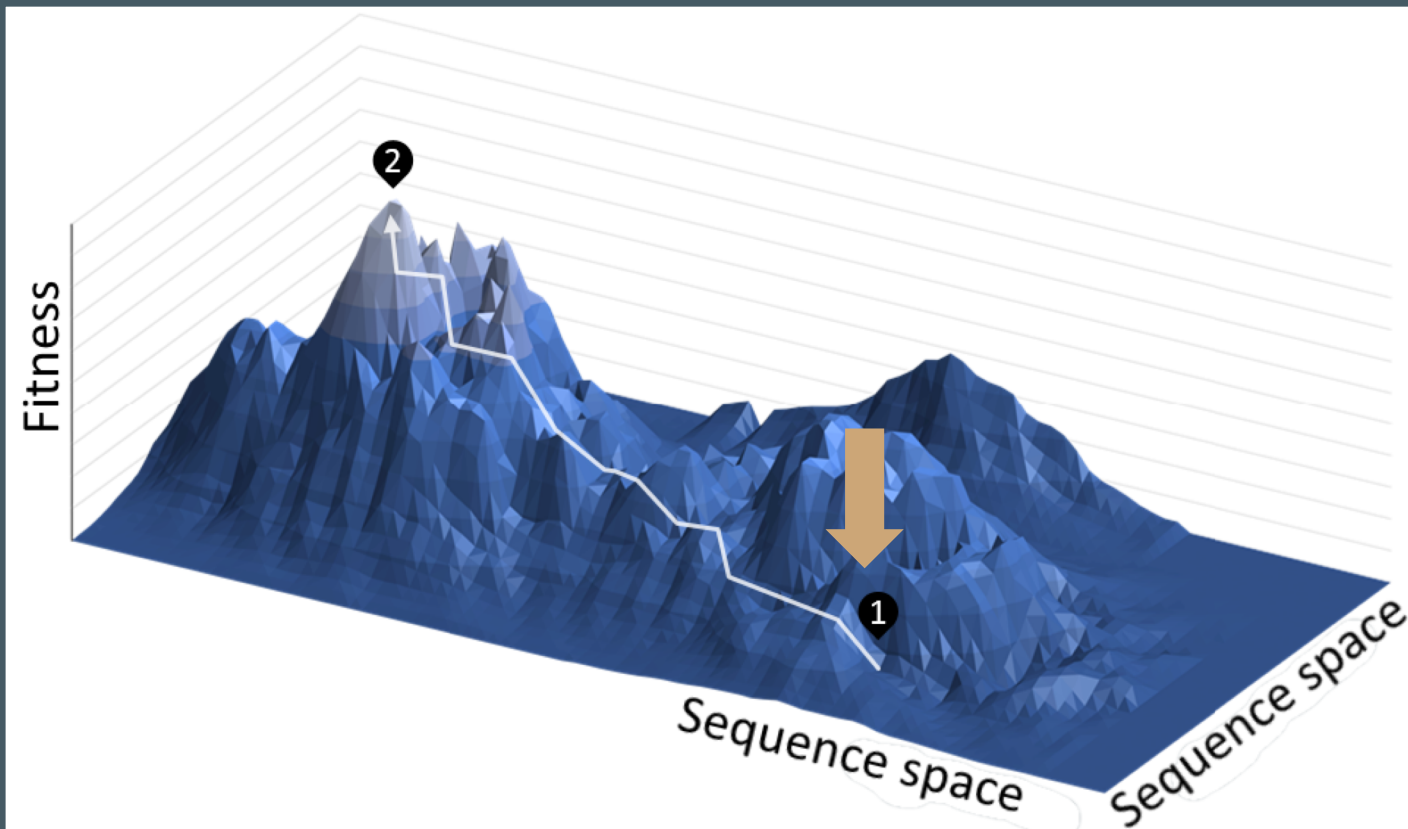
**Generated Aptamer
Sequences**

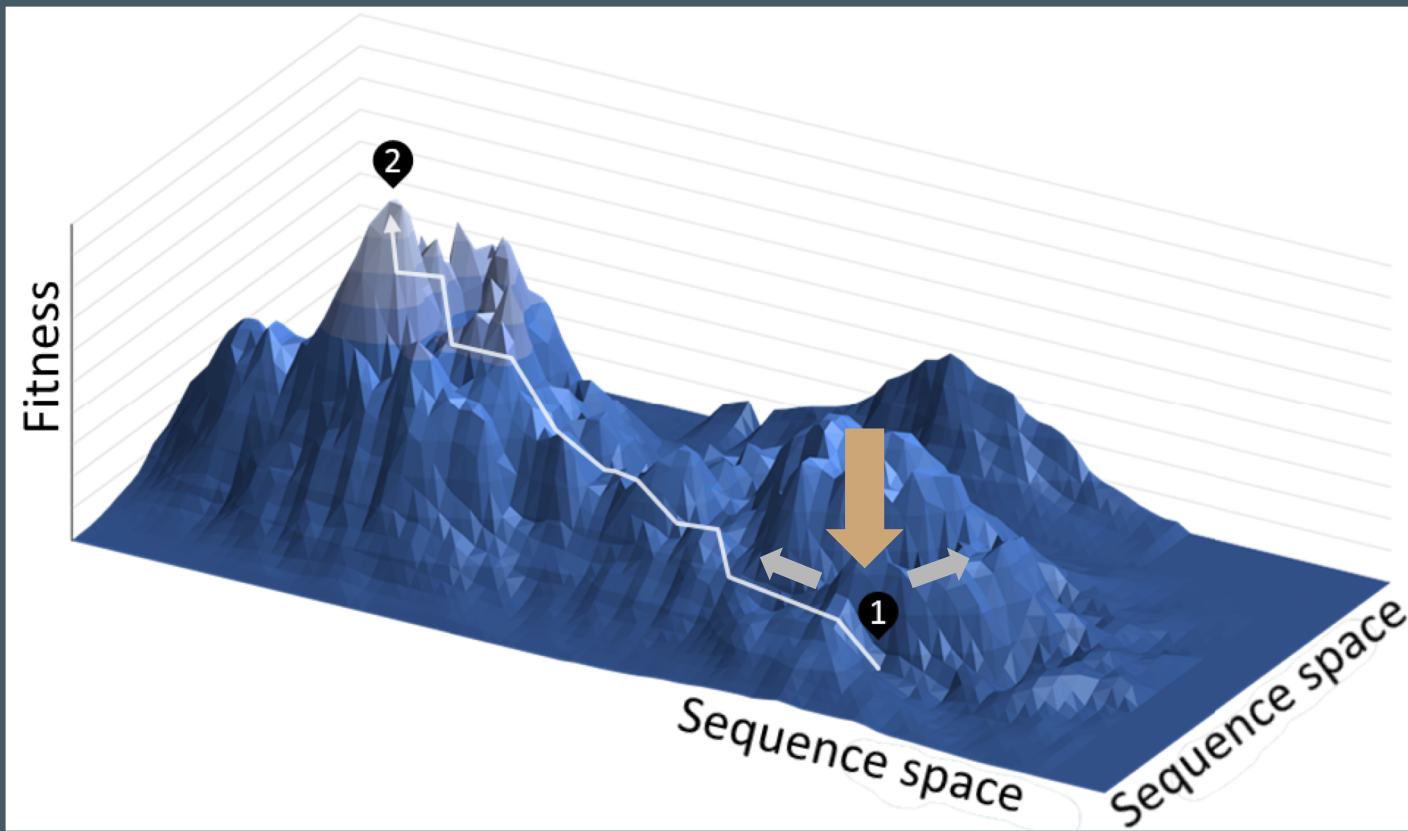


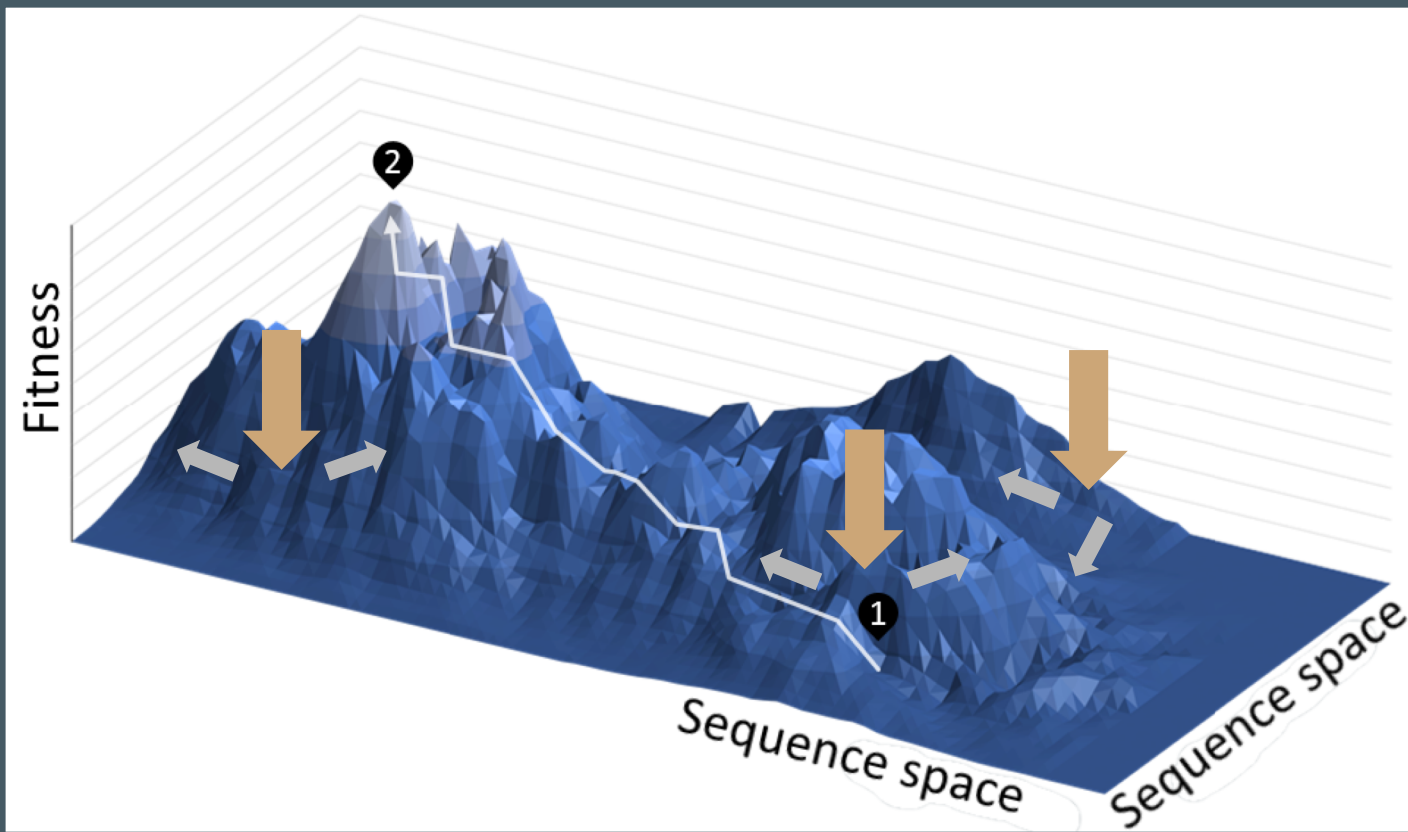
**RNA Design
Algorithm**











Preliminary Performance

16 threads $\Rightarrow \approx 2\text{-}4\text{x}$ speedup

Scientific ML to Augment Experimental Validation

- Training Data: First round of experimental candidate validation
- Biophysics-informed NN to model aptamer-target binding (expensive to determine experimentally)
- Input: 4 (number of nucleotides – A, U, C, G) x n (length of desired aptamer)
- Output: Binding Affinity
- NN Interpretation: Network weights indicate importance of specific positions and domains on molecule

Citations

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- Dykeman, E. C. An implementation of the Gillespie algorithm for RNA kinetics with logarithmic time update. *Nucleic Acids Res* 43, 5708–5715 (2015).
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