

SELEXzyme

Evolving DNAszymes for Target Sequences

02-601 Project Presentation

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December 2, 2020

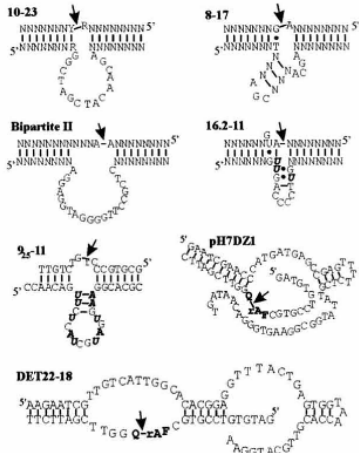
Summary

1. DNAzymes
2. SELEX and Genetic Algorithms
3. SELEXzyme

What is a DNAzyme?

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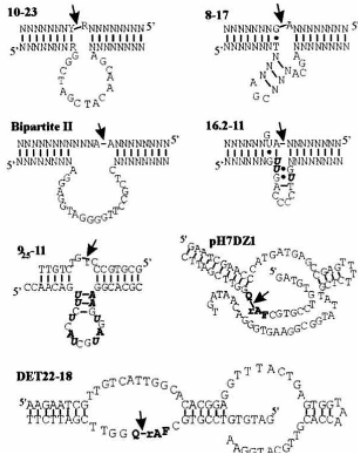
B Representative RNA-cleaving deoxyribozymes



- ▶ Short DNA sequences with catalytic activity

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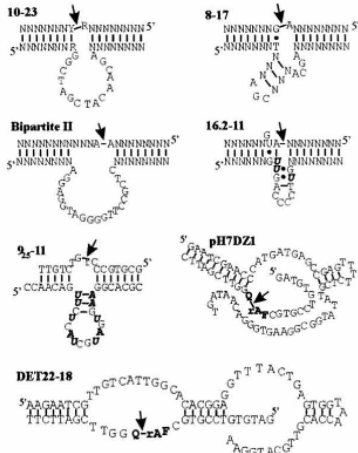
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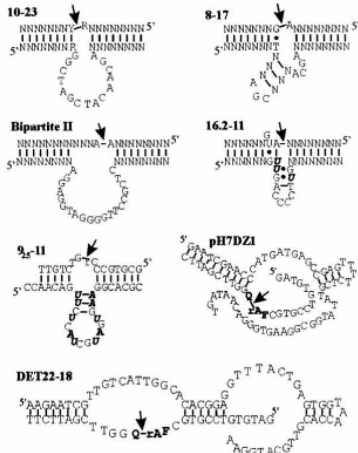
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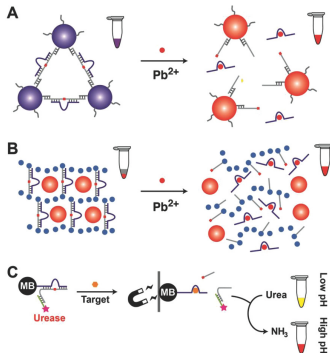
B Representative RNA-cleaving deoxyribozymes



- ▶ Short DNA sequences with catalytic activity
- ▶ Often cut target nucleotide sequences
- ▶ Can have tertiary structure
- ▶ Never before observed *in vivo*

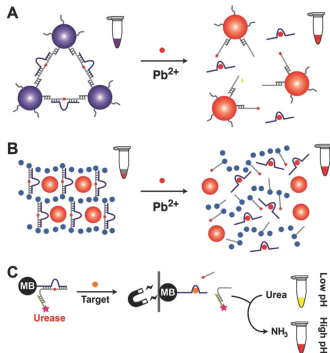
Why Care About DNazymes?

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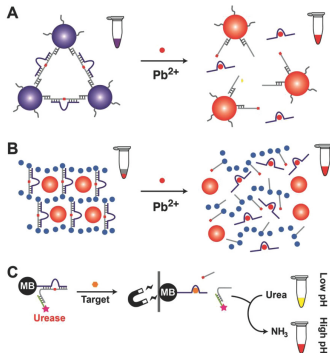
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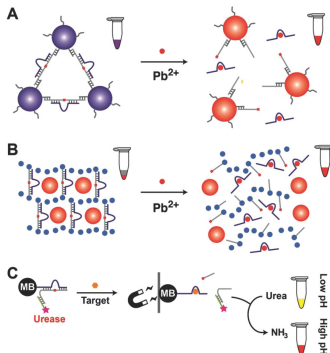
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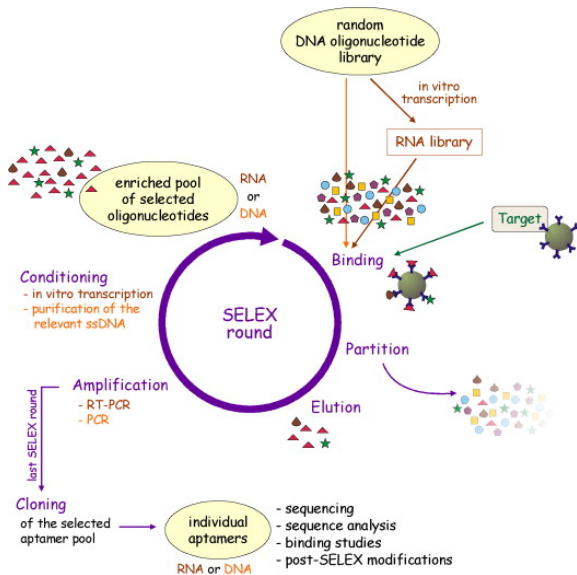
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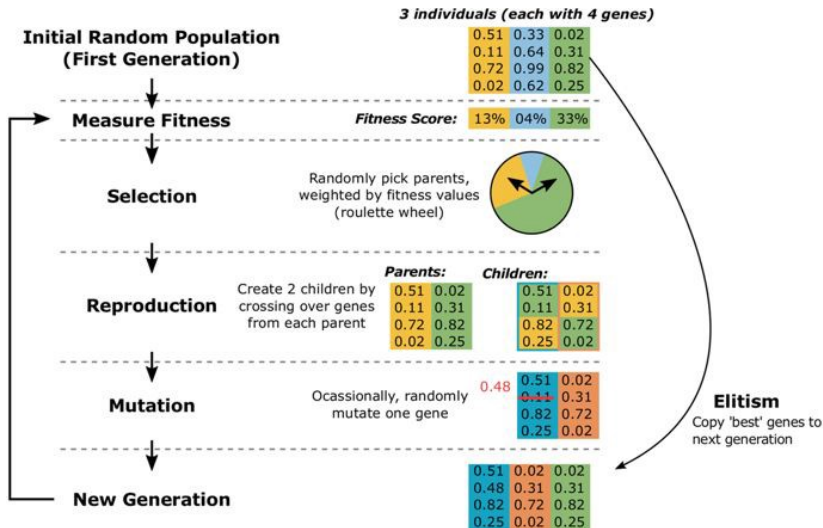


- ▶ Easy to synthesize, efficient production, highly active
- ▶ Chemical sensors, motors, therapeutics
- ▶ Can encode logic into DNAzyme constructs
- ▶ Often combined with DNA Aptamers i.e. DNA antibodies

How Do You Design DNAzymes?



Genetic Algorithms Simulate SELEX



My Project

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- ▶ GA to evolve possible DNAzymes that target a user-defined sequence

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```
09:38 AM ~/Project_02601/genetic_algorithm (main) 0.1.5
./genetic_algorithm -target test.fna -output dnazymes.fna
generations: 30 / 30 [=====] 100.00% 8s
Reached Max Iterations 30
Final Generation Fitness Summary
lin..... 0.28
5% Quart ..... 0.8431372549019608
Mean..... 0.8330886607782734
5% Quart ..... 0.8431372549019608
Max..... 0.8627458908392157
Std. Dev ..... 0.83992185843247186
CoV..... 0.84792392965876239

09:38 AM ~/Project_02601/genetic_algorithm (main) 0.1.5
→ head dnazymes.fna
Sequence_266 | Fitness:0.28
AATATAGATTAATTATCACTCTACGCCGATTAGCAGCCGTACGGGGTGT
Sequence_106 | Fitness:0.5304615304615304
AATATAGATTAATTATCACTCTACGCCGATTAGCAGCCGTACGGGGTGT
Sequence_495 | Fitness:0.5769230769230769
AATATAGATTAATTATCACTCTACGCCGATTAGCAGCCGTATAGGATGT
Sequence_322 | Fitness:0.6153046153046154
AATATAGATTAATTATCACTCTACGCCGATTAGCAGCCGTACGGGGTGT
Sequence_446 | Fitness:0.62
AATATAGATTAATTATCACTCTACGCCGATTAGCAGCCGTACGGGGTGT
```

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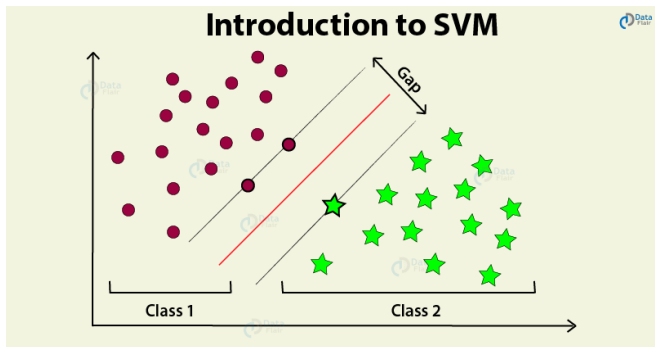
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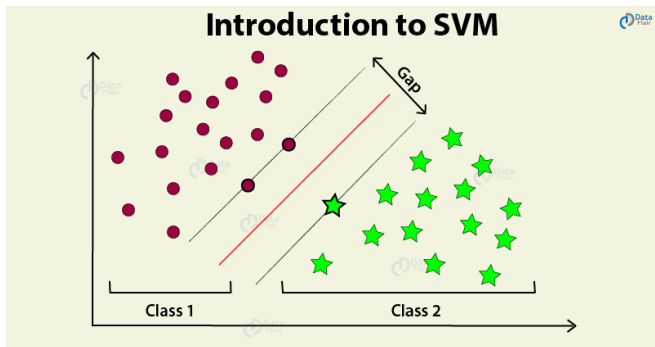
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- ▶ Smith-Waterman alignment score to user target sequence
- ▶ Probability of being a DNAzyme from the ML model
- ▶ Use an SVM model, good for simplicity vs quality trade-off
- ▶ Model trained on known DNAzymes, DNA aptamers, Promoters and simulated data



[J RNAi Gene Silencing](#). 2005 Oct; 1(2): 88–96.

Published online 2005 Oct 14.

PMCID: PMC2737201

PMID: [19771209](#)

Design of efficient DNazymes against muscle AChR α -subunit cRNA *in vitro* and in HEK 293 cells

[Amr Abdelgany](#),¹ [M Khabir Uddin](#),^{2,3} [Matthew Wood](#),⁴ [Kazunari Taira](#),^{2,5} and [David Beeson](#)^{1,*}

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- Computationally generated vs. *in vitro* screened DNazymes

Validation

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- Computationally generated vs. *in vitro* screened DNAzymes
- Similar sequence composition (high alignment score)
- *in vitro* screened DNAzymes should have high fitness values

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References II



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