# Molecular Computation A DNA-Based Model for Solving Mathematical Problems 

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## Topics

- What is DNA computing?
- What are the prerequisites for creating a DNA computing model?
- The two phases of the project
- Phase 1: Testing DNA strand binding
- The Geneseo problem
- Phase 2: Modeling the problem
- Future work


## What is DNA Computing?

- An application of nanotechnology
- First developed in 1994 by Leonard Adleman
- Uses single stranded DNA molecules to represent the variables in a mathematical problem
- Selective hybridization then allows for the isolation of the correct answer



## Why DNA?

- DNA has the ability to compute in parallel
- Standard computers compute in series
- This gives DNA the ability to sort through massive sets of data much quicker than a standard computer
- The key is simultaneous hybridization of DNA in solution

Example: Adding Numbers
$5+3,4+2,3+6$
Standard Computer:
$5+3=8$
$4+2=6$
$3+6=9$
Parallel:
$5+3=8$
$4+2=6$
$3+6=9$

## Prerequisites

- Method for generating sequences of DNA to represent all the variables of a given problem
- Must also generate "well-behaved" strands
- Procedure for validating this method
- Strands that mis-pair when hybridizing will create errors in a DNA problem


## Phase I

- Generated sequences using a computer algorithm developed by Dr. Anthony Macula
- Sequences were then synthetically prepared by Invitrogen
- Validated efficacy of the algorithm using SYBR Green I molecular dye
- This Dye binds to the minor groove of double stranded DNA (dsDNA) only


## SYBR Green

- Place the generated strands in solution together
- Measure fluorescence to see if there is dsDNA present
- If there is notable fluorescence when it is not expected a DNA strand will be discarded and not used in the final experiment


## Fluorescence Experiments

Construct S14/C15


Construct S9/S10


Conclusion: SYBR Green was effective in screening for appropriate binding. The algorithm used to generate the sequences was efficient at producing "well-behaved" strands.

## Other SYBR Experiments

Combined Data for SYBR Green as a function of Base Pairs


- 65.3C
- 71C
- 75.1C
- 80.1C
- 85.1C
- 73.3C
$\triangle 78.1 \mathrm{C}$
- 68.1C


## The SAT Problem

- Short for Satisfiability
- A series of logic clauses connected by "and" statements
- Each clause must be true for the entire series to be true
- Each Variable is represented by two strands: One for TRUE and one for FALSE

In a SAT problem all clauses must be true!
Example:

1) $X 1$ or $X 2$
2) $\sim \mathrm{X} 1$ or X 5
3) $\sim A X$ or $X 3$ or $X 4$
4) $X 3$ or $\sim X 5$
5) $X 4$ or $X 5$
6) $\sim \mathrm{X} 3$ or $\sim \mathrm{X} 4$
7) $\sim \mathrm{X} 2$ or X 3

It is easy to see that these problems can get incredibly complex as more clauses are added.

Answer: $\mathrm{A} 1=\mathrm{T}, \mathrm{A} 2=\mathrm{T}, \mathrm{A} 3=\mathrm{T}$, $\mathrm{A} 4=\mathrm{F}, \mathrm{A} 5=\mathrm{T}$

## Phase II Modeling the Problem

- The first step is to create all the possible answers to the problem
- The individual DNA strands must be linked together to produce all possible combinations
- Ex:

10 strands to code for $\mathbf{T}$ or $\mathbf{F}$ for 5 Variables
Each strand is 16 nucleotides long there are $2^{5}=32$ possible "solution" strands of length 80 nucleotides ( 16 nucleotides * 5variables)

## DNA Strands

- Library Sequences ( $5^{\prime}$ - $3^{\prime}$ )
- C C T T T T T T T T T T T T T T, T1
- T T T C C A A T T T C C T T A T, F1
- A ACAACCAAACCAAAA, T2
- A A A T C CTCTTTTCAAA, F2
- A C A C A C A C T T T T A C T T, T3
- ACTATCACAAA TA A A, F3
- C T T A C T A T T C A T T C A T, T4
- TA A C C T A C C T C T C C T T, F4
- C T A T A C C A T C A A T T A T, T5
- T A A T T C TC A A C A T T T A, F5


## Building the Answers

- DNA polymerase extends a DNA molecule by adding complementary bases to a primer
- We exploit this capability to create all combinations of the variable strands



## Connecting the Pieces

- Polymerase Chain Reaction (PCR): Repetitive heating and cooling of DNA sample to allow DNA polymerase to extend all the molecules
- Using complements to each new variable position all possible combinations of strands are created one PCR reaction at a time
- What is this slide talking about?


## Stepwise PCR



## Future Work

- The PCR reactions produce all 32 combinations, but it also creates their complements
- We need single-stranded DNA
- Use Biotin and Streptavidin to separate



## Future Work

- Once all strands are single stranded the problem can be solved
- Bind complement sequences that make the first clause True to Streptavidin, which is also associated with metallic beads on a column
- Strands with the right combination will adhere to the column
- Pass the captured strands through successive columns representing TRUE for each clause in the problem
- Anything remaining at the end codes for the answer
- Sequence the strand


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