Building Bacterial Computers to Solve Satisfiability Problems

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Abstract

We designed bacterial computers to solve satisfiability (SAT) logic problems using 5 base frameshift suppressor tRNAs. Mathematical analyses of SAT problems guided our construction. We built a physical model of a suppressor tRNA, cloned eleven suppressor tRNAs and their cognate mutated RFPs. We measured the function of three generations of devices as part of an iterative design/construct/test/redesign process.

Satisfiability (SAT) Problems

SAT problems are the oldest NP-complete problems. A SAT problem determines whether a set of inputs can satisfy a series of logical clauses consisting of two (2-SAT) or three (3-SAT) literals connected by OR operators. MAX SAT problems ask how many of logical clauses consisting of two (2-SAT) or three (3-SAT) literals are satisfied.

SAT problems are satisfied when exactly two distinct tRNAs suppress one mRNA. DnaE, as a single clone encodes multiple clauses and reports MAX SAT solutions.

Analysis of SAT Problems

We analyzed 2- and 3-SAT problems with Mathematica to identify unsatisfiable problems and to visualize SAT problems graphically that are not satisfied by a particular input. We classified SAT problems by rough distribution of each problem, meaning how many inputs satisfied a certain number of clauses in a problem.

Frameshift Suppression

Frameshift mutations alter the reading frame prevent protein production. tRNAs that contain four base and five base anticodons (Anderson et al. 2002) can suppress frameshift mutations. At right is a physical model we fabricated of a 5 base frameshift suppressor tRNA.

Solving SAT Problems in Bacteria

Suppressor tRNAs are inputs processed by frameshift suppressor leaders (FSL) in reporter genes. We designed FSLs to count how many logical clauses are satisfied in a MAX 2-SAT or MAX 3-SAT problem. The logical clause (G OR r) can be encoded by an 11 base pair sequence NNNNgggmmnn. Only one tRNA binding an mRNA can restore the reading frame; no tRNA binding retains the frameshift.

Construction

We designed and constructed eleven 5 suppressor tRNAs and eleven cognate RFP genes. We evaluated a series of promoters to quantify their output. We counted the frequency of all 11 5mers in eleven cognate RFP genes. We evaluated a series of promoters to quantify their output. We counted the frequency of all 11 5mers in eleven cognate RFP genes. We evaluated a series of promoters to quantify their output. We counted the frequency of all 11 5mers in eleven cognate RFP genes.

Results

We designed, built, and tested three versions of our frameshift suppression test modules. The three iterations of devices allowed us to measure the impact of promoters and positioning of the tRNAs.

Automation Scale for Bacterial Computers

Our bacterial computer lends itself to different levels of automation as tradeoffs between human intervention and operations carried out by the bacteria. In the least automated level, each bacterial clone encodes a single literal while in the highest level of automation a single clone encodes multiple clauses and reports MAX SAT solutions.

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