

# A Max 1s Problem in DNA Computing via Genetic Algorithms

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## One-Page Summary

Consider the difficulty of designing DNA sequences such as that of the human genome which codes for approximately 100,000 proteins. Even a small protein of 300 amino acids is encoded in a sequence space of  $20^{300} \approx 10^{390}$ . (A “sequence space” being the number of possible sequences of a particular length). It appears that no DNA library can be made large enough to allow one-step selection of an average, functional gene. What if it would be possible to carry out the selection in a few steps while still keeping the computing time moderately short?

Recently, some very important complex biological problems that use genetic materials have been attacked [2] by the means of *in vitro* evolution that utilizes repeated cycles of variation and selection. This paper addresses a challenging Max 1s problem, via genetic algorithms based on *in vitro* evolution techniques. Genetic algorithms normally manipulate bitstrings on silicon computers using operations of pointwise mutation and crossover. Therefore, they are well suited to DNA implementation [1, 3].

The DNA implementation of the Max 1s problem is carried out by the following outline.

## DNA Genetic Algorithm for Max 1s Problem

Begin with a diverse initial population of candidates.

1. Evaluate fitness by hybridizing candidates to target strands and physically separating them on a 2-DGGE gel.
2. Select and purify more fit candidates to breed.
3. Amplify fit candidates with pointwise mutation and reserve 50%.
4. Breed candidates, using crossover.
5. Combine reserved and bred candidates, to obtain a new generation.

Repeat process.

## References

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- [2] A. Crameri, S. A. Raillard, E. Bermudez, and Willem P. C. Stemmer. DNA shuffling of a family of genes from diverse species accelerates directed evolution. *Nature*, 391(6664):288–291, January 15, 1998.
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