DNA Starts to Learn Poker

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Abstract. DNA is used to implement a simplified version of poker. Strategies are evolved that mix bluffing with telling the truth. The essential features are (1) to wait your turn, (2) to default to the most conservative course, (3) to probabilistically override the default in some cases, and (4) to learn from payoffs. Two players each use an independent population of strategies that adapt and learn from their experiences in competition.

1 Introduction

The long-term goal is to use DNA to construct special purpose computers. Their special purpose is to learn game-playing strategies adapting to the strategies of opponents, even while opponent's strategies are also changing and adapting. It is clear that many real-world problems have this nature --- and it is equally clear that no general method is known for these problems. The ultimate payoff for our research is a method for finding adaptive game-theoretic strategies. The ultimate aim is to use DNA to encode game strategies that improve over time and adapt to the strategies of other players. In the medium term, this is to be addressed for the game of poker.

This project demonstrates the necessary DNA laboratory techniques for an example from a textbook on game theory (49). This is a simplified version of poker, but it still involves probabilistic strategies of bluffing versus truth- telling and calling versus folding. The essential features are to wait your turn, to default the most conservative course, to aggressively override this in some contexts, and to learn from the payoffs obtained. Each of two players competes using a large population of strategies that adapt and learn from their experiences in competition.

We employ laboratory evolution of DNA (3-5, 9,13,20,58-61), whiplash PCR (22, 30, 38,39,55), and the evolutionary computation paradigm from conventional computing (2,12,21,23,25-28,35, 40,51,52,62,63). All three techniques been used before, but have never been combined. One obtains massively parallel nanoscale computers where communication is not dependent on a myriad of fixed physical connections, but rather on pattern matching of information encoded in independent free-floating molecules.

!.1 The Advantages of DNA For Computing

Computations of evolving strategies seem particularly well suited to DNA implementation (4-8,20,41-46,59-61).

1. Estimated answers for a particular problem can be encoded in DNA molecules using binary representation.
2. Selection by fitness, and breeding via mutation and crossover, can be implemented by laboratory procedures, as demonstrated in (59-61).
3. Evolutionary computation, like natural evolution, benefits from tolerance of error (18, 19), requiring only that selection be correlated with fitness.
4. Massive parallel processing of up to 10^{18} independent bytes of data is a characteristic of DNA laboratory processes (about one milligram). This is comparable to[1] projected next-generation silicon computers (24).
5. DNA laboratory procedures can multiplex[2] many simultaneously evolving populations at no extra cost. Multiplexing permits large-scale sampling of the distribution of possible population evolutions.
6. A very large amount of information storage is available using DNA. For example, the entire Internet contains about the same amount of data as a milligram of DNA[3].

[1] Assuming one laboratory operation per minute.

[2] In multiplexing, populations are combined, independently and uniformly processed, and separately recovered.

2 Where Do Game Strategies Come From?

A game is a situation in which two or more players make moves (or plays). The reward received by a player for its moves depends in part on the moves made by the other player(s). The broad applicability of game theory not only ensures its importance, but also explains why game theory is unlikely to produce general methods for finding good strategies[4]. Consider poker. While we admire the accomplishments of game theory, we regret that equilibrium and hyper-rationality are so often unrealistically assumed. Playing competitive poker, for example, seems to be a dynamic process of adapting one's strategies to exploit the mistakes of opponents. Regrettably, neither of these two features is usual in game-theoretic analysis. We depart from what has been the mainstream of game theory in that we focus on the dynamics of play and strategy creation, rather than on the statics and the various equilibrium concepts (e.g., Nash and its refinements). A recent commentary in Nature (?) nicely captures our perspective:

> "Of course, the main problem with Nash equilibria is still there: they may exist, but how does one reach them? . . . .We are in a situation akin to the beginning of mechanics: we can do the statics, but we don't have the dynamics."

Some of our prior research provided application
We are led to using evolutionary computation because: (I
(II) Its robustness under change or uncertainty is importa
changes as opponents evolve their own strategies.

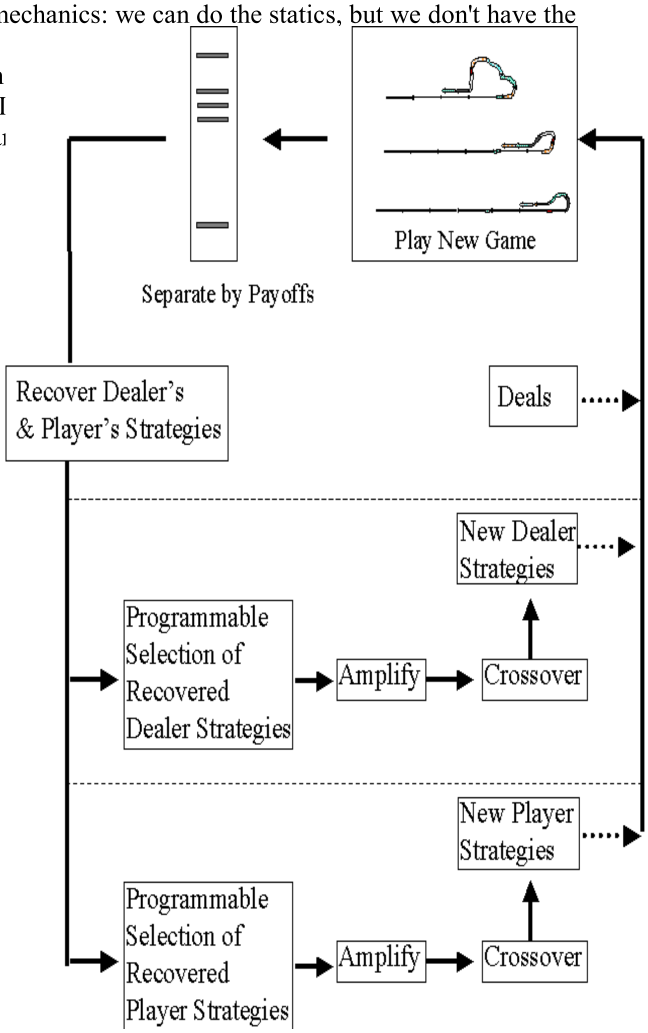

Separate by Payoffs
Play New Game
Recover Dealer's & Player's Strategies
Deals
New Dealer Strategies
Programmable Selection of Recovered Dealer Strategies
Amplify
Crossover
New Player Strategies
Programmable Selection of Recovered Player Strategies
Amplify
Crossover

Fig. 1. Evolving poker playing strategies.

2.1 Complexity of Seeking Game Strategies

The complexity of the problem of finding good strategies can be indicated in the following way. Roughly speaking, all interesting games have exponentially many possible strategies. As for finding good strategies, no definite procedures are known which can consistently outperform simple enumeration. This is analogous to the complexity of seeking solutions or approximations for NP-complete problems, plus extra difficulties arising from dynamically changing situations.

3 Simplified Poker via DNA

In this paper, we use an very simplified version of poker taken from a game theory textbook (49). Even so, it incorporates bluffing, calling, and folding --- all of which must be done with varying probabilities, if good payoffs are to be achieved.

> There is a Dealer and a Player. Each contributes $1 into the pot to start one hand of play. The Dealer deals a single card, an Ace or a 2, so that only the Player can see it. If it is an Ace, the Player must add $1 and say "Ace." If the card is a 2, the Player may say "2," losing the hand, or may add $1 and bluff by saying "Ace." If the Player has said "Ace," it becomes the Dealer's turn. The dealer may choose to fold, losing the hand, or may add $1 and call. At this point the Player shows the card and wins the hand if it is an Ace, and loses if it is a 2.

[3] The Internet is estimated to contain 9 x 10^{16} bytes (32). One gram of single-stranded DNA is approximately 1.8x 10^{21} nucleotides or about 10^{22} bytes.

[4] A strategy is a set of instructions for all possible situations that can be encountered in a game.

3.1 Strategies Are Learned by Playing Trillions of Simultaneous Hands Using DNA

Our DNA based implementation of playing poker is organized as shown in Figure 1. This gives a broad overview of three independent but linked processes. The overall approach of selection by fitness, adding variation by crossover, is similar to in-vitro evolution (1,5,11,14,16,36).

At the top, differing strategies compete, and the resulting histories of play are separated by outcomes.

In the middle, the many dealer-strategies are evaluated and selected by using a procedure based on payoffs achieved. This must be done carefully. Many selection criteria are possible, and it is foolish to insist on consistently high payoffs. Population size is restored by amplifying the selected strategies. Then, crossover induces variation within the population of strategies. Finally, the new dealer strategies are entered into another round of competition.

At the bottom, the other player uses a similar process, but with an independent method of selection.

3.2 Encoding Strategies in DNA Strands

The Player's strategies are encoded in single-stranded DNA as shown at the top of Figure 2. This DNA strand consists of four pairs of labeled regions, with pairs separated by "stoppers." The roles of the various regions will be explained shortly. It is important to note that all of the Player's strategy strands are identical except in one variable region, labeled SAY 2'. This region will vary throughout the Player's population of strategies. Its purpose, as we will see, is to implement diverse probabilities of bluffing.

The Dealer's strategies are similarly encoded, having one variable region labeled FOLD' to implement various probabilities of calling.

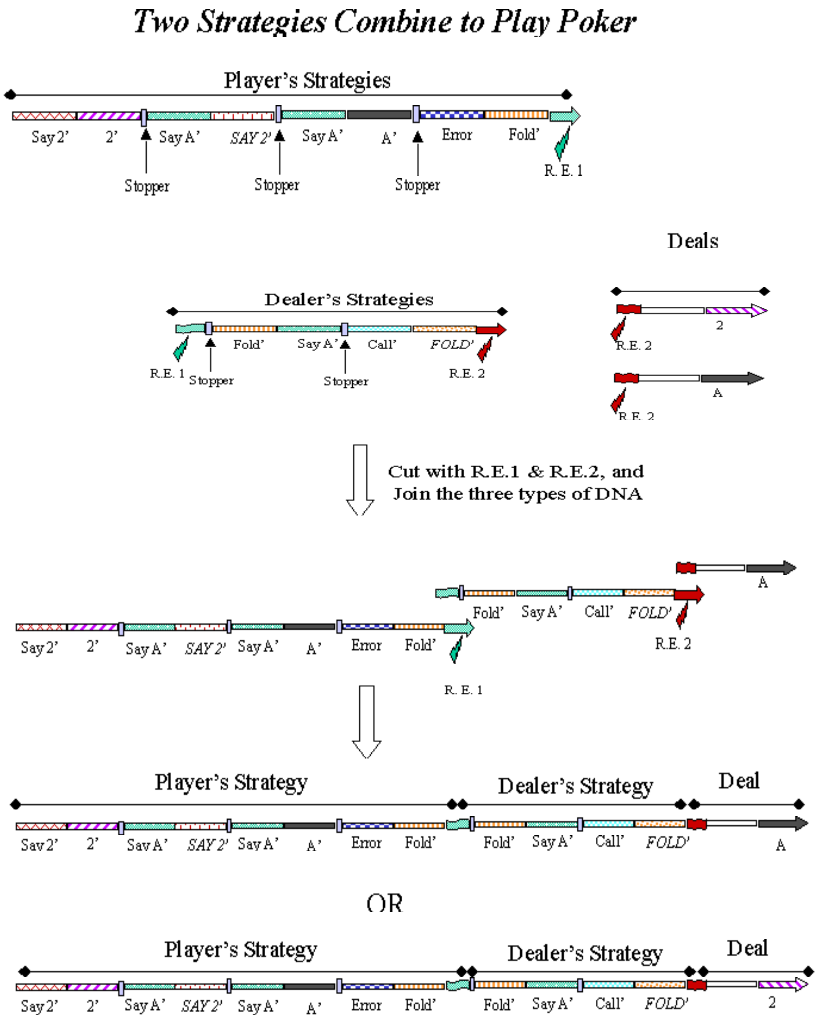
The cards to be dealt are Ace and 2, shown with unlabeled spacers at their left (labeled Deals in Figure 2).

Restriction enzymes, R.E. 1 and R.E. 2, cut DNA strands at specific locations, where indicated. This facilitates first joining Dealer strategy strands to Player strategy strands to Deal strands; and to later sever these strands so they can be individually recovered (separated by length using gel electrophoresis).

Two situations can result, as shown at the bottom of Figure 2. They differ by ending with A or with 2. Of course, the variable regions are not predictable in advance. These variable regions will probabilistically determine the course of the play.

3.3 The DNA Sequences Used

The specific DNA sequences used are shown in Table 1. These sequences are based on (32) where they were used in Whiplash[5] PCR, which is similar to the play of one Hand of simplified poker using two fixed strategies.



l
g. 2. A Player's and a Dealer's strategy join a deal for a hand of poker.

[5] Sometimes called hairpin or banjo PCR.

Table 1.

Names	Size	Sequences
A (Ace)	15-mer:	5′CCGTCTTCTTCTGCT3′
A′	15-mer:	5′AGCAGAAGAAGACGG3′
2	15-mer:	5′TTCCCTCCCTCTCTT3′
2′	15-mer:	5′AAGAGAGGGAGGGAA3′
Say A′	15-mer:	5′CGTCCTCCTCTTGTT3′
Say 2	15-mer:	5′CCCCTTCTTGTCCTT3′
SAY 2′	**15-mer:**	**Random with T,G,& C**
Fold′	15-mer:	5′TGCCCCTCTTGTTCT3′
FOLD′	**15-mer:**	**Random with T,G,& C**
Call′	20-mer:	5′CTCCTCTTCCTTGCT CTTCTCCCTT3′
Error	10-mer:	5′TCCCCTTGTG3′

3.4 Whiplash PCR Plays a Hand of Poker

At the top of Figure 3 below, two strategies are combined with a dealt Ace. The rest of the figure shows how the play of the hand can result in two possible outcomes, depending on whether the Dealer decides to fold or call. Figure 4 is almost the same, showing the play of a hand when a 2 is dealt.

Having been dealt an Ace, the Player must say "Ace." This is accomplished using DNA in the following way. The sequence encoding A at the end of the DNA strand strongly pairs [6] with its Watson-Crick complementary sequence A'. This enables DNA polymerase to extend the strand by appending the sequence Say A'. Extension halts at a "stopper." To continue extension into a stopper region (encoded with 4 A-bases) would require dTTP, which is withheld from the reaction. Raising the temperature disrupts interstrand pairing. Recooling begins the Dealers turn.

The Dealer must decide to call or fold. This is an IF-THEN-ELSE type decision, but we implement it in the form, "By default, fold, but if the probability is large enough, change your mind and call." That is, in the part of Figure 3 labeled Dealer Folds, the Dealer's strategy encodes this situation and extends the DNA strand with the Fold sequence. After heating followed by cooling, the Fold sequence may or may not pair with the FOLD' sequence, as at the bottom of Figure 3. If and only if pairing occurs, the DNA strand is extended by the Call sequence, essentially changing the Dealer's decision from Fold to Call.

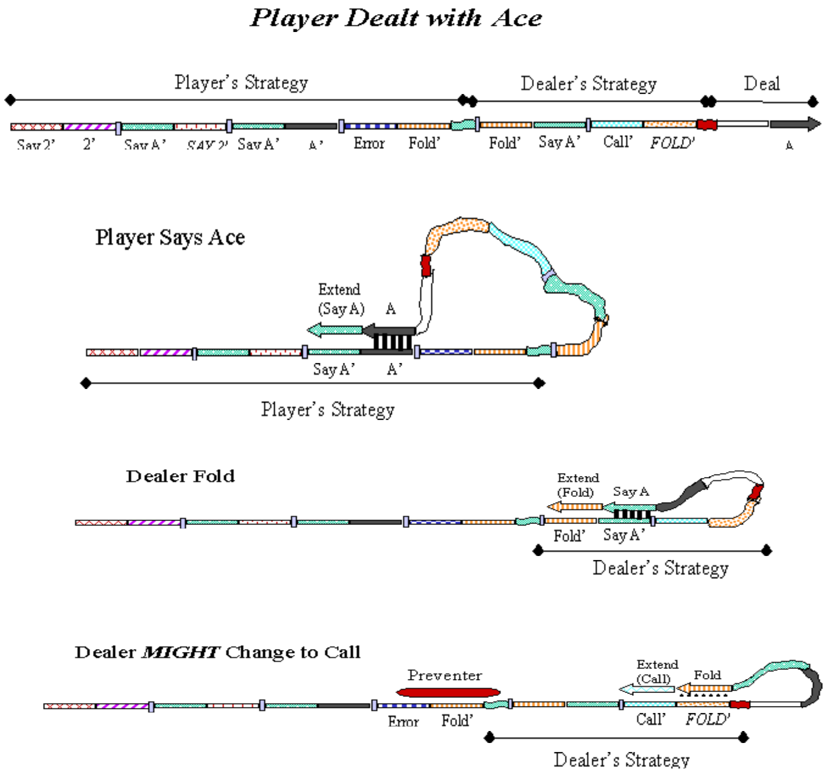


Fig. 3 Player is dealt an Ace.

Success of pairing depends on the FOLD' sequence, which is generally different for different Dealer strategy strands. Therefore, the population of Dealer's strategies will generally produce some fold outcomes and some call outcomes. These outcomes are later used to select strategies by payoffs. Thus, it is the FOLD' sequences within Dealer's strategy strands that do the adapting. The FOLD' sequences in the initial population of strategies are randomized during the synthesis of Dealer's strategy strands.

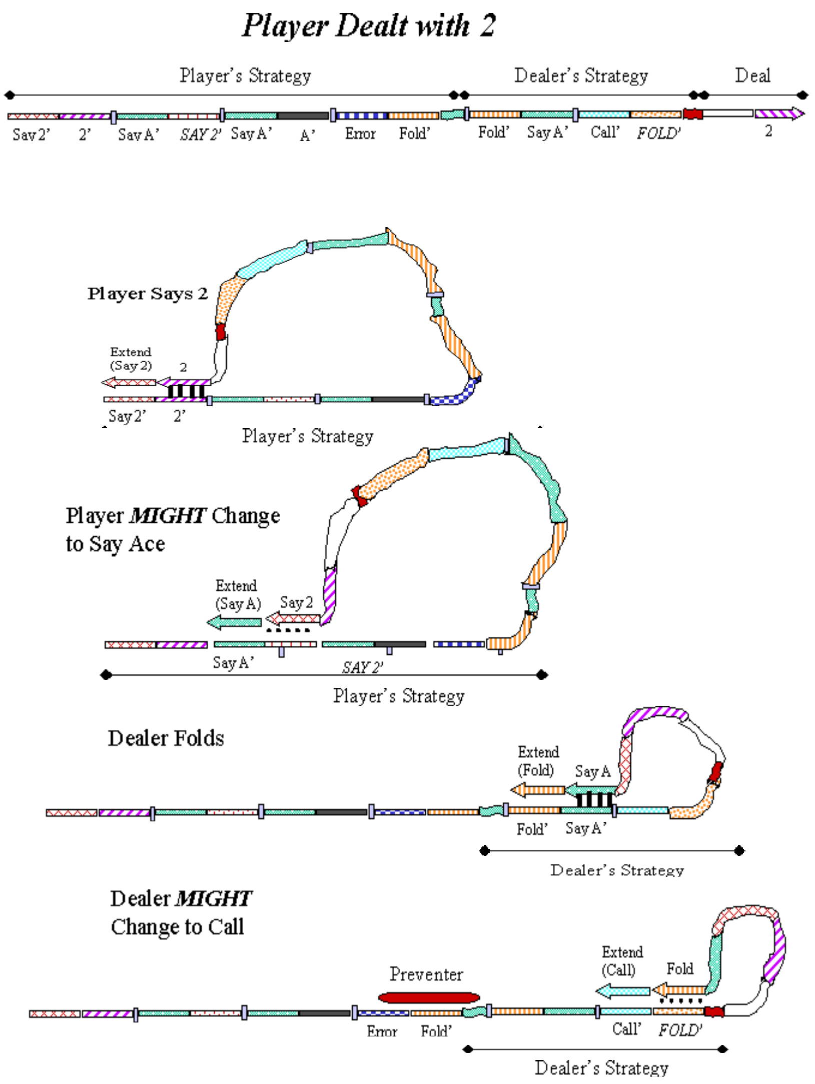
[6] In Watson-Crick complementary pairing within double stranded DNA, each base A in one strand pairs with a base T in the other strand, and similarly, each base G pairs with a base C. Any such pairings tend to hold two strands together.

3.5 Regular Poker Would Use Similar Techniques

A “Wait Your Turn” feature is also shown in the last step in Figure 3. Strictly speaking, this feature is not needed in simplified poker, but we wish to test it because it is needed in other games where players may take several turns. In essence, the Player’s strategy is prepared to react to folding, but must not react before there is a chance for the Dealer to change from Fold to call. Thus, as we cool the DNA we include a Preventer stand that preferentially (at higher temperature) pairs as shown in the Player’s strategy. Should prevention fail, we would detect the presence of the Error sequence in some outcomes.

In regular poker decisions are similar but somewhat more complex. For example, the Dealer’s decision in Figure 3 would become the following. “By default, I fold, but append a copy of the hand I have been dealt. If my hand is good enough to match an evolved criterion, I can change my mind and call. But I append another copy of my hand and if it is good enough, I make a small raise. An additional comparison can result in a larger raise, etc.

Fig. 4. Player is dealt a 2.



g. 4. Player is dealt a 2.

3.6 The Dealer and Player Independently Evolve Their Strategies

So far, we have explained how DNA laboratory techniques are able to pair off Dealer strategies and Player strategies along with a deal of an Ace or a 2. The result is a DNA strand recording the entire history of the play of one hand of simplified poker. So far, we have elaborated on the top part of Figure 1. We now go on to explain how the Dealer and the Player can independently evolve their populations of strategies.

Figure 5 A (the extrinsic form of the game of simplified poker, plus an error output) contains all five possible game histories, along with their payoffs, positive or negative, for the Dealer. The left side corresponds to Figure 3 and the right side to Figure 4. Figure 5 A also reflects the different final lengths of the DNA strands encoding each of the histories.

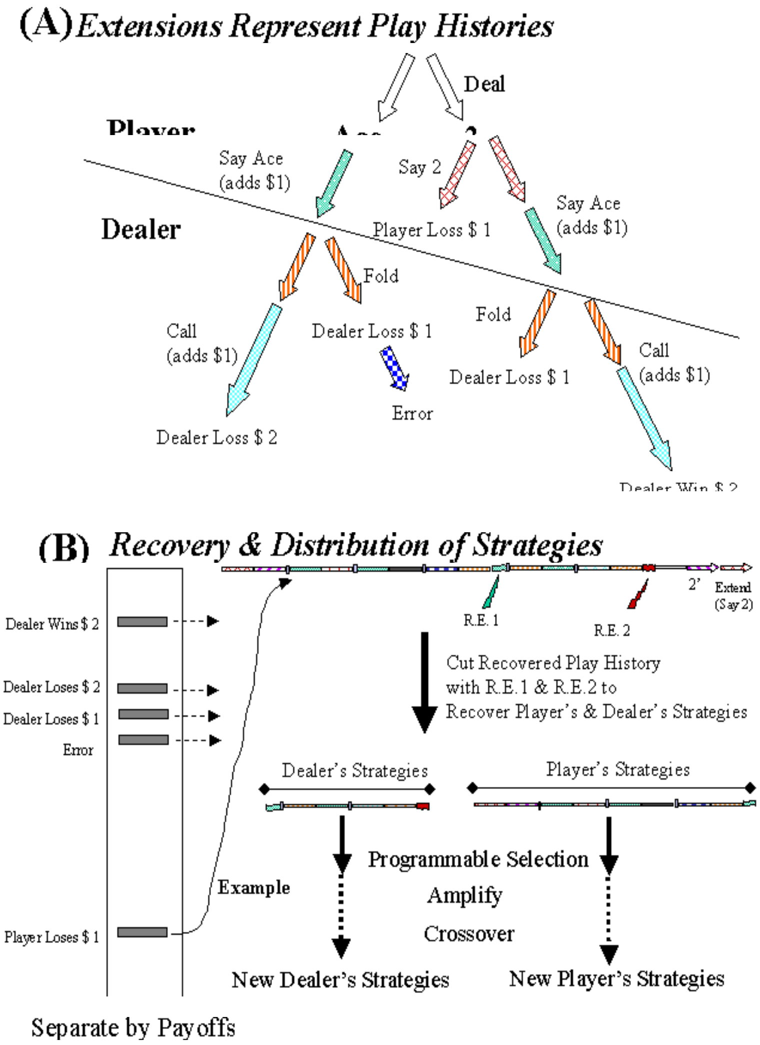
Differing lengths make it convenient to physically separate histories using denaturing gel electrophoresis. Readout is provided by quantifying the amounts of DNA in each band of the gel. Other techniques could also be used, for example the 2d-DGGE techniques that we have used in evolutionary computations (4-5, 20, 59-61).

Physical separation gel is indicated on the left of Figure 5 B. Each lane of the gel corresponds to a different payoff. What follows is that for each possible payoff the Dealer receives a quantified sample of the strategies that led to the given payoff. These samples are obtained by literally cutting the bands from the gel and extracting the DNA from them. The Dealer is then able to recombine strategies in various dilutions of her own choosing. Using this freedom of choice, and a chosen amount of crossover to explore further variations, the Dealer produces a new generation for strategies that will hopefully improve her net payoff. Improvement cannot be guaranteed, of course, because the Player is independently striving for the opposite outcome.

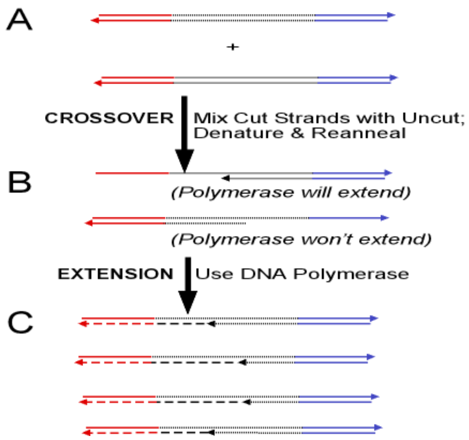
3.7 Implementation of Crossover

The most common recombining of genetic information in evolutionary computation is single point crossover (2). Here, the beginning part of an offspring's genetic material comes from one parent and the rest from a second parent[7].

Laboratory procedures are available for crossover (47, 48). Our method (5, 59-61), shown in Figure 6, is designed to accommodate highly variable regions. It begins with double stranded PCR product obtained restoring population size. Part of the PCR product is reserved. The unreserved DNA strands are cut at random locations about once per strand[8] and then combined with the reserved strands. The mixture is denatured (strands are melted apart) and allowed to reanneal (cool down). This allows single strands to recombine in various configurations. Some of these configurations are suitable for completing crossover.



g. 5. Each branch of the game tree gives different DNA lengths.



Recall that the ends of the DNA strands encode PCR primer sites. This means the rightmost (3') end is designed to Watson-Crick pair to its complement in correct alignment at a relatively high temperature during cooling. Thus, a truncated Players' or Dealers' strategies DNA strand can pair in proper alignment with an intact complement of a different DNA strand. As shown in Figure 6B (top), some of the truncated DNA strands may additionally pair well at their

[7] Multiple-point, multiple-parent crossover could be easily obtained by iterating single-point crossover.

[8] We use the enzyme *DNAase I* to mostly nick (cut only one strand) double stranded PCR product. Strand nicking could also be done by other enzymes or chemicals.

other (3’) ends. When this happens, they can be extended to full length using DNA polymerase. The result is single-point crossover. Many undesired products not shown in Figure 6 are also formed in the crossover reactions. But virtually none of the undesired products achieve the same length as the original DNA strands. Therefore, the desired single-point crossover products can be purified by length using denaturing gel electrophoresis.

3.8 Experimental Results

We have constructed the two ssDNAs to represent the two possible plays shown in Figures 3 and 4. Currently, demonstration of whiplash PCR is in process. Preliminary experimental results will be presented in the meeting.

4 Anticipated Directions

We attempt to address some game theoretic questions on the evolution of strategies for simplified poker. For simplified poker the questions can also addressed by analytic means, whenever possible, and by computer simulation. However, computer simulation would be difficult for populations as large as using DNA.

The main outcome sought is to gain confidence in the DNA encodings and techniques that could be applied to more challenging games, especially poker. We will address questions such as the following. Is equilibrium maintained once it is induced? If one party uses an equilibrium strategy, will the other party evolve to equilibrium? If one party does a poor job of learning strategies, does the other party exploit this? What are good choices for programmable selection in evolving strategies? Will they result in obtaining equilibrium? If so, how fast? How much does crossover help? What crossover rates are best?

Thus, we have cited many more questions than answers. However, we hope to provide a *technique* for answering such questions---namely, taking advantage of the massive parallelism of DNA computing to test huge numbers of strategies in competition and to improve them based on their outcomes.

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