#### **Build a Game Playing Agent**

### Opening Book using Genetic Algorithm

I decided to develop an opening book using a genetic algorithm. The custom agent was also augmented to use this opening book.

## 1. Process for collecting statistics to build your opening book, and the rollout procedure.

The opening book I constructed attempted to find the best moves for every possible game state from an empty board. Notation clarification: from here onwards let player\_0 represent the player that starts the game with an empty board.

A genetic (evolutionary) algorithm used was:

- For each starting board position, construct a large pool of *genomes*. A genome is a sequence of actions [move\_1, move\_2, ..., move\_n], where each move\_i corresponds to one ply for player\_0. Thus, a genome of length n corresponds to n rounds in the Isolation game.
  - Note: Each genome is initially generated as a sequence of random <u>legal</u> actions on an empty starting board with no opponent. Also, move\_1 in each genome is the starting board position.
- ii) for each starting position:

for generation in range(number of generations):

for genome\_i in genome\_pool:

- Evaluate the fitness of genome\_i by simulation a game against an opponent (player\_1) that chooses a random initial move and then follows the minimax algorithm with search depth of 3 thereafter.
- In the simulated games, player\_0 chooses moves sequentially from the elements of genome\_i. Once the moves from genome\_i have been exhausted, player\_0 follows the minimax algorithm with search depth of 3 thereafter.
- If the next move suggested by genome\_i is invalid for the current board state, player\_0 substitutes it for the move suggested by the minimax algorithm.
- The fitness of genome\_i is tuple: (player\_0's utility at final game state, number of turns to complete the game)

Sort the genomes by their fitness (prioritizing winning in fewest turns) and discard the worst k\_percentile (where k is based on learning\_rate)

Generate k\_percentile new genomes by splicing:

- The splicing strategy chooses two parents based on a weighted random sample of genome\_pool, where the weights give preference to genomes with higher fitness.
- The spliced child genome contains moves from the two parent genomes in alternating order (as illustrated below).

• Check if the new child genome is a legal sequence of moves (starting on an empty board, with no opponent). If the new genome is not legal, the splicing process is repeated with a different sample of parents.

The new spliced genomes are added to the genome pool.

Lastly, a small percentage of the genomes from the genome\_pool are mutated by replacing a randomly (uniform) chosen move with another legal move. Note: the mutation of a move may affect the legality of subsequent moves in the genome's sequence. So, more than one (random) mutation per genome may be necessary to preserve the genome's legality.

I decided to run this algorithm using 2 sets of hyperparameters:

Strategy 1:	Strategy 2:
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Genome length =  $\underline{\mathbf{5}}$  Genome length =  $\underline{\mathbf{10}}$  Genome Pool Size = 2000 Genome Pool Size = 2000 Number of Generations = 50 Number of Generations = 50 Learning Rate = 0.25

Mutation Rate = 0.05 Mutation Rate = 0.05

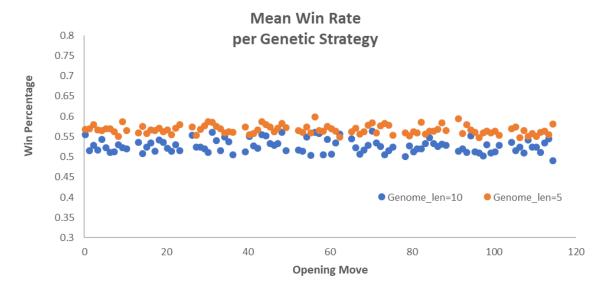
The heuristic used with minimax algorithm for all experimentation is the (#my\_moves - #opponent\_moves) heuristic.

## 2. Experimental Results

For each starting position, each genome from the final genome\_pool for the two strategies above was tested against 100 opponents. The 100 opponents (player\_1) each chose a random initial move and followed the minimax algorithm with search depth of 3 thereafter. The starting

player (player\_0) followed the actions in the genome until exhausted; and used the minimax algorithm with search depth of 3 thereafter.

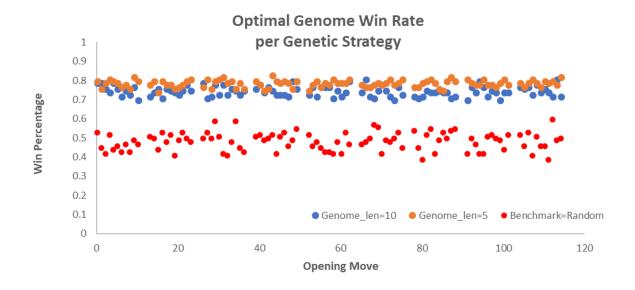
The chart below shows the <u>average</u> win rate across all genomes for each starting position.



We can see that Strategy 1 consistently outperforms Strategy 2. I suspect longer genomes require a greater number of generations to improve performance.

The chart below shows the win rates for the <u>best performing</u> genome for each starting position.

For the benchmark, we set player\_0 to randomly select from legal actions for the first 5 plies; and use the minimax algorithm with search depth of 3 thereafter. The benchmark for each starting position was also tested against 100 opponents (as above).



The average win rate (across all starting positions) for the benchmark is 49.38%. The average win rate for the best genomes from Strategy 1 is 78.75%. The chart above also shows that Strategy 1 consistently out performs the random benchmark against the 100 opponents (as defined previously).

So, the 5-ply opening book I created is made up of these best performing genomes from the genetic Strategy 1, for each starting position.

# 3. What opening moves does the book suggest? What is player 2's best reply?

According to my experiments, some examples of opening strategies that were able to achieve close to 80% win-rates are:

- Opening Move: 47 -> Action.NNE -> Action.ENE -> Action.ESE -> Action.SSW (win-rate 81%)
- Opening Move: 114 -> Action.SSE -> Action.ESE -> Action.ESE -> Action.SSE (win-rate 80%)
- Opening Move: 43 -> Action.NNW -> Action.NNE -> Action.ESE -> Action.WSW (win-rate 80%)
- Opening Move: 56 -> Action.NNE -> Action.WSW -> Action.WSW -> Action.SSW (win-rate 79%)

Opening Move: 114

Below are the board representations of the moves above

Opening Move: 47

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As expected, one successful strategy for replies by player\_1 is to visit one (or more) of the cells in player\_0's opening move sequence before player\_0. In my current implementation, this forces player\_0 to resort to the mini-max algorithm (same as player\_1), and thus drives player\_0's win-rate closer to 50%.

Below are some other move sequences that defeat the opening moves discussed above:

• Player 1 = Initial Move: 47

Player 2 = Move Sequence: 60 -> NNE -> ENE -> SSW

• Player 1 = Initial Move: 114

Player 2 = Move Sequence: 3 -> NNE -> NNE -> NNE -> WSW

• Player 1 = Initial Move: 43

Player 2 = Move Sequence: 78 -> SSW -> SSE -> WSE -> NNE

• Player 1 = Initial Move: 56

Player 2 = Move Sequence: 66 -> NNE -> WSW -> SSE -> WSW

I suspect more robust performance can be achieved from this opening book strategy by increasing the number of generations in the genetic algorithm (keeping the other model hyperparameters same).