

GENETIC ALGORITHMS IN THE SEARCH FOR OPTIMAL KUHN POKER STRATEGIES

Dissertation Abstract - MSc in Computer Science

Author:

Paula LÓPEZ POZUELO

Supervisor:

Dr. Robin HIRSCH

This dissertation examines the search for intelligent computer strategies in the game of Kuhn Poker, a simplified Poker variant that is played between two players with a three-card deck.

A Genetic Algorithm (GA) was fully implemented to do this, as well as a Kuhn Poker game, and they were both combined to evolve strategies for the players. The effects of different types of population initialization, selection and crossover were studied.

The results show that Genetic Algorithms can be quite efficient at generating winning strategies against a particular player by modeling its behaviour. For instance, in a game against a standard player, the best strategies evolved made \$0.23 on average if playing first and \$0.32 if playing second (the second player generally has an advantage), in a game with \$1 bets.

Some of the computer player strategies produced displayed bluffing and sandbagging behaviours as a means to take advantage of the opponent's habits - highlighting the importance of deceptive game-play in Poker.

Through the use of co-evolution, in which two populations were trained against each other, strong strategies capable of winning against a multitude of different players were found. Additionally, a mixed approach between co-evolution and population breeding against fixed opponents was suggested, and successfully implemented, for the evolution of even fitter strategies.

More complex variants of the Kuhn Poker model were implemented and examined, in which players were allowed to place different amounts of bets, bet more than once or both.

Tournament and Rank selections were found to perform significantly better than Roulette-Wheel selection, converging faster towards better performing strategies (average wins of \$0.08 in 100 generations versus \$0.02 in 500 generations). A uniformly random initialization of the first population performs slightly better than a purely random one, while ensuring an equal distribution of values throughout the chromosomes. Finally, Uniform and One Point crossover performed similarly, however, the former was used due to a slightly improved performance against some models.

September 3, 2015