

# ***IBC: Individual Based Choice***

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***Abstract*** — Genetic Algorithms seek to solve optimization problems by implementing bioinspired techniques that simulate the evolution of living beings. This work explores a particular aspect of these techniques and proposes an individual mate choice criteria for the mating phase, called IBC. The main idea is to delegate the choice of the mate to the individuals, seeking to obtain a positive incidence in the evolution of the individuals throughout the generations. The choice criteria is codified within the chromosome, so it participates of the evolutionary process, giving each individual its own criteria. Experimental comparison between IBC, Rank and Binary Tournament show a positive tendency for the proposed technique.

***Keywords:*** Artificial Intelligence, Genetic Algorithms, Evolutionary Algorithms, IBE, Mating Strategies.

## I. INTRODUCTION

Part of the mere essence of Artificial Intelligence is its constant observation of human and animal behaviors. The evolutionary algorithms area especially, finds its inspiration in natural phenomenons of race perpetuation. Evolution, despite environmental changes, is believed to always maintain immutable natural laws. One of evolution root mechanisms (some of which unchangeable) is the survival of the fittest. The survival of the fittest individual settles a selection strategy of individuals from one generation to another. Moreover, it is observed in natural processes such as mating selection, a choosing strategy of which individual is best fitted to perpetuate genetic codes with. Which means that in nature itself exists a choosing mechanism allowing individuals to decide with whom to reproduce, and a selection mechanism setting up which ones will be the best to perpetuate their characteristics, according to environmental conditions.

It is worth noticing that in the case of genetic algorithms[1], there is no real mating mechanism, since only selection[2], is actually performed, omnipresently, leaving little participation to the individual in evolution dynamics. In other words, mate choosing criteria don't depend on individuals, and are equally adopted by the whole population in evolution. Clearly, this pure selection choosing allows a better control of the experiment and makes easier comparing different characteristics.

Classic mating selection criteria are: binary tournament and rank [2] and [3]. Both select individuals from the population, without allowing the individual to particularize its choice. For instance, in Kai Song Goh research[4], a binary tournament is used for mating selection when implementing an evolutionary algorithms with sexual reproduction. Normally, selection criteria remain through generations and their efficiency is proved [1]. In this article, the two best known selection processes are compared: binary tournament and Rank, with the choosing criteria proposed, named IBC (Individual Based Choice).

The technique proposed IBC, comes from the intuitive idea of having more choice criteria than mating selection. This choice criteria is customized for every individual to express its preferences when choosing which partners to breed with. It means that every individual will bear in its chromosome a sequence we will call choice feature to determine its preferences when choosing mate. Furthermore, as this choice feature is part of the individual chromosome (be heard as domain feature) then, choice feature lying within the evolution process, it will be changeable through generations.

IBC extends the simple chromosome of every individual with this choice feature, that is to say with the sequence that reflects mating preferences. This sequence has to reflect an individual's mating desire with three possible options:

- The mate has specific genes identical to the selector.
- The mate has specific genes contrary to the selector
- Absolute indifference of the selector to the characteristics of the mate's specific genes.

To some extent, this choice feature reflects the compatibility an individual would have with a mate selected for breeding. A quantitative value is defined for compatibility, setting which mate is the fittest for an individual, according to its preferences.

On the other hand, in this study the fitting function only applies to domain feature, since basis selection has to be rooted in specific characteristics of the individual. Its preferences are more likely to be part of its interaction with the community, which means a social and cultural concept, than a genetic feature. Additionally the IBC chromosome, made with choice and domain features, will have crossing points so that they will allow both characteristics to vary through generations.

## II. THE PROPOSAL

Selection, crossing and mutation mechanisms are generally implemented as omnipresent mechanisms that take

actions and make decisions as far as reproduction and generation survival are concerned.

An **Individual Based Choice (IBC)** is proposed, setting in every individual's hands the responsibility of mate selection. This way, the individuals are defined as independent beings, with their own criteria. Including choice feature, each individual sees its preferences changing through the evolutionary process, creating new sequences representing the criteria out of breed and parents' mutation.

### A. Choice mechanism

**Definition 1.** An IBC  $C_E$  chromosome is a sequence composed of genes that codify the problem or domain feature  $[g_1, g_2 \dots g_n]$  and a sequence with values between  $\{-1, 0, 1\}$  and that codifies the individual's preferences or choice feature  $[e_1, e_2 \dots e_n]$

$$C_E = [e_1, e_2 \dots e_n, g_1, g_2 \dots g_n]$$

For instance, simple chromosomes as:

$$\begin{matrix} C_1 = [ & 1 & , & 0 & , & 0 & , & 1 & , & 1 \\ C_2 = [ & A & , & B & , & D & , & O & , & 1 \\ C_3 = [ & \# & , & \$ & , & * & , & @ & , & 1 \end{matrix}$$

*Domain Features*

Could be represented as IBC chromosomes this way:

$$\begin{matrix} C_{E1} = [ & 1 & , & 1 & , & 1 & , & 1 & , & 1 & , & 1 & , & 0 & , & 0 & , & 0 & , & 1 \\ C_{E2} = [ & 1 & , & 0 & , & -1 & , & 0 & , & A & , & B & , & D & , & O & , & 1 \\ C_{E3} = [ & -1 & , & -1 & , & -1 & , & -1 & , & \# & , & \$ & , & * & , & @ & , & 1 \end{matrix}$$

*Choice Feature*                      *Domain Feature*

### Definition 2. Be

$$C_E = [e_1, e_2 \dots e_n, g_1, g_2 \dots g_n].$$

If  $e_i = 1$  then the individual  $C_E$  prefers breeding with individuals with the same value for  $g_i$  gene. If  $e_i = -1$ , the individual prefers breeding with individuals with a different value for  $g_i$  gene. And if  $e_i = 0$  then, it is indifferent to him the value for  $g_i$  gene.

It is to be noticed that through its choice feature, the individual expresses the characteristics he expects from his mate, whether similar, different or indifferent to his.

An IBC chromosome choice feature has the same length as its domain feature so that the individual can express his preference for each feature or gene composing chromosome.

### Definition 3. Be two IBC chromosomes,

$$\begin{matrix} C_{E1} = [e_{11}, e_{12} \dots e_{1n}, g_{11}, g_{12} \dots g_{1n}] \\ C_{E2} = [e_{21}, e_{22} \dots e_{2n}, g_{21}, g_{22} \dots g_{2n}] \end{matrix}$$

IBC  $C_{E1}$  compatibility regarding IBC  $C_{E2}$   $Comp(C_{E1}, C_{E2})$  is expressed as:

$$C_{12}(g_{1i}, g_{2i}, e_{1i}) = \begin{cases} 1 & \text{if } e_{1i} = 1 \text{ y } g_{1i} = g_{2i} \\ 1 & \text{if } e_{1i} = -1 \text{ y } g_{1i} \neq g_{2i} \\ 0 & \text{in contrary case} \end{cases}$$

$$Comp(C_{E1}, C_{E2}) = [\sum(C_{12}(g_{1i}, g_{2i}, e_{1i}))]*100/m$$

Where  $m$  is the quantity of values in the choice feature different from zero.

Let's take a look at calculating compatibility between two specific chromosomes:

$$\begin{matrix} C_{E1} = [ 1 , 1 , 0 , -1 , A , B , C , B ] \\ C_{E2} = [ 1 , 0 , 0 , -1 , A , C , C , A ] \end{matrix}$$

$$\begin{matrix} C_{12}(g_{11}, g_{21}, e_{11})=1 & \text{because } e_{11}=1 \text{ y } g_{11}=g_{21} \text{ (A=A)} \\ C_{12}(g_{12}, g_{22}, e_{12})=0 & \text{because } e_{12}=1 \text{ y } g_{11} \neq g_{21} \text{ (B \neq C)} \\ C_{12}(g_{13}, g_{23}, e_{13})=0 & \text{because } e_{13}=0 \\ C_{12}(g_{14}, g_{24}, e_{14})=1 & \text{because } e_{14}=-1 \text{ y } g_{11} \neq g_{21} \text{ (B \neq A)} \end{matrix}$$

$$Comp(C_{E1}, C_{E2}) = (1+0+0+1) * 100/3 = 66,6\%$$

### B. Choice mechanism applied to Evolution

Having already defined a mechanism allowing calculation of two IBC chromosomes, let's see how this concept participates in an evolutionary algorithm. During the selection phase, every individual decides which mate fits to breed with instead of the better known mechanisms of binary tournament and rank. The general algorithm is:

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Random initialization of IBC population of n size
While there is no evolution ending condition
  For each individual CEi of the population
    For each individual CEj / i != j
      Calculate Comp(CEi, CEj)
    CEi chooses CEj with highest compatibility
  Breeding CEi y CEj (two random cut points)
  Mutate sons with low probability
  Reduce to half population for fitness
  
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Once the mate is chosen, thanks to compatibility, a crossing is performed with two random cut points, and two new IBC chromosomes (blend from parents) are generated. It two folds the next generation's population, which is thus to be reduced with the fitness function. As the choice feature is part of the chromosome, the engendered individuals may have a choice feature made of a blend of their parents. This way, the choice criteria is as well transmitted as part of the individual.

### III. THE EXPERIMENT

#### A. Implementing strategies

Experimental comparison is centered on the well known “knapsack problem”, using the two best known selection strategies [3] in genetic algorithms. This way, both selection methods are compared with the Individual Based Choice on a simple genetic algorithm:

- Binary Tournament with substitution
- Rank
- Individual Based Choice (IBC)

It is worth stressing that these methods will use the same crossing and mutation processes in order to concentrate the evolution results [4] and to compare only the selection methods with IBC.

##### 1) Crossing:

This experiment carried on with random points crossover. W. Spears y K. De Jong experiment [6] concludes that the quantity of points to be used and their distribution (uniform or random) depends a lot on the problem to be resolved, reason for the great importance left to this regard.

With the IBC chromosome, specifically, there is a small detail when using only one random point crossover. Figure 1 pictures the problem to be considered:

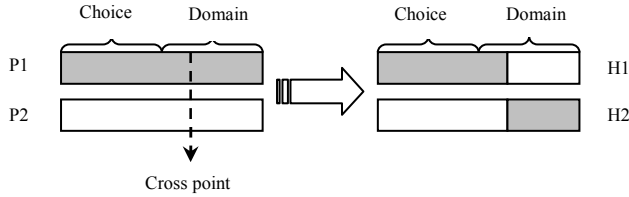


Figure 1. One point crossover in IBC chromosome

In figure 1 we can observe that son 1 inherits all of the father’s choice feature, whereas son 2 will get all of the father’s domain feature. But there did exist a change in domain feature. With only one point, this will always happen: either information is mixed in choice feature, or it is mixed in domain feature, but both feature never mix with each other.

In order to support genetic material mixing, it was decided to use two random points crossover.

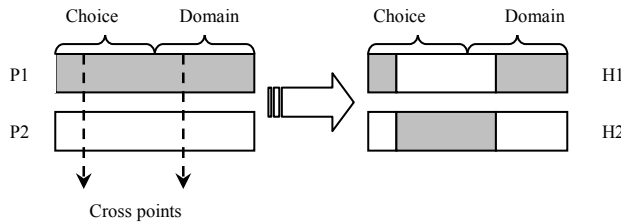


Figure 2. Two point crossover in IBC chromosome

Now, in figure 2 we can observe that using two points the opportunity of genetic material exchange in individual’s both features is increasing.

##### 2) Mutation

Taking into account the possibility that the strategies implemented are affected differently by mutation probability, it was decided to determine experimentally the best value for this factor for each one of the methods.

The experiment consisted in resolving 10 times a simple knapsack problem with each strategy (tournament, Rank and IBC). In each one of these races, a different mutation rate was registered, between [0.03,0.3].

According to previous considerations, it is intended to compare each one of the methods in positive conditions, to avoid explaining any difference in results by sensitivity of the evolution elements.

#### B. The Problem

The knapsack problem is a quite well known NP hard problem, and it is one of the most used to test and compare simple and multipurpose evolutionary algorithms [5] and [7]. For this research, it was decided to define three knapsack problems, varying from one another only in the quantity of available elements.

- Problem1=250, weight between [0,20] and max. 1666
- Problem2=500, weight between [0,20] and max. 3333
- Problem3=750, weight between [0,20] and max. 5000

It is worth stressing that the maximum weight of the knapsack corresponds to the formula (Number of Items\*max. value of Item)/3. Intending to avoid knapsacks with maximum weights superior to the sum of the weights of the available items.

To resolve these problems using the implemented AG, binary chromosomes were codified, where every position of the chromosome or gene indicate whether the item is present or not in the knapsack. This codification is one of the most used to represent solutions to problems such as chromosomes of an evolutionary algorithm.

##### C. Experimental test

The experimental test consists in resolving each of the previously proposed problems with each of the choice methods. Below is to be found the configurations used by the different methods in every test:

TABLE I. BINARY TOURNAMENT WITH SUBSTITUTION

Binary tournament with substitution	Problem 1 (250)	Problem 2 (500)	Problem 3 (750)
Number of individuals	500	700	900
Mutation probability	0.03	0.03	0.03
Generations	100	100	100



Comparing IBC box and whisker plots versus both of the other methods, it is observed that the solutions it offers are superior in each of the cases, showing a symmetrical and concentrated distribution regarding the median, managing stability when reaching superior solutions yet maintaining individuals diversity.

Additionally, it is observed that the solutions offered by IBC maintain a wider spreading than the other methods, although it also tends to curb progressively.

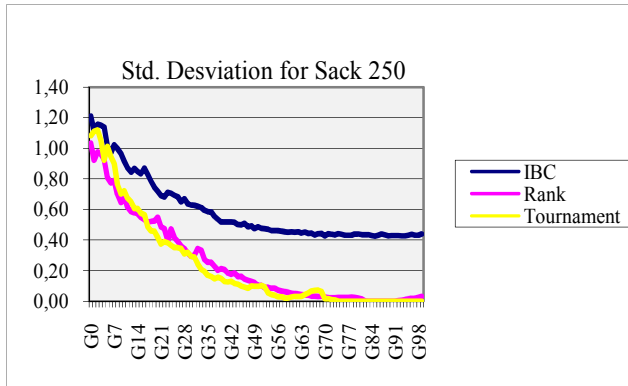


Figure 6. Standard deviation in the three selection methods

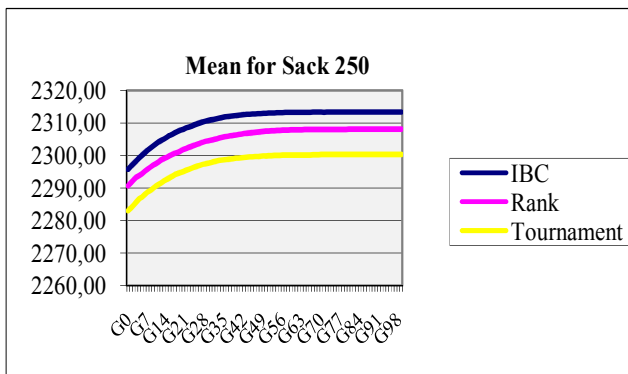


Figure 7. Median for the three selection methods

Comparing the arithmetic medians of the 3 methods it is obvious that in every generation IBC is superior to the others, yet in its worst solutions.

## V. CONCLUSIONS AND RECOMMENDATIONS

Proposing previously a new selection criteria, which according to the proposed specification, is better said a choice criteria, it was intended to reflect the specific preferences of each individual of the population, when choosing mate. As fitness function doesn't apply to choice feature, but to domain feature, it is impossible to assert there is evolution for choices. Nevertheless, it is definitely possible to assert that this feature is shared between different individuals, and changes through generations. It could be said, at least empirically that under this mating strategy, individuals preferences are conditioned by the fittest preferences, for they are the ones who breed and mutate.

Through generations, trend patterns or group preferences might be observed, appearing or disappearing without any optimal value, not even local or even less global. In studies to come, this problem will be approached in order to intend to characterize this social behavior which is probably present in the population due to the choice feature.

On the other hand, in all of the tests performed, since the first generation, with an average of fitness, IBC is superior to tournament and Rank in 50 runs for 3 experiments. We have a strong empirical presumption that for the knapsack problem, IBC is offering better results.

## VI. STUDIES TO COME

First of all, it is to be considered carrying out experiments with different problems. What would be IBC behavior in competitive problems? Would the results be as satisfactory in bigger problems?

On the other hand, it would be convenient to measure the efficiency of the choice method in a mutual compatibility, that is to say, when an individual makes a choice, he has to be sure he is also the chosen's preference. It is linked to another point to be tested, being a choice within a restricted population, as a simulation of age and gender. How would these populations co-evolve?

Moreover, we should evaluate the incidence of mutation in individuals' evolution when applying IBC. We have the intuition it has little incidence in evolutionary process.

Eventually, a crossover operator was implemented with 2 random points, without forcing any of them in the choice and domain features. What would be the consequences of always crossing genetic material on domain and choice?

In the current implementation of IBC, each individual seeks in the entire population until he finds the fitting mate. A faster approach to this seeking process would be that the individual seek in a limited part of the population and choose one from this small group of individuals. What would happen if we introduced a neighborhood concept?

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