Taming the 0/1 knapsack problem with monogamous pairs genetic algorithm

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ABSTRACT

This paper defines and explores a somewhat different subclass of genetic algorithm (GA) – a *monogamous pairs genetic algorithm (MopGA)* for solving the 0/1 knapsack problems (0/1-KP). The MopGA incorporates two important operations borrowed from social monogamy: pair bonding and infidelity at a low probability. Unlike conventional GAs, same pairs of parents (monogamous parents) are re-mated at each generation until their bonds expire. Nonetheless, this monogamy rule may be violated at the presence of infidelity. Our technique emphasizes on the thorough exploitation of the current search region via pair bonding, while allowing sufficient exploration to other unknown regions via infidelity. Consequently, MopGA is able to preserve higher population diversity by shielding offspring under the monogamous parents from population-wide selection pressure and restrictive mating strategy. As a side benefit from economical use of selection mechanism, the MopGA is computationally more efficient, especially when dealing with high-dimensionality 0/1-KPs. The empirical results on 0/1-KPs also show considerable performance in favour of the proposed methodology in terms of solution quality.

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1. Introduction

The 0/1 knapsack problem (0/1-KP) is one of the most studied NP-hard combinatorial problems in the last few decades (Azad, Rocha, & Fernandes, 2014; Khuri, Bäck, & Heitkötter, 1994; Wang, Wang, & Xu, 2012a). It has practical applications in numerous areas including budget control, telecommunication, resource allocation, VLSI design, and project selections, to name but a few.

The classical 0/1-KP can be defined as: Given a set of M items with p_j and w_j representing the profit and weight of each item j, respectively; the goal is to choose a subset of the items such that its total profit is maximized without exceeding the knapsack capacity, C. The problem can be formulated as:

$$\text{maximize} \quad \sum_{j=1}^{M} p_j x_j$$

$$\text{subject to} \quad \sum_{j=1}^{M} w_j x_j \leq C,$$

$$x_j \in \{0, 1\}, \quad j = 1, 2, \ldots, M \tag{1}$$

where x_j is a binary decision variable with $x_i = 1$ if item j is included in the knapsack, 0 otherwise. Without loss of generality, it may be assumed that all weights and profits are positive, all weights are smaller than C, and the overall weight of items exceeds C.

In early KPs literature, the exact algorithms are often adopted. For example, Mansi, Alves, Valério de Carvalho, and Hanafi (2012) propose an exact algorithm for solving the bi-level 0/1-KP. They use linear relaxation method to compute good feasible solutions. Additionally, they also describe a dynamic programming procedure which finds integer optimal solution. The proposed method successfully outperforms other state-of-the-art approaches. In the meantime, utilizing dynamic programming and partitioning the original discounted 0/1-KP into several easier sub-problems based on core concept of the original KP also lead to promising results (Rong, Figueira, & Klamroth, 2012).

More recently, heuristic algorithms are gaining popularities among KPs researchers. The main advantage of heuristic approaches is that approximate solutions can usually be found within reasonable time frame. The genetic algorithm (GA) has been one of the most widely employed candidate in this light. For instance, Khuri et al. (1994) propose GA for solving the 0/1 multiple KP with relatively large test problems. Shen, Xu, and Huang (2011) improve a dual population GA by introducing greedy

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approach and sub-group competition for tackling the 0/1-KP. Nonetheless, the tests are not extensive enough to conclude the efficacy of the proposed methodology. Meanwhile, the 0/1-KP has also been solved using a quantum GA with mutation operation, sine and cosine functions for encoding chromosomes, and adaptive adjustment of rotation angle (Wang, Guo, Xiang, & Mao, 2012b). The proposed method produces better quality solution owing to its ability in maintaining higher population diversity.

The other evolutionary algorithms adopted for solving the KPs include, but not limited to the ant colony optimization (He & Huang, 2011), cuckoo search algorithm (Feng, Jia, & He, 2014), amoeboid organism algorithm (Zhang et al., 2013), artificial fish swarm algorithm (AFSA) (Azad et al., 2014), and harmony search (Zou, Gao, Li, & Wu, 2011).

Unfortunately, the challenges of solving the problem within reasonable time frame increases proportional to its dimensionality (complexity). To make matter worse, solution quality also degrades accordingly. Given these considerations, a monogamous pairs genetic algorithm (MopGA) is proposed. The main aim of this paper is to uncover the use of *pair bond (monogamy)* and occasional infidelity inspired by social monogamy into genetic algorithm.

Unlike traditional GAs, parents in MopGA form an enduring partnership over a predefined number of generations. Bonded or monogamous parents continue to breed until their bond expires. Then, selection of new parents for the next cycle of pair bonding takes place. As a result, selection mechanisms are used sparingly. Offspring compete only with their siblings for survival into the next generation. At times, infidelity forces exchange of genetic materials across the entire population. Broadly, the two factors, namely pair bonding and infidelity control the depth of exploitation and exploration of the search space, respectively. Improvement in performance is achieved through:

1. Increasing exploitation of search space via pair bonding.
2. Preserving higher population diversity by shielding offspring under the monogamous parents from population-wide selection pressure and restrictive mating strategy.

Additionally, as a side benefit from economical use of selection mechanism, the MopGA is computationally more efficient, especially when dealing with high-dimensionality problems.

It is worth noting that even though an initial attempt was made using monogamous GA to solve numerical optimization problems by Lim and Khader (2013), the present work differs from its predecessor in many ways, especially on the architectural construction of the algorithm.

The rest of the paper is organized as follows: We begin by introducing the biological concepts of monogamy, which inspires the present work in Section 2. This is followed by the motivation for monogamous GA in Section 3. Thereafter, we present some previous works directly or indirectly related to monogamy in GA (Section 4). Section 5 is devoted to detailed description of MopGA. The ensuing section (Section 6) presents the experimental results and discussion in solving a large set of 0/1-KPs, including 14 low-dimensional problems (low-*D*, less than 40 items) and 11 high-dimensional problems (high-*D*, over 100 items). Finally, the paper concludes in Section 7 with promising avenues for future work.

2. Monogamy and inspiration

A social organization in which the female and male organisms breed exclusively with each other, albeit the presence of extrapair copulations or infidelity is refer to as *monogamy* (Hatchwell, Russell, Ross, & Fowlie, 2000; Young & Wang, 2004). Socially monogamous birds often display selective, though not exclusive affiliation, copulation, biparental care of offspring, and nest sharing (Schuiling, 2003).

Studies have shown that the duration of pair bonding and age are the two main determinants for reproductive success in long-term monogamous bird species (Griggio & Hoi, 2011). They find that longer pair bond period leads to more successful breeding attempts, hatching and fledging.

On the other hand, numerous hypotheses have been proposed for the existence of infidelity in monogamous society. Among the well-known ones are the good genes and future partnerships hypotheses (Ramsay, Otter, Mennill, Ratcliffe, & Boag, 2000). Broadly, the former suggests that traits that will increase survival or reproductive success of offspring are favoured and the latter looks for potential mates.

In the context of neurobiology, Resendez and Aragona (2013) suggest that monogamous pair bonds are formed and maintained by a balance between mu- and kappa-opioid receptors [1] activation. It has been shown that animal sees negative or harmful stimuli as aversion, whereas positive ones as reward under the influences of endogenous opioid transmission. Likewise, when bond is seen as rewarding, then an enduring relationship is formed (Resendez & Aragona, 2013).

Fascinated by natural monogamous mating system, this work draws inspiration from the fact that modern human society, some species of rodents (Young, Gobrogge, Liu, & Wang, 2011), lizards (Leu, Kappeler, & Bull, 2011), fish (Oldfield & Hofmann, 2011), and 90% of bird species are monogamic (Schuiling, 2003).

Biological interest in social monogamy has grown enormously in the recent years, but has yet been integrated with the evolutionary computation as a process of search and optimization. For instance, in conventional GAs, parents change partners at every generation. Taking the cue from nature, this paper proposes a monogamously structured GA.

3. Motivation for monogamous GA

In MopGA, pair bond is introduced to strengthen the exploitation of search space between pairs of parents during the evolutionary process. The effect of pair bond is expanded via repeated applications of crossover operations that spread across multiple generation steps. The reasons behind pair bonding in GA are:

1. In GAs, crossover is regarded as the main genetic operator (Goldberg, 1989; Holland, 1975).
2. Offspring inherit genetic materials from their parents through crossover. However in general, offspring do not always surpass the fitness values of their parents. The same parents pair may produce fitter or even weaker offspring from each crossover operation all by chance.
3. As suggested by De, Pal, and Ghosh (1998), a crossover acts as an exploitation operator. Similarly, our technique emphasizes on the thorough exploitation of the current search region via pair bonding before exploring new ones.
4. Finally, De Jong and Spears (1992) state that higher exploratory power can be achieved by applying crossover operation multiple times over several generations.

It is worth noting that the effect of mutation is ignored since in common GA practices, mutation rate, P_m is usually kept low, e.g. $P_m = 0.001$ (De Jong & Spears, 1992). Therefore, we only pay considerable attention to crossover as the main reproduction operator supported by pair bonding.

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[1] Opioid receptors are a group of G protein-coupled receptors with opioid as ligands. They are widely distributed in the brain, spinal cord and digestive tract.