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Sexual selection and evolution of male and female choice in genetic algorithm

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Variety and diversity of population are essential for convergence to global optimal in genetic algorithm. In this study, the concepts of fitness distribution, expected and cumulative fitness distribution, reproduction rate and loss of diversity are defined for a sexual selection mechanism, and their performance of this type of selection mechanism is studied theoretically. Then a genetic algorithm based on this selection mechanism and penalty function are utilized for solving multidimensional 0/1 knapsack problems. Computational experiments are conducted on the proposed technique compared with some commonly used selection mechanisms for solving multidimensional 0/1 knapsack problems from the literature.

Key words: Genetic algorithm, multidimensional knapsack problems, penalty function, sexual selection.

INTRODUCTION

In the biological evolution that Darwin (1888) introduced, natural selection is a process consisting of three ingredient principle: variation, heredity and chromosome selection. There is an unsettled question in evolutionary biology (Judson and Normak, 1996), "What selective forces maintain sexual reproduction and genetic recombination in nature"? (Smith, 1987).

In many kinds of natural selection, males are chosen by females in order to mate and create offspring, thus males have to contest with each other in order to be selected as mates. Female choice for male is an extensively approved method by which females take advantage of their reproductive success in offspring quality.

The first research to provide a possible solution to the problem of selection for maladaptive behaviors is introduced by Fisher (1958). He proposed that if a gene for a convinced trait becomes genetically connect to the preference for it, then the trait will become more common to match the female's preference for it, giving a reason to maladaptive behaviors becoming common in males. Kirkpatrick (1982) developed an analytic model of sexual selection. In the sexual selection that Kirkpatrick

considered, the male of the species donate only gametes to the next generation, hence the trait and preference loci are not sex-linked and dwell on different chromosomes and the genetic system is single. There is a strong confirmation that the specialization of chromosomes is principally by gender bunch (Kimura, 2000).

The division of the population into multiple preference categories is another attractive result. The female's preference for different traits could split the males so that each group would 'specialize' in meeting the preference for one trait at the expense of meeting preferences for another (Todd and Miller, 1991).

Genetic algorithm (GA) is a search optimization technique that mimics some of the processes of natural selection and evolution (Holland, 1975). Since GA is extracted from natural evolution, then gender is one of the most crucial elements in the GAs.

Gender of GA can be categorized into two well known components; the standard GA (Goldberg, 1989; Holland, 1975) and the theory of sexual selection (Allenson, 1992; Freeman and Herron, 2001; Lis and Eiben, 1997; Rejeb and AbuElhaja, 2000; Stearns and Hoekstra, 2001; Vrajitoru, 2002). These simulations consist of adding an extra attribute of gender to the chromosome, and a constraint avert for crossover between the same sex chromosomes are considered.

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Jalali and Lee (2012a) introduced a new sexual selection. In their technique, the population is divided into two groups of males and females.

Raghuwanshi and Kakde (2006) studied a GA with species and sexual selection beads using the real coding. Their approach views every female chromosome as niche in population and formation lays its foundations on the Euclidean distance between the male and female chromosomes.

Sanchez-Velazco and Bullinaria (2003) presented a gendered GA simulation model inspired by sexual selection and gender separation in which crossover only occurs between opposite-sex chromosome and the evaluation, selection, and mutation strategies of the GA are functions of gender, and thus a scheme of intra-gender competition and cross-gender cooperation evolved. During the sexual selection, the female chromosome is selected by the tournament selection while the male chromosome is selected based on the hamming distance from the selected female chromosome, fitness value or active genes. In another study conducted by Jalali and Lee (2012b) a fuzzy genetic algorithm based on this technique for selection mechanism was suggested. They used some nonlinear numerical functions and by considering the results from each test function, they showed that the proposed technique of grouping the male and female chromosomes alternately outperforms other grouping techniques of sexual selection mechanisms.

In this study, the sexual selection mechanism which was presented by Jalali and Lee (2012a) is considered and theoretically the concepts of fitness distribution, expected and cumulative fitness distribution, reproduction rate and loss of diversity are surveyed for this selection mechanism. Then a GA based on this selection mechanism and penalty function are utilized for solving multidimensional 0/1 knapsack problems.

The rest of the paper is organized as follows. Subsequently, a theoretical analysis of the sexual selection in GA is given. A GA based on sexual selection and penalty function for solving multidimensional knapsack problem (MKP) is then proposed. Thereafter, the results of computations of the benchmark deflates from the literature are presented. Finally, a brief conclusion is given.

SEXUAL SELECTION

In a classical GA, chromosomes reproduce asexually: any two chromosomes may be parents in crossover. Gender division and sexual selection here inspire a model of gendered GA in which crossover takes place only between chromosomes of opposite sex.

Let $P = \{C_1, C_2, \dots, C_N\}$ is the population at generation T ; the function $f_i: C_i \rightarrow R$ is called fitness value for chromosome C_i . One of the most important parameters

of quality of chromosome measured is fitness value.

Hamming distance: If $C_i = \{c_{i1}, c_{i2}, \dots, c_{im}\}$ and $C_j = \{c_{j1}, c_{j2}, \dots, c_{jm}\}$ are two chromosomes of population P , the hamming distance between C_i and C_j is:

$$HD(C_i, C_j) = \sum_{k=1}^m d(c_{ik}, c_{jk}) \tag{1}$$

where $d(c_{ik}, c_{kj}) = 0$ if $c_{ik} = c_{jk}$ and $d(c_{ik}, c_{kj}) = 1$ otherwise.

Active gene: The active gene that is denoted by $Act(C_i)$ is number of none zero genes in chromosome C_i (Jalali and Lee, 2012a). For example, let $C_i = (1,0,0,1,0,1,0,1,0,0,0,1,0,0)$ is a chromosome, then $Act(C_i) = 6$.

Tournament selection size t is a technique for selecting chromosomes in GA which works as follows: at first, t chromosomes are selected randomly from the population and then the best chromosome from this group is copied into the intermediate population.

Inspired by the non-genetic sex-determination system existed in some species of reptiles, including alligators and some turtles where sex is determined by the temperature at which the egg is incubated, the population is divided into two groups, male (50% of the population) and female (50% of the population), so that the male and female can be selected in an alternate way. In each generation, the layout of selection of male and female are different. In this research, a relation between the fitness value, hamming distance and active gene as in biological systems affecting the selection procedure is proposed.

During the sexual selection, the female chromosome is selected by tournament selection size t from female category. This chromosome is called female-sex. The male chromosome is selected as follows: choose some number t of chromosomes randomly from the male category and then the hamming distance between these chromosomes and female-sex chromosome are calculated. The chromosome with maximum hamming distance is selected for crossover with female-sex. This chromosome is called male-sex. When hamming distances are calculated, maybe some chromosomes have the same hamming distance and this number is the maximum hamming distance. In this condition, the fitness value of these chromosomes is considered and the best chromosome is selected. If the best fitness value belongs to more than one chromosome, a third parameter 'active gene' is considered and the chromosome with the highest

active gene is considered for male-sex. Otherwise one of them is selected randomly for male-sex (Jalali and Lee, 2012a).

The rest of this chapter is analyses of fitness distribution, reproduction rate and loss of diversity for this sexual selection. In this study, we use some definitions and theorems that were considered by Blickle and Thiele (1995) for the survey of performance sexual selection mechanism in GA.

Fitness distribution: The function $s: R \rightarrow Z_0^+$ allots to each fitness value $f \in R$ the number of chromosomes in a population P bearing this fitness value. s is called the fitness distribution of a population P (Blickle and Thiele, 1995).

Expected fitness distribution: s^* denotes the expected fitness distribution after applying the selection method to the fitness distribution s (Blickle and Thiele, 1995).

Cumulative fitness distribution: let n be the number of unique fitness value and $f_1 < f_2 < \dots < f_n$ ($n \leq N$) the ordering of the fitness values. $S(f_i)$ denotes the number of chromosomes with fitness value f_i or worse and is called cumulative fitness distribution (Blickle and Thiele, 1995).

$$S(f_i) = \begin{cases} 0 & i < 1 \\ \sum_{j=1}^{j=i} s(f_j) & 1 \leq i \leq n \\ N & i > n \end{cases} \quad (2)$$

Reproduction rate: The reproduction rate $R(f)$ denotes the ratio of the number of chromosomes with a certain fitness value f after and before selection.

$$R(f) = \begin{cases} \frac{s^*(f)}{s(f)} & s(f) > 0 \\ 0 & s(f) = 0 \end{cases} \quad (3)$$

where s^* denotes the expected fitness distribution after applying the selection method to fitness distribution s (Blickle and Thiele, 1995).

Loss of diversity: The loss of diversity L_d is the ratio of chromosomes of a population that is not selected during the selection phase.

Theorem 1: If the reproduction rate $R(f)$ increases

monotonously in f , the loss of diversity of a selection method is:

$$L_d = \frac{1}{N} (S(f_z) - S^*(f_z)) \quad (4)$$

where f_z denotes the fitness value such that $R(f_z) = 1$ (Blickle and Thiele, 1995).

Theorem 2: The expected fitness distribution after performing sexual selection on the distribution s is:

$$s^*(f_i) = \begin{cases} 2^t N \left(\left(\frac{s(f_i)}{N} \right)^t - \left(\frac{s(f_{i-1})}{N} \right)^t \right) & 1 \leq i \leq \frac{N}{2} \\ 2^t N \left(\left(\frac{s(F_i)}{N} \right)^t - \left(\frac{s(F_{i-1})}{N} \right)^t \right) & \frac{N}{2} < i \leq N \end{cases} \quad (5)$$

where F_i is analogue fitness value of male chromosome C_i with the best hamming distance from female-sex.

Proof: If $1 \leq i \leq N/2$ tournament selection is used for female chromosomes. Suppose $S^*(f_i)$ is number of chromosomes with fitness f_i or worse after applying selection method. The probability for selecting a chromosome with fitness value or worse is $2 \left(\frac{S(f_i)}{N} \right)$ and since tournament is repeated for $N/2$ then $S^*(f_i) = 2^t N \left(\frac{S(f_i)}{N} \right)^t$. By definition cumulative fitness distribution $S(f_i) = s(f_i) - s(f_{i-1})$ then for expected fitness value is:

$$s^*(f_i) = S^*(f_i) - S^*(f_{i-1}) = 2^t N \left(\frac{S(f_i)}{N} \right)^t - 2^t N \left(\frac{S(f_{i-1})}{N} \right)^t \quad (6)$$

Let $N/2 < i \leq N$, if F_i is considered like fitness value for chromosomes in tournament we obtain:

$$s^*(f_i) = 2^t N \left(\frac{S(HD_i)}{N} \right)^t - 2^t N \left(\frac{S(HD_{i-1})}{N} \right)^t \quad (7)$$

Theorem 3: The reproduction rate of sexual selection is:

$$R(f_i) = \begin{cases} \frac{2^t}{N^{t-1}} (S(f_i)^{t-1} + S(f_i)^{t-2} S(f_{i-1}) + \dots + S(f_{i-1})^{t-1}) & S(f_i) > 0 \\ 0 & S(f_i) = 0 \end{cases} \quad (8)$$

Proof: This is obtained by reproduction rate and Equation (6):

$$R(f_i) = \frac{s^*(f_i)}{s(f_i)} = \frac{s^*(f_i) - s^*(f_{i-1})}{S(f_i) - S(f_{i-1})} = \frac{2^t N \left(\frac{S(f_i)}{N}\right)^t - 2^t N \left(\frac{S(f_{i-1})}{N}\right)^t}{S(f_i) - S(f_{i-1})}$$

$$= \frac{2^t \left(\frac{S(f_i)^t - S(f_{i-1})^t}{S(f_i) - S(f_{i-1})}\right)}{N^{t-1}} = \frac{2^t}{N^{t-1}} (S(f_i)^{t-1} + S(f_i)^{t-2} S(f_{i-1}) + \dots + S(f_{i-1})^{t-1})$$

Theorem 4: The loss of diversity of sexual selection is:

$$L_d = \begin{cases} 2^t \left(\frac{S(f_z)}{2^{t-1} N}\right) - \left(\frac{S(f_z)}{N}\right)^t & 1 \leq i \leq \frac{N}{2} \\ 2^t \left(\frac{S(F_z)}{2^{t-1} N}\right) - \left(\frac{S(F_z)}{N}\right)^t & \frac{N}{2} \leq i \leq N \end{cases} \quad (9)$$

where f_z denotes the fitness value such that $R(f_z) = 1$ and F_z is analogue fitness value of male chromosome C_i with the best hamming distance from female_sex such that $R(F_z) = 1$.

Proof: Suppose $1 \leq i \leq N/2$

$$L_d = \frac{2}{N} (S(f_z) - S^*(f_z)) = 2 \left(\frac{S(f_z)}{N} - \frac{S^*(f_z)}{N} \right) = 2 \left(\frac{S(f_z)}{N} - \frac{2^t N \left(\frac{S(f_z)}{N}\right)^t}{N} \right)$$

$$= 2^t \left(\frac{S(f_z)}{2^{t-1} N} - \left(\frac{S(f_z)}{N}\right)^t \right)$$

For $N/2 < i \leq N$, the proof follows the same pattern.

GENETIC ALGORITHM FOR MULTIDIMENSIONAL KNAPSACK PROBLEM

The Multidimensional Knapsack Problem (MKP) is a general statement of any 0-1 integer problem with nonnegative coefficients. It is formulated as follows:

$$\text{Maximize } f(x_1, x_2, \dots, x_n) = \sum_{j=1}^n p_j x_j \quad (10)$$

$$\text{Subject to } \sum_{j=1}^n w_{ij} x_j \leq c_i \quad i = 1, \dots, m$$

$$x_j \in \{0,1\} \quad j = 1, \dots, n$$

with $p_j > 0, w_{ij} \geq 0, c_i \geq 0$

Where n is the number of objects and m is the number of knapsacks, w_{ij} is the consumption of resource i for object j , c_i is the capacity of i th knapsack, p_j is the profit associated with object j , and x_j is the decision variable with object j (Djannaty and Doostar, 2008).

Genetic algorithms maintain a population of solution and use selective breeding and recombination strategies to generate better and better solution. As applied to the MKP, most GAs are based on the some heuristic approaches. These approaches are used to generate an initial population of solution, and then genetic operators such as crossover and mutation are applied to construct new, hopefully improved, solutions.

Chu and Beasley (1998) presented a GA approach which to date seems to be one of the best heuristics yet found for the MKP. In their technique, an n-bit binary string was used as the representation of solutions to the MKP and a repair operator was used to transform infeasible solutions to feasible solutions.

The performance of this approach was not as good as that of Chu and Beasley (1998). For controlling infeasible solution, Khuri et al. (1994) utilized a fitness function that uses a graded penalty term to penalize infeasible chromosomes. Their implementation allowed infeasibly bred strings to participate in the search since they do contribute information. Some researchers showed GAs are suitable for solving large knapsack problems (Chu, 1997; Chu and Beasley, 1997; Hinterding, 1994; Khuri et al., 1994; Olsen, 1994; Rudolph and Sprave, 1996; Thiel and Voss, 1994).

Hoff et al. (1996) showed how a proper selection of parameters and search mechanisms lead to an implementation of GA that yields high quality solutions for MKP. Simões and Costa (2001) presented an empirical study that compares the performances of the transposition based GA and the classical GA solving the 0/1 knapsack problem and they claimed transposition is always superior to crossover.

Djannaty and Doostar (2008) considered a hybrid of GA and Dantzig algorithm based on a strong initial population was created to solve single knapsack problems. They used some penalty functions for control infeasibility solution. An improved GA for the MKP is introduced by Raidl (1998). In this method, a bit string based GA for the MKP has been improved by introducing a pre-optimized initial population, a repair, and a local improvement operator. Neoh et al. (2010) presented a layered encoding structure and they used a hybrid GA and partial swarm optimization for 0/1 knapsack problems. Genetic algorithm must be modified to solve

problems. Our modified GA for the MKP is as follows.

Encoding and fitness function

Binary encoding is used and the values of all variables x_j are sorted in a bit string of length n , that means $x_j \in \{0,1\}^n$. However, this representation is direct and easy but a string might represent an infeasible solution and this infeasible solution needs to be considered. One way to do this is by discarding infeasible strings and ignoring infeasible regions of the search space. Another technique is the employment of penalty functions combined into the objective function (Goldberg, 1989; Michalewicz, 1992; Richardson et al., 1989).

Since penalty function and its coefficients is effective on premature convergence and infeasible final solution, then selection of penalty function is not easy. Some penalty functions which has been used in GA for uni-dimensional knapsack problem was compared by Olsen (1994). Khuri et al. (1994) utilized a simple fitness function that used a penalty function to penalize infeasibly bred strings for some standard test problems.

Rudolph and Sprave (1996) presented a GA for MKP such that neighboring method was utilized for parent selection and infeasible solutions were penalized as that of Khuri et al. (1994). Thiel and Voss (1994) used a hybrid of GA and Tabu Search with local search operators for controlling infeasible solutions.

In this research, the following fitness function is used:

$$\text{Maximize } f(x_1, x_2, \dots, x_n) = \sum_{j=1}^n p_j x_j - s \cdot \max\{p_j\} \quad (11)$$

where $s = |\{j \mid \sum_{j=1}^n w_{ij} x_j > C_i\}|$ (Khuri et al., 1994).

Selection

Selection is an important parameter in GA, which directs the GA to the solution by preferring chromosomes with high fitness over low-fitted ones. In other word, selection is the result of competition process between chromosomes to determine which chromosomes are used to form new ones. Selection is obtained by preferring fitter chromosomes to make sure that good properties are carried forward to the next generation.

Various selection schemes are utilized in GA namely: roulette-wheel, tournament selection, stochastic universal sampling, sigma scaling, Boltzmann selection, ranking selection, steady state selection, elitism selection, local selection, group selection, subset selection, action selection, truncation selection, multilevel selection,

directional selection, stabilizing selection, disruptive selection, clonal selection and sexual selection.

In this paper, sexual selection (SXS) which is considered and this method is compared with Roulette-wheel (RW), tournament selection (TS), Stochastic universal sampling (SUS), linear ranking selection (LR), Truncation selection (TRS)

Crossover

Chu and Beasley (1996, 1997) showed overall performance of GAs that are selected for MKP is frequently proportionately insensitive to the special select of crossover operator. In this study, the uniform crossover operator is considered as the default crossover operator.

Uniform crossover operator by exchanging genes between two chromosomes based on a set of positions defined by a mask in which both the number of positions to be exchanged and the positions themselves are randomly determined (Chou et al., 2001). Syswerda (1989) compared uniform crossover to traditional one-point and two-point crossover by several means including comparing the performance of each crossover method on several optimization problems.

Chou et al. (2001) claimed uniform crossover, used with p_c (probability of crossover) of 1.0 to be the best performing crossover method in terms of solution quality. Dengiz et al. (1997) used a specialized form of uniform crossover with repair to make sure each offspring was feasible according to their implementation. Eshelman and Schaffer (1991) noted that uniform crossover was much less likely than one-point or two-point crossover to produce the same offspring from the same parent.

Mutation

Mutation is one of the important parameters in GA. Usually, mutation is used after a crossover in GA. If chromosomes in the GA are the same in the generation, after crossover the offspring will be the same parent and GA will be converge to local optimum. The mutation operator is used for keeping diversity in the population of chromosomes and avoiding premature convergence. There are some methods for mutation, however in this study binary encoding was used. A binary mutation procedure is performed to mutate some randomly selected bits in the chromosome, that is, it causes these chosen bits to change from 0 to 1 or vice versa.

COMPUTATIONAL EXPERIMENT

Experiment design

The experimental runs reported here are performed by using a

Table 1. Comparison error and time (second) for selection methods with $n = 100$ variables, $m = 5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$.

m	n	Ratio	Benchmark	E./T.	SXT	RW	TS	LR	SUS	TRS
5	100	0.25	24197.20	Error	1.27	2.68	1.42	2.48	2.11	2.41
				Time	8.31	6.21	7.25	11.17	12.10	10.17
		0.50	43252.90	Error	1.13	2.40	1.38	2.31	2.10	2.30
				Time	8.05	6.05	7.12	10.98	11.13	10.01
		0.75	60471.00	Error	1.48	2.33	1.25	1.98	1.90	2.11
				Time	7.83	5.98	6.95	10.31	11.01	9.87
10	100	0.25	22601.90	Error	1.15	2.77	1.53	2.33	2.25	2.69
				Time	9.12	7.31	8.17	12.14	12.48	11.35
		0.50	45659.10	Error	1.53	2.18	1.47	2.12	2.08	2.53
				Time	8.35	6.85	7.11	11.21	12.32	10.72
		0.75	59555.60	Error	1.39	2.10	1.36	2.08	1.98	2.27
				Time	8.21	6.45	7.05	11.19	11.31	10.41
30	100	0.25	21654.60	Error	1.52	2.88	1.89	2.74	2.44	2.93
				Time	16.51	14.36	15.53	18.96	18.04	18.19
		0.50	41431.30	Error	1.47	2.78	1.63	2.65	2.37	2.62
				Time	15.93	13.73	14.81	18.03	18.16	17.81
		0.75	59199.10	Error	1.35	2.22	1.45	2.15	2.03	2.44
				Time	15.61	13.40	15.42	17.52	17.65	17.80

genetic algorithm with a population size of 50, a mutation rate $p_m = 1/L$ where L is length of chromosomes, crossover rate $p_c = 0.50$. Sexual selection (SXS) is considered as the default selection operator. This method is compared with Roulette-wheel (RW), tournament selection (TS), stochastic universal sampling (SUS), linear ranking selection (LR) and truncation selection (TRS). Uniform crossover is considered as the default crossover operator.

A benchmark data set of 270 multidimensional knapsack problems (MKPs) was proposed in Chu and Beasley (1990, 1996, 1998) and was widely used in the literature for the testing of MKP algorithms. These problems are available in OR-Library (Beasley, 1990, 1996; <http://mscmga.ms.ic.ac.uk/info.html>). The problems are generated with $n = 100, 250, 500$ variables, $m = 5, 10, 30$, constraints, and tightness ratios $\alpha = 0.25, 0.50, 0.75$. This set of problems contains 27 different problem sets, each having 10 randomly generated instances, thus a total of 270 problems. Each test problem is tested on the GA for 30 times with a maximum of 10^4 generations per each run. All algorithms are coded in C++ and run on a Pentium IV with 2.00 GHz CPU and 2.00 GB of RAM.

COMPUTATIONAL RESULTS

The benchmark data set tested in this research inclusive of 270 problem instances on multidimensional knapsack problems proposed by Chu and Beasley (1998). These problem instances have been extensively utilized in the literature for the testing of MKP algorithms. These problems include $n = 100, 250, 500$ variables and $m = 5, 10, 30$ constraints and for each category variables three

tightness ratios are considered as $\alpha = 0.25, 0.50, 0.75$. These set of problems contains 27 different problem sets, each having 10 randomly generated instances, thus a total of 270 problems.

In these problem set, w_{ij} was drawn from discrete uniform generator $U(0, 1000)$ and the right hand side coefficients $c_i, i \in \{1, \dots, m\}$, were set using

$c_i = \alpha \sum_{j=1}^m w_{ij}$ where α is the tightness ratio, and $\alpha = 0.25$ for the first ten problems, $\alpha = 0.5$ for the next ten problems, and $\alpha = 0.75$ for the last ten problems. The objective function coefficients $p_j, j \in \{1, \dots, n\}$ were correlated to w_{ij} and are generated

as $p_j = \alpha \sum_{i=1}^m \frac{w_{ij}}{m} + 500e_j$ where $e_j, j \in \{1, \dots, n\}$ is a real number drawn from the continuous uniform generator $U(0, 1)$ (Chu and Beasley, 1998).

Table 1 reports the comparison results for selection methods on the MKPs with $n = 100$ variables, $m = 5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$ when the algorithm terminates at 10^4 generations.

Benchmark column represent the average results for each category of MKPs that were reported (Beasley, 1990, 1996). Error is calculated as $Error = |B - Re|$

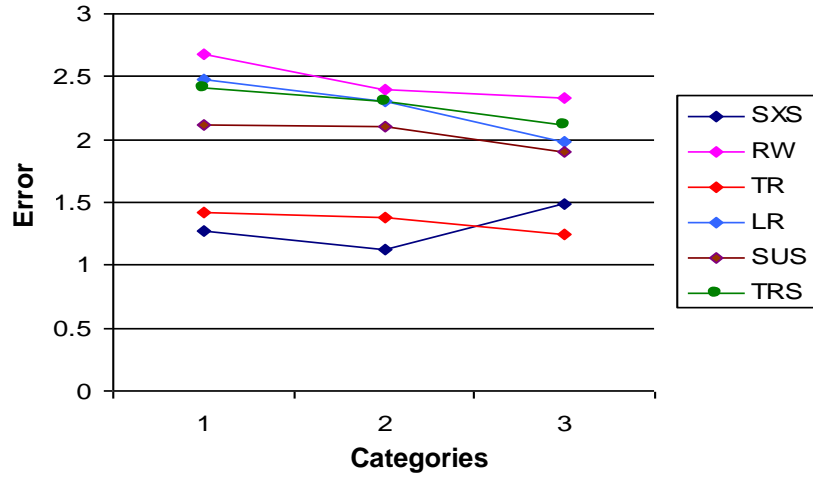


Figure 1. Error comparison for m=5 and n=100.

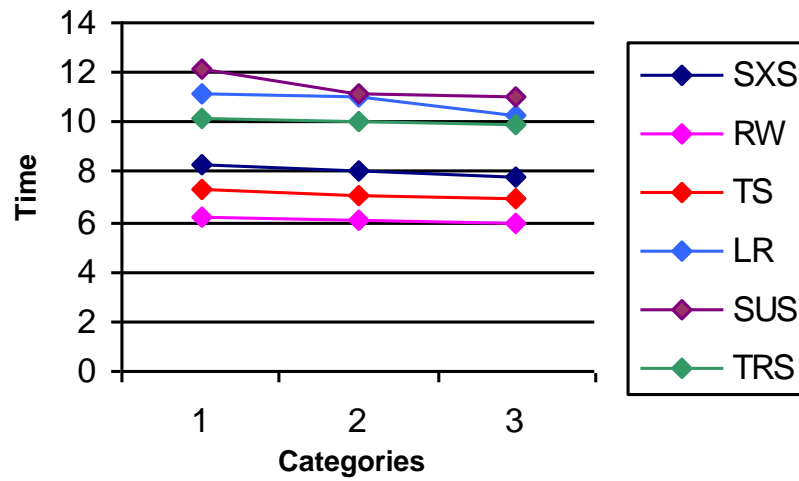


Figure 2. Time comparison for m=5 and n=100.

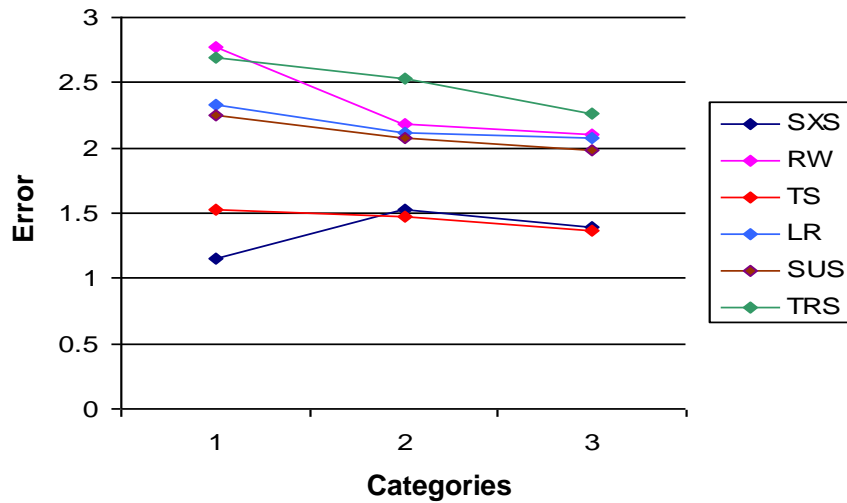


Figure 3. Error comparison for m=10 and n=100.

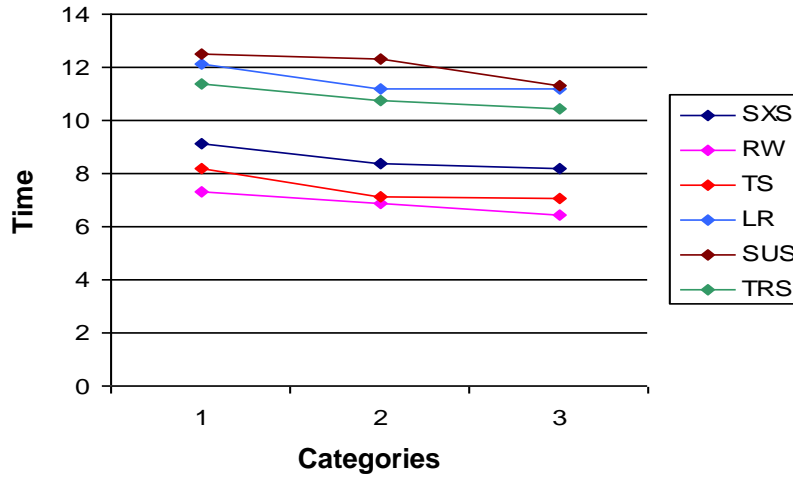


Figure 4. Time comparison for $m=10$ and $n=100$.

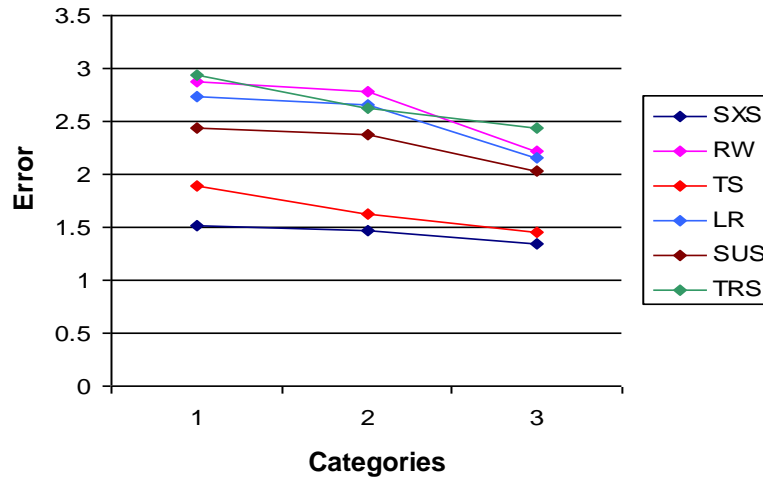


Figure 5. Error comparison for $m=30$ and $n=100$.

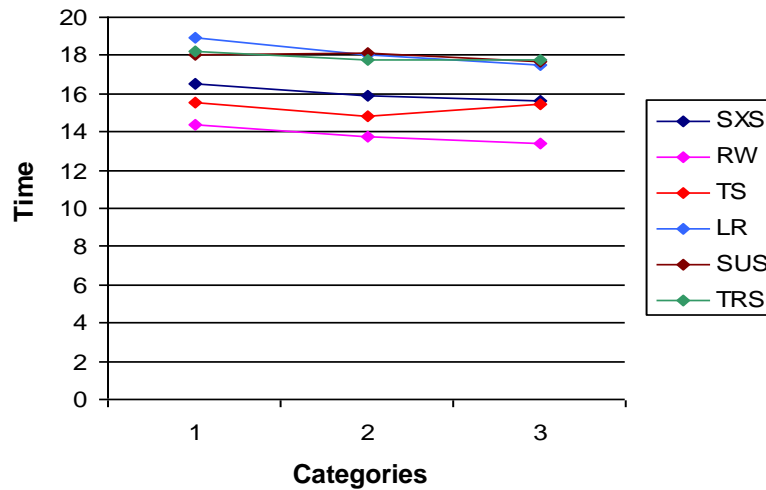


Figure 6. Time comparison for $m=30$ and $n=100$.

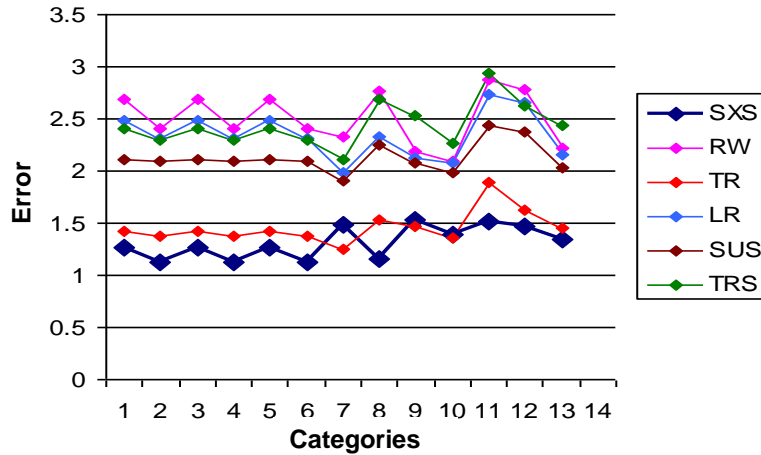


Figure 7. Error comparison for $m=5, 10, 30$ and $n=100$.

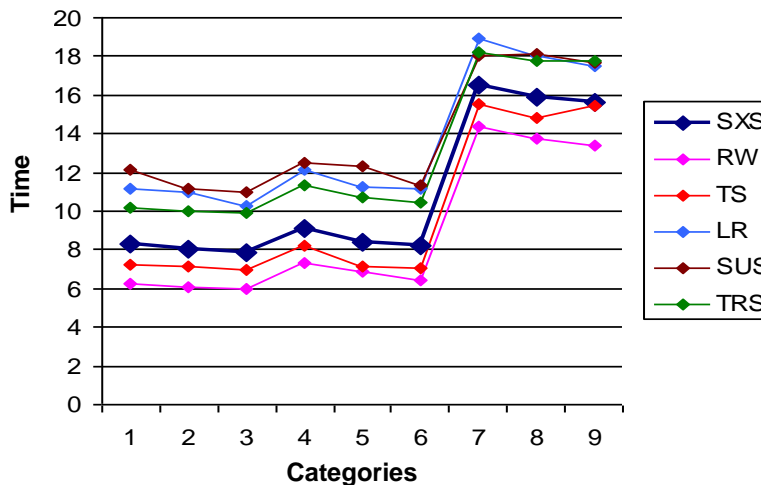


Figure 8. Time comparison for $m=5, 10, 30$ and $n=100$.

where B is average of benchmark results and Re is average of results that was obtained by algorithms for the same category. The row time represent the total time (second) used at 10^4 generation.

The horizontal axis in Figures 1 to 6 represent the error and time (second) for MKPs, respectively so that $m=5, 10, 30$ and $n=100$. The comparison results for selection methods on the MKPs with $n=100$ variables, $m=5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$ are represented together in Figures 7 and 8.

Table 2 reports the comparison results for selection methods on the MKPs with $n=250$ variables, $m=5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$ when the algorithm terminates at 10^4 generations. The horizontal axis in Figure 9 until 14 represent the error and time for MKPs respectively so that $m=5, 10, 30$ and

$n=250$.

Summary of comparison results for selection methods on the MKPs with $n=250$ variables, $m=5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$ are represented together in Figures 15 and 16.

Table 3 reports the comparison results for selection methods on the MKPs with $n=500$ variables, $m=5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$ when the algorithm terminates at 10^4 generations. The horizontal axis in Figures 17 to 22 represent the error and time for MKPs, respectively so that $m=5, 10, 30$ and $n=250$.

Summary of comparison results for selection methods on the MKPs with $n=500$ variables, $m=5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$ are represented together in Figures 23 and 24. As can be

Table 2. Comparison error and time (second) for selection methods with $n = 250$ variables, $m = 5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$.

m	n	Ratio	Benchmark	E./T.	SXT	RW	TS	LR	SUS	TRS
5	250	0.25	60409.70	Error	5.02	7.41	6.17	7.21	6.90	7.95
				Time	14.90	12.70	13.82	17.01	17.15	16.81
		0.50	109284.60	Error	4.83	6.27	5.65	6.42	6.03	7.12
				Time	13.62	11.43	12.53	16.22	16.35	15.56
		0.75	151555.90	Error	4.31	5.60	5.23	5.15	5.12	6.48
				Time	12.23	10.68	11.72	15.23	15.37	14.91
10	250	0.25	58993.90	Error	6.21	8.93	7.41	8.50	7.97	8.12
				Time	18.43	16.56	17.45	21.19	21.30	20.62
		0.50	108706.40	Error	5.97	7.45	7.02	7.15	6.63	7.90
				Time	17.52	15.27	16.31	19.63	19.72	19.31
		0.75	151330.40	Error	5.31	7.17	6.50	6.83	5.97	6.53
				Time	16.21	14.96	15.10	19.21	19.42	18.81
30	250	0.25	56875.90	Error	8.11	10.35	9.31	9.89	9.15	10.82
				Time	35.83	33.82	34.90	38.17	38.30	37.91
		0.50	106673.70	Error	7.60	9.30	8.54	8.93	8.20	10.15
				Time	34.17	32.01	33.12	37.32	37.50	36.21
		0.75	150443.50	Error	6.12	8.51	7.29	7.77	7.41	9.11
				Time	31.59	29.87	30.91	35.11	35.18	32.53

Table 3. Comparison error and time (second) for selection methods with $n = 500$ variables, $m = 5, 10, 30$, constraints and tightness ratios $\alpha = 0.25, 0.50, 0.75$.

m	n	Ratio	Benchmark	E./T.	SXT	RW	TS	LR	SUS	TRS
5	500	0.25	120615.50	Error	6.30	8.41	7.63	8.05	7.95	9.61
				Time	26.27	24.17	25.12	29.23	30.05	28.21
		0.50	219503.10	Error	5.79	7.96	6.90	7.53	7.05	8.75
				Time	24.61	22.12	23.52	27.18	27.41	26.31
		0.75	302354.90	Error	5.41	7.08	6.58	6.81	6.25	9.23
				Time	22.40	20.43	21.37	25.91	26.05	24.19
10	500	0.25	118565.50	Error	7.95	10.12	9.67	9.85	9.41	10.71
				Time	35.32	32.17	33.41	37.12	37.31	36.17
		0.50	217274.60	Error	7.03	9.21	8.95	8.95	8.16	9.65
				Time	32.81	29.89	31.78	34.18	34.29	33.90
		0.75	302556.00	Error	6.45	8.35	8.04	7.96	7.60	8.50
				Time	30.21	28.01	29.15	32.67	33.01	32.15
30	500	0.25	115473.50	Error	10.31	12.45	12.60	11.41	11.05	12.15
				Time	67.35	65.14	66.21	70.14	70.31	69.51
		0.50	216156.90	Error	9.95	12.23	11.72	10.96	10.17	11.41
				Time	63.75	61.56	62.63	66.73	66.82	65.72
		0.75	302353.40	Error	8.20	11.01	10.56	10.05	9.45	11.23
				Time	61.24	59.13	60.17	65.04	65.28	63.24

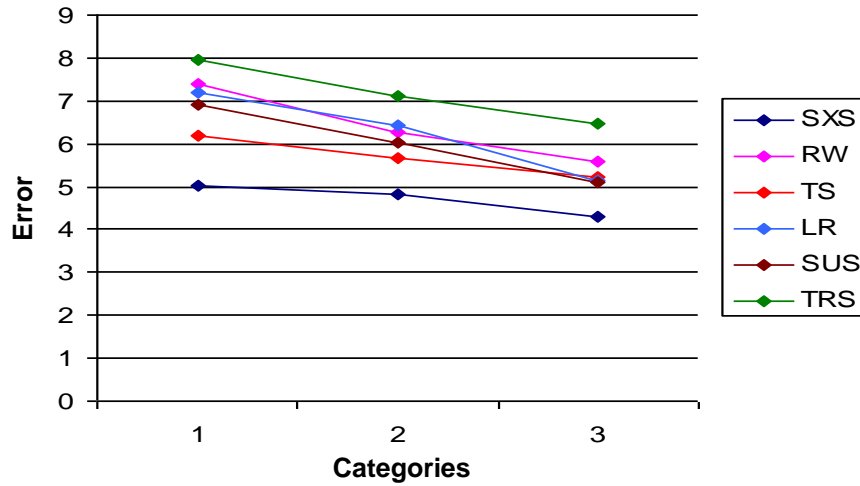


Figure 9. Error comparison for m=5 and n=250.

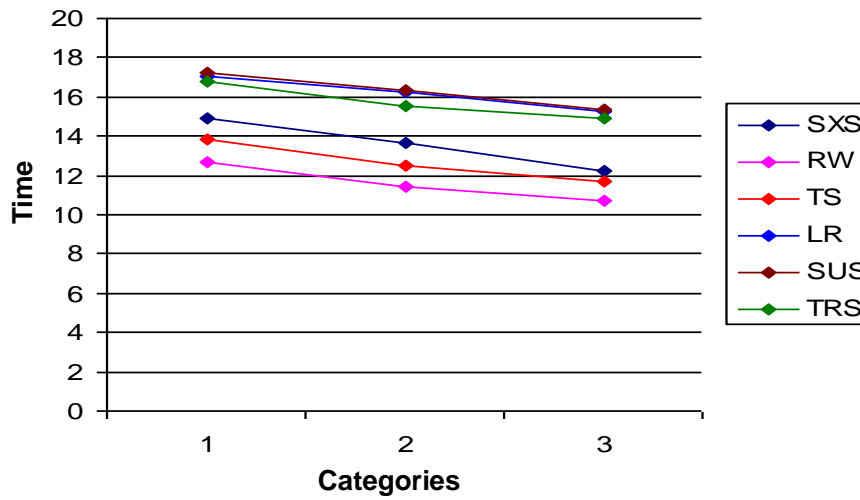


Figure 10. Time comparison for m=5 and n=250.

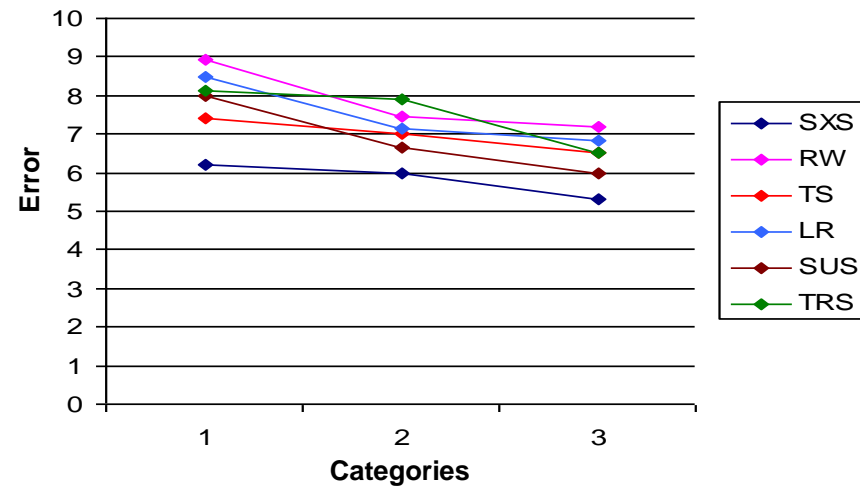


Figure 11. Error comparison for m=10 and n=250.

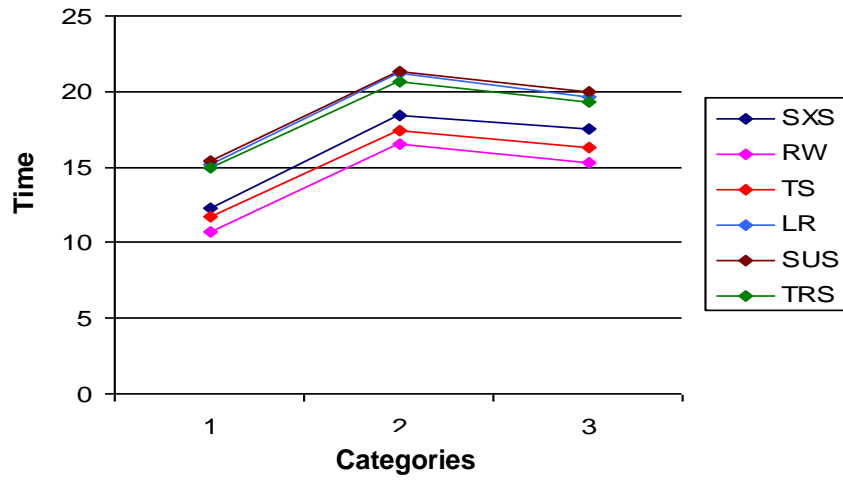


Figure 12. Time comparison for $m=10$ and $n=250$.

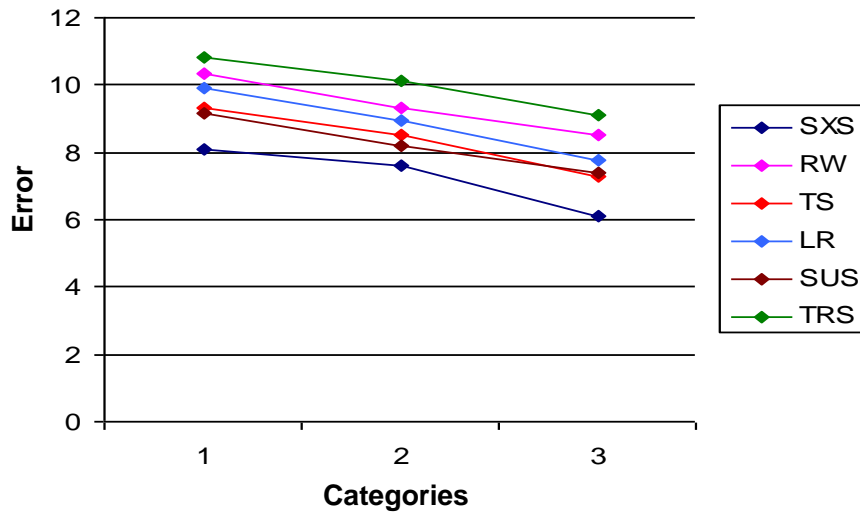


Figure 13. Error comparison for $m=30$ and $n=250$.

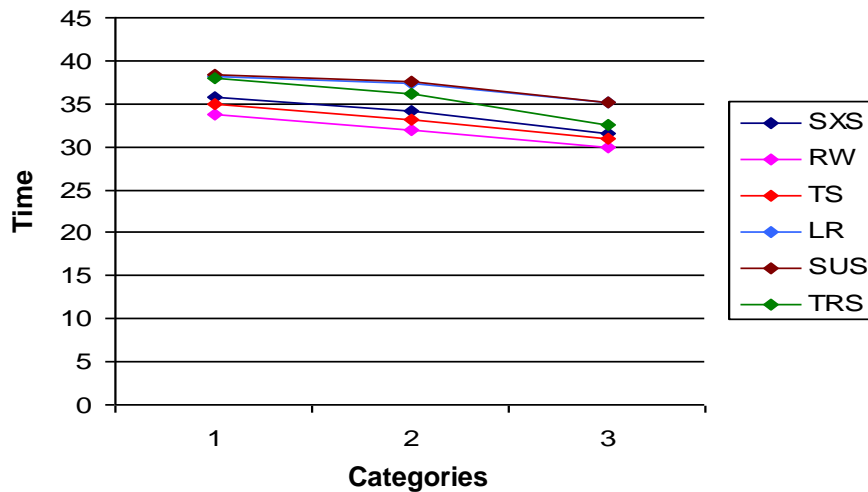


Figure 14. Time comparison for $m=30$ and $n=250$.

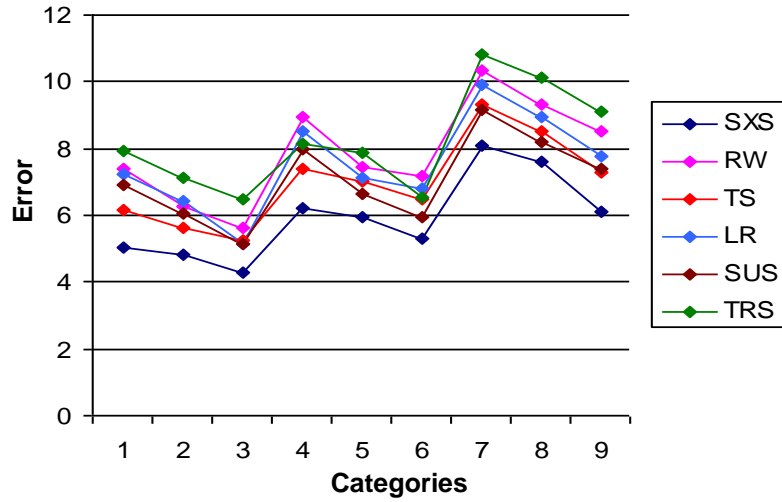


Figure 15. Error comparison for $m=5, 10, 30$ and $n=250$.

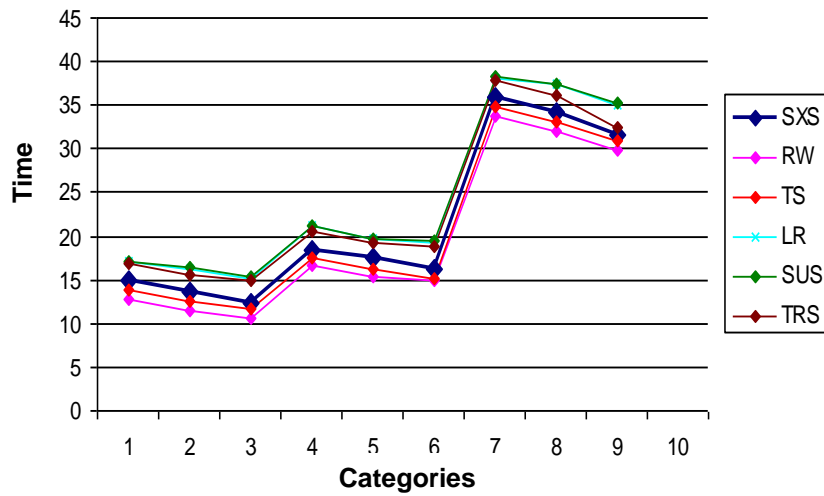


Figure 16. Time comparison for $m=5, 10, 30$ and $n=250$.

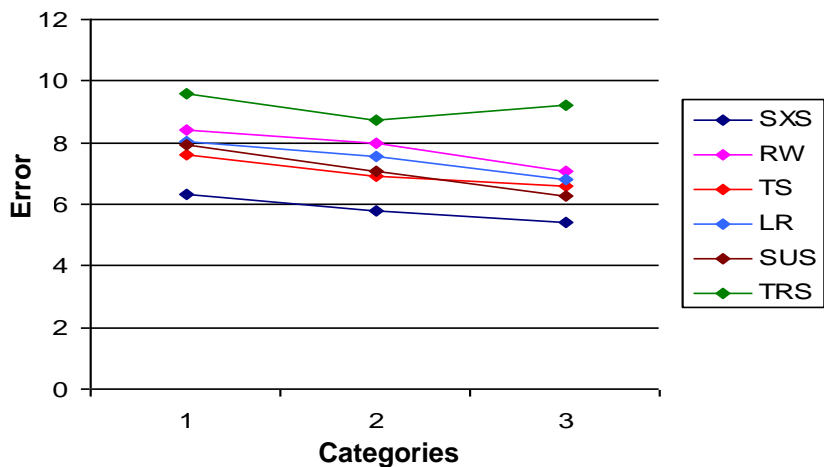


Figure 17. Error comparison for $m=5$ and $n=500$.

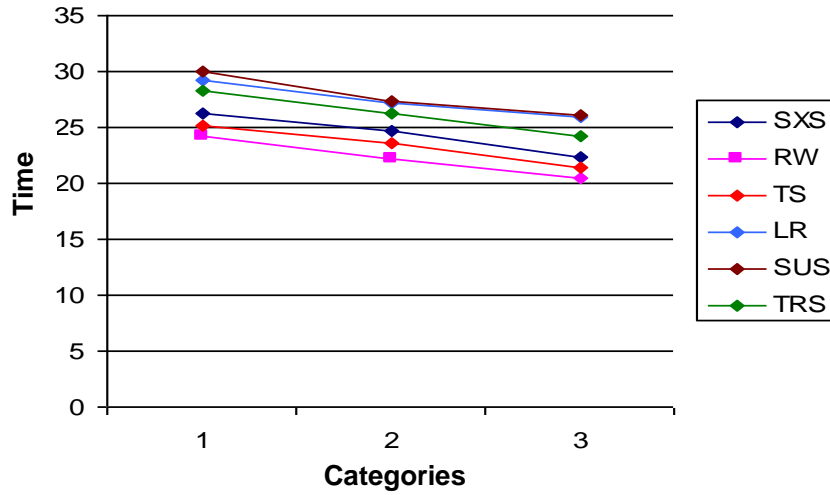


Figure 18. Time comparison for $m=5$ and $n=500$.

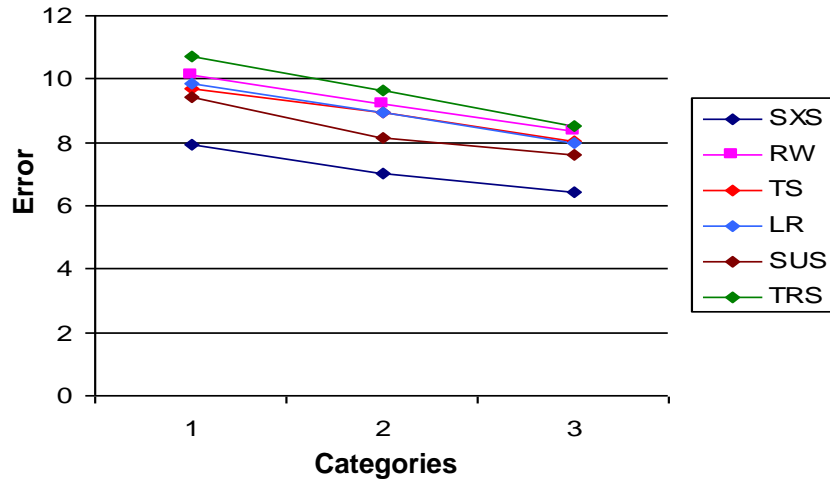


Figure 19. Error comparison for $m=10$ and $n=500$.

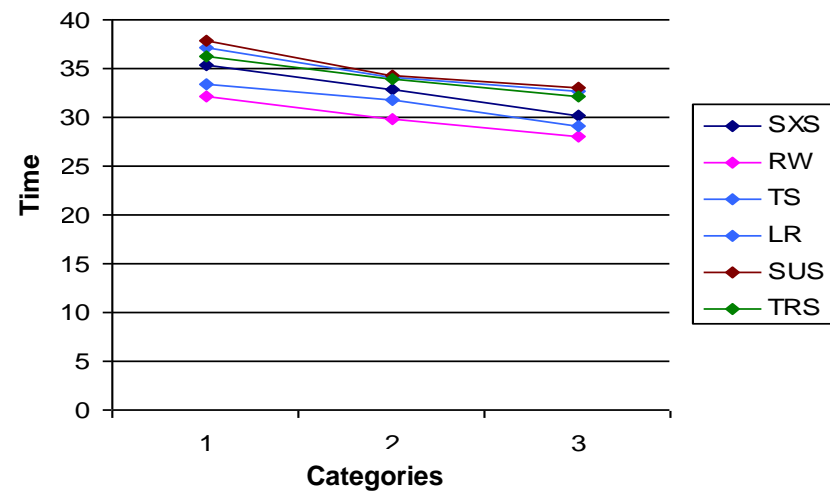


Figure 20. Time comparison for $m=10$ and $n=500$.

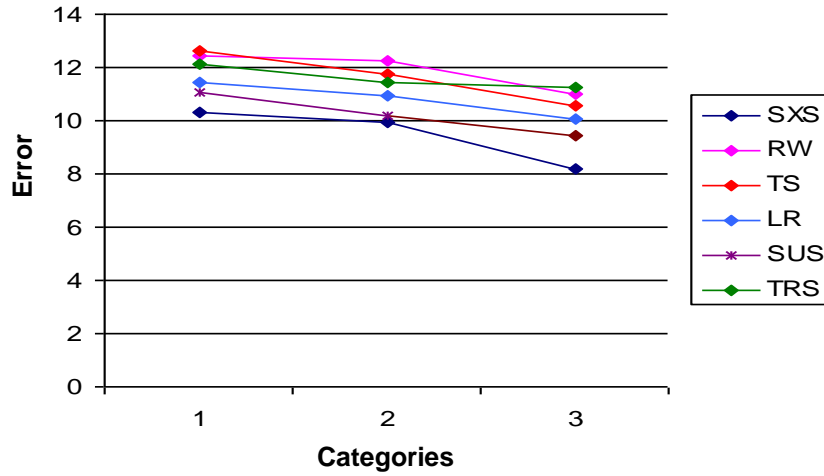


Figure 21. Error comparison for m=30 and n=500.

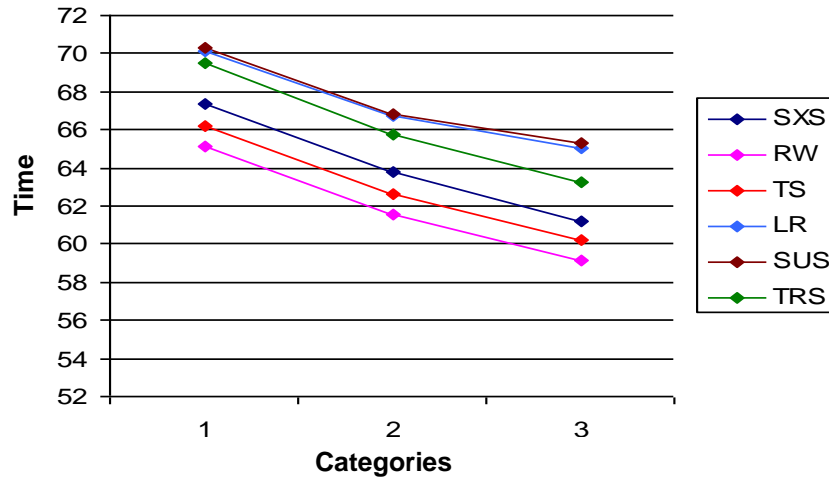


Figure 22. Time comparison for m=30 and n=500.

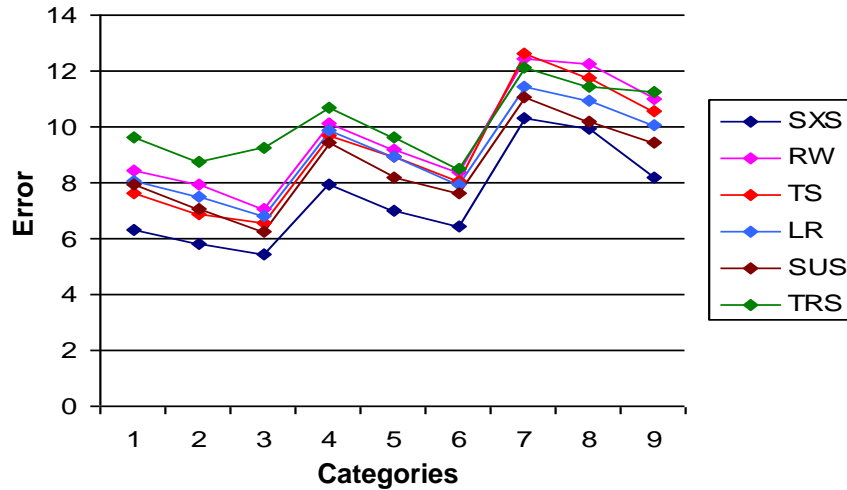


Figure 23. Error comparison for m=5, 10, 30 and n=500.

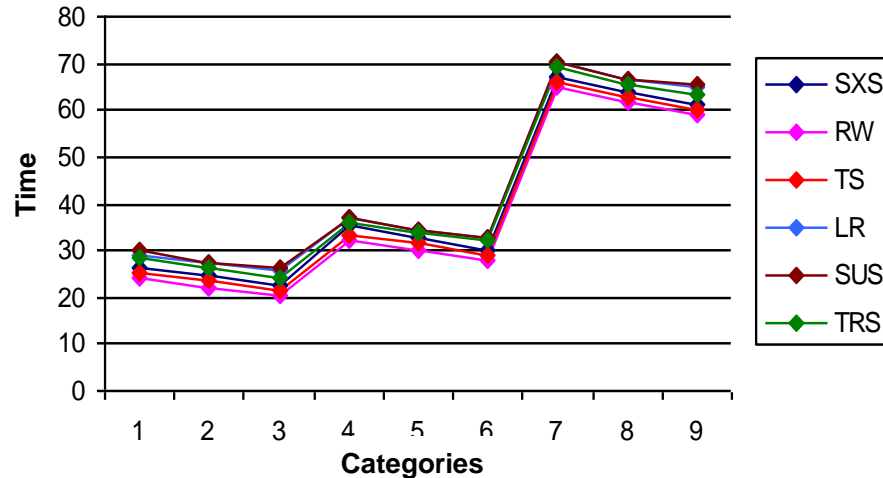


Figure 24. Time comparison for $m=5, 10, 30$ and $n=500$.

seen, it is clear that sexual selection for MKPs has a major advantage over other selection methods.

REFERENCES

- Allenson R (1992). Genetic algorithm with gender for multi-function optimization: Technical Report EPCC-SS92-01: Edinburgh Parallel Computing Centre.
- Beasley JE (1990). OR—Library: Distributing Test Problems by Electronic Mail. *J. Oper. Res. Soc.* 41:1069-1072.
- Beasley JE (1996). Obtaining Test Problems via Internet. *J. Glob. Opt.* 8:429-433.
- Beasley JE, Chu PC (1996). A Genetic Algorithm for the Set Covering Problem. *Euro. J. Oper. Res.* 94:392-404.
- Blickle T, Thiele L (1995). A Comparison of Selection Schemes used in Genetic Algorithm. Technical Report 11, Comp. Engin. Commu. Net. Lab (TIK), Swiss Federal Institute of Technology (ETH) Zurich, Gloriastrasse 35, CH-8092 Zurich.
- Chou H, Premkumar G, Chu CH (2001). Genetic Algorithms for communications network design—an empirical study of the factors that influence performance. *IEEE Trans. Evolu. Comp.* 5:236-249.
- Chu PC (1997). A Genetic Algorithm Approach for Combinatorial Optimisation Problems. PhD Thesis, University of London.
- Chu PC, Beasley JE (1997). A Genetic Algorithm for the Generalised Assignment Problem. *Comp. Oper. Res.* 24:17-23.
- Chu PC, Beasley JE (1998). A genetic Algorithm for the multidimensional Knapsack Problem. *J. Heur.* 4(1):63-86.
- Darwin C (1888). *The Origin of Species by Means of Natural Selection, or The Preservation of Favoured Races in the Struggle for Life*. London: Murray, sixth edition.
- Dengiz B, Altiparmak F, Smith AE (1997). Local search genetic algorithm for optimal design of reliable networks. *IEEE Trans. Evolu. Comp.* 1:179-188.
- Djannaty F, Doostar S (2008). A Hybrid Genetic Algorithm for the Multidimensional Knapsack Problem. *Int. J. Contemp. Math. Sci.* 3(9):443-456.
- Eshelman L, Schaffer D (1991). Preventing premature convergence in genetic algorithms by preventing incest. In *Proceeding of the Fourth Inter. Conf. Gene. Algo.* San Mateo, Calif: Morgan Kaufman Publishers, pp. 115-122.
- Fisher RA (1958). *The Genetical Theory of Natural Selection*. Dover, New York, 2nd edition. Freeman S, Herron JC (2001). *Evolutionary Analysis*: Prentice-Hall.
- Goldberg DE (1989). *Genetic Algorithms in search, Optimization and Machine Learning*: Addison-Wesley.
- Hinterding R (1994). Mapping, Order-independent Genes and the Knapsack Problem, in *Proceeding of the 1st IEEE Inter. Conf. Evolu. Comp.* Orlando, pp. 13-17.
- Hoff A, Løkketangen, A, Mittet I (1996). *Genetic Algorithms for 0/1 Multidimensional Knapsack Problems*. Working Paper, Molde College, Britveien 2, 6400 Molde, Norway.
- Holland JH (1975). *Adaptation in natural and artificial systems*. Ann Arbor: The University of Michigan Press.
- Jalali Varnamkhasti M, Lee LS (2012a). A Genetic Algorithm Based on Sexual Selection for the Multidimensional 0/1 Knapsack Problems. *Inter. J. Modern Phys.: Confer. Ser.* 9(2012):422-431
- Jalali Varnamkhasti M, Lee LS (2012b). A Fuzzy Genetic Algorithm Based on Binary Encoding for Solving Multidimensional Knapsack Problems, *Hindawi Publishing Corporation J. Appl. Math.* p. 23.
- Judson OP, Normak, BB (1996). Ancient asexual scandals *Trends in Evolution. Ecology* 11:41-46.
- Khuri S, Back T, Heitkotter J (1994). The Zero/One Multiple Knapsack Problem and Gene. *Algo. In the Proceedings of the 1994 ACM Sympo. Appl. Comp.* pp. 188-193.
- Kimura D (2000). *Sex and Cognition*. Cambridge, MA: MIT Press.
- Kirkpatrick M (1982). Sexual selection and evolution of female choice. *Evolution* 36(1):1-12.
- Lis J, Eiben AE (1997). A multi-sexual genetic algorithm for multiobjective optimization. In *Proceedings of the 1997 IEEE Inter. Conf. Evolu. Comp.* pp. 59-64.
- Michalewicz Z (1992). *Genetic Algorithms + Data Structures = Evolution Programs*: Springer, Berlin.
- Neoh SC, Norhashimah M, Lim CP, Abdul Aziz Z (2010). A GA-PSO Layered Encoding Evolutionary Approach to 0/1 Knapsack Optimization. *Int. J. Innov. Comp. Inf. Cont.* 6(8):3489-3505.
- Olsen AL (1994). Penalty Functions and the Knapsack Problem. In *Proceeding of the 1st Inter. Conf. Evolu. Comp.* pp. 559-564.
- Raghuwanshi MM, Kakde OG (2006). Genetic algorithm with species and sexual selection. In *Proceedings of IEEE Conf. Cyber. Intel. Syst. Bangkok, Thailand*, pp. 1-8.
- Raidl GR (1998). An Improved Genetic Algorithm for the Multiconstrained 0-1 Knapsack Problem.
- Rejeb J, AbuElhaja M (2000). New gender genetic algorithm for solving graph partitioning problems. In *the Proceedings of the 43rd IEEE Midwest Symp. Circuits Syst.* 1:444-446.
- Richardson JT, Palmer MR, Liepins G, Hilliard M (1989). Some guidelines for genetic algorithms with penalty functions. In *Proceedings of the 3rd Inter. Conf. Gene. Algo.*, Morgan Kaufmann Publishers, San Mateo, CA, pp. 191-197.
- Rudolph G, Sprave J (1996). Significance of Locality and Selection Pressure in the Grand Deluge Evolutionary Algorithm. *Parallel Problem Solving from Nature IV. Proceedings of the Inter. Conf.*

- Evolu. Compu., Lecture Notes in Computer Science, Springer pp. 686-694.
- Sanchez-Velazco J, Bullinaria JA (2003). Sexual selection with competitive/co-operative operators for genetic algorithms. In proceedings of IASTED Inter. Conf. Neural Net. Compu. Intel., Cancun, Mexico, pp. 191-196.
- Simões A, Costa E (2001). An Evolutionary Approach to the Zero/One Knapsack Problem: Testing Ideas from Biology. In the Proceedings of the Fifth Inte. Conf. Artif. Neural Net. Gene. Algo. (ICANNGA), Prague, Czech Republic, pp. 22-25.
- Smith MJ (1987). The Evolution of Sex. Cambridge Univ. Press, UK.
- Stearns SC, Hoekstra RF (2001). Evolution. Oxford: Oxford University Press.
- Syswerda G (1989). Uniform Crossover in Genetic Algorithms. In Proceeding of the Third Inter. Conf. Gene. Algo. San Mateo, Calif: Morgan Kaufman Publishers, pp. 2-9.
- Thiel J, Voss S (1994). Some Experiences on Solving Multiconstraint Zero-One Knapsack Problems with Genetic Algorithms. INFOR 32:226-242.
- Todd PM, Miller GF (1991). On the sympatric origin of species: Mercurial mating in the quicksilver model. In the Proceedings of the 4th Inter.Conf. Gene. Algo., San Mateo,CA: Morgan Kaufmann, pp. 547-554.
- Vrajitoru D (2002). Simulating gender separation with genetic algorithms. In Proceedings of the Gene. Algo. Evolu. Compu. Conf. (GECCO 2002), pp. 634-641.