An Novel Artificial Immune Systems Multi-objective Optimization Algorithm for 0/1 Knapsack Problems

Wenping Ma[1], Licheng Jiao[1], Maoguo Gong[1], and Fang Liu[2]

[1] Institute of Intelligent Information Processing, P.O. Box 224, Xidian University, Xi'an 710071, China
wpma@mail.xidian.edu.cn, maoguo_gong@hotmail.com
[2] School of Computer Science and Technology, Xidian University, Xi'an 710071, China

Abstract. Based on the concept of Immunodominance and Antibody Clonal Selection Theory, This paper proposes a new artificial immune system algorithm, Immune Dominance Clonal Multiobjective Algorithm (IDCMA), for multiobjective 0/1 knapsack problems. IDCMA divides the individual population into three sub-populations and adopts different evolution and selection strategies at them, but the update of each sub-population is not carried out all alone. The performance comparisons among IDCMA, SPEA, HLGA, NPGA, NSGA and VEGA show that IDCMA clearly outperforms the other five MOEAs in terms of solution quality.

1 Introduction

Since 1960s, the multiobjective optimization problems have attracted more attentions from researchers in various fields[1]. With the appearance of evolutionary algorithms and its lucubrating, it attracts comparative attentions as a novel method solving multiobjective optimization problems: Schaffer put forward VEGA.[2] Horn et al's NPGA and Srinivas et al's NSGA attracted more attentions[3]. In recent years, a lot of newly improved algorithms were proposed, such as Zitzler's SPEA[4]. Just like evolutionary algorithms, artificial immune system (AIS) constructs new intelligent algorithms with immunology terms and fundamenta.l[5]

After describing the multiobjective 0/1 knapsack problem in Section 2, a novel multiobjective optimization algorithm for the multiobjective 0/1 knapsack problem, Immune Dominance Clonal Multiobjective Algorithm (IDCMA), is put forward in Section 3. Section 4 is the simulation analyses.

2 The Multiobjective 0/1 Knapsack Problems

The multiobjective knapsack problem considered here is defined in the following[4]

Given a set of m items and a set of n knapsacks, with $P_{i,j}$ = profit of item j according to knapsack i , $w_{i,j}$ = weight of item j according to knapsack I, c_i = capacity of knapsack i. Its mathematic model:

Y. Hao et al. (Eds.): CIS 2005, Part I, LNAI 3801, pp. 793 – 798, 2005.

$$\begin{aligned} &max. \qquad y = f(x) = \left(f_1(x), f_2(x), \ldots, f_n(x)\right) \\ &subject\ to \quad \sum_{j=1}^{m} w_{i,j} \square x_j \le c_i, x = (x_1, x_2, \ldots, x_m) \in \{0,1\}^m \end{aligned} \tag{1}$$

find a vector $x = (x_1, x_2, \ldots, x_m) \in \{0,1\}^m$, such that $\forall i \in \{1,2,\ldots,n\}; \sum_{j=1}^{m} w_{i,j} \square x_j \le c_i$ and for which $f(x) = (f_1(x), f_2(x), \ldots, f_n(x))$ is maximum, where $f_i(x) = \sum_{j=1}^{m} p_{i,j} \bullet x_j$ and $\boldsymbol{x_j} = 1$ if item $\boldsymbol{j}$ is selected.

A 0/1 knapsack problem is a typical NP-hard problem. The dynamic programming can not search the satisfactory solutions with the feasible computation time and cost. As a result, we should find effective search method.

3 Solving Multiobjective 0/1 Knapsack Problems Based on IDCMA

Beginning with explanation of some terms used in IDCMA

Antigen: In artificial immune system, antigens refer to problems and its constraints.

Antibody: Antibodies represent candidates of the problem. For the multiobjective 0/1 knapsack problem, every candidate adopts binary coding with the length m, each binary bit represents the value of variable $x_i \mid i \in [1, m]$.

Antibody-Antigen Affinity: In AIS, it generally indicates values of objective functions or fitness measurement of the problem.

Antibody-Antibody Affinity: The reflection of the total combine power locates between two antibodies. In this paper, we compute the antibody-antibody affinity as reference [6]. Namely, if the coding of an antibody $\boldsymbol{a_i}$ is '1 1 0 0 0 0 1 0', and the coding of another antibody $\boldsymbol{a_{di}}$ is '1 1 0 1 0 1 1 0', then the antibody-antibody affinity between $\boldsymbol{a_i}$ and $\boldsymbol{a_{di}}$ is $6 + 3^2 + 2^2 = 19$.

Immune Dominance: For the multiobjective 0/1 knapsack problem, the antibody $\boldsymbol{a_i}$ is an immune dominance antibody in antibody population $A = \{a_1, a_2, \cdots, a_{n_b}\}$, if there is no antibody $\boldsymbol{a_j}$ $(\boldsymbol{j} = 1, 2, \cdots \boldsymbol{n_b} \wedge \boldsymbol{j} \neq \boldsymbol{i})$ in population $\boldsymbol{A}$ satisfied

$$(\forall k \in \{1,2,\cdots n\}\ f_k(e^{-1}(\boldsymbol{a}_j)) \ge f_k(e^{-1}(\boldsymbol{a}_i))) \wedge (\exists l \in \{1,2,\cdots n\}\ f_l(e^{-1}(\boldsymbol{a}_j)) > f_l(e^{-1}(\boldsymbol{a}_i))) \tag{2}$$

So the immune dominance antibodies are the Pareto-optimal individuals in current population.

Clonal Operation: In AIS, the clonal operation to the antibody population $\boldsymbol{A}(k)$ is defined as:

$$Y(k) = T_c^C(A(k)) = [T_c^C(a_1(k)) \quad T_c^C(a_2(k)), \quad \cdots \quad , T_c^C(a_{n_b}(k))]^{\mathrm{T}} \tag{3}$$

where $T_c^C(\boldsymbol{a}_{ci}(k)) = \boldsymbol{I}_{ci} \times \boldsymbol{a}_{ci}(k)\ \ i = 1, 2 \cdots N$, $\boldsymbol{I}_{ci}$ is a q_{ci}-dimensional identity row vector.

Immune Differential Degree: The Immune Differential Degree denotes the relative distribution of an immune dominance antibody. Namely, assuming that there are n_d immune dominance antibodies in current population, f_{kl} is the value of the K-th objective function of the l-th antibody. The Immune Differential Degree of the l-th antibody a_l can be calculated as follow:

$$d_l^* = \min\left\{ d_l(m) = \sqrt{\sum_{k=1}^{q}\left(\frac{\phi(f_{kl})-\phi(f_{km})}{\phi(f_{kl})}\right)^2} \;\middle|\; l=1,2,\cdots n_d;\ m=1,2,\cdots n_d \wedge m \neq l \right\} \tag{4}$$

where $\phi(\bullet)$ is an incremental function without the value of zero.

Inspired from the immuodominace of the biology immune system and the clonal selection mechanism, IDCMA is based on clonal selection with immune dominance and clone anergy for the multiobjective 0/1 knapsack problems which can be implemented as follows:

Step 1: Give the termination generation $G_{\max}$, the size of Immune Dominance Antibody population n_{d}, the size of Generic Antibody population n_{b}, the size of Dominance Clonal Antibody population n_{t}, and clonal scale n_{c}. Set the mutation probability p_{m}, recombination probability p_{c} and coding length c. Randomly generate the original antibody population $\boldsymbol{A}(0)=\{\boldsymbol{a}_1(0),\boldsymbol{a}_2(0),\cdots\boldsymbol{a}_{n_b}(0)\}\in \boldsymbol{I}^{n_b}$, k:=0;

Step 2: Modify $\boldsymbol{A}(k)$ with the greedy repair method as reported in reference [4], obtain the antibody population $\boldsymbol{A}(k)$ which satisfies the constrained conditions.

Step 3: According to the antibody-antigen affinities of all the antibodies in $\boldsymbol{A}(k)$, constitute population $\boldsymbol{DT}(k)$, if the number of antibodies in $\boldsymbol{DT}(k)$ is no larger than n_{d}, let Immune Dominance Antibody population $\boldsymbol{D}(k)$=$\boldsymbol{DT}(k)$, go to Step6; otherwise go to Step4;

Step 4: Compute the Immune Differential Degrees in population $\boldsymbol{DT}(k)$;

Step 5: Sort all the antibodies in $\boldsymbol{DT}(k)$ by descending of their Immune Differential Degrees, and select the first n_{d} antibodies to constitute $\boldsymbol{D}(k)$;

Step 6: If k=$G_{\max}$, export $\boldsymbol{D}(k)$ as the output of the algorithm, Stop. Otherwise, replace the immune dominance antibodies in $\boldsymbol{A}(k)$ by new antibodies generated randomly. Then marked the antibody population as $\boldsymbol{B}(k)$;

Step 7: Select an immune dominance antibody $\boldsymbol{a}_{di}$ randomly from $\boldsymbol{D}(k)$. Compute the antibody-antibody affinities between the antibodies in $\boldsymbol{B}(k)$ and the antibody $\boldsymbol{a}_{di}$.

Step 8: Sort all the antibodies in $\boldsymbol{B}(k)$ by descending of their antibody-antibody affinities, select the first n_{t} antibodies to constitute the Dominance Clonal Antibody population $\boldsymbol{TC}(k)$, and other antibodies to constitute the Immune Anergy Antibody population $\boldsymbol{NR}(k)$.

Step 9: Implement the Antibody Clonal Operation $T_{\mathrm{c}}^{\mathrm{C}}$ at $\boldsymbol{TC}(k)$ and get the antibody population $\boldsymbol{CO}(k)$ after clonal operation.

Step 10: Implement the recombination operation at $\boldsymbol{CO}(k)$ with the probability p_{c} and get the antibody population $\boldsymbol{CO}'(k)$.

Step 11: Implement the mutation operation at $\boldsymbol{CO}'(k)$ with the probability p_{m} and get the antibody population $\boldsymbol{COT}(k)$.

Step 12: Combine the populations $\boldsymbol{COT}(k)$, $\boldsymbol{D}(k)$ and $\boldsymbol{NR}(k)$ to form the antibody population $\boldsymbol{A}(k+1)$, $k:=k+1$, go to Step 2.

4 Simulations

In order to validate the algorithm, we compare the algorithm with another five algorithms. They are Zitzler's Strength Pareto Evolutionary Algorithm (SPEA)[4], Schaffer's Vector Evaluated Genetic Algorithm(VEGA)[7], Hajela's and Lin's genetic algorithm (HLGA)[8], the niched Pareto genetic algorithm (NPGA)[9] and Srinivas' and Deb's Nondominated Sorting Genetic Algorithm (NSGA)[10]. This paper selects the performance measure ς in [11].The test data sets are available from the authors[4], where two, three, and four objectives are taken under consideration, in combination with 250, 500, 750 items. The parameters setting of IDCMA are:

The halt generation $G_{\max}$=500, immune dominance antibody population size $n_{\mathrm{d}}=100$, antibody population size $n_{\mathrm{b}}=100$, dominance clonal antibody population size $n_{\mathrm{t}}=50$, clonal scale $n_{\mathrm{c}}=300$, coding length $c= m$ where m is the number of terms, mutation probability $p_{\mathrm{m}}=2/c$, recombination probability $p_{\mathrm{c}}=1$. Thirty independent runs of IDCMA are performed per test problem. The test problems and reported results of SPEA, HLGA, NPGA, NSGA and VEGA are directly gleaned from Zitzler' website: http://www.tik.ee.ethz.ch/~zitzler/testdata.html/.

The direct comparisons of IDCMA with the other algorithms based on the ς measure from 30 runs are depicted using box plots, as shown in Figure 1. A box plot provides an excellent visual result of a distribution. The upper and lower ends of the box are the upper and lower quartiles, while a thick line with the box encodes the median. Dashed appendages summarize the spread and shape of the distribution.

As the Figure 1 shows, IDCMA achieves the best assessments among these multiobjective EAs. It covers 100% of the nondominated solutions found by HLGA with all the nine test problems, and covers 100% of the nondominated solutions found by NPGA with seven of the nine test problems, and covers 100% of the nondominated solutions found by VEGA with eight of the nine test problems, and covers 100% of the nondominated solutions found by NSGA with seven of the nine test problems, and covers 100% of the nondominated solutions found by SPEA with six of the nine test problems; For 2 knapsacks and 500 items 100% are covered, as the same as 2 knapsacks and 750 items. For 4 knapsacks and 250 items at least 81% are covered. And for other six test problems at least 91% are covered. Vice versa, those algorithms cover less than 2% of the IDCMA outcomes in all 270 runs. Therefore IDCMA can find solutions that are closer to the Pareto-optimal front than those produced by other five algorithms.

Figure 1 reveals the superiority of IDCMA over the compared MOEAs in terms of robustness and nondominated solution quality. The experimental results reveal that IDCMA outperforms SPEA, HLGA, NPGA, NSGA and VEGA, especially for problems with a large number of items or a large number of knapsacks. IDCMA also performs well for various numbers of knapsacks.

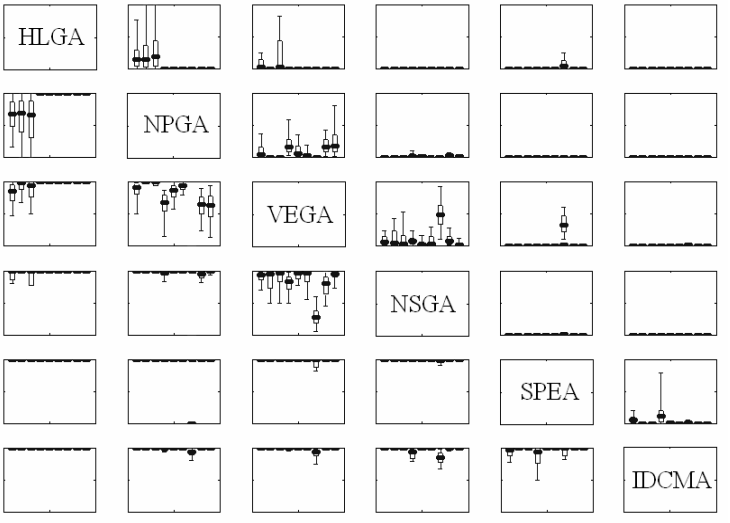

Fig. 1. Box plots based on the ς measure. Each rectangle contains nine box plots representing the distribution of the ς values for a certain ordered pair of algorithms; the three box to the left relate to 2 knapsacks and (from left to right) 250,500,750 items; correspondingly the three middle box plots relate to 3 knapsacks and the three to the right to 4 knapsacks. The scale is 0 at the bottom and 1 at the top per rectangle. Furthermore, each rectangle refers to algorithm $\boldsymbol{A}$ associated with the corresponding row and algorithm $\boldsymbol{B}$ associated with the corresponding column and gives the fraction of $\boldsymbol{B}$ covered by $\boldsymbol{A}$ ($\varsigma(\boldsymbol{A},\boldsymbol{B})$).

5 Concluding Remarks

In this paper, a novel algorithm for the multiobjective 0/1 knapsack problem, Immune Dominance Clonal Multiobjective Algorithm is put forward, which is inspired by the concept of immunodominance and the clonal selection theory. From the numerical results of the metrics, Coverage of Two Sets, we draw a conclusion quantificationally that solutions obtained from IDCMA dominate those obtained from SPEA, HLGA, NPGA, NSGA and VEGA obviously. Especially for problems with a large number of items or a large number of knapsacks, the dominance of IDCMA is more obvious. Namely, for the discontinuous Pareto-optimal fronts or the isolated optimal point, IDCMA can construct and find them while the other algorithms seem incapable sometimes. At the same time, IDCMA is much better than the other five algorithms from the distributions of the solutions.

References

1. Hwang, C. and Yoon, K.: Multiple Attribute Decision Making: Methods and Applications, Spinger-Verlage, Berlin, (1981)
2. Schaffer, J.D.: Multiple objective optimization with vector ecaluated genetic algorithms. PhD thesis, Vanderbilt University (1984)

3. Abido, M.A.: Environmental economic power dispatch using multiobjective evolutionary algorithms. IEEE Trans. Power Systems, Vol.18, No. 4, November (2003)
4. Zitzler, E., Thiele, L.: Multiobjective Evolutionary Algorithms: A Comparative Case Study and the Strength Pareto Approach. IEEE Trans. Evolutionary Computation. Vol. 3, No. 4, November (1999)
5. Jiao Licheng, Du Haifeng.: Artificial immune system: progress and prospect (in Chinese). ACTA ELECTRONICA SINICA, Vol.31, No.10, (2003) 1540-1548
6. Carlos A.Coello Coello and Nareli Cruz Cortss.: An Approach to Solve Multiobjective Optimization Problems Based on an Artificial Immune System. In: Jonathan Timmis and Peter J. Bentley (editors). Proceedings of the First International Conference on Artificial Immune Systems (ICARIS'2002), 212-221, University of Kent at Canterbury, UK, September, 9-11 (2002)
7. J. D. Schaffer.: Multiple objective optimization with vector evaluated genetic algorithms, in Proceedings of an International Conference on Genetic Algorithms and Their Applications, J. J. Grefenstette, Ed., Pittsburgh, PA, July 24-26 (1985) 93-100, sponsored by Texas Instruments and U.S. Navy Center for Applied Research in Articial Intelligence (NCARAI)
8. P. Hajela and C.- Y. Lin.: Genetic search strategies in multicriterion optimal design, Structural Optimization, vol. 4, June (1992)99-107
9. J. Horn and N. Nafpliotis.: Multiobjective optimization using the niched pareto genetic algorithm, IlliGAL Report 93005, Illinois Genetic Algorithms Laboratory, University of Illinois, Urbana, Champaign, July (1993)
10. N.Srinivas and K.Deb.:Multiobjective optimization using nondominated sorting in genetic algorithms, Evolutionary Computation, vol.2, no.3, (1994) 221-248
11. Eckart Zitzler. Evolutionary Algorithms for Multiobjective Optimization: Methods and Applications. A dissertation submitted to the Swiss Federal Institute of Technology Zurich for the degree of Doctor of Technical Sciences. Diss. Eth No. 13398 (1999)
12. Gong, M.G., Du, H.F., Jiao, L.C., Wang, L.: Immune Clonal Selection Algorithm for Multiuser Detection in DS-CDMA Systems. Springer-Verlag, LNCS 3339, (2004) 1219-1225
13. Jiao, L.C., Gong, M.G., Shang, R.H., DU, H.F., Lu, B.: Clonal Selection with Immune Dominance and Anergy Based Multiobjective Optimization. Springer-Verlag, LNCS 3410, (2005) 474–489
14. Gong, M.G., Jiao, L.C., Liu, F. and Du, H.F.: The Quaternion Model of Artificial Immune Response. Springer-Verlag, LNCS 3627, (2005) 207–219