

A New Ant Colony Optimization Algorithm: Three Bound Ant System

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Since its introduction, ant colony optimization (ACO) algorithms and especially the MAX-MIN ant system (MMAS) [4] are found to be well suited for many challenging optimization problems. Our theoretical analyses of MMAS allowed us to create the new algorithm, named the three bound ant system (TBAS), which has lower computational complexity and at the same time retains and even improves the quality of constructed solutions. In this paper, TBAS is briefly explained and experimentally explored in the terms of algorithmic speedup and solution quality. Some distinctive characteristics of TBAS with regard to MMAS are:

- three pheromone bounds (the lower bound τ_{LB} , the upper bound τ_{UB} , and the contraction bound $\tau_{CB} = \omega \cdot \tau_{UB}$),
- occasional pheromone contractions, instead of regular evaporations,
- its unique pheromone reinforcement procedure,
- the initial pheromone value is equal to the lower pheromone bound.

In the solution construction procedure, TBAS uses well known random proportional rule identically as it is used in MMAS (and many other ACO algorithms). TBAS uses all the parameters as MMAS does, although some parameters TBAS uses somewhat different (e.g. parameter ρ that is used in MMAS for pheromone evaporation), and has additional parameter ω , where $\tau_{LB}/\tau_{UB} \leq \omega \leq 1$.

The pheromone update procedure of TBAS starts with the pheromone reinforcement and is followed by the pheromone contraction procedure, only in the case that some pheromone trail outgrows the upper pheromone bound τ_{UB} . During the pheromone reinforcement it is necessary to choose one or many solutions whose components will be rewarded with the additional pheromone values. For that, different strategies like iteration best, κ -best or max- κ -best can be used [2]. All the components of the chosen solution s^{bs} are reinforced in the TBAS according to the expression (1), where in the first iteration $Q_0 = 1$, and afterwards in the i -th iteration Q_i is modified by $Q_{i+1} = Q_i/(1 - \rho)$. The pheromone contraction multiplies all the pheromone trails and Q_i with $\omega' = \tau_{UB}/\tau_{max} \cdot \omega$ and enforces that every pheromone trail τ_c is inside the interval $[\tau_{LB}, \tau_{CB}]$.

$$\tau_c = \tau_c + \frac{Q_i}{f(s^{bs})}, \forall c \in s^{bs} \quad (1)$$

Because of different pheromone update procedures, TBAS has lower computational complexity than MMAS. In the case when precomputed values of $\tau_c^\alpha \cdot \eta_c^\beta$ are stored in the lookup table (LUT), to speedup the algorithm, the

TBAS has the additional advantage since it is often sufficient to recompute pheromone trails only for components affected by the pheromone reinforcement. The actual speedup of TBAS over MMAS, for equal number of iterations and equal common parameters, depends on optimization problem, algorithm's implementation, parameters, etc, and can vary from negligible to highly significant. According to [3] the time spent in the pheromone update procedure can take up to 90% of the total running time of the algorithm. In order to show a possible speedup of TBAS over MMAS we chose an optimization problem and parameter settings for which we expected significant speedup. Experiments were conducted on instances of ATSP with sizes ranging from 53 to 5000 available at <http://www2.research.att.com/~dsj/chtsp/> and <http://comopt.ifl.uni-heidelberg.de/software/TSP LIB95/>. The both algorithms shared the same source code, except for the pheromone update procedure and the same parameters ($\alpha = 1.3$, $\beta = 4$, $\rho = 0.02$, the favorite nodes list size was set to 40, etc.), with exception of $\omega = 0.03125$ which exist only in TBAS. Experiments carried on the HP 6830s laptop have shown that speedup ratio in the case when the number of ants $m = 10$ is between 2 and 18, and for $m = 1000$ the speedup ratio was between 1.01 and 1.2 (i.e. TBAS was 1% to 20% faster than MMAS), etc.

To explore TBAS in the terms of solution quality, the experimental comparison of TBAS and MMAS were conducted on 55 instances of the quadratic assignment problem (QAP) [4,1] from QAPLIB with sizes ranging from 15 to 256 locations. The algorithms were compared without local optimization and with 2-opt local optimization after 10000 iterations, in every category with two parameter settings. For MMAS the parameters were set to commonly recommended values and reinforcement strategy was tuned by comprehensive experimentation. For TBAS the parameters were copied from MMAS, and then the parameters ω and $\vartheta = \tau_{LB}/\tau_{UB}$ were tuned based on p^{QAP} probability [1]. The experiments were repeated 100 times and median values were used. In both categories TBAS clearly outperformed MMAS which were confirmed with very high statistical significance with Friedman test and various post hoc procedures.

The newly proposed TBAS has special theoretical relation with MMAS, and has experimentally proved itself competitive with MMAS in both algorithmic speedup and solution quality.

References

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