

## Multiple Ant Colony Optimizations for Stereo Matching

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### Abstract

The stereo matching problem, which obtains the correspondence between left and right images, can be cast as a search problem. The matching of all candidates in the same line forms a 2D optimization task, which is an NP-hard problem in nature. Two characteristics are often utilized to enhance the performance of stereo matching, i.e. concurrent optimization of several scan-lines and correlations among adjacent scan-lines. Such correlations are considered to be posterior, which require several trails for their discovery. In this paper, a Multiple Ant Colony based approach is proposed for stereo matching because of the Ant Colony optimization's inherent capability of relation discovery through parallel searching. The Multiple Ant Colony Optimization (MACO) is efficient to solve large scale problems. For stereo matching, it evaluates sub-solutions and propagates the discovered information by pheromone, taking into account the ordering and uniqueness constraints of candidates in images. The proposed algorithm is proved to be able to find the optimal matched pairs theoretically and verified by experiments.

**Keywords:** Multiple Ant Colony Optimizations, Stereo Matching, Iteration, Constraints.

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### 1. INTRODUCTION

The purpose of computer stereo vision is to obtain depth information of objects with the help of two or more cameras. Generally speaking, there are four steps to accomplish it, which are image pre-processing, matching primitive defining & extracting, feature matching and disparity refining. The image pre-processing includes image enhancement and epipolar rectification; the second step includes the definition of feature and its extraction; disparity refining is to get a smooth depth map in which sub-pixel interpolation is involved for example. Feature matching has been one of the most challenging research topics in computer vision.

The stereo matching problem [1-7], that is to obtain a correspondence between right and left images, can be cast as a search problem. When a pair of stereo images is rectified, corresponding points can be searched within the same scanline, this is a two dimensional (2D) optimization, which can be shown as a NP-hard problem [3]. An optimization method, such as Dynamic Programming (DP)[2,8-16], Simulated Annealing(SA) [17], Genetic Algorithm(GA)[18],

max-flow[19], graph-cut [3,20], etc., can be used to find the optimal or sub-optimal solutions with different efficiency.

Baker [1] describes a fast, robust, and parallel implementable edge-based line-by-line stereo correlation scheme. Based on the fact that a connected sequence of edges in one image should be a connected sequence of edges in the other, a cooperative procedure to deal with edge correspondences is proposed. The dynamic programming algorithm performs a local optimization for the correlation of individual lines in the image, and the edge connectivity is used to remove miscorrelations.

Ohta [8] defines two different searches, intra-scanline and intera-scanline search. The intra-scanline search can be treated as finding a matching path on 2D search plane whose axes are the right and left scanlines. Vertically connected edges in the images provide consistency constraints across the 2D search planes. Inter-scanline search in a 3D search space, with a stack of the 2D search planes, needs to utilize the vertically connected edge information. Dynamic programming is used in both searches.

Birchfield [2] proposes a new algorithm based on three heuristic functions. During the matching the occluded pixels are allowed to remain unmatched, the information between scanlines is propagated by a postprocessor. The global post-process propagates reliable disparities to the regions with unreliable disparities.

Bobick [4] develops a stereo algorithm that integrates matching and occlusion analysis into a single process. After highly-reliable matches, the ground control points (GCPs) are introduced. The matching sensitivity to occlusion-cost and algorithmic complexity can be significantly reduced. The use of ground control points eliminates both the need for biasing the process towards a smooth solution and the task of selecting critical prior probabilities describing image formation.

Raymond [10] proposes the use of a multi-level dynamic programming method to solve the matching problem of stereo vision. At level 1, the line segment pairs that have a very high local similarity measure are selected for the matching process. By considering the geometric properties between the matched and the unmatched line segments, a global similarity measure is calculated for each unmatched line segments pair, and then the second level starts.

In [Kim 13], first, a new generalized ground control points (GGCPs) scheme is introduced, where one or more disparity candidates for the true disparity of each pixel are assigned by local matching using the oriented spatial filters. Second, it performs optimization both along and across the scanlines by employing a two-pass dynamic programming technique. Combined with the GGCPs, the stability and efficiency of the optimization are improved significantly.

[Sorgi 15] presents a symmetric stereo matching algorithm, based on the bidirectional dynamic programming scanline optimization. The Sum of the Squared Differences (SSD) map is treated as a decoding trellis and inspected twice: the forward optimization produces the optimal path from the upper left to the lower right corner, and the backward optimization produces the optimal path from the lower right back to the upper left corner. The final operation, a consistency check between the selected forward and backward optimal paths, can produce an occlusion-robust matcher without defining an empirical occlusion cost.

[Sung 16] proposes a stereo matching algorithm which employs an adaptive multi-directional dynamic programming scheme using edge orientations. Chain codes are introduced to find the accurate edge orientations which provide the DP scheme with optimal multidirectional paths. The proposed algorithm eliminates the streaking problem of conventional DP based algorithms, and estimates more accurate disparity information in boundary areas.

On the assumption that the neighboring elements have consistent match values, in [Zitnick 5], local support area that determines which and to what extent neighboring elements should contribute to averaging is introduced. An iterative algorithm updating the match values by diffusing support among neighboring values and inhibiting others along similar lines of sight is proposed. After the match values have converged, occluded areas are explicitly identified and the final results are obtained.

Marr and Poggio [9] present two basic assumptions for a stereo vision algorithm. The first assumption, uniqueness assumption, states that at most a single unique match exists for each pixel if surfaces are opaque; The second one, continuity assumption, states that disparity values are generally continuous, i.e., smooth within a local neighborhood.

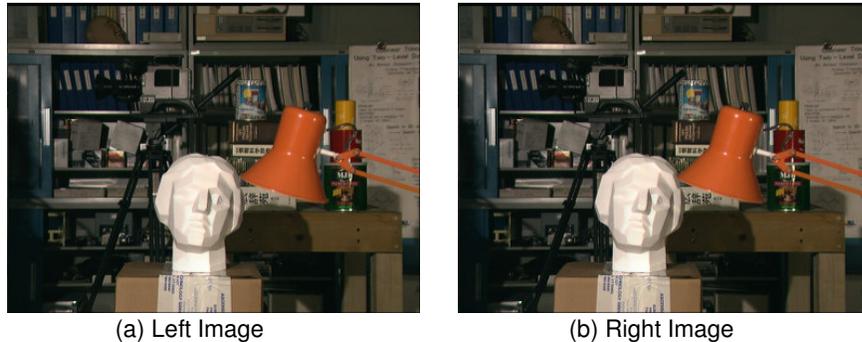
[Scharstein 6, Brown 7] reviews the development in decades. In [Leung 12, Selzer 14], the process is speeded up with special data structure. All the articles mentioned above have the following common characteristics. 1) There are two kinds or levels of optimization, the local one which accomplishes the optimization in the corresponding scanline and the global one which finds the best solution among all scanlines. 2) Based on the Marr's assumptions, many constraints must be obeyed, for example, ordering constraint, uniqueness constraint and bi-directional monotonicity constraint. 3) To get the global optimal solution, the reliability should be propagated. How to propagate the reliability is skillful. In [8], the optimization function is update by the inter-scanline information; in [4, 13], the preprocessed GCPs are introduced; in [5, 10], the iteration is used to remove the wrong matches or enhance the correct matches; in [2], a postprocessor is employed to remove wrong matches after the optimization.

In this paper, the expected merits of a good algorithm for stereo matching are analyzed. Then a new multiple ant colony optimization (MACO) method is proposed to solve the stereo matching problem, and the convergence of the proposed algorithm is also discussed. In the last part the experiments show the results of the algorithm.

## 2. PRELIMINARIES

Stereo matching is still an open task to be investigated. The following two questions are argued firstly in this paper.

- Marr's assumptions is correct, but dose it need to be obeyed during the optimizing process?
- The reliability propagation is necessary, but how to get more reliable one and how to do?



**FIGURE 1:** Tsukuba Pairs

One pair of standard test images for stereo algorithm is shown in Fig.1. Supposed the size of epipolar rectified image is  $K$  by  $L$ , there are  $N$  features (the features can be point, line, curve and area) on the  $k^{th}$  ( $k=1\dots K$ ) scanline of left image and  $M$  features on the  $k^{th}$  scanline of right image. A matrix  $L \times L$ , named as similarity matrix, stores all possible matches on the  $k^{th}$  scan line. The element at  $(n^{th}, m^{th})$  is the Sum of Absolute Differences (SAD) similarity of the feature on  $(k^{th}, n^{th})$  in left image and the feature on  $(k^{th}, m^{th})$  in right image. In the similarity matrix, only  $N$  by  $M$  elements are meaningful, the others are zero. If minimum & maximum parallax restraint is considered, define  $v_n$  as the search space of the  $n^{th}$  feature in the left image, all  $v_n$  ( $n=1\dots L$ ) form a banded region (actually,  $n$  should be from 1 to  $N$ , to simplify statement and not loss of the generality, in this paper  $n=1\dots L$ ), as the white banded region shown in Fig.2, marked with notation  $\Omega$  (including  $\Omega'$ , in which every element is zero, marked as the black area) in this paper. The  $d_{min}$  and  $d_{max}$  represent the minimum and maximum parallax respectively. The parallax on the dot black line is zero. One similarity matrix corresponds to a specific scan line, and then  $K$  similarity matrixes are available, That is to say there are  $K$  tasks to be optimized in the stereo matching (every one is a sub-task).

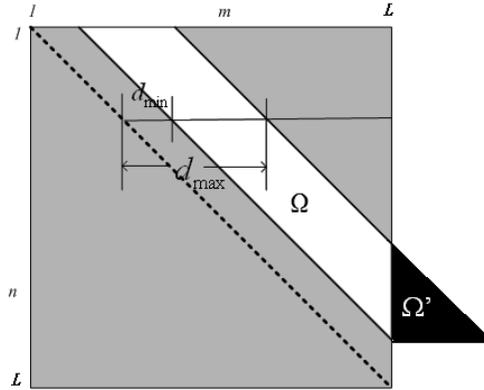


FIGURE 2: Similarity Region

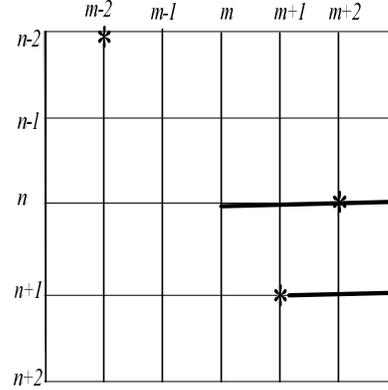


FIGURE 3: Constraints in Matching Process

### 2.1 Constraints during the Optimization

The dynamic programming algorithm requires the uniqueness and ordering constraints [11]. The current state is undoubtedly decided by the state of the previous result, when the matching error occurs in the previous stage, it will directly affect the current stage of the match. There is no opportunity to rectify this error in the later match if the simple DP is used.

In the matching process what's happened if the ordering and uniqueness constraints are exerted? In the  $k^{th}$  scanline, suppose there are 3 features at  $n-2^{th}$ ,  $n^{th}$ ,  $n+1^{th}$  columns of left image and 5 features from  $m-2^{th}$  to  $m+2^{th}$  columns of right image. The matching process is illustrated by Fig.3, in which  $d_{min} \leq m-n \leq d_{max}$  is satisfied. Set the features at  $n-2^{th}$  is the best match with one at  $m-2^{th}$ , then the possible matchers with  $n^{th}$  can be found from  $m^{th}$  to  $m+d_{max}^{th}$  as marked with a dark black line. If there is no match with  $n-1^{th}$  features and the  $n^{th}$  is matched with  $m+2^{th}$ , considering the ordering constraint, the match with the  $n+1$  can only be found from  $m+3$  to  $m+1+d_{max}$ . If there is a wrong math between the  $n^{th}$  and  $m+2^{th}$ , the abuse of such constraints will miss the correct math between the  $n+1^{th}$  and  $m+1^{th}$ ! Clearly we cannot trust the ordering constraint based on maybe false assumptions, the same as the uniqueness constraint.

- In this paper, during the procedure of matching, the only constraint is the minimum & maximum parallax constraint.

Such strategy is good for finding more real matches, simplifying the computation and promoting the parallelism greatly. That is to say the sub-optimization can start from random position instead of the rigid left-top or right-bottom corner.

### 2.2 Reliability Propagation

In literature[4,13], GCPs are used to increase the real match probability, GCPs not only generate a sufficient number of seed pixels for guiding the subsequent matching process, but also remarkably reduce the risk of false match. It is known that the false matches in GCPs could severely degrade the final matching results. In practice, the reliability of GCPs/GGCPs is far away from expectation. The ordering and uniqueness constraints may propagate the error and make the result worse, additionally, the GCPs must be identified before the DP optimization process, but how to automatically get more reliable GCPs?

The vertical edges information among scanlines may be the most frequently considered one. Vertical edges, especially the edges with high threshold, are robust features, that is to say the possibility of an edge which finds the correct match is high. There is no any priori-knowledge about which edge of the right image is matched with one of the left image. Every vertical edge are discretized by sacnlines, so many features are fomed. According to the large probability hypothesis, most of the features on the vertical edge in the left image will be matched with the features in the same edge in the right image. That is to say after the optimization of features sharing the same vertical edge, if the matching results are voted, the matched edge in the right image can be identified. **This information is posterior, means that this information only can be obtained after every sub-optimization.** Such automatically obtained knowledge is relative

reliable and should be propagated to the sub-matching process, so the feedback or iterative idea should be introduced into the whole optimizing procedure. The confirmed matching edges after voting can serve as the GCPs for the next optimization. **The first contribution of this paper is that such voted GCPs are obtained automatically during the optimization procedure.**

### 3. PARALLEL ACO Based STEREO MATCHING

An ideal stereo matching algorithm should have three merits, first the ordering and uniqueness constraints are ignored during the optimizing process but the result must satisfy such constraints; second the optimizing process of every line is relatively independent, so every process can be done concurrently; third if two scanlines share the same vertical edge, the hint of vertical edge should be exploited to enhance the certainty of every line's optimization next time, That is to say the reliability should be propagated. To sum up, a parallel, iterative and feedback algorithm is proposed in this paper.

Ant-based system is recently developed for the solution of combinatorial optimization problems [21]. After this the Ant Colony Optimization (ACO) emerged. In ACO, an ant builds a solution to a combinatorial optimization problem by exploiting pheromone trails and heuristic information. The main characteristics of the ACO are inherent parallelism, stochastic nature, adaptability, and the use of positive feedback. Paper [22] shows that ACO is always better than Genetic Algorithm (GA) and Simulated Annealing (SA), if the parameters are selected properly.

When dealing with complex and large-scale issues, a single-group ant colony optimization algorithm is prone to be slow and premature. The parallel multiple Ant Colony Optimization (MACO) algorithms can be exploited through the acceleration of the construction procedure. Various parallel approaches [23-28] are proposed to promote the efficiency with the help of communication and parallelism. Most parallelization models can be classified into fine-grained, in which the population of ants is separated into a large number of very small sub-populations, and coarse-grained models, in which the population of ants is divided into few sub-populations. [Bullnheimer 23] introduces two parallel implementations called the Synchronous Parallel Implementation (SPI) and the Partially Asynchronous Parallel Implementation (PAPI). SPI is based on a master-slave paradigm in which every ant finds a solution in the slaves and sends the result to the master. When the solutions are available the master updates the pheromone information and sends the updated information back to all slaves. PAPI is based on the coarse-grained model in which information is exchanged among colonies every fixed number of iterations. The simulation indicates that PAPI performs better than SPI in terms of running time and speedup. [Talbi 24] presents a parallel model for ant colonies to solve the Quadratic Assignment Problem. The programming style used is a synchronous master/workers paradigm. During every iteration, the master broadcasts the pheromone matrix to all the workers. Each worker receives the pheromone matrix, constructs a complete solution, and sends the found solution to the master. When the master receives all the solutions, it updates the pheromone, and then the process is iterated. In [Rahoual 25], the Set Covering Problem is solved by master/slaver colonies. Each ant process is set on an independent processor. The master process sends the necessary information (pheromone) to each ant. In [Randall 26], several parallel decomposition strategies, Parallel Independent Ant Colonies, Parallel Interacting Ant Colonies, Parallel Ants, Parallel Evaluation of Solution Elements, Parallel Combination of Ants and Evaluation of Solution Elements, are examined. These techniques are applied to Traveling Salesman Problem (TSP). In [Chu SC 27], the artificial ants are partitioned into several groups. Seven communication methods for updating the pheromone between groups are proposed. In [Ellabib 28], a performance study is carried out to evaluate the effectiveness of the exchange strategies and demonstrate the potential of applying MACO to solve the Vehicle Routing Problem with Time Windows. Experiments using the proposed assessment technique demonstrate that the exchange strategies have a considerable influence on the search diversity. The results indicate that the multiple colony system approach outperforms the single colony.

As mentioned above, the total stereo matching consists of many sub-optimization problems, and every sub-task can be optimized at the same time. So in this paper single ACO is employed to solve a sub-task. As mentioned above there are some relationship among sub-optimizations if the scanlines share the same vertical edge. Based on the large probability assumption voting can be

used to decide the correctness of all sub-solutions after the optimization of all sub-tasks are finished. This posterior knowledge requires a master to gather the results of slavers and get the best one by evaluation. When a good result is obtained by voting, it is propagated iteratively to enhance reliability. In this paper, a parallel MACO is employed. It is based on the master-slaver mode that the parallel slaver optimizes every sub-problems and the master broadcasts the pheromone formed according to the results from slavers.

### 3.1 Construction of MACO

The constructed MACO for stereo matching is introduced in this section by means of the following definitions.

- Definition of Pheromone

It is a 2D optimization for every sub-task to find the best matchers. In literature [33], the 2D optimization can be cast as a path finding problem. All possible paths in a search space should be stored at a pheromone matrix. The search space of sub-optimization task is  $\Omega$ , which consists of  $v_n (n=1, \dots, K)$ . Suppose that in some iteration, the best matched pair is the  $n^{th}$  and  $m^{th}$  features.

All possible match feature with the  $n+1^{th}$  feature is in  $v_{n+1}$  if there is. It means there are  $d_{max} - d_{min}$  possible choices, so as every element in  $v_n$ . Actually without the ordering and uniqueness constraint, the number of all possible choices is independent with the position in  $v_n$ . The pheromone matrix  $\tau_{ijp}$  is defined, Where  $i=1, \dots, L-1, j, p=1 \dots d_{max} - d_{min}$ . The size of pheromone field matrix is with a dimension of  $(L-1) \times (d_{max} - d_{min}) \times (d_{max} - d_{min})$ .

- Definition of Heuristic Information

Heuristic information is used for an ant to choose the correct match, the bigger value of similarity the higher possibility of a match. If the best match pair is the  $n^{th}$  and  $m^{th}$  features, all possible match with the  $n+1^{th}$  feature is all elements in  $v_{n+1}$ . Which one is the most likely match with the  $n+1^{th}$  feature depends on whose SAD is the smallest one from  $m+1+d_{min}$  to  $m+1+d_{max}$ . In this paper, the heuristic Information is defined as the SAD if all SAD values in  $v_{n+1}$  are not equal to zero, clearly heuristic information satisfies  $0 < \eta_{min}$ .

- Probability Decision

In search domain  $\Omega$ , set the ant at the position  $x_i^j \in v_i$ . According to the following probability, it will select  $x_{i+1}^p \in v_{i+1}$  according to Equation (1).

$$p_{jp} = \begin{cases} \frac{\tau(i, x_i^j, x_{i+1}^p)^\alpha \eta(x_{i+1}^p)^\beta}{\sum_{l \in x_{i+1}} \tau(i, x_i^j, x_{i+1}^l)^\alpha \cdot \eta(x_{i+1}^l)^\beta}, & \max(x_{i+1}^l) > \theta \\ 0 & , \text{others} \end{cases} \quad (1)$$

where  $i=1, \dots, L-1; j=i+d_{min}, \dots, i+d_{max}; l, p=i+1+d_{min}, \dots, i+1+d_{max}$ .  $\alpha, \beta > 0$  are the weight parameters for pheromone and heuristic information;  $\tau(i, x_i^j, x_{i+1}^p)$ , simply note as  $\tau_{ijp}$ , is the pheromone value between  $x_i^j \in v_i$  and  $x_{i+1}^p \in v_{i+1}$ ;  $\eta(x_{i+1}^l)$  is the heuristic information of  $x_{i+1}^l$ ;  $\max(x_{i+1}^l)$  is the maximum value in  $v_{i+1}$ ;  $\theta$  is the threshold for occlusion, refer to section 5.1.

- Definition of Exchanged Information

The images are shown in Fig.4 with Canny operator, the 26<sup>th</sup>, 30<sup>th</sup>, 37<sup>th</sup> row are marked as white solid line, dotted line, stippling line respectively. There are two edges named  $B, E$  as marked in Fig.4 (a), and  $\beta, \epsilon$  in Fig. 4 (b). The 26<sup>th</sup>, 30<sup>th</sup> scanlines pass through the  $B, E$  edge and the 37<sup>th</sup> doesn't. In the similarity matrix corresponding to the 26<sup>th</sup> scan line, if the  $B$  feature in left image matches with  $\beta$  in the right image, and so as the left  $E$  with the right  $\epsilon$  feature, then in the 30<sup>th</sup> similarity matrix, the same match should exist, while the phenomena do not exist

between the 30<sup>th</sup> and 37<sup>th</sup> similarity matrix. Clearly the relationship among sub-optimization relies on whether the scan lines share the same vertical edge. It means that there are some uncertain relationships among every sub task.

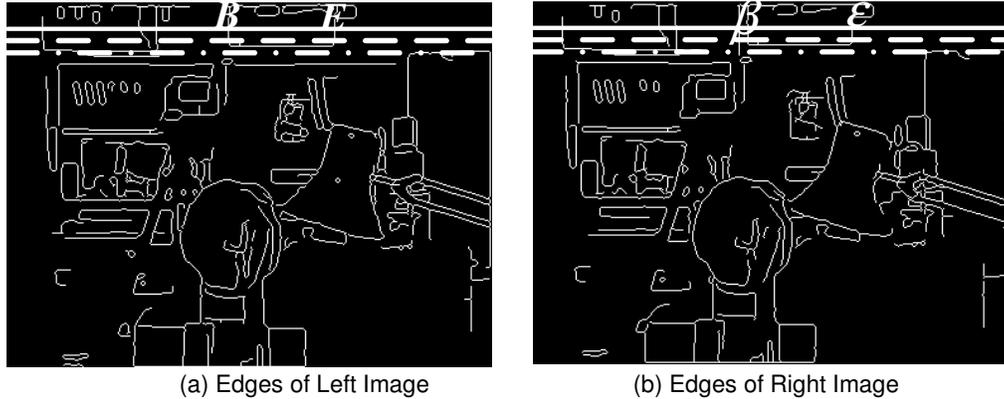


FIGURE 4: Edges Images

The master collects all solutions of every sub-task and votes to get the most probably matched vertical edge. In order to broadcast this possibly existed information to impact the process of the next iteration, the pheromone, corresponding to these voted edges, is selected as the exchange information between master and slavers. We know that the behavior of an ant is indirectly and possibly influenced by pheromone. The exchanged information (constructed pheromone) acts as a kind of soft GCPs indeed, avoiding the shortcomings of the hard one. **The second contribution of this paper is that the soft GCPs (pheromone) are used.**

In order that the optimization of the next generation can be induced by the master, the pheromone corresponding to the same edge decided by voting should be increased. Take the edge named  $B$  of left image for example, assume it crosses with the 11<sup>th</sup> to 40<sup>th</sup> scanlines, that is to say there are 30 features, among which there are 26 features matched with the same edge  $\beta$  of the right image. According to the big probability assumption,  $\beta$  edge of the right image should be the real matched edge with left  $B$ . In order to propagate this information, the pheromone matrix  $T_{\max}^k$  ( $k = 1, \dots, K$ ) is constructed in which the values corresponding to matched edge are  $\tau_{\max}$  and the others are 0. Take the 11<sup>th</sup>, 12<sup>th</sup> scan line for example, the 99<sup>th</sup>, 100<sup>th</sup> column crossed with  $B$  edge, the 119<sup>th</sup>, 120<sup>th</sup> column with  $\beta$ , That is to say the best matched pairs are (99<sup>th</sup>, 119<sup>th</sup>) and (100<sup>th</sup>, 120<sup>th</sup>). So in  $T_{\max}^{11}$ , all pheromone recording the connection with (99<sup>th</sup>, 119<sup>th</sup>) are  $\tau_{\max}$ , and the others are zero, as well as (100<sup>th</sup>, 120<sup>th</sup>) in  $T_{\max}^{12}$ . **The exchanged pheromone is re-constructed instead of directly getting from one of the best solutions of sub-task, which is the third discrimination with the past articles.**

- Pheromone Updating

Every isolated ant colony fulfilling every sub-task has its own pheromone updating strategy. While in MACO, the pheromone updating process consists of two parts, local and global updating. The local updating, the same as the single ACO, is done after every generation is finished, shown as Equation (2). The global updating, which reflects the influence of the master, is done after all colonies are finished, shown as Equation (3). That is to say that the pheromone of every colony must be influenced not only by itself but also the master when each iteration is finished.

The Local pheromone updating procedure can be described as follows after a generation is finished.

$$\forall(i, j, p) : \tau_{ijp}(n) \leftarrow (1 - \rho) \cdot \tau_{ijp}(n) \tag{2}$$

if  $J(R_a) < J(\hat{R})$  then  $\hat{R} \leftarrow R_a$

$$\forall(i, j, p) \in \hat{R} \tau_{ijp}(n+1) \leftarrow \tau_{ijp}(n) + \rho \cdot g(\hat{R})$$

where  $0 < \rho < 1$  is the evaporation rate;  $J(R_a)$  is the energy of path belonging to the  $a^{th}$  ant;  $\hat{R}$  is the best matched pairs at present; the boundary function  $g(\hat{R})$  returns the pheromone matrix corresponding to  $\hat{R}$ . Every element after update must obey  $0 < \tau_{\min} \leq \tau_{ijp}(n+1)$ .

The global pheromone updating procedure is executed in two phases, an evaporation phase where a fraction of the all sub-task's pheromone evaporates, and a reinforcement phase where the pheromone is increased corresponding to a better solution which the master thinks. Take the  $k^{th}$  colony for example, the update rule is:

$$\forall(i, j, p) : \tau_{ijp}(n) \leftarrow (1 - \mu) \cdot \tau_{ijp}(n) \tag{3}$$

$$\tau_{ijp}(n+1) = \tau_{ijp}(n) + \mu \cdot T_{\max}^k$$

Where  $k = 1, \dots, K$ ;  $0 < \mu < 1$  is the evaporation rate,  $\mu = 0$  means the new pheromone totally comes form the master, and  $\mu = 1$  means the new pheromone ignored the information form master; Every element must obey  $\tau_{\min} \leq \tau_{ijp}(n+1)$ . The new global updated pheromone works as the initial value of every sub-task, means one iteration is finished;  $T_{\max}^k$  is the reconstructed pheromone for the  $k^{th}$  colony by master.

### 3.2 Flow Chart

The flow chart of MACO is illustrated as Fig.5, the slavers and the master are marked as different shading respectively, where  $\tau_{jk}^0 = \tau_{\min}$  is the initial pheromone matrix to all sub-tasks. At the beginning, set  $T_{\max}^k = 0$ , firstly every sub-task gets initial pheromone matrix of this iteration according to Equation (3), and then the isolated colonies start its own optimization (inner loop), in which the local pheromone updating is done according to Equation (2) after every generation is finished. After all sub-tasks are finished, the master evaluates all solutions and constructs every  $T_{\max}^k$ , the outer loop starts again. This process is iterated until a stopping criterion is met.

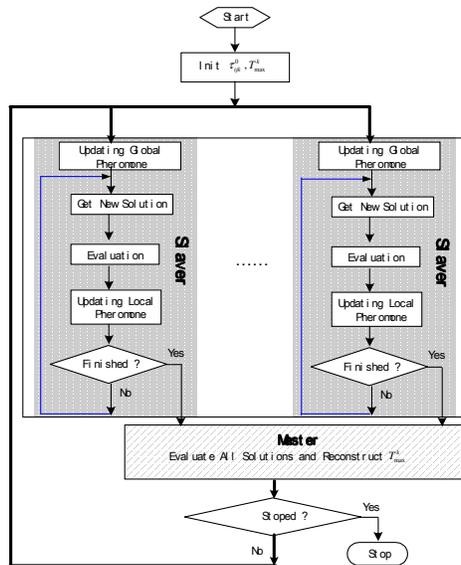


FIGURE 5: Flow Chart of MACO

## 4. CONVERGENCE PROOF

The convergence proof of single colony can refer to literature [29, 30, 31]. The MACO is based on the single colony, and with the help of mutual communication. The convergence has dealings with not only how every colony is defined but also how the information is interacted. Based on literature [33], the convergence proof of this paper is the following.

Set  $\tau_{ijp}(n)$  represent the pheromone after iterated  $n$  times,  $\hat{R}(n)$  represent the optimal path iterated  $n$  times later, and  $\hat{J}(n)$  be the energy function value. A stochastic process  $X(n) = \{\tau_{ijp}(n), \hat{R}(n), \hat{J}(n)\} (n = 1, \dots)$  is defined. It can be deduced that  $X(n)$  depends on new status and current status merely. Therefore,  $X(n)$  is an inhomogeneous Markov chain in discrete time.

**Lemma 1:** let  $T_0$  be the initial pheromone value of every sub-task. Supposing that pheromone evaporation coefficient obeys  $0 < \rho < 1$ , for arbitrary pheromone  $\tau_{ijp}$ , it holds  $\tau_{\min} \leq \lim_{x \rightarrow \infty} \tau_{ijp}(n) \leq (\rho+1) \cdot g(R^*)$ , where  $\tau_{\min}$  and  $(\rho+1) \cdot g(R^*)$  is the lower and upper bound of pheromone.

**Proof :**

Let  $R^*$  be the best matched pairs, after  $n$  generations the arbitrary  $\tau_{ijp}$  meets

$$\tau_{ijp}(n) \leq \left( \prod_{i=1}^n (1-\rho) \right) \cdot T_0 + \sum_{i=1}^{n-1} \left( \prod_{j=i+1}^n (1-\rho) \right) \cdot g(R^*)$$

When  $n \rightarrow \infty$ , we get

$$\lim_{n \rightarrow \infty} \tau_{ijp}(n) \leq \lim_{n \rightarrow \infty} \left[ \prod_{i=1}^n (1-\rho) \right] \cdot T_0 + \lim_{n \rightarrow \infty} \left[ \sum_{i=1}^{n-1} \left( \rho \prod_{j=i+1}^n (1-\rho) \right) \right] \cdot g(R^*)$$

The first factor is  $\lim_{n \rightarrow \infty} \left[ \prod_{i=1}^n (1-\rho) \right] = \lim_{n \rightarrow \infty} (1-\rho)^n = 0$

The second factor is  $\lim_{n \rightarrow \infty} \left[ \sum_{i=1}^{n-1} \left( \rho \prod_{j=i+1}^n (1-\rho) \right) + \rho \right] = \rho + \lim_{n \rightarrow \infty} \left[ \rho \sum_{i=1}^{n-1} (1-\rho)^{n-i} \right] = \rho + 1$ , then we have

$$\lim_{n \rightarrow \infty} \tau_{ijp}(n) \leq \tau_{\max} = (\rho+1) \cdot g(R^*)$$

Function  $g(x)$  has bound, so  $\tau_{ijp}$  is limited by  $(\rho+1) \cdot g(R^*)$  after  $n$  interactions.

Set the initial value of some elements  $\tau_{ijp}$  to be  $\tau_{\min}$ , and its value is not increased, after a generation although we have  $\tau_{ijp} = (1-\rho) \tau_{\min} < \tau_{\min}$ , actually it is obliged to lower bound  $\tau_{\min}$ .

Finally, we get  $\tau_{\min} \leq \tau_{ijp}(n) \leq (\rho+1) \cdot g(R^*)$ . □

**Lemma 2:** Set the initial value of every sub-task as the exchanged pheromone according to the master, for arbitrary pheromone  $\tau_{ijp}$ , it also holds  $\tau_{\min} \leq \lim_{x \rightarrow \infty} \tau_{ijp}(n) \leq (\rho+1) \cdot g(R^*)$

**Proof :**

At the end of generation optimization of sub-task, the arbitrary  $\tau_{ijp}$  meets  $\tau_{\min} \leq \lim_{x \rightarrow \infty} \tau_{ijp}(n) \leq (\rho+1) \cdot g(R^*)$ . Set the max value of pheromone from master is  $(\rho+1) \cdot g(R^*)$ , the initial value of next generation is the result according to Equation (3), after evaporation we get

$$\tau_{ijp}^{new}$$

$\tau_{\min} \leq \tau_{ijp}^{new} \leq (1-\mu) \cdot (\rho+1) \cdot g(R^*)$ , if the pheromone  $\tau_{\min}$  is enhanced, then it meets

$\tau_{\min} + \mu \cdot (\rho+1) \cdot g(R^*) \leq \tau_{ijp}^{new} \leq (1-\mu) \cdot (\rho+1) \cdot g(R^*) + \mu \cdot (\rho+1) \cdot g(R^*)$ , if the pheromone which is  $\tau_{\min}$  is not enhanced, then it meets

$$\tau_{\min} \leq \tau_{ijp}^{new} \leq (\rho+1) \cdot g(R^*)$$

Set  $\tau_{ijp}^{new}$  as initial value, according to **Lemma 1**, after  $n$  steps, arbitrary  $\tau_{ijp}$  holds  $\tau_{\min} \leq \lim_{x \rightarrow \infty} \tau_{ijp}(n) \leq (\rho+1) \cdot g(R^*)$ . That is to say the new initial value has the lower and upper bound. □

**Lemma 3:** Heuristic information  $\eta$  has a bound, that is,  $\eta_{\min} \leq \eta \leq \eta_{\max}$ .

**Proof :** According to the definition of heuristic information, firstly, the minimum value of  $\eta$  is above zero , and set the search windows to be  $R$  by  $T$ , then the maximum value of SAD is  $R \times T \times 255$ .  $\square$

**Theorem 1:** Set  $W \in Z^+$  , for an arbitrary  $n \geq W$  , if there exists  $\tau_{\min}(n) > 0$  to guarantee  $\tau_{ijp}(n) \geq \tau_{\min}(n) > 0$  , the inhomogeneous Markov process in discrete time  $X(n) = \{\tau_{ijp}(n), \hat{R}(n), \hat{J}(n)\}$  will be convergent at the optimal status  $(\tau_{ijp}[R^*], R^*, J^*)$  with probability one when  $n \rightarrow +\infty$  , where  $R^*$  represents the optimal path;  $J^*$  the minimal energy function value, and  $\tau_{ijp}[R^*]$  is defined as follows:

$$\tau_{ijp}|_{R^*} = \begin{cases} \tau_{\max} & (i, j, p) \in R^* \\ 0 & \text{others} \end{cases}$$

**Proof :** According to Equation (1), there exists  $p_{jp} = \frac{\tau(i, x_i^j, x_{i+1}^p)^\alpha \eta(x_{i+1}^p)^\beta}{\sum_{l \in x_{i+1}} \tau(i, x_i^j, x_{i+1}^l)^\alpha \cdot \eta(x_{i+1}^l)^\beta}$  . Set  $N = d_{\max} - d_{\min}$ .

According to lemma 1, lemma2, lemma3 and  $\tau_{ijp}(n) \geq \tau_{\min}(n) > 0$  , the following holds:

$$p_{jp}(n) \geq \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^\alpha \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^\beta$$

Then, the probability of an artificial ant producing a solution (including the optimal solution  $R^*$  ) after  $n$  steps iterations is  $\hat{p} \geq \hat{p}_{\min}^M = \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^{M \cdot \alpha} \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^{M \cdot \beta} > 0$  , where  $M < +\infty$  is the maximal length of the sequence. The minimal probability of Markov chain  $X_n$  being convergent at the optimal solution  $X_n^*$  after  $n$  steps iterations can be given by [11]:

$$\hat{P}^*(n) = 1 - (1 - \hat{p})^n \geq 1 - \left( 1 - \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^{M \cdot \alpha} \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^{M \cdot \beta} \right)^n$$

When  $n \rightarrow +\infty$  , considering the second term of  $\hat{P}^*(n)$  ,  $\left( 1 - \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^{M \cdot \alpha} \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^{M \cdot \beta} \right)^n$  and taking the

logarithm and limit of this product we obtain

$$\begin{aligned} & \lim_{n \rightarrow \infty} \log \left( 1 - \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^{M \cdot \alpha} \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^{M \cdot \beta} \right)^n \\ &= \sum_{n=W}^{\infty} \log \left( 1 - \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^{M \cdot \alpha} \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^{M \cdot \beta} \right) \\ &\leq - \sum_{n=W}^{\infty} \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^{M \cdot \alpha} \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^{M \cdot \beta} = -\infty \end{aligned}$$

Therefore,  $\lim_{n \rightarrow \infty} \left( 1 - \left( \frac{\tau_{\min}(n)}{N \cdot \tau_{\max}} \right)^{M \cdot \alpha} \cdot \left( \frac{\eta_{\min}}{\eta_{\max}} \right)^{M \cdot \beta} \right)^n = 0$  . Then  $\lim_{n \rightarrow \infty} \hat{P}^*(n) = 1$  , that is, when  $n \rightarrow +\infty$  ,  $X_n$  will be

convergent at the optimal status  $(\tau_{ijp}[R^*], R^*, J^*)$  with probability one.  $\square$

**Reasoning 1.** For every colony of multi colonies, after information exchange, in the worst case, the probability of finding the best solution is bigger than that of the single colony.

**Proof :** Due to the pheromone and heuristic information limits  $\tau_{\min}$  ,  $\tau_{\max}$  ,  $\eta_{\min}$  ,  $\eta_{\max}$  , and set  $N = d_{\max} - d_{\min}$ . A trivial lower bound<sup>[29]</sup> can be given as

$$p_{\min} \geq p_0 = \frac{\tau_{\min}^\alpha \eta_{\min}^\beta}{(N-1)\tau_{\max}^\alpha \eta_{\max}^\beta + \tau_{\min}^\alpha \eta_{\min}^\beta}$$

For the derivation of this bound we consider the following “worst case” situation: the pheromone trail associated with the desired decision is  $\tau_{\min}, \eta_{\min}$ , while all the other feasible choices (there are at most  $N - 1$ ) have an associated pheromone trail of  $\tau_{\max}, \eta_{\max}$ .

When the pheromone is updated by the master, in “worst case”, the elements whose value is  $\tau_{\max}$  is increased, according to the Equation (1), a new lower bound can be given as

$$p'_{\min} \geq p'_0 = \frac{\tau_{\min}^{\alpha} \eta_{\min}^{\beta}}{(1-\mu)(N-2)(\tau_{\max})^{\alpha} \eta_{\max}^{\beta} + ((1-\mu)\tau_{\max} + u\tau_{\max})^{\alpha} \eta_{\max}^{\beta} + \tau_{\min}^{\alpha} \eta_{\min}^{\beta}}$$

The denominator of  $p'_0$  is

$$\begin{aligned} & (1-\mu)(N-2)(\tau_{\max})^{\alpha} \eta_{\max}^{\beta} + ((1-\mu)\tau_{\max} + u\tau_{\max})^{\alpha} \eta_{\max}^{\beta} + \tau_{\min}^{\alpha} \eta_{\min}^{\beta} \\ & = (1-\mu)(N-2)(\tau_{\max})^{\alpha} \eta_{\max}^{\beta} + \tau_{\max}^{\alpha} \eta_{\max}^{\beta} + \tau_{\min}^{\alpha} \eta_{\min}^{\beta} \end{aligned}$$

Clearly, it is smaller than the denominator of  $p_0$ . That is to say the probability of finding best solution is bigger than the single colony. □

**Reasoning 2.** The colony in MACO can find better solutions after information exchanged.

**Proof:** Heuristic information is unchanged with iteration. In order to simplify the description, and don not lose generality, set  $\eta(x_{i+1}^p) = 1$ , in the  $i^{th}$  colony, the pheromone of the  $j^{th}$  and  $p^{th}$  feature is  $\tau(i, x_i^j, x_{i+1}^p) = \tau_m$ , and they are true match pair. In current generation, the actual matched feature is the  $j^{th}$  and  $s^{th}$  feature, its corresponding pheromone is  $\tau(i, x_i^j, x_{i+1}^s) = t'_{\max} > \tau_m, v \neq p$ , then the probability of selecting the  $p^{th}$  feature is

$$p_{jp} = \frac{\tau_m^{\alpha}}{sum + t'_{\max}{}^{\alpha} + \tau_m^{\alpha}}, \text{ where } sum \text{ is the summary of pheromone of the others } d_{\max} - d_{\min} - 2.$$

After voting, suppose the master thinks the  $j^{th}$  feature should be matched with  $s^{th}$  feature, then its will increase the pheromone being  $\tau(i, x_i^j, x_{i+1}^p) = (1-\mu) \cdot \tau_m + \mu \cdot \tau_{\max}$ , then the probability of selecting  $p^{th}$  feature is

$$\begin{aligned} p'_{jp} &= \frac{((1-\mu)\tau_m + \mu t_{\max})^{\alpha}}{(1-\mu)^{\alpha}(sum) + (1-\mu)^{\alpha} t'_{\max}{}^{\alpha} + ((1-\mu)\tau_m + \mu t_{\max})^{\alpha}}, \text{ simplify the equation, we get} \\ p'_{jp} &= \frac{(\tau_m + (1/(1-\mu) - 1)t_{\max})^{\alpha}}{sum + t'_{\max}{}^{\alpha} + (\tau_m + (1/(1-\mu) - 1)t_{\max})^{\alpha}}, \text{ because } (\tau_m + (1/(1-\mu) - 1)t_{\max})^{\alpha} > \tau_m^{\alpha} \text{ and} \\ & sum + t'_{\max}{}^{\alpha} > 0, \text{ so } p'_{jp} > p_{jp}. \end{aligned}$$

The probability is bigger after master influenced, that is to say the colony in MACO can find better solutions after information exchanged. □

Every sub-optimization is a not-convex and the total optimization target is consistent, the master broadcasts the better pheromone to induce the optimizing process of every sub-task. Every sub-task is convergent, so the algorithm proposed in this paper can find the global best solution with probability one.

## 5. SIMULATION

### 5.1 Optimization Target

Given energy function, the proposed algorithm can be used to find the best match in every  $\Omega$  space. Just as what's said above, every sub-task finishes optimization according to its own energy function and master's guidance, and the master gathers all solutions from sub-tasks and evaluates them to get exchanged information. The local and global energy functions are defined in this section.

The function must have the following two traits. Firstly, because of the change of viewpoint, some features in left image cannot match with any one in right image, so the occlusion should also be considered. If the maximum similarity with  $n^{th}$  feature is  $\theta'$  and  $\theta'$  is smaller than threshold  $\theta$ , then we can conclude that the counter feature with  $n^{th}$  is occluded. Secondly, the ordering and

uniqueness constraint are all ignored during the optimization procedure. So there is a special phenomenon that one feature of left image may be matched with many features of right image, called collision in this paper and it must be forbidden.

Suppose there are  $N$  features on  $k^{th}$  ( $k=1...K$ ) line of left image and  $M$  features on  $k^{th}$  line of right image. Because of occlusion and collision, there are  $L$  real matches. Refer to literature [2], local energy function for the  $k^{th}$  sub-task is defined as Equation (4).

$$\min J_k = - \left( \sum_{i=1}^L D(x_i^j) - k_{occ} N_{occ} - k_{coll} N_{coll} \right) \tag{4}$$

where  $x_i^j \in R^*$ ,  $R^*$  represent the best path;  $N_{occ}$  is the number of occlusion;  $k_{occ}$  is the penalty coefficient of occlusion;  $N_{coll}$  is the number of collision;  $k_{coll}$  is the penalty coefficient of collision; function  $D$  is the similarity of SAD. It is clear such definition is to encourage more match and punish the unmatched and the collided case.

The vertical edge is discretized by every sub-task. Based on large probability, most of features matched with discretized point of left edge will lie on the same edge of right image. After voting the corresponding edges are decided, the pheromone is reconstructed according to the voting results. The target of master is to get the most consistent voting results. Set  $L_i > R_i$ , the energy function for the master is:

$$\min J_{global} = \frac{1}{N} \sum_{i=1}^N \left( \frac{L_i - R_i}{L_i} \right) \tag{5}$$

where,  $N$  is the number of vertical edges of left image;  $L_i$  is the length of  $i^{th}$  edge in left image;  $R_i$  is the quantity of matched features in right edge which corresponds to the  $i^{th}$  left edge after voting.

### 5.2 Depth Restoration

The MACO is implemented by the multi-thread technology on PC. The resources are limited, so the quantity of sub-groups is limited. Set 10 colonies in a group (the maximum length of  $L_i$  is 10), 5 ants in every colony, information exchange every 10 generation. When  $J_{global}$  is smaller than 0.2 the whole optimization procedure is stopped. The matching primitive is the intensity and window size of the SAD is  $9 \times 9$ .

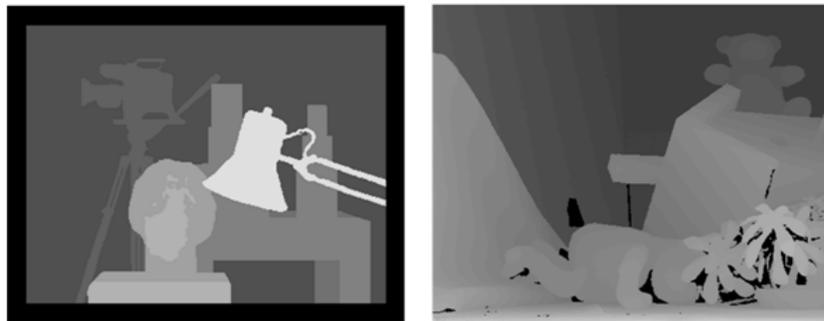
$\alpha$	$\beta$	$\rho$	$k_{occ}$	$k_{coll}$	$\mu$	$\theta$
2	0.5	0.6	1	1	0.6	0.2

TABLE 1: Parameters for depth Restoration

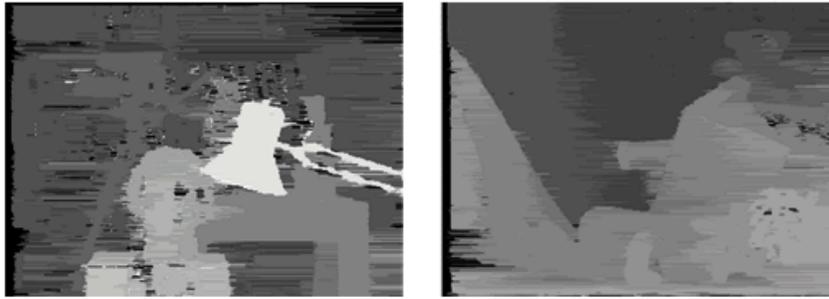
To obey the ordering and uniqueness constraint, after the whole procedure is finished, such constraints is obliged to the final results.

Because of the exhaustive parallelism (there are no any constraints among sub task optimization but minimum & maximum parallax restraint), the start point can be at arbitrary  $n^{th}$  feature (if the ordering or uniqueness constraints are exerted, such merits will no longer exist). So during the sub-task, the start position can be variable at every generation, this manner can eliminate the collision.

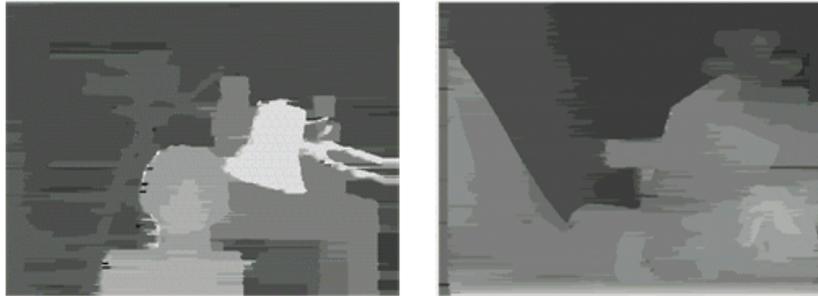
In Fig.6, the tests and comparisons are shown. Clearly, the result is better than DP, but there are big step to improve.



a) True Depth Map of Tsukuba、Teddy



b) Results of DP



c) Results of this paper

**FIGURE 6:** the Results of Depth Map

## 6. CONCLUSIONS

This paper presented a parallel, iterative and feedback MACO method for stereo matching. In this method the slaver optimizes every sub-task, which is the target to find the best matchers along every scan-line. During the iterative process, the master gathers and analyzes the results from sub-groups the results, decides the matched edge based on voting, and then reconstructs the pheromone corresponding to the matched edges, feeds the pheromone field back to the sub-task. Each sub-optimization problem starts a new matching process under the reconstructed pheromones until the stopping criterion is met. The proposed method has two outstanding merits. Firstly, this method makes full use of the matching problem of parallelism, that each relatively independent sub-task can be solved in parallel. Secondly, also makes full use of a posteriori information. Besides, the reconstructed pheromones which reflects the result of voting plays the role of soft GCPs, avoiding the misleading of hard GCPs, theory and experiments show that this idea is better than the dynamic programming algorithm with hard GCPs. The convergence proof of the proposed method gives the strong support for its application. Finally, there are problems, such as the efficiency, parameter tuning and other issues should be resolved.

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