An Automated Tracking Algorithm for Quantitative Group Behavior Studies

Haishan Wu
School of Computer Science, Fudan University
Zhangheng Road. Shanghai, P. R. China
hswu@fudan.edu.cn
+86-159 0092 2460

ABSTRACT
In this paper, we present an automated algorithm for tracking large groups of targets. To quantitatively investigate the behaviors in group context, it is vital to measure the motion trajectories of each target. This is task is challenging because large numbers of interacting targets lead to frequent occlusions. The proposed method first automatically detects the targets from video sequences, and then tracks the detections vial solving a global optimization problem. Several parameters of the proposed method can be determined automatically. Using this approach, we successfully measured the motion trajectories of large numbers of *Mycoplasma mobile*, which may facilitate the biologist to explore their gliding behavior in group context.

Author Keywords
Group behavior, multi-target tracking.

INTRODUCTION
Behavior of organism groups, such as human crowds, insect swarms and bacterial groups, is a fascinating natural phenomenon. Quantitative investigation of such behavior may lead new insights to the underlying interaction mechanism. Tracking a group of targets by human visual inspection is obviously very laborious and tedious, and thus developing an automated algorithm for measuring individual motion trajectories will be of great value.

With one video camera, target tracking involves two steps: target detection in each frame and detection association in consecutive frames. Most current tracking approaches [1] are used to track single or several targets. When handling large numbers of targets in a group, frequent occlusions in video sequences will result in challenges in both object detection and identity association. Recently, several approaches were proposed to track different organism groups [2][3][4]. The main drawbacks of these methods are

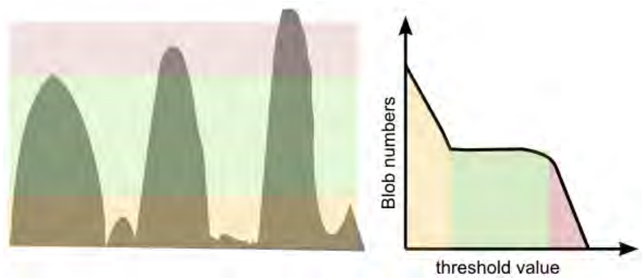

Figure 1. Threshold selection.

that their performances were highly dependent on the parameter selections, most of which should be determined empirically.

In this paper, we present an automated tracking algorithm for quantitative group behavior studies. It is able to detect the targets with occlusions automatically by utilizing the statistical information of detected blobs. It then associates the detections across frames by solving a linear assignment problem, which is designed to handle the occlusions and solved efficiently by using Hungarian algorithm.

METHODS
Taking the video sequences as input, we first removed the background in each frame, which was estimated as the time average of the whole sequences. We then segmented the targets by a global threshold, which was chosen automatically in the following way: we first found the smallest and largest pixel values in each frame, which were denoted by p_s, and p_l, respectively; then the threshold was then chose from [p_s, p_l], and the numbers of the detected blobs were counted. As shown in Figure 1, the numbers of detected blobs decreases when the threshold is too large, and too small threshold will lead to large numbers of blobs, because many of them are tiny pieces. The numbers of detected blobs are almost unchanged if the threshold is proper. Such threshold is selected to segment the targets from backgrounds.

We then associated the detections between two successive frames. We formulated this problem as a linear assignment problem, which was solved by minimizing the assignment costs. Let $C(i,j)$ be the cost by assigning the *i-th* detection in *t* frame to the *j-th* detection in *t+1* frame. We used the Euclidean distances between them to define the cost matrix *C*, then the optimal assignment matrix A was obtained by solving the following optimization problem:

$$A = \arg\min \sum_{i=1}^{N_i} \sum_{j=1}^{N_j} C(i,j)A(i,j)$$

$$subject\ \ to\ \ \sum_{i=1}^{Ni} A(i,j) = 1\ , \sum_{j=1}^{N_j} A(i,j) = 1$$

A is a binary matrix with entries 1 (association) and 0 (otherwise)[4]; N_t and N_{t+1} are the detection numbers in *t* and *t+1 th* frame. Generally, $N_t \neq N_{t+1}$ because of occlusions and false positive detections *et.*, and therefore one detection in current frame might not be assigned to one detection in the next frame. We overcame this difficulty by the following way: for any detection without assignment, its position in next frame was predicted by the velocity in current frame, which were regarded as a new detection, and the corresponding track was labeled as prediction status. If a track remained prediction status for several frames (5 to10 in our experiment) would be terminated. Experiment results demonstrated that this method could result in more complete and accurate tracks.

RESULTS

The gliding behavior of *Mycoplasma mobile* has attracted the attention of many biologists [5][6]. With a video of 700 frames, we here applied our method to measure the motion trajectories of a large group of *Mycoplasma mobile* comprising nearly one hundred individuals. The results were shown in Figure 2 and Figure.3.

CONCLUSION

We presented an automated method for measuring the motion trajectories of organism groups. This method is general-purpose and thus applicable to other tracking tasks, such as moving locust groups [7]. One future work is developing machine learning methods to mine the acquired data.

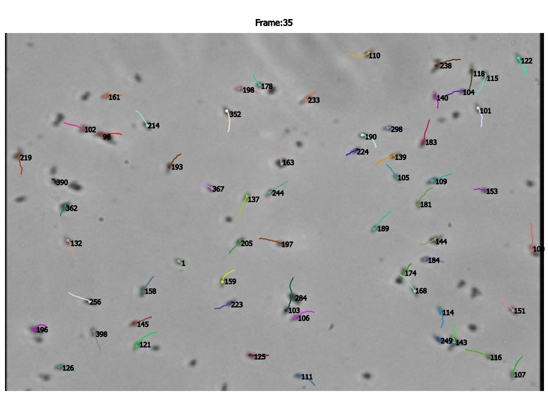

Figure 2. Tracking large number of *Mycoplasma mobile.* Round dots denote the detected positions in current frame.

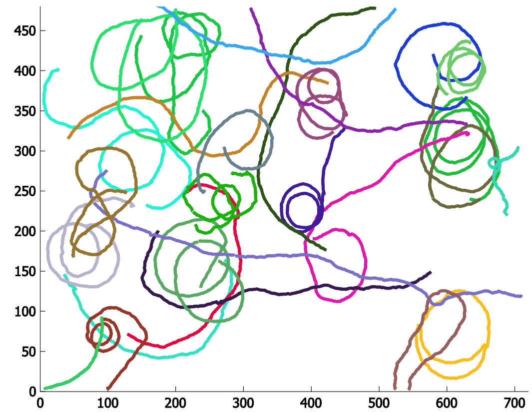

Figure 3. Twenty-four acquired trajectories with lengths longer than 300 frames are shown. Different colors represent different individuals.

REFERENCES

1. Yilmaz, A., Javed, O., Shah, M., Object tracking: A survey. *ACM Computing Surveys*, *38*, 4 (2006).
2. Betke, M., Hirsh, D.E., Bagchi, A., Hristov, N.I., Makris, N.C., Kunz, T.H., Tracking Large Variable Numbers of Objects in Clutter, In *IEEE Proc. ICCV 2007.*
3. Branson, K., Robie, A., Bender, J., Perona, P., Dickinson, M. High-throughput ethomics in large groups of *Drosophila*. *Nature Methods*, *6*, 6 (2009), 451-457.
4. Jaqaman K, Loerke D, Mettlen M, Kuwata H, Grinstein S, Schmid SL, Danuser G. Robust single-particle tracking in live-cell time-lapse sequences. *Nature Methods*, *5*, 8 (2008), 695-702.
5. Uenoyama, A. and Miyata, M.. Gliding ghosts of *Mycoplasma mobile*. *PNAS*, *102*, 36 (2005), 12754-12758
6. Jaffe, J.D. and Miyata, M. and Berg, H.C., Energetics of gliding motility in *Mycoplasma mobile*. *Journal of bacteriology*, *186*, 13 (2004).
7. Buhl, J., Sumpter, D. J. T., Couzin, I. D., Hale, J. J., Despland, E., Miller, E. R., & Simpson, S. J.. From disorder to order in marching locusts. *Science*, *312*, 5778 (2006), 1402-1406.