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Learning to rank biological motion trajectories ☆

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ABSTRACT

Many feature transforms have been proposed for the problem of trajectory matching. These methods, which are often based on shape matching, tend to perform poorly for biological trajectories, such as cell motion, because similar biological behavior often results in dissimilar trajectory shape. Additionally, the criteria used for similarity may differ depending on the user's particular interest or the specific query behavior. We present a rank-based distance metric learning method that combines user input and a new set of biologically-motivated features for biological trajectory matching. We show that, with a small amount of user effort, this method outperforms existing trajectory methods. On an information retrieval task using real world data, our method outperforms recent, related methods by ~9%.

1. Introduction

While it is generally accepted that the motion of cells can be affected by environmental factors, such as the presence of tumors, inflammation within blood vessels, and various types of treatments, the specific factors that influence particular cell types are not yet fully understood. For example, the subset of T lymphocytes known as natural killer T (NKT) cells are known to be important for inflammation and disease response within the liver and have the ability to destroy various foreign objects, including tumor cells [1]. However, the underlying signals responsible for NKT cells to change direction and speed are still largely unknown. One method of investigation is to analyze cell trajectories from *in vivo* microscopy imagery. Automatic cell detection and tracking algorithms (e.g., [2,3]) have advanced to the point of reliability to become commercially available, and the once-manual process of accumulating vast numbers of cell trajectories from video has been greatly simplified. Statistics collected from these cell trajectories provide data for initial efforts towards high-level cell motion behavior analysis. Current approaches include estimating, for example, the number of cells tracked, percent of moving cells, and velocity characteristics [4]. However, these metrics may be insufficient for discriminating between biologically important behaviors. Consider the four primary behaviors displayed by cells (depicted in Fig. 1):

- *Sentinel*. This is the most common behavior, also known as sentry or patrolling [1]. The cell appears to move randomly and will often change direction without an apparent destination. This lack of directed motion indicates that no chemical signals have been detected.
- *Directed*. The cell moves continuously through a single sinusoid, presumably towards a detected signal. Depending on the surrounding vasculature, the cell may appear to zig-zag through multiple sinusoids attempting to reach the location of the signal.
- *Tumbling*. The cell moves through a sinusoid, stops, and reverses direction, potentially multiple times in succession. One theory is that tumbling cells have moved past the location of a detected signal and are returning. This may occur if the signal is weak or attached to another cell.
- *Stopped*. The cell remains motionless for a long period of time, usually adhering to the wall of a blood vessel. Cells generally do not stop within sinusoids; it is believed that stopped cells are responding to chemical signals.

The motion pattern of a cell, or more interestingly, the change in behavior under a new influence, may give insight into the environmental factors that affect cell behavior. A deep understanding of cell responses in different conditions could lead to better treatments for diseases or tumors. Experiments for understanding cell motion behavior have moved beyond the simple velocity metrics and towards comparing trajectories from cells under different conditions. Manually searching through databases of cell trajectories to detect patterns is impractical, so methods from automated trajectory matching have been applied to this problem.

Trajectory matching methods are popular in a number of domains, particularly surveillance and sketch recognition. Generally, the approach is to devise a trajectory-based distance metric to be either used for clustering or direct similarity comparisons. A variety of approaches have been proposed [5]. For example, Bashir et al. [6] described each trajectory by a sequence of sub-trajectories, where each sub-trajectory was represented by the coefficients obtained from principal component analysis (PCA). The PCA components were used with spectral clustering to group trajectories, and matching was

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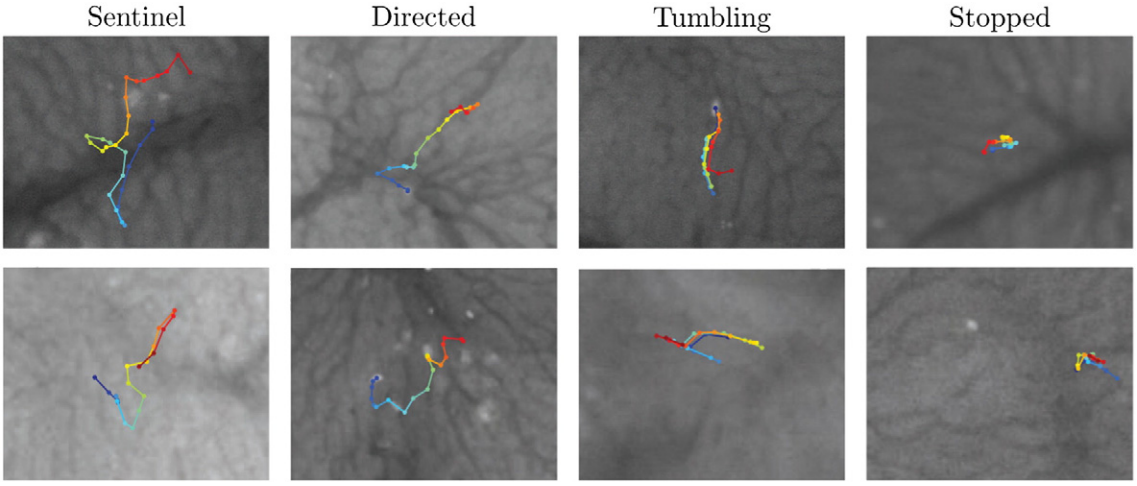

Fig. 1. Each column shows two examples of the primary cell motion behaviors. Color indicates start (blue) and end (red) of motion. Trajectories which display similar biological behavior may appear visually dissimilar.

performed through a combination of clustering and string matching. Another method [7] uses histograms to model the directional probability of a trajectory and perform a coarse clustering; point-to-point distances were used for finer matching. Anjum and Cavallaro [8] cluster trajectories in multiple feature spaces and fuse the clusters from each feature space to obtain a higher-level final clustering. Separate from clustering, some approaches focus on a similarity measure between trajectories. Vlachos et al. [9] transformed the trajectories into a rotation-, translation-, and scale-invariant space for handwriting recognition. Jiang et al. [10] modeled each trajectory as a Hidden Markov Model and used the Bayesian information criterion as a dissimilarity measure. Hsieh et al. [11] modeled trajectories as both a syntactic string representation and Bézier curve approximation and compared instances using a combination of the edit distance between string representations and the point-to-point distance between the longest common subsequence of the Bézier curves.

The variety of approaches highlights both the importance and difficulty of the problem of trajectory matching. One aspect in common among all these approaches is the focus on trajectory shape. Trajectory matching for cells is complicated by the fact that two cells that exhibit similar biological behavior do not necessarily display similar trajectory shapes. For example, consider the examples of the "Sentinel" motion shown in Fig. 1. An expert in cell motion analysis would visually identify these as similar patterns, even though, in isolation, the trajectory shapes are quite dissimilar. We demonstrate that shape-centric methods fail to identify this type of similarity.

In this work, we address this problem by: (1) developing a set of basic features motivated by cell behavior and (2) leveraging user input for distance metric learning on trajectories. A typical motion analysis task includes finding semantically similar trajectories given a database of trajectories and a query. With our approach, the database of trajectories are represented using biologically-motivated features and the analyst encodes his knowledge by rating a small number of examples from the database. From this input, we derive a distance metric over the set of trajectories and present the database items sorted by relevance. This rank-based learning method follows the approach previously applied to other information retrieval tasks, such as web page ranking, or, in the biomedical domain, eye cataract grading from images [12]. In Section 2, we describe a set of biologically-motivated features, and in Section 3 we describe how these features are incorporated into a learning framework for trajectory matching. In Section 4, we show results on a trajectory matching problem using NKT cell data, and, in Section 5, show how these results can be used to inform further biological experiments.

2. Biological trajectory features

Given a trajectory $T=\{p_0, p_1, \ldots, p_{n_T-1}\}$ generated from some process, such as automated cell tracking, where each $p_i=\langle x_i, y_i\rangle$ is one of n_T temporally-sequential points in image coordinates, we transform T into a feature space which incorporates both speed and shape. Trajectory shape is described in both local and global terms. The local shape features describe changes of direction throughout the trajectory with a set of syntactic symbols. The global shape features captures the overall scope of the trajectory.

2.1. Local shape

Similar to the approach of Hsieh et al. [11], a trajectory T is represented by a subset of points, Q_T, having high curvature or significant directional changes, called *control points*. For each point $p \in T$, curve angle, $\alpha(p)$ is calculated as follows:

$$\alpha(p) = cos^{-1}\frac{||p-p^+||^2 + ||p-p^-||^2 - ||p^-,p^+||^2}{2||p-p^-||||p-p^+||} \quad (1)$$

where p^- and p^+ refer to points (temporally) before and after p, respectively. These points are selected to meet the criteria $d_{min} \le \|p-p^-\| \le d_{max}$ and $d_{min} \le \|p-p^+\| \le d_{max}$. To improve the local curve angle estimates, d_{min} and d_{max} are selected to balance the effect of noisy point locations with an accurate estimate of the local curve angle. We set d_{min} and d_{max} to $|T|/20$ and $|T|/15$ respectively. Points in T which satisfy $\alpha(p) \le T_\alpha$ are candidates for Q_T. We follow [11] and set $T_\alpha = 150^\circ$. To reduce redundant shape information within Q_T, control points are required to be at least d_{min} apart. If two points are closer than d_{min}, the point with the smaller curvature (higher $\alpha(p)$) is removed from Q_T. Finally, the first and last points in T, p_0 and p_{n_T-1}, are included in Q_T.

Next, a syntactic label is given to each point in Q_T that incorporates both curve angle and curve direction. For each point p and its neighboring points q_p^- and q_p^+, sequentially before and after, respectively, in Q_T, we calculate the curve direction at p based on the vectors $\mathbf{q_p^-}\,\mathbf{p}$ and $\mathbf{q_p^-}\,\mathbf{q_p^+}$:

$$\theta(p) = \begin{cases} \text{clockwise}, & \text{if } \mathbf{q_p^-}\,\mathbf{p} \otimes \mathbf{q_p^-}\,\mathbf{q_p^+} > 0 \\ \text{counterclockwise}, & \text{otherwise} \end{cases} \quad (2)$$

where $\otimes$ denotes the cross product of the vectors. Additionally, for each p in Q_T, we calculate the angle $\alpha(p)$ using Eq. (1) replacing p^- and p^+