A Framework for Multiscale Comparison of Three-dimensional Trajectories Based on the Maxima on Curvature Scale Space

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Abstract

In this poster we present a multiscale comparison method for three-dimensional trajectories. In order to deal with the problem that zero-crossings of curvature cannot be determined for space curve, we focused on the maxima of curvature. In experiments we demonstrate that reasonable correspondences were obtained on the simple but noisy trajectories.

Keywords:

Multivariate time series, Multiscale analysis, Trajectory mining.

Introduction

This poster presents a multiscale comparison method for three-dimensional trajectories. We propose to use the maxima of curvature instead of zero-crossings (inflection points) for splitting a trajectory into subtrajectories (segments), so that a segment-based multiscale matching scheme can be applied for 3D trajectories whose curvature is by nature signless.

Methods

Let us denote by $c(t) = \{x(t), y(t), z(t)\}$ a 3D trajectory composed of three time series $x(t)$, $y(t)$ and $z(t)$. The trajectory at scale σ, denoted by $C(t, \sigma)=\{X(t, \sigma), Y(t, \sigma), Z(t, \sigma)\}$, can be obtained by the discrete convolution of $x(t)$ and the modified Bessel function $In(\sigma)$ of order n as follows [1].

$$X(t,\sigma) = \sum_{n=-\infty}^{+\infty} e^{-\sigma} In(\sigma) \cdot x(t-n)$$

Similar treatment applies to $Y(t, \sigma)$ and $Z(t, \sigma)$. By changing σ, we can represent $c(t)$ at various observation scales.

Next, we split $C(t, \sigma)$ into segments based on the places of curvature maxima. Due to smoothing, the number of maxima monotonically decrease when scale increases. Maxima are successively linked from the top scale to bottom scale based on the minimal distance criterion to trace segment hierarchy.

After that, the best set of segment pairs that satisfies both of the following conditions are searched over all scales: (1) By concatenating all segments, the original trajectory must be completely formed without any gaps or overlaps. (2) The sum of segment dissimilarities over all segment pairs are minimized. We define the dissimilarity between two segments as follows.

$$d(a_m^{(k)}, b_n^{(h)}) = \left|v(a_m^{(k)})\right|\left|v(b_n^{(h)})\right| \times \cos dist(v(a_m^{(k)}), v(b_n^{(h)})) \\ + \gamma \{\cos t(a_m^{(k)}) + \cos t(b_n^{(h)})\}$$

where $a_m^{(k)}$ denotes the m-th segment at scale k of trajectory A, $b_n^{(h)}$ denotes the n-th segment at scale h of trajectory B, $v(a_m^{(k)})$ denotes a 3D vector connecting both ends of $a_m^{(k)}$, cosdist() denotes the cosine distance between two vectors, and cost() denotes a cost function for merge of segments.

Results

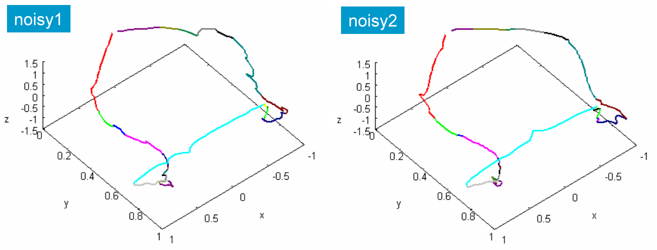

Figure 1-Noise trajectories

We generated two noisy trajectories by adding Gaussian noise to a 3D synthetic curve. Figure 1 shows their matching results, where matched segments are represented in the same color. We could confirm that their structural similarity was successfully captured in a global scale if there existed local differences at fine scales caused by noise.

Conclusions

We have presented a multiscale comparison method for 3D trajectories. Future work include quantitative evaluation of the performance and application to the real medical data.

This work is supported in part by the Grant-in-Aid for Young Scientists (B) (#20700140) by MEXT, Japan.

References

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