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Analysis of human motion variation patterns using UMPCA

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ABSTRACT

The rapid development of motion capture technologies has greatly increased the use of human motion data in many applications. This has increased the demand to have an effective means to systematically analyze those massive data in order to understand human motion variation patterns. This paper studies one typical type of motion data, which are recorded as multi-stream trajectories of human joints. Such a high dimensional multi-stream data structure makes it difficult to directly perform visual comparisons or simply apply conventional methods such as PCA to capture the variation of human motion patterns. In this paper, a high order array (tensor) is suggested for data representation, based on which the Uncorrelated Multilinear Principal Component Analysis (UMPCA) is applied to analyze the variation of human motion patterns. A simulation study is presented to show the superiority of UMPCA over PCA in preserving the cross-correlation among multi-stream trajectories. The effectiveness of UMPCA is also demonstrated using a case study for analyzing vehicle ingress test data.

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1. Introduction

In recent years, increasing interest in the analysis of human motion data has been driven by a wide range of applications in different fields. In the athletics field, for example, Li et al. (2006) presented a multistep algorithm to automatically detect and recognize athletes' sporting actions in a long video with a dynamic background. Knudson (2013) introduced the concept of Qualitative Movement Diagnosis (QMD) to improve athletes' performance and reduce their risk of injury by visually observing video recordings of their motion. In the medical field, gait analysis, which uses motion data to analyze patients' walking patterns, is used to assist doctors' clinical diagnosis and treatment decisions. For example, Kay et al. (2000) discussed the impact of postoperative gait analysis on the assessment of treatment outcomes and planning on-going care. In the automotive industry, Masoud et al. (2016) presented a systematic framework for using human ingress motion trajectories to predict customers' ingress discomfort ratings for improving vehicle design. Although these applications may have different objectives in terms of the usage of motion data, some common questions are often encountered during data analysis. For example, what are the

typical motion variation patterns among different participants? Which time segments in a long video would be related to motion patterns of interest? Which particular joints and moving directions will reflect a normal or abnormal motion pattern of interest? The main goal of this paper is to use a systematic way to provide reasonable answers for these sorts of questions. In other words, analyzing human motion variation patterns in the ingress motion means to find the joints, motion directions (X, Y and Z) and time segments that suggest the highest variability among all subjects performing the ingress motion. A noteworthy point is that variability in this context is defined among different subjects performing the ingress motion. Furthermore, it is important to capture the cross-correlation structure among the joints in order to have more thorough understanding of the motion's mechanism, which is studied in detail in Section 3.

There are various ways to analyze human motion variation patterns. One simple way to analyze motion patterns of tested subjects is to replay the recorded motion videos multiple times and use visual comparison. In Cook et al. (2003), for instance, gait analysis experts visually compared 3D joint motion trajectories of patients having cerebral palsy to the "normal" motion trajectories to assess patients' need for surgery. This approach is effective in the existence of simple motions where the observer knows what type of pattern they are looking for (i.e. the walking motion of an unhealthy individual compared to that of a healthy one). However, in many other applications, such as vehicle ingress, the motion data is

much more complex. The ingress motion data involves multiple joints moving in a 3D space. As shown in Fig. 1(a), the ingress motion data of one subject are recorded for numerous joints such as ankles, elbows, back vertebrae etc., where the location of each joint over time in 3D moving directions is referred to as a joint trajectory, as shown in Fig. 1(b). In this paper, the trajectories of these multiple joints are referred to as multi-stream trajectory data. Considering such a high dimensional data, it is extremely cumbersome, if even possible, to extract the motion patterns among different subjects by visually comparing the recorded motion videos of individual subjects. Consequently, the conclusions regarding motion patterns via visual comparison could be highly subjective. Therefore, having an effective methodology to automatically analyze motion variation patterns is critically needed for reducing tedious data exploration efforts and avoiding subjective bias.

Principal Component Analysis (PCA) is a commonly used method for analyzing variation patterns. If the analysis of motion data is based on a single trajectory, PCA can be applied directly. For example, the motion data of the right ankle joint trajectory shown in Fig. 1(b) can be represented by a matrix, where each row vector represents the right ankle joint trajectory of one participant, and the number of rows represents the number of tested participants.
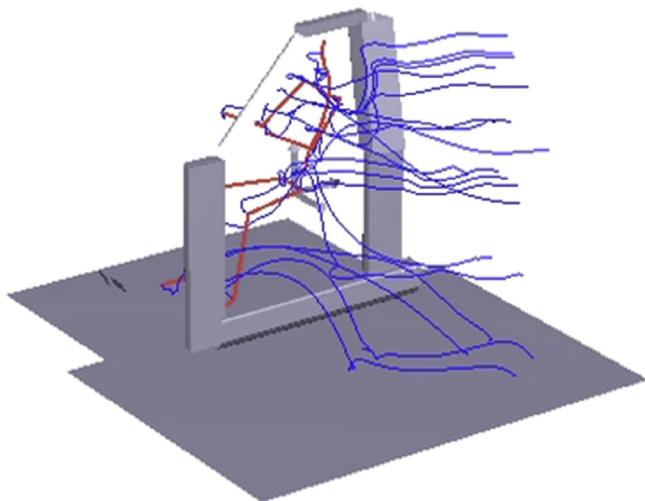
(a) Multi-stream trajectories
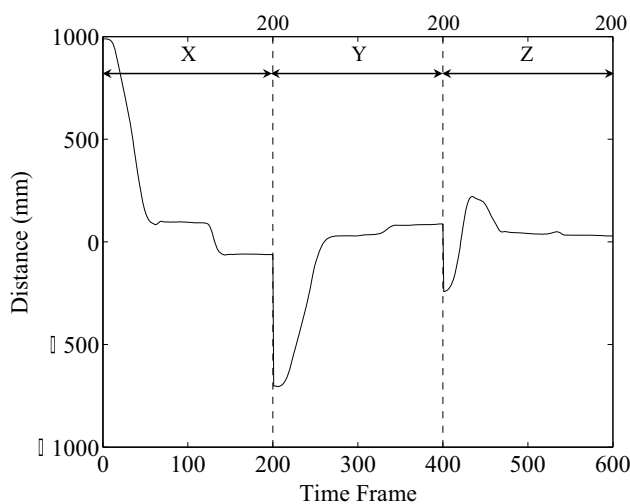
(b) The right ankle joint trajectory

Fig. 1. Ingress motion data of one participant.

Without manipulating the structure of the data, it is not plausible, however, to directly apply the conventional PCA method to multistream trajectories. One naïve way to apply PCA to such data is to combine the multistream trajectories into one high-dimensional vector before applying PCA. For example, if the ingress dataset has N participants with K joints recorded for each participant, and each joint trajectory has M data points, then the new dataset will be represented by a matrix of size N × MK. This means that we combine the M-dimensional vectors of all the K joints for one subject together and consider them as one vector. PCA can subsequently be applied to this matrix to estimate the eigenvectors and extract the significant variation patterns indicated by larger eigenvalues. A PCA analysis of this kind is known as stack-up PCA (Mason et al., 2001; Bharati et al., 2004). Using this stack-up method on human motion data arises two issues that affect the performance of PCA method in providing accurate estimates of the eigenvectors; thus misrepresenting the true variation patterns. First, the number of variables (columns) will highly likely exceeds the number of subjects (rows) i.e. MK > N. Second, it is obvious that some of the joints are highly correlated. In the ingress motion context, this means that the locations of joint A in X, Y and Z directions (trajectories) are correlated to those of joint B, for instance. In this case, if joint A's motion has high variability across the subjects, then joint B must have the same behaviour. This will help find groups of joints that are highly variable in a specific part of the motion; thus having more interpretable results. The problem of stack-up PCA is that since all the joints are combined together, it fails to capture the correlation specially if there is a negative correlation among some joints while the other joints are positively correlated. This problem will be thoroughly discussed and demonstrated in Section 3.

Several authors have pointed out the inefficacy of the stack-up PCA method in these situations (He et al., 2005; Paynabar et al., 2013; Yan et al., 2015). These issues motivate us for utilizing a novel methodology that can analyze the variation patterns without manipulating the correlation structure of the data. Therefore, another type of data representation avoiding the stack-up procedure can be more effective for variation analysis.

In this paper, a high-order array is used to represent the multistream trajectory data, and the Uncorrelated Multilinear Principal Component Analysis (UMPCA) method (Lu et al., 2009) is subsequently applied to analyze variation patterns in human motion. It is then shown that using a high-order representation followed by the UMPCA method can preserve the original spatiotemporal correlation structure of the multistream structured data; therefore, it can provide more efficient dimension reduction and feature extraction compared to the PCA method.

The remainder of this paper is organized as follows. Section 2 provides a brief review of the UMPCA method and considers how this method can be used for human motion analysis. In first part of Section 3 a simulation study is presented to demonstrate the superiority of the UMPCA method over PCA in capturing the variation of human motion patterns in multistream datasets. In the second part of Section 3, the use of UMPCA is illustrated for selecting a few important joints, directions, and time segments from massive ingress motion data, which contribute most significantly to motion variations among the tested participants. Section 4 provides concluding remarks.

2. Methods

2.1. Basic notation of multistream algebra

This section introduces the basis of using a high-order tensor representation for multistream trajectory data. A tensor is a