

Quantifying biomechanical motion using Procrustes motion analysis

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Abstract

The ability to quantify and compare the movements of organisms is a central focus of many studies in biology, anthropology, biomechanics, and ergonomics. However, while the importance of functional motion analysis has long been acknowledged, quantitative methods for identifying differences in motion have not been widely developed. In this article, we present an approach to the functional analysis of motion and quantification of motion types. Our approach, *Procrustes Motion Analysis* (PMA) can be used to distinguish differences in cyclical, repeated, or goal-directed motions. PMA exploits the fact that any motion can be represented by an ordered sequence of postures exhibited throughout the course of a motion. Changes in posture from time step to time step form a trajectory through a multivariate data space, representing a specific motion. By evaluating the size, shape, and orientation of these motion trajectories, it is possible to examine variation in motion type within and among groups or even with respect to continuous variables. This represents a significant analytical advance over current approaches. Using simulated and digitized data representing cyclical, repeated and goal-directed motions, we show that PMA correctly identifies distinct motion tasks in these data sets.

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1. Introduction

The analysis of motion is a central focus of many studies in biology, anthropology, biomechanics, and human factors. These studies typically quantify the relationship between structure and function for a particular task, and compare this relationship among groups of individuals. Some examples include identifying species-specific locomotion differences (e.g., Vilensky, 1987; Larson et al., 2000); the effect of body scaling on functional traits (e.g., Demes et al., 1999); determining the link between structure, performance, and fitness

(e.g., Arnold, 1983; Wainwright, 1994); and examining age, gender, and body size effects on posture and reach performance (Chaffin et al., 2000).

A crucial aspect of functional motion analysis is the ability to quantify and identify alternate movement strategies for a specific task. This is particularly important in human motion studies, because more than one movement strategy can be used to accomplish the same objective (e.g., Straker, 2003). While the importance of alternate movement techniques has long been acknowledged in certain fields (e.g., motor control research, and ergonomic lifting studies), quantitative methods for identifying motion strategies have not been widely developed (reviewed in Park et al., 2005).

Recently, Park et al. (2005) proposed a method for identifying alternate movement techniques for goal-directed tasks. Using three-dimensional, whole-body motion data, they examined the relative contributions of

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joint degrees of freedom and compared the utilization patterns between tasks and individuals. While this approach provides a quantitative means of identifying human motion strategies, it is limited to the analysis of goal-directed tasks. As a result, it cannot be used to examine the full breadth of motion data exhibited by humans and other organisms. For example, complex motions such as running and jumping, and cyclic motions such as swinging a golf club, are common in functional morphological studies but cannot be quantified and identified using their approach (see Park et al., 2005).

Because these motion types are of vital importance to many biomechanical studies, it is critical that a general approach to motion analysis is developed. In this study, we present a general approach to the functional analysis of motion and quantification of motion types that can distinguish differences between cyclical, repeated, or directed motions. The approach, *Procrustes Motion Analysis* (PMA), exploits the fact that any motion can be represented by an ordered sequence of postures exhibited throughout the course of a motion. Changes in posture from time step to time step form a trajectory through a multivariate data space, which represents a specific motion. By evaluating the size, shape, and orientation of these motion trajectories, it is possible to examine variation in motion type within and among groups or with respect to continuous variables (e.g., motion relative to age). Below we describe the PMA procedure, and demonstrate its ability to detect differences between distinct arm and body motions for both simulated and captured motion data.

2. Methods

2.1. Motion trajectory quantification

Because motion is an ordered sequence of postures through time, simply quantifying the posture at each time step and identifying postural differences over time accurately represents a motion. To quantify posture we use geometric morphometric methods (Bookstein, 1991; Adams et al., 2004). First, we record the x , y , z positions of p anatomical landmarks on a set of individuals during each time step of a motion or motions (for 3-dimensional landmarks, more than 3 non-colinear landmarks should be used). Landmarks typically identify underlying bony structures to estimate joint centers, or are other anatomical features that represent the overall shape of an individual (e.g., eyes, nose, etc.). Each configuration of landmarks is then treated as a $p \times 3$ matrix of coordinates and represents the posture of an individual at a given time step during a motion, using the landmark coordinates as variables ($3p$). Postures are standardized for differences in scale, position, and

orientation by superimposing them through a Generalized Procrustes Analysis (GPA: Rohlf and Slice, 1990). GPA centers each configuration at the origin, scales each to unit-centroid size, and optimally rotates each configuration so corresponding points align as closely as is possible. After GPA superimposition, each standardized posture is represented as a point in a curved shape space (of $3p-7$ dimensions: Rohlf, 1996). To perform standard multivariate analyses, these are then projected into a linear tangent space that contains the same number of dimensions, $3p-7$ (i.e., projection, but not dimension reduction: Rohlf, 1996, 1999). Thus, after standardization and projection, each posture is represented by a set of $3p-7$ shape variables in linear tangent space, which are used to compare shape variation within and among groups of individuals (e.g., Adams and Rohlf, 2000; Adams, 2004).

A useful feature of geometric morphometrics is that the shape variables quantitatively describe the position of each individual in the multivariate tangent space. In tangent space, similar configurations of points (corresponding to individuals in similar postures) are close together. By capturing the same individual repeatedly throughout a motion, a sequence of postures is generated that corresponds to distinct points in tangent space. Connecting this ordered sequence of postures defines a trajectory through tangent space that describes the path of a particular motion. A general schematic representing this procedure is found in Fig. 1.

2.2. Statistical assessment of motion trajectories

The motion trajectories described above quantify how posture changes throughout a motion. It is important to recognize however that these trajectories can differ in a number of ways. First, the manner in which posture changes throughout a motion may differ between motions (i.e., motion trajectories differ in *shape*). Alternatively, two motions may have similar trajectory shape, but the extent of one motion path may be greater than that of another (i.e., motion trajectories differ in *size*). Finally, two motions may differ in their orientation relative to the body (i.e., motion trajectories differ in *orientation*). Our approach statistically examines all of these components.

To extract the size, shape, and orientation parameters for each trajectory, we perform a GPA superimposition of the motion trajectories (Fig. 2). First, the shape variables for each posture at each time step of an individual motion are concatenated into a single vector representing a trajectory. Trajectories are then standardized for position, size, and orientation through Procrustes superimposition (see above). During this superimposition, we retain the size and orientation information for further analysis. The size of each motion trajectory is calculated as centroid size: the

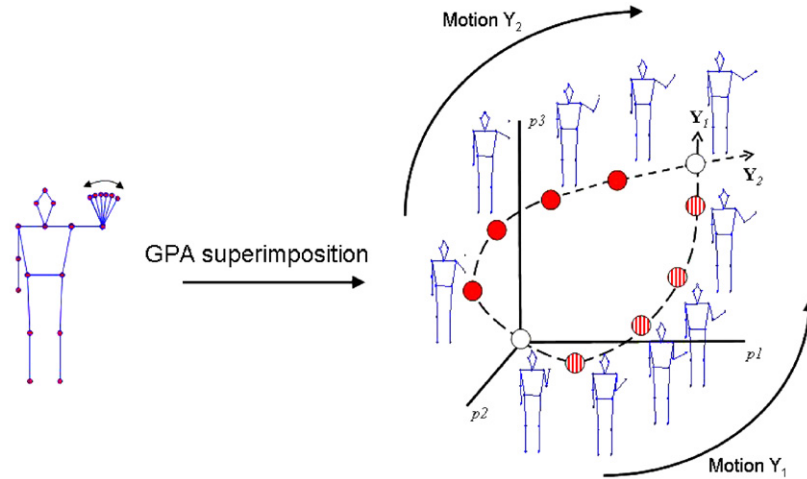


Fig. 1. A schematic diagram representing a sequence of postures digitized throughout a motion. After GPA superimposition, each posture corresponds to a point in a multivariate data space (Note: actual data are in a data space of considerably higher dimension). A sequence of postures quantitatively describes a trajectory through the space, which represents the motion. In this schematic example, two distinct arm-waving motions are shown. Both motions begin and end at the same points (open circles), but the two motion trajectories differ (closed and hatched circles), demonstrating that each is a distinct motion trajectory (Y_1 and Y_2).

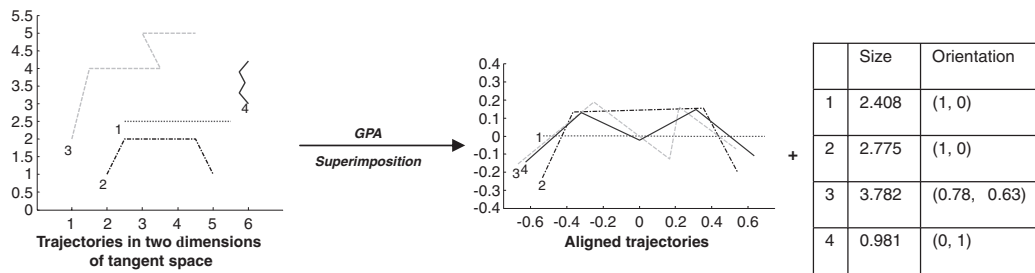


Fig. 2. Trajectories are standardized for position, size, and orientation through Procrustes superimposition. Size and orientation information are retained for further analysis.

square-root of the sum of squared distances between postures and the trajectory centroid in the multivariate space (Bookstein, 1991). The orientation of each trajectory is described by the principal axis of the trajectory data based on a principal components analysis. The set of variables describing each trajectory after superimposition define its shape (see Fig. 2).

Typically, a general linear model analysis (e.g., ANOVA) is performed to statistically compare groups. Unfortunately, this is not possible when comparing motion trajectories, because the high dimensionality of trajectory shape information precludes the use of standard designs due to lack of sufficient degrees of freedom (because the number of landmarks \times the number of time steps used to quantify motion trajectories typically exceeds the number of individuals). We therefore used an alternative approach based on the difference in values between trajectories. Our method uses Mantel tests of matrix correlation (Mantel, 1967) to evaluate the association between trajectory attributes represented in a dissimilarity matrix and a hypothesis

(design) matrix. For trajectory shape, we calculated the pairwise Euclidean distance between trajectories ($D_{ij} = \sqrt{(Y_i - Y_j)^2}$), where Y_i is the set of shape variables for the i th motion trajectory. Calculating all possible pairwise comparisons generates a distance matrix, D_{shape} . Similarly, D_{size} was found as the absolute value between pairs of trajectory sizes ($D_{ij} = |\text{Size}_i - \text{Size}_j|$), and differences in orientation, D_{orient} , were found by calculating the angle between principal vectors ($\theta_{ij} = \cos^{-1}[\text{PC1}_i^T \text{PC1}_j]$). To ensure that θ_{ij} incorporated vector direction, the starting point of each trajectory was projected onto its principal axis, and the difference between the sign of these projected points was used to determine whether θ_{ij} or $\theta_{ij} = \pi - \theta_{ij}$ should be used.

We compared the size, shape, and orientation dissimilarity matrices to a hypothesis matrix that designated known groups of trajectories. Design matrices representing groups contain values of ‘0’ and ‘1’, with ‘0’ representing groups trajectories in the same group and ‘1’

representing trajectories from different groups. The Mantel correlation between a distance matrix and a binary design matrix tests whether the variation between groups is larger than variation within groups, and therefore is analogous to an analysis of variance (Legendre and Legendre, 1998). An advantage of our approach however, is that it is not constrained to group comparisons. The Mantel test can also be used to examine trajectory attributes relative to continuous variables (e.g., a design matrix of peak compression forces for individuals) through correlation with a distance matrix of the continuous data.

2.3. Empirical examples

We illustrate our PMA approach using both simulated and digitized data sets. Two simulated data sets

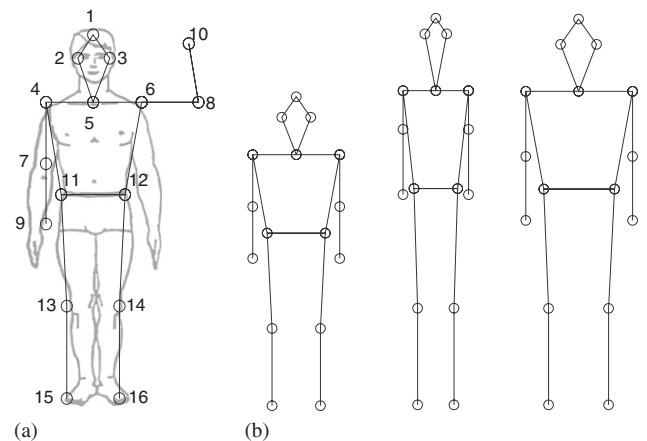


Fig. 3. (a) Landmarks used in the analyses. 1 = top of head, 2 = left tragon, 3 = right tragon, 4 = left acromion, 5 = suprasternum, 6 = right acromion, 7 = left humeral epicondyle lateral, 8 = right humeral epicondyle lateral, 9 = left radial styloid, 10 = right radial styloid, 11 = left iliac crest, 12 = right iliac crest, 13 = left femoral epicondyle lateral, 14 = right femoral epicondyle lateral, 15 = left lateral malleolus, 16 = right lateral malleolus. (b) Subjects 1, 2 and 3 used in the simulation study.

were based on two-dimensional human figure data from an average male human (Tilley, 1993; Department of Defense (DOD-HDBK-743A), 1991), represented by 16 landmarks in a standing posture (Fig. 3). Three specimens were created: two with identical body proportions but different size, and the third with similar size but differing body shape. Twenty individuals for each of the three body types were generated by incorporating isotropic noise at each landmark with variance set to 0.15 (relative to size). For the first simulated data set, we generated cyclic and repeated motion data by depicting back-and-forth articulations of the left arm. Twenty time steps were used to produce each of seven motions (Fig. 4). Five of these motions (A–E) represented distinct motion types. The remaining two motions (F and G) were not distinct motion types, but rather differed from a previous motion only by orientation or size, respectively. An additional 3% digitizing error was incorporated to simulate realistic motion capture data.

Simulated data for the seven cyclical motion types were statistically examined using our PMA procedure. First, a principal coordinates analysis of the double-centered similarity matrix for trajectory shape was performed to visualize separation of the motions by the shape of their trajectories. We then calculated the distance matrices for size, shape, and orientation of motion trajectories, and determined whether motion trajectory attributes varied significantly between motion types using the Mantel test of matrix correlation. Pairwise multiple comparisons were then performed to determine whether specific motion types differed from one another with respect to shape (e.g., motion A vs. motion B, etc.) Additional pairwise comparisons were performed to determine whether motions designed to differ in their extent were significantly different in the size of their trajectories and whether motions designed to differ in their orientation relative to the body differed significantly in trajectory orientation. Analyses were performed in NTSYSpC (Rohlf, 2000), and Matlab (Mathworks, 2000).

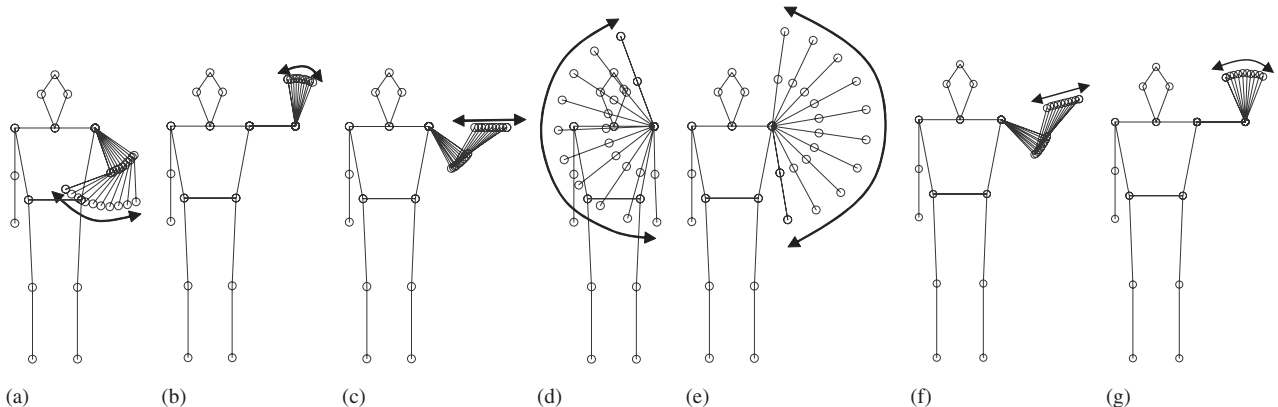


Fig. 4. (a–g) The seven motions modeled in the simulated analysis and replicated in the digitized human figure data.

The second simulated data set contained five distinct alternative motion paths (H–L) for the goal-directed task of touching a target using the left arm (Fig. 5). Thirty replicates of each motion were simulated over 20 time steps, using an additional 1.8" digitizing error in hand position. Alternative motion trajectories were compared using PMA and Mantel tests of matrix correlation and pairwise multiple comparisons as described above.

The final data set contained digitized data for two distinct motions performed by eight human subjects. All subjects participated in this experiment as volunteers. Each subject performed 10 squat lifts and 10 stoop lifts (Fig. 6), in a manner similar to Park et al. (2005). Fourteen body landmarks were placed as in Fig. 3 (only 1 head landmark was used), and the motions of each individual were tracked in three-dimensions using a Ascension MotionStar magnetic tracking system sampling at 60 Hz. A total of 25 time frames (time steps) were used to quantify each motion. The two lifting types were compared using PMA and Mantel tests of matrix correlation as described above.

3. Results

When the shapes of cyclical and repeated motion trajectories from the first simulated data set were examined, distinct clusters of motion types were observed (Fig. 7a). These results imply that the shape of motion trajectories differed among motions, and that different motions form discrete groups or motion ‘types’. Examining the average motion trajectory for each motion type in the first two principal dimensions of shape confirmed these differences, demonstrating that motions differed largely in their degree of curvature (Fig. 7b). Using the Mantel test, we found significant differences in the shape of motion trajectories between motion types (Table 1). Pairwise multiple comparisons found that all motion types differed significantly in their trajectory shape (Table 1). Additionally, pairwise comparisons revealed that, with the exception of motions C and F, all motion types were different from one another in the shape of their trajectories, (Table 2). This was noteworthy, as motions C and F differed only in their orientation relative to the body. Examining

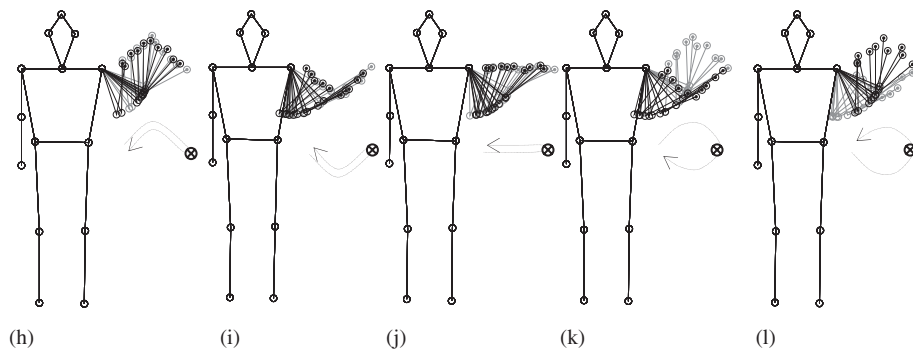


Fig. 5. (h–l) The five simulated reaches, representing alternative movement techniques for accomplishing a goal-directed task (target indicated).

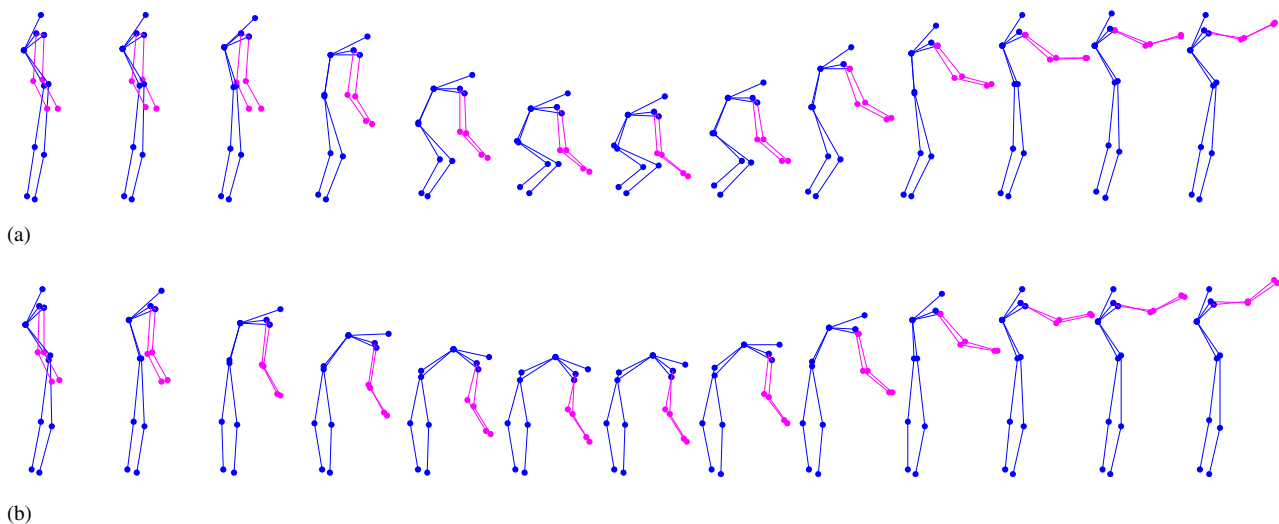


Fig. 6. Schematic representations of (a) squat lifting and (b) stoop lifting, as used in digitized data example.

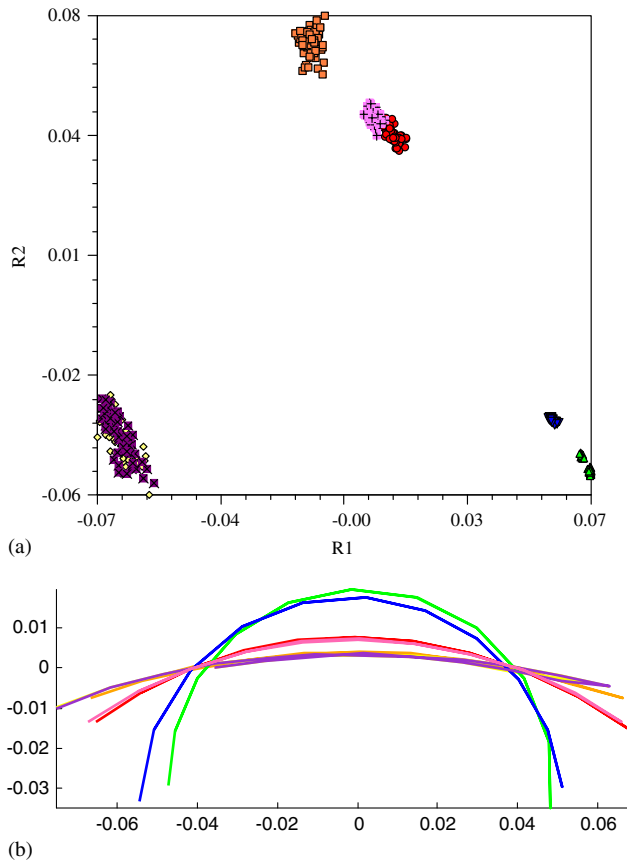


Fig. 7. (a) The first two principal axes of trajectory shape for simulated data. The first two factors represent 90.92% of the total variation in the data set. (b) Average trajectories for each motion type type for the simulated data.

Table 1
Mantel results for simulated data sets

Simulated data	Z-value	P-value
Shape	50 928.03	0.001
Orientation	1880.33	0.001
Motion B v. G	1114.26	0.001
Motion C v. F	4198.52	0.001
Size	40 668.52	0.001
Motion B v. G	6416.03	0.001
Motion C v. F	-38.84	0.664

Table 2
Mantel results for pairwise comparison of groups for the simulated data

	A	B	C	D	E	F	G
A	1						
B	5460.907	1					
C	7073.393	7046.193	1				
D	7106.446	6913.336	7075.963	1			
E	7098.593	6850.799	7063.612	7000.361	1		
F	7074.178	7046.05	-27.128	7075.820	7063.826	1	
G	3094.114	4840.599	7105.233	7061.185	7031.201	7099.736	1

Z-values in bold are significant at ($P < 0.05$).

motions of similar type but different extent (motions B and G) revealed a significant difference in the size of their motion paths (Table 1). As anticipated, a significant size effect was not found between motions C and F, which were generated to differ only in the motion’s orientation relative to the body. Both sets of motions, those differing in their extent and those differing in their orientation, were found to differ significantly in the orientation of their trajectories. This is of particular importance in the case of motions C and F, which were not found to differ in the shape of their trajectories in the simulated analysis.

When goal-directed motions from the second digitized data set were examined, we found significant differences in the size ($r = 0.604$, $P = 0.001$), shape ($r = 0.543$, $P = 0.001$), and orientation ($r = 0.605$, $P = 0.001$) of the five alternative goal-directed motion paths (Fig. 8). Further, pairwise comparisons revealed that all goal-directed motion paths differed from one another in each of these attributes, with the exception of the orientation of motions K and L.

Finally, comparisons of the three-dimensional digitized data from the stoop lift and squat lift experiment revealed significant differences between these groups in both the shape of the motion path ($Z = 916$, $P = 0.001$) as well as their orientation ($Z = 418$, $P = 0.001$). These results imply that the manner in which stoop lift and squat lifts were performed differ biomechanically. This difference was illustrated in both the PCA plot of trajectory shape (Fig. 9a) as well as the average motion path for each motion type (Fig. 9b).

Taken together, these results demonstrate that PMA was capable of distinguishing between alternative cyclical and repeated motions, between alternative motion trajectories for goal-directed tasks, as well as for more complicated three-dimensional motion paths.

4. Discussion

The ability to identify alternate movement strategies is a critical task in human motion studies, yet quantitative techniques to achieve these tasks have only recently been

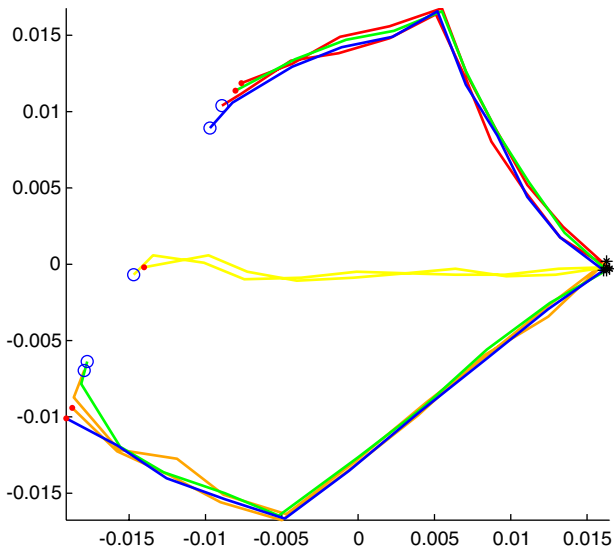
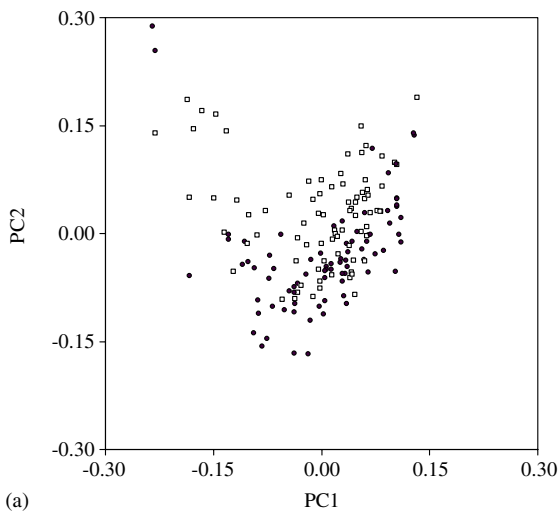
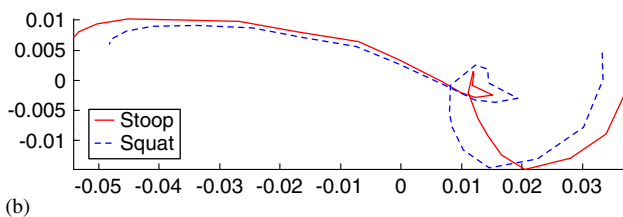


Fig. 8. Average trajectories for each motion type. The starting point is indicated by a red dot and the target is indicated by a black asterisk. Motion types are depicted as: red = H; orange = I; yellow = J; green = K; blue = L. (This article can be viewed in colour at www.sciencedirect.com)



(a)



(b)

Fig. 9. (a) The first two principal axes of trajectory shape for the digitized data. The first two factors represent 66.2% of the total variation. Open symbols are stoop lifts, closed symbols are squat lifts. (b) Average trajectories for each motion type (stoop lifts and squat lifts) for the digitized data.

explored (e.g., Park et al., 2005) In this article, we described Procrustes Motion Analysis (PMA) as a general approach for analyzing functional motion data.

Using simulated and real human data sets, we demonstrated that PMA correctly distinguished distinct motion tasks for cyclical, repeated, and goal-directed motion paths, as well as for more complicated three-dimensional motions. Further, PMA was able to identify distinct motions that differed only in their size or orientation relative to the body, as well as motions that differed in the overall shape of their motion paths. Thus, our procedure correctly identified small execution differences between motions when they existed.

Previous methods for motion quantification examined the relative contributions of joint degrees of freedom to compare utilization patterns between tasks and individuals (Park et al., 2005). While this represents a significant step towards the quantification of motion, several aspects limit its general utility. First, the use of *K*-means cluster analysis assumes that variation in motion is discrete (see Park et al., 2005). Motions that vary across a continuum cannot be examined. Second, this approach only considers joint motion that directly impacts end-effector trajectory. Compensatory balance and stability motions are ignored. Most importantly, this method can only be used to quantify goal-directed tasks. Cyclic or repeated motions cannot be evaluated. Our approach exhibits none of these shortcomings. In this study, we demonstrated PMA for the comparison of groups of motions. However, PMA can also be used to examine continuous variation in motion trajectories. Here, one simply uses a design matrix that incorporates differences in some continuous variable, such as peak compression force or age, and performs Mantel tests of motion trajectory attributes versus this design matrix (for design matrix formulation see Legendre and Legendre, 1998). Additionally, PMA can incorporate both end-effector and compensatory body motions. Finally, it can be used for cyclic and repeated motions, as well as for goal-directed tasks. This represents a significant analytical advance over current approaches.

Motion analysis has also been considered in the field of quantitative morphology (geometric morphometrics). Here, motions were quantified as vectors (Adams, 1999a, b) or periodic functions in shape space (Slice, 1999, 2002, 2003), and differences in these parameters were examined. While these methods correctly recognized that an ordered sequence of postures represents a trajectory in shape space, they failed to provide a complete analysis of motion trajectories, because generalizing these approaches to more than a few landmarks or more than 2-dimensions is challenging. Because PMA examines the size, shape, and orientation of motion trajectories without reliance on curve-fitting or dimension reduction approaches, it more completely captures motion variability, and is therefore of more utility than these previous methods.

It is worth noting that PMA is not limited to the analysis of landmark-based data, but can also be used to

evaluate joint angles and other types of continuous biomechanical data. There are two ways in which this can be accomplished. First, PMA can be used in conjunction with standard kinetic and kinematic approaches, by quantifying the same motions simultaneously with both procedures. When combined in this manner, PMA provides a complementary tool for assessing variation in biomechanical motion. Second, standard kinetic and kinematic variables could be used to represent the motion itself, and be treated as input data in the PMA procedure. This allows covariation in a set of kinematic variables to be incorporated in the analysis, and can be compared to traditional analyses of kinematic variation to yield additional insight. Further theoretical development of this second approach is ongoing.

PMA offers a means of testing biological and anthropological hypotheses of functional variation in motion. This general procedure is an effective method of identifying different motion types by evaluating the shape, size, and orientation components of motion trajectories.

Acknowledgments

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