Linear and Nonlinear Subspace Analysis of Hand Movements During Grasping

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Abstract— **This study investigated nonlinear patterns of coordination, or synergies, underlying whole-hand grasping kinematics. Prior research has shed considerable light on roles played by such coordinated degrees-of-freedom (DOF), illuminating how motor control is facilitated by structural and functional specializations in the brain, peripheral nervous system, and musculoskeletal system. However, existing analyses suppose that the patterns of coordination can be captured by means of linear analyses, as linear combinations of nominally independent DOF. In contrast, hand kinematics is itself highly nonlinear in nature. To address this discrepancy, we sought to to determine whether nonlinear synergies might serve to more accurately and efficiently explain human grasping kinematics than is possible with linear analyses. We analyzed motion capture data acquired from the hands of individuals as they grasped an array of common objects, using four of the most widely used linear and nonlinear dimensionality reduction algorithms. We compared the results using a recently developed algorithm-agnostic quality measure, which enabled us to assess the quality of the dimensional reductions that resulted by assessing the extent to which local neighborhood information in the data was preserved. Although qualitative inspection of this data suggested that nonlinear correlations between kinematic variables were present, we found that linear modeling, in the form of Principle Components Analysis, could perform better than any of the nonlinear techniques we applied.**

I. Introduction

Complex hand movements underly a diverse variety of everyday activities. The execution of these movements demands the coordinated control of more than 25 degrees of freedom in the hand, which can be considered to correspond to the angles of the joints whose rotations parametrize the poses of the hand during the executed kinematic trajectory. However, both everyday experience and the scientific literature on the neural and biomechanical control of movement make it clear that we are not able to independently control each of these degrees of freedom (DOF), either consciously or automatically. Rather, there is ample evidence that this is due to couplings at the biomechanical, motor and neural levels [1], [3], [6], [8], [9], [11], [13], [12], [5], [17], [20]. The notion of *hand synergies* has been proposed to explain the neural, motor, and biomechanical coordinations between the DOF at respective hierarchical levels. A synergy is a collection of nominally independent DOF that are organized into a collective entity acting in union to execute a task, such as to find a maximally stable grasp configuration.

Because the parametric combination of a small number of hand synergies can explain variation in a larger number of variables (e.g., joint angles, muscle activations), these synergies can be regarded as implementing a form of dimensionality reduction (DR). The latter refers to a class of machine learning algorithms aimed at transforming the data so as to reduce the number of variables required to specify each configuration while retaining content in the original signal. DR is effective when the observed data is not distributed uniformly, but instead possesses lower dimensional structure that can be captured as relations among the original variables.

Previous research has analyzed kinematic, force and EMG data during grasping, yielding strong evidence that lower dimensional structures exist at multiple stages of the motor control hierarchy, and providing an explanation of time-dependent grasping data in terms of synergies, which consist of linear transformations of the original variables (joint angle variables, in the case of interest) that are able to effectively capture the observed variations (here, measured kinematic trajectories).

To date, however, the analyses in these investigations have focused exclusively on linear patterns of coordination, corresponding to linear subspace models of dimensionality reduction (most notably principle component analysis, PCA), whereas motor control and kinematics of the hand are nonlinear [9]. This suggests that instead of analyzing the corresponding DOF using *linear* subspace representations, it could be advantageous to employ models that can capture *nonlinear* patterns of coordination underlying hand movements, however this has not been previously tested.

To investigate this, we analyzed hand kinematics using a dataset describing joint angle trajectories obtained from motion capture data during object grasping. We analyzed this data using four different linear and nonlinear dimensionality reduction algorithms, and assessed the quality of each using an algorithm-independent measure of the extent to which each lower-dimensional representation preserved neighborhood information in the data.

II. Methods

We analyzed 20-dimensional kinematic temporal trajectories of the hands of six individuals performing 12 different grasps, using data from a published and publicly available database. We quantified the ability of four different linear and nonlinear dimensionality reduction (DR) algorithms to capture the information in this data by using these algorithms to reduce dimensionality from the original 20 to a smaller number D, with $1 < D \leq 20$. We compared the results of

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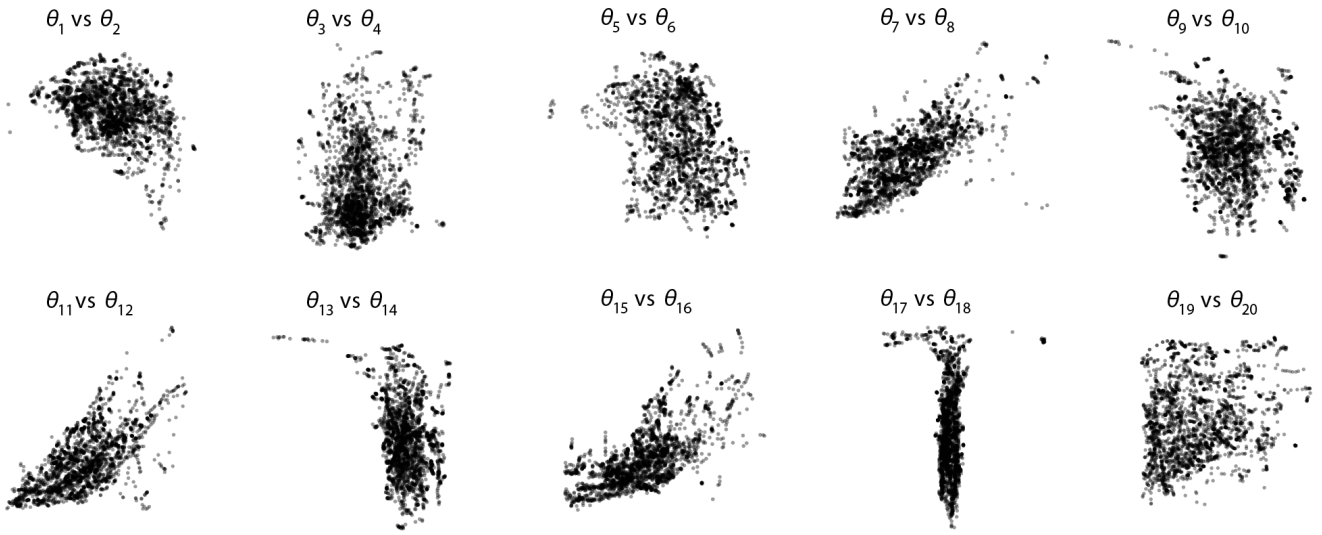

Fig. 1. Visualizations of the preprocessed data obtained by projecting it onto successive pairs of dimensions. The visualizations are suggestive of significant correlations between dimensions, and appear to evidence nonlinear trends, notably in projections onto $(\theta_{17}, \theta_{18})$, $(\theta_{15}, \theta_{16})$, and $(\theta_{13}, \theta_{14})$. These observations provided empirical motivation to the nonlinear analyses investigated here.

these methods using a DR quality metric derived from prior literature.

A. Data

The data consists of 276 trials of kinematic trajectories in the form of 20 time-dependent joint angles of the hand recorded during object grasping. The data we used was obtained from the DLR human grasping database (www.handcorpus.org), which consists of optical motion capture recordings during whole-hand grasping of a subset of objects used in prior research of Santello et al. [13]. Each trial consists of a trajectory measured while an individual grasped a specified object in a prescribed way. Six different individuals, 23 different objects, and two tasks are represented, yielding the total of 276 trajectory exemplars. Each such trajectory is described by a time-varying set of joint angles. The trajectories of joint angles (in radians) consist of $n_f \times n_a$ matrices, where n_f is the number of discrete-time frames of data ($n_f \approx 250$) for each trial, and n_a is the number of joint angles ($n_a = 20$).

B. Analysis and dimensionality reduction algorithms

We first preprocessed the data, by performing an infilling procedure to replace missing components of data vectors (less than 1% of the total data), using mean values to replace the missing values. We combined data from all subjects, grasps, and objects into a single data matrix. Since this data was highly correlated in time, and excessively large for our analysis, we downsampled the data in time by a factor of 20. The resulting preprocessed data is visualized in Fig. 1, where it was projected onto successive dimension pairs in the original data space.

The data was subsequently analyzed using dimensionality reduction (DR), a transformation of the data that aimed to reduce (from 20) the number of variables in each frame while retaining content in the original signals. We compared four different algorithms for this purpose. We briefly describe them here:

Principle components analysis (PCA): This procedure performs a linear orthogonal transformation of the variables, rendering them largely uncorrelated, then reduces dimensionality by retaining only $D < 20$ variables with the highest variance over the dataset [4]. In our application, it is implemented by applying singular value decomposition (SVD) to the evolving hand posture data captured during interaction. The SVD determines orthogonal matrices U and V and a diagonal matrix Σ such that $X = U\Sigma V^T$ (here T denotes transpose). U consists of joint angle variables that define eigenpostures of the hand [8], [13], while V consists of temporal weightings of the eigenpostures, yielding a sequence of values defines the contribution of each eigenposture at each successive time index. The diagonal entries of matrix Σ are the singular values, and indicate the relative amount of variance explained by each eigenposture-temporal weighting pair.

Polynomial Kernel PCA: This algorithm performs a similar task to that of PCA, except that a kernel transformation is used in order to efficiently compute the result of applying PCA to a dataset consisting of the original variables and nonlinear combinations thereof [15]. The kernel function of the algorithm, $K(\mathbf{x}, \mathbf{y})$, determines the effective nonlinearities that are implemented by the algorithm. In a first version of Kernel PCA, we employed a polynomial kernel, of the form $K(\mathbf{x}, \mathbf{y}) = (\mathbf{x}^T\mathbf{y} + 1)^q, q > 0$.

Radial Basis Function Kernel PCA: In this version of Kernel PCA, we employed a radial basis function (Gaussian) kernel, yielding a higher complexity DR model that can be thought of as incorporating nonlinearities of all orders in the reduction algorithm. The kernel is $K(\mathbf{x}, \mathbf{y}) =$

$\exp(-\frac{||\mathbf{x}-\mathbf{y}||^2}{\sigma^2})$.

Neural Network (Nonlinear) PCA: This algorithm consists of an artificial neural network-based auto-encoder that is used to perform the DR transformation [10]. The network is trained, with both weights and inputs estimated using a variant of the backpropagation algorithm. The training algorithm estimates a mapping from the lower-dimensional space (represented by the network inputs) to the higher dimensional space (captured through the outputs).

In each of these algorithms, the number D of reduced dimensions enters as a parameter that can be freely selected. The quality of the dimensionality reduction is assumed to depend on both the choice of algorithm and the dimensionality, D. We used custom software together with published Matlab toolboxes in order to perform the Dimensionality Reduction of the data using these algorithms [18], [16]. We then implemented and applied a DR quality metric (described below) in order to evaluate and compare the results.

C. Comparing DR algorithms

Performing a fair comparison of the quality of dimensionality reduction algorithms is not straightforward, since each such algorithm has been designed to be optimal with respect to a specific and largely algorithm-defining criterion. Several evaluation methods have been proposed in prior literature [19], [2], [18]. Here, we used a quality measure based on the co-ranking matrix [7], which measures the extent to which the DR algorithm being evaluated preserves the rank-ordered distance to other points in the dataset.

The algorithm is computed as a function of the distance matrices of the original and dimensionally reduced data. If the original data consists of data vectors $\mathbf{y}_i$, where $\mathbf{y} = (y_1\ y_2\ \ldots\ y_N)$ and i indexes the data instance (in our dataset, $y_i = \theta_i$, the ith joint angle), then the distance matrix is

$$\delta_{ij} = ||\mathbf{y}_i - \mathbf{y}_j||$$

Similarly, if the lower-dimensional data consists of vectors $\mathbf{x}_i$, where $\mathbf{x} = (x_1\ x_2\ \ldots\ x_D)$, then the corresponding distance matrix is

$$d_{ij} = ||\mathbf{x}_i - \mathbf{x}_j||$$

The next step is to compute the rank matrices P and R corresponding to the distance matrices δ and d. These encode the rank order of points in the respective datasets, and are given by

$$P_{ij} = |\{k : \delta_{ik} < \delta_{ij} \text{ or } (\delta_{ik} = \delta_{ij} \text{ and } 1 \leq k < j \leq N)\}|$$

$$R_{ij} = |\{k : d_{ik} < d_{ij} \text{ or } (d_{ik} = d_{ij} \text{ and } 1 \leq k < j \leq N)\}|$$

where $|A|$ denotes the cardinality of the set A. Then the co-ranking matrix q, which measures the degree of coincidence in the rank order of points before and after transformation, is computed by

$$q_{kl} = |\{(i,j)|P_{ij} = k \text{ and } R_{ij} = l\}| \qquad (1)$$

The interpretation is as follows: the more of the large values of elements in the co-ranking matrix that concentrate toward the diagonal, the greater the distance over which information in high dimensional matrix is preserved by the low dimensional one. Furthermore, errors at small values of the rank can be regarded as more important than those at large rank values. This is because small rank errors indicate the capability of the DR algorithm to map data (here, hand postures) that are similar to points that are near to each other. For this reason, we use a co-ranking based quality measure, $Q(K_{\max})$, which counts the number of points that remain within the same set of $K_{\max}$ nearest neighbors after transformation. It is computed by averaging the co-ranking matrix over increasing values of K up to $K_{\max}$

$$Q(K_{\max}) = \frac{1}{K_{\max}} \sum_{K=1}^{K_{\max}} \frac{1}{KN} \sum_{i=1}^{K} \sum_{l=1}^{K} q_{kl} \qquad (2)$$

In our evaluation, we fixed a value of $K_{\max} = 5$ based on preliminary testing, and computed the quality of Q for each algorithm for each value of the number of reduced dimensions, D.

III. Results

We performed dimensionality reduction of the data for all possible values of the target number of dimensions, $1 < D \leq 20$, and all algorithms, then computed the co-ranking based quality measure using Equation 2.

The results consist of the values of the quality measure $Q(D)$ for each algorithm, at each possible values of the reduced number of dimensions, D. They are shown in Figure 2, which captures the performance of each respective algorithm for at each level of reduction. As is apparent from the the figure, the linear DR algorithm (PCA) fared better at all values of $D > 3$. Among the nonlinear algorithms, Radial Basis Function Kernel PCA perfomed best, but was typically at least 5% worse than PCA. The results obtained from Nonlinear PCA fluctuated as a function of the number of reduced dimensions, D. It is possible that this is attributable to instances in which the NLPCA algorithm became trapped in a local minimum of the neural network error surface.

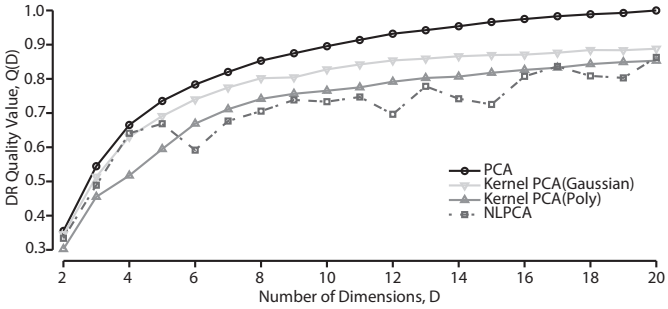

Fig. 2. Dimensionality reduction quality $Q(D)$ for each algorithm as a function of the number D of reduced dimensions.

IV. Conclusions

The results presented here indicated that PCA was able to perform dimensionality reduction of higher quality than was obtained with any of the nonlinear DR algorithms investigated. In contrast, Fig. 1, which presents projections of the original raw data onto pairs of dimensions, appears to provide evidence of nonlinear correlations in the kinematic data, notably through scatterplots of $(\theta_{17}, \theta_{18})$, $(\theta_{15}, \theta_{16})$, and $(\theta_{13}, \theta_{14})$. A number of potential explanations could be proposed. First, PCA is based on an orthogonal transformation, which preserves Euclidean distance. This may suggest that the Euclidean distance based quality function we used, $Q(D)$, was somewhat biased in favor of PCA. Another possible explanation is that PCA was able to capture linear correlations in the data more efficiently than was possible with the nonlinear algorithms, although this requires further investigation. An alternative quality measure that could be used to evaluate the DR techniques in this application is that of sensorimotor efficiency (SME) [14], which connects to information theoretic ideas. The basic idea behind this approach is to capture the amount of information transmitted by hand shape about the target to be grasped, which might make better use of the additional information about grasping that is available in this dataset. Several other nonlinear DR algorithms, including t-Distributed Stochastic Neighbor Embedding and Local Linear Embedding, were not used here, due to difficulties posed in computing the quality measure $Q(D)$. It is plausible that better results would have been obtained with these. Finally, biomechanical constraints could be introduced more explicitly as a means of providing prior knowledge to guide this analysis. We intend to investigate these possibilities in future work.

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