# Generalized Principal Motion Analysis: Classification of Sit-to-Stand Motions

Tomoyuki Iwasaki, Shogo Okamoto, Yasuhiro Akiyama, and Yoji Yamada

*Department of Mechanical Systems Engineering, Nagoya University, Nagoya, Japan*

*Abstract*—**We propose a generalized principal motion analysis (GPMA) method for analyzing temporally evolving motions of redundant systems, such as human motions. GPMA finds base functions, which are called principal motions, that maximally separate distinctive types of motions and that weaken the effects of repeated errors within each type of motion. As an example of human motions, we measured 15 types (3 participants $\times$ 5 conditions) of sit-to-stand motions by a camera-based motion capture system. Each type of motion was repeated 10 times. We then compared GPMA and PMA in terms of their ability to classify the type of motions. GPMA correctly classified all types of motions, whereas PMA correctly classified only 81% of them, which shows that GPMA has a better ability to classify motions.**

*Index Terms*—**principal motion analysis, time-series data**

## I. INTRODUCTION

Techniques to distinguish human motions are important for a variety of applications including security and sports science. A human motion is composed of the time-series data of multiple variables such as joint angles. We exemplify sit-to-stand motions from a chair. It is a dynamic motion of the total joint motions of the lower limbs and the trunk, which requires the load on the lower-limb joints during the postural change from sitting to standing position. In human motion detection problems, typically, statistics computed from the motion data are discussed. For the analysis of sit-to-stand motions, Anan et al. [1] and Turcot et al. [2] divided each motion into a few phases and compared several characteristic values of joint variables for each phase. Christiansen et al. [3] and Samman et al. [4] discussed the time-series data for each joint variable. Thus, many previous studies did not aim to analyze multivariate motion data continuously and statistically. The maximum joint moments during the sit-to-stand motions have been also typically discussed [5], [6].

Human motions are sometimes analyzed by principal motion analysis (PMA) [7], [8]. This method can reduce dimension without losing the information of interlocked multiple degrees of freedom of redundant systems. Hence, PMA has been leveraged for solving the problems of redundant motion systems including motion generation of animated robots [7] and classification of human motions [9]. However, PMA is affected by the variation in inter-individual motion and, therefore, it may not correctly classify human motions of multiple participants.

In this work, we improved PMA and propose a generalized principal motion analysis (GPMA) method that is robust to the effects of motion repetition errors. We analyzed the sit-to-stand motions of knee-pain holders as an example of human motions and then compared the capabilities of GPMA and PMA. Especially, we evaluated their ability to classify sit-to-stand motions recorded by a camera-based motion capture system.

## II. ANALYSIS METHODS

### A. Notion of Motion Variables

Suppose that a human motion at a certain moment is represented by $p$ joint angles. For joint $i$ ($i = 1, ..., p$) at $k$-th trial ($k = 1, ..., k'$), the time-series data vector $\boldsymbol{\theta}_{ik}$, which is aligned to the data length $u$, is given as

$$\boldsymbol{\theta}_{ik} = (\theta_{ik1}, ..., \theta_{ikl}, ..., \theta_{iku})^{\mathrm{T}}. \tag{1}$$

Using this, we create an extended column vector $\boldsymbol{x}_k$ as

$$\boldsymbol{x}_k = (\boldsymbol{\theta}_{1k}{}^{\mathrm{T}}, ..., \boldsymbol{\theta}_{ik}{}^{\mathrm{T}}, ..., \boldsymbol{\theta}_{pk}{}^{\mathrm{T}})^{\mathrm{T}}. \tag{2}$$

Here, $\boldsymbol{x}_k^{(s)}$ represents a time-series column vector of the experiment participant $s$ ($s = 1, ..., s'$) at trial $k$ and $\bar{\boldsymbol{x}}$ represents the mean value of the motions of all the experiment participants. If the dataset contains $s'k'$ trials, the time-series data of all the motions are represented by a matrix $\boldsymbol{X}$ ($\in \mathbb{R}^{s'k' \times pu}$), as follows:

$$\boldsymbol{X} = (\boldsymbol{x}_1^{(1)} - \bar{\boldsymbol{x}}, ..., \boldsymbol{x}_k^{(s)} - \bar{\boldsymbol{x}}, ..., \boldsymbol{x}_{k'}^{(s')} - \bar{\boldsymbol{x}})^{\mathrm{T}}. \tag{3}$$

### B. Principal Motion Analysis (PMA)

Park et al. [7] extended the principal component analysis (PCA) method to make it applicable to time-series data and achieved a representation of human motions with a reduced number of variables. PCA is a multivariate analysis method that identifies the combinations of correlated variables, which are called principal components. These components, which are calculated from the same data pool, are linearly independent of each other.

PMA interlocks the variables along the temporal dimension as well as among multiple variables. The combination of interlocked variables in the temporal direction is called the principal motion. PMA is a linear analysis method, and it is possible to interpret the meanings of the obtained principal motions.

From the eigenvector expansion of covariance matrix $\boldsymbol{X}^{\mathrm{T}}\boldsymbol{X}$,

$$\boldsymbol{X} \sim \boldsymbol{Y}\boldsymbol{V}^{\mathbf{T}}, \tag{4}$$

where $\boldsymbol{Y} = (\boldsymbol{y}_1^{(1)}, ..., \boldsymbol{y}_{k'}^{(s')})^{\mathrm{T}}$ is a score matrix that represents how much each observed motion includes the information of each principal motion and $\boldsymbol{V} = (\boldsymbol{v}_1, ..., \boldsymbol{v}_q, ..., \boldsymbol{v}_r)$ is a principal motion matrix composed of $r$ eigenvectors corresponding to the $r$ largest eigenvalues. $\boldsymbol{v}_q \ (\in \mathbb{R}^{s'k' \times 1})$ is the $q$-th principal motion vector. Any motion is represented by a linear combination of the principal motion vectors weighted by the corresponding scores:

$$\boldsymbol{x}_k^{(s)} \sim \boldsymbol{V} \boldsymbol{y}_k^{(s)}. \tag{5}$$

### C. Generalized Principal Motion Analysis (GPMA)

We extended the linear discriminant analysis (LDA) method, a generalized form of PCA, to make it applicable to time-series data and propose a (GPMA) method. LDA finds the reduced space of observed samples so that the variance between individuals is increased and that within individuals is decreased. Therefore, in the motion analysis of multiple participants, GPMA can emphasize individual differences and depress the factors caused by repetition errors within individuals.

A motion matrix of experimental participants $\boldsymbol{A} \ (\in \mathbb{R}^{s' \times pu})$ is computed as

$$\boldsymbol{A} = (\bar{\boldsymbol{x}}^{(1)} - \bar{\boldsymbol{x}}, ..., \bar{\boldsymbol{x}}^{(s)} - \bar{\boldsymbol{x}}, ..., \bar{\boldsymbol{x}}^{(s')} - \bar{\boldsymbol{x}})^{\mathrm{T}}, \tag{6}$$

where $\bar{\boldsymbol{x}}^{(s)}$ is the mean of the motions of each participant. Moreover, a matrix of repetition errors within individuals $\boldsymbol{B}$ $(\in \mathbb{R}^{s'k' \times pu})$ is computed as

$$\boldsymbol{B} = (\boldsymbol{x}_1^{(1)} - \bar{\boldsymbol{x}}^{(1)}, ..., \boldsymbol{x}_k^{(s)} - \bar{\boldsymbol{x}}^{(s)}, ..., \boldsymbol{x}_{k'}^{(s')} - \bar{\boldsymbol{x}}^{(s')})^{\mathrm{T}}. \tag{7}$$

Let the covariance matrices $\boldsymbol{A}^{\mathrm{T}}\boldsymbol{A}$ and $\boldsymbol{B}^{\mathrm{T}}\boldsymbol{B}$ of $\boldsymbol{A}$ and $\boldsymbol{B}$ be $\boldsymbol{C}$ and $\boldsymbol{D}$, respectively. Then, we regularize these matrices and obtain $\boldsymbol{C}_r$, $\boldsymbol{D}_r$, respectively. A principal motion matrix $\boldsymbol{V}$ and a score matrix $\boldsymbol{Y}$ are obtained from the eigenvector expansion of $\boldsymbol{D}_r^{-1}\boldsymbol{C}_r$. Motion $\boldsymbol{x}_k^{(s)}$ is approximated by a linear combination of the principal motions as well as by PMA:

$$\boldsymbol{x}_k^{(s)} \sim \boldsymbol{V} \boldsymbol{y}_k^{(s)}, \tag{8}$$

where $\boldsymbol{y}_k^{(s)}$ is a row vector of the score matrix $\boldsymbol{Y}$.

### III. Data collection of sit-to-stand motions

We recorded sit-to-stand motions of people under some controlled conditions. In the first condition, three healthy male participants normally stood up from a chair. In the other conditions, they imitated the motion of those with light or severe pain on either the right or the left knee. Before the imitation, they received a lesson on stand-up motions of patients with knee impairment. The level of pain was adjusted by the imbalance ratio of body weight support. In the light pain condition, the participant loaded his weight on the foot of the supposedly healthy side by $10-20$ % compared to the affected side. In the severe pain condition, the healthy side supported more weight than that of the affected side by $30-40$ %. Each condition was repeated 10 times. In total, three participants performed sit-to-stand motions under five conditions and then the motions of 15 people were imaginarily prepared.
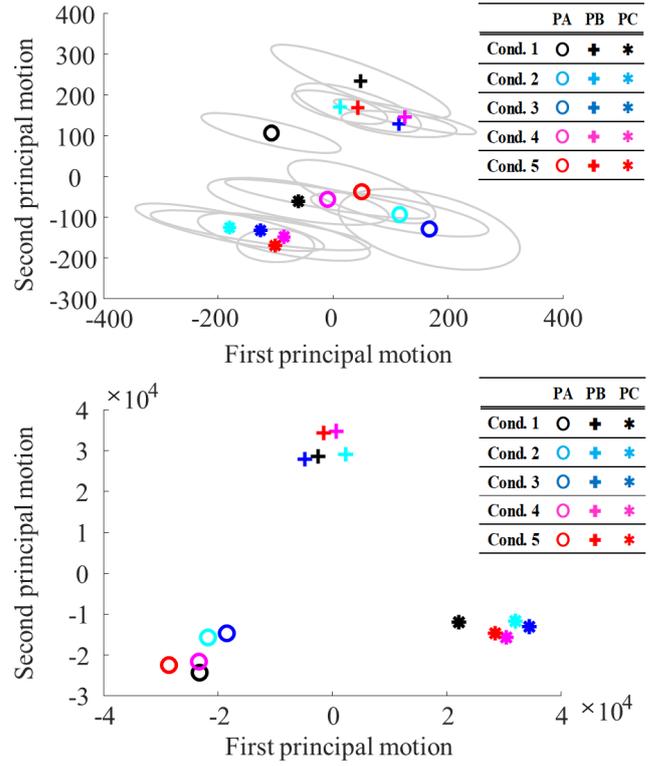


Fig. 1. Scatter plots of the first and second principal motion scores of the PMA (top) and GPMA (bottom). The markers indicate the mean scores, whereas the ellipses indicate the standard deviations. Here, PA, PB, and PC stand for participant A, B, and C, respectively. Condition 1: helthy; condition 2: light pain on the left knee; condition 3: severe pain on the left knee; condition 4: light pain on the right knee; condition 5: severe pain on the right knee. The ellipses of GPMA are invisible because they are extremely small.

Sit-to-stand motion is a full-body motion with upper body and lower limb motions. Therefore, the joint angles measured in this experiment were trunk forward angles and hip flexion angles as upper-body angles, and knee flexion angles and ankle dorsiflexion angles as lower-limb angles. We defined the beginning and the end of the sit-to-stand motion as follows. The beginning of the sit-to-stand motion was defined as a point when the trunk forward angular velocity reached 5 deg/s in 0.4 s. The end of the sit-to-stand motion was when either the left or the right hip joint angle reached its maximum extension.

### IV. Results

Fig. 1 shows the distribution of the first and second principal motion scores for PMA (top) and GPMA (bottom). Both figures show the distribution of first and second principal motion scores on the principal motion plane. The markers in the figures represent the mean scores among 10 trials for each combination of the condition and participant. The ellipses represent their standard deviations.

We tested whether arbitrary pairs of 15 motions could be statistically distinguished. Using the PMA scores, we could statistically classify 85 of 105 $(_{15}\mathrm{C}_2)$ pairs (MANOVA, $p < 0.05$). On the other hand, using the GPMA scores, we could

correctly classify all types of motion pairs. In the result of the PMA (top of Fig. 1), the ellipses of the standard deviations were large, whereas in the result of the GPMA (bottom of Fig. 1), they were extremely small. GPMA decreased the repetition errors within individuals and identified the principal motions, which increased the statistical differences between individuals. GPMA exhibits a good ability to classify the motions of individuals.

## V. Conclusions

We proposed a generalized principal motion analysis (GPMA) method to improve the capability of the principal motion analysis (PMA) method. In the result of the performance test of sit-to-stand motions recorded by a camera-based motion capture system, GPMA correctly classified all the participants' motions, whereas PMA correctly classified only 81 % of them.

## References

[1] M. Anan, K. Shinkoda, K. Suzuki, M. Yagi, T. Ibara, and N. Kito, "Do patients with knee osteoarthritis perform sit-to-stand motion efficiently?," Gait & Posture, vol. 41, pp. 488–492, 2015.

[2] K. Turcot, S. Armond, D. Fritschy, P. Hoffmeyer, and D. Suva, "Sit-to-stand alterations in advanced knee osteoarthritis," Gait & Posture, vol. 36, pp. 68–72, 2012.

[3] C. L. Christiansen and J. E. Stevens-Lapsley, "Weight-bearing asymmetry in relation to measures of impairment and functional mobility for people with knee osteoarthritis," Archives of Physical Medicine and Rehabilitation, vol. 91, pp. 1524–1528, 2010.

[4] M. A. Samman, B. J. Schwaiger, M. C. Gallo, T. M. Link, A. L. Zhang, S. majumdar, and R. B. Souza, "Abnormal joint moment distributions and functional performance during sit-to-stand in femoroacetabular impingement patients," Physical Medicine & Rehabilitation, vol. 9, pp. 563–570, 2017.

[5] K. Yamakawa, S. Okamoto, R. Kubo, N. Yamada, Y. Akiyama, and Y. Yamada, "Knee pain patient simulation for recommendation of sit-to-stand handrail positions," IEEE Transactions on Human-Machine Systems, 2019.

[6] C. Qiu, S. Okamoto, N. Yamada, Y. Akiyama, and Y. Yamada, "Patient simulation: Handrail position for knee-OA patients considering physical burden and stability," Proceedings of IEEE Global Conference on Life Sciences and Technologies, pp. 12–13, 2019.

[7] F. C. Park and K. Jo, "Movement primitives and principal component analysis," On Advances in Robot Kinematics, pp. 97–106, 2004.

[8] N. Yamada, S. Okamoto, H. Okumura, Y. Yamada, K. Isogai, and K. Kawakami, "Similarities and differences in manual stretching of physical therapists for equinovarus," Proceedings of IEEE/SICE International Symposium on System Integration, pp. 490–495, 2014.

[9] K. Mishima, S. Kanata, H. Nakanishi, T. Sawaragi, and Y. Horiguchi, "Extraction of similarities and differences in human behavior using singular value decomposition," IFAC Proceedings Volumes, vol. 43, pp. 436–441, 2010.