Alignment and parameterization of single cycle motion data

Kate Duquesne[1]. Joris De Roeck[1]. Jose-de-Jesus Salazar-Torres[2]. Emmanuel Audenaert[1,3,4,5].

[1] *University Ghent, Department Human Struct & Repair, Ghent, Belgium*
(e-mail: kate.duquesne@ugent.be, joris.deroeck@ugent.be, Emmanuel.audenaert@ugent.be).

[2] *Nemours/A.I. duPont Hospital For Children, Wilmington, Delaware, US*
(email: Jose.Salazar@nemours.org)

[3] *Ghent University Hospital, Department Orthopaedic Surgery & Traumatology, Corneel Heymanslaan 10, B-9000 Ghent, Belgium*

[4] *Department of Trauma and Orthopedics, Addenbrooke's Hospital, Cambridge University Hospitals NHS Foundation Trust, Hills Road, Cambridge CB2 0QQ, UK*

[5] *Department of Electromechanics, Op3Mech Research Group, University of Antwerp, Groenenborgerlaan 171, Antwerp 2020, Belgium*

Abstract: Motion capturing systems produce a large amount of information on the motion of individuals. A growing number of data reduction techniques have been developed to reduce the amount of data while keeping relevant information. An overview that compares and identifies the advantages and disadvantages of these methods on cyclic motion data is, however, lacking. Therefore, this study aims to assess the features of different data reduction techniques by applying them to a large public gait data set. Due to the periodicity of cyclic data, an individual cycle can be isolated and analyzed. The analysis of single cycles requires pre-processing steps to segment and align the individual cycles. The latter is needed to isolate the amplitude variability. Three alignment procedures with different complexity, namely Linear Length Normalization (LLN), Piecewise LNN (PLLN) and Continuous Registration (CR), are assessed based on the amount of resulting variation. Subsequently three data reduction techniques (i.e. Principal Component Analysis (PCA), Principal Polynomial Analysis (PPA) and Multivariate Functional PCA (MFPCA)) are applied to the aligned single gait cycles. The data reduction techniques are evaluated based on the in-sample error, the out-of-sample error, the compactness and the computation time to produce a model. The curves aligned with CR have the lowest remaining variation and thus the lowest amount of remaining phase variation. The differences between the different data reduction techniques appear to be minimal. PPA shows to be the most compact and is therefore recommended when compactness is crucial and out-of-sample performance is less essential. The use of MFPCA is advised when one wants to include data from different sources. PCA is suggested when computation time is key.

Keywords: PCA, Variability, Statistics, Cyclic motion, Human Gait, Single cycle

1. INTRODUCTION

Motion Analysis can already be traced back hundreds of years but started to grow out to a scientific discipline with the pioneering work by photographer Eadweard Muybridge on animal locomotion (Baker, 2007). The progress in technology results in more efficient measurements and provides specialists with a large amount of reliable information (Sutherland, 2002). For traditional data analytics methods, analyzing these large volumes of motion data might become cumbersome (Phinyomark et al., 2018). To this end, a growing number of techniques for data parameterization or data reduction were developed. For cyclic motion data, an overview of the advantages and disadvantages is, however, lacking. Therefore, this study aims to compare the features of different data reduction techniques by applying them to a large public data set. A section on related work is included to support the choice of the selected data reduction techniques.

1.1 Related work

Analyzing cyclic motion, can be performed in two ways. Either one can isolate and analyze a single cycle or one can study a repeated series of motion cycles in time. As the former is typically used in literature and requires another approach than the latter, the latter is not included in this study.

A typical example of cyclic motion is human gait. In gait analysis, a single cycle is called a gait cycle (Taborri et al., 2016). Analyzing gait cycles requires several pre-processing steps to isolate and align the segmented cycles. The latter is needed as within a sample of single-cycle gait curves, there is both amplitude and phase variation (Chau et al., 2005; Forner-Cordero et al., 2006; Sadeghi et al., 2000). When describing gait variation, one typically refers to amplitude variability (Chau et al., 2005). Without correction for phase variation, simple point-by-point averaging of the joint angle curves diminishes useful curve features and misrepresents the temporal position of the landmarks (Chau et al., 2005).

Consequently, to compare the joint angles on a point-by-point basis, temporal alignment techniques are needed. Linear Length Normalization (LLN) linearly compresses/expands the time axis of the gait data such that the duration of all the gait cycles is the same (Helwig et al., 2011). However, temporal differences between events remain present. To improve upon this alignment, piecewise LLN (PLLN) divides the time-series in subphases at specific landmarks and aligns each subphase with the corresponding subphase of the template (Helwig et al., 2011). LLN and PLLN both belong to the category 'landmark registration'. These methods suffer from a number of potential drawbacks (Ramsay et al., 2009b). The landmarks can be concealed in some of the curves, and identifying their timing may involve tedious interactive graphical procedures. Additionally, landmark based registration typically uses only a limited set of landmarks, which leaves large parts of the curves unregistered (Ramsay et al., 2009b). Therefore, Continuous Registration (CR) that uses the entire curve rather than their values at specified points is developed (Chau et al., 2005; Crane et al., 2010; Ramsay et al., 2009b; Sadeghi et al., 2003).

Following the pre-processing, the dataset can be parameterized. The traditional approach is to apply Principal Component Analysis (PCA) (De Roeck et al., 2020; Luksys et al., 2018; Milovanović & Popović, 2012). PCA is a linear data reduction technique that creates a new set of orthogonal and independent variables (principal component (PC) vectors) by making linear combinations of the original possibly correlated variables. Subsequently, the original data is expressed as linear combinations of the PCs. In PCA, the data points of each curve are assumed to be independent of each other (Warmenhoven et al., 2017).

Different non-linear alternatives to PCA have been developed (Hou et al., 2009; Van Der Maaten et al., 2009; Zhang et al., 2018). However, for these non-linear techniques the out-of-sample extension, volume-preservation and invertibility are often hurdles (Zhang et al., 2018). Principal Polynomial Analysis (PPA) overcomes these hurdles by modelling the directions of maximal variance by means of curves, instead of the straight lines used in PCA (Laparra et al., 2014).

Functional PCA (FPCA) forms another appealing alternative to PCA. FPCA is the equivalent of PCA in the functional domain (Warmenhoven et al., 2021) and can be used to examine multiple variables simultaneously (Happ & Greven, 2018). To indicate the primary modes of variation, Multivariate Functional Principal Component Analysis (MFPCA) uses eigenfunctions, whereas PCA and PPA use eigenvectors (Ramsay et al., 2009a).

The amount of data reduction techniques has grown over the last decades. However, a reliable overview of the advantages and disadvantages of these different techniques for cyclic motion data is missing. Therefore, in this study, we present a benchmarking experiment in which we selected parameterization techniques based on their ability to produce statistical models that are generative and may be used for data augmentation. In addition, these three selected parameterization techniques (i.e. PCA, PPA and MFPCA) allow for a tight control during the construction of the statistical model. Before applying the parameterization techniques, optimal curve correspondence is recommended. Three different alignment techniques (LLN, PLLN or CR) are, therefore, evaluated.

2. MATERIALS AND METHODS

To compare the different methodologies applicable to single cycle analysis, we use the comprehensive gait database from *(Schreiber & Moissenet, 2019)*. The data is processed using the Anybody musculoskeletal modelling package (Anybody Technology A/S Aalborg, Denmark) to obtain 6 joint angles, namely hip flexion-extension, hip abduction-adduction, hip external-internal rotation, knee flexion-extension, ankle plantar-dorsi flexion and subtalar eversion-inversion.

2.1 Pre-processing

Before parameterization can be performed, a single motion cycle must be isolated, normalized and aligned. To isolate separate cycles, the fundamental periods of the knee flexion curves are estimated using the Fourier transform. The knee flexion curve is chosen as reference, due to the large amplitude differences.

The next step is to remove the phase variation by aligning the cycles. Three different alignment techniques, namely LLN, PLLN and CR, are applied and evaluated. To obtain the LLN version of the cycles, the cycles are normalized to 101 points. For the PLLN procedure, the two peaks and the valley in-between or the single swing peak of the knee flexion curves are chosen as additional landmark(s) to subdivide the knee flexion cycle in subphases. Subsequently, the subphases are linearly expanded/ compressed to match the length of the corresponding subphases of a template. The other joint angle curves are subdivided and scaled using the parameters from the corresponding knee flexion curve. For the CR procedure, the CR implementation in MATLAB (MathWorks, Natick, Massachusetts, United States of America) of Ramsay et. al (2009a) is used with 17 Fourier basis functions and a roughness parameter of 10. The three alignment procedures are compared based on the remaining variation. The Root Mean Square Error (RMSE) between the registered curves and their corresponding mean curve are a measure for this variation (Crane et al., 2010). The mean RMSE is calculated as follows:

$$mean\ RMSE_{reg} = \frac{1}{N}\sum_{j=1}^{N}\sqrt{\frac{1}{N_t}\sum_{i=1}^{N_t}\left(c_{reg}(i,j) - c_{reg,mean}(i)\right)^2} \quad (1)$$

with c_{reg} and $c_{reg,mean}$ respectively a registered curve and the mean of the registered curves, N the number of training samples and N_t the number of points where the c_{reg} and $c_{reg,mean}$ are evaluated. To compare the RMSEs for the different alignment techniques, the Kruskal-Wallis test is used. Post hoc comparison is performed using the Bonferroni post hoc multiple comparison test. The complete pre-processing and statistical analysis of the alignment procedures is performed in MATLAB (MathWorks, Natick, Massachusetts, United States of America).
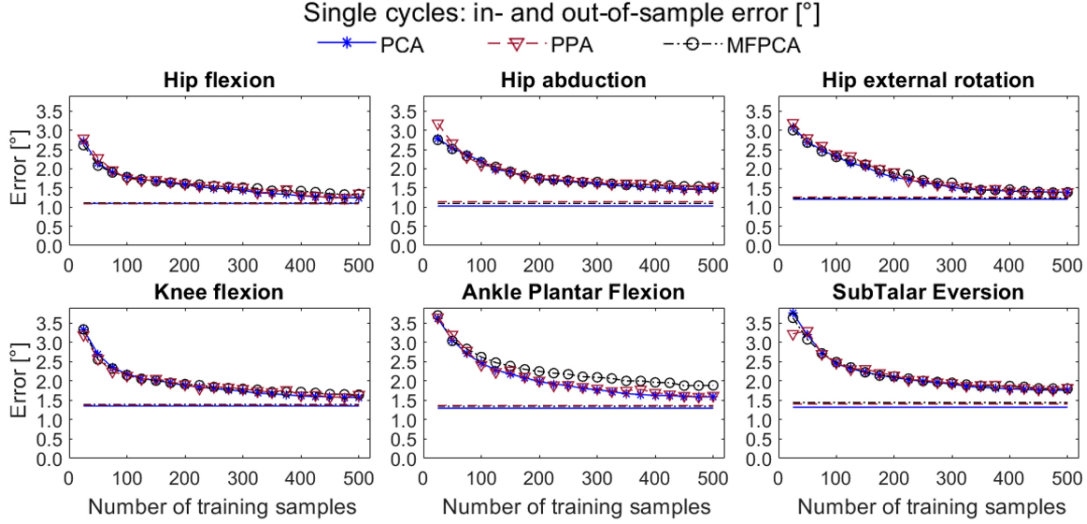
Figure 1 Single cycle analysis: the in-sample errors (horizontal lines) when all possible samples are included during training and the out-of-sample errors for different amounts of training samples included during training for the six different joint angle curves.

2.2 Parameterization

Principal Component Analysis, Principal Polynomial Analysis and Multivariate Functional Principal Component Analysis are applied to the aligned curves set to test their performance. The amount of meaningful variance for PCA is determined based on the rank of roots permutation test (Vieira, 2012). For PPA and MFPCA, the same amount of variance is retained as in corresponding case of PCA. For PCA, an in-house developed algorithm, implemented in MATLAB is used. For PPA, the implementation of Laparra (2014) in MATLAB (MathWorks, Natick, Massachusetts, United States of America) is used. The maximum allowed polynomial degree of the principal components curve is optimized using nested cross-validation. For MFPCA, the MFPCA implementation in R (The R foundation, Vienna, Austria) by Happ and Greven (2018) is adopted. In this particular application, a univariate basis expansion to represent the joint angle curves needs to be chosen. In our case cubic B-splines are chosen (Warmenhoven et al., 2021; Zernicke et al., 1976). The number of basis functions is defined so that the knee flexion curves of the training set are represented with a mean RMSE lower than 0.5°, while the error does not decrease with more than 5% when including one additional basis function. The mean RMSE is calculated as follows:

$$mean\ RMSE_{spl} = \frac{1}{N}\sum_{j=1}^{N}\sqrt{\frac{1}{N_t}\sum_{i=1}^{N_t}\big(c(i,j) - c_{spl}(i,j)\big)^2}\quad (2)$$

with c and c_{spl} respectively, the knee flexion curve and the approximated knee flexion curve, N the number of training samples and N_t the number of points where the c and c_{spl} are evaluated.

The different parameterization techniques are evaluated based on the in-sample error (accuracy), the out-of-sample error (generalization), the resulting model compactness and the computation time to build the model. The in-sample error is calculated using the two equations below:

$$\|c_r - c_{or}\|_{RMSE,j} = \sqrt{\frac{1}{N_t}\sum_{i=1}^{N_t}(\|c_r(i,j) - c_{or}(i,j)\|)^2}\quad (3)$$

$$in - sample\ error = \frac{1}{N}\sum_{j=1}^{N}(\|c_r - c_{or}\|_{RMSE,j})\quad (4)$$

with c_r the reconstructed curves, N_t is the number of time points where the curves are evaluated, N the number of samples on which the model is trained and evaluated. For PCA and PPA, the c_{or} are the original curves. For MFPCA, the c_{or} the approximations of the original curves. The out-of-sample error is calculated using the equations (3) and (4) where N is the number of samples in the test set. Additionally, the equality in variance of the out-of-sample error, a measure for the stability of the models, is tested using the Barlett's test. A Bonferroni correction is applied to perform the pair-wise comparisons. The statistical analysis is performed in MATLAB (MathWorks, Natick, Massachusetts, United States of America).

3. RESULTS

3.1 Pre-processing

Curve alignment has an important impact on the remaining variation. CR aligned curves have a statistically lower RMSE than LLN and PLLN aligned curves for respectively four and five out of six joint angle curves. The mean RMSEs of the different gait curves after the three different alignment techniques are shown in table 1.

3.2 Parameterization

For the parameterization, the in- and out-of-sample errors for PCA, PPA and MFPCA are not noticeably different (figure 1). The out-of-sample errors do not considerably improve when more than 300 training samples are included during training. PPA and PCA have a statistically different variance for the most numbers of training samples included (figure 2). The rank of roots statistical test indicates that when all samples are used to build a model, 94.7% of the variance is meaningful. This is captured with 20, 19 and 18 principal components for PCA, MFPCA and PPA respectively. The creation of the forward model required 1.5 s for PCA, 139.5s for PPA and 10 s for MFPCA on a Laptop PC with Intel(R) Core(TM) i7-6700HQ CPU @ 2.60GHz.

Table 1 Single Cycle Analysis: the mean RMSE between the registered curves and the corresponding mean of the registered curves for the curves aligned with LLN, PLLN and CR for the different joint angle curves.

[°]	LLN			PLLN			CR		
Hip flexion	36.2		"	34.7		°	25.4	"	°
Hip abduction	5.1	*		6.0	*	°	4.85		°
Hip external rotation	16.9			17.0			17.1		
Knee flexion	32.1		"	28.2		°	17.9	"	°
Ankle plantarflexion	15.3	*	"	18.4	*	°	10.1	"	°
Subtalar eversion	21.0	*	"	22.0	*	°	19.6	"	°

Statistically significant differences between LLN and PLLN, LLN and CR and PLLN and CR are indicated by respectively *, ",° for P<0.05 calculated with Kruskal-Wallis and a Bonferroni correction.
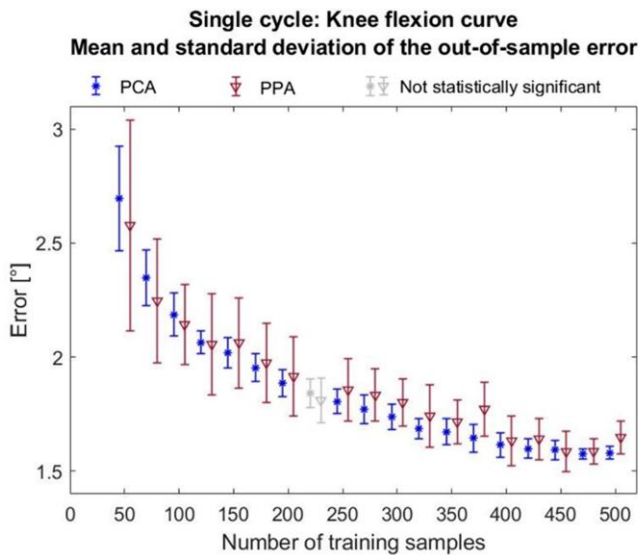

Figure 2 Single cycle analysis: the out-of-sample errors (with standard deviations) for the knee flexion curve for PCA and PPA models trained on different amounts of training samples. The colored markers indicate a statistical difference between the variances of PCA and PPA models trained.

4. DISCUSSION

Human locomotion is characterized by inter- and intra-subject variability. Capturing the inter-subject variation in a statistical model allows to study this variation efficiently. PCA, PPA and MFPCA trained models give very similar in- and out-of-sample errors. MFPCA and PPA are slightly more compact than PCA. Although the mean out-of-sample error of PPA is about equal to those of PCA, for some combinations of joint angle curve and number of training samples the variation is statically higher, indicating that PPA is less stable. Furthermore, the computation time of PPA is drastically higher. Independent of the parameterization technique, the creation of a model that generalizes to the whole able-bodied population requires at least 300 training samples. For the alignment step in the pre-processing of the single cycles, CR outperformed LLN and PLLN in removing phase variability.

FPCA is the equivalent of PCA in the functional domain. It handles the continuity of the data by approximating the curves with a number of basis functions. This smoothens that data. Thus, for densely regularly sampled variables FPCA is equivalent to PCA with an additional smoothness parameter (Warmenhoven et al., 2021). Hence, it is no surprise that MFPCA shows very comparable results to PCA. However, (M)FPCA has several advantages over PCA. It allows to include data from several sources with different sampling rates or sparce data of different dimensions (Happ & Greven, 2018; Warmenhoven et al., 2021). In addition, while PCA runs into difficulties in high dimensions, FPCA provides a more informative way of examining the sample covariance structure (Shang, 2014).

Different non-linear alterative to PCA exist (Hou et al., 2009; Van Der Maaten et al., 2009; Zhang et al., 2018). One of them is PPA (Laparra et al., 2014). In contrast to other non-linear alternatives, PPA has several attractive features for gait analysis such the out-of-sample extension, volume-preservation and invertibility. Nevertheless, PPA is found to be to less stable than PCA. In addition, PPA has a high computational need due to its current dependency of iterative steps makes it less useful to date.

In addition, a comment must be made on the amount of variance to be retained in a statistical model. Traditionally, when performing data reduction 95% of the variance is retained. However, kinematic data is often noise rich data. Therefore, it is interesting to use a permutation test to determine how many principal components are meaningful. For the single cycle data aligned with CR, the rank of roots test identified that 94.7% of the variance is meaningful. PPA is able to capture the meaningful variance with the fewest components. This result cannot be easily compared to other studies as the compactness of a model depends on the size of the training set. As a consequence, it is difficult to compare the compactness of different models trained on different training sets.

Another important finding relates to the isolation of amplitude variability. Joint angle curves aligned with CR demonstrate a statically lower remaining RMSE between the registered curve and the mean of registered curves than joint angle curves aligned with LLN or PLLN. This indicates that CR removes statistically more phase variation. Sadeghi et al. (2003) found similar results when comparing LLN with CR. In addition, they showed that the curve's structural characteristics were not greatly modified. Besides the lower variability, another advantage of CR is that it makes use of the different types of joint angle curves while preserving the time-relation between these different joint angle curves. In contrast, the alignment procedure of PLLN is determined on one type of joint angle curve.

Alongside alignment, the selection of a representative gait cycle is of importance for single cycle analysis. In many gait analysis studies this problem is solved by choosing one gait cycle from the middle of the recording sequence or by averaging several cycles from the middle (Djurić-Jovičić & Miler-Jerković, 2011). Jacobsen and Rasmussen (2019) advocated another possibility. They estimated the mean

pattern of a joint angle curve by fitting a Fourier series to the corresponding series of cycles (Jacobsen & Rasmussen, 2019). In addition, using a series of cycles allows to study intra-subject variability. The latter is often used to identify the presence of a pathological condition (Morgan & Noehren, 2018). In our study, we used the gait cycles from Schreiber and Moissenet (2019) dataset and assumed they provided representative gait cycles.

The strengths of this study are that all the techniques are applied on the same large public dataset which allows for an easy comparison (Phinyomark et al., 2018). However, our findings need to be interpreted in the context of some limitations. In this review, the parameterization and alignment is focused on amplitude variability. However, the phase variability might also be of interest as it might contain information about the control of gait parameters and the stability (Chau et al., 2005; Forner-Cordero et al., 2006). Additionally, only one way of PLLN alignment is implemented. The influence of using another curve as reference or using other landmarks was not determined.

5. CONCLUSION & RECOMMENDATIONS

In conclusion, this paper presented a comparison between different popular and/or recently emerged techniques to align and parameterize single cycle motion data. We conclude that CR achieves better curve correspondence than LLN and PLLN. Non-linear techniques for parameterization are interesting from a mathematical point of view and appear to perform well. Yet, on large datasets the difference with traditional PCA is minimal. For applications which require high compactness and in which the out-of-sample performance is less crucial, we recommend the use of PPA. To create a statistical model from samples from different sources, we suggest the use of MFPCA. When compactness is less crucial though computation time is, the use of PCA is advised. Finally, this paper presents the methods for the analysis of single cycles. In future work, we will also evaluate the analysis of a series of cycles.

AUTHOR CONTRIBUTIONS

KD, JD and EA designed the algorithms. KD and EA performed the statistical analysis. KD, EA and JS wrote the manuscript. All authors contributed to the manuscript revision and approved the submitted version.

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