



A method for developing biomechanical response corridors based on principal component analysis



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ABSTRACT

The standard method for specifying target responses for human surrogates, such as crash test dummies and human computational models, involves developing a corridor based on the distribution of a set of empirical mechanical responses. These responses are commonly normalized to account for the effects of subject body shape, size, and mass on impact response. Limitations of this method arise from the normalization techniques, which are based on the assumptions that human geometry linearly scales with size and in some cases, on simple mechanical models. To address these limitations, a new method was developed for corridor generation that applies principal component (PC) analysis to align response histories. Rather than use normalization techniques to account for the effects of subject size on impact response, linear regression models are used to model the relationship between PC features and subject characteristics. Corridors are generated using Monte Carlo simulation based on estimated distributions of PC features for each PC. This method is applied to pelvis impact force data from a recent series of lateral impact tests to develop corridor bounds for a group of signals associated with a particular subject size. Comparing to the two most common methods for response normalization, the corridors generated by the new method are narrower and better retain the features in signals that are related to subject size and body shape.

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1. Introduction

The fidelity of the responses of human surrogates used for injury prediction, such as crash test dummies and human finite element models, has usually been assessed by comparing surrogate responses to biomechanical response corridors. These corridors describe the population variability in a particular mechanical response (e.g., force produced by impacting a body region) measured in biomechanical tests involving human cadavers or other surrogates such as animals, volunteers etc. Such response corridors are typically developed using a process that involves (1) normalizing response data to account for inter-subject variability in physical characteristics, (2) aligning the data to account for phase variability in measured experimental responses, and (3) constructing a corridor based on point wise distributions of the normalized and aligned data (e.g., ± 1 standard deviation at each point in time).

Besides the naïve eyeballing method (ISO) without numerical analysis, the most common approaches to response normalization

include equal-stress equal-velocity normalization (Eppinger et al., 1984) and impulse–momentum normalization (Mertz, 1984). Equal stress–equal velocity normalization uses dimensional analysis along with the assumption that all subjects are geometrically similar to derive relationships between fundamental parameters (mass, length, time). Additional assumptions of equal density and modulus of elasticity among subjects allow all relationships between fundamental parameters to be normalized to a reference based solely on a ratio of subject mass to reference mass. Impulse–momentum normalization assumes that subject response is described by a simple mechanical model, usually a spring–mass system, and determines relationships between stiffness and mass of a reference and a subject. Mass relationships are typically expressed as the ratios of the experimentally determined effective mass of a body region to the average effective mass of the sampled population. Assumptions of geometric similitude and equal modulus of elasticity across a population are then commonly applied, allowing stiffness ratio to be expressed as a ratio of lengths. Later

implementations of impulse–momentum normalization have used slightly more complex mechanical models and stiffness ratios determined from experimental data (Viano et al., 1989, Moorhouse et al. 2013). Another implementation is to use a deformation energy approach (Donnelly et al., 2014). However, some of these approaches assume a relationship between body characteristics and response or require information that may not be available, like deformation of a body region. Those restrictions motivate us to develop a statistical method that models the relationship between body characteristics and response signals without using any other information. A statistical method is preferred since it considers the uncertainties and can be used to generate corridor limits with different confidence levels.

Existing methods for response normalization are based on assumed relationships between a subject and a reference, such as similar geometry or that the response of a body region can be described by a simple mechanical model. In practice, these assumptions are violated to varying degrees. Subjects from the same population may not be geometrically similar, modulus varies with factors like age for different tissues, the data needed to fit mechanical models may not be available, and the validity of even simple mechanical models for a particular response is often difficult to prove with the small sample sizes typically present in experimental studies involving cadavers.

In this paper, we propose a method for generating response corridors that models the variability in univariate response histories with anthropometric variables and uses these models along with target values for the anthropometric variables to develop a corridor. This method involves aligning signals using established methods, performing a principal components analysis (PCA) on the aligned data, modeling the relationships between principal component (PC) features and subject anthropometry, performing Monte Carlo simulation on these models to generate sets of PC features associated with a target anthropometry, reconstructing curves using these PC features, and generating corridors from the reconstructed data. A demonstration of this method using recently reported impact force data from lateral impact tests on whole seated cadavers is provided, and corridors generated with and without considering the effects of subject anthropometry are compared. A comparison of corridors generated using traditional scaling techniques to corridors generated using the PCA/regression/Monte Carlo simulation approach is also provided.

2. Corridor development methods

2.1. Align data

As a first step, signals from different subjects are shifted in the time domain to align overall phase response. The most common approach, and the approach used in this paper is to find the time shift that maximizes the alignment of the i th subject relative to the reference subject using a similarity metric (Venables and Ripley, 2002). In the paper, n subjects' response signals are represented as a matrix $F_{n \times p} = [f_1 \dots f_i \dots f_n]^T$ and its vector $f_i \in \mathbb{R}^{p \times 1}$ denotes the signal from subject i signal with p sampling points. The cross-correlation coefficient between subject i ($i \neq 1$) and the reference subject 1 is calculated as:

$$r_{i1}(\tau) = \frac{\sum_j (f_1(j) - \mu_1^f)(f_i(j + \tau) - \mu_i^f)}{\sqrt{\sum_j (f_1(j) - \mu_1^f)^2} \sqrt{\sum_j (f_i(j + \tau) - \mu_i^f)^2}} \quad (2.1)$$

where μ_i^f is the average of all sampling points of subject's signal f_i , and τ is the shifted time to align subject i to subject 1. The optimal shifted time τ_i^* for subject i maximizes its cross-correlation

coefficient, i.e.,

$$\tau_i^* = \operatorname{argmax}_{\tau} \{r_{i1}(\tau)\}. \quad (2.2)$$

By following the same procedure to align all other subjects with subject 1, the aligned signals are represented as a matrix $Y_{n \times p} = [y_1 \dots y_i \dots y_n]^T$, where $y_i(j) = f_i(j + \tau_i^*)$ ($j = 1, \dots, p$). Let $\bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$ represent the average signal of n aligned subjects, and $x_i = y_i - \bar{y}$ denote the deviation of subject i 's signal from the average signal. Then, the matrix $X_{n \times p} = [x_1 \dots x_i \dots x_n]^T$ represents all n subjects' deviation from the mean response.

2.2. Principal component analysis

Principal component analysis (PCA) (Jolliffe, 2002) is used as an orthogonal linear transformation to obtain a reduced dimension of features that can describe the original subject signals accurately and efficiently. The linear transformation is formed by a set of eigenvectors $u_k = [u_{k1} \dots u_{kp}]^T \in \mathbb{R}^{p \times 1}$ ($k = 1, \dots, q$; $q \leq p$) sorted based on the descending order of eigenvalues λ_k , which are obtained via the singular value decomposition (SVD) of the sample covariance matrix $X^T X$. Here, SVD is used since the sample size is rather small. By projecting x_i on the k th eigenvector, a PC feature (also commonly called a PC score), $z_{ik} = x_i^T u_k$ is obtained. In this paper, z_{ik} is called a PC feature whose variance is equal to eigenvalue λ_k . If q eigenvectors are applied on x_i , we can obtain q PC features for subject i , denoted as $z_i = [z_{i1} \dots z_{iq}]^T \in \mathbb{R}^{q \times 1}$. The percentage of the variance represented by these q PC features is denoted as C_q , which is calculated as follows:

$$C_q = \frac{\sum_{k=1}^q \lambda_k}{\sum_{k=1}^p \lambda_k} \times 100\%. \quad (2.3)$$

By setting a threshold η on C_q , i.e., $C_q > \eta\%$, we can determine the minimum q , which decides how many PC features are essentially needed to represent $\eta\%$ of the total variance of the original signals.

To see how well q PC features represent original signals, each signal can be reconstructed in the time domain and compared to the corresponding aligned original signal. For subject i , the approximated signals based on these q PC features are reconstructed by:

$$\hat{y}_i = \sum_{k=1}^q \hat{x}_i(k) + \bar{y} \quad (2.4)$$

where $\hat{x}_i(k) = z_{ik}^T u_k$ indicates the contribution of the k th PC feature z_{ik} to the approximation signal \hat{y}_i in the time domain. The variance of approximation errors by using these q PC features is $E[\hat{y}_i - y_i]^2 = \sum_{k=q+1}^p \lambda_k$, which is limited to $(1 - \eta\%)$ of the total variance of the original signals.

2.3. Stepwise regression

To further analyze the effects of subject anthropometry, a stepwise regression approach is used to model the relationships between q PC features and subject anthropometry measurements. Because the PCA transform is an orthogonal linear transform, the resulting PC features are mutually independent. As a result, individual regression models can be built for q PC features separately.

To analyze the effect of anthropometry variables on the k th PC feature, the regression model is written as:

$$z_{ik} = \sum_{j=1}^r w_{ij} \beta_{kj} + \varepsilon_{ki}, k = 1, 2, \dots, q, \quad (2.5)$$

where w_{ij} ($i=1,\dots,n; j=1,\dots,q$) represents the j th anthropometry variable measurement of subject i , i.e., matrix $W = \{w_{ij}\} \in \mathbb{R}^{n \times r}$ represents all anthropometry measurements of n subjects with r attributes. β_{kj} ($j=1,\dots,r; k=1,\dots,q$) is the regression model coefficient representing the anthropometry measurement j 's contribution to the k th PC feature. ε_{ki} ($i=1,\dots,n; k=1,\dots,q$) is the normally distributed residual error with mean 0 and variance ξ_k^2 .

2.4. Construct corridor limits

To assess the effect of considering subject anthropometry on corridors, corridor bounds were generated with and without the use of regression models. The detailed procedures of each approach are discussed in the following two subsections.

2.4.1. Construct corridor limits without using regression models

To construct corridor limits without considering the effects of subject anthropometry, we assume all the subjects' responses are from the same probability distribution and leverage the normal distribution of PC features. The steps for constructing the corridor limits using q PC features are:

Step 1: For the k th PC feature ($k=1,\dots,q$), z_{ik} , calculate its sample mean and sample variance over n tested subjects as: $\hat{\mu}_k = \frac{1}{n} \sum_{i=1}^n z_{ik}$

$$z_{ik}; \hat{\sigma}_k^2 = \frac{1}{n-1} \sum_{i=1}^n (z_{ik} - \hat{\mu}_k)^2.$$

Step 2: Based on above estimated mean and variance, apply the normal distribution of $z_{ik} \sim N(\hat{\mu}_k, \hat{\sigma}_k^2)$ to perform a Monte Carlo simulation, which generates N samples (a large integer number) for the k th ($k=1,\dots,q$) PC feature, i.e., $\tilde{z}(k) = \{\tilde{z}_{ik}\}, i = 1, 2, \dots, N$. The notation of “ \sim ” in the paper denotes the simulated PC features or the surrogate signals used in Eq. (2.6) below.

Repeat step 1 and step 2 for all q PC features.

Step 3: Based on Eq. (2.6), construct N surrogate signals by using all generated q PC features of $\tilde{z}_{ik}(i = 1, \dots, N; k = 1, \dots, q)$:

$$\tilde{\mathbf{y}}_i = \sum_{k=1}^q \tilde{z}_{ik} \mathbf{u}_k + \bar{\mathbf{y}} \tag{2.6}$$

The row vector of $\tilde{\mathbf{y}}_i^T (i = 1, 2, \dots, N)$ represents subject i 's signal, based on which the matrix $\tilde{\mathbf{Y}}_{N \times p}$ is formed to represent all N surrogate signals. Each column vector of $\tilde{\mathbf{Y}}_{N \times p}$ is denoted as $\tilde{\mathbf{y}}(j) (j = 1, 2, \dots, p)$, which represents the j th sampling data of all the surrogate N signals.

Step 4: Calculate the corridor limits by using the pointwise quantile of the surrogate signals on each sampling data point j

($j = 1, \dots, p$):

$$UCL_j = q_{1-\alpha/2}(\tilde{\mathbf{y}}(j)), LCL_j = q_{\alpha/2}(\tilde{\mathbf{y}}(j)) \tag{2.7}$$

where function $q_\tau(v)$ represents the τ th quantile of random variable v .

2.4.2. Construct the corridor limits by incorporating regression models

If subject anthropometry variables are significant predictors of PC features then narrower corridor limits can be generated for a particular set of anthropometry measurements (see comparisons in Subsection 3.4). The steps for developing corridor limits that consider subject variables are:

Step 1: Apply PCA, calculate the k th ($k=1,\dots,q$) PC feature z_{ik} for each subject i ($i=1,\dots,n$) by projecting signal \mathbf{x}_i on the k th eigenvector \mathbf{u}_k . q is so determined that $C_q < \eta\%$ is satisfied under a given threshold $\eta\%$, where C_q is defined in Eq. (2.3)

Step 2: Based on Eq. (2.5), run stepwise regression for each PC feature with r anthropometry measurements as the independent variables. Specifically, the feed forward variable selection approach is taken to sequentially select the critical anthropometric measurements for each PC feature. The estimated regression coefficients and the corresponding standard errors are denoted as $\hat{\beta}_{kj}$ ($j=1,\dots,r$) and $\hat{\xi}_k$, respectively. The expected prediction of the k th PC feature is calculated by $\hat{\mu}_k^r = \sum_{j=1}^r w_{ij} \hat{\beta}_{kj}$.

Step 3: Simulate N samples for the k th PC feature (denoted as \tilde{z}_{ik}) based on the normal distribution $N(\hat{\mu}_k^r, \hat{\xi}_k^2)$.

Step 4: Reconstruct N simulation curves according to Eq. (2.6).

Step 5: Calculate the pointwise quantile according to Eq. (2.7).

3. Case study and analysis results

3.1. Data source

As a demonstration, the methods described above were applied to pelvis impact force data collected in a recent study in which the lateral aspects of nine seated post-mortem human subjects (PMHS) were impacted with a segmented wall in a manner that reproduced important aspects of the loading of the body in a side impact crash (Wood et al., 2014). Each of the impact segments was instrumented to record applied force. The body dimensions of the PMHS used in this study were characterized using standard methods (NHTSA, 2014). Anthropometric measurements considered in the regression analysis are listed in Table 1.

Table 1 Available anthropometric measurements.

| Subject index | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
|----------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| BMI (kg/m ²) | 27.59 | 13.98 | 16.49 | 17.04 | 20.55 | 25.51 | 26.91 | 24.07 | 26.74 |
| Stature (cm) | 157 | 167 | 163 | 168 | 160 | 160 | 160 | 180 | 172 |
| Mass (kg) | 68 | 39 | 43.8 | 48.1 | 52.6 | 65.3 | 68.9 | 78 | 79.1 |
| Vertex to symphysis (cm) | 84 | 86 | 86 | 81 | 85 | 86 | 79 | 81 | 80 |
| Waist height (cm) | 74 | 101 | 86 | 103 | 93.5 | 99 | 91.5 | 100 | 106 |
| Tibiale height (cm) | 44 | 48 | 48 | 50 | 47.5 | 31 | 41.5 | 45 | 51 |
| Shoulder breadth (cm) | 37 | 37 | 36.9 | 37.7 | 40.1 | 39 | 40 | 43 | 39.2 |
| Waist breadth (cm) | 38 | 23 | 25.3 | 27.5 | 29.9 | 33 | 35.5 | 35.5 | 36.8 |
| Hip breadth (cm) | 39 | 33 | 31.5 | 32 | 32 | 35.5 | 36 | 34.6 | 38.7 |
| Forearm hand length (cm) | 26 | 23 | 39 | 40 | 46.5 | 46 | 39.5 | 44 | 50 |
| Waist depth (cm) | 20 | 18 | 17.4 | 16.6 | 15.4 | 18.5 | 21.5 | 25 | 19 |
| Effective pelvis mass (kg) | 25.3 | 11.9 | 10.1 | 9.9 | 16.6 | 18.6 | 19.2 | 21.2 | 18.7 |

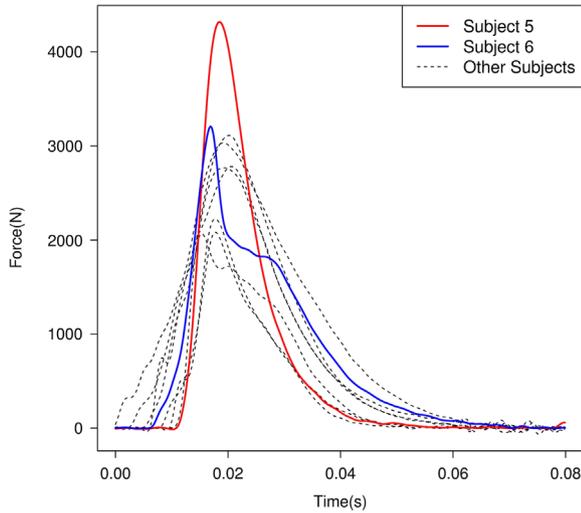


Fig. 1. Aligned signals.

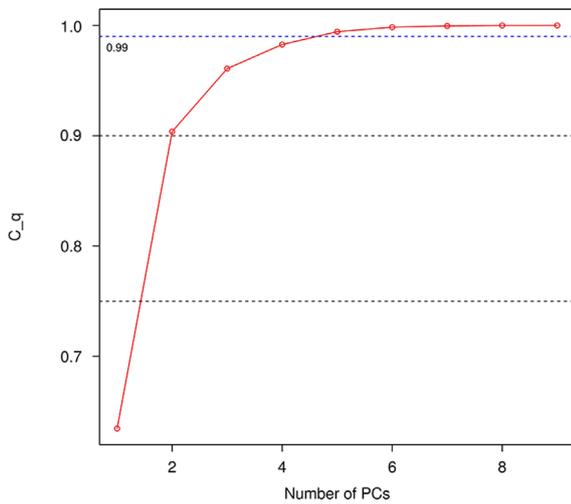


Fig. 2. Cumulative variance contribution of PCs.

The aligned pelvis force signals of nine subjects are shown in Fig. 1. The common pattern shared by nine signals is that the signal starts from zero and increases to its central peak, and thereafter decreases to zero at the end. In contrast, the signal for Subject 5 shows a significant central peak whose maximum is over 4 kN, which is much higher than the other signals, and the signal for Subject 6 has a “shoulder” shape within the sampling period from 20 ms to 30 ms.

3.2. PCA

PCA was conducted on the nine subjects' signals. The resulting contribution of each PC to the cumulative variance, C_q , is shown in Fig. 2. The required number of PCs decided by the pre-set threshold of $\eta=99\%$ was reached by the 5th PC ($q=5$). Limiting the number of PCs simplifies the corridor generation process, especially when responses from more subjects are added. The resultant PC scores are shown in Table 2. For new observations to be added to the study, if we were comparing a new response to the distributions of previous responses, i.e. detecting outliers, new observations would be directly projected into the PC space by using the eigenvectors calculated from existing observations. If we

Table 2
PC scores.

| PC scores | PC1 | PC2 | PC3 | PC4 | PC5 |
|-----------|---------|---------|-------|-------|-------|
| Subject 1 | -10,317 | 3993 | 335 | -2254 | -1344 |
| Subject 2 | 7731 | 2750 | 1349 | 2055 | -1811 |
| Subject 3 | 10,317 | 725 | -1223 | -1424 | 215 |
| Subject 4 | 10,086 | -674 | -1165 | -1216 | 442 |
| Subject 5 | -2816 | -12,591 | 1010 | -18 | -428 |
| Subject 6 | -1064 | 2702 | 5043 | 11 | 132 |
| Subject 7 | -3553 | 1665 | -2142 | 1332 | 406 |
| Subject 8 | -7142 | 710 | -1948 | 662 | 258 |
| Subject 9 | -3243 | 720 | -1258 | 852 | 941 |
| Mean | 0 | 0 | 0 | 0 | 0 |
| STD | 7563 | 4926 | 2269 | 1403 | 1023 |

were to develop a new corridor by combining all the data, we would re-run the PCA.

To interpret the PCA results, the contribution of the first PC feature is visualized in Fig. 3(a) and (d). The reconstructed signal by the first PC feature, i.e., $\hat{\mathbf{x}}_i(1) = z_i^T \mathbf{u}_1$, is shown in Fig. 3(a), and (d) shows $\hat{\mathbf{x}}_i(1) + \bar{\mathbf{y}}$. The first PC feature can be interpreted as the representation of the overall profile shape variations among nine subjects.

Similarly, the contribution of the second PC feature, i.e., $\hat{\mathbf{x}}_i(2) = z_i^T \mathbf{u}_2$ ($i=1, \dots, 9$) is visualized in Fig. 3(b), which shows Subject 5 is quite different from other subjects especially around the central peak area. To further interpret the second PC feature, Fig. 3(e) compared the reconstructed Subject 5's signal by using the first two PC features plus the average signal, i.e., $\hat{\mathbf{x}}_5(1) + \hat{\mathbf{x}}_5(2) + \bar{\mathbf{y}}$ with that by only using the first PC feature plus the average signal, i.e., $\hat{\mathbf{x}}_5(1) + \bar{\mathbf{y}}$. Based on the comparison in Fig. 3(e), the second PC feature mainly contributes to signal variation around the central peak area. In this test dataset, subject 5 shows an excessive difference around the central peak area from other 8 subjects.

The similar analysis is conducted for the third PC feature. Fig. 3(c) shows the reconstructed signal $\hat{\mathbf{x}}_i(3) = z_i^T \mathbf{u}_3$ by only using the third PC feature, which indicates Subject 6 is significantly different from other subjects. To obtain a better comprehension of the third PC feature, Fig. 3(f) compares the reconstructed signal of $\sum_{k=1}^3 \hat{\mathbf{x}}_6(k) + \bar{\mathbf{y}}$ by using the first 3 PC feature plus the average signals with that of $\sum_{k=1}^2 \hat{\mathbf{x}}_6(k) + \bar{\mathbf{y}}$ by using the first 2 PC feature plus the average signals. Fig. 3(f) reveals a unique “shoulder shape” that is mainly contributed by the third PC feature, which results in the difference between Subject 6 and other subjects in Fig. 3(e).

3.3. Regression analysis on anthropometry variables

The anthropometry variables may be highly linear correlated and make the results of regression analysis plausible. Therefore, one variable is removed from each pair of highly correlated variables (over 0.6 linear correlation coefficients) prior to the regression analysis. To characterize the relationship between the impact force signals and the subject anthropometry variables listed in Table 2, regression models were built for the first five PC features. Instead of arbitrarily picking anthropometry measurements, a stepwise linear regression was used to determine which variables are significant to be included in the model. At each step, the variable leading to the largest adjusted R^2 was kept until a maximum of three anthropometric variables were selected. The number of anthropometric variables used in the regression was limited to three to avoid over fitting considering a relatively high

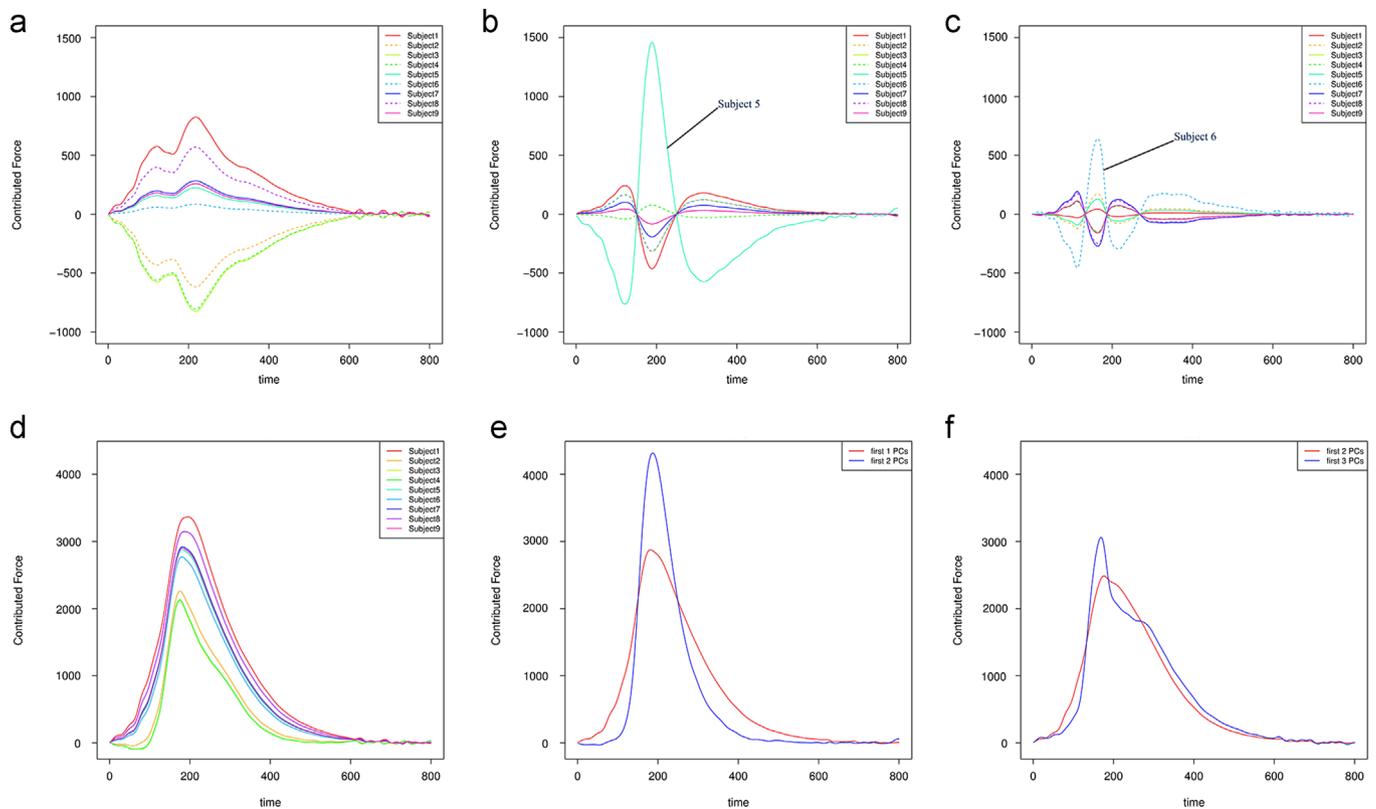


Fig. 3. (a) The first PC's contribution for all subjects. (b) The second PC's contribution for all subjects, (c) The third PC's contribution for all subjects, (d) The reconstructed signals from PC1 for all subjects, (e) The reconstructed signal from PC1 and that from PC1–PC2 for Subject 5, (f) The reconstructed signal from PC1–PC2 and that from PC1–PC3 for Subject 6.

Table 3
Stepwise regression model and the selected anthropometry measurements.

| Response | β_{k0} | β_{k1} | β_{k2} | β_{k3} | R^2 | Adjusted R^2 |
|----------|------------------------------------|---|--|---------------------------------------|--------|----------------|
| PC1 | Intercept 157575.9* (53744.2) | Waist breadth – 1375.2** (245.0) | Vertex to symphysis – 968.8 (478.7) | Shoulder breadth – 861.6 (620.0) | 0.9033 | 0.8452 |
| PC2 | Intercept 34823.4 (27581.6) | Hip breadth – 2077.1 (1063.6) | Waist breadth 843.5 (570.3) | Tibiale height 234.6 (273.6) | 0.4839 | 0.1743 |
| PC3 | Intercept – 42041.28 (16682.13) | Vertex to symphysis 536.30* (168.29) | Tibiale height – 202.10* (73.07) | Waist height 68.91 (44.81) | 0.8241 | 0.7186 |
| PC4 | Intercept – 9876.52 (11532.27) | Waist height 94.79 (60.51) | Shoulder breadth 202.80 (272.58) | Stature – 42.38 (91.92) | 0.4612 | 0.1379 |
| PC5 | Intercept 45868.68 (18921.17) | Mass 226.04* (75.45) | Hip breadth – 851.99* (303.62) | Shoulder breadth – 770.03 (346.66) | 0.6981 | 0.517 |

Standard deviations are in parentheses. “*” or “**” denotes variables with p -values smaller than 0.05.

dimension of anthropometry measurements ($r=11$) compared to a fewer number of tested subjects ($n=9$). If more subjects were added, more variables could be used in the regression equations.

Table 3 presents the selected anthropometric measurements and their corresponding estimated coefficients, where R^2 and adjusted R^2 (denoted as R^2_{adj}) are used to indicate the regression fitting performance. For the first and the third PC features, both R^2 and R^2_{adj} are much higher than that of other PCs, suggesting an adequate model for predicting these two PC features based on the selected dimensions. For PC 1, higher waist breadth was associated with higher pelvis force ($p < 0.05$) and vertex to symphysis and tibiale height were significantly associated with the third PC. The “shoulder” shape shown in Fig. 1 was associated with the third PC score and with larger vertex to symphysis distance and smaller tibiale height. In contrast, no variable was significantly associated

with PC 2, which is related to the peak at 20 ms. As a result of this and because the PC score of Subject 5 was an extreme of the distribution on scores on PC 2, the PCA and regression method generates a corridor that does not include the peak in the response for Subject 5, as shown in Fig. 4 and discussed below.

3.4. Corridor bounds with and without considering subject anthropometry

Fig. 4 illustrates corridor limits representing the 2.5th and 97.5th quantiles (i.e., spanning the central 95%) and plus-minus-one standard deviation of the data, generated by Monte-Carlo simulations based on the estimated distributions of 5 PC features without considering subject anthropometry. Fig. 4(a) shows the 1000 simulated signals and the associated corridor limits (dashed

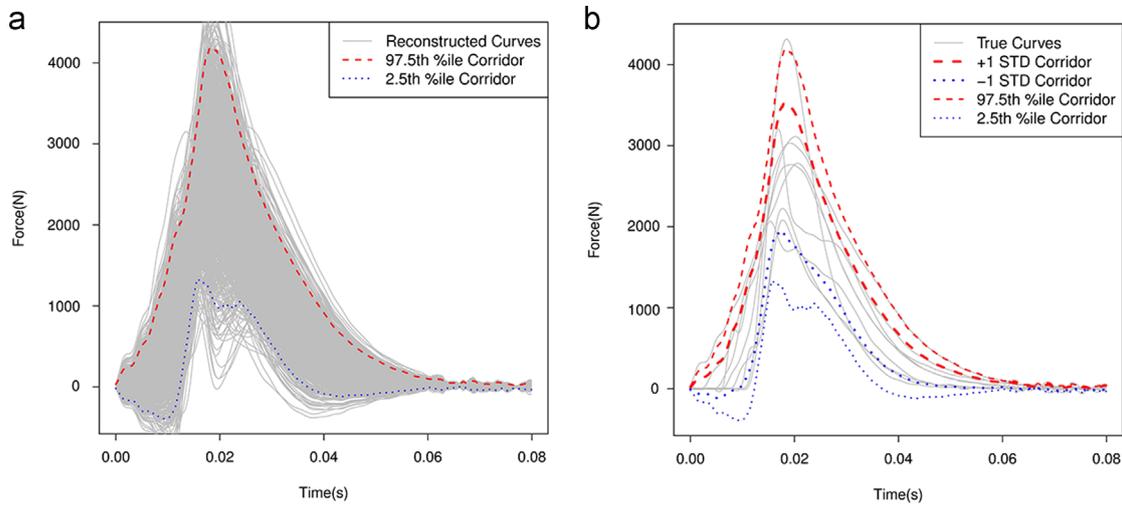


Fig. 4. (a) Corridor limits with simulated signals. (b) Corridor limits with original signals.

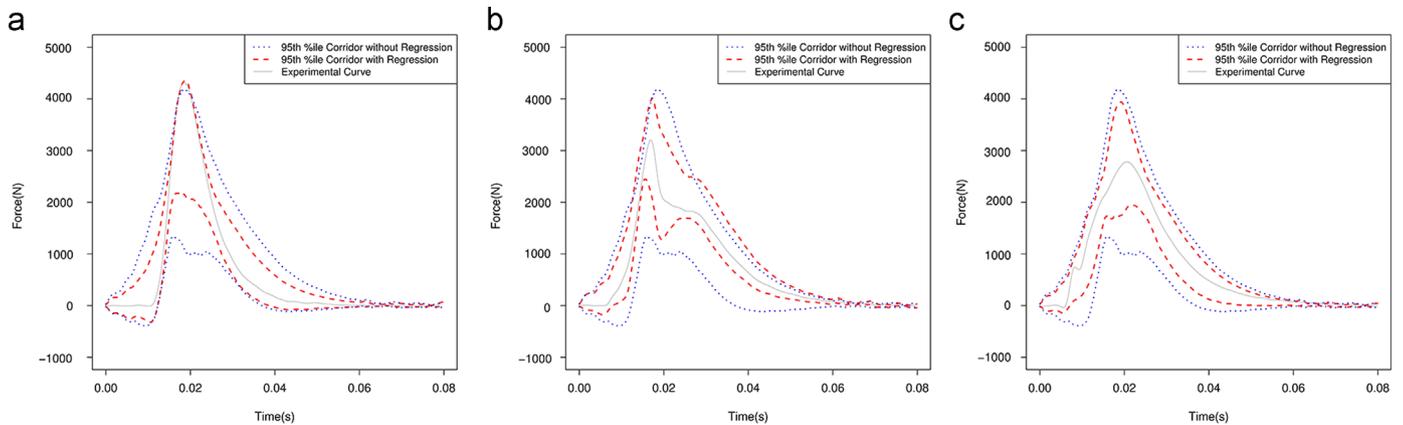


Fig. 5. (a) Effect of using regression models to construct corridor limits for subjects whose body dimensions are similar to Subject 5. (b) Effect of using regression models to construct corridor limits for subjects whose body dimensions are similar to Subject 6. (c) Effect of using regression models to construct corridor limits for subjects whose body dimensions are similar to Subject 7.

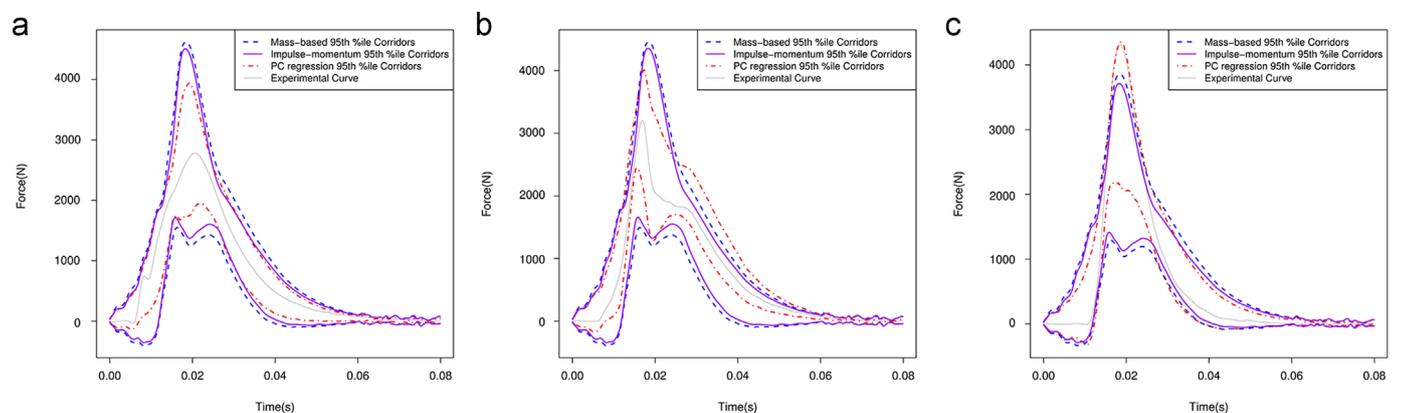


Fig. 6. (a) Comparison between different corridor construction methods for Subject 7. (b) Comparison between different corridor construction methods for Subject 6. (c) Comparison between different corridor construction methods for Subject 5.

line). Fig. 4(b) shows the comparison between the estimated corridor limits (dashed lines) and the original signals (solid lines). The estimated corridor limits cover the original signals except a small portion of the signal from Subject 5 at the central peak area.

Fig. 5 compares corridor bounds constructed using the PCA/regression/Monte Carlo simulation approach with significant

predictors of PC features shown in Table 1 for pelvis force responses from Subject 5 (Fig. 5a), Subject 6 (Fig. 5b), and Subject 7 (Fig. 5c). These subjects had responses that were typical, had a relatively high peak at ~20 ms or had a shoulder shape. Because the responses are significantly associated with body dimensions, corridor limits constructed using the regression models can better

reflect the shape of subject responses than those developed without using the regression models. The “narrower corridor” reflects a smaller variance under the same confidence level. However, a smaller variance does not necessarily generate a better corridor if it fails to reflect the signal profile shape due to a substantial bias error.

3.5. Comparison with corridor bounds generated by scaling techniques

As indicated above, scaling techniques, such as equal-stress, equal velocity scaling (Eppinger et al., 1984) or impulse–momentum scaling (Mertz, 1984) based on dimensional analysis or assumed mechanical models are commonly used to either normalize responses to account for variability in body size or to scale a corridor from one reference size to another (e.g., scaling a corridor that represents a midsize male response to a corridor that represents a small female). In contrast, the approach developed in this manuscript is based entirely on relationships between signal responses and anthropometry variables that exist in the experimental dataset.

Fig. 6 compares corridors generated by the PCA/regression/Monte Carlo simulation approach with the body dimensions from Subjects 5, 6, and 7 to corridors generated using equal-stress equal velocity scaling based on whole-body mass and impulse–momentum scaling based on hip breadth and the effective mass of the pelvis. Table 1 provides the subject characteristics and effective masses used in the scaling processes. In each case, the PCA/regression/Monte Carlo approach results in corridor limits that are narrower and can better reflect the shape of the original signal. As shown in Fig. 6(b), PCA/regression/Monte Carlo captures shoulder shape from Subject 6, while the other methods do not. Fig. 6(c) shows that although Subject 5's high central peak is not covered by any of the estimated corridor limits, PCA/regression/Monte Carlo better captures the peak shape than the traditional scaling methods.

4. Discussion

The PCA, regression, and Monte Carlo simulation approach to corridor development is a departure from traditional techniques for response corridor development that involve normalizing and scaling experimental responses to a particular reference size (e.g., the small female). In particular, the PCA, regression, and Monte Carlo is based entirely on empirical data than either dimensional analysis and/or assumed relationships between size and response described by simple mechanical models. Because of this difference, the PCA, regression, and Monte Carlo approach should result in corridors that more accurately describe the target response as long as there are sufficient experimental data that can be used in corridor development. If sufficient data do not exist, then scaling approaches to corridor development, and in particular newer scaling approaches like those proposed by Moorhouse (2013) and Donnelly et al. (2014), may offer improved performance, provided that the deformation data required by these approaches are available.

The method described in this paper aligns data in the time domain to an arbitrarily selected reference response prior to performing PCA, similar to the alignment approach proposed by Maltese et al. (2002). However, such an approach can bias results if a reference response does not represent the average response. Alternative approaches that address this issue by aligning all signals to the mean signal or segments of a mean signal have been proposed (Donnelly and Moorhouse, 2012, Nusholtz et al. 2013, Gayzik et al., 2015). These methods can be implemented with the PCA, regression, and Monte Carlo simulation approach described in this paper without any loss of generality. When implementing

any alignment method, the relationship between the phase shift produced by the alignment and subject body dimensions should be explored. If such relationships exist, then consideration should be given to statistically modeling them and implementing the resulting statistical models as phase shifts on the corridor developed following Monte Carlo simulation. Another alternative approach is to perform the analyses in the spectral domain with a windowed transform of the sensor data which should be insensitive to the location of the rise and peaks in the time domain.

The proposed method is applicable when signals have similar shape and are well aligned. Also, the PCA method works well when signals are smooth. Otherwise other techniques such as wavelets or Fourier transformation are suggested. For example, the Discrete Fourier Transform represents the signals as a combination of sine/cosine functions with a range of frequencies. However, PCA is more efficient than alternative methods in which the basis functions are predefined, allowing the signals to be represented at a given level of fit with fewer coefficients, simplifying the regression step. On the other hand, all the above analysis assumes normality of PC features. Before applying the proposed method, normality checks such as qq-plot or Shapiro-Wilk's tests are suggested.

Similar to other current methods for corridor development, the PCA, regression, and Monte Carlo simulation method can generate corridors that encompass responses that are physically unrealistic, such as the negative force-values prior to 0.01 s shown in Figs 4 and 5. When corridors encompass physically unrealistic results, truncation of the corridors should be considered.

In each case, the proposed PCA/regression/Monte Carlo approach results in the corridor limits that not only have a narrower band but also can better reflect the shape of the original signal. The meaningful improvement associated with the current approach is that it produces corridors that are directly related to characteristics of the experimental data (e.g., the shoulder shape shown in Fig. 5(b)). This is in contrast to traditional approaches for developing corridors, which average out aspects of curves related to subject anthropometry by applying the same normalization factor to an entire curve and then developing a corridor by taking the mean \pm SD of a set of responses normalized in this manner at each point in time.

Corridor limits constructed using the methods described in this paper can be used for outlier detection by using a leave-one-out cross-validation technique where corridors are developed using all but one signal and the remaining signal is compared to the resulting corridor. Similarly, the method can be used to compare a subsequent response to a corridor developed from previous responses. However, further work is needed to set a reasonable criterion to evaluate signal's performance with respect to given corridor limits for the purposes of outlier detection.

A novel approach to generate response corridors for associated target body dimensions was developed. Unlike the traditional scaling and normalization approaches that assume relationships between response and anthropometry based on dimensional analysis or simple mechanical models-based relationships, the new method is based solely on statistical models derived from empirical data. An application of the new approach showed that it results in corridors that are narrower than traditional approaches to corridor development and captures curve shapes that are affected by body dimensions. (3992 Words).

Conflict of interest statement

We wish to draw the attention of the Editor to the following facts which may be considered as potential conflicts of interest and to significant financial contributions to this work.

We confirm that the manuscript has been read and approved by all named authors and that there are no other persons who satisfied the criteria for authorship but are not listed. We further confirm that the order of authors listed in the manuscript has been approved by all of us.

We confirm that we have given due consideration to the protection of intellectual property associated with this work and that there are no impediments to publication, including the timing of publication, with respect to intellectual property. In so doing we confirm that we have followed the regulations of our institutions concerning intellectual property.

We understand that the Corresponding Author is the sole contact for the Editorial process (including Editorial Manager and direct communications with the office). He/she is responsible for communicating with the other authors about progress, submissions of revisions and final approval of proofs. We confirm that we have provided a current, correct email address which is accessible by the Corresponding Author and which has been configured to accept email from sunwbgt@umich.edu.

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.jbiomech.2016.07.034>.

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