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Short communication

# A point-wise normalization method for development of biofidelity response corridors

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ABSTRACT

An updated technique to develop biofidelity response corridors (BRCs) is presented. BRCs provide a representative range of time-dependent responses from multiple experimental tests of a parameter from multiple biological surrogates (often cadaveric). The study describes an approach for BRC development based on previous research, but that includes two key modifications for application to impact and accelerative loading. First, signal alignment conducted prior to calculation of the BRC considers only the loading portion of the signal, as opposed to the full time history. Second, a point-wise normalization (PWN) technique is introduced to calculate correlation coefficients between signals. The PWN equally weighs all time points within the loading portion of the signals and as such, bypasses aspects of the response that are not controlled by the experimentalist such as internal dynamics of the specimen, and interaction with surrounding structures. An application of the method is presented using previously-published thoracic loading data from 8 lateral sled PMHS tests conducted at 8.9 m/s. Using this method, the mean signals showed a peak lateral load of 8.48 kN and peak chest acceleration of 86.0 g which were similar to previously-published research (8.93 kN and 100.0 g respectively). The peaks occurred at similar times in the current and previous studies, but were delayed an average of 2.1 ms in the updated method. The mean time shifts calculated with the method ranged from 7.5% to 9.5% of the event. The method may be of use in traditional injury biomechanics studies and emerging work on non-horizontal accelerative loading.



## 1. Introduction

In the field of injury biomechanics, there is a continuous need for robust techniques to generate biofidelity response corridors (BRCs). BRCs provide a representative range of time-dependent responses from multiple experimental tests of a parameter from multiple biological surrogates (often cadaveric). Since BRCs ideally represent fundamental behavior of some tested population, more general than a single experimental test, they are an essential input for the design of models whether they are physical, such as anthropomorphic test devices (ATDs), or computational, such as finite element models. In the past, many BRC corridors were simply drawn by eye by bounding a set of data using a series of straight lines (Kent et al., 2006; Lobdell et al., 1973). There is a need for methods that can be consistently applied without subjective input to various loading scenarios, from traditional blunt impacts in the horizontal plane to emerging applications based on vertical loading. The desired output is a corridor with well-defined boundaries based on robust statistical principles.

The scope of this work is focused on single parameter, time-history corridors. Numerous methods have been presented on this subject (Yoganandan et al., 2014). Seminal work in injury biomechanics essentially employed a visually estimated average to draw straight line corridors encapsulating data (Kroell et al., 1974; Viano et al., 1989). Many studies have employed a straightforward mean and standard deviation calculation at each time point for all data in a set (Yoganandan et al., 2004). The open source software "Correlation and Analysis" or CORA, is an objective curve evaluation software that calculates corridors based on a set of signals.

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These corridor calculations can be done using two methods, either generating inner and outer corridors that are set percentages of the mean signal maximum, or using the mean and standard deviation of an input set of signals, without further alignment (Gehre et al., 2009; Gehre and Shahlschmidt, 2011). In the area of objective curve comparison, the fixed inner and outer corridors from CORA have been documented in a recent ISO standard (ISO/TS 18571) (Barbat et al., 2013). While representative of the peaks, fixed corridors overestimate variance in the dataset particularly when signal magnitudes are low, such as in the loading and unloading phases (Maltese et al., 2002; Viano, 1989).

Other, arguably more sophisticated techniques have been used to shift signals forward or backward in time to minimize variance in the set prior to calculating corridors. Raymond et al. (2009) selected time = 0 of all signals as the time when the signal reached 10% peak, then aligned all data to that time prior to calculating mean and standard deviations. Maltese et al. (2002) used a time alignment method that minimizes the cumulative variance of the signals. The method outlined a set of rules for different types of signals (i.e. acceleration, force, displacement) adding versatility and repeatability, and making it one of the more frequently referenced methods e.g. (Yoganandan and Pintar, 2005). However, that method requires subjective selection of one signal as the standard for alignment.

Recently, Nusholtz et al. (2013) published a technique that generates a representative curve (RC, essentially the mean) and evaluates repeatability within a system and reproducibility between systems. Time alignment is achieved by iteratively maximizing the cross correlation of all signals within a data set. This process obviates the need for subjective selection of a standard signal. While the paper also introduces statistical checks for repeatability and reproducibility within and between sets, the present work focuses only on the RC calculation.

The purpose of the current work is to improve the method used to calculate the Representative Curve (RC) outlined in Nusholtz et al. (2013) which can be applied to single parameter, time-dependent biomechanical response data for the generation of BRCs from PMHS data. We introduce modifications of two key parts of the Nusholtz et al. method. First, the proposed method limits correlation calculation to the loading portion of the curve, and second, the calculation of the correlation coefficients between signals is done using point-wise normalization (PWN).

## 2. Methods

Prior to BRC generation, biomechanical data are typically scaled to a target body habitus using methods such as equal stress-equal velocity (Eppinger et al., 1984) or impulse-momentum (Mertz, 1984; Viano, 1989). This paper assumes that such measures have been completed prior to BRC generation.

Because the methods of Nusholtz et al. forms the foundation of this work, a brief review of the process is included. Further details can be found in Appendix C of Nusholtz et al. (2013). The technique begins with a set of time history signals of a response parameter from multiple tests with identical sample rates. As described in Nusholtz et al. (2013) the mean to mean technique is used to calculate a representative curve (RC). The heart of this approach is the calculation of a cross correlation coefficient (CCC) between signals, shown below in Eqs. (1) and (2a). For ease of comparison with Nusholtz et al. (2013), the notation $p$ is used here for the joint cross correlation coefficient. The notation CCC is meant to represent the maximized coefficient $p$, which occurs at time $\tau$.

$$p(x,y) := p(x,y,\tau) \tag{1}$$

$$p(x,y,h) = \frac{\int x(t)y(t+h)dt}{\sqrt{\int x^2(t)dt \int y^2(t)dt}} \tag{2a}$$

$$p(x,y,h) = 1 - \int \frac{\sqrt{(x(t)-y(t+h))^2}}{\sqrt{x(t)^2}+\sqrt{y(t+h)^2}}dt \tag{2b}$$

Here, $x(t)$ and $y(t)$ are two time-valued signals within the data set, and $h$ is an arbitrary shift in time. The iterative technique used in Nusholtz et al. (2013) is preserved in this study, wherein a $p$ value is determined for all pairings in the set, and then the two best-correlated signals are averaged. Signals are iteratively included in the average based on how well they correlate, until a representative curve is calculated. This is the close of the first iteration, and results in $RC_1$. $RC_1$ is then used as the seed signal and the process is repeated until the CCC values do not change, resulting in an optimized RC.

The principal modification introduced in this work is that correlation coefficients are calculated using PWN (Eq. (2b)), resulting in the modified correlations that are termed $CCC_L$. The PWN technique weighs all time points equally: each value in the resulting vector is normalized by the maximum difference that can occur between the two signals at that time point (sum of absolute values). To clarify, the term normalization used within PWN calculation (Eq. (2b)) should not be confused with its well-known definition in the study of injury biomechanics related to population variation. The entire calculation is subtracted from unity because it is a sum of squares difference, and unlike Eq. (2a), better matches between curves will approach zero. The use of PWN was needed because Eq. (2a) aligns truncated signals at their peaks. This is an artifact of Eq. (2a) (the numerator is largest when peaks are aligned) and artificially increases variance between signals particularly early in the event. To calculate the RC, the iterative technique described above is again followed. The point-wise standard deviation of the signals after alignment provides the corridors for the BRC.

To apply this method to high rate biomechanical data, it was desirable to use *only the loading portion of the curve* since time-dependent variation of unloading response generally increases with increasing strain rate. The loading portion was defined as the time between the initiation of the test and the time at which the dependent mechanical variable (e.g. force or moment) reached the local maximum of the greatest magnitude. The definition was different for acceleration data however. In that case, the end of loading was considered the time at which the integrated signal (velocity) reached the local maximum of greatest magnitude. This exception was made for acceleration signals to indicate the time when kinematics of the subject were no longer under the influence of the source of loading.

To demonstrate this method, biomechanical impact data originally published by Maltese et al. (2002) was used. Two sets of human cadaver data (lower spine acceleration and thorax lateral force), from lateral sled impacts into a rigid wall at 8.9 m/s were downloaded from the Biomechanics Test Database maintained by the National Highway Traffic Safety Administration (NHTSA) (NHTSA, 2014). The PMHS in these tests had a mean age of $67.9 \pm 8.8$ years, weight of $68.5 \pm 15.4$ kg and included 2 female and 6 males for a total of 8 specimens. Data were accessed using the NHTSA Signal Browser software version 1.3.6.2. The data was scaled to a target mass of 76 kg using the equal stress, equal velocity method (Eppinger et al., 1984) and filtered using CFC 180 and CFC 1000 on lower spine acceleration and thorax lateral force respectively. The data was resampled to a common sampling frequency of 10 kHz.

The signals were time aligned using the PWN method described above. The BRC was generated using the RC (mean of the signals after optimized alignment), and a corridor that represented $\pm$ one standard deviation of the mean response. Resampling, time alignment, and BRC generation was performed using MATLAB version 2014a. For comparison purposes, the mean and standard deviation curves from Figs. A1 and A5 in Maltese's paper (Maltese et al., 2002), for the rigid test condition, were digitized using MATLAB version 2014a.

## 3. Results

The results of the study are found in Fig. 1. The left side of the figure shows acceleration data whereas the right shows the force data. These two exemplar sets were selected to demonstrate how the loading portion is identified in acceleration vs. other types of biomechanical data (e.g. force). In the upper panels of the plot, red circles identify the end-time for the loading phase of each signal. Only the portion of the signal to the left of the red circle was used in the alignment; however the full signal was used to calculate the BRC. The lower panels of the plot show the raw data curves in cyan which reflect the optimized signal alignment. The bold face black curve shows the RC, with the standard deviation represented above and below.

The average magnitude of the time shift for the lower spine acceleration and thorax force data was 4.5 ms and 5.7 ms respectfully. Note in this example, time traces were shifted independently of one another. Assuming a 60 ms event, these shifts represent 7.5% to 9.5% of the total event time. The algorithm ran six iterations for the acceleration based event and four iterations for the force based event before reaching the convergence criteria (no change in sum of $CCC_L$).