

A METHODOLOGY FOR GENERATING OBJECTIVE TARGETS FOR QUANTITATIVELY ASSESSING THE BIOFIDELITY OF CRASH TEST DUMMIES

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Paper Number 13-0138

ABSTRACT

A set of analysis tools and a procedure are presented for generating objective biofidelity targets derived from post-mortem human subject (PMHS) test response data and quantitatively assessing the biofidelity of crash test dummies. Using response time history data from PMHS tests (Maltese et al., 2002), this paper presents a methodology for creating PMHS response targets that have a statistical basis and then using those targets for quantitative evaluation of crash dummy biofidelity. The first step in the methodology is to normalize the response data to remove variation associated with anthropometric differences and match the size of the dummy to be assessed (e.g., 50th percentile male). After the data is normalized the phase differences are minimized for all responses using the cross-correlation functions and the Lagrange Multiplier technique. The resulting phase-adjusted set of time histories can be averaged, point by point, to obtain a “typical” response. The average phase shift is utilized to locate the mean PMHS response in time. The typical response, or mean curve, can then be bracketed with plus and minus one standard deviation curves resulting in a biofidelity target specification for a dummy response. A single average standard deviation value is used to encompass the mean curve rather than using the point by point standard deviation values, which eliminates “necking” at crossing points. To quantitatively determine the quality of the dummy biofidelity, each dummy response is evaluated for biofidelity in terms of shape and magnitude (SM) and phase (P). First, phase differences between the dummy and mean PMHS response are minimized by using the cross-correlation function to find the phase shift, or lag, that minimizes the squared difference between the two curves. Then the difference between the phase-minimized dummy response and the target mean is measured using a cumulative variance ratio (DCV/CCV) to describe

the response shape and magnitude biofidelity. In addition, the dummy phase response biofidelity is assessed utilizing a ratio of the minimizing lag (dummy phase shift) divided by a standard acceptable lag. The acceptable lag is found by shifting the PMHS mean curve in time with respect to itself and determining the lag between the shifted and unshifted PMHS mean curves that results in a DCV/CCV equal to 1.0. The values for shape and magnitude biofidelity (SM) and phase biofidelity (P) are combined using a root mean square (RMS) methodology (the resultant or orthogonal vector addition) to provide a sense of the total biofidelity quality of each channel time history. The RMS values for each response measurement are averaged for each test condition to obtain the test condition rank; the test condition ranks are averaged to obtain the body region rank; and the body region ranks are averaged to obtain the External or Internal Biofidelity Rank; the External and Internal Biofidelity Ranks are then averaged to obtain the Overall Biofidelity Rank. Results consist of example PMHS biofidelity targets for lateral sled impact tests and two side impact dummies are ranked using this revised BioRank system.

INTRODUCTION

In 2002 Rhule et al. presented a new Biofidelity Ranking System (BRS) which quantifies 1) the ability of a dummy to load a vehicle as a cadaver does - External Biofidelity and 2) the ability of a dummy to replicate those cadaver responses that best predict injury potential - Internal Biofidelity. External Biofidelity is calculated using measures of the environment that the dummy and human subject are loading (i.e., thorax load wall force); Internal Biofidelity is calculated using measures from the dummy or human subject response. The essence of the biofidelity rank lies in the comparison of each selected dummy response to its corresponding mean human subject response. Equation 1 shows the calculation presented in 2002

for generating biofidelity ranks, where R (also known as DCV/CCV) is the ratio of the cumulative variance between the dummy response and mean human response (DCV) over the cumulative variance between the mean human response and the mean plus one standard deviation (CCV) (Morgan et al., 1986, Rhule et al., 2002).

$$B = \frac{\sum_{j=1}^m V_j \left(\frac{\sum_{k=1}^n \sqrt{R_{j,k}}}{n} \right)}{\sum_{j=1}^m V_j} \quad (1)$$

where

B = Biofidelity Rank, either External or Internal
 R = Response Measurement Comparison Value (DCV/CCV)
 V = Test Condition Weight
 j = test condition
 k = response measurement
 m = number of test conditions
 n = number of response measurements per test condition

For any given response measurement in a biofidelity test the R value is calculated and its square root is taken to provide a biofidelity score for that response measurement. The \sqrt{R} value represents the difference between the dummy response and the PMHS mean response in multiples of standard deviation, and thus a lower value represents better biofidelity.

In 2009 Rhule et al. presented updates to the BRS, including removal of all Test Condition Weights and inclusion of all available internal PMHS or dummy measures, not just those used for injury criteria. Internal dummy measures for which there are matching human subject response targets are useful for biofidelity evaluation. The Test Condition Weights were justifiably criticized for being subjective and were removed from the algorithm. A rigorous assessment of the relevance of the tests selected for biofidelity evaluation and the robustness of their corresponding human subject response targets should occur prior to using the objective Biofidelity Ranking System. Equation 2 shows the calculation presented in 2009 for generating biofidelity ranks.

$$B = \frac{\sum_{i=1}^l \left(\frac{\sum_{j=1}^m \left(\frac{\sum_{k=1}^n \sqrt{R_{i,j,k}}}{n} \right)}{m} \right)}{l} \quad (2)$$

where

B = Biofidelity Rank, either External or Internal
 R = Response Measurement Comparison Value (DCV/CCV)
 i = body region
 j = test condition
 k = response measurement
 l = number of body regions
 m = number of test conditions
 n = number of response measurements per test condition

Since the 2009 presentation of the BRS, updates have been made to include an approach for minimizing phase differences among PMHS responses prior to generating human subject response targets as well as an independent measure of dummy phase biofidelity. This paper provides a set of tools and a procedure for generating objective biofidelity targets derived from post-mortem human subject test response data and quantitatively assessing the biofidelity of crash test dummies using an improved BRS.

METHODS

Biofidelity target generation and dummy ranking involves normalizing the PMHS data to a standard size, minimizing phase differences among multiple PMHS time histories, building human subject response targets, and scoring crash test dummy biofidelity using the BRS. The Results section of the paper presents an exemplar set of data after performing each step in the methodology, ending with example biofidelity ranks for two side impact crash test dummies.

Normalization

The first step in the methodology is to normalize the response data to remove variation associated with anthropometric differences and match the size of the dummy to be assessed (e.g., 50th percentile male). Moorhouse (2013) quantified the effectiveness of several methods of normalization by applying them to various sets of data. The methods evaluated include mass-based normalization as described by Eppinger et al. (1984) and impulse momentum-based normalization as described for single mass systems (e.g., sled & drop tests) by Mertz (1984) and for two-mass systems (e.g., pendulum tests) by Viano (1989).

Moorhouse developed a potential improvement to the impulse-momentum based normalization technique

by using an estimate of the effective stiffness calculated from the response data. The calculation for effective stiffness is shown in Equation (3):

$$\int F dx = \frac{1}{2} k_{eff} x_{max}^2 \Rightarrow k_{eff} = \frac{2 \int F dx}{x_{max}^2} \quad (3)$$

where k_{eff} is the effective stiffness, F is the force during impact, and x_{max} is the maximum displacement during the impact. The value of standard effective stiffness is estimated by first calculating the ratio of each subject's effective stiffness to its characteristic length (e.g., chest breadth for a thoracic side impact). Then the average ratio is determined and multiplied by the characteristic length of the population to which the data is to be normalized.

Example results of the normalization effectiveness evaluation are shown in Figure 1, where the effective mass-effective stiffness technique for normalizing PMHS response data resulted in the greatest improvement of signal groupings as indicated by the $\%CV_{ellipse}$ value (see Moorhouse 2013). The effective mass-effective stiffness method for normalizing PMHS response data yielded the smallest $\%CV_{ellipse}$ value in 21 out of 26 signal groups examined, and is selected as the technique of choice for normalizing data prior to building mean response curves in this study.

Phase Optimization

After the data is normalized, the phase differences among all responses are simultaneously minimized using an optimization technique (Donnelly and Moorhouse 2012) based on the cross-correlation function and the Lagrange Multiplier method. The phase shifts, or lags, of each PMHS curve are also averaged to locate the mean curve with respect to time zero so that appropriate timing of the response is not lost.

Kang et al. (2012) utilized the technique to perform phase optimization on rear impact PMHS data and present examples of mean response curves constructed prior to and after phase optimization (Figures 2 and 3, respectively). The mean response curve after phase optimization, shown in Figure 3, is much more like each individual PMHS response than is the non-phase optimized mean response curve of Figure 2.

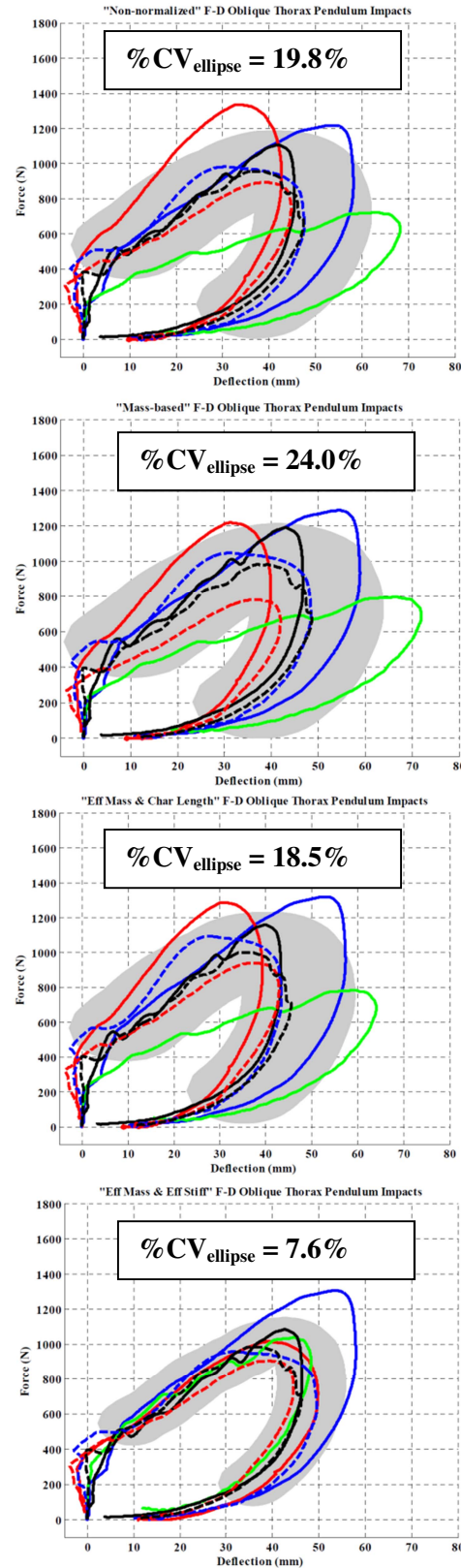


Figure 1. Results from Moorhouse (2013) evaluation of normalization methods as compared to the non-normalized PMHS data

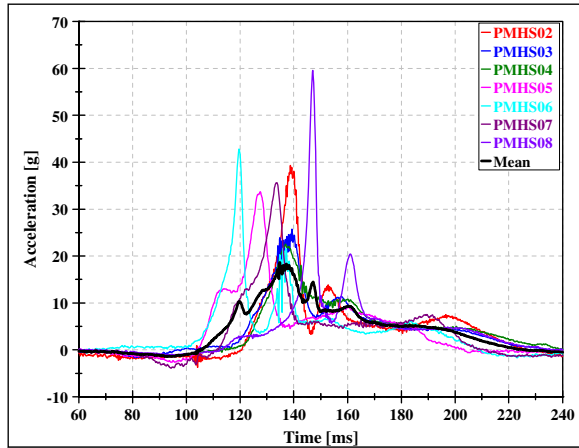


Figure 2. PMHS and mean (solid black line) responses before phase optimization

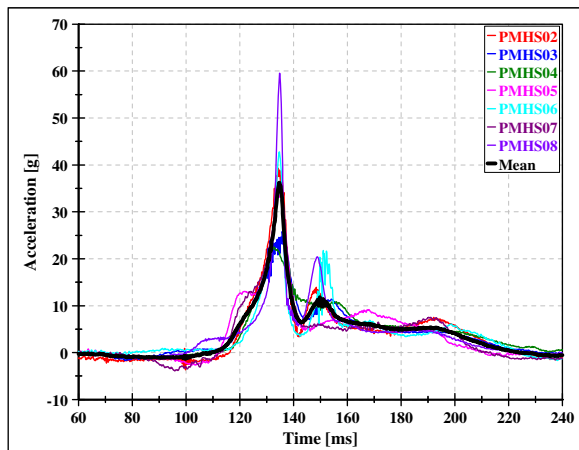


Figure 3. PMHS and mean (solid black line) responses after phase optimization

It should be noted that the timing of the responses can be affected by the normalization process since time is normalized as well as force, acceleration and deflection. Therefore normalization is performed prior to phase optimization. Performing phase optimization prior to normalization would be moot since the normalization would alter the timing of the signals, possibly causing the need for phase optimization to be performed again. Further, the optimization technique provides the time shifts that are averaged to locate the mean curve in time, and normalizing after this is accomplished would invalidate the location in time of the mean curve.

Target Building

Mean Response Curve The resulting phase-adjusted set of time histories can be averaged, point by point, to obtain a “typical” response.

The Mean Response and Standard Deviation Tolerance Curves The typical response, or mean curve, can then be bracketed with plus and minus one standard deviation curves resulting in a biofidelity target specification for a dummy response. Standard deviation curves obtained by using the point by point standard deviation values often result in “necking” at points where the original curves happen to be similar in value: usually where PMHS curves cross. To eliminate this issue, a single standard deviation value is obtained by averaging the point by point standard deviation values, and the single average standard deviation value is used to encompass the mean curve. Also, to focus on the most relevant portion of the target, the standard deviation curves are only calculated for the upper 80% of the mean response (i.e., for values of the mean response that are greater than 20% of the peak magnitude of the mean curve).

Figures 4 and 5 show examples of one standard deviation curves calculated at each point and averaged across all points, respectively. It should be noted that these mean and standard deviation curves will ultimately be used to calculate the CCV portion of the DCV/CCV value used to obtain \sqrt{R} (Rhule et al., 2002, 2009) for the assessment of dummy biofidelity (see next section), and that for this calculation it does not matter whether the standard deviation is calculated at each point or the average standard deviation is used because the resulting CCV values will be the same. Although the resulting \sqrt{R} values are not affected, using the average standard deviation makes the targets look more uniform.

Biofidelity Assessment

In the previously published versions of the BRS (Rhule et al. 2002; 2009), a dummy’s biofidelity was assessed by calculating the \sqrt{R} for the dummy response, regardless of the relative timing between the dummy response and the PMHS biomechanical response target. However, Moorhouse et al (2012) recently identified some cases where the calculation of the \sqrt{R} value in this manner does not produce an outcome that accurately reflects the relative biofidelity of the dummies being evaluated. In particular this can occur when the PMHS and dummies exhibit short duration high peak responses, and the timing of the dummy response differs from the PMHS target.

Consider a PMHS response target with a large magnitude force peak such as seen in Figure 6, and

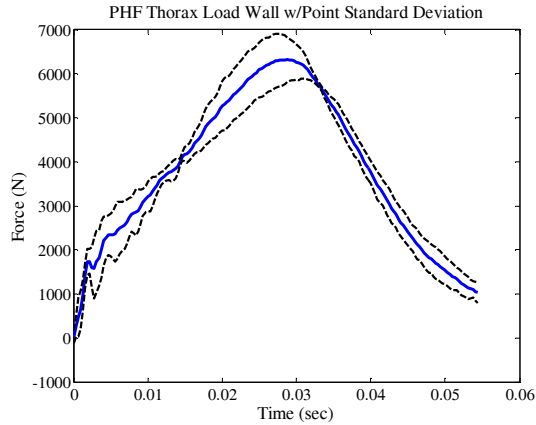


Figure 4. Thorax load wall PMHS mean response curve (thick blue) and plus- and minus-one standard deviation (thin black) targets (calculated at each point in time) for padded high speed flat wall (PHF) tests (Maltese et al., 2002)

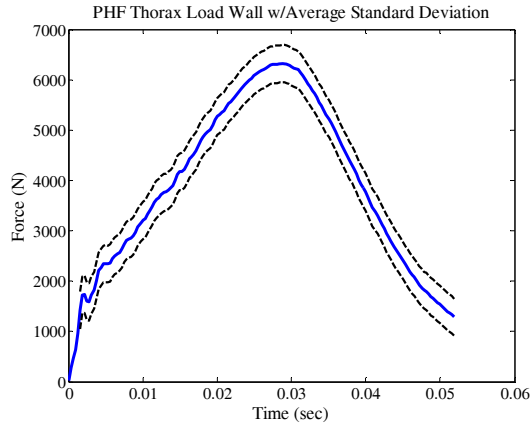


Figure 5. Thorax load wall PMHS mean response curve (thick blue) and plus- and minus-one standard deviation (thin black) targets (averaged across all points) for padded high speed flat wall (PHF) tests (Maltese et al., 2002)

three different dummies that are being compared to that PMHS target. Dummy 2 has a force peak similar in magnitude but out of phase and the other two dummies have essentially no force peak. Clearly a dummy that exhibits the proper force response, even if out of phase, is superior to one that generates no comparable force response, but the \sqrt{R} values as calculated using the methods from Rhule et al. (2002, 2009) indicate only slightly better biofidelity for Dummy 2 (Figure 6). However, if the phase differences between each dummy and the mean PMHS response curve are first minimized prior to calculating the \sqrt{R} value, the score of Dummy 2 improves and more clearly demonstrates the best biofidelity (Figure 7).

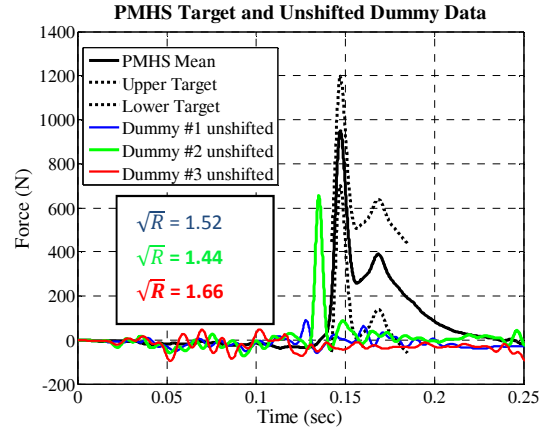


Figure 6. PMHS response target and three different dummy responses (unshifted), of which only one contains a peak response similar to that of the target, but out of phase. \sqrt{R} values are shown.

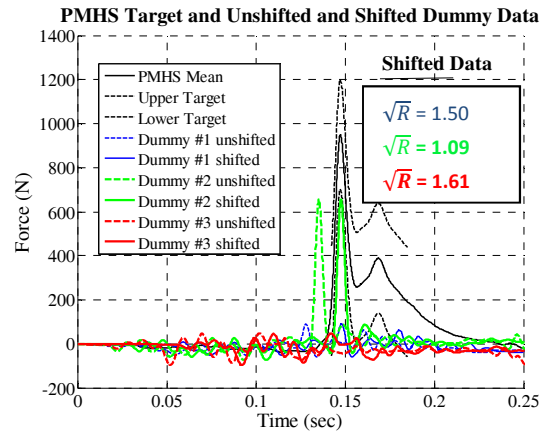


Figure 7. PMHS response target and three different dummy responses (unshifted and shifted shown). \sqrt{R} values for shifted curves are shown.

Note that minimizing phase differences prior to calculation of \sqrt{R} effectively assesses a dummy's biofidelity with respect to shape and magnitude only, and does not account for differences in the timing of the dummy response. However, with advanced restraints and countermeasures of modern vehicles the timing of a dummy response is also important and should be accounted for in a dummy's biofidelity assessment.

The example provided in Figures 6 and 7, along with the need to account for the timing of the dummy response, identifies the need for an improved method for assessing dummy biofidelity. An improvement to the BRS which accomplishes this is presented below.

Shape and Magnitude (SM value) In order to assess a dummy's biofidelity with respect to response shape and magnitude, the \sqrt{R} calculation (Rhule et al., 2002, 2009) is performed after the dummy response is phase-minimized with respect to the mean PMHS response curve. The phase minimization is accomplished using the cross-correlation function to find the phase shift, or lag, that minimizes the squared difference between the two curves, and then the dummy response is shifted toward the PMHS mean response by that amount. The resulting \sqrt{R} value between the shifted dummy response and the PMHS mean response is referred to as the Shape and Magnitude Response Comparison Value (SM). The SM value represents the difference between the dummy response and the PMHS mean response in multiples of standard deviation similar to the \sqrt{R} value in previous versions of the BRS (Rhule et al., 2002; 2009), although the SM value only considers differences in shape and magnitude. Note that this calculation is only performed for the upper 80% of the mean PMHS response, which is the portion of the response for which the standard deviation curves were generated.

Phase (P value) In order to quantitatively assess the biofidelity of the phasing of a dummy response, a ratio metric is developed in which the minimizing lag (dummy phase shift) is divided by a standard acceptable lag such that large ratios represent poor phasing and small ratios represent good phasing. The acceptable lag is found by shifting the PMHS mean curve in time with respect to itself and determining the lag between the shifted and unshifted PMHS mean curves that results in a \sqrt{R} value equal to 1.0. The absolute value of the minimizing dummy lag is divided by this standard acceptable lag to obtain a measure of phase quality. If the value of this ratio, the Phase Response Comparison Value (P), is less than 1.0, the dummy phasing is within a tolerance of one standard deviation of the PMHS mean response curve. If P is larger than 1.0, the value relates to multiple standard deviations in the same sense that multiples of the \sqrt{R} value relate to a standard deviation.

Channel Biofidelity For each response measurement, or channel, selected for biofidelity assessment there will be a Phase Response Comparison Value (P) and a Shape and Magnitude

Response Comparison Value (SM). The values for phase biofidelity, P, and shape and magnitude biofidelity, SM, are combined using a root mean square (RMS) methodology (the resultant or orthogonal vector addition) to provide a sense of the total biofidelity quality of each channel time history. The root mean square methodology is appropriate because each part, the P and the SM, measures biofidelity independently and without any interaction between the two. This is analogous to vector components in space where the resultant of the X and Y components is the magnitude of the vector. Note that both the P and the SM values are based on multiples of one cumulative standard deviation of the mean PMHS time history and thus have the same units and can be combined.

Biofidelity Rank Calculation For illustration purposes, Figures 8 and 9 show a schematic of how the Internal and External Biofidelity Ranks are calculated. For instance, if two test conditions (TC1 and TC2 in Figures 8 and 9) are selected to assess a dummy's biofidelity, and each test condition includes three internal thorax measurements (CH1, CH2, and CH3 in Figure 8), and one internal measurement for each of the abdomen and pelvis body regions (CH4 and CH5 in Figure 8), the internal biofidelity ranking schematic would look like Figure 8. Similarly, if one external measurement was recorded for each of two test conditions, the external biofidelity ranking schematic would look like Figure 9. For each response measurement there is a Phase Response Comparison Value (P) and a Shape and Magnitude Response Comparison Value (SM), which are combined using the RMS method for each response measurement (RMS in Figures 8 and 9). For each test condition the RMS values are averaged. For example, the RMS values for response measurements CH1, CH2 and CH3 are averaged to get the biofidelity rank for test condition 1 (TC 1) in Figure 8. Moving up Figures 8 and 9 to the body region level (orange, blue, and purple shading for thorax, abdomen, and pelvis body regions, respectively), each body region rank consists of the average of the test condition ranks. To obtain the Overall Internal (or External) Biofidelity Rank, the body region ranks are averaged. To obtain the Overall Biofidelity ranks, the Overall Internal and External Biofidelity Ranks are averaged.

	Overall Internal Biofidelity Rank									
Body Region	Thorax Rank						Abdomen Rank		Pelvis Rank	
Test Condition	TC 1			TC 2			TC 1	TC 2	TC 1	TC 2
Response Measurement	CH1	CH2	CH3	CH1	CH2	CH3	CH4	CH4	CH5	CH5
SM and P for each Response	SM P	SM P	SM P	SM P	SM P	SM P	SM P	SM P	SM P	SM P
RMS of SM and P	RMS1	RMS2	RMS3	RMS4	RMS5	RMS6	RMS7	RMS8	RMS9	RMS10

Figure 8. Schematic of how Internal Biofidelity Ranks are calculated

	Overall External Biofidelity Rank					
Body Region	Thorax Rank		Abdomen Rank		Pelvis Rank	
Test Condition	TC1	TC2	TC1	TC2	TC1	TC2
Response Measurement	CH1	CH1	CH2	CH2	CH3	CH3
SM and P for each Response	SM P	SM P	SM P	SM P	SM P	SM P
RMS of SM and P	RMS1	RMS2	RMS3	RMS4	RMS5	RMS6

Figure 9. Schematic of how External Biofidelity ranks are calculated

RESULTS

The padded high speed flat wall (PHF) and rigid low speed flat wall (RLF) test conditions from Maltese et al. (2002) were selected to illustrate the usage of the tools for generating PMHS response targets and the procedure for assessing dummy biofidelity. Each step of the new tool box is illustrated using the RLF thorax deflection responses.

Normalization

Figures 10 and 11 show the non-normalized and normalized responses, respectively, of the three PMHS for the thorax deflection measurement in the RLF test condition.

Phase Optimization

Figure 12 shows the normalized PMHS thorax deflection responses after optimizing the phase responses.

Target Building

After the PMHS responses are normalized and the phase differences are minimized, the PMHS mean curve is calculated at each point in time (black curve in Figure 13) and the point-by-point standard deviations are averaged for the upper 80% of the mean PMHS response (black dotted curves in Figure 13) and plotted along with the mean PMHS

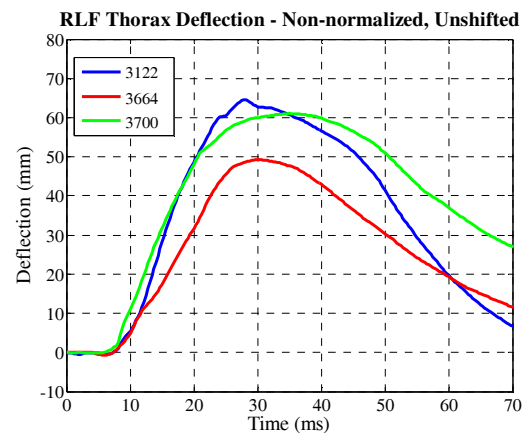


Figure 10. Non-normalized thorax deflection responses for three PMHS in RLF test condition.

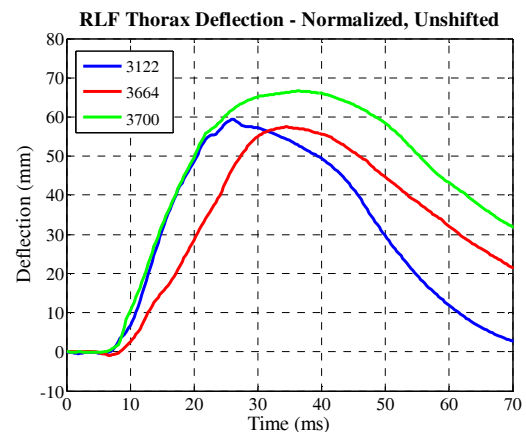


Figure 11. Normalized thorax deflection responses for three PMHS in RLF test condition.

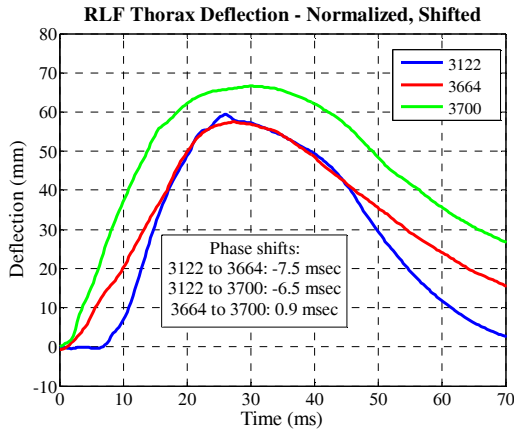


Figure 12. Normalized thorax deflection responses for three PMHS in RLF test condition after minimizing phase differences

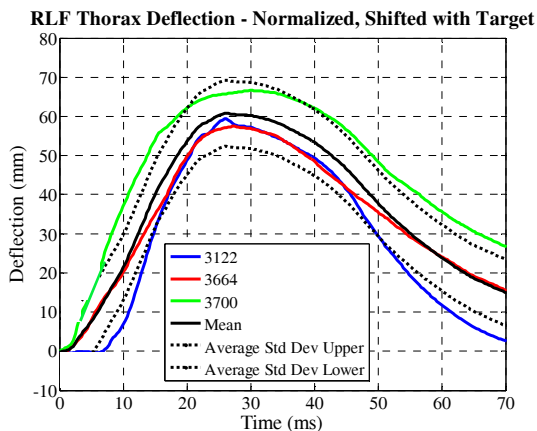


Figure 13. Mean and average standard deviation PMHS response target for RLF thorax deflection with three normalized and shifted PMHS curves

curve. The mean and average standard deviation curves represent the PMHS response and dummy biofidelity target.

Biofidelity Assessment

To assess dummy biofidelity, the dummy response is first phase-minimized with the mean PMHS response. Figure 14 shows the PMHS response target with the dummy curve unshifted (dashed pink) and shifted by 6 ms (solid pink) to minimize the phase difference. Also shown in Figure 14 is the \sqrt{R} value for the unshifted curve (as calculated in previous versions of the BRS), the \sqrt{R} value for the shifted dummy curve (SM value), the ratio of the dummy lag and the mean curve lag (P), and the RMS value. Note that the quantitative assessment of dummy biofidelity for this response would yield a value of 1.1 (\sqrt{R}) using the previous BRS and a value of 0.9 (RMS) using the new methodology.

The entire set of PHF and RLF targets with shifted dummy responses and P and SM values are shown in the appendix.

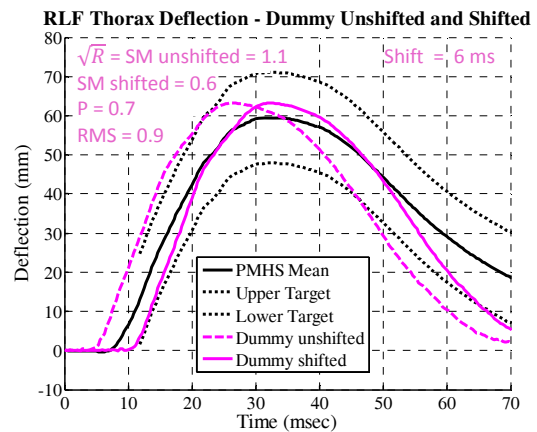


Figure 14. PMHS response target with a dummy curve unshifted and shifted with BRS values for RLF thorax deflection

Biofidelity Rank Calculation

Figures 15-18 show the SM, P, and RMS values for each response measurement included in the demonstration of the updated BRS for Dummies A and B. The External Biofidelity response measurements include thorax, abdomen and pelvis load wall forces. The Internal Biofidelity responses include T1 and T12 lateral accelerations, the average of the upper and lower thorax half chest deflections, mid abdomen half deflection and pelvis lateral acceleration. Any P or SM value over 2.0 is highlighted in red, indicating a response that varies from the mean PMHS by more than two cumulative standard deviations.

Both dummies exhibit better Internal Biofidelity than External Biofidelity, probably because they were designed to be biofidelic in measurements related to injury criteria – typically those internal to the dummy. It appears that the thorax of both dummies could be improved in the shape/magnitude component of their external biofidelity responses, indicated by the SM values over 2.0; however, the phase biofidelity is good. The abdomen and pelvis of both dummies performed well (under 2.0) in both shape/magnitude and phase for one test condition and poorly in both shape/magnitude and phase for the other test condition. The RMS values for each response measurement appropriately reflect the combined biofidelity of the shape/magnitude and phase components.

		Dummy A External Biofidelity Rank					
		2.53					
Body Region		Thorax		Abdomen		Pelvis	
		3.07		2.07		2.44	
Test Condition		PHF	RLF	PHF	RLF	PHF	RLF
		3.89	2.26	3.22	0.91	3.21	1.66
Response Measurement		Thorax Plate		Abdomen Plate		Pelvis Plate	
		SM	P	SM	P	SM	P
		3.72	1.14	2.19	0.55	2.34	2.20
		1.33	1.00	1.33	1.00	1.33	1.00
RMS of SM and P		3.89		2.26		3.21	
		3.89		2.26		3.21	

Figure 15. SM, P, and RMS values for Dummy A for each external biofidelity response measurement, and biofidelity ranks for test condition, body region and external biofidelity levels.

		Dummy A Internal Biofidelity Rank									
		1.42									
Body Region		Thorax						Abdomen		Pelvis	
		1.19						1.97		1.08	
Test Condition		PHF			RLF			PHF	RLF	PHF	RLF
		1.05			1.33			1.53	2.41	1.21	0.96
Response Measurement		T1 Lat	T12 Lat	Thx Defl	T1 Lat	T12 Lat	Thx Defl	Abd Defl	Abd Defl	Pelvis Lat	Pelvis Lat
		SM	P	SM	P	SM	P	SM	P	SM	P
		0.69	0.00	0.60	1.46	0.86	0.21	0.59	1.93	1.08	0.11
		0.60	1.46	0.86	0.21	0.59	1.93	1.08	0.11	0.60	0.67
		1.48	0.40	2.34	0.56	1.16	0.35	0.85	0.44	1.48	0.40
RMS of SM and P		0.69		1.58		0.89		2.02		1.09	
		0.69		1.58		0.89		2.02		1.09	

Figure 16. SM, P, and RMS values for Dummy A for each internal biofidelity response measurement, and biofidelity ranks for test condition, body region and internal biofidelity levels.

		Dummy B External Biofidelity Rank					
		2.95					
Body Region		Thorax		Abdomen		Pelvis	
		3.34		2.20		3.30	
Test Condition		PHF	RLF	PHF	RLF	PHF	RLF
		4.26	2.42	3.51	0.89	4.51	2.09
Response Measurement		Thorax Plate		Abdomen Plate		Pelvis Plate	
		SM	P	SM	P	SM	P
		3.96	1.57	2.42	0.11	2.63	2.33
		0.85	0.28	3.69	2.60	1.84	1.00
RMS of SM and P		4.26		2.42		3.51	
		4.26		2.42		3.51	

Figure 17. SM, P, and RMS values for Dummy B for each external biofidelity response measurement, and biofidelity ranks for test condition, body region and external biofidelity levels.

Dummy B Internal Biofidelity Rank																				
1.53																				
Body Region	Thorax						Abdomen			Pelvis										
1.37																				
Test Condition	PHF			RLF			PHF	RLF	PHF	RLF										
1.24																				
1.49																				
1.47																				
3.01																				
1.05																				
0.89																				
Response Measurement	T1 Lat Acc		T12 Lat Acc		ThxDefl		T1 Lat Acc		T12 Lat Acc		ThxDefl		Abd Defl		Abd Defl		Pelvis Lat Acc		Pelvis Lat Acc	
SM P																				
0.56 0.15																				
0.55 1.46																				
1.59 0.12																				
0.62 0.93																				
0.92 1.50																				
1.56 0.32																				
1.45 0.26																				
2.84 1.00																				
0.99 0.35																				
0.88 0.11																				
RMS of SM and P	0.58		1.56		1.59		1.12		1.76		1.59		1.47		3.01		1.05		0.89	

Figure 18. SM, P, and RMS values for Dummy B for each internal biofidelity response measurement, and biofidelity ranks for test condition, body region and internal biofidelity levels.

Table 1 shows that the External Biofidelity Rank of Dummy A is better than that of Dummy B and their Internal Biofidelity Ranks are comparable since they do not differ by more than 0.2 (Rhule et al, 2009). Overall, the Biofidelity Rank of Dummy A is better than that of Dummy B.

Table 1.
Biofidelity Ranks for Dummies A and B

	Dummy A	Dummy B
External	2.53	2.95
Internal	1.42	1.53
Overall	1.98	2.24

DISCUSSION

Normalization

The example of force-deflection curves presented in Figure 1 of the Methods section provides an excellent representation of the benefit of effective stiffness normalization.

Phase Optimization

If we assume that time zero in an impact test event is established by initial contact with the PMHS, it is likely that subjects with excessive body fat will have response data that occurs later in time than will the response data from slender subjects with minimal body fat, and vice versa. If these response curves are not phase-optimized the resulting point by point mean curve will have a broad time duration and possibly a lower magnitude. Phase optimizing allows for the mean curve to be more typical of the basic structural

response characteristic of the musculoskeletal system. The Phase Optimization method (Donnelly and Moorhouse, 2012) retains all of the phase lag information among all of the PMHS and it is used to establish the average time zero for the mean curve.

Target Building

The development of a statistically-based PMHS target using a point by point mean and standard deviation has been suggested in the past (Maltese et al, 2002; Rhule et al, 2002, 2009). When the magnitude of the response data is very nearly the same at a point in the time history, perhaps at a point where multiple response curves cross, the standard deviation can be very small. This can result in “necking” where the target created by the plus and minus standard deviation is very small. This feature in a plot of the PMHS target does not affect the mathematical calculation of the \sqrt{R} value (or SM); however, this disconcerting feature can be eliminated by plotting the average standard deviation. The average standard deviation is found by summing all the point by point standard deviations for the upper 80% of the mean PMHS response and dividing by the total number of data points included. Again, this does not affect the calculation of the \sqrt{R} value but does provide a better feel for the quality of an overplotted dummy curve.

Biofidelity Assessment

Figure 19 provides another illustration of why minimizing the phase differences between the dummy response and the mean PMHS response is necessary to obtain an accurate assessment of the biofidelity of a dummy response. Because the SM is calculated relative to the upper 80% of the mean

PMHS curve (note the start and end points of the standard deviation curves), the portion of the unshifted dummy curve (dotted blue line) that is assessed occurs after the main dummy response and is not very meaningful. When the phase difference between the dummy response and the mean PMHS response is minimized, the portion of the shifted dummy response (solid blue line) that is assessed is much more appropriate and meaningful. The SM value for the shifted curve (0.59) compared to that of the unshifted curve (1.17) reflects the better fit of the dummy response after minimizing the phase difference, while the P value (1.93) quantifies the biofidelity of the phase response of the dummy.

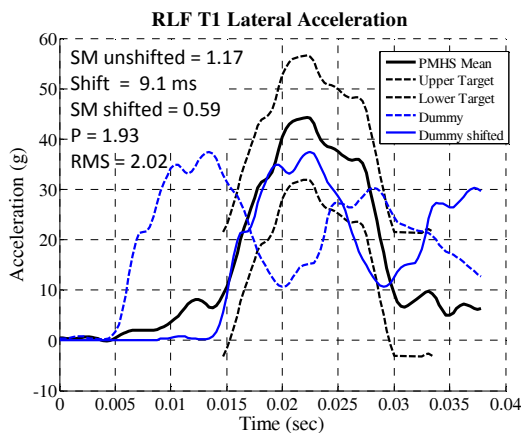


Figure 19. Unshifted and shifted response curves for Dummy A with biofidelity target for RLF T1 Lateral Acceleration

The RMS value for the RLF T1 lateral acceleration for Dummy A is 2.02, which is much different

from the 1.17 SM value for the unshifted curve (which represents the \sqrt{R} that would have been calculated in previous versions of the BRS). When the dummy phase response is poor, as it is in this case, the quantitative biofidelity assessment value for the response measurement (RMS) will show a larger difference from its predecessor, \sqrt{R} , as compared to when the dummy phase response is good. By individually assessing the biofidelity of dummy phase and shape/magnitude responses, the biofidelity assessment is more meaningful since the SM values (and thus RMS values) are now more appropriately calculated. Furthermore, the additional phase biofidelity information helps to indicate more specifically where improvement to the dummy response is needed.

Figure 20 shows the External Biofidelity assessment schematic for Dummy A using \sqrt{R} values, as would have been done using the 2009 version of the BRS. Notice that the External Biofidelity Rank of 2.83 unshifted is not very different compared to that of the 2.53 for Dummy A using the shifted data of the new methodology (Figure 15). This is because the two methods will produce similar results for well-conditioned responses (i.e., not highly out of phase or very short duration high peak responses), while the new method is able to much more accurately quantify the biofidelity for those dummy responses that exhibit some of these issues. Since this occurrence is relatively rare it is unlikely that previously published biofidelity ranks need to be re-calculated.

		Dummy A External Biofidelity Rank					
		2.83					
Body Region		Thorax		Abdomen		Pelvis	
		3.18		2.57		2.76	
Test Condition		PHF	RLF	PHF	RLF	PHF	RLF
		4.07	2.28	3.77	1.36	3.83	1.68
Response Measurement		Thorax Plate	Thorax Plate	Abdomen Plate	Abdomen Plate	Pelvis Plate	Pelvis Plate
unshifted SM		4.07	2.28	3.77	1.36	3.83	1.68

Figure 20. \sqrt{R} values for external biofidelity response measurements of Dummy A (2009 version of BRS), and biofidelity ranks for test condition, body region and external biofidelity levels.

SUMMARY

A set of tools are presented that can be applied to a set of PMHS responses, in sequence, to obtain a biofidelity target. The updated Biofidelity Ranking System is also presented for quantitatively assessing the biofidelity of a dummy as compared to the PMHS targets for phase and for shape and magnitude.

The tools are:

- Normalization for modifying PMHS response data to better represent a 50th percentile male human (or other target population).
- Phase Optimization based on all permutations of the cross-correlation functions and the Lagrange Multiplier method to find the best phase fit simultaneously for all PMHS response curves as well as determine the average PMHS phase shift to locate the mean curve in time.
- Target Building creates a PMHS response target that is statistically based and can be used to quantitatively assess the quality of a dummy response, or multiple dummies' responses.
- The Biofidelity Ranking System (BRS) has been updated to include the Shape and Magnitude Response Comparison Value, SM, the Phase Response Comparison Value, P, and the Channel Biofidelity Value, RMS. These features improve the quantitative assessment of internal and external dummy biofidelity quality.

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Appendix

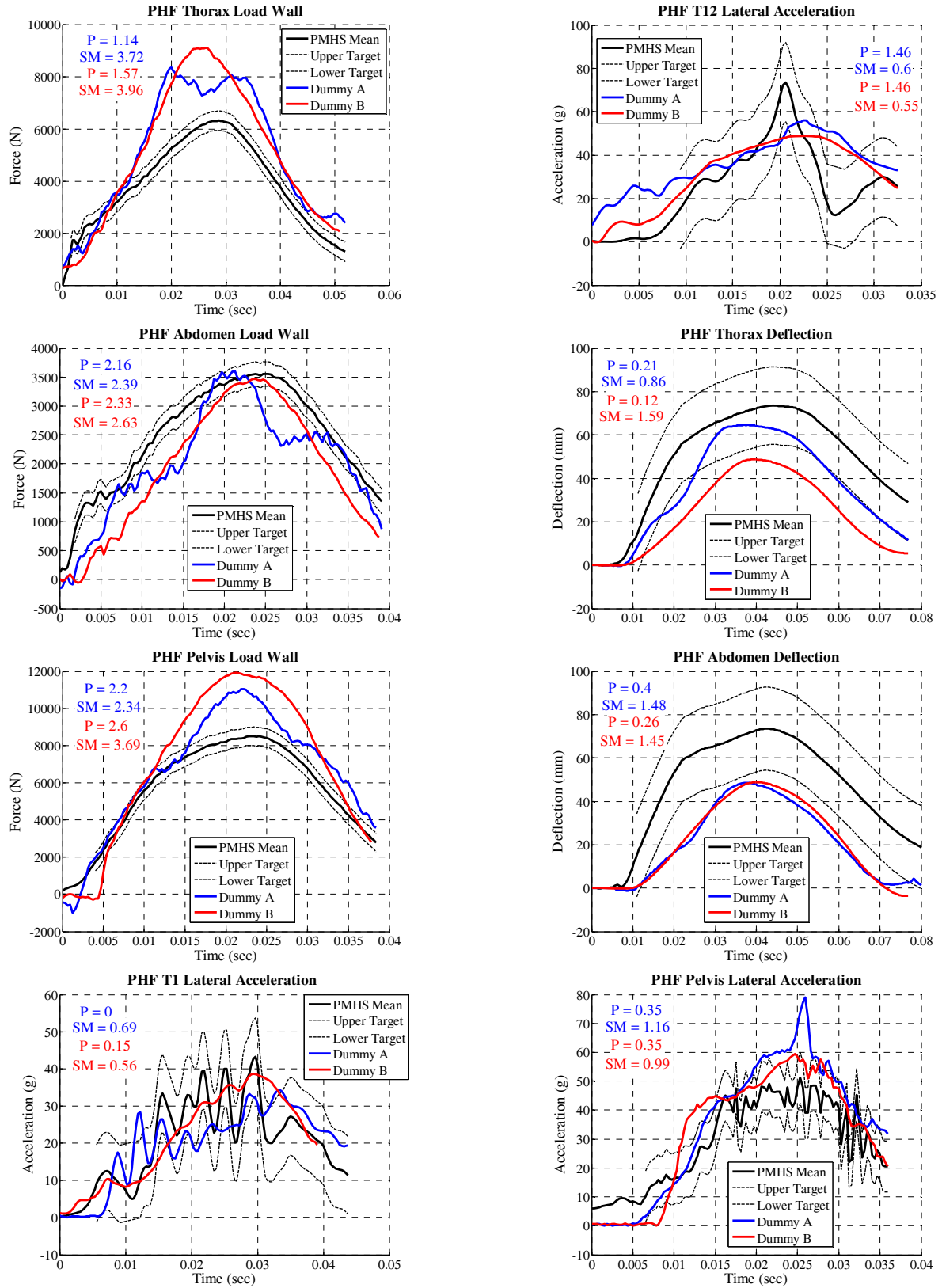


Figure A1. PMHS mean and average standard deviation targets with two side impact dummy responses for Padded High Speed Flat Wall sled tests (Maltese, 2002)

Appendix

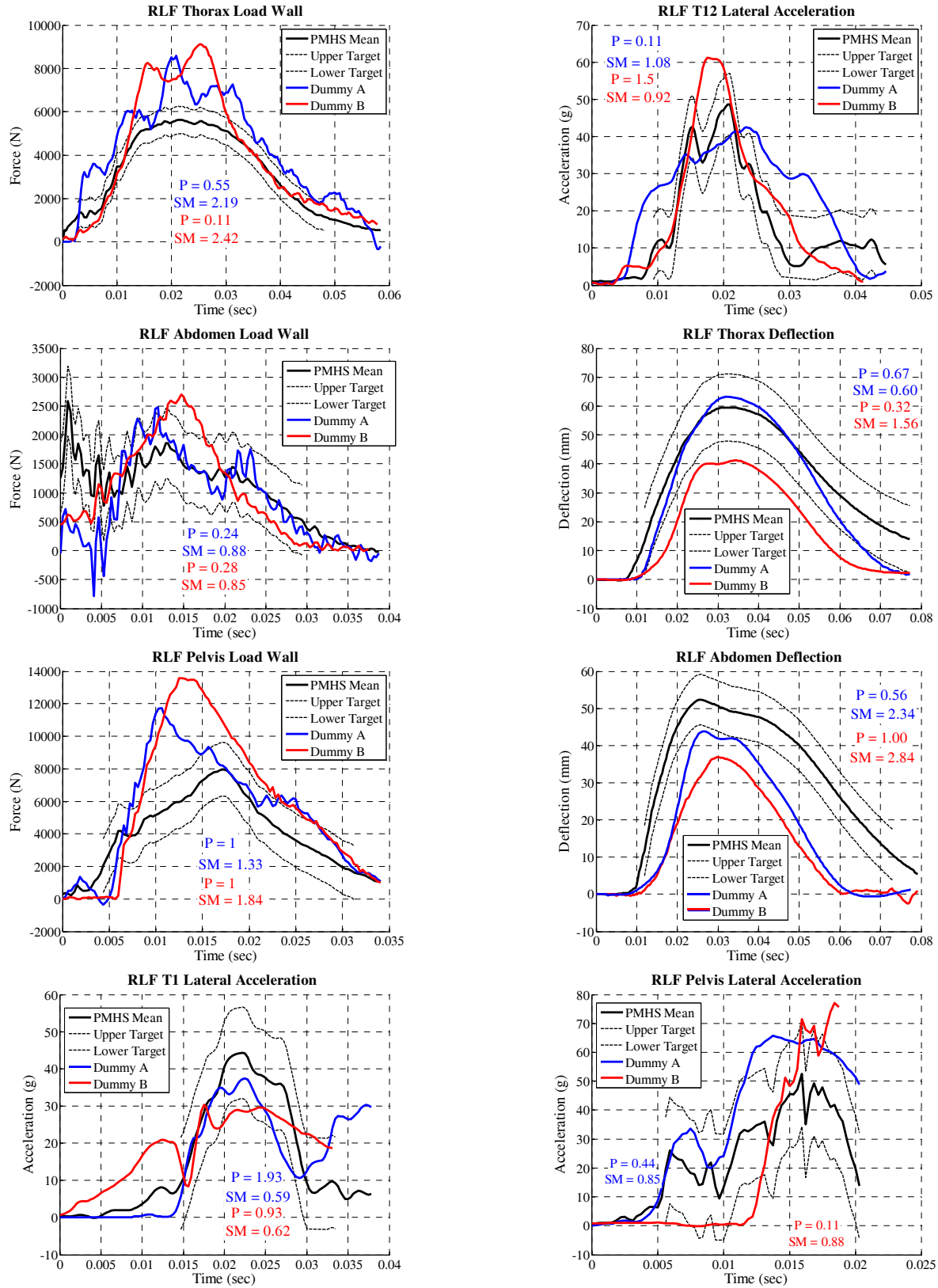


Figure A2. PMHS mean and average standard deviation targets with two side impact dummy responses for Rigid Low Speed Flat Wall sled tests (Maltese, 2002)