IRC-18-12 IRCOBI conference 2018

# Improvements to NHTSA's Biofidelity Ranking System and Application to the Evaluation of the THOR 5<sup>th</sup> Female Dummy

Heather Rhule, Jim Stricklin, Kevin Moorhouse, Bruce Donnelly

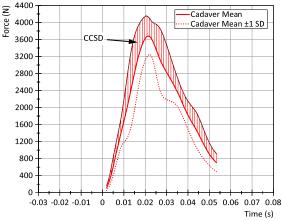
#### I. INTRODUCTION

The US National Highway Traffic Safety Administration's (NHTSA) Biofidelity Ranking System (BRS), originally developed in 2002 [1], is a method to quantitatively assess the biofidelity of crash test dummies in an objective manner, providing a fair comparison of multiple dummies. The BRS was previously updated in 2009 [2] and in 2013 [3] to improve the system based on feedback and findings from continued use. This paper discusses ongoing efforts to further improve the system, and details the methods used to evaluate the biofidelity of the THOR 5<sup>th</sup> Female dummy.

#### II. METHODS

## Cadaver Cumulative Standard Deviation (CCSD) and Dummy Cumulative Absolute Difference (DCAD)

The foundation of the BRS is the quantitative comparison of a dummy response curve to the mean cadaver response curve. Previously, this comparison was equal to the square root of the ratio of the *Dummy Cumulative Variance* over the *Cadaver Cumulative Variance* (*DCV/CCV*), where large values represented poor biofidelity and small values represented good biofidelity. This comparison has been modified for the THOR 5<sup>th</sup> dummy evaluation to be the ratio of the *Dummy Cumulative Absolute Difference* over the *Cadaver Cumulative Standard Deviation* (*DCAD/CCSD*), essentially removing the squaring of the differences at each point in time and the square root of the ratio. To calculate the *CCSD*, the digitized one standard deviation values from the cadaver mean curve are summed (Fig. 1a). To calculate the *DCAD*, the digitized absolute differences between the cadaver mean curve and the dummy response curve are summed (Fig. 1b).



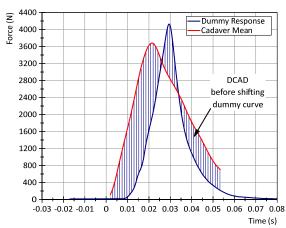


Fig. 1a. Calculating CCSD.

Fig. 1b. Calculating DCAD.

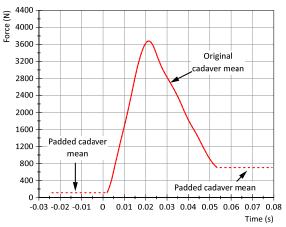
When large differences between the dummy response and the cadaver mean response occur, the previously used VDCV/CCV was larger than the DCAD/CCSD ratio due to the squaring and square root. Now the DCAD/CCSD reflects a more straightforward measure of the difference between the two curves and represents multiples of standard deviation (e.g. DCAD/CCSD = 2 means the average dummy response is 2 standard deviations from the mean cadaver response). Because the absolute differences are not squared, an averaged standard deviation tolerance band can be used to encompass the cadaver mean curve without changing the CCSD calculation (incorrectly stated in 2013 [3]).

H. Rhule (email: heather.rhule@dot.gov; tel: 937-666-3320) is a Biomechanical Engineer and K. Moorhouse, Ph. is Chief of the Applied Biomechanics Division at the NHTSA Vehicle Research and Test Center in East Liberty, Ohio, USA. J. Stricklin is a Research Engineer at the Transportation Research Center Inc., Ohio, USA. B. Donnelly, PhD is a Research Engineer at Biomechanics Research Associates, Ohio, USA.

IRC-18-12 IRCOBI conference 2018

## Shape and Magnitude (SM) and Phase (P) Values

As in the previous version of the BRS, each dummy response curve is assessed for shape and magnitude (*SM*) and phase (*P*) biofidelity [3]. To quantitatively assess the biofidelity of the phasing of a dummy response, a ratio metric is used in which the *Dummy Minimising Phase Shift* (*DMPS*) is divided by a standard *Acceptable Phase Shift* such that large ratios represent poor phase biofidelity and small ratios represent good phase biofidelity. However, the most current BRS used to evaluate the THOR 5<sup>th</sup> Female computes these quantities differently. The *Acceptable Phase Shift* is now found by repetitively shifting the cadaver mean curve in time, with respect to itself, until the sum of the <u>absolute differences</u> between the shifted and unshifted curves equals or exceeds *CCSD*. Since the cadaver mean curve has a finite length, the curve must be padded before shifting. The beginning of the curve is padded with the value of the first data point and the end of the curve is padded with the value of the last data point (Fig. 2a). The absolute differences between the shifted padded curve and the unshifted padded curve are summed over the portions of the curves that overlap with the original cadaver mean curve (Fig. 2b). Depending on the shape of the cadaver mean curve, this method can produce a different *Acceptable Phase Shift* with a left shift versus a right shift. Thus, the cadaver mean curve is shifted in the direction of the dummy response curve being evaluated. For example, for the dummy response curve shown in Fig. 1b, the cadaver mean curve would be shifted to the right when finding the *Acceptable Phase Shift*.



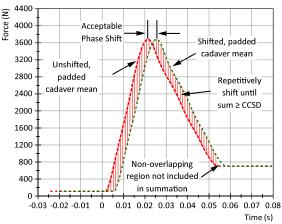


Fig. 2a. Padding the cadaver mean curve.

Fig. 2b. Calculating Acceptable Phase Shift.

To find the *Dummy Minimising Phase Shift* in the current BRS to evaluate the THOR 5<sup>th</sup> Female, the dummy response curve is phase minimised with respect to the cadaver mean curve <u>such that the minimum  $RMS_t$  value is found</u> where  $RMS_t = V(SM_t^2 + P_t^2)$ ;  $SM_t = DCAD/CCSD$ ;  $P_t = Dummy$  Phase Shift/Acceptable Phase Shift; and t is the phase shift of the dummy curve with respect to the cadaver mean response curve. Previously, the phase minimisation was accomplished using cross correlation to find the phase shift that minimised the sum of the squared differences between the two curves. However, not only do various statistics programs perform cross correlation slightly differently, certain curve shapes can cause the cross correlation function to give anomalous results. To remedy this, the dummy curve is repetitively shifted in time and the  $SM_t$ ,  $P_t$ , and  $RMS_t$  are recalculated at each time shift, until the minimum  $RMS_t$  is identified (which could result from either a left shift or a right shift) (Fig. 3). The DMPS is the phase shift that results in the minimum  $RMS_t$ . The minimum  $RMS_t$  method of finding the DMPS is currently being evaluated against other methods and will be discussed in a future publication.

Then, SM is calculated, where SM = DCAD/CCSD at the DMPS (Fig. 3). Previously, the SM value was only calculated for the upper 80% of the cadaver mean response curve (i.e. for values of the mean response greater than 20% of the peak magnitude of the mean curve) due to a carryover from the quantitative assessment of various normalization methods, using cumulative %CV (coefficient of variation). The upper 80% was used for this previous %CV assessment because small magnitudes of the mean would misleadingly skew the %CV. However, since the entire mean response curve is important for evaluating biofidelity, and the %CV is not needed for that, SM for the THOR  $5^{th}$  Female evaluation was calculated over 100% of the mean response curve.

It is important to note that only the meaningful portion of the mean response curve should be used to evaluate biofidelity (e.g. should not include excessive amounts of quiescent data in the "tails" of the response). Guidelines for defining the meaningful portion of the response curve are being considered for a future publication.

IRC-18-12 IRCOBI conference 2018

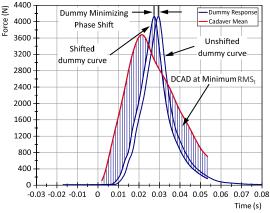


Fig. 3. Finding minimum RMS<sub>t</sub> and Dummy Minimising Phase Shift.

The *P* value is the ratio of the *DMPS* (Fig. 3) over the *Acceptable Phase Shift* (Fig. 2b). An *SM* or *P* value less than 1.0 indicates that the dummy shape and magnitude or phasing, respectively, is within a tolerance of one standard deviation from the cadaver mean response. An *SM* or *P* value greater than 1.0 indicates that the dummy shape and magnitude or phasing, respectively, is some multiple of one standard deviation from the cadaver mean response.

As in the previous version of the BRS, for each dummy response of a given biofidelity test, a total biofidelity score is calculated using a root mean square methodology:  $RMS = V(SM^2 + P^2)$ . The RMS values for each dummy response measurement (channel of data) are combined to obtain the test condition, body region, and overall biofidelity ranks. Although the external and internal biofidelity of a dummy are both important, it is not necessary to evaluate them separately, as previously done [3]. External and internal biofidelity measures were grouped together within each test condition for the THOR 5<sup>th</sup> Female biofidelity evaluation. However, it is important for the analyst to consider whether the measurements (external or internal), the response targets and test conditions used to evaluate the biofidelity of the body regions selected are meaningful and appropriate for the dummy being evaluated. For the BRS to provide meaningful results, the analyst must understand how the calculations are performed as well as the effect of selecting certain test measurements, response targets, and test conditions for biofidelity evaluation. This will be discussed further in a future publication.

### III. REFERENCES

- [1] Rhule, H., et al., Stapp Car Crash J, 2002.
- [2] Rhule, H., et al., Enhanced Safety of Veh, 2009.
- [3] Rhule, H., et al., Enhanced Safety of Veh, 2013.