ANALYSIS OF COUPLING EFFECTS IN SEATED BODY BIODYNAMIC RESPONSES TO MULTI-AXIS VIBRATION

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Introduction

The biodynamic responses of seated body exposed to whole-body vibration (WBV) have been mostly studied under single-axis vibration, except for a few very recent studies. The responses to single-axis fore-aft and vertical vibration have shown considerable sagittal plane motions and magnitudes of cross-axis responses. The reported biodynamic responses to multi-axis vibration, however, suggest negligible coupled effects of multi-axis vibration[1,2], although coupled motions of the body are clearly perceived by subjects and observed by experimenters[3]. This raises concerns over suitability of the data analysis method used in deriving multi-axis vibration biodynamic responses. This study examines the current data analysis method, primarily based on H_1 estimator, and an alternate H_3 estimator for analyses of responses to uncorrelated multi-axis vibration. The relative effectiveness of the H_3 estimator in emphasizing the coupling effects of multi-axis vibration is demonstrated through analyses of apparent mass (APMS) and seat-to-head-transmissibility (STHT) data to dual-axis (*xz*) vibration.

Methods

Majority of the studies have reported biodynamic responses derived using the H_1 method based on cross-spectral density (CSD) of the measured signals, such that:

$$H_{kl} = \frac{S_{a_k b_l}}{S_{a_k}} \; ; k=x, y, z \text{ and } l=x, y, z \tag{1}$$

Where $H_{kl}(j\omega)$ defines the complex direct (*k=l*) or cross-axis (*k≠l*) APMS or STHT function, $S_{a_k b_l}$ is CSD of the response (force measured at the driving-point or the head acceleration along direction *l*, *l=x,y,z*) and the input acceleration a_k (*k =x,y,z*) with auto-spectral density of S_{a_k}. A few studies have also employed power-spectral density (PSD) or root-mean-square (RMS) methods, which yield identical magnitude results under single axis vibration. Using the linear system theory, the total response along each axis under multi-axis vibration can be considered as the sum of both the direct- and cross-axis responses to individual axis, such that:

$$\bar{H}_k = \frac{S_{a_k \bar{b}_k}}{S_{a_k}} = \sum_l \frac{S_{a_k b_{kl}}}{S_{a_k}} \tag{2}$$

Where $\bar{H}_k$ is total biodynamic response along axis *k*, $S_{a_k \bar{b}_k}$ defines CSD of total response to input along *k*, $S_{a_k b_{kl}}$ is CSD of either direct (*k=l*) or cross (*k≠l*) component of response along *k* to single axis excitation along *l* and b_{kl} is response along *k* due to excitation along *l*. In multi-axis experiments, the vibrations applied along individual axis are uncorrelated ($S_{a_k a_l} = 0$), which would lead to $S_{a_k b_{kl}} = 0$ (*k≠l*). Consequently, the biodynamic responses derived using H_1 method would not account for the contributions of the cross-

axis components observed under single axis vibration. The PSD method considers auto-spectral density of response alone and could thus appropriately account for cross-axis components, while it would not provide the phase data. Alternatively, the H_3 estimator combines the advantages of both the H_1 and PSD methods, by incorporating the cross-axis components and providing the phase information, and is given by:

$$H_k = \sqrt{\frac{S_{a_k \bar{b}_k}\ S_{\bar{b}_k}}{S_{a_k}\ S_{\bar{b}_k a_k}}} \tag{3}$$

The suitability of H_3 estimator is investigated through analyses of STHT and APMS data acquired with 9 seated subjects exposed to individual *x* and *z*-axis and combined *xz* axes.

Results

Fig. 1 compares the mean vertical APMS and STHT responses obtained under single-axis vibration using the H_1 method, and under dual-axis vibration using H_1 and H_3 estimators. The dual-axis responses derived using H_1 are quite comparable to the single-axis responses, particularly in APMS, as reported[1,2]. The H_3 method, on the other hand, shows greater coupling effect of the dual-axis vibration by emphasizing contributions due to cross-axis responses observed under single-axis vibrations, which are evident at lower frequencies. The results obtained using H_3 method also support the response attained through superposition of direct and cross axis responses to single-axis vibration[3]. The H_3 method is thus considered better suited for the analysis of biodynamic response data to uncorrelated multi-axis vibration and the study of coupling effects.
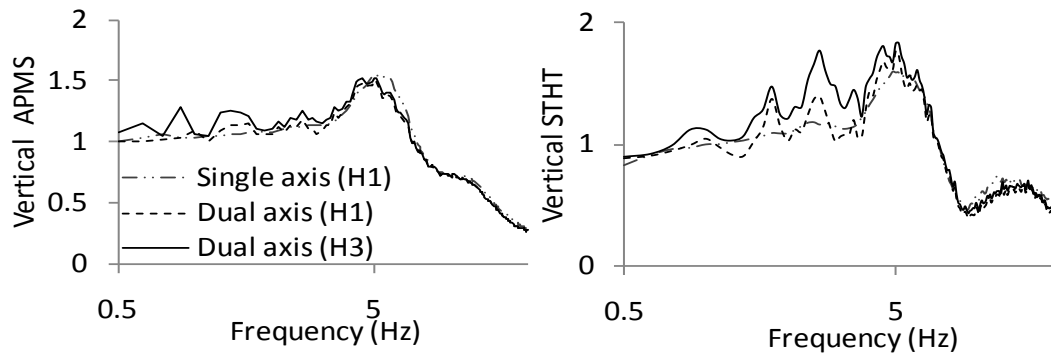

Fig. 1: Comparisons of single- and dual-axis vertical APMS and STHT responses.

References

1. Hinz B, Blüthner R, Menzel G, Rützel S, Seidel H and Wölfel Horst P (2006). Apparent mass of seated men – Determination with single and- and multi-axis excitation at different magnitudes. J. Sou & Vib, 298, 788-809.

2. Mansfield N J and Maeda S (2007) The apparent mass of the seated human exposed to single-axis and multi-axis whole-body vibration. J. Biomechanics, 40, 2543-2551.

3. Mandapuram S, Rakheja S, Boileau P-É, Maeda S and Shibata N (2009) Apparent mass and seat-to-head transmissibility responses of seated occupants under single and dual axis horizontal vibration. Prod. 4th Whole-Body Vib Injury Conf, 33-34.