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# THE EFFECT OF ANATOMICAL LANDMARK MISPLACEMENT ERRORS ON TRUNK JOINT ANGLES MEASUREMENT

[1] Hossein Rouhani, [1]Sara Ayatollahzadeh, [2]Richard Preuss, [1]Kei Masani and [1]Milos R. Popovic
[1]Rehabilitation Engineering Laboratory, Institute of Biomaterials and Biomedical Engineering, and Toronto Rehabilitation Institute, University of Toronto, Canada
[2]School of Physical & Occupational Therapy, McGill University, and the Constance Lethbridge Rehabilitation Centre site of the Centre de recherche interdisciplinaire en réadaptation (CRIR), Canada;
email: hossein.rouhani@utoronto.ca , web: www.toronto-fes.ca

## SUMMARY

Trunk kinematics is being recently studied using multi-segment trunk models to assess the small angular motions among vertebrae. Because of such small ranges of angular motion, the measurement errors can considerably affect the assessed 3D joint angles. A major type of measurement errors is the anatomical landmark misplacement error that affects the axes of the segment's anatomical frame. The present study aimed at investigating the effect of anatomical landmark misplacement errors on the assessment of 3D joint angles in a multi-segment trunk model. Six healthy subjects performed forward trunk bending and six cameras recorded the trajectory of 22 reflective markers on the anatomical landmarks of seven segments of their trunk. Simulated markers misplacement errors were added to the original recorded data and the relative errors in the 3D range of angular motion of the trunk joints were calculated. The induced errors in the sagittal ranges of motion in all joint were ignorable (<1%). However, the induced errors in the frontal and transverse ranges of motion in all joints were much larger (over 13%) because of the small original ranges of motion. Although these latter errors were still small, they should be considered carefully when the results of the analysis are used for clinical decision making.

## INTRODUCTION

Trunk and vertebral column motions measurement have been of interest in a variety of clinical evaluations for patients with low back pain [1], spinal cord injury [2], etc. Thanks to development of more accurate motion-capture systems, recently, the flexible trunk complex can be considered as several segments and their kinematics can be studied separately [3]. In such multi-segment trunk models, 3D kinematics of each segment is measured based on recording the trajectory of at least three anatomical landmarks on the segment forming an anatomical frame. Usually, reflective markers are placed on these landmarks and their trajectory during trunk bending is recorded by motion-capture systems (e.g., cameras). Among different types of experimental errors, anatomical landmarks misplacement errors made by examiner while palpation have been considered as a major source of error in assessment of 3D joint angles, through affecting the axes orientation of the segments' local anatomical frame [4]. Such induced errors have been widely discussed for lower limb joints [5], but were never assessed for multi-segment trunk joints. When several segments are considered in the trunk model, the range of motion of the joints among them is small. Therefore, the anatomical landmark misplacement errors may considerably affect the calculated 3D joint angles [6], and their influence must be assessed in clinical measurement protocols with a specific trunk motion.

This study aimed to investigate how the anatomical landmark misplacement errors, in kinematics measurement of multi-segment trunk, affect the calculated 3D joint angles among trunk segments.

## METHODS

*a) Measurement protocol*

Six young healthy subjects participated in this study. They sat on a chair with 75% of their thigh length supported on the chair. A multi-segment trunk model was considered composed of upper thoracic (UT), mid-upper thoracic (MUT), mid-lower thoracic (MLT), lower thoracic (LT), upper lumbar (UL), lower lumbar (LL), and sacral (SC) segments. 22 10-mm reflective makers were placed on their skin over the vertebral column such that every 3 markers could record the 3D orientation of each segment separately according to Figure 1. A target was placed in front of the subject in the sagittal plane. Subjects were asked to bend their trunk to touch the targets by their head. The target's height and distance were adjusted based on each subject's height to achieve a total 45 deg of angular motion of the whole trunk when the head reaches the target. Six cameras (Vicon, UK) recorded markers trajectories at 120 Hz. The same experimental data as in [3] was used.

*b) Data Analyses*

Every three markers over a segment formed a local coordinate system (also used as segment's anatomical frame) and the 3D joint angles between consecutive segments were calculated based on joint coordinate system (JCS) convention [5]. Based on our previous studies [6], anatomical landmark misplacement errors were modeled as a Gaussian error with dispersion of 7 mm at each of the two directions on the skin surface in vicinity of the bony landmark on which the marker was placed. This error was set constant during each trial. For each trial of each subject, this random error was added to the marker trajectory and the erroneous 3D joint angle was calculated (as an angular curve during trunk bending). Then, the difference between the range of erroneous and original angles divided by the original range was calculated as the relative error (%). This simulation was repeated 20 times for each trial of each subject and then the relative errors were averaged over all simulations, all trials, and all subjects.

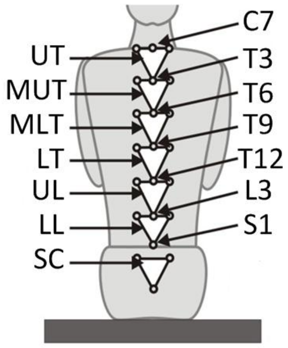


*Figure 1. Marker placement on trunk anatomical landmarks [3]. Markers in both sides of the vertebral column were installed 10 cm apart.*

**RESULTS AND DISCUSSION**

The range of angular motion (ROM) of joints between neighbor trunk segments (UT~MUT, MUT~MLT, MLT~LT, LT~UL, UL~LL, and LL~SC), in the sagittal, frontal, and transverse planes are presented in Table 1. According to Table 1, the joints between lumbar segments and LL~SC joint had a major contribution (76%) in the trunk bending in the sagittal plane, and the joints between thoracic segments had a minor contribution. However, during forward bending of the trunk, the angular motions in the frontal and transverse planes were similar among all trunk joints (1.2 to 2.5 deg). The relative errors in measurement of these ROMs due to anatomical landmark misplacement errors are presented in Table 2. The marker misplacement errors caused ignorable errors in the joints ROM in the sagittal plane (<1%). However, due to the small amplitude of the joints ROMs in the frontal and transverse planes while bending forward in the sagittal plane, the induced relative errors in the frontal and transverse ROMs were much larger (over 13%). Although these relative errors might still be considered as small, more caution should be exercised when this data is interpreted, in particular if this interpretation is used to base clinical decisions.

**CONCLUSIONS**

The effect of the anatomical landmark misplacement errors on assessment of the 3D joint angles among trunk segments was investigated during forward bending of the trunk (similar to reaching tasks). In a multi-segment trunk model, the relative error induced in the range of angular motion of all joints in the sagittal plane was ignorable (<1%). However, the relative error induced in the joints angular motion in the frontal and transverse planes during forward bending of the trunk was much larger (over 13%). Although these latter errors were still small compared to the joints range of angular motion, they should be considered with caution especially if this data is used for clinical assessments.

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*Table 1. The range of angular motion (ROM) of the joints between trunk segments (Segment1~Segment2) in the sagittal, frontal and transverse planes. ROMs are presented in degree as mean±SD among subjects.*

| | UT~MUT | MUT~MLT | MLT~LT | LT~UL | UL~LL | LL~SC |
|---|---|---|---|---|---|---|
| Sagittal | 4.2 ± 1.4 | 4.5 ± 2.3 | 3.7 ± 1.1 | 7.6 ± 3.9 | 15.5 ± 6.2 | 15.9 ± 5.7 |
| Frontal | 1.6 ± 1.0 | 1.2 ± 0.9 | 1.3 ± 0.3 | 1.8 ± 0.2 | 2.1 ± 0.7 | 1.9 ± 0.9 |
| Transverse | 2.1 ± 1.4 | 1.6 ± 0.6 | 2.4 ± 0.6 | 2.5 ± 0.9 | 2.2 ± 0.7 | 1.6 ± 0.5 |

*Table 2. The errors propagated in ROMs of the joints between trunk segments (Segment1~Segment2) due to on anatomical landmark misplacement errors. The relative ROM errors in the sagittal, frontal and transverse planes are presented in percentage of the original ROM as mean±SD among subjects.*

| | UT~MUT | MUT~MLT | MLT~LT | LT~UL | UL~LL | LL~SC |
|---|---|---|---|---|---|---|
| Sagittal | 0.5 ± 0.3 | 0.5 ± 0.2 | 0.8 ± 0.2 | 0.4 ± 0.2 | 0.2 ± 0.1 | 0.2 ± 0.1 |
| Frontal | 4.6 ± 1.4 | 7.2 ± 2.4 | 7.9 ± 2.3 | 4.5 ± 1.9 | 3.7 ± 1.7 | 11.5 ± 5.4 |
| Transverse | 2.1 ± 0.9 | 3.5 ± 1.6 | 1.7 ± 1.5 | 3.5 ± 2.2 | 8.4 ± 2.9 | 13.2 ± 7.8 |