

# Simulation-Based Morphing of Personalized Models of the Torso for Scoliosis Brace Design – Preliminary Results

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**INTRODUCTION:** Computational and personalized design of braces for patients suffering from adolescent idiopathic scoliosis is a subject that has not been extensively studied and faces several unknowns. One of the most challenging tasks is the development of patient-specific biomechanical models of the torso. The first step required in order to build a personalized model is the acquisition of the patient’s specific geometry, i.e., the bones and joints of the skeleton. To this end, this study morphs a template torso model into patient-specific data in the following way: We start by acquiring x-rays, and we annotate personalized landmarks. Then, we use as template a biomechanical torso model consisted of a multibody dynamic system coupled with FEM and we proceed to the morphing in two steps. First, an initial tuning by adjusting the global scale of the model and finally a finer one, taking into account local deformations.

**METHODS:** Frontal and sagittal x-rays of five young patients with a mild scoliotic curve were obtained (normal-dose x-rays for one patient, low-dose for the other four). We obtained oral and written consent according to national guidelines and the Helsinki Declaration, and with approval of the local ethics committee study (No H-17034237). The vertical range of the low-dose x-ray machine was limited; therefore, for tall patients we obtained two lateral and two sagittal images, which were stitched together by clinical experts. On each stitched x-ray, we selected the center point of each vertebra, along with a supplementary point on a line parallel to the upper end-plate of the vertebra and passing through the center point. Thus, we can define the position and orientation of vertebrae on both frontal and sagittal planes. We then leverage a reference torso model [1], which we deform to match the patients’ geometry. Initially, we scale the model. The scaling coefficients in the longitudinal and sagittal axes are calculated according to the height difference between T1 and L5. The scaling coefficient in the frontal axis is calculated according to the maximum distance between the sixth pair of ribs. Finally, we deform the reference torso model to match the patient’s landmarks, by solving a constrained equilibrium problem. In this deformation step, we impose soft constraints for the center points and orientations of the vertebrae, and we constrain the lateral rotation of the pelvis to match the measured one. For the axial rotation of vertebrae, we estimate the apical axial rotation as  $0.52 * \text{Cobb angle}$  [2], and we define a rhythm in order to distribute the axial rotation to the rest of the vertebrae.

**RESULTS SECTION:** A total of five patients’ x-rays were used in this study. In order to validate our work, we captured frontal and sagittal images of the deformed model and we used widely accepted anatomical parameters for comparisons between our result and the x-rays. The parameters are found and explained in [3]. For validation, we used the patient with normal-dose x-rays. This is also used in [3], and next we compare error measurements:

	RH5-10	RVA6-10	RVAD6-10	RSD	AVB_R	MT Cobb	TL/L Cobb	AVTThorax	AVTLumbar	LL	TK
Shayest [3]	6.3 mm	6.6	10.2	6 mm	0.22 (ratio)	-	-	-	-	-	-
Normal x-ray	9 mm	4.7	7.4	1 mm	0.23 (ratio)	2	5	1 mm	3 mm	2	7

Table 1: Error comparison between our method and [3]. Units are in degrees unless stated differently.

Table 2 summarizes the average error of the remaining four patients. Note that, for low dose x-rays, some parameters such as the rib hump or the thoracic kyphosis angle are impossible to measure with precision, so we discard them from the comparisons.

	RH5-10	RVA6-10	RVAD6-10	RSD	AVB_R	MT Cobb	TL/L Cobb	AVTThorax	AVTLumbar	LL	TK
Low dose x-rays	-	5.1	2.2	1.1 mm	0.03 (ratio)	2.5	3	1.1 mm	2 mm	3.2	-

Table 2: Average error of four patients with low dose x-rays. Units are in degrees, unless stated differently.

**DISCUSSION:** As depicted in the two tables and the figure, the errors between our results and the x-rays are minimal, especially in the parameters that describe the full torso (MT Cobb angle, etc.). RVAD is an important measure for scoliosis as it illustrates the downward tilt of the ribs on the convex side compared with the concave one. The highest average error obtained is less than 7.5 degrees. The highest errors in the method are found in the RVA. We cannot achieve an exact match, as we apply a rigid transformation and we do not actually deform the bones; however, the accuracy achieved is sufficient for our target application. Furthermore, we have applied our methodology only to patients with moderate scoliosis, none with severe scoliotic curves. Usually, these patients need surgery, as the brace treatment is not sufficient for their case. Finally, the proposed methodology requires manual input for the landmark annotation, which could be a source of error. Fortunately, the use of soft constraints in the simulation allows a significant tolerance in the selection of landmarks.

**SIGNIFICANCE:** This study provides a step towards the development of patient-specific biomechanical models and computational design of personalized scoliosis braces.

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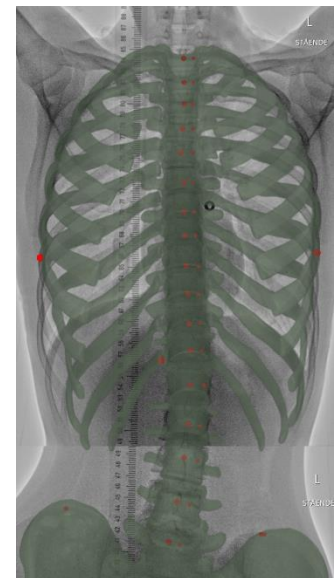


Fig. 1: A patient’s x-ray with the annotated landmarks and on top the morphed geometry drawn green semitransparent.