

# Comparison of deviations in SAR prediction between highly detailed and proper simplified human models at 7T

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## Introduction

Using RF simulations of human models are one current approach to stay within the given SAR limits for in-vivo MR examinations [1]. This approach, however, requires a thorough understanding of any consequences of remaining differences between the used model and the actual patient's geometry or structure. The consequences of this generalization regarding intensity and location of possible hotspots, i.e. for high RF frequencies, are still in exploration [2, 3].

In this work, deviations in the SAR prediction caused by simplification of the model are compared to deviations between highly detailed models, which do or do not reflect the actual patient. Since simplification allows reduction in calculation times, this may pave the road to individualized SAR prediction.

## Methods

All simulations have been performed in CST MicrowaveStudio [4] using a 7T birdcage head coil [5], fed at two ports, exciting a circularly polarized mode. As human models, the virtual family man and woman [6], with a cubic voxel-size of 2 mm, were used. At this isometric resolution, the male whole body model has a size of 270x141x902 and the female whole body model has a size of 252x139x817. These models provide a variety of over 80 different tissue types with about 45 dielectric properties in the whole body. Of these tissues, 49 represent the head of the model, providing 25 dielectric properties [7]. All the models have been positioned with their head centered in the head-coil and facing upward. For evaluation, the specific absorption rate (SAR) was calculated at 298.2 MHz for 1W input power. For the comparison, these values have been normalized to archive the same mean magnetic field in a certain cross-section of the model's head. For both models it is evaluated how much the extent can be truncated to reduce the models size. In addition, different tissues inside the model have been combined to further simplify and accelerate the calculation. The resulting E-fields of the different simplification steps of the female model are compared to the E-fields of the unmodified male model. This provides an indication of the inaccuracies induced by such model simplifications compared to commonly accepted inter-individual differences.

## Results

Assuming that the full female model is the actual subject to be examined, it is used as a reference. A reasonable truncation of this model and an additional simplification of the tissue structure have been determined (cf. fig1) resulting in deviations of the global and local SAR of below 1%. This is consistent with previous results on the virtual family male model [8]. There are similarities with the male model regarding the SAR pattern. A comparison of the SAR-distribution in cross-sections through one of the three highest hotspots of the female model can be seen in fig2. These are very similar to the patterns in the male model. A direct comparison between different simplifications of the model of the virtual family woman and the unmodified virtual family man is shown in table1. Considering the three highest ranked hotspots of both models, a similar position of the first two hotspots is observable. Only the third hotspot is at a different position inside the model's head. Furthermore, the intensities of the models' hotspots differ by about  $\pm 10\%$  between the models.

## Discussion

It has been shown that model simplifications such as reduced extension and reduction of tissue types are feasible and may allow the creation of human models, which are more similar to the actual subject. Quantitative results show only very minor impact of the simplification. In addition, similarities between different models have been demonstrated, suggesting that individual SAR prediction may be possible by selection of a proper model that is close to the actual subject's geometry. Quantitative differences between the "large" and "small" model used here, show that patient size differences seem to have a larger effect than the model simplifications introduced here.

model	model-weight [kg] (head)	power loss [W] (head)	global SAR [W/kg] (head)	TOP3 local SAR (10g) [W/kg] + position (x,y,z)[m]		
vf_woman (reference)	4.2	584.8	138.1	470.6 (0.040, 0.010, -0.027)	378.4 (0.000, -0.054, -0.033)	368.5 (0.020, 0.057, -0.027)
vf_woman (truncated)	4.2	577.6	136.4	464.8 (0.040, 0.010, -0.027)	373.7 (0.000, -0.054, -0.033)	363.9 (0.020, 0.057, -0.027)
vf_woman (muscle shoulders)	4.2	584.8	138.2	471.0 (0.038, 0.012, -0.027)	379.3 (0.000, -0.054, -0.033)	376.5 (0.020, 0.057, -0.027)
vf_man (unmodified)	5.0	610.6	122.3	520.2 (0.040, 0.018, -0.027)	380.6 (0.000, -0.046, -0.051)	336.1 (0.008, 0.006, 0.075)

Table 1: Overview over power loss and SAR values of the virtual family woman, for truncation and tissue simplification compared to the virtual family man.

## Acknowledgement

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## References

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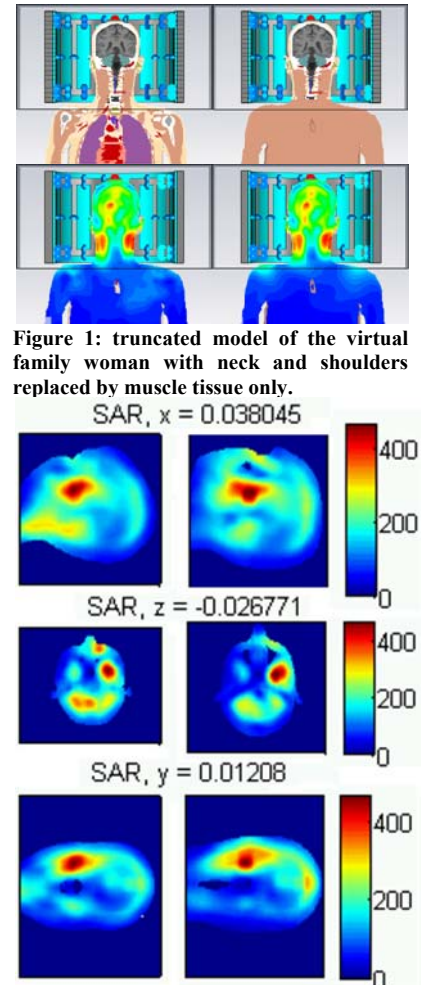


Figure 1: truncated model of the virtual family woman with neck and shoulders replaced by muscle tissue only.

Figure 2: Comparison of the SAR distribution of the virtual family woman (left) with the virtual family man (right) in three cross-sections through a hotspot.