A Robust Concept for Real-Time SAR Calculation in Parallel Transmission

H. Homann[1], P. Börnert[2], O. Dössel[1], and I. Graesslin[2]
[1]Institute of Biomedical Engineering, Karlsruhe Institute of Technology, Karlsruhe, Germany, [2]Philips Research Europe, Hamburg, Germany

Introduction The estimation of the local specific absorption rate (local SAR) in parallel transmission MRI systems is a challenging problem. For a given transmit array, the SAR depends on the RF waveforms used on the different channels. Real-time calculations of the local SAR based on generic patient models allow optimizing the safety margin [1]. On the other hand, the SAR also depends on patient-specific parameters, such as the body size and shape, sex, and the body position relative to the transmit elements [2]. A possible solution to this problem is the use of patient-specific SAR models.
However, in a clinical setting, it is not practical to generate a specific SAR model for every patient. Instead, a large number of different body models needs to be considered for a robust estimation of the worst-case SAR. This study suggests an approach for the efficient real-time calculation of the worst-case local SAR when using a large number of body models for robust RF safety assessment.

Methods SAR estimation in parallel transmit MRI systems can be achieved by superposition of the pre-simulated electric fields. The electric fields E can be stored as a local power sensitivity matrix $Q \sim E^H \cdot E$ for each mesh cell and weighted with the respective waveform I to calculate the local SAR [3]. However, it is not necessary to calculate the local SAR for each cell of a body model. Instead, a clustering approach can be used to identify a mesh cell i where the SAR is smaller than in another cell j for all RF waveforms I (Eq. 1). These mesh cells can be excluded from the calculation of the maximum SAR. This yields a significant model compression [4] when using an additive SAR overestimation ε term (Eq. 2) and can be solved by calculation of the smallest eigenvalue λ_{min} of $Q_j - Q_i$ (Eq. 3).

$$SAR(cell\ i) \leq SAR(cell\ j) \quad \forall I \quad (1)$$

$$\Leftrightarrow I^H Q_i I \leq I^H (Q_j + diag(\varepsilon)) I \quad \forall I \quad (2)$$

$$\Leftrightarrow -\varepsilon \leq \lambda_{min}(Q_j - Q_i) \quad (3)$$

In this study, this clustering approach is applied twice to improve the SAR calculation efficiency when using multiple body models. The algorithm consists of the following steps: 1) Clustering according to [4] is performed for every single body model in order to reduce the computational effort of the following steps. 2) The local matrices Q of several models are combined to a generalized model in order to represent different anatomies and/or body positions. The generalized model gives an upper bound of the SAR. 3) The clustering algorithm is applied for a second time to further compress the generalized model.
Simulations were performed for an 8-channel 3T body coil [5] using the finite-differences time domain method (XFDTD, Remcom Inc., PA, USA). Multi-model clustering was performed for two cases: a) using the Visible Human [6] at 18 positions of the model relative to the TX array and b) using body models generated from 6 volunteers representing different anatomies [7]. The SAR overestimation term ε was defined as a percentage of the maximum local SAR in any of the models at quadrature excitation.

Results and Discussion The original number of SAR cells was 750,000 for the Visible Human and 310,000 – 540,000 for the volunteer models. The local SAR for the Visible Human at different stations of the patient is shown in Fig. 1. The first clustering step (using ε=10%) reduced the number of cells in the Visible Human model to 83 – 5,190, depending on the station, and to 223 – 2,365 for the different volunteer models. The second clustering step resulted in a further reduction of the required number of cells, as shown in Fig. 2 as a function of ε. Using ε=10% in the second clustering step yields a compression of the generalized models by approximately 85% for both cases. Further improvement can be obtained by higher ε.
For the Visible Human, several patient positions were no longer included in the reduced generalized model. This means that the maximum local SAR does not occur at the respective patient position for any waveform. For the reduced generalized model generated from the volunteer models, such a relation was not found. This means that the maximum SAR can occur in any of the volunteers, depending on the waveforms. Overall, the memory requirements as well as loading and calculation times are drastically reduced.

Conclusions The presented approach removes the redundancy between multiple body models. The calculation time is almost independent of the number of models used. This allows for efficient and robust local SAR estimation in parallel transmit MRI. The approach can be applied for real-time safety assessment or for fast iterative optimization of the RF waveforms for SAR reduction.

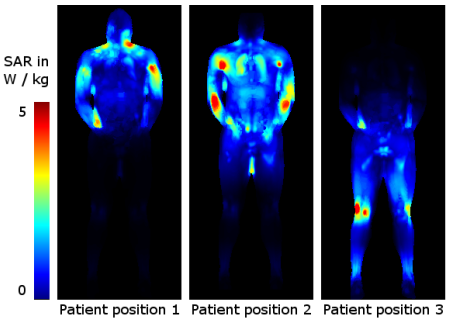

Fig. 1: Projections of the SAR simulated for the Visible Human at different model positions for quadrature excitation.

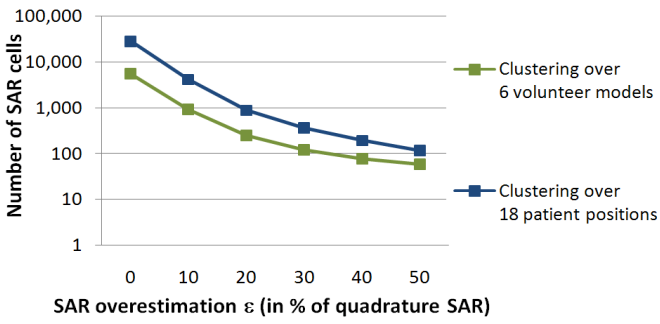

Fig. 2: Number of remaining mesh cells for the real-time SAR estimation as a function of the overestimation term ε in the second clustering step.

References

[1] I. Graesslin, Proc. ISMRM 2008, p.74
[2] W. Liu, Appl.MR 29:5-18 (2005)
[3] I. Graesslin, Proc. ISMRM 2010, p. 3873
[4] M. Gebhardt, Proc ISMRM 2010, p.1441
[5] P. Vernickel, MRM 58:381-389 (2007)
[6] "Visible Human Project" 1996, NLM
[7] H. Homann, Proc. ISMRM 2010:3874