

Multi-body-model Method for Design of Mismatch-insensitive SAR-aware Parallel Transmit RF Pulses

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TARGET AUDIENCE: Researchers and engineers interested in RF safety and parallel transmit

PURPOSE: At higher fields, shorter electromagnetic wavelengths result in increased sensitivity of local SAR distributions to intersubject anatomical variations. Due to the present lack of availability of in-vivo SAR mapping methods, numerical simulation using a realistic coil model and patient-matched body model is the approach of choice for local SAR estimation. To address increased mismatch sensitivity at higher field strengths, one approach is to create dense body model libraries spanning a wide range of anatomies, tissue properties, and positions within coil. Such an approach has previously been intractable due to the extreme computational demands given the number of combinations that must be considered. We propose a simple strategy for reducing the necessary density of the library – the use of multiple body models for SAR estimation – and a time-efficient implementation of this multi-body-model concept. By taking the M most closely matched models from a relatively sparse library and considering the SAR over all voxels of all M models, we show that one can largely reverse the significant error that arises when using just a single closest match model from this sparse library. With this approach of multi-body-model SAR estimation, one need only construct a relatively sparse body model library but still be guaranteed a relatively small error in SAR estimation.

THEORY: The standard method to account for local SAR during pulse design is to require that $\max_{v \in \mathcal{V}} (\mathbf{b}^H \mathbf{Q}_v \mathbf{b}) \leq \psi$ where \mathbf{Q}_v is the n -gram spatially averaged local SAR matrix at voxel v within a single body model \mathcal{V} (assumed to be closely matched to the patient) and ψ is the n -gram local SAR regulatory limit. In the proposed method, we use a stricter constraint on local SAR by requiring that $\max_{v \in \{\mathcal{W}_1, \dots, \mathcal{W}_M\}} (\mathbf{b}^H \mathbf{Q}_v \mathbf{b}) \leq \psi$ where $\mathcal{W}_1, \dots, \mathcal{W}_M$ correspond to M body models from a sparser library, each with a moderate amount of mismatch. Mathematically, these two approaches are identical, as the multi-model approach merely results in an increase in the total number of SAR matrices by a factor of M . In practice, however, the Virtual Observation Points (VOP) [1] based approach for optimization (presently, the most commonly used SAR-aware pTx pulse design method) has the drawbacks of long computation time for the compression as well as an increase in the number of VOPs which increases duration of the optimization. Instead, we use the recently developed IMPULSE algorithm [2] which allows for optimization directly without a compression precomputation step and scales favorably with total number SAR matrices.

METHODS: We used an 8-channel loop array to simulate (SEMCAD X) electric fields at 298 MHz (7T) using nine different body models for estimation (Figure 1). Using diffeomorphic registration [3], we created a body model “Ellie” as a hybrid between the Ella and Billie body models from the Virtual Family collection; Ellie is then treated as the patient. We then built densely sampled (\mathcal{V}) and sparsely sampled (\mathcal{W}) libraries, each consisting of body models generated by combining Ella and Billie with different morph factors (0 corresponding to Billie and 1 corresponding to Ella) and different amounts of displacement from isocenter in the right-left axis. The dense library consist of body shapes constructed using morph factors of 0.25 and 0.75 and offcenter displacements of either 1 cm or 3 cm. Each of these body models is relatively well matched to the patient Ellie (morph factor of 0.5, displacement of 2 cm). The sparse library consists of the original Billie and Ella models (morph factors of 0 and 1) with displacements of 0 cm or 4 cm, corresponding to less well matched models. The minimum SAR RF pulse (3-spoke small-tip angle, 5% flip angle inhomogeneity tolerance) to excite the central axial slice (shown in Figure 1, \mathcal{P}) was computed with the IMPULSE method [2] using different sets of body models from either the patient, the dense library or the sparse library. With the patient and dense library, a single model was used and with the sparse library varying numbers of models were used. In each case, the true peak local SAR for the optimized pulse was computed on the Ellie model to assess performance. Each optimization used the same B1+ maps taken from simulation on Ellie that are assumed to be patient-matched as would be the case in in-vivo B1+ mapping.

RESULTS: The results for each optimization are shown in Figure 2. The ideal situation using the patient’s true SAR produces a peak local SAR of 1.70 W/kg. With a single model from the dense library the optimized SAR ranges from 1.95-2.24 W/kg. From the sparse library, if a single model is used, the optimization performs poorly, producing a SAR as large as 4 W/kg. When additional models are incorporated, performance improves to a degree that is comparable with the use of single model from the dense library. In particular, using the models $\mathcal{W}_1, \mathcal{W}_2, \mathcal{W}_4$ produced a SAR of 2.03 W/kg, very similar to the best closely matched model (\mathcal{V}_1).

DISCUSSION: The results indicate that the multi-body-model method is a simple and practical method (assuming the use of IMPULSE) of avoiding patient-to-body-model mismatch errors without requiring an excessively dense library. The pulse optimization seeks to achieve destructive interference among the estimated electric fields to mitigate SAR hotspots. With misestimation of these electric fields due to model mismatch, constructive interference may actually result in an increase in true SAR. With additional models, the pulse will be optimized in such a way that destructive interference occurs in *all* models. This makes the optimization more conservative but more robust and thus limits the occurrence of inadvertent constructive interference. It is important to note, however, that the multi-model approach can become overly conservative with too many models (eg. 4) leading to higher SAR.

CONCLUSION: This multi-body-model approach motivates future investigations of the effect that various parameters such as anatomy, position within coil, and electric properties of tissue have on SAR estimation. Further analysis into the influence that closeness of match has on the optimal number of body models in pTx pulse design will help guide construction of a body model library that is sufficiently sparse without significant loss of accuracy in SAR prediction.

References: [1] Eichfelder. MRM 2011;66:1468–1476 [2] Pendse, 5008, ISMRM 2015 [3] Jin, Phys. Med. Biol. 57 (2012) 8153–8171

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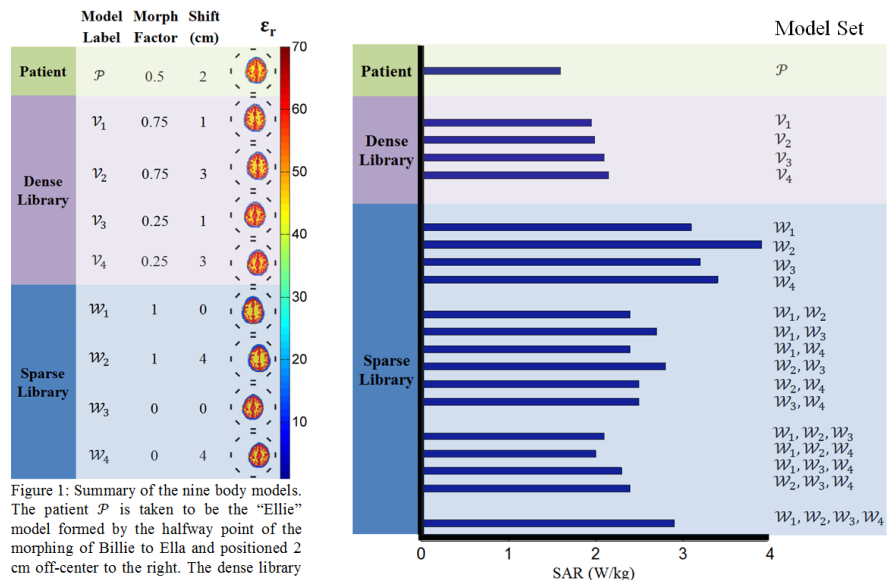


Figure 1: Summary of the nine body models. The patient \mathcal{P} is taken to be the “Ellie” model formed by the halfway point of the morphing of Billie to Ella and positioned 2 cm off-center to the right. The dense library \mathcal{V} consists of four models that match the patient very closely, while the sparse library \mathcal{W} consists of models with higher mismatch.

Figure 2: True patient SAR achieved by the optimum pulse when using a particular set of models for SAR estimation during optimization