Fast, Accurate Calculation of Maximum Local N-Gram Specific Absorption Rate

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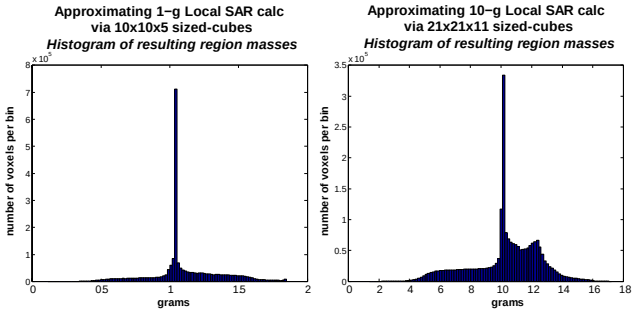
INTRODUCTION. SAR is a major concern in both single-channel and parallel transmission. Being able to quickly and accurately calculate maximum *N*-gram local SAR is crucial in order to evaluate the energy deposition characteristics of various pulses. In contrast with low-res human models that lack many tissue compartments and where tissue-boundaries are overly-smoothed, high-resolution models permit accurate localized SAR calculations. Unfortunately, due to the fine resolution of such models, calculating the average *N*-gram SAR arising at each spatial location is a computationally intractable problem when straightforward region growing methods are employed. Often, practitioners simply perform averages over *N*x by Ny by Nz sets of voxels that approximately cover N grams of tissue, but we show that this frequently leads to averaging over regions whose masses differ greatly from the intended N grams, and thus lead to inaccurate local SAR estimates. We pose a rapid algorithm that is faster than even the inaccurate cube-averaging method, yet always finds an N-gram region to average over, thus ensuring N-gram SAR estimation accuracy.

Fig 1: Approximating N-gram regions with a fixed (Nx by Ny by Nz) cube at every spatial location.
This shows how dense the regions are that the fixed-cube method will average over.
We see that the regions being averaged over often deviate largely from the intended N-gram densities.

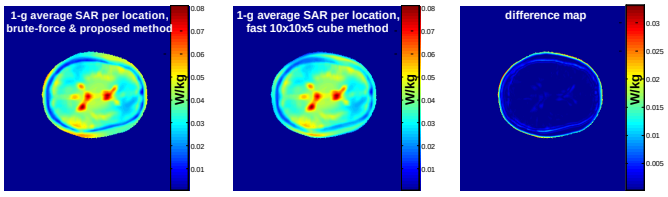


It is evident that using a fixed cube does not lead to averaging over true 1-g and 10-g regions at all spatial ocations in the head model. This is especially true in the 10-g case, where hundreds of thousands of voxels are averaged over 11-16 grams, rather than the intended 10-g.

METHODS & RESULTS. **Maximum local N-gram SAR**. Suppose SAR in W/kg due to a given excitation pulse has been calculated for all spatial locations **r** in a head model; we thus have SAR(**r**), $\forall$r $\in$ Head. Safety standards require the calculation of maximum local N-g SAR. To accomplish this, a box-shaped N-gram region has to be determined that is centered around each **r**, and then for each **r**, SAR values within this N-gram region are averaged and the result is recorded, which thus obtains $SAR_{N\text{-}gram}(\mathbf{r})$ $\forall\mathbf{r}$; maximum local N-gram SAR then simply equals $\max_{\mathbf{r}} SAR_{N\text{-}gram}(\mathbf{r})$. Here we focus on a fast accurate method to compute $SAR_{N\text{-}gram}(\mathbf{r})$ $\forall\mathbf{r}$ for arbitrary N.

Method I: brute-force region growing. For each **r**, create a small box around the voxel being considered and record its mass. If mass is too low, grow the box. In the 1x1x2 mm^3 head model here, there are ~2.5 million voxels [2]; voxels are small and thus contain only several mg of tissue. Thus this region growth method yields highly-accurate boxes whose masses are within several milligrams of the intended N grams, so averages computed over each region yield accurate N-gram SAR. Unfortunately, this method is incredibly slow (see Table I). Further, while the N-gram region surrounding each **r** will *not* change based on the pulse being evaluated, remembering all such 2.5 million regions (each of which contains hundreds to thousands of voxels, depending on N) requires 10+ GB of memory, meaning that "lookup-table" methods are also infeasible. This means that slow region growths must be performed *each* time a pulse is being evaluated, making this method infeasible for all but the lowest-resolution models.

Fig 2: 1-g SAR maps per spatial location for one transverse slice of the head model
Here, fixed-cube-averaging leads inaccurate 1-g SARs at the edges of the head
Deep inside the brain, it yields nearly the same estimates as the brute-force & proposed methods



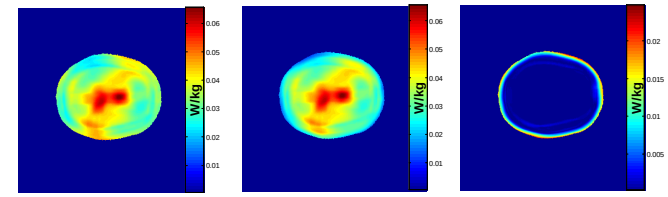
1-g average SAR per spatial location determined by brute-force region growth and the proposed rapid accurate method

Estimated 1-g average SAR per spatial location determined by rapid 10 x 10 x 5 voxel method, where regions are not always close to 1-g in density

Difference in SAR between the methods. The fast 10 x 10 x 5 voxel averaging has underestimated the SAR of edge locations.

Method II: using fixed-sized cubes to proxy for N-gram regions. For each **r**, simply average SAR values within an (Nx by Ny by Nz) box around **r**. Choose Nx, Ny, and Nz such that for most locations, the box approximates an N-gram region. This method is feasible, because a dynamic region does not need to be grown for each **r**. However, for many **r**, the fixed-size cube fails to index an N-gram region: thus averages end up being computed over regions that do not contain N grams of tissue, which impairs our ability to accurately determine $SAR_{Ngram}(\mathbf{r})$. Fig. 1 shows the pitfall of this method when (10x10x5)-voxel & (21x21x11)-voxel are used as proxy for 1-g and 10-g regions in our head model. The histograms show that for most **r**, the fixed cubes do indeed index regions close to N grams: but note that for tens of thousands of **r**, the cubes end up indexing regions that contain far from N grams worth of tissue. Thus this method has sacrificed SAR estimation accuracy for speed (see Table I).

Fig 3: 10-g SAR maps per spatial location for one transverse slice of the head model
Here, fixed-cube-averaging leads inaccurate 10-g SARs at the edges of the head
Deep inside the brain, it yields nearly the same estimates as the brute-force & proposed methods



10-g average SAR per spatial location determined by brute-force region growth and the proposed rapid accurate method

Estimated 10-g average SAR per spatial location determined by rapid 22 x 22 x 11 voxel method, where regions are not always close to 10-g in density

Difference in SAR between the methods. The fast 22 x 22 x 11 voxel averaging has underestimated the SAR of edge locations.

Method III: proposed fast, accurate method for determining N-gram regions based on coding theory. As we have seen, *rapidly* finding an *accurate* N-gram region around each **r** is non-trivial. In two dimensions, counting the number of grid points inside a square of a given radius is called Gauss's Circle Problem and has defied an elegant representation. The dual to Gauss's Circle Problem is to find a set of grid points of a given size with the smallest possible circumscription; it is similarly difficult. We face a somewhat more difficult problem because we are in 3D, we need to generate boxes rather than spheres, and the grid points in this case have weights, i.e., the voxelized volumes have known and generally *unequal* masses. For any given center position **r**, we would like to be able to find a set of voxels that indexes N grams and resembles a cube. To accomplish this, we form a list of grid positions in order of distance from the origin. This can be interpreted as a "universal" list of offsets from any given position **r**. Then to find the set of voxels of interest, we choose the shortest prefix of the list that gives sufficient total mass. One possible implementation—given a location **r**, the mass per voxel around **r**, and this universal list—is to form a voxel mass vector and then search the cumulative sum of the voxel mass vector for the number of voxels needed to form the set. From Table I and Fig. 2 & 3, we see that this proposed method finds the exact same regions as the brute-force method (thus yielding equivalent $SAR_{Ngram}(\mathbf{r})$), while having a runtime than is in fact less than that of even the inaccurate fixed-cube method.

Table I: Performance & Runtime of Local N-Gram SAR Calculation Methods Relative to Accurate but Intractable Brute-Force Region Growth (Method I)

1-gram SAR case	Normalized Region Mass Error	Normalized $SAR_{Ngram}(r)$ error (over all **r**)	Runtime
Method II: Fixed-sized 10x10x5 cube as proxy for a 1-gram region	27%	13%	173 seconds
Method III: Proposed Coding-Theoretic based fast N-gram method	0%	0%	73 seconds

CONCLUSION. A fast accurate method for calculating maximum local N-gram SAR has been demonstrated: it obtained the accuracy of the intractably-long brute-force region-growth method while having a runtime faster than even the inaccurate fixed-size-cube averaging method.

[1] Katscher et al. NMR Biomed '06;19:393-400. [2] Angelone et al. ISMRM '06, pg. 881.