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 Nx 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.

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), r ∈ 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 SARavg(r) = Vmax r∈r \text{sar(r)} max; maximum local N-gram SAR then simply equals max r SARavg(r). Here we focus on the N-gram region determination step to compute SARavg(r )\text{for arbitrary N} 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 small, grow the box. In the 1x1x2 mm³ 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. 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.

Method II: using fixed-sized cubes 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 SARavg(r). Fig. 1 shows the pitfalls 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).

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 defined 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 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 list 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 SARavg(r)), while having a runtime that 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)

<table>
<thead>
<tr>
<th>Method I</th>
<th>Normalized Region Mass Error</th>
<th>Normalized SARavg(r) error (over all r)</th>
<th>Runtime</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fixed 10x10x5 cube as proxy for a 1-g region</td>
<td>27%</td>
<td>13%</td>
<td>173 seconds</td>
</tr>
<tr>
<td>Proposed Coding-Theoretic based fast N-gram method</td>
<td>0%</td>
<td>0%</td>
<td>73 seconds</td>
</tr>
</tbody>
</table>

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