

## Fusion of Anatomical and Functional Information in Neuroimaging

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### Introduction

The spatial resolution displayed by brain SPECT images is rather limited, if compared with the resolution of the corresponding anatomical images (MR or CT images).

To some extent this fact limits the diagnostic potential of the functional SPECT scans of the brain [1]. For instance, it may be difficult to distinguish between low tracer uptake due to a functional deficit, where brain tissue still exists, from low uptake generated by focal atrophy, where tissue is lost and replaced by CerebroSpinal Fluid (CSF). In the pathologies where both phenomena occur the interpretation of SPECT images may be problematic.

In the last few years the so called iterative reconstruction methods [2–3–4] have been found to represent a valuable tool for a thorough exploitation of the informational content of the acquired functional data (the SPECT projections). However, the computational burden associated with these techniques is rather high, since at each iteration step a simulation of the data collection process is performed by applying the so called projector, denoted by  $A$ , to the current iterate. At the software level, this action is realized by a suitable routine containing features and parameters which must be customized to the specific SPECT system, to the acquisition protocol and, even, to the particular object which is being recovered.

Sometimes the quality of the reconstructions does not reward adequately for the related management, programming and computational efforts. Substantial improvements along this line can originate from a higher quality acquisition technology (for instance, by using the more expensive PET) or from imposing some structural constraints on the SPECT image (e.g., the statistical constraints of the Bayesian methods [5–6–7]).

The present contribution investigates some ways of imposing deterministic constraints of anatomical type on a SPECT image while preserving its original functional content.

### T1 Weighted MR Images of the Brain

For a given patient, the quality of the SPECT image of brain blood flow can be relevantly improved by using the structural information contained in the T1 weighted MR scan of the same subject.

In fact, the T1 weighted MR images of the brain display a spatial resolution much higher than that of the corresponding SPECT images and, moreover, on the basis of known structure-to-function relationships exhibit some analogies and correspondences with the functional maps of brain blood flow. In particular, the contrast between CSF and brain tissue (gray matter of the cortex) in a T1 weighted MR image is similar to what is expected in a blood flow SPECT image. For a given patient the signal gradients are located in the same locations. The key idea is to transfer the high resolution information of the MR to the SPECT image.

### The Fusion Algorithm

We begin by detailing the fusion algorithm in a framework of iterative reconstruction, where the projector  $A$  is needed. Subsequently, a simpler and computationally cheaper approach will be proposed.

In the context of iterative reconstruction one obtains the unknown three dimensional (3D) tracer distribution  $f$  by solving the huge linear system

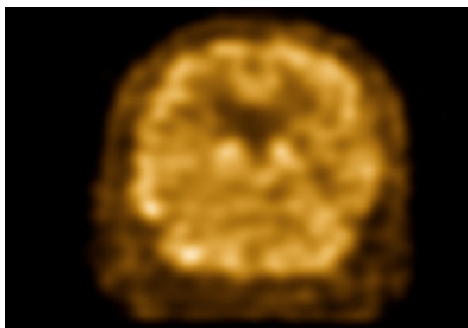
$$g = A f \quad (1)$$

where  $g$  are the SPECT data (the so called projections). Because of the extremely large size of

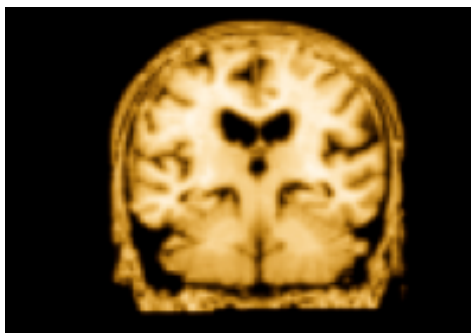
system (1), a sensible approximation for  $f$  is obtained by means of an iterative algorithm, such as the Conjugate Gradient (CG) [4]–[8] or the Ordered Subset Expectation Maximization algorithm (OSEM) [9–10]. The number of performed iterations is chosen in such a way as to obtain an acceptable trade-off between noise and resolution. Let  $f_{opt}$  be the conventional optimal solution of problem (1) obtained in that way (Figure 1 (a)).

**Figure 1.** Coronal slices cut in anatomical correspondence from the SPECT and MR images of the same subject: (a) slice from  $f_{opt}$ , blood flow map; (b) slice cut from  $m$ , T1 weighted MR image coregistered and resampled to the SPECT

(a)



(b)



The proposed fusion technique requires both the SPECT data  $g$  and a T1 weighted MR image of the same patient. The following steps must be performed:

Step 1) The selected iterative reconstruction algorithm generates  $f_{opt}$ .

Step 2) The MR image is accurately coregistered to the SPECT  $f_{opt}$ .

Step 3) The coregistered version of the MR image is denoted by  $m$ . It must be resampled in order that a voxelwise correspondence between  $m$  and  $f_{opt}$  exists. Since fat activity in the T1 weighted MR  $m$  is very high and has no counterpart in the

SPECT, it is convenient to threshold the MR image by zeroing all activity higher than that of white matter. Then, the voxel values in  $m$  must be scaled so that the total activity in  $m$  equals the total activity in  $f_{opt}$  in corresponding volumes. In Fig 1

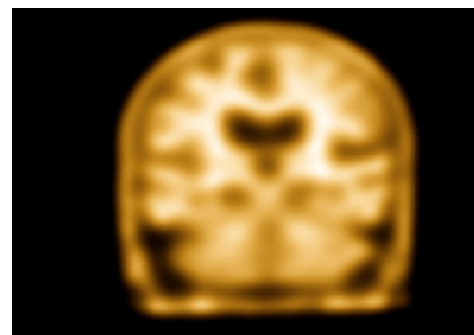
(b) a coronal slice cut from  $m$  is shown.

Step 4) By applying the projector  $A$  to  $m$ , generate the synthetic data  $gm = A m$ . Such data correspond to what one collects if the MR-like activity distribution  $m$  is placed inside the SPECT scanner. Step 5) Apply the same iterative algorithm (same iteration number) to reconstruct the data  $gm$ . Denote the result by  $m_{opt}$ . It represents a sensible

estimate of what the conventional tools (SPECT scanner + the reconstruction algorithm) would be able to recover, should the activity map  $m$  be really present in the scanner. In Figure 2 (a) a coronal slice cut from  $m_{opt}$  is shown.

**Figure 2.** Coronal slices in anatomical correspondence and cut from: (a)  $m_{opt}$  the visible part of  $m$ ; (b)  $h$ , the invisible part of  $m$

(a)



(b)



Step 6) Evaluate the difference  $h = m - m_{opt}$ . The image  $h$  represents what the conventional tools are not able to recover. In Fig 2 (b) a coronal slice cut from  $h$  is shown.

Step 7) Following to the idea of adding to  $f_{opt}$  something of what we would have never been able to see, even if really present, we generate the

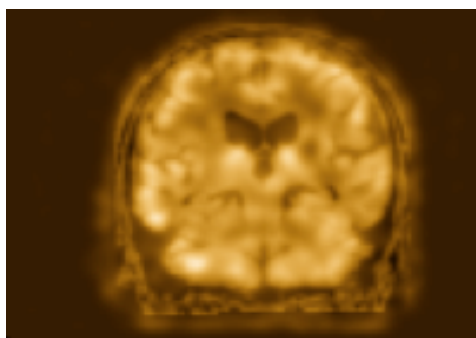
enhanced image

$$e_{opt} = f_{opt} + k h, \quad (2)$$

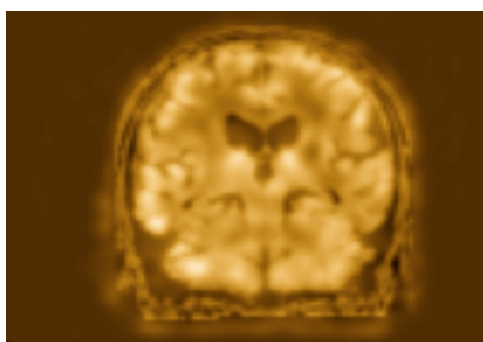
where  $k$  tunes the influence of the MR on  $e_{opt}$ . Once  $f_{opt}$  and  $h$  have been obtained at the cost of two conventional SPECT reconstructions, the tuning of the parameter  $k$  can be performed rather quickly since the computational cost of evaluating (2) is negligible. Good quality images are obtained with  $k$  values of the order of unity. In Fig 3 (a)–(b) two coronal slices cut from two  $e_{opt}$  images are shown, respectively obtained with  $k=0.6$  and  $k=0.9$ .

**Figure 3.** Coronal slices cut from the functional images enhanced with the structural information derived from MR: (a)  $e_{opt}$  obtained with  $k = 0.6$ ; (b)  $e_{opt}$  obtained with  $k = 0.9$

(a)



(b)



A simpler version of the proposed fusion algorithm is suggested by the Frequency Encoding technique (FE) [11] and replaces the computationally demanding steps 4) and 5) with the less onerous recipe of generating  $m_{opt}$  by filtering  $m$  with a Gaussian filter whose width is comparable with the effective spatial resolution achieved in  $f_{opt}$ . Once  $m_{opt}$  is obtained as a smoothed version of  $m$ , the steps 6) and 7) can be performed. An evaluation of price in

accuracy paid for this computational shortcut will be performed in the future.

## Discussion

It can be shown that  $h$  contains only high spatial frequencies, that the sums of the counts in  $h$  and in relevant portions of it vanish and that this is not true for Regions Of Interest (ROIs) whose dimensions are comparable with or smaller than the SPECT resolution length. This is obvious in the case of the FE version of algorithm, but also holds for the iterative version. Then, on the basis of the enhancement scheme (2) and of the properties of  $h$ , it can be shown that  $e_{opt}$  contains the same functional activity as  $f_{opt}$  (no foreign counts are added)

and that the original functional activity may only be displaced to some extent. The displacement may be more relevant for low counts and is always negligible for high counts. In any case it is always comparable with the SPECT resolution length.

An inspection of the enhanced images indicates that the original SPECT activity is “shaped” by the features coming from the MR image; such features represent an anatomical framework which helps an accurate localization of functional activity, provided that the coregistration has been satisfactory. Moreover, a significant improvement in spatial resolution, with appreciable corrections for the so called partial volume effects, is observed in the definition of the boundaries between CSF and the gray matter of the cortex. The reason for that resides in the fact that the template represented by the MR image displays signal gradients consistent in sign and location with what one expects from the corresponding functional activity.

A thorough analysis of the properties of enhanced images generated by the fusion technique proposed here, with particular emphasis to what happens in the cases of mismatch between structure and function can be found in [12].

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