

# A Time-Averaged Projection Matrix Approach to Motion Compensation

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## Abstract

One approach to motion compensation in reconstruction from emission data is to modify the existing data to approximate, as best we can, what the data would have been had the detected motions not occurred and then to process that modified data vector  $y$  in the usual way, using the formulation  $y = Px$ . Here the matrix  $P$  contains the probabilities associated with the motion-free case. Here we suggest a different approach, appropriate for non-rigid motion, in which there is no modification of the data. The problem again has the form  $y = Px$ , but now it is the matrix  $P$  that depends on the motion. The main points are: 1) how we process the data does not depend on when the data was recorded or on where the patient was at the time the data was recorded; 2) all the motion information is contained in the probabilities in  $P$ , which depend only on how long the patient was in a given position and not on when that happened; 3) the matrix  $P$  is a time-weighted average of the projection matrices pertaining to a single motion-free period, so it is likely that great accuracy in specifying each of these individual matrices is not crucial; detailed non-rigid motion models may then not be necessary. The discussion here is an amplification of [1]. The idea of using the time-averaged projection matrix also occurs in [2]. A similar approach has recently been announced in [3].

## 1 The Goal

The objective in emission tomography is to estimate, at least approximately, the spatial distribution of radionuclide within the patient. When there is no patient motion, this distribution is static, with respect to the fixed ambient space of the room, and can then be described by a nonnegative function  $f(s)$  of the continuous two- or three-dimensional spatial variable  $s$ , scaled so that, for a given region  $A$ ,

the integral  $\int_A f(s)ds$  is the expected number of emissions within  $A$  during the scan. When there is patient motion, the distribution changes over time, with respect to the fixed ambient space of the room, and is best described as a spatio-temporal function  $f(s, t)$ . Our goal, in the case of motion, is to estimate, at least approximately, the function  $f(s, 0)$ .

## 2 The Motion-Free Case

For  $j = 1, \dots, J$ , let  $V_j$  be a small subset of  $s$ -space. Typically,  $V_j$  will be a pixel or voxel. Let  $r_j$  be the radionuclide within  $V_j$  at the start of the scanning, called the  $j$ -th *emission element* in [2]. In the motion-free case,  $r_j$  will remain within  $V_j$  throughout the scanning time. Then  $x_j = \int_{V_j} f(s)ds$ , the expected number of emissions from  $r_j$ , is proportional to the size of  $r_j$ . Our approximation of  $f(s)$  is then the column vector  $x$  with entries  $x_j$ . The objective is to estimate  $x_j$ , for each  $j$ . Our data are the counts  $y_i, i = 1, \dots, I$ , received at the detectors. We assume that we know  $P_{ij}$ , the probability that an emission from  $V_j$  is detected at the  $i$ th detector. When we calculate  $P_{ij}$ , we make the implicit assumption that  $V_j$  is so small that an emission anywhere within  $V_j$  will have the same probabilities of detection at the various detectors.

## 3 The EM Algorithm

Because the various approaches to motion correction are usually discussed in the context of iterative reconstruction, it is helpful to exhibit one particular method, the EM algorithm. Beginning with a positive vector  $x^0$ , and having calculated  $x^k$ , the  $k$ -th estimate of  $x$ , we let

$$x_j^{k+1} = x_j^k s_j^{-1} \sum_{i=1}^I P_{ij} \frac{y_i}{(Px^k)_i}, \quad (3.1)$$

where  $s_j = \sum_{i=1}^I P_{ij}$ . The sum on  $i$  in Equation (3.1) is called the *back-projection step*, the sum on  $j$  that occurs in the calculation of  $(Px^k)_i$  is called the *forward-projection step*, and, for convenience, we assume that  $s_j = 1$ . These steps also occur as part of the block-iterative RBI-EMML and OSEM iterative algorithms.

## 4 The Case of Patient Motion

When there is motion during the scanning process, the radionuclide  $r_j$  that is initially within  $V_j$  may move. We denote by  $V_j^t$  the region of space occupied, at time  $t$ , by

the region of the body that initially occupied  $V_j$ ; so  $V_j^0 = V_j$ ; we do not necessarily assume that  $V_j^t$  is a voxel, even when  $V_j^0$  is. We denote by  $P_{ij}^t$  the probability that an emission from within  $V_j^t$  will be detected at the  $i$ th detector.

Note that, when we take the  $V_j^0$  to be voxels, we need not assume that  $V_j^t$  is again a voxel, but rather a region into which the portion of the body originally in  $V_j^0$  has moved. We assume either that  $V_j^t$  is small enough so that the detection probabilities are identical throughout  $V_j^t$ , or, that the radionuclide occupying  $V_j^t$  is distributed uniformly throughout  $V_j^t$ . We allow for the possibilities that  $V_j^t$  may consist of two or more non-contiguous regions, and that the regions of the body initially in distinct  $V_j$  and  $V_m$  may come to occupy the same  $V_j^t$  at a later time; that is, we can have  $V_j^t = V_m^t$ . The point is simply that we need to know what the probabilities of detection are at all points within the body, and the location, at time  $t$ , of the region initially within  $V_j$ . If  $V_j^t$  consists of two non-contiguous small regions, but, at time  $t$ , the radionuclide  $r_j$  resides in only one of the two regions, we cannot know that a priori, and must the  $r_j$  is distributed uniformly throughout  $V_j^t$ . In short, from a mathematical standpoint, the effect of motion is only to change the probabilities.

## 5 The Time-Averaged Projection Matrix

As motion occurs, and the radionuclide moves, the probability that an emission from  $r_j$ , at time  $t$ , will be detected at the  $i$ th detector, is  $P_{ij}^t$ . Therefore, the probability that an emission from  $r_j$  will be detected at the  $i$ th detector is

$$Q_{ij} = \int_{t=0}^{t=1} P_{ij}^t dt. \quad (5.1)$$

The matrix  $Q$  with entries  $Q_{ij}$  is the *time-averaged projection matrix*.

The photon counts  $y_i$  then have expected value  $(Qx)_i = \sum_{j=1}^J Q_{ij}x_j$ . We can then estimate  $x_j$  using any of the standard approaches, such as likelihood maximization.

## 6 The Discrete Motion Model

We assume now that the motions have been identified, through the use of the visual tracking system (VTS) and, perhaps, the data itself. We assume, in addition, that the motions occur at finitely many times  $0 < t_1 < t_2 < \dots < t_{M-1} < 1$ , with  $t_0 = 0$  and  $t_M = 1$ . For motions that extend over a period of time, such as the respiratory cycle and heart creep, this model imposes a discretization of the movement into finitely many stages. For each  $m = 1, \dots, M$  the intervals  $[t_{m-1}, t_m)$  are periods that are

motion-free; the matrix  $P^m$  is the projection matrix associated with  $[t_{m-1}, t_m)$  and  $d_m = t_m - t_{m-1}$  is the duration of that period. The matrix  $Q$  is the time-weighted average of the  $P^m$ ; specifically,

$$Q_{ij} = \sum_{m=1}^M d_m P_{ij}^m,$$

for each detector (or line of response)  $i = 1, \dots, I$  and each voxel  $j = 1, \dots, J$ . Once we have determined  $Q$  we solve  $y = Qx$  in the usual fashion, using, say, the EM algorithm, or a block-iterative version, such as RBI. The important point is that how we process the data does not depend on when the data was recorded nor on where the patient was at the time the data was recorded!

## 7 The Fulton-Meikle Approach

In [3] Fulton and Meikle present a closely related approach. In iterative reconstruction, having found the  $k$ th estimate of  $x$ , denoted  $x^k$ , we typically forward projection into data space and compare the results with the measured data; that is, we calculate

$$(Px^k)_i = \sum_{j=1}^J P_{ij} x_j^k,$$

for each  $i$ . Their approach is to modify this forward projection step to incorporate motion.

For each  $m = 1, \dots, M$  and  $j = 1, \dots, J$ , let  $g = g(j, m)$  be the index of the voxel occupied, at pose  $m$ , by emission element  $r(j)$ , so that  $g(j, 0) = j$ , and let  $h = h(j, m)$  be the index of the emission element that, at pose  $m$ , occupies the  $j$ -th voxel. So we have  $h(g(j, m), m) = j$ , for each  $j$  and  $m$ . Their forward projection is

$$\sum_{m=1}^M \sum_{j=1}^J d_m P_{i,j} x_{h(j,m)}^k. \quad (7.1)$$

We can rewrite 7.1 as

$$\sum_{j=1}^J \left[ \sum_{m=1}^M d_m P_{i,g(j,m)} \right] x_j^k. \quad (7.2)$$

Therefore, 7.2 becomes  $(Qx^k)_i$ .

They then use  $(Qx^k)_i$  in place of  $(Px^k)_i$  in the forward-projection step. Their back-projection step is unchanged. For example, their EM algorithm would now be

$$x_j^{k+1} = x_j^k \sum_{i=1}^I P_{ij} \frac{y_i}{(Qx^k)_i}. \quad (7.3)$$

Note that they calculate  $(Qx^k)_i$  not by calculating  $Q$ , but by moving the entries of  $x^k$  prior to forward projection. This may be a more efficient way to do the forward projection, than using  $Q$  explicitly, but, since they do not actually compute  $Q$ , they use  $P$  in the back-projection step. This puts their algorithm outside the framework of the theory of the EM algorithm and raises the question of convergence. Nevertheless, their results suggest that this is a useful approach. As we shall see, we can also use  $Q$  in the back-projection step without explicitly calculating  $Q$ .

## 8 Backprojecting Using $Q$

Suppose that we wish to implement the EM algorithm, using  $Q$  instead of  $P$ ; that is, we want the iterative step to be

$$x_j^{k+1} = x_j^k \sum_{i=1}^I Q_{ij} \frac{y_i}{(Qx^k)_i}. \quad (8.1)$$

We perform this calculation in the following way.

Given  $x^k$  and  $Qx^k$ , initialize  $z = (z(1), \dots, z(J))$  as the zero vector. Let

$$a_j = \sum_{i=1}^I P_{ij} \frac{y_i}{(Qx^k)_i},$$

for  $j = 1, \dots, J$ . For  $m = 1, \dots, M$  and  $j = 1, \dots, J$ , do

$$z(h(j, m)) \leftarrow z(h(j, m)) + d_m a_j.$$

Then

$$x_j^{k+1} = x_j^k z(j),$$

for each  $j$ . The advantages are that we do not have to calculate  $Q$ , and perform only a single back-projection step, in calculating the vector  $a$ . The movements involved in determining the entries of the vector  $z$  are analogous to those Fulton and Meikle use in the forward-projection step.

## 9 The Reyes-Malandain-Koulibaly-Darcourt Approach

In [2] the authors consider the possibility of including a respiratory model in the reconstruction process, thereby allowing the use of all the acquired data, without the need for extra hardware. Their approach is to extend the matrix of probabilities to

account for motion and voxel deformation. The resulting matrix of probabilities is  $Q$ , and their approach is identical to the time-averaged projection matrix method of [1] discussed previously.

## 10 Summary

Let  $r_j$  denote the  $j$ -th emission element, that is, the radionuclide material contained within the region  $V_j$  at the beginning of the scan. When motion occurs, this material  $r_j$  may move, and the attenuator may move, so the probability  $P_{ij}$  that an emission from  $r_j$  will be recorded at  $i$  changes. Correcting for motion may involve moving the data, which is reasonable for rigid motion, but problematic for non-rigid motion. For the non-rigid case, we may move the estimates of the intensities during the forward-projection step in iterative reconstruction, as in [3], or, as in [2], view the intensities as static and the probabilities as time-dependent, and compute the time-averaged probability matrix  $Q$ .

In [3] the  $Q$  is not explicitly used; the forward-projection step calculates  $(Qx^k)_i$  by moving the estimated intensities, and the back-projection step uses the original probability matrix  $P$ . Convergence is then a concern. Calculating  $Q$  explicitly may be more costly, but it does allow for expansion and contraction due to motion, and does not necessarily require a model by which each voxel moves to another voxel. In either approach, we still need to model how the various portions of the body distort as the patient moves.

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## References

- [1] Byrne, C. (2004) A new approach to motion compensation, *preprint*.
- [2] Reyes, M., Malandain, G., Koulibaly, P., and Darcourt, J. (2005) Respiratory Motion Correction in Emission Tomography Imaging, *Eighth International Meet-*

*ing on Fully Three-dimensional Image Reconstruction in Radiology and Nuclear Medicine.*

- [3] Fulton, R., and Meikle, S. (2005) Reconstruction of Projection Data Corrupted by Rigid or Non-rigid Motion, *MIC-05, Puerto Rico*, poster **M10-1**.