# An Automated Method for the Alignment of Image Pairs 

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The computer comparison of two images of the same organ requires proper alignment of the images before further computer processing. This alignment can be achieved by (a) fixing patient position during the study, (b) alignment methods using analytical transformations, or (c) operator interaction. We propose an automated method based upon the cross-correlation between projections of the images. With fast Fourier transforms, the algorithm becomes computationally cheap.

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#### Abstract

The computer comparison of two images obtained under varying physiological conditions (different tracers, time-phased studies, etc.) requires proper alignment of images before further processing. Fixing a patient position during various phases of the study restricts the number of views obtained (1-3). Alignment methods that use analytical transformations within the computer require reference markers placed on the patient (4), and operator interaction is inefficient and expensive in terms of personnel and machine time ( 5 , 6). Hence the need for a rapid, noninteractive method.

We present an automated alignment method that permits patient movement between images and does not require reference markers or operator interaction. Given a pair of images of the same organ-say ventilation and perfusion views of a lung-the computer identifies the translation required to align the images. The algorithm is accurate and requires only modest computer time and memory storage.


## METHODS

We assume that the two images are scaled to the same size, and that one is not rotated with respect to the other. Data windows are first applied to the original images to enhance the information at the center of the image field and to suppress the influence of the background information always present near the edge of the field. These data windows are, in fact, weighting functions. Although we have chosen the Hann window (commonly called the "Hanning" window), many others are available ( 7,8 ).

The required horizontal and vertical translations are identified separately. The two images are first projected in the vertical dimension, producing two sequences that are then cross-correlated.

[^0]The peak value of this cross-correlation function corresponds to the horizontal shift (lag) of one image with respect to the other. Similarly, the horizontal projections of the windowed images are cross-correlated to identify the vertical lag. Finally, using these lags, the second image is shifted to superimpose it with the first, completing the alignment.

To formalize the procedure mathematically, let the two images be represented as $x(i, j)$ and $y(i, j)$ where $\mathrm{i}, \mathrm{j}=0,1, \ldots, N-1$ are the coordinates of the discrete image plane within the range of interest, with outside values all at zero. Since identification of the vertical and horizontal lags is computationally similar, consider the case involving vertical projection (horizontal lag) only. Let the vertical projections of $x(i, j)$ and $y(i, j)$ be denoted as $p(i)$ and $q(i)$, respectively, where

$$
\begin{aligned}
& p(i)=\sum_{j=0}^{N-1} x(i, j) \cdot w(i, j) \\
& q(i)=\sum_{j=0}^{N-1} y(i, j) \cdot w(i, j)
\end{aligned}
$$

and the Hann window, $w(i, j)$, extended to two dimensions, is given by

$$
w(i, j)=0.25 \cdot\left\{1-\cos \left(\frac{2 \pi i}{N}\right)\right\}\left\{1-\cos \left(\frac{2 \pi j}{N}\right)\right\}
$$

The cross-correlation function, $\phi_{\mathrm{pq}}(\mathrm{m})$, between $\mathrm{p}(\mathrm{i})$ and $\mathrm{q}(\mathrm{i})$ is defined as

$$
\phi_{p q}(m)=\frac{1}{N} \sum_{i} p(i) q(i+m)
$$

where " $m$ " is the shift index or lag (9). The cross correlation function can be directly evaluated when the number of lags is small. However, when one wishes to evaluate this function for many values of " $m$ ", Fourier transform methods should be used, thereby exploiting the computational advantage offered by the fast Fourier transform (FFT) (9,10). It is easy to demonstrate that the Fourier spectrum $\Phi_{\mathrm{pq}}(\mathrm{k})$, of the cross-correlation function $\phi_{\mathrm{pq}}(\mathrm{m})$ is related
to the projections by

$$
\Phi_{\mathrm{pq}}(\mathrm{k})=\mathrm{P} *(\mathrm{k}) \mathrm{Q}(\mathrm{k})
$$

where $P(k)$ and $Q(k)$ are the Fourier spectra of $p(i)$ and $q(i)$, respectively, and $P^{*}(k)$ is the complex conjugate of $P(k)$. Thus, the function can be evaluated in the following manner:

$$
\phi_{\mathrm{pq}}(\mathrm{~m})=\operatorname{IFFT}\left[\mathrm{FFT}\{\mathrm{p}(\mathrm{i})\}^{* F F T}\{\mathrm{q}(\mathrm{i})\}\right]
$$

where IFFT represents the inverse FFT.
The required shift is identified by performing a peak search of $\phi_{\mathrm{pq}}$. The location of the peak corresponds to the horizontal lag, $\mathrm{l}_{\mathrm{h}}$, that yields the maximum correlation between the two projections. [From the definitions, it follows directly that $\phi_{\mathrm{pq}}(-\mathrm{m})=\phi_{\mathrm{pq}}(N$ $-\mathrm{m})$.] By performing a similar cross-correlation in the horizontal dimension, a vertical lag, $l_{v}$, is found, which then maximizes the correlation between the two images. To accomplish alignment, we now shift the second image by the horizontal and vertical lags, displacing $y(i, j)$ to $y\left(i-l_{h}, j-l_{v}\right)$. If the shifting is performed in place, indexing should proceed in the direction opposite to the lag to avoid overwriting the image data.

Assuming the image matrix to be sufficiently sampled (say 64 $\times 64$ or larger), the need to accommodate fractional sample shifts can be ignored. Otherwise an interpolation procedure must be incorporated into the final shifting step.

The shift performance can be visually evaluated by the computer operator to provide a qualitative measure of the goodness of fit of the aligned images. A more objective performance measure of goodness of fit is provided by the coefficient of correlation

$$
r=\frac{N^{2} \Sigma x y-\Sigma x \Sigma y}{\left[N^{2} \Sigma x^{2}-(\Sigma x)^{2}\right]^{1 / 2}\left[N^{2} \Sigma y^{2}-(\Sigma y)^{2}\right]^{1 / 2}}
$$

As can be seen, the correlation of an image with a shifted version of itself (perfect correlation) yields $r=1$, whereas completely uncorrelated processes yield $\mathrm{r}=0$.

## RESULTS

The performance of the algorithm can be illustrated by a typical ventilation/perfusion study in one patient. The tracers were Xe -


FIG. 1. Pair of images following alignment. Top left: posterior ventilation equilibrium image with $\mathrm{Xe}-133$ gas; right: aligned posterior Tc-99m MAA image. Bottom left: ventilation image with superimposed perfusion edges, right: perfusion image with superimposed ventilation edges.

133 gas and Tc-99m MAA, and repositioning of the patient was necessary to provide for anterior and posterior projections, both laterals, and four $45^{\circ}$ oblique views. Computer data acquisition and subsequent image pair alignment were performed on a laboratory computer system. The alignment program was written in Fortran IV and required approximately 30 sec to execute without hardware multiply/divide.

In Fig. I the normal posterior ventilation equilibrium image (upper left) is aligned with the posterior perfusion image (upper right), which shows a defect in the left lateral lobe. The images are repeated below, each with the image edges of the other superimposed. Edges are calculated using a method based upon a threshold and gradient technique.

In Fig. 2 (same format as Fig. 1) are shown the anterior ventilation washin image and the anterior perfusion image for the same patient. The grossly abnormal washin study fails to prevent acceptable alignment.

## DISCUSSION

The proper alignment of two scintigrams presents a significant problem because patient movement often occurs between images during the collection of an optimal clinical study. Our approach does not require either operator interaction or reference markers. The method decomposes a two-dimensional cross-correlation problem into two one-dimensional ones, by cross-correlating projections of the windowed images rather than cross-correlating the windowed images directly. The computational advantage offered by the fast Fourier transform makes the algorithm computationally cheap.

This decomposition is performed for two reasons: (a) onedimensional cross-correlation allows the use of one-dimensional fast Fourier transform routines, and (b) the projection of the images generates sequence lengths that can be accommodated in the memories of most nuclear medicine computers, which a row-byrow organization would not do. We thus avoid the need for a fast Fourier transform designed for externally stored data (11-13).

The alignment algorithm identifies the shifts required of one image to maximize its correlation with the other. In the absence


Fig. 2. Pair of images following alignment. Top left: $\mathrm{Xe}-133$ anterior ventilation washin image; right: aligned anterior Tc-99m MAA image. Bottom left: ventilation image with superimposed perfusion edges; right: perfusion image with superimposed ventilation edges.
of noise and lung defects, the shifts provide perfect correlation, but the presence of defects in the lung fields complicates the problem. In the case of matched defects, maximizing the correlation will yield the proper lags, but in Fig. 2 there was gross mismatching. In this case a single lung was cross-correlated with its matching member in the perfusion image, and the method still worked. Hypothetically, the method would have failed if the contralateral perfusion image had also shown as massive a defect as was present in the ventilation image. There appears to be no general solution, short of external reference markers, to this potential problem.

We have assumed no rotation of one image with respect to the other, and this has not generated serious problems to date. In the more general problem of image-pair alignment, however, it must be considered (14,15).*

Our method also assumes that both images are scaled to the same size. If this is not the case, scale parameters for the coordinate system of the second image ( $\mathrm{i}, \mathrm{j} \rightarrow \alpha \mathrm{i}, \beta \mathrm{j}$ ) could be included in the cross-correlation to account for this, with $\alpha$ and $\beta$ determined by iteration. It would be far preferable, however, to control image size by instrument calibration.

In our experience the algorithm described herein has performed well in aligning ventilation/perfusion image pairs over a wide class of $\mathrm{V} / \mathrm{Q}$ disorders. This could be anticipated because images of the lungs usually exhibit strong correlation. Otherwise the method could be less than ideal. Application of the algorithm to other image pairs will require a careful investigation by the user.

## FOOTNOTE

* One solution to this problem is an iterative scheme in which cross-correlations are computed at various angles of rotation about some arbitrary, preselected point in the image matrix. The rotation aspect of the extended algorithm could then be incorporated into the projection step of the current alignment algorithm. Because an extra degree of freedom (rotation) has been introduced, improved correlations would be expected.


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