An Automated Method for the Normalization of Scintigraphic Images

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The computer comparison of two images of the same organ requires normalization of the images. We propose an iterative, automated method of normalization that is highly insensitive to structural modifications in the images. The normalization factor is calculated by maximizing the number of sign changes in the scanned subtraction image with a unidimensionnal optimization method. This algorithm is efficient, computationally cheap, and can be implemented on most nuclear medicine data-processing systems.

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The comparison of two scintigraphic images of the same organ explored under varying conditions (different tracers, various physiological or pharmacological interventions, etc.) is a routine problem in nuclear medicine. If performed automatically, it first necessitates a proper alignment of the images if they have been acquired in different spatial conditions. Some interactive or automated methods that have been developed for nuclear medicine or other imaging techniques are available for this purpose (*1–5*). Second, the registered images must be normalized to compare the local activities by subtraction or other processing techniques. When the second image is different from the reference one because of defects or active zones, the normalization step is difficult to carry out and no general automated method has been proposed to handle it. In this paper, an iterative, automated method of image normalization is described. The method is shown to be theoretically consistent, and several representative examples show it to be insensitive to image modifications.

METHOD

We assume that the two images (reference and unnormalized images) either have been acquired in similar geometrical conditions or have been first scaled to the same size and superimposed.

Consider two images A(i,j) and B(i,j) of a radioactive organ, where i,j = 1,2,... N are the coordinates of the digitized image. If the relative distribution of the radioactivity within the organ does not vary, we have: A(i,j) = NF. B(i,j), where NF is the normalization factor. Let D(i,j) = A(i,j) − NF. B(i,j) be the subtraction image between A and normalized B images. Because of the presence of noise, the D(i,j) values are not equal to zero but exhibit random fluctuations, either positive or negative. Let R be the number of sign changes in the sequence of the values of D(i,j), scanned line by line or column by column (for example, in the sequence +−−+++−+−, R = 5). For the calculation of NF, we propose to maximize R with respect to this parameter. Such a method can be derived from the following nonparametric statistical considerations in the case of similar images. If there are enough counts (more than 20) in every pixel of A(i,j) and B(i,j), the radioactive Poisson noise has a symmetric distribution in the pixels of these images, and the D(i,j) values have a zero mean symmetric distribution. When the normalization is not correct, the D(i,j) distribution remains symmetric but incurs a nonzero mean, so that the expected value of R will be smaller (*6*). R therefore becomes a similarity criterion between the images A(i,j) and B(i,j). It must be maximized to find the NF value. This can be performed iteratively with a unidimensionnal optimization method such as the Fibonacci or the golden section (*7*).

RESULTS

NF calculations were carried out on a laboratory computer system* connected with an array processor†. The unidimensionnal Fibonacci search program was written in FORTRAN IV. The number of sign changes in the subtraction images was calculated by the array processor at each iteration. Convergence was achieved in approximately 15 iterations for an initial search interval of 0.1–10. Thus, NF was estimated with an absolute precision of 0.01 [equal to the ratio of the initial search interval to the 15th number of the Fibonacci series (*8*)]. Calculations required respectively 1, 2, and 8 sec in format 64 × 64, 128 × 128, and 256 × 256.

The performance of the algorithm was studied on scintigrams

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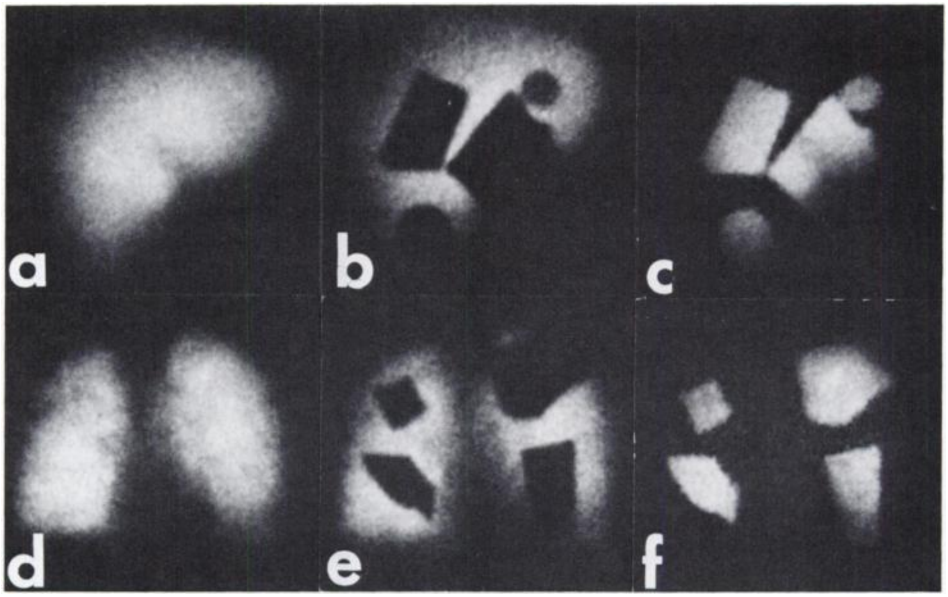

FIG. 1. Examples of normalization. a: reference liver-phantom image, b: modified, normalized phantom image, c: subtraction image a–b; d: reference lung image, e: modified normalized lung image, f: subtraction image d–e.

of a liver phantom (Tc-99m) and lungs (Tc-99m MAA). Reference images were modified by setting absorbant materials on the phantom or patients. Illustrative results are shown in Table 1 and Fig. 1, with images a, b, d, and e in Fig. 1 corresponding respectively to results designated P1, P5, L1, and L5 in Table 1. All these liver-phantom and lung images were acquired sequentially with short acquisition times (<100 sec), without any change of the acquisition parameters but with different imaging times. Therefore the true NF values were derived from the ratio of these imaging times. This procedure was validated a posteriori by the following facts: Images P2,P3 and L2,L3 differed only from images P1 and L1 because of the imaging times (without any shield). When the images P2,P3 and L2,L3 are compared respectively with P1 and L1, the ratios of the total number of counts are 6.11, 1.51, 4.09, 1.35. These values come close to the corresponding true NF values of 6.11, 1.51, 4.10, 1.34 (see Table 1). This fact validates the use of the ratios of the acquisition times as true NF values in these particular experimental conditions.

No influence of the acquisition format (64 × 64 or 128 × 128) on NF values was found when images were acquired in both formats. Calculated NF values appear very close to true NF values. Subtraction images c and f in Fig. 1 illustrate this fact pictorially.

The influence of wrong alignment of images on NF values was studied by translating the liver phantom through 0, 0.5, 1, 1.5 cm. The corresponding estimated values were 1.33, 1.38, 1.29, 1.21 for a true NF value of 1.33.

TABLE 1. TRUE AND CALCULATED NF VALUES

Image	Total number of counts	Modification of image	True NF values	Calculated NF values
P1*†	488 473	—	—	—
P2	79 930	no	6.11	5.93
P3	323 954	no	1.51	1.49
P4	258 761	yes+	1.51	1.50
P5	182 843	yes++	1.51	1.50
L1*†	363 639	—	—	—
L2	88 960	no	4.10	4.00
L3	269 301	no	1.34	1.34
L4	249 820	yes+	1.34	1.32
L5	179 377	yes++	1.34	1.33

* P1 to P5 are liver-phantom images, L1 to L5 are lung images (128 × 128 format).

† P1 and L1 correspond to reference phantom and liver images used for NF calculations.

DISCUSSION

The computer comparison of two aligned images requires a normalization step in order to correct the images for variable acquisition parameters such as the injected activity, acquisition time, spectrometric window, detection efficiency, etc. It must be emphasized that the two images can be very different but must contain some part where the assumption A(i,j) = NF. B(i,j) remains valid. Otherwise normalization would be meaningless. If there is no change in the repartition of the tracer within the explored organs, the ratio of the total number of counts in the images is classically used as a normalization factor. This method does not work properly when significant changes occur in the images. For example such a method applied to images L1 and L5 (Table 1) leads to a NF value of 2.03, which is very different from the theoretical value of 1.34. When modifications occur, the normalization is usually carried out by visually selecting with a lightpen an unchanged area of interest in the image; the ratio between the two total counts in this zone gives the NF value (*9*). Such a method is operator-dependant; the unchanged zones are often difficult to determine and only a part of the image is used. Skretting (*10*) has proposed an iterative method working from the pixel values of a zone of interest, but it is suitable only for superimposed radioactive organs.

Our approach is automated, does not require any operator interaction, and can be applied in spite of both positive and negative changes in the whole image. The method is based on the maximization of the number of sign changes in the scanned subtraction image between the reference and the normalized image. The computation time is very short and therefore such a method can be implemented on most commercial nuclear medicine data-processing systems (at least with 64×64 and 128×128 formats), even if no array processor is available.

The Fibonacci optimization procedure was used because of its well-known efficiency, but other methods such as the golden section could be convenient. Our method works with the sign changes in the images, and therefore is not influenced by the amplitude of the modifications (in terms of local activity). Thus, NF calculated values remain very close to the true ones even if the images are dramatically modified (compare images b and e in Fig. 1). This method might be less powerful in the case of low-count images because of the asymmetric shape of the Poisson law. Nevertheless NF values still fall close to theoretical in images P2 and L2 (Table 1), which correspond to noisy images. The criticality of incorrect image alignment on NF calculated values was studied and demonstrated the need for a proper superposition of images before calculations are made.

The entire digitized images were used for the calculation of R. When active zones represent only a small part of the field of detection, one could do better to select a more restricted part of the image. This is not in fact a limitation of this method since zones need not be selected with great precision. The maximization of R permits an efficient normalization of nuclear medicine images. Registration problems (translation, rotation) can also be solved from the optimization of this criterion, with the expected benefit of great insensitivity to image modifications. The comparison of sign-change methods with correlation ones for image registration is currently under investigation in our laboratory.

FOOTNOTES

*IMAC 7300, CGR Médecine Nucléaire (French version of ADAC System 1).

† AP120B, Floating Point System.

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