FAST MULTIMODALITY IMAGE MATCHING

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#### ABSTRACT

The diagnostic potential of medical images obtained at different times or from complimentary imaging modalities may be augmented by objective, accurate matching of the different data sets. Correlation analysis offers a powerful<br>technique for the computation of technique for the computation of<br>translation, rotation, and scaling rotation, and scaling differences between image data sets, especially in the case of complimentary images containing similar but not exact information. So far, this technique suffers from the drawback of high computational expense. We have computational expense. We have<br>reformulated this approach, yielding a fast, computationally much less expensive algorithm. Reduction of computation time is about seventy five percent.

### INTRODUCTION

Advanced medical imaging modalities such as nuclear medicine imaging (single photon and positron emission, positron emission,<br>nonoclonal antibodies), radiolabeled monoclonal antibodies), resonance spectroscopy, radiographic CT, and high resolution US duplex scanners provide<br>precise anatomic/pathologic and anatomic/pathologic functional data. As information is complimentary, the diagnostic potential can be augmented by combinations of single data sets. Due to the different nature of the displayed parameters, resulting in non-matching geometrical structures, and problems arising from non-uniform scale factors, viewing non-uniform scale factors, viewing<br>angles, and planes of images obtained at<br>different times or from different different times or from modalities, combining or overlaying different images requires the detection<br>of 3-dimensional translational and 3-dimensional translational and rotational shifts of the image planes adjustments of scale factors, and subsequent transformation of the images into a common frame.

Our goal was to develop an image matching system based on correlation analysis  $(1,2)$  which computes the three dimensional translation, rotation, and

scale factors necessary to determine the correspondence between complimentary image data sets with high precision and low computational expense. The work described herein discusses computation of<br>the translational and rotational the translational differences in two dimensions when using PET and NMR image data having equivalent scale.

At present, the predominant method for combining multimodality information relies on the vision of an expert human observer. Although this method is subjective, and therefore the precision<br>or reproducibility is not high, or reproducibility is not satisfactory results can be obtained if structures are similar and patient positioning differences are limited to positioning differences are finited to<br>two dimensional translations and two dimensional translations and<br>rotations. The quantitative combination of two complete sets of images with limited structural similarities and tilted image planes requires computer support. Past approaches to support. Past approaches to<br>multimodality image combination included the use of rigid head fixation devices<br>containing markers(3), edge detection containing markers(3), edge detection techniques(4), and iterative techniques(4), and iterative<br>correlation analysis(2), none of them however offering satisfactory results.

Current correlation analysis approaches are limited, as the coupling of the registration variables requires an iterative, computationally expensive algorithm. The solution described here<br>improves upon past work by first improves upon past work decoupling the translational and rotational components, thus eliminating the iterative part of the algorithm and significantly reducing the computational expense.

#### METHODS

Translation invariant information is derived from the input images and used to compute the rotational difference between them. This rotational difference is then applied to one of the input images, followed by a two dimensional cross correlation to compute

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the translational offset. This translation is then applied to the rotationally equivalent images to rocationally equivalent images to<br>produce the final matching images. The results of the matching can be evaluated by using highpass filter to find edges from one of the matched images and superimposing them over the other.<br>Translation in the time domain is a

phase shift in the frequency domain, so translation invariant information can be obtained by computing the power spectra of the input images. Conversion of the translation invariant power spectra to polar coordinates and then cross correlating yields the rotational difference.

Initially we computed the power spectra of the input image data using a two dimensional FFT, and then resampled two dimensional FFT, and then resampled<br>the spectra in polar coordinates to find<br>the rotational difference. Such an the rotational difference. Such an approach worked only on test images having much wider bandwidth than *ei* ther the PET or NMR images. The bandwidth of the PET and NMR images are<br>so narrow that most of the power is so narrow that most of the power is<br>concentrated in the the very low<br>frequencies close to DC. Computing the frequencies close to DC. rotational difference from the power spectra requires sampling the power spectra along a circle centered about the DC component. The larger the radius of the circle, the higher the rotational<br>sensitivity. Narrow band image data Narrow band image data has all the energy concentrated in a circle of small radius so rotational sensitivity is poor when resampling in polar coordinates from a rectangular grid.

The problem of poor rotational sensitivity has been solved by computing<br>the Fourier coefficients using a discrete Fourier Transform. The two one dimensional sequences of radial power spectra are then cross correlated, and the peak location indicates the rotational difference. The rotational resolution is proportional to the number<br>of angular samples of the power of angular samples of the spectra. computing 256 samples as is done in our project yields an angular resolution of approximately 1.4 degrees.

The rotation angle between two images cannot be determined unless the center of rotation is specified beforehand. Our algorithm computes the rotation angle necessary to orient the images in parallel(7). Thus the center of rotation is the center of the spatial domain image matrix.

The calculated rotational difference<br>ompensated in the NMR image, is compensated in the NMR image, yielding rotationally equivalent<br>images. A two dimensional cross correlation analysis determines the translational shift.

Currently we are using bilinear

interpolation to rotate the image data prior to computing the translation distances. This interpolation does introduce some errors into the rotated image, however since the NMR image is of much better quality than the PET image, the rotation is applied to the NMR image such that information loss is not noticeable.<br>The comput:

computational expense of correlational image registration depends upon the size of the search space. For iterative techniques each combination of rotation and scale requires three two dimensional Fourier transforms. If the best match is searched over a twenty<br>degree range at two degree intervals, and degree range at two degree intervals, and over a scale range from 0.8 to 1.2 at intervals of 0.05, then 297 twodimensional Fourier transforms must be Our approach requires six two dimensional Fourier transforms and six one dimensional transforms, obviously a considerable savings.

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