

Development of Automated Image Stitching System for Radiographic Images

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Introduction

X-ray images are very useful in diagnosing fractured bones or joint dislocation, looking for injury or arthritis, and in guiding orthopedic surgery for joint replacement and fracture reductions.

Conventional X-ray equipment can only provide a limited visual field. For high-resolution and larger image using the conventional screen-film technique, special cassettes and films of limited sizes are utilized. Sometimes, using one X-ray image is not enough to detect any abnormality in the human body. To produce images containing the whole body parts, digitized images from the cassettes and films which contain portions of the body parts can be assembled. For example, in conventional radiography, a large image can be assembled from the X-ray images of multiple exposures with a small spatial overlap. This technique is commonly referred to as stitching.

Image stitching is the process of overlapping two or more images taken at different viewpoints and different times to generate a wider viewing panoramic image. It consists of image registration and an image blending process. In image registration, portions of adjacent or consecutive images are modeled to find the merge position and the transformation which aligns the images [1]. Once the image has been successfully matched, a panorama image will be created to make a wider viewing so that the images are matched and merged seamlessly.

Image stitching plays an important role in panorama creation, super resolution image formation, medical image analysis [2, 3], and many other computer vision applications

[1]. Image stitching can be classified into feature-based and direct-based registration methods. Direct-based methods are based on pixel-to-pixel matching to maximize a measure of image similarity to find a parametric transformation between the two images [1, 4, 5].

Feature-based methods first extract distinctive features such as a corner in the two images to match these features and establish a global correspondence by comparing the feature descriptors; then, images are warped according to parametric transformations that are estimated from those correspondences [4]. Direct methods have the advantage of using all of the available image data and hence can provide very accurate registration, but being iterative methods, they require initialization. Unlike direct methods, feature-based methods do not require initialization, but they are timeconsuming, and for the majority of cases, finding features inside component images are difficult [6]. Some other methods are the combination of the two mentioned methods [1, 4, 5].

Direct- or pixel-based methods using the full image content are the most interesting methods in current research. Theoretically, these are the most flexible of the registration methods since, unlike all the other methods mentioned, they do not start by reducing the gray-level image to relatively sparse extracted information but use all of the available information throughout the registration process [1, 4, 5].

Kumar et al. [7] proposed a method for stitching medical image using histogram matching coupled with the sum of squared difference to overcome the drawback of featurebased method for image alignment. Although their method improves the efficiency of the similarity measure and search, they still have increasing complexity, and the degrees of freedom of the transformation are increased. Furthermore, hence, the sum of the squared difference method is not differentiable at the origin; it is not well suited to gradient descent approaches [1, 4].

Yu and Mingquan [8] adopted the grid-based registration method for the medical infrared images. They used the sum of

the squared difference metric to measure the similarity between the pixels in the two images. In order to improve the registration accuracy and reduce the computational time, they divided the registration process into two steps. The first step is rough registration, which records the best registration point position, while the second step is precise registration. With the current best registration point as the center, the template moves n grids and computes the square of difference of the corresponding pixels in the two images. The processing time decreased slightly by using the two steps, but still suffers from the complexity. An alternative to taking intensity differences is to perform correlation, i.e., to maximize the product (or cross-correlation) of the two aligned images [8].

Čapek et al. [9] utilized the point matching method together with the normalized correlation coefficient (NCC) to evaluate a similarity measure of the X-ray image. They claim that their method gave precise and correct results, but the time taken for processing is long.

The NCC score is always guaranteed to be in the range $[-1, 1]$, which makes it easier to handle in some higher-level applications (such as deciding which patches truly match). However, the NCC score is undefined if either of the two patches has zero variance. In fact, its performance degrades noisy low-contrast regions.

Correlation is a basic statistical approach to direct-based image registration. It is usually used for template matching or pattern recognition. It is a match metric, i.e., it gives a measure of the degree of similarity between an image and a template. This similarity measure method has been widely used because it can be computed using the fast Fourier transform (FFT); thus, for combining large images of the same size, it can be implemented efficiently. Furthermore, both direct correlation and correlation using FFT have costs which grow at least linearly with the image area [4].

Correlation filters are a direct-based method that has found applications in automatic target recognition [10] and biometric identification [11, 12]. The simplest form of correlation

filter is known as the matched spatial filter (MSF) [13, 14]. It performs well at detecting a reference image corrupted by additive white noise, but this technique suffers from distortion variance, poor generalization, and poor localization properties. The reason for this poor performance is because MSF uses a single training filter to generate broad correlation peaks [11]. This shortcoming is addressed by introducing another correlation filter known as a synthetic discriminant function (SDF). It is a linear combination of MSFs. It linearly combines a set of training images into one filter, which further allows users to constrain the filter output at the origin of the correlation filter [15]. These prespecified constraints are also known as “peak constraints.” SDF filters provide some degree of distortion in variance, but like MSFs, they result in large side lobes and broad correlation peaks that make localization difficult.

To reduce the large side lobes observed in SDFs and to maximize peak sharpness for better object localization and detection, minimum average correlation energy (MACE) filters were introduced. A MACE filter minimizes the average correlation energy of the correlation outputs from the training images while producing a sharp peak for the training object patterns [16–18]. This results in a correlation plane value very close to zero, except at the location of the trained object.

Based on the attributes of the MACE filter, we develop a stitching method, the details of which will be presented in the following sections. The proposed system employs correlation filters to find the best-matched position for two X-ray images that will be combined to form a single image

In this paper, a robust method is proposed for medical image stitching which uses MACE filter and peak-to-side lobe ratio as a similarity measure. In our experiment, it is assumed that there exists enough overlapping between adjacent images not less than 30 % so that precise stitching can be achieved. Our method proves its efficacy in matching accuracy and challenging processing time. The main method

and the algorithm are discussed in “[Image Stitching Method](#)”, “[Experiment and Results](#)” describes our experiment and presents the results. Discussion of the result is presented in “[Performance Evaluations](#)” section. Conclusions are presented in “[Conclusion](#).”

Image Stitching Method

The image stitching method functional flow presented in this paper is shown in Fig. 1. The components of the functional flow depicted in Fig. 1. It consists of seven components: (1) image preprocessing—this repository consists of input images after applying the pre-image processing strategy; (2) frequency domain transformation—the main function of this processor is to convert real-time domain values of images into frequency domain; (3) image filter computing—this processor implements MACE filter and produces a correlation plane of the input images; (4) correlation filter module—it actually takes the input test image and MACE filter correlation plane of the input object and finds the relation between them; (5) time domain transformation—this employs a logic that transforms the frequency domain values to time domain values; (6) peak-to-side lobe ratio calculation—this processor enhances the correlation peak and uses its logic to measure the performance of a filter and enhance the decision making to find the best match in the two images; (7) image stitching module—this utilizes the information received from all processors to create the panoramic image and output of the stitched image. These modules are explained in detail in forthcoming sections.

Image Preprocessing

Intensities in the images are highly sensitive to external factors such as illuminations. These external factors affect the distribution of intensities in the histogram of the images, which in turn affects the matching accuracy to a great extent. In order to make intensities relatively insensitive to the particular contrast, brightness of

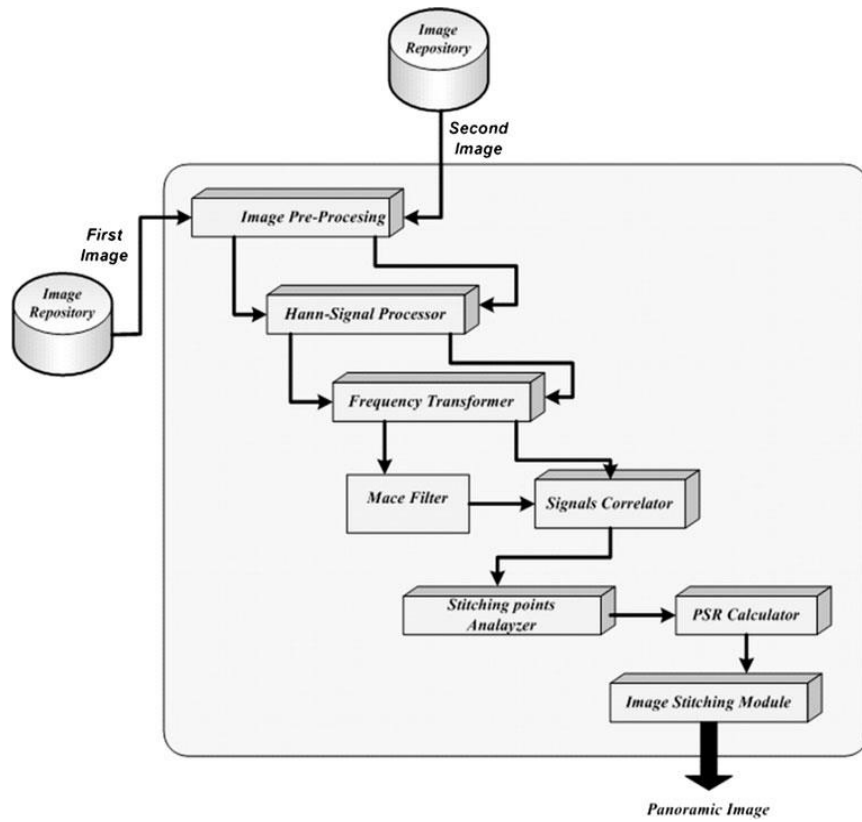


Fig. 1 Image stitching workflow

the original image, etc., we apply a histogram equalization with a flat envelop on the image to redistribute the intensities throughout the image. Then, the equalized image is Fourier-transformed.

Full text is available at :

<http://www.ncbi.nlm.nih.gov/pubmed/22610151>

<http://link.springer.com/article/10.1007/s10278-012-9483-5>