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Registration and analysis for images couple: Application to mammograms

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1 Abstract

In the scientific world, signal analysis and especially image analysis is a very active area, due to the variety of existing applications, with issues such as file compression, video surveillance or medical image analysis. This last area is particularly active. The number of existing devices and the number of images produced cause the availability of a large amount of information to be processed by practitioners. Computers give now an opportunity to assist them.

In this thesis, the problem addressed is the development of a computer-aided diagnosis system (CAD) based on conjoint analysis of several images, and therefore on the comparison of these medical images. The particularity of our approach is to look for evolutions or aberrant new tissues in a given set, rather than attempting to characterize, with a strong *a priori*, the type of tissues. This problem allows to apprehend one aspect of the analysis of a medical file performed by experts which is the study of a case through comparison and evolution detection. This task is not easy when automation is concerned. The human eye performs quasi-automatically treatments that we have to replicate.

The methodology proposed is carried out within the application context of the development of a CAD applied to mammograms. The first step when a couple of images are involved is to perform an adapted registration. Any automated comparison of signals requires an alignment of similar components present on the pictures, that is to say a registration phase, so that they occupy the same space on the two images. If no registration is applied, it is difficult to localize and compare regions of interest on the two images, as differences of size, orientation or other distortions may have occurred. As the registration is never perfect, we must take into account the level of uncertainty and develop a comparison method able to distinguish registration error and real small differences between comparable tissues. In many applications, the assessment of similarity used during the registration step is also used in the interpretation step that yields to prompt suspicious regions. In our case, registration is assumed to match the spatial coordinates of similar anatomical elements.

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The projection of a 3D reality onto a 2D image causes differences due to the orientation of the observed tissues, and will not allow to analyze a pair of shots with a simple difference between images. Before comparing some region on the two images, we need to determine where this area is located on both images. In order to reach a significant registration, a referent image is computed from control points based on anatomical features that can be extracted automatically in a robust way on the images. Then the second image of the couple is realigned on the referent image, using a coarse-to-fine approach as an expert could do. This approach allows both rigid and non-rigid transforms with a not too high computation complexity.

This 2-step registration methodology is inspired by the mechanism of expert mammogram reading that performs a pre-attentive observation, which is global, before focusing on different local significant landmarks of the breast. This approach can be applied to nearly all other medical images where a contextual location has to be found before a more precise registration.

The registration starts with a rigid and global transformation of the image, where translation and rotation are performed in order to refer to the same coordinate systems in both the floating image and reference image. A common coordinate system is defined in the two images. This part is based on the extraction of anatomical primitives of the breast. We adopt the most robust landmarks, which are the breast contour, the nipple, and the pectoral muscle. The second step is then a local registration. The methods we propose, intend to simulate the deformation due to the image point of view and to the breast compression, including *a priori* knowledge on the internal physics of the breast. The most important contribution is to consider general registration is decomposed in two linear 1D registration, considering some specific direction or considering an angle measure. Then, it is based on very fast structuring methods. This methodological framework allows a computational cost lower than methods analyzing the set of pixels to generate a complex registration. Nevertheless the composition of different transforms we propose enables the definition of complex deformation fields. The simple linear model can be improved using a quadratic approximation of the theoretical breast deformation. Different transformations are elaborated and evaluated to obtain an adapted and robust registration of the processed images. The references used can be adapted to other context according the expert use. In our case we obtained the registration of all points of the breast using only relevant primitives. It produces a complex deformation field, fast to estimate and non-rigid.

After minimizing the location differences on the images, the analysis of tissues evolution is performed. Most of the existing solutions are based on the characterization of what is “normal” or “typical” and on what is representative of an “abnormal” phenomenon previously learned at a well-adapted level (pixel, shape, texture, characteristic vector, etc). These methods can be very specific and bring complex solutions. The proposed method is not based on texture learning or shape segmentation. Our idea is different; it relies on a pixel level representation that makes it possible to identify original distributions or new elements.

As a pixel is characterized by the neighborhood distribution of basis elements, comparison is integrating richer information than a simple characteristic and then it is simple and adaptive. The information representation is done at pixel level. The basis elements represent all the clustered patterns included in the images. Our method is based on a sparse representation of the signal in order to obtain a restricted number of significant components well suited with respect to the patient. The elements are chosen to enhance what is rare and what is new with respect to current elements. The resulting codebook controls simplicity and integration of original (rare) elements, and a bag of words methodology makes it possible to compare two images with this new referential.

The images are reinterpreted, not as a set of pixels with different brightness, but as patterns representative of the entire image, enabling a new decomposition of the images. The advantage of such a representation is that it allows to highlight some specific aspect of the signal, and to analyze the image under a new perspective the information necessary for the diagnosis aid. In order to detect tissue anomalies, the comparison of two images can be done either in a pairwise pixel comparison, integrating patches content around each pixel and codebook components or by computing the distance between local distribution vectors of patterns associated with each image of the pair. These approaches are evaluated and compared.

The method has been tested on a mammogram temporal pair database. A pair is a couple of images in oblique view, with the same resolution. This evaluation allows to compare the different approaches elaborated during this Ph.D work to determine the better representation of information for each problematic.

Our results are embedded in a CAD reproducing as much as possible the perceptual human behavior, in an efficient way in order to have an acceptable computation time. The registration is based on anatomical primitives for location and performs a deformation inspired by practitioner mammogram reading, including a priori knowledge on the internal physics of the breast. It is based on very fast methods and highlights image structure.

For the analysis, we measure an evolution appearing in the tissues by comparing them to tissues from the same patient. An important point is the choice of the learning set. Many works try to use universal dictionaries. The variability of inter-patient tissues in a mammogram is such that this choice is rarely judicious. It seems more appropriate to carry out the building of the codebook from the patient file itself in order to offer a good specificity. The differences that may occur can be either due to noise or to ill parts, but only a medical expert can label the area as ill or not.

This thesis has been carried out in the LIPADE laboratory of University Paris Descartes (SIP team, specialized in image analysis) and in collaboration with the Fenics Company (designer of diagnosis aid stations for the analysis of mammograms) under a Cifre convention. The convergence of the research fields of those teams led to the development of this document.