

Non Rigid Registration for Building 3D Anatomical Atlases

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Abstract

This paper presents a general scheme for the building of anatomical atlases. We propose to use specific and stable features, the "crest lines" or ridge lines which are automatically extracted from 3D images by differential geometry operators. We have developed non-rigid registration technics and got encouraging results for the building of a first atlas of the crest lines of the skull based on several CT-Scan images of different patients.

1 Introduction

In order to improve the diagnosis and the therapy planning, the physician needs to compare 3D medical images coming from Computed Tomography, Magnetic Resonance Imagery or Nuclear Medicine with anatomical atlases.

Nevertheless, anatomical atlas books are only two-dimensional and very few of them give a quantitative information about the localization of features or their variations among patients as [TT88]. By using image processing tools applied to very precise 3D medical images, we could build very accurate 3D atlases with quantitative results.

In this paper, we present such a project. After a presentation of the general scheme, we detail the type of features used in the atlas and describe a non-rigid registration algorithm. At last, we show the first encouraging results of the automatic building of an atlas of the crest lines of the skull.

2 General scheme

Our project may be decomposed into two parts:

- *the atlas building*: a set of representative objects (for instance, healthy patients) are registered. By

making comparisons between these data, the registration algorithm seeks for some features that are shared by the reference set (or a significant subset). The features "average" will then compose the atlas. A statistical analysis will determine the "acceptable difference" in relation to the atlas.

- *the atlas use*: the registration algorithm permits to compare the second set of data (for instance, a pathological patient) and the atlas. The statistical parameters give precious information about the level of "abnormality".

Such an atlas would allow to localize very precisely, especially if anatomists have thoroughly labelled a lot of elements as in [SHP⁺93]. Quantitative results could also be sent to a diagnosis module to detect some pathologies. For now, we plan to integrate the 3D visualization of the skull atlas in the craniofacial surgery simulation testbed developed in the Epidaure project [DSCP94], in order to help the physician to plan operations.

3 The atlas structure

Raw medical images are stored in a discrete 3D matrix $I = f(x, y, z)$. By thresholding I , isosurfaces of organs are computed (for instance, the surface of the skull for CT-Scan, of the brain or the face for MRI). The problem is then to compute specific features of these surfaces. We can use *surface features* based on mean and Gaussian curvatures, *line features* as ridge lines or skeletons, *point features* as the "extremal points" [Thi93] or a combination of the three.

We decided first to use only line features: the "crest lines" introduced in [TG93]. They are defined (except at umbilics) as the successive loci of a surface whose largest principal curvature is locally maximal in the

direction of its principal direction. Let k_1 be the principal curvature whose curvature is maximal in absolute value and \vec{t}_1 the associated principal direction, each point of a crest line verifies $\vec{\nabla} k_1 \cdot \vec{t}_1 = 0$. These lines are automatically extracted from an isosurface by the “marching lines” algorithm [TG93].

Furthermore, crest lines are anatomically meaningful: in figure 1, crest lines represent the salient lines of the skull and they follow the convolutions of the brain.

4 The registration algorithm

The 3D curves registration algorithm is the key point of our scheme: given two sets S and S' , we want to find which lines C_i of S (or portions of lines) correspond to which lines (or portions) of S' .

Two difficulties arise: the number of lines of each set is quite important (several hundreds) and the registration between S and S' is not rigid. Our algorithm follows the steps of the “iterative closest point” introduced in [Zha92] and [BM92].

- *Point matching*: each point of S is linked with its closest neighbour in S' according to the Euclidean distance. We also plan to use in the distance computation the differential curve or surface parameters. We apply some heuristics to make the links symmetrical and consistent along the curves.

With these couples of points, two coefficients are computed: p_i^j and p_j^i which are the proportion of the curve i of S matched with the curve j of S' and vice versa. Thus, by thresholding, $p_i^j \geq thr$ and $p_j^i \geq thr$, we can determine the curves “registered” at thr percent. For instance, curves can be considered completely registered when $p_i^j \geq 0.5$ and $p_j^i \geq 0.5$.

- *Least-squares transformation*: as the registration is not rigid and even not affine, we try to register S and S' with a 2-order polynomial transformation by a least-squares method.

We tried to use higher order polynomials but large unexpected undulations then occur. 2-order polynomial transformations give accurate registration but we are not able to decompose them into intuitive physical meaning transformations such as rotation, translation or scaling. Notice that at each iteration, we compose the transformation with a 2-order polynomial and so, we obtain after n iterations a 2^n -order polynomial transformation.

- *Updating*: the transformation is applied, then the algorithm iterates again or stop according to several criteria (mean value of the distance distribution between matched points, stability of the registration coefficients p_i^j and p_j^i , threshold on the matrix norm $\|T - I_d\|$ where T is the transformation and I_d the identity matrix).

By incrementing the threshold value thr at each iteration, for instance, from 0 to 0.5 by step of 0.05 and by taking only in account the matched point couples (M, M') belonging to “registered” curves at thr percent, the algorithm tends to improve the registration of already matched curves and to discard isolated ones. Moreover, we can begin to apply rigid transformations to align the two sets of lines, then affine transformations to scale them and, at last, quadratic transformations to refine the registration.

5 Results

We applied this algorithm to two sets of the longest crest lines (for easier visualization) of the skulls of two different patients. Notice in figure 2 that the number of lines of the two sets (42 and 31 lines with 5659 and 4816 points) and their shape (as the nose) are different and also that the two skulls are quite shifted.

One set of lines S is then deformed to be registered with the second S' . To evaluate the result, we display in figure 2 (right) the registered lines of S' and S after deformation. The matched points are linked by segments. The registration takes a few minutes on a DEC-Alpha workstation. The algorithm detects and matches similar lines (12 lines) as the orbits, the mandible, the nose, the temples and the occipital foramen. Even if the lines are not perfectly superimposed, linked points appear very accurate. In figure 2 middle, we show the registered lines of the set S' and of the set S not deformed.

Then, we registered, two by two, 6 sets of lines extracted from CT-Scan images of different dry skulls (520 lines, 18000 points per set on average) and we searched for the lines common to all the sets. We found 48 subsets of similar lines (figure 3) including the mandible, the nose or the orbits which can be then automatically labelled. More results are presented in a research report [STA94]. Now, we work on how to average the common lines and to compute statistical parameters.

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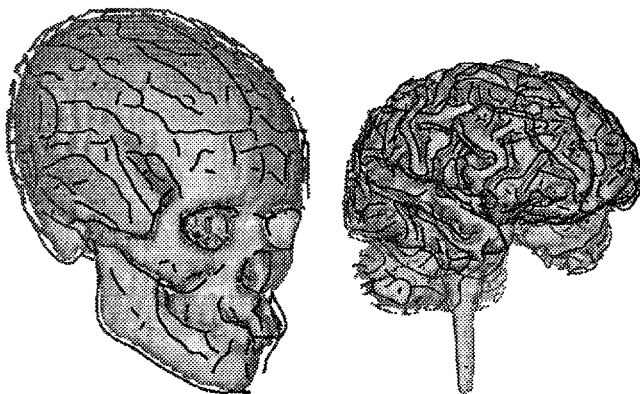


Figure 1: Crest lines of a skull and of a brain.

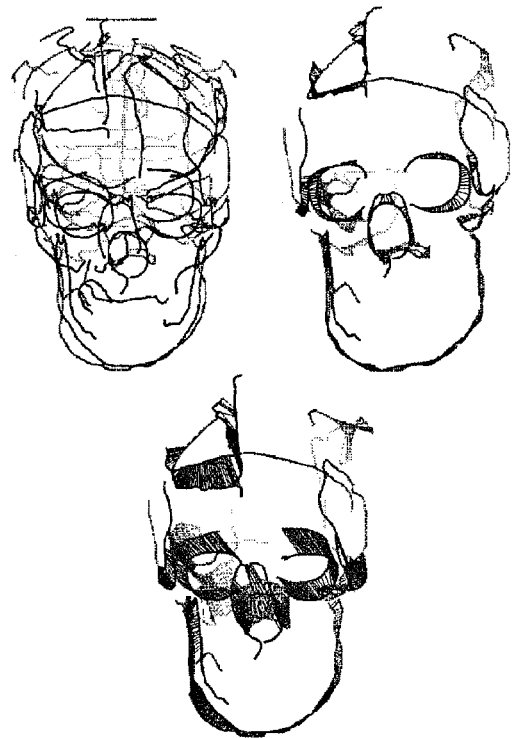


Figure 2: Left: The longest crest lines of the two skulls superimposed. Right: Registration of similar lines after the deformation. Middle: Registration of similar lines in their original position.

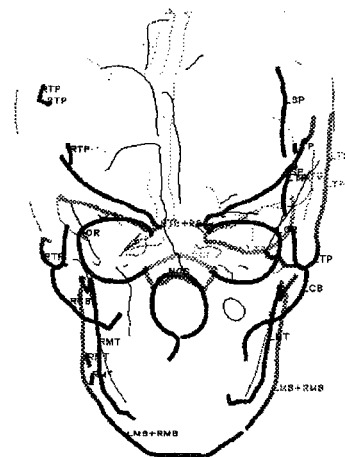


Figure 3: On the skull, 48 subsets of common lines have been automatically extracted from 6 different CT-Scans. Some of them have been automatically labelled and highlighted.