

CLARCS, a C++ Library for Automated Registration and Comparison of Surfaces: Medical Applications

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Abstract. In this paper we present the methods implemented in the CLARCS (C++ Library for Automated Registration and Comparison of Surfaces) library. This library allows some basic and high level processing on free-form surfaces, represented as point sets or meshes. Three methods are the “building bricks” of CLARCS; they allow (i) the rigid/affine/non-linear registration of two point sets, (ii) the computation of the mid-sagittal plane of one point set, (iii) the computation of a mean point set from several point sets, and the variability around this mean. These methods are all based on a common methodological framework, in which the point sets/meshes are represented either as a Gaussian mixture model or as a draw of such a model. We propose some applications of the methods implemented in CLARCS on different sets of medical data.

1 Introduction

In medical image processing, the most widely used methods are voxel-based, which means that their required input data must be (most often) 3D arrays of grey values. Some important issues with this kind of data include the large memory needed to store them, the large run time of standard algorithms to process them, the choice of data type to code the grey value of a voxel or the sometimes problematic orientation of the volumes. Thanks to the increase of 3D rendering and computational capacities of computers in the last few years, new surface based processing methods have emerged as an alternative to standard voxel-based techniques. In this context, the VisAGeS team at INRIA/INSERM (<https://www.irisa.fr/visages>) has proposed a set of computational tools that have been implemented in a software library called CLARCS (C++ Library for Automated Registration and Comparison of Surfaces).

In this paper, we outline the methods implemented in CLARCS (Section 2) and we provide some potential medical applications of these (Section 3): assessment of dysmorphology in craniosynostosis and plagiocephaly and construction of a statistical shape model of thalami for deep brain stimulation (DBS).

2 Overview of CLARCS

In the first subsection below, we briefly describe some of the best known libraries or software working on point sets, meshes or surfaces. In the second subsection, we describe the functions implemented in CLARCS.

2.1 Related software for surface processing

There exists a bunch of commercial software allowing for some basic (*e.g.* import/export, visualisation) and higher level (*e.g.* registration) processing on surfaces, such as Amira (<http://www.amira.com>), or Rapidform (<http://www.rapidform.com>), but it is often difficult to know what methods are implemented therein, and always costly to acquire the software.

Some freeware are specifically dedicated to high level geometric computation (*e.g.* CGAL, <http://www.cgal.org>) or high level visualisation (*e.g.* ParaView, <http://www.paraview.org>, and VTK, <http://www.vtk.org>) of surfaces, but we restrict our brief overview here to software which allow surface registration/comparison in a broad sense. The Point Cloud Library (or PCL, <http://pointclouds.org>) and MeshLab (<http://meshlab.sourceforge.net>) are two such software/libraries, but they only implement rigid registration. FreeSurfer (<http://surfer.nmr.mgh.harvard.edu>) allows non-linear registration of surfaces, but is limited to brain (cortical) data (using a specific atlas for this purpose).

Some freely available state-of-the-art software with a larger range of applications include:

- TPS-RPM [4]: <http://noodle.med.yale.edu/~chui/tps-rpm.html>
- TPS-L2 [15]: <http://code.google.com/p/gmmreg>
- CPD [20]: <https://sites.google.com/site/myronenko/research/cpd>
- SPHARM [22]: <http://www.enallagma.com/SPHARM.php>
- weighted-SPHARM [5]: <http://www.stat.wisc.edu/~mchung/software/software.html>

We have experimentally found the first three methods to be most often unable to cope with large (more than 100,000 points) point sets, while the two others impose strong topological constraints on the surfaces to register (they must be closed). The methods implemented in CLARCS allow the processing of large point sets (often needed to encode highly convoluted/complex anatomical structures) without topological constraints, in an efficient and fast way. From a methodological point of view, a strong advantage of these methods over most of

the abovementioned ones is the unified computational framework they are based on, as outlined below. Finally, to our knowledge, there is no freely available software allowing the computation of the symmetry plane of approximately bilateral surfaces, and the assessment of asymmetries thereof.

2.2 CLARCS

CLARCS is a C++ library for surface processing and analysis which has been developed at IRISA (<http://www.irisa.fr>) since 2007. CLARCS is mainly composed of three basic algorithms allowing (i) the rigid/affine/non-linear registration of two point sets, (ii) the computation of the mid-sagittal plane of one point set, (iii) the computation of a mean point set from several point sets, and the variability around this mean. These algorithms are building bricks that can be combined to allow higher-order surface processing such as computation of pointwise asymmetry fields and statistical analysis thereof within or between populations. The three algorithms rest on a common methodological framework, that we briefly outline here. We refer the reader to the corresponding papers for a deeper insight into these algorithms. Let us first define the following pseudo-distance between point sets X^1 and X^2 :

$$\delta^2(X^1, X^2) = \min_{A, T} \left[\sum_{x_i \in X^1} \sum_{x_j \in X^2} A_{i,j} \|x_i - T(x_j)\|^2 + 2\sigma^2 \sum_{i,j} A_{i,j} \log(A_{i,j}) + \alpha L(T) \right]$$

with $\forall i \sum_j A_{i,j} = 1$ and $\forall i, j A_{i,j} \geq 0$

Computing $\delta^2(X^1, X^2)$ is a minimisation problem involving the unknown transformation T linking the two point sets, and the unknown $\text{card}(X^1) \times \text{card}(X^2)$ matrix A . The constraints on this matrix allows it to encode the point-to-point correspondences between the point sets in a *fuzzy* way. The cost function can be seen as the sum of (i) a data-attachment term, (ii) a barrier (smoothing) function, which convexifies the cost function, and (iii) a regularity constraint on the unknown transformation. The relative strength of the three terms is weighted by the positive scalars $2\sigma^2$ and α .

It is enlightening to notice that this minimisation problem is actually the maximum a posteriori (MAP) problem consisting of finding the transformation T best superposing the two point sets, when one makes the hypotheses that (i) each point x_i of X^1 is independently drawn from a Gaussian mixture model (GMM) (whose means are the points $T(x_j)$ of $T(X^2)$, whose covariance matrices are equal to $\sigma^2 I$, I being the identity 3×3 matrix, and whose mixture weights are equal) and (ii) T is a random variable with a distribution of the form $\propto \exp(-\alpha L(T))$. With this probabilistic view, X^1 can be interpreted as a *noised* version of $T(X^2)$, σ being the standard deviation of this noise.

This MAP problem can typically be solved using the Expectation-Maximisation (EM) algorithm, which leads to the following iterative two-step algorithm:

- **E-step:** $\forall i, j \tilde{A}_{i,j} = \frac{\exp[-\|x_i - \tilde{T}(x_j)\|^2 / (2\sigma^2)]}{\sum_k \exp[-\|x_i - \tilde{T}(x_k)\|^2 / (2\sigma^2)]}$
- **M-step:** $\tilde{T} = \arg \min_T \sum_{i,j} \tilde{A}_{i,j} \|x_i - T(x_j)\|^2 + \alpha L(T)$

This EM algorithm can be shown to converge monotonically to an (at least) local maximum of the MAP criterion or, equivalently, to an (at least) local minimum of the aforementioned cost function. Actually, the two steps of the EM algorithm are exactly the same as those obtained when minimising this cost function with respect to A and T in turn.

The formulation of the E-step helps to understand why the matrix A encodes the point-to-point correspondences: when the transformation T is known, $\tilde{A}_{i,j}$ is the posterior probability that the point x_i has been drawn from the mixture component with centre $T(x_j)$. The E-step simply consists in computing these $\text{card}(X^1) \times \text{card}(X^2)$ probabilities. On the contrary, solving the M-step is highly dependent on the type of transformations considered.

Below, we show how this generic algorithm can be instantiated to lead to the three basic methods implemented in CLARCS.

Rigid/affine/non-linear registration. When T is set to be rigid and $\alpha = 0$ (*i.e.* no prior on the rigid transformation), the MAP problem boils down to a maximum likelihood (ML) problem. Several closed-form solutions exist for the M-step, using typically the unit quaternions or the singular value decomposition. This results in what was termed the EM-ICP algorithm by Granger & Pennec [14]. An earlier variant of this algorithm was devised by Rangarajan *et al.* and termed the RPM algorithm [21].

We built on the EM-ICP algorithm to propose some adaptations for non-linear registration. In previous works, we showed how to use the normals in addition to the point coordinates [19], and how to enforce some constraints on the point-to-point correspondences [9]. We also showed how to solve the M-step when considering a model of locally affine transformations [19, 9] or when using the Reproducing Kernel Hilbert Space (RKHS) theory and the Fourier analysis to build the model [10]. Finally, we showed how to obtain symmetric consistency when using this last transformation model [10].

Symmetry plane computation. When T is set to be a reflection, $\alpha = 0$ (*i.e.* no prior on the reflection) and when $X^1 = X^2$, the EM algorithm allows to compute the plane best superposing the left and right parts of $X^1 = X^2$ [7]. Needless to say, this assumes that $X^1 = X^2$ is (at least) approximately *bilateral*. Our specific contribution was to propose a closed-form for the M-step, relying on the parametrization of the unknown reflection plane using its unit normal and distance to the origin of the coordinate system [7]. Non-linear registration of the point set with its flipped image with respect to the approximate symmetry plane allows the pointwise mapping of asymmetries [8].

Atlas construction. The problem here is to find a point set M best representing a set of n point sets X^1, \dots, X^n . We defined it as:

$$M = \arg \min_X \sum_{i=1, \dots, n} \delta(X, X^i)$$

If T is set to be a similarity (rigid transformation plus uniform scaling), it is possible to devise an iterative algorithm converging to an (at least) optimum of this criterion, in which the point-to-point correspondences, the mean point set (which turns out to be the mean shape in this case where T is defined as a similarity) and the unknown transformations linking the n point sets and the mean point set are estimated in turn. However, in such an approach, point-to-point correspondences are likely to be meaningless; this is why we proposed to establish these correspondences using non-linear transformations while computing the mean shape using similarities. The resulting iterative algorithm can no longer be shown to converge, but behaves well in practice [6]. Once the algorithm has converged, it is straightforward to perform PCA on the residuals.

Implementation details. These three algorithms were implemented within a **multiscale** framework. As previously noted by Granger & Pennec, the σ parameter allows to deal with the correspondences in a fuzzy way, leading to a smoother criterion to minimise. When σ is infinitely small, their EM-ICP algorithm is simply the ICP algorithm of Besl & McKay, hence the name [2]. This leads to the idea of devising a scheme in which several EM algorithms are successively run with decreasing σ values, with a large starting value when the point sets to register are far from each other. We also used *kd*-trees, for **increased speed**, and a cut-off distance between the points x_i and $T(x_j)$, above which they are eliminated from the estimation of the transformation, for increased speed and **robustness to outliers**.

3 Applications

3.1 Quantification of skull asymmetries in craniosynostoses

Synostosis is the union of two or more separate bones to form a single bone (Merriam-Webster). Cranial synostosis, or craniosynostosis is a rare congenital disease which consists in the premature fusion of one or several cranial sutures. The last medical condition is typically met in conjunction with a hundred of syndromes, among which are Apert or Crouzon. On the contrary, the etiology of isolated (nonsyndromic) craniosynostosis is largely unknown. Early detection and treatment of craniosynostosis is crucial, as hindered skull growth can lead to increased intracranial pressure and thus alteration of normal brain development [23].

It is expected that improved characterisation of the dysmorphology of the skull associated with craniosynostosis could help understanding its cause(s), improving its diagnosis (e.g. lambdoid synostosis may be easily confounded with

deformational plagiocephaly) and even improving its treatment. In this context, of particular interest are the unilateral coronal synostoses, as it is not clear whether the left and right coronal synostoses are due to the same factors.

We propose to characterise the dysmorphology of one skull with unilateral left coronal synostosis by assessing its pointwise asymmetry. This assessment is based on the computation of an *approximate* symmetry plane, from which the left-right differences (asymmetries) can be evaluated (cf. Fig. 1). The outer surface of the skull was computed using manual grey-level thresholding, mathematical morphology and the marching cube algorithm from a CT scan. The point set is a triangular mesh of a complete skull made up of about 140,000 cells and 82,000 points.

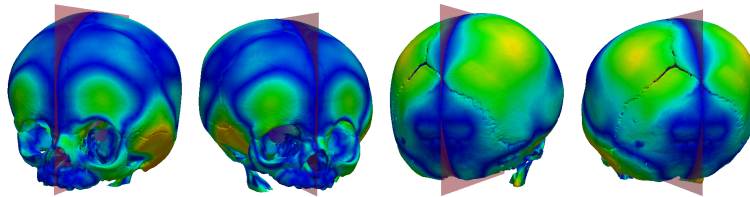


Fig. 1. Evaluation of pointwise asymmetries on a skull with craniosynostosis. We display the norm of the asymmetry field. Strong asymmetries are visible on the temporal bone, the posterior part of the parietal bone and the supraorbital part of the frontal bone.

3.2 Quantification of skull asymmetries in deformational plagiocephaly

Since the inception of the "back to sleep" recommendations in the early 90s to reduce sudden infant death syndrome, the incidence of positional (i.e. nonsynostotic) plagiocephaly has drastically increased [18, 16]. Plagiocephaly consists of the flattening of one side of the head, with aesthetics consequences, and potential altered brain development [17]. Objective assessment of plagiocephaly should help diagnosis and follow-up of this condition [3].

We propose to characterise the deformational plagiocephaly of one skull using the same computational tools as in the previous section (cf. Fig. 2). The outer surface of the skull was computed using manual grey-level thresholding, mathematical morphology and the marching cube algorithm from a CT scan. The point set is a triangular mesh of a complete skull made up of about 200,000 cells and 137,000 points.

3.3 Building statistical shape models of deep grey nuclei

Deep brain stimulation (DBS) was initially targetted to the ventral intermediate thalamus to reduce tremor in patients with Parkinson's disease [1]. Since

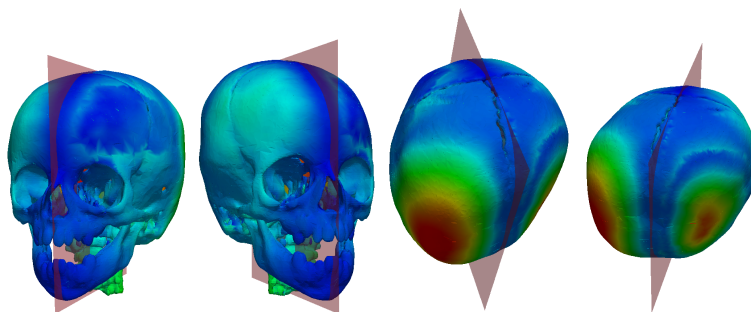


Fig. 2. Evaluation of pointwise asymmetries on a skull with deformational plagiocephaly. We display the norm of the asymmetry field. Strong asymmetries are visible on the posterior part of the parietal bone and on the superior part of the occipital bone.

then, alternative targets have emerged, such as the subthalamic nucleus (STN), globus pallidus interna, which appear to be comparatively efficient in this context [12]. The indications for DBS have also been extended to drug-resistant epilepsy, dystonia, Tourette syndrome or even obsessive compulsive disorders, using the caudate and accumbens nuclei (for instance) as targetted structures. An improved knowledge of the anatomy of these subcortical structures is key to optimise pre-operative planning and to assess treatment efficacy.

In this context, statistical shape models (SSMs) are extremely useful as they allow to help the segmentation of the structures of interest in MR images, in which typical pulse sequences make it hard to distinguish these nuclei based on the grey values alone [11].

As an illustration, we propose to build a statistical shape model of the thalami (Fig. 4) which were manually segmented together with six other deep brain structures (cf. Fig. 3) by a trained neuroanatomist using itk-SNAP (<http://www.itk-snap.org>) in 10 patients with Parkinson's disease. For each patient, the seven pairs of segmented structures were stored in a 3D image with discrete labels. The surfaces of the structures were computed using the marching cube algorithm. The points sets representing the left and right thalami are triangular meshes with sizes of about 10,000 cells and 5,000 points.

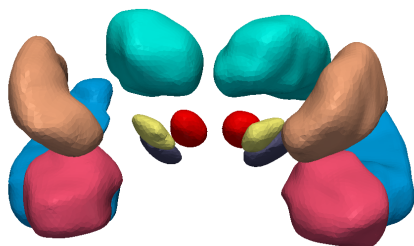


Fig. 3. Front view of seven deep brain structures. Cyan: thalamus, orange: putamen, magenta: amygdala, blue: hippocampus, red: red nucleus, yellow: STN, purple: substantia nigra.

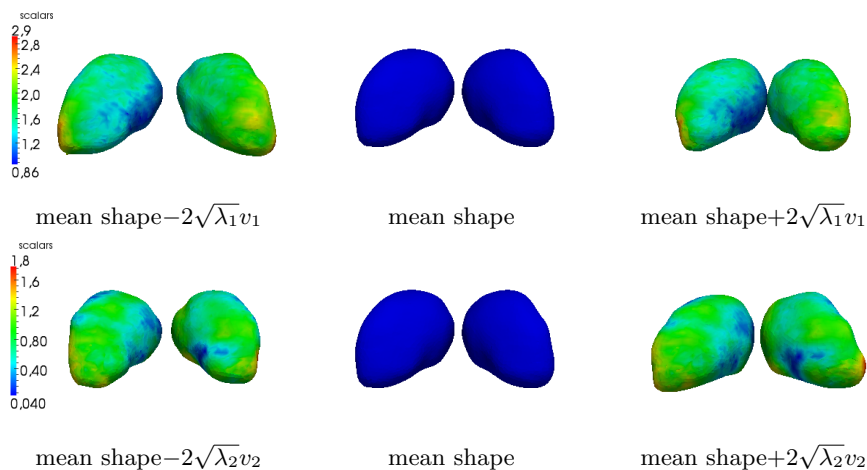


Fig. 4. Mean shape and first two modes of variation on left and right thalami. The colour maps the norm of the displacement (in mm) of each point along the first (top row) and second (bottom row) mode of variation ($\pm 2\sqrt{\lambda_i}v_i$) around the mean shape.

4 Discussion & Conclusion

In this paper, we presented the CLARCS library and its three building bricks, namely: (i) the rigid/affine/non-linear registration of two point sets, (ii) the computation of the mid-sagittal plane of one point set, and (iii) the computation of a mean point set from several point sets. We also gave some possible applications of CLARCS. Some other applications can be found in the full papers describing the methods implemented in CLARCS, for instance:

- the construction of a statistical shape model of the osseous labyrinth [6] and the caudate nuclei [10]
- the estimation of the mean pointwise brain asymmetry in male right-handed subjects and the comparison with situs inversus subjects [6] and with chimpanzees [13]
- the estimation of the mean pointwise facial asymmetry in males and females, and the comparison thereof [8]

With its new, robust and fast methods for surface processing, CLARCS opens interesting perspectives with medical applications. For instance, the non-linear registration of two point sets of about 200,000 points each runs in less than 5 minutes on a recent standard personal computer (3GHz).

The implementation of the framework of CLARCS is compatible with the well-known visualization toolkit VTK (<http://www.vtk.org>), thus it is possible to insert CLARCS specific methods into more general VTK pipelines.

We plan to distribute CLARCS as an open-source library, but this step will require some code refactoring, thus CLARCS will be first available as an external plugin of the future version of MedInria (<http://med.inria.fr>) that will be released in early September 2011.

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