Multiple Registration and Mean Rigid Shapes – Application to the 3D case – Xavier PENNEC
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Multiple Registration and Mean Rigid Shapes Application to the 3D case

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Abstract

We present in this article a multiple registration algorithm to compute the mean rigid shape of a set of possibly incomplete k-tuples in any dimension. Synthetic and real experiments in molecular biology and medical imaging illustrate the validity and utility of the method.

1 Introduction

To study the shape of an object, it is common to describe the object by a fixed number k of characteristic features in order to obtain a k-tuple $(x_1, \dots x_k)$. Two objects have the same form if there exists a transformation that superimposes them, and thus identifies their "characteristic" k-tuples.

General studies focus on k-tuples of points and their form under rigid transformation with possibly scaling (Kendall, 1989; Goodall, 1991; Le and Kendall, 1993). There are fewer works dealing with more general transformations, and most applications concern 2D landmarks (Bookstein, 1991; Small, 1988). In computer vision and medical imaging, however, some more complex features can appear (like lines, frames…), and we need to work in 3D. This type of constraints is also shared in structural biology, when it comes to the tertiary structure of the proteins.

We have already presented algorithms for recognition and registration of two observations for 3D substructure matching of proteins and registration of medical images based on extremal points (Pennec and Ayache, 1994; Thirion, 1994; Pennec and Thirion, 1996). We are interested here in multiple registration of n observations and the definition of a mean shape based on point features under rigid transformations.

We present in the first part a characterization of expected and mean rigid shapes which is basically the generalization to nD of some 2D result of Ziezold, (1989, 1994). We show that the mean rigid shapes can be computed independently after a multiple registration step of the k-tuples, and propose an iterative method to solve the multiple registration problem. In the real world, however, we have to cope with missing data and thus incomplete k-tuples. We propose another iterative scheme that allows to solve this problem. This theoretical framework is illustrated in molecular biology and medical imaging with the creation of a model of the heme binding motif and a model of the head of a patient based on extremal points.

1.1 Expected and mean elements in metric spaces

This theory of expectation in metric spaces was introduced in (Frechet, 1948). Let *dist* be an distance on a manifold $\mathcal{M}$ and $\mathbf{x}$ a random feature of probability density function (pdf) $p_{\mathbf{x}}$ (in the parameter space). The expected square distance of a deterministic feature y with the random feature $\mathbf{x}$ is defined by

$$\sigma_{\mathbf{x}}^2(y) = E(\operatorname{dist}(y, \mathbf{x})^2) = \int_{\mathcal{D}} \operatorname{dist}(y, x)^2 . p_{\mathbf{x}}(x) . dx \tag{1}$$

If $\sigma_{\mathbf{x}}^2(y)$ is finite for all y, we call every feature $\bar{x}$ minimizing $\sigma_{\mathbf{x}}^2$ an expected feature, and we denote by $\mathbb{E}(\mathbf{x})$ the set of all expected features of the random feature $\mathbf{x}$. We have thus

$$\mathbb{E}(\mathbf{x}) = \arg \inf_{y \in \mathcal{M}} \left(E(\operatorname{dist}(y, \mathbf{x})^2) \right) \tag{2}$$

If there is at least one expected feature $\bar{x}$, then $\sigma_{\mathbf{x}} = \sigma_{\mathbf{x}}(\bar{x})$ is called the standard deviation of $\mathbf{x}$ and $\sigma_{\mathbf{x}}^2$ the variance. In general, the existence and uniqueness of the expected value are not ensured. In a very similar way, we can define the set of empirical means of features $x_1, \ldots x_n$ by

$$\mathbb{M}(\{x_i\}) = \arg \inf_{y \in \mathcal{M}} \left(\sum_i \operatorname{dist}(y, x_i)^2 \right) \tag{3}$$

More generally, the “mean deviation” at order α is define by

$$\sigma_\alpha(y) = (E(\operatorname{dist}(y, \mathbf{x})^\alpha)^{1/\alpha} = \left(\int_{\mathcal{M}} \operatorname{dist}(y, x)^\alpha . p_{\mathbf{x}}(x) . dx \right)^{1/\alpha} \tag{4}$$

If this function is finite over $\mathcal{M}$, the features $\bar{x}_\alpha$ minimizing it are called central features of order α. To be more practical, we obtain the modes of the pdf for $\alpha = 0$, the median features for $\alpha = 1$, of course the mean or expected features for $\alpha = 2$, and the “barycenter” of the support of the pdf (which is a compact set) if the mean deviation is finite for $\alpha = \infty$. This can also be applied to define the empirical central features at any order.

2 Rigid shapes in $\mathbb{R}^m$

We consider in this article point features in $\mathbb{R}^m$ and investigate the shape of a k-tuple of such landmarks under rigid transformations. In order to simplify the notations, we note $\mathcal{M} = \mathbb{R}^m$ the manifold of features and $\mathcal{G}$ the rigid motion group.

A rigid transformation of $\mathbb{R}^m$ is represented by a translation vector $t \in \mathbb{R}^m$ and a rotation matrix $(m \times m)$ R satisfying $R.R^\top = R^\top.R = I_d$ and $\det(R) = +1$. We denote by $f = (R; t)$ such a transformation. The action of the group on the features is simply $f \star x = R.x + t$.

An object can be represented by a k-tuple $X = (x^{(1)}, \ldots x^{(k)}) \in \mathcal{M}^k$ of features. The action of the transformation group $\mathcal{G}$ on k-tuples is simply $f \star X = (f \star x^{(1)}, \ldots f \star x^{(k)})$. The *rigid* *shape* of this object is characterized by the relative position between features of the k-tuple, i.e. the quotient space $\mathcal{M}^k/\mathcal{G}$: two objects have the same shape if they are congruent modulo $\mathcal{G}$ (*i.e.* if there exist a rigid transformation $g \in \mathcal{G}$ such that $Y = g \star X$).

2.1 Distances on points, k-tuples and rigid shapes

Let $X = (x^{(1)}, \dots x^{(k)})$ and $Y = (y^{(1)}, \dots y^{(k)})$ be two k-tuples of points. We define the distance between these k-tuples by the classical square formula

$$D(X, Y)^2 = \sum_{h=1}^{k} d(x^{(h)}, y^{(h)})^2$$

where d is the Euclidean distance between points. If we consider the k-tuples X and Y as "points" in $\mathcal{M}^k = \mathbb{R}^{m \times k}$, then D is the classical Euclidean distance. In order to obtain a distance in the shape space, we need to minimize this distance on k-tuples over all possible transformations[1]:

$$d_k(\tilde{X}, \tilde{Y}) = \inf_{f \in \mathcal{G}} \left(D(f \star X, Y) \right)$$

2.2 Mean shapes

Extending the formalism of section 1.1 to rigid shapes, we define the set of mean shapes of the set of shapes $\{\tilde{X}_i\}_{i=1}^n$ as

$$\tilde{\mathbb{M}}(\{\tilde{X}_i\}) = \arg \inf_{\tilde{M} \in \mathcal{M}^k/\mathcal{G}} \left\{ \sum_{i=i}^{n} d_k(\tilde{M}, \tilde{X}_i)^2 \right\} \tag{5}$$

In terms of k-tuples, we can write this equation:

$$\mathbb{M}(\{X_i\}) = \arg \inf_{M \in \mathcal{M}^k} \left\{ \inf_{(f_1, \dots f_n) \in \mathcal{G}^k} \left\{ \sum_{i=1}^{n} D(M, f_i \star X_i)^2 \right\} \right\} \tag{6}$$

We note that if $M \in \mathbb{M}(\{X_i\})$, then any k-tuple of the form $M' = f \star M$ is also a instance of the mean shape. The problem we are confronted with is thus two-folded: find both a k-tuple M representing the mean shape and a set of transformations f_i that register the k-tuple X_i with it. In fact, we can extend the results of Ziezold (1989, 1994) and solve first for the multiple registration problem, and then for the mean shape.

2.3 Multiple registration and optimal positions

A central notion to decouple the multiple registration from the mean shape problem is the optimal position. The k-tuples $X_1, \dots X_n$ are in optimal position to each other if their positions realize the minimum of their relative distances:

$$\sum_{1 \leq i < j \leq n} D(X_i, X_j)^2 = \inf_{(f_1, \dots f_n) \in \mathcal{G}^k} \left\{ \sum_{1 \leq i < j \leq n} D(f_i \star X_i, f_j \star X_j)^2 \right\}$$

[1]Due to the lack of space, all the proofs of this paper will appear in a forthcoming research report.

Theorem 1 *$M \in \mathbb{M}$ represents a mean shape if and only if*

- *there exists a set of rigid transformations $(f_1, \ldots f_n)$ such as the k-tuples $f_1 \star X_1, \ldots f_n \star X_n$ are in optimal position and*
- *considering the k-tuples as vectors: $M = \frac{1}{n}\sum_{i=1}^{n} f_i \star X_i$*

In this case, the variance is $s^2 = \frac{1}{n^2} \sum_{1 \le i < j \le n} D(f_i \star X_i, f_j \star X_j)^2.$

Let $\{X_i = (x_i^{(1)}, \ldots x_i^{(k)})\}_{i=1}^{n}$ be a set of n k-tuples. We call centroid of a k-tuple X_i the barycenter of its points $\bar{x}_i = \frac{1}{k}\sum_{h=1}^{k} x_i^{(h)}$. The corresponding centered k-tuples is then $Y_i = (y_i^{(1)}, \ldots y_i^{(k)})$ with $y_i^{(h)} = x_i^{(h)} - \bar{x}_i$.

Theorem 2 *Optimal positions exist and the centroids of the k-tuples correspond in such a position. The remaining criterion to maximize for rotations is then:*

$$F = \sum_{i,j} tr\left(R_i.H_{i,j}.R_j^\top\right) \qquad with \qquad H_{i,j} = \begin{cases} \sum_{h=1}^{k} y_j^{(h)}.{y_i^{(h)}}^\top & if\, i \neq j \\ 0 & if\, i = j \end{cases} \tag{7}$$

2.3.1 A closed form solution for the simple registration problem

In the case of two k-tuples (simple registration), the criterion reduces to $F = 2\text{tr}\left(R_2^\top.R_1.H_{2,1}^\top\right)$ since $H_{1,2} = H_{2,1}^\top$. As the solution is defined up to a rotation (if R_1 and R_2 are solutions, then $R_0.R_1$ and $R_0.R_2$ also are), we are usually looking for the transformation $R = R_2^\top.R_1$ from the first k-tuple to the second one. Closed form solutions are well known using the singular value decomposition (SVD) or using quaternions for 3D points. We recall here the result of the SVD method of :

Theorem 3 *Let $U.D.V^\top = K$ be a singular value decomposition of K. Assuming that the singular values are sorted by decreasing value, the maximum of the criterion $G = tr(R.K^\top)$ is reached over all rotations for*

$$R = U.S.V^\top \qquad with \qquad S = diag(1, \ldots 1, \det(U).\det(V))$$

with the value $G_{opt} = tr(D.S)$. The maximum is unique if $rank(K) \ge m - 1$.

2.3.2 An iterative scheme for the multiple registration problem

As in the simple registration case, we observe first that if the set of rotations $\{R_1, \ldots R_n\}$ maximizes the criterion $F = \sum_{i,j} \text{tr}\left(R_i.H_{ij}.R_j^\top\right)$, then the set $\{R_0.R_1, \ldots R_0.R_n\}$ also maximize the criterion with the same value. The second step is to isolate in the criterion the influence of a single rotation R_l: we have indeed

$$F = 2F_l + \sum_{i \neq l}\sum_{j \neq l} \text{tr}(R_i.H_{i,j}.R_j) \qquad \text{with} \qquad F_l = \text{tr}\left(\sum_i R_l.H_{l,i}.R_i^\top\right)$$

The basic idea is to maximize the criteria F_l according to the rotation R_l only. Since the second part of the global criterion F does not depend upon R_l, its value is fixed during the optimization of F_l, whereas the value of F_l is increasing. The value of the global criterion F is thus always increasing, and since we optimize on a compact set (SO_m^n), it converges to a local maximum.

We note that starting by registering independently each k-tuple Y_i with the first one (with for instance $R_1 = I_d$) maximizes the criterion F_1. Then, we iteratively maximize over R_l the criterion $F_l = \text{tr}(R_l.(\sum_i R_i.H_{i,l})^\top)$. We consider that the maximum is reached when the value of the global criterion increases less than a given threshold in one pass on each index.

The maximum reached can be verified experimentally to be global by several computations with different starting point (start to register with Y_i instead of Y_1) and/or a randomization of the order of maximization.

2.4 Extension to incomplete k-tuples

In the real world, however, there are often missing data and thus incomplete k-tuples: some usually stable features can be mismatched, highly displaced or simply forgotten in the extraction scheme in one or a few observations. It would be inauspicious to simply dismiss these features since they can bring useful information in most of the cases.

We consider thus that a missing point in a k-tuple X can correspond to any point location in another k-tuple Y: if there are p missing points, the k-tuple can be viewed as a p-plane in $\mathcal{M}^k$. In order to keep a standard representation, we associate to the k-tuple $X = (x^{(1)}, \dots x^{(h)})$ a binary vector ε_X such that $\varepsilon_X(h)$ is 1 if the point exists and 0 if the point is missing. The "distance" between incomplete k-tuples can thus be written:

$$D(X,Y)^2 = \sum_{h=1}^{k} \varepsilon_X(h).\varepsilon_Y(h).d(x^{(h)}, y^{(h)})^2$$

This is not really a distance since the triangular inequality is not verified and this is null if the associated p-plane and q-plane intersect. However, this corresponds to the distance on k-tuples we define above if there is no missing data, and the distance of a full k-tuple (the mean one for instance) to an incomplete one is the Euclidean distance from a point to a p-plane. We can thus define the set of mean k-tuples as above (equation 6).

Unfortunately, if we could theoretically separate the multiple registration from the mean shape computation, we cannot separate the rotation and translation parts in the multiple registration criterion. Since we now have to optimize on a non compact set, we prefer to use another (simpler) iterative scheme: assuming that we have an initial multiple registration, we can compute a mean k-tuple M (with $m^{(h)} = \{\sum_{i=1}^n \varepsilon_{X_i}(h).(R_i.x_i^{(h)} + t_i)\}/\{\sum_{i=1}^n \varepsilon_{X_i}(h)\}$), which can now be used to minimize criterion (6) for the simple registration of each k-tuple with M. We iterate this process until convergence or a maximum number of iterations.

The initial registration can be obtained by using the previous algorithm with sub-k-tuples that are present in all observation or more easily with a "naive" registration of all k-tuples with the first one.

3 Experiments

Synthetic experiments showed that the two iterative process converge (to the numerical precision of the machine) in about 5 iterations. The incomplete scheme does not give a sensible improvement of the mean shape precision if only a few points are missing, but turns out to be more and more interesting as the number of missing points increases and/or the number n of k-tuples increases. Indeed, the first method is not any more usable if the number of *globally* common points is too small (we need for instance at least 3 points to register in 3D), and its computational complexity increases in n^2 whereas it is linear for the second method.

3.1 Mean shape of the Heme binding motif

We present here an application in molecular biology: the globin family collects proteins of many different organisms. Their amino acid homology can be as low as 16%. However, their 3D structure is still related and constitutes the globin fold. It is mainly composed of α helices that form a pocket for the active site which in myoglobins and hemoglobins binds a heme group. The motif constituted by the amino acids binding the heme in 9 globins was extensively studied in (Lesk and Chothia, 1980). We used the correspondences given in this study and the atoms coordinates from the Protein Data Bank to determine the mean shape of the binding motif.

A collection of such models of motifs would allow to routinely scan each newly determined structure of protein or help protein design by providing reliable parts of the structure.

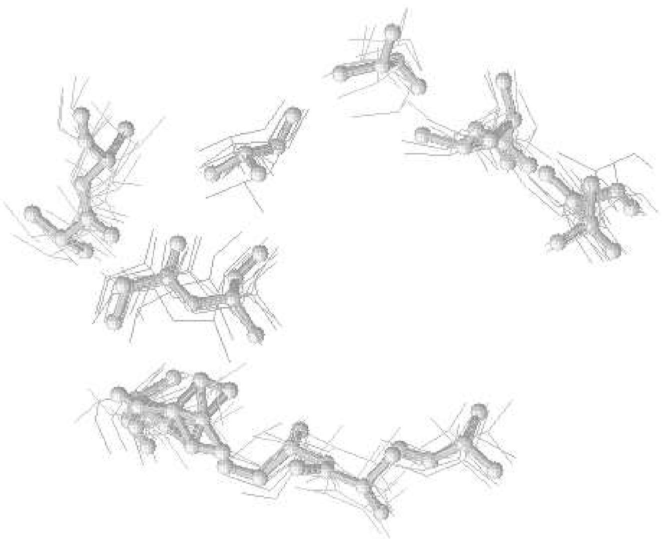

Figure 1: The 16 amino acids from 9 globins of the active site are represented by their 4 backbone atoms (bindings are lines). The mean shape of the motif is displayed in balls and sticks. On the bottom-left of the figure, a compact group of atoms represents two alternative (and exclusive) positions of an amino-acid: k-tuples are incomplete.

3.2 Model of a single patient based on Extremal points

In 3D medical imaging, the identification and measurement of meaningful features, or landmarks, is much more difficult and can become a bottleneck of the shape studies if done by hand. we believe that extremal points are good landmarks candidates thanks to their automatic extraction. The remaining problem is to discriminate meaningful features from spurious or uninteresting ones. In fact, the saliency of features is their stability across a wide range of observations for a given "object". We are thus confronted to a multiple matching and registration problem in the presence of noise and outliers. Once meaningful features have been identified and matched in different observations, it is interesting to merge their observations in order to obtain a model that incorporate all meaningful information and has a reduced noise. The shape of this model can then be studied, compared with others, used to determine if a similar shape is present in an observation (among other objects or outliers for instance), etc.

The experiment is performed on 24 3D MRI images of the head of the same patient (courtesy of Pr. Ron Kikinis). We register each pair of images and look for maximal cliques of correspondences between the whole set of images. This process is rather time consuming and can certainly be improved, but we focus here on the following step: multiple registration and fusion, whose results are presented in figure 2. The 24 sets of highly incomplete k-tuples where registered and merged using the second method within a few seconds. In order to have a more complete model, we add to each extremal point the standard deviation of the observations, which gives an idea of the geometrical stability or accuracy of this feature, and its probability of observation (the percentage of images where it was observed).

The next step in such an experiment would be to repeat this operation on several patients independently, and then look for the similar or affine shape based on these models. We could then characterize extremal points that are anatomically stable and incorporate them into an atlas.

4 Conclusions

We observe in this study that multiple registration and mean shape estimation problems can be solved efficiently in any dimension with a reasonable computational cost. Several tracks are left open, the first being the extension of this scheme to similarities and affine transformations. Another very interesting point would be to generalize the theory to other types of geometric features, such as oriented points, lines, frames... Last but not least, an automatic analysis of shapes should include a powerful and reliable *multiple matching* algorithm in order to automatically determine the landmarks correspondences.

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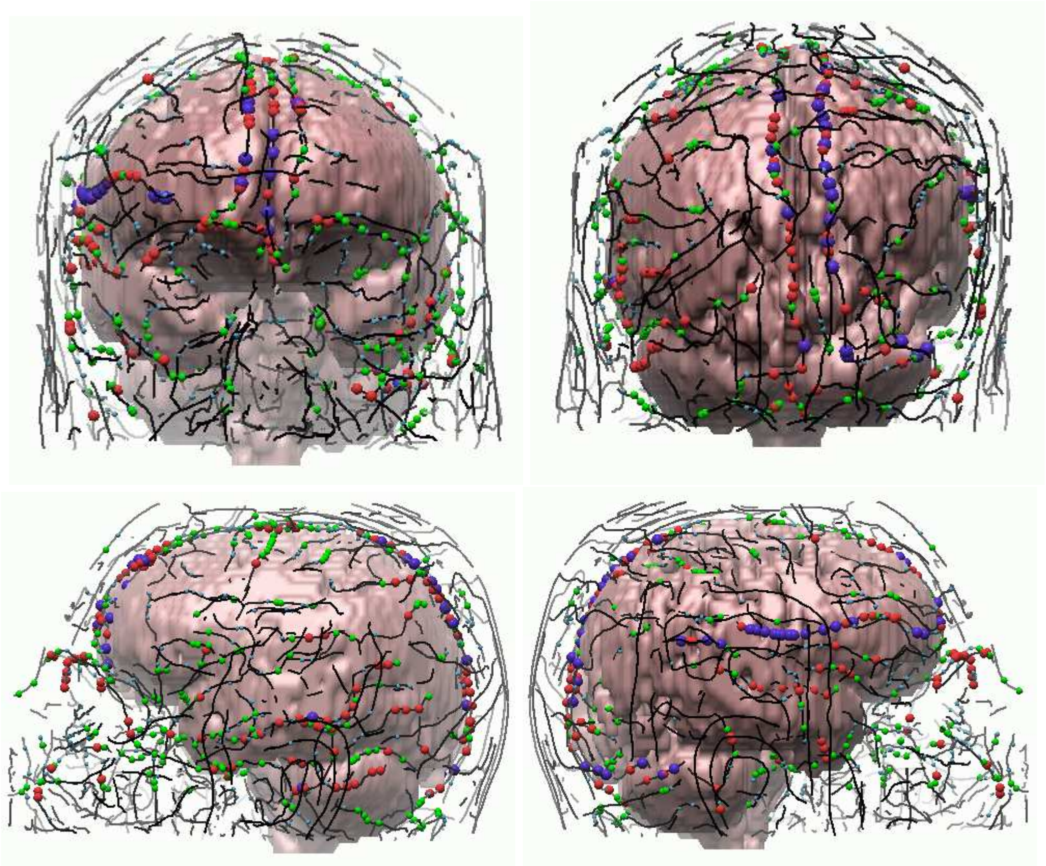

Figure 2: The surface of the brain is displayed along with the crest lines extracted from the first image. The most stable frames of the model are represented by spheres colored from decreasing stability order (and size) in purple, red, green and blue. Top line from left to right: front and rear views of the head. Bottom line: left and right views.

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