

A Combinatorial Method for 3D Landmark-Based Morphometry: Application to the Study of Coronal Craniosynostosis*

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Abstract. We present a new method to analyze, classify and characterize 3D landmark-based shapes. It is based on a framework provided by oriented matroid theory, that is on a combinatorial encoding of convexity properties. We apply this method to a set of skull shapes presenting various types of coronal craniosynostosis.

1 Introduction

Since three decades, *Geometry Morphometrics* has revolutionized the quantitative analysis of the variation of the shape of anatomical structures [1]. It can be defined as a collection of methods that process directly the coordinates of *landmarks*, in 2D or in 3D, rather than with traditional distance or angle measurements. The landmarks, which are in general points, can be defined by experts in anatomy or can be automatically computed by geometrical feature extraction algorithms. Landmark-based morphometry methods are now used in many medical applications but they present some important drawbacks as emphasised in [7,6].

In the *superposition methods*, many schemes of alignment have been proposed to superimpose the sets of landmarks (e.g. Procrustes, matching of a specified edge, etc.). The morphometrical result is then directly related to the alignment scheme itself, which is often selected by guessing the potential variability of the shape. Moreover, in some cases, the alignment scheme may result in transforming a strictly local deformation into a global one (*Pinocchio effect* [4]).

In the *deformation methods*, the difficulty is to define an appropriate class of transformations to warp a set of landmarks toward another. If the class is too general, the reference shape may deform to anything without any geometrical consistency. On the contrary, if the transformation is too constrained, there may be no accurate registration. In both cases, the transformation parameters will not properly characterize the shape deformation. Many mathematical formulations have been proposed but they remain difficult to assess and interpret as we do not know the potential variability of the shape.

Linear distance-based methods as the Euclidean Distance Matrix Analysis do not require to define any geometrical transformation to align or deform the shape. Nevertheless, the results which are based on inter-landmark distances are quite

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difficult to understand. The practitioner, indeed, does not only want not to know that the shape of an anatomical structure has varied by a quantity, but also to graduate this quantity on a standard scale and to localize the deformation. And even if some procedures to identify the most influential landmarks were proposed [3], this kind of methods remains little used for medical applications.

In this paper, we propose to encode 3D landmark configurations as oriented matroids, a combinatorial mathematical structure which was developed over the past forty years [2]. The idea is to code all the relative 3D positions of points of the shape, without taking into account the distances between them. As in linear distance-based methods, no alignment or deformation is to be computed. Using tetrahedra orientations in the shape, we obtain a vector of discrete values (-1 or 1) which characterizes the structure of the shape, independently of its size, its position, or more generally of any linear isomorphism of the space (see Section 2). The mathematical structure allows one to detect structural changes in a shape such as the crossing of a landmark through the plane defined by three others, and more generally all convexity properties involving subsets of landmarks. In Section 3, we introduce some theoretical and computational method to analyze and compare those shape representations. Let us point out that the discretization allows to perform a morphometrical analysis, without any numerical error or approximation. We show in Section 4 a clinical application to the classification of coronal craniosynostosis, yielding simple formal/geometrical/combinatorial characterizations of the classes within the studied set of individuals.

2 Combinatorial Structure of a 3D Model

Let E be a finite set of n labels. Let M be a set of n points labelled by E in the real affine space of dimension 3. We call M a *model*. We assume that these n points are in general position, meaning that every subset of E having four elements is a basis of the affine space. We call *basis* such a subset $B = \{a, b, c, d\}$. Let \mathcal{B} be the set of all bases. For the sake of formal simplicity, we assume that E and \mathcal{B} are linearly ordered. Hence every element $B = \{a, b, c, d\}_<$ of \mathcal{B} is ordered, and we denote $B = abcd$. Then, for instance, \mathcal{B} can be ordered lexicographically.

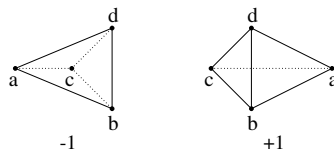


Fig. 1. The two possible orientations of tetrahedron $abcd$ given by $\chi_M(abcd)$

Every basis B in \mathcal{B} gets a sign in $\{+1, -1\}$, called *orientation* or *sign* of B in M , and denoted $\chi_M(B)$. It is defined as the orientation of the tetrahedron formed by the four points in B with respect to the ordering of B and a chosen orientation of the space. See Figure 1.

Equivalently, in linear algebra terms, and in computational terms, $\chi_M(B)$ is the sign of the determinant of the 4×4 matrix whose columns give the coordinates of the points in a canonical basis of the space, that is:

$$\chi_M(abcd) = \text{sign} \left(\text{determinant} \begin{pmatrix} 1 & 1 & 1 & 1 \\ x_a & x_b & x_c & x_d \\ y_a & y_b & y_c & y_d \\ z_a & z_b & z_c & z_d \end{pmatrix} \right).$$

Let χ_M be the list of signs of elements of \mathcal{B} in M , with respect to the linear ordering of \mathcal{B} , that is $\chi_M = [\chi_M(B_1), \chi_M(B_2), \chi_M(B_3) \dots]$. We call χ_M the *chirotope* of M . We consider χ_M as a vector in the real space $\mathbb{R}^{\mathcal{B}}$ of dimension $|\mathcal{B}|$; and for a vector x of this space, $x(B)$ denotes the value of x at coordinate B .

Figure 2 shows an example of M on 5 points labelled by $1 < 2 < \dots < 5$. The following table shows the ordered list of bases and their signs:

basis	1234	1235	1245	1345	2345
sign	-1	-1	+1	-1	-1

yielding the chirotope $\chi_M = [-1, -1, +1, -1, -1] \in \mathbb{R}^5$.

Figure 3 shows another example M' on 5 points with the same labels. The chirotope of M' is $\chi_{M'} = [+1, -1, +1, -1, -1]$. In comparison with M from Figure 2, the point 1 has crossed the plane 234 (and no other plane spanned by points of the model). That is why χ_M and $\chi_{M'}$ differ only with the sign of the basis 1234. Also, for example, it can be read from the chirotope if the point 1 belongs or not to the convex hull formed by the other points.

Observe also that if a point moves in M without crossing a plane spanned by other points, then χ_M does not change. The properties encoded by χ_M do not depend directly on numerical measures (distances, angles...), and this combinatorial encoding rather describes the “structural shape” of the point set.

The properties of χ_M are known as the *uniform oriented matroid theory* [2]. This rich mathematical theory is forty years old and can be seen as a combinatorial abstraction of linear algebra. In the case of real points, the oriented matroid defined by χ_M is a mathematical structure which is combinatorial (i.e. defined on a finite set), encodes the relative positions of the points of M , and catches in particular all their convexity properties¹.

In this paper, we use this information to compare models, labelled by a same set, practically given by landmarks. Formally, we fix a set \mathcal{M} of models M labelled by E , and we study the set of χ_M , for $M \in \mathcal{M}$.

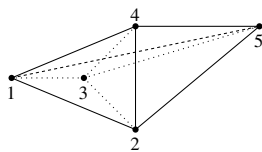


Fig. 2. A model M . Full lines belong to the front part of the convex hull; light dashed lines belong to its back part; the medium dashed line 15 is inside the convex hull.

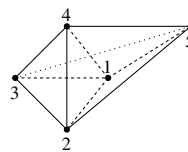


Fig. 3. A model M' obtained from M by moving 1 inside the tetrahedron 2345. The lines 12, 13, 14 and 15 are now inside the convex hull.

¹ We mention that the case where points may not be in general position leads to a possible 0 sign for the values $\chi_M(B)$, and to the general theory of oriented matroids. In this paper, for the sake of clarity and concision, we focus on the uniform case.

3 Method of Analysis

3.1 General Scope

The main concept to compare models in \mathcal{M} is the following. For a subset \mathcal{D} of \mathcal{B} , and two vectors x and y in $\mathbb{R}^{\mathcal{B}}$, we define the *distance between x and y w.r.t. \mathcal{D}* as

$$d_{\mathcal{D}}(x, y) = (1/2) \cdot \sum_{B \in \mathcal{D}} |x(B) - y(B)|$$

which is, mathematically, a distance for projections onto the space $\mathbb{R}^{\mathcal{D}}$. In what follows we make the abuse to call $d_{\mathcal{D}}$ a distance in $\mathbb{R}^{\mathcal{B}}$ even when $\mathcal{D} \neq \mathcal{B}$. Observe that the distance $d_{\mathcal{D}}$ between two chirotopes χ_M and $\chi_{M'}$ equals the number of bases in \mathcal{D} having different signs in M and M' .

Let us now consider a partition of \mathcal{M} in two classes $\mathcal{M} = \mathcal{C} \uplus \mathcal{C}'$, or, more generally, a partition into k classes $\mathcal{M} = \mathcal{C}_1 \uplus \dots \uplus \mathcal{C}_k$. Such a partition can be given by the experts that provided the models (e.g. four known medical types for skulls as in Section 4). On the other hand, such a partition can be built using the chirotopes of the models without any other preliminary knowledge. Note that if classes satisfying automatic unsupervised classification criteria match classes given by experts, then it means that the combinatorial data captures some geometrical properties that characterize the classes in which the experts are interested, and yields a formal characterization of those classes.

Once a partition is given, either by experts or by automatic classification, a second step is to characterize classes using the less possible information from the chirotopes. For instance, we look for a few bases whose signs allow to determine if a model belongs to a given class or not. In terms of applications, those bases should be significant, providing either a mathematical formal confirmation of criteria used by experts, or new properties pointing out typical features of the class that would interest experts.

3.2 Automatic Classification

Given a set \mathcal{C} of models, the *barycenter* $m_{\mathcal{C}}$ of \mathcal{C} is the vector in $\mathbb{R}^{\mathcal{B}}$ whose coordinate at basis B is the mean of the signs of models in \mathcal{C} at basis B , that is:

$$m_{\mathcal{C}}(B) = \frac{1}{|\mathcal{C}|} \sum_{M \in \mathcal{C}} \chi_M(B).$$

We say that the partition $\mathcal{M} = \mathcal{C} \uplus \mathcal{C}'$ satisfies the *k-means criterion* if for every $M \in \mathcal{M}$ we have: $M \in \mathcal{C}$ if and only if $d_{\mathcal{B}}(\chi_M, m_{\mathcal{C}}) < d_{\mathcal{B}}(\chi_M, m_{\mathcal{C}'})$, and $M \in \mathcal{C}'$ if and only if $d_{\mathcal{B}}(\chi_M, m_{\mathcal{C}}) > d_{\mathcal{B}}(\chi_M, m_{\mathcal{C}'})$. Of course, this criterion directly extends to a partition into k classes.

Various clustering algorithms can be used to build automatically a partition into classes satisfying criteria such as the above one. The most classical one consists in initializing arbitrary classes, computing the barycenters for each class and move a model to an other class if it is closer to the barycenter of this other class than to the barycenter of its initial class. Repeating this procedure until

stability yields a partition satisfying the k-means criterion. Then, one may test many initializations and select an “optimal” classification.

For lack of space, we just mention that such an algorithm allows to detect “mean” individuals among the classes, characterized by “mean” chirotopes, and that other clusterisation algorithms can be used (e.g. k-medoids).

3.3 Characterization of Classes

Assume that a partition $\mathcal{M} = \mathcal{C} \uplus \mathcal{C}'$ is given. We now look for simple and significant combinatorial criteria defining this partition.

Formally, in this paper, we will build classes depending on three parameters: a set \mathcal{D} of bases, a vector x in the space $\mathbb{R}^{\mathcal{B}}$, and a real value l . We define

$$\mathcal{C}_{\mathcal{D},x,l} = \{M \in \mathcal{M} \mid d_{\mathcal{D}}(\chi_M, x) \leq l\}.$$

This set can be considered as the set of model chirotopes contained in a “ball” in the space $\mathbb{R}^{\mathcal{B}}$, centered at x and of radius l for the distance $d_{\mathcal{D}}$.

Practically, we look for a subset \mathcal{D} of \mathcal{B} the smallest possible for simplicity, for a vector x in $\mathbb{R}^{\mathcal{D}}$ with coordinates in $\{-1, +1\}$, and for an integer value l , such that $\mathcal{C}_{\mathcal{D},x,l}$ is equal to class \mathcal{C} . In this combinatorial setting, a model M belongs to the class \mathcal{C} if and only if there are at most l bases B in \mathcal{D} such that $\chi_M(B) \neq x(B)$. Hence, \mathcal{D} serves as a significant set of bases, x as the characteristic values of these bases for \mathcal{C} , and l as a threshold value to the fact that a model fits this characteristic values.

As an example of particular interest, consider the case where \mathcal{D} consists of a single basis $\mathcal{D} = \{B\}$. Then x is given by a single sign, say $x(B) = +1$. Then a model M belongs to \mathcal{C} if and only if $\chi_M(B) = +1$, and it belongs to \mathcal{C}' if and only if $\chi_M(B) = -1$. Equivalently, we have $\mathcal{C} = \mathcal{C}_{\{B\},+1,0}$. In this case, the sign of B determines if M belongs to \mathcal{C} or not. We say that B is *totally discriminant* for the class \mathcal{C} . This is the most simple possible characterization of a class.

The problem is to detect such parameters \mathcal{D}, x, l . Let us use the following procedure. For a basis B , we define the *discriminability* of B as $\tau(B, \mathcal{C}, \mathcal{C}') = |m_{\mathcal{C}}(B) - m_{\mathcal{C}'}(B)| / 2$. This value belongs to $[0, 1]$. The closer to 1 this value is, the more significant the basis B is for the class \mathcal{C} . The extreme case is $\tau(B, \mathcal{C}, \mathcal{C}') = 1$, implying that $m_{\mathcal{C}}(B) = +1$ and $m_{\mathcal{C}'}(B) = -1$ (or the inverse), and then, by definition of $m_{\mathcal{C}}$ and $m_{\mathcal{C}'}$, that every model in \mathcal{C} (resp. \mathcal{C}') has value $+1$ (resp. -1), meaning that B is totally discriminant for \mathcal{C} and \mathcal{C}' . On the contrary, $\tau(B, \mathcal{C}, \mathcal{C}') = 0$ can be obtained for instance when B has the same sign in every model in \mathcal{M} , or also at the limits when B has a random sign; hence we cannot expect B to be significant to describe \mathcal{C} .

We can order the bases in \mathcal{B} according to their discriminability. This ordering allows a computation to search parameters \mathcal{D}, x, l . Indeed, from the computational viewpoint, there may be a huge number of elements in \mathcal{B} (any set of four landmarks is a basis), and hence a non-affordable number of subsets \mathcal{D} to test. Considering only bases with high discriminability allows to restrict the number of subsets to be tested, while focusing on the information that has some chance to be significant. So we consider bases having the highest possible

discriminability to build a set \mathcal{D} and an integer l as required. The values $x(B)$ determining x are naturally given by the signs of $m_{\mathcal{C}}(B) - m_{\mathcal{C}'}(B)$ for $B \in \mathcal{D}$.

Observe that if a partition $\mathcal{M} = \mathcal{C}_1 \uplus \dots \uplus \mathcal{C}_k$ is given and such parameters are known for every class \mathcal{C}_i in the partition, then we have two independent criteria to detect a class: first the direct criterion provided by the parameters characterizing \mathcal{C}_i , secondly the negation of the criteria determining that a vector belongs to another class \mathcal{C}_j , $j \neq i$.

4 Applications to Coronal Craniosynostosis

Coronal craniosynostosis is a rare infant pathology in which one of the two coronal sutures of the skull prematurely fuses by ossification. We can distinguish between left (LUCS), resp. right (RUCS), uni-coronal craniosynostosis when only one side is affected and the bilateral case (BCS) when both sides are fused. It is essential to use 3D morphometric tools to quantify and analyze precisely the deformation of the skull shape in this pathology. In [5], the authors used classical landmark-based tools (Procrustes and Principal Component Analysis) to study a database of the International Craniosynostosis Consortium and assess the (a)symmetry of the pathology. We could test our new morphometric method on the same data and we propose below some preliminary results.

The clinical database is composed of CT-Scan images of 40 children diagnosed with non syndromic coronal craniosynostosis (LUCS=8 / RUCS=17 / BCS=15) and 20 unaffected individuals of the same age. Anatomy experts pointed 41 landmarks on these CT-Scan and added 92 semilandmarks along predefined curves, as illustrated on Figure 4. No alignment or spatial normalization was performed.

To compute the $\binom{133}{4}$ tetrahedron signs, it takes about 6 hours on a standard PC. This process is performed only once. The k-means clustering itself takes about 30 seconds on a standard PC, but one wants to run it multiple times (1000 in our application) with different starting positions.

First, we present results obtained by using the whole set of 133 landmarks. We started off by testing if the four classes given by the experts (BCS, LUCS, RUCS and Unaffected) satisfy the k-means criterion. This criterion is satisfied by these four classes, so we can assume that the premature fusion of sutures

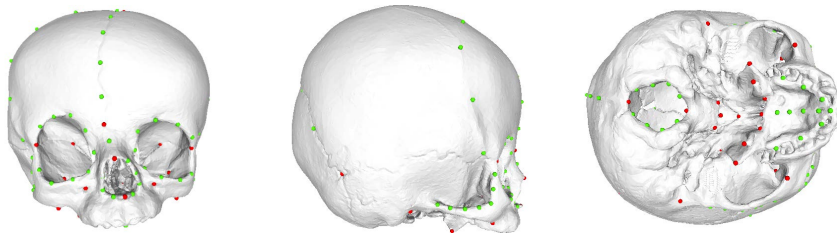


Fig. 4. Illustration of the 133 3D landmarks (RUCS skull shown here). Anatomical landmarks are in red and curve semilandmarks are displayed in green.

corresponds to changes in the skull shape chirotopes. We applied the k-means algorithm to find a partition of the 60 individuals in 4 clusters which minimizes the sum of distances between the individuals and the barycenter of their class. The algorithm returns exactly the classes defined by the experts, strengthening the above observation. With this result we obtain also for every class \mathcal{C} the closest individual of the barycenter of \mathcal{C} .

Let \mathcal{C} be a class among BCS, LUCS, RUCS and Unaffected. We denote by \mathcal{C}' the set of all the individuals which are not in \mathcal{C} . We computed the discriminability $\tau(B, \mathcal{C}, \mathcal{C}')$ for every basis B and class \mathcal{C} . For every class there exist several bases which are totally discriminant. Precisely there are 147 such bases for BCS, 15,667 such bases for LUCS, 5,064 such bases for RUCS, and 7 such bases for Unaffected. So for each class we have many simple characterizations (direct criterion and negation of the criterion of the others classes).

In a second time we used only the 41 anatomical landmarks. The first reason is to focus only on what has a real anatomical meaning and a precise anatomical definition. The second reason is to speed up all the calculus as it reduces the number of tetrahedra from $\binom{133}{4} = 12,457,445$ to $\binom{41}{4} = 101,270$.

The k-means algorithm yields a partition into 4 clusters which match exactly the 4 classes given by the experts, except for one individual among the 60.

There exist bases which are totally discriminant for LUCS (22 bases) and RUCS (4 bases). The four bases for RUCS all contain the *bregma* (intersection of the coronal and the sagittal suture) and the *lambda* (intersection of the sagittal and lambdoidal sutures). Each basis contains a third landmark in the median sagittal plane. This third landmark is the *nasion* for two bases and the *nasale* for the two other bases. For each basis, the fourth landmark is a point of the right part of the cranial base. For each of these bases, if we replace the fourth landmark by the symmetric landmark with respect to the median sagittal plane, we obtain one of the 22 bases which are totally discriminant for LUCS. Figure 5 shows one of the four basis totally discriminant for RUCS and the symmetric basis which is totally discriminant for LUCS.

For BCS, there is no totally discriminant basis. Let us detail one characterization we obtained, among other ones. We found two tetrahedra B_1 and B_2 such that an individual is BCS if and only if both the orientations of these tetrahedra are -1 . That is $\text{BCS} = \mathcal{C}_{\{B_1, B_2\}, x, 0}$ for $x(B_1) = x(B_2) = -1$. Their discriminabilities are high and equal 0.89 and 0.91. These two tetrahedra share two landmarks. Let us denote $B_1 = 1234$ and $B_2 = 1256$. Figure 6 shows these two tetrahedra on some BCS model, and Figure 7 details their positions for the BCS class. Figure 8 shows the other possibilities, available for models in the other classes. The involved landmarks are: the left *anterior clinoid process* (1); the left *asterion* (posterior end of the parietomastoid suture) (2); the left and the right *fronto-zygomatic junction* at orbital rim (4 and 3 respectively); the anterior *nasal spine* (5); and the left external *auditory meatus* (6).

For the unaffected individuals, we found (for instance) a slightly more involved characterization: a set \mathcal{D}_2 , with five bases having discriminabilities between 0.85 and 0.875, such that this class equals $\mathcal{C}_{\mathcal{D}_2, y, 2}$ for some $y \in \{-1, +1\}^{\mathcal{B}}$. That is:

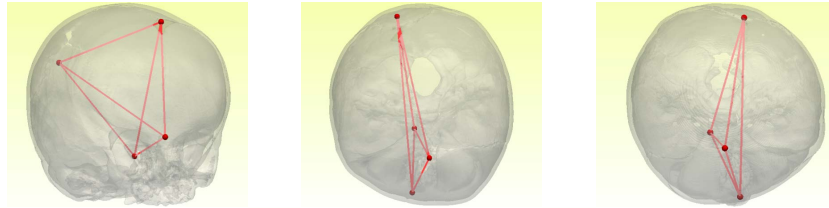


Fig. 5. One of the 4 bases totally discriminant for the RUCS (left and middle) and the basis obtained by symmetry which is totally discriminant for the LUCS (right)

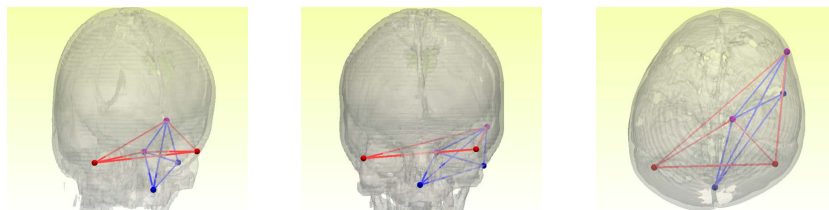


Fig. 6. The two tetrahedra (red and blue) which give a characterization for BCS

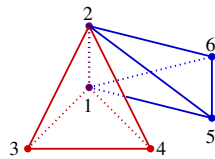


Fig. 7. The orientations $[-1, -1]$ of B_1 (red) and B_2 (blue) characterize BCS

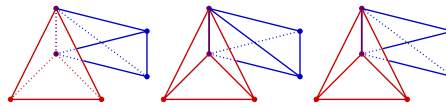


Fig. 8. The other possible orientations $[-1, +1]$, $[+1, -1]$, and $[+1, +1]$ (from left to right), available for non-BCS models.

x is unaffected if and only if there exist at least three bases in \mathcal{D}_2 such that the signs of these bases are the same in x and y .

Finally, we point out that the formal/geometrical/combinatorial characterizations above are obtained with respect to a given whole set of models, and may depend noticeably on this initial data. However, they raise the question of medical anatomical interpretations.

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