# MULTILEVEL STATISTICAL SHAPE MODELS: A NEW FRAMEWORK FOR MODELING HIERARCHICAL STRUCTURES

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## ABSTRACT

Statistical shape models are commonly used in various applications of computer vision. Nevertheless, these models are not well adapted to hierarchical structures. This paper proposes a solution to this problem by presenting a general framework to build multilevel statistical shape models. Based on multilevel component analysis, the idea is to decompose the data into a within-individual and a between-individual component. As a result, several sub-models are deduced and can be treated separately, each level characterizing one sub-model. In this paper, we present a multilevel model of the human spine. The results show that such a modelization offers more flexibility and allows deformations that classical statistical models can simply not generate.

***Index Terms***— Statistical shape models, multilevel modeling, hierarchical structures, spine

## 1. INTRODUCTION

Statistical shape models (SSM) are commonly used in various applications of computer vision. These deformable models were proposed by Cootes *et al.* [1] in the context of the active shape model approach, which goal was to segment objects in images. The novelty was to globally constrain the shape of the objects so that, based on observations, the model can only synthesize plausible instances of the object.

In several biomedical applications, the collected data is comprised of hierarchical structures where the objects are associated to groups depending on one another. A practical example of such a structure is the human spine. Indeed, the vertebral column is comprised of vertebræ, linked to one another. Traditional statistical models can hardly deal with this dependance between items since all points are treated identically whether they belong to the same sub-structure or not. Nevertheless, in the case of the spine, works such as [2] have represented the link between adjacent vertebræ with an articulated model.

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In the literature, only a few studies were dedicated to hierarchical models. In [3], the authors proposed a hierarchical formulation of active shape models. Their approach is based on the hierarchical representation of a shape in terms of its wavelet transform. Then, a principal component analysis is performed on the wavelet coefficients. Finally, one object is divided into sub-models that are recursively divided. The interest here is to have sub-models with only few parameters.

Another hierarchical framework was developed in [4]. The authors defined a hierarchical statistical shape model, including a global model of the lung and a series of sub-models, to hierarchically guide the segmentation. Actually, the global model is used to initialize the segmentation and the resulted segmentation is refined with a sub-model. The sub-models are independant and are determined by an affinity propagation method to cluster the samples into homogeneous groups. Recently, a similar work was presented in [5], but the sub-models are deduced with a clustering technique based on criteria derived from a principal factor analysis.

For all of these methods, the model is hierarchical, *i.e.* several levels of representation are considered, but there is actually no link between the levels of the model.

The main contribution of this paper is to propose an extension of statistical shape models adapted to hierarchical structures, where the objects depend on one another. Various methods for the analysis of multilevel data are presented in the literature (*e.g.* multilevel regression [6]). However, in our framework, we are interested in the multilevel component analysis [7]. We illustrate our purpose with the case of the human spine. Traditional SSM allow global deformations of the spine, which is suitable for normal anatomical variations. However, it does not deal well with discontiuities in the vertebra sequence. Nevertheless, discontinuities can appear in various pathologies (*e.g.* vertebral compression caused by osteoporosis, displacements caused by spondylolisthesis, *etc.*) and numerous particular situations can arise (*e.g.* patients having spinal fusion surgery, *etc.*). Current models are not a suitable answer to these issues given that it is only possible to represent global deformations. Therefore, we present in this paper a general modeling framework adapted to any situation

of that type. We demonstrate that a multilevel model is a promising solution to represent hierarchical structures in a more general and flexible way than current models.

## 2. METHODS

In this section, we first present how to reconstruct a data matrix from a multilevel decomposition with multilevel component analysis. Then, we will extend these notions to decompose a statistical shape model in multiple levels.

### 2.1. Multilevel Component Analysis (MCA)

Principal component analysis (PCA) is a key step for building most statistical shape models. Here, we need however to deal with an extension of PCA: the multilevel component analysis.

The concept of MCA was introduced in [7] as an extension of PCA for hierarchical structures. If we consider a model with 2 levels, the idea is to decompose the data into a within-individual and a between-individual component. Let us assume a sample with $N$ items, divided into $K$ groups of size $K_k$. An item $i$ belonging to the group $k$ according to the variable $j$ is denoted by: $x_{ijk}$, with $i \in [1, \ldots, K_k]$, $k \in [1, \ldots, K]$, and $j \in [1, \ldots, J]$. Based on the Cronbach and Webb's model [8], $x_{ijk}$ can be decomposed into a within-group and a between-group term, such as:

$$x_{ijk} = x_{\bullet j \bullet} + (x_{\bullet jk} - x_{\bullet j \bullet}) + (x_{ijk} - x_{\bullet jk}), \qquad (1)$$

where $x_{\bullet j \bullet} = \frac{1}{N} \sum_{k=1}^{K} \sum_{i=1}^{K_k} x_{ijk}$, and $x_{\bullet jk} = \frac{1}{K_k} \sum_{i=1}^{K_k} x_{ijk}$. In the relation (1), $(x_{\bullet jk} - x_{\bullet j \bullet})$ is the between-group term, while $(x_{ijk} - x_{\bullet jk})$ is the within-group one.

Let $X_k$ be a $K_k \times J$ matrix characterizing the data belonging to the group $k$. MCA allows to retrieve the matrix $X_k$ with respect to the decomposition presented at the equation (1). Such a multilevel modelization implies:

$$X_k = 1_{K_k} m^T + 1_{K_k} d_{B,k}^T \Phi_B^T + D_{W,k} \Phi_W^T + E_k, \qquad (2)$$

where $m$ is a $J \times 1$ vector representing the overall mean, $1_{K_k}$ denotes a $K_k \times 1$ vector with each element equal to one, $d_{B,k}$ stands for a $R_B \times 1$ vector containing the $R_B$ between component scores of group $k$, $\Phi_B$ represents a $J \times R_B$ matrix of the between principal components, $D_{W,k}$ is a $K_k \times R_W$ matrix of the $R_W$ within component scores of group $k$, $\Phi_W$ denotes a $J \times R_W$ matrix of the within principal components for the group $k$ and, finally, where $E_k$ is a $K_k \times J$ matrix of residuals for the group $k$.

The interest of MCA is that the parameters of the equation (2) can be determined separately. It is demonstrated in [7] that respecting $1_{K_k}^T D_{W,k} = 0_{R_{W,k}}$ and $\sum_{k=1}^{K} K_k d_{B,k} = 0_{R_B}$, allows to deal with the 3 terms (constant, between-group, within-group) of the model separately. This aspect will be the basis for building a multilevel model.

Let us note that MCA can be extended to more levels by adding an extra decomposition term for each level.

### 2.2. Multilevel Statistical Shape Model (MSSM)

Let us consider a set of objects (or shapes) where each of them has an influence on the others. An example of such a hierarchical structure could be the human spine, where all the vertebræ are linked together. In the proposed modelization, each object of the hierarchical structure can be viewed as a group at the first level. Let us assume a sample of $K$ hierarchical structures characterized by $I$ objects. Each group of the model stands for an object and contains the $K$ instances of it in the sample. This hierarchical representation is illustrated at Fig. 1.

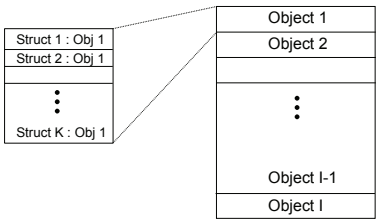



**Fig. 1**: Multilevel representation of $K$ hierarchical structures composed of $I$ objects

Let us assume that an object is represented according to $J$ variables. Usually, these variables are point coordinates. Then, by considering 2 levels, a deformable model for any object (shape) $x_i$ with $i \in [1, \ldots, I]$ can be determined by:

$$x_i = \bar{x} + \phi_W d_{W,i} + \phi_B d_{B,i}, \qquad (3)$$

where $\bar{x}$ is a column-vector of size $J$ standing for the mean computed over all the objects in the sample, $\phi_W$ denotes the $J \times R_W$ matrix containing the within-group principal components, $d_{W,i}$ is a $R_W \times 1$ vector representing the weights controlling the deformation of the within-group term, $\phi_B$ stands for the $J \times R_B$ matrix representing the between-group principal components, $d_{B,i}$ is the $R_B \times 1$ vector of weights controlling the deformation of the between-group term.

Let $X$, be a $N \times J$ matrix including all the objects of the sample ($N = KI$). First, the within-group parameters are obtained after a particular decomposition of the matrix $X$. This decomposition consists in mean-centering all the submatrices $X_i$ of size $K \times J$, where $X_i$ is the partition of the matrix $X$ belonging to the group $i$. This decomposition is given by: $X_{c,i} = X_i - 1_K m_i^T$, where $m_i$ is a $J \times 1$ vector describing the mean induced by the matrix $X_i$ over the $J$ considered variables. Let $X_c$ be the matrix resulting from the vertical concatenation of matrices $X_{c,i}$. Since this matrix represents the within-group variations of the model, the matrix $\phi_W$ is composed of the eigen vectors of the covariance matrix related to $X_c$. Furthermore, the variance of the weights $d_{W,i}$, which limits the deformation of the within-group submodel, is determined by the eigen values of the covariance matrix related to $X_c$.

In order to determine the between-group parameters of the model, let us substract the overall mean of the matrix $X$. Let

$\tilde{X}$ be this matrix. Let us note $\tilde{X}_i$, the partition of the matrix $\tilde{X}$ belonging to the group $i$. Moreover, let us consider the $I$ vectors $\tilde{m}_i$, each of them representing the mean of the associated matrix $\tilde{X}_i$. In fact, these vectors characterize the between-group differences. Therefore, we note $M$, the matrix resulting from the vertical concatenation of the vectors $\tilde{m}_i$. As a consequence, the matrix $\phi_B$ of the between-group principal components is built by the eigen vectors of the covariance matrix related to $M$. In addition, the deformation limits of the between-group sub-model are given by the eigen values of the covariance matrix related to $M$.

The concepts of MSSM can naturally be extended to a greater number of hierarchical levels. Since a group stands for an object, the extra levels are between-group terms. We can generalize the relation (3) in accordance with:

$$x_i = \bar{x} + \phi_W d_{W,i} + \sum_{l=2}^{L} \phi_{B_l} d_{B,i_l}, \tag{4}$$

where $L$ is the number of levels and $i_l$ is the index of the group to which the object belongs at the level $l$.

## 3. RESULTS AND DISCUSSION

In this section, we propose to illustrate the interest of applying a MSSM to the modelization of the human spine. The spine can be viewed as a combination of 4 consecutive curves in the sagittal plane: the cervical lordosis, the thoracic kyphosis, the lumbar lordosis and the sacral kyphosis. Therefore, we can assume that vertebræ belonging to the same curve are correlated. Moreover, all the vertebræ are linked together. The usual statistical models in the literature do not take into account the dependance between vertebræ. The aim of multilevel modeling is to assume such a link.

To perform our tests, we used a sample of 100 patients. We considered 17 vertebræ, *i.e.* T1 to L5. Each vertebra is represented according to 6 points of reference in a three-dimensional space. These points are the center of inferior and superior endplates, and the inferior and superior extremities of pedicles. Two decompositions are studied. The first one is characterized by 2 levels. Each group of the level 1 stands for a vertebra type. The last level is characterized by one group where all the vertebræ are represented. In the second decomposition, one level is added and is characterized by two groups. The first one includes the lumbar vertebræ. The thoracic vertebræ compose the second group.

### 3.1. Variability Decomposition and Explained Variance

The analysis of the variability decomposition is important for two reasons. On the one hand, it is a measure to assess if a MSSM is relevant and fits with the data. On the other hand, the variability decomposition permits to select the number of levels to consider.

Let us define $SSD_{tot}$, the sum of squared differences between the vertebræ and the overall mean. Similar to ANOVA (ANalysis Of VAriance) and if we use the notation of the relation (1), we can write:

$$\begin{aligned} SSD_{tot} &= \sum_{j,k} K_k \left(x_{\bullet jk} - x_{\bullet j\bullet}\right)^2 + \sum_{i,j,k} \left(x_{ijk} - x_{\bullet jk}\right)^2 \\ SSD_{tot} &= SSD_{between} + SSD_{within} \end{aligned} \tag{5}$$

With the equation (5), it is now possible to determine the partition of the total variability according to a within-group and a between-group term. This relation can naturally be extended to 3 or more levels. Table 1 shows the decomposition of the total data variability. Globally, the results indicate that the magnitude of the within-group (13.34%) and the between-group variability (86.66%) is sufficient and makes the use of a MSSM relevant when the spine is studied. Actually, for the 2-level model, each group at level 1 stands for a vertebra type. Therefore, the within-group variability represents the variability between identical vertebræ but on different patients. As a result, the between-group variability is greater.

| Levels | Var. With. (%) | Var. Between (%) | |
|---|---|---|---|
| 2 | 13.34 | 86.66 | |
| 3 | 13.34 | 27.69 | 58.98 |

**Table 1**: Decomposition of the total variability

Computing the proportion of explained variance according to the number of principal components gives information on how to select the MCA components. Usually, the number of principal components is chosen in respect to a given percentage of the total variance explained by the components. Naturally, the within-group and the between-group sub-models have to be distinguished.

The results for the 2-level model reveal that for a given percentage of total variance, the within-group sub-model requires more principal components than the between-group sub-model, despite the fact that 86.66% of the model is between-group information. To give an order of magnitude, let us assume that our multilevel model has to capture 95% of the total variance. This way, the within-group sub-model requires 8 principal components while the between-group sub-model is characterized by only 2 principal components.

### 3.2. Model Deformation

The aim of this section is to study the deformation of the within-group and between-group sub-models. The results are provided for the 2-level model. Fig. 2 illustrates the deformations along the first principal component for, respectively, the within-group and the between-group sub-models. The deformation weights used at Fig. 2 depend on the within-group and between-group standard deviations $\sqrt{\sigma_{W_1}}$ and $\sqrt{\sigma_{B_1}}$ along

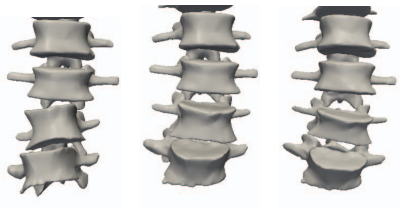
the first principal component. The analysis of Fig. 2 demonstrates that the first principal component of the within-group sub-model is associated with the elongation of the spine. Furthermore, this component characterizes a curve appearing in the part of thoracic vertebræ. Concerning the between-group sub-model, the results reveal that its first principal component is associated to the elongation of the vertebræ themselves. Therefore, the position of the vertebræ can vary along this component and can be influenced by the position of the others. This way, the between-group characterizes a link between vertebræ. This aspect of the modelization is very important since a classic SSM is not able to represent this deformation.



(a) $-2\sqrt{\sigma_{B_1}}$ (b) $-3\sqrt{\sigma_{W_1}}$ (c) $\bar{x}_i$ (d) $+3\sqrt{\sigma_{W_1}}$ (e) $+2\sqrt{\sigma_{B_1}}$

**Fig. 2**: Deformations of the within-group and the between-group sub-models along the first principal component around the mean $\bar{x}_i$ (for better visualization, dense vertebrae models were fitted to the modelled points).

Fig. 2 offers an illustration of deformations allowed by a multilevel model. These variations are associated with normal anatomical variations and could probably also be obtained using a conventional SSM. However, there are clinically relevant cases where conventional SSM would break down (*e.g.*, cases with discontinuity of the spine). Let us consider Fig. 3 to illustrate our point. The spine at the center is simply a mean shape of the model. On the left, we have represented a particular deformation of the two inferior vertebræ (L4 and L5). Indeed, the multilevel model allowed a representation of a case that we can assimilate to a vertebral dislocation that could be caused by a scoliosis. Similarly, the illustration on the right shows a compression of vertebræ L4 and L5. As a consequence, multilevel models seem to be relevant for the study of pathologies such as: osteoporosis, scoliosis, or spondylolisthesis. These particular deformations are made possible thanks to the between component of the multilevel model and could therefore not have been generated with a SSM. Numerous other examples can be generated. With Fig. 3, we aim to demonstrate that for many applications, multilevel modeling is of great interest.



(a) Dislocation (b) Normal (c) Vertebral compression

**Fig. 3**: Some clinically relevant deformations of the spine

## 4. CONCLUSION

Multilevel statistical shape models are suitable for modeling objects belonging to a hierarchical structure. We have demonstrated the interest of our framework by building several MSSM of the human spine. First, the results showed that each sub-model represents a large proportion of data variability, which suggests that the use of a MSSM is relevant. Furthermore, a MSSM offers more flexibility which means that it can represent deformations which would not not be practical to model using a conventional SSM. In the future, we plan to validate our framework as part of a medical application. Other organs could also be considered.

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