

# SHAPE-AWARE 3D INTERPOLATION USING STATISTICAL SHAPE MODELS

F. Bernard<sup>1,2,3,\*</sup>, L. Salamanca<sup>2</sup>, J. Thunberg<sup>2</sup>, F. Hertel<sup>1</sup>, J. Goncalves<sup>2,4</sup>, P. Gemmar<sup>3</sup>

<sup>1</sup>CHL, Luxembourg, LU <sup>2</sup>LCSB, UL, Esch-sur-Alzette, LU <sup>3</sup>Trier University of Applied Sciences, Trier, DE <sup>4</sup>University of Cambridge, Cambridge, UK

**Background:** The reconstruction of surfaces from (few) points has many applications (e.g. visualisation or surgery planning). In variational interpolation [1], a 3D surface is reconstructed from few 2D contours under a surface smoothness assumption. Statistical shape models (SSMs) are more powerful priors for surface reconstruction. The difficulty is that the correspondence problem and model fitting need to be solved at the same time, which is usually done with the Iterative Closest Point (ICP) algorithm (or variants thereof) with discrete correspondences [2, 3, 4]. In contrast, Coherent Point Drift (CPD) [5] uses probabilistic correspondences for (robust) affine, rigid or nonlinear point-set registration.

**Aims:** Based on CPD, we present a shape-aware interpolation scheme for surface reconstruction from a sparse set of points by employing an SSM as prior.

**Methods:**  $\otimes$  is the Kronecker product,  $\text{vec}(\mathbf{A})$  stacks all columns of matrix  $\mathbf{A}$  into a column vector and  $\text{diag}(\mathbf{a})$  returns a matrix with vector  $\mathbf{a}$  on the diagonal.

Given is a set of  $K$  training shapes  $\mathbf{X}_k \in \mathbb{R}^{N \times 3}$ , each formed by the points  $\{x_i \in \mathbb{R}^3\}_{i=1}^N$  (vertices of green surfaces in Fig. 1(b)). Let  $\mathbf{y}(\alpha) = \bar{\mathbf{x}} + \Phi\alpha$  be the point distribution model (PDM), where  $\bar{\mathbf{x}}$  is the mean shape obtained from averaging  $\mathbf{x}_k = \text{vec}(\mathbf{X}_k) \in \mathbb{R}^{3N}$  over all  $k$ ,  $\Phi \in \mathbb{R}^{3N \times M}$  conveys  $M$  modes of variation of shapes  $\mathbf{x}_k$ , and  $\alpha \in \mathbb{R}^M$  is the deformation parameter. Let  $y_i(\alpha) \in \mathbb{R}^3$  be the  $i$ -th point ( $1 \leq i \leq N$ ) of the PDM. We assume that the shapes are already aligned or pose information is modelled directly into the PDM. The proposed methodology aims at using the PDM to reconstruct the full shape from (sparse) surface points  $\mathcal{P} = \{p_j \in \mathbb{R}^3\}_{j=1}^P$  (red points in Fig. 1(b)) by finding  $\alpha$ , as shown in Fig. 1(c).

Assume each point  $p_j$  is generated with probability  $p(i) = \frac{1}{N}$  by the  $i$ -th component of a Gaussian Mixture Model, where each PDM point  $i$  represents a Gaussian centred at  $y_i(\alpha)$  with covariance  $\sigma^2 \mathbf{I}_3$  (cf. Fig. 1(a)), i.e.  $p(p_j | \alpha, \sigma^2) = \sum_{i=1}^N p(i) \mathcal{N}(p_j | y_i(\alpha), \sigma^2 \mathbf{I}_3)$ . Thus, the probability that the  $i$ -th component has generated  $p_j$  for given  $\alpha$  and  $\sigma^2$  is  $p(i | p_j, \alpha, \sigma^2) \propto \exp(-\frac{1}{2\sigma^2} \|p_j - y_i(\alpha)\|^2)$ . Assuming each  $p_j$  as i.i.d., to obtain  $\alpha$  we need to maximise the log-likelihood function  $L(\alpha, \sigma^2) = \sum_{j=1}^P \ln p(p_j | \alpha, \sigma^2) = \sum_{j=1}^P \ln \sum_{i=1}^N p(i) \mathcal{N}(p_j | y_i(\alpha), \sigma^2 \mathbf{I}_3)$ . To obtain tractability, the generating Gaussian  $i$  for each  $p_j$  must be known. So we consider the expected complete-data log-likelihood [5] instead, which leads to  $Q(\alpha, \sigma^2, \alpha_{\text{old}}, \sigma_{\text{old}}^2) = \sum_{j=1}^P \sum_{i=1}^N p(i | p_j, \alpha_{\text{old}}, \sigma_{\text{old}}^2) \ln[\frac{1}{N} \mathcal{N}(p_j | y_i(\alpha), \sigma^2 \mathbf{I}_3)]$ . By introducing  $\mathbf{P} = \mathbf{I}_3 \otimes [p(i | p_j, \alpha_{\text{old}}, \sigma_{\text{old}}^2)] = \mathbf{I}_3 \otimes [p_{ji}] \in \mathbb{R}^{3P \times 3N}$ ,  $\mathbf{p} = \text{vec}([p_1 \dots p_P]^T) \in \mathbb{R}^{3P}$ , and dropping constants,  $Q(\alpha, \sigma^2, \alpha_{\text{old}}, \sigma_{\text{old}}^2) = -\frac{3}{2} P \ln \sigma^2 - \frac{1}{2\sigma^2} (2\bar{\mathbf{x}}^T \text{diag}(\mathbf{1}_{3P}^T \mathbf{P}) \Phi \alpha - 2\mathbf{p}^T \mathbf{P} \Phi \alpha + \alpha^T \Phi^T \text{diag}(\mathbf{1}_{3P}^T \mathbf{P}) \Phi \alpha)$ . Using Expectation Maximization (EM), we iteratively estimate parameters  $\alpha$  and  $\sigma^2$ . In the E-step, for all  $i, j$  we compute  $p(i | p_j, \alpha_{\text{old}}, \sigma_{\text{old}}^2)$

given  $\alpha_{\text{old}}$  and  $\sigma_{\text{old}}^2$ . In the M-step we re-estimate the parameters using the expressions obtained by taking partial derivatives of  $Q$ , which for parameter  $\alpha$  results in  $[\Phi^T \text{diag}(\mathbf{1}_{3P}^T \mathbf{P}) \Phi + \sigma^2 \Sigma_{\text{PDM}}^{-1}] \alpha = \Phi^T \mathbf{P}^T \mathbf{p} - \Phi^T \text{diag}(\mathbf{1}_{3P}^T \mathbf{P}) \bar{\mathbf{x}}$ , where a Gaussian prior  $\mathcal{N}(\alpha | \mathbf{0}, \Sigma_{\text{PDM}})$  is additionally imposed upon  $\alpha$  ( $\Sigma_{\text{PDM}} \in \mathbb{R}^{M \times M}$  is the covariance of the training data in the  $M$ -dimensional subspace). The variance parameter is given by  $\sigma^2 = \frac{1}{3P} (\mathbf{p}^T \text{diag}(\mathbf{P} \mathbf{1}_N) \mathbf{p} - 2\mathbf{p}^T \mathbf{P} \mathbf{y}(\alpha) + \mathbf{y}(\alpha)^T \text{diag}(\mathbf{1}_{3P}^T \mathbf{P}) \mathbf{y}(\alpha))$ . **Results:** Using a compound PDM of ten brain structures created from  $K=17$  training shapes, we compare the proposed method to ICP for fitting the PDM to  $\mathcal{P}$ . For each of the 17 shapes, we synthetically sample  $2.4 \cdot 10 = 80$  instances of  $\mathcal{P}$ , where each  $\mathcal{P}$  contains  $n_c \in \{2, 3\}$  partial contours per brain structure in  $n_b \in \{3, 4, 5, 6\}$  out of ten brain structures. For each of the  $2.4 = 8$  configurations we perform 10 draws. As such, for some of the structures there is no surface point in  $\mathcal{P}$ , i.e. during reconstruction these structures are interpolated from the other structures by the PDM.

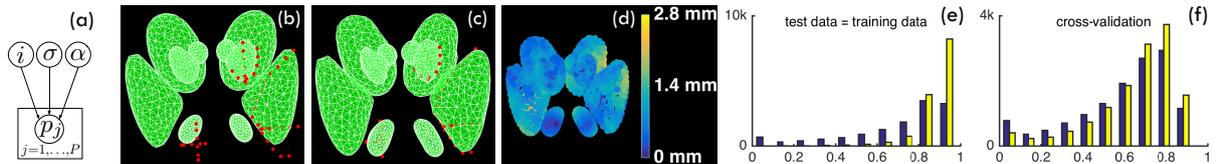
Fig. 1(e) and (f) reveal that the proposed method (yellow) outperforms ICP (blue) with respect to the Dice overlap (DSC) to the ground truth shape.

**Conclusions:** The proposed probabilistic approach outperforms the commonly used ICP algorithm for matching a PDM to a sparse set of points. Our experiments have revealed that when the test shape is also used for creating the PDM (Fig. 1(e)) all brain structures can be reconstructed with very high quality, even if no surface points of some of the brain structures are specified. However, using cross-validation (Fig. 1(f)) reveals that there is room for improvement w.r.t. generalisation.

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## References:

- [1] Heckel, F. *et al.*: Interactive 3D medical image segmentation with energy-minimizing implicit functions. *Computers & Graphics*, 35(2), 275-287, Apr 2011
- [2] Barratt, D.C. *et al.*: Instantiation and registration of statistical shape models of the femur and pelvis using 3D ultrasound imaging. *MIA*, 12(3), 358-374, 2008
- [3] Zheng, G. *et al.*: Kernel regularized bone surface reconstruction from partial data using statistical shape model. *IEEE EMBS*, 6579-6582, 2006
- [4] Fleute, M., Lavallée, S.: Building a complete surface model from sparse data using statistical shape models: Application to computer assisted knee surgery. *MICCAI*, 1998
- [5] Myronenko, A., Song, X.: Point Set Registration: Coherent Point Drift. *IEEE TPAMI*, 32(12), Dec 2010



**Figure 1:** (Best viewed on screen when zoomed in). Graphical model (a); PDM (green) and  $\mathcal{P}$  (red): before fitting (b); after fitting (c); ground truth error of PDM after fitting (d); DSC histograms (e) and (f) of ICP (blue) and our method (yellow).