

球面パラメータ空間での適応的なサンプリングを用いた MDL法の改良

徐 睿^a 周 向榮^b 平野 靖^a 橘 理恵^c 木戸 尚治^a 藤田 広志^b

^a 山口大学大学院医学系研究科 〒755-0097 山口県宇部市常盤台 2 丁目 16-1

^b 岐阜大学大学院医学系研究科 〒501-1194 岐阜市柳戸 1-1

^c 大島商船高等専門学校情報工学科 〒742-2193 山口県大島郡周防大島町小松 1091-1

E-mail: xurui@yamaguchi-u.ac.jp

あらまし 統計形状モデルは有効的な手法と認められ、医用画像のセグメンテーションに使用されている。統計形状モデルの構築では、各形状の対応点の決定が重要な課題であり、近年MDL法を用いた手法が提案した。MDL法の有効性が証明されたが、決定した対応点で構成したメッシュは元の形状メッシュより精度が低い。この問題を解決するため、球面のパラメータ空間で適応的なサンプリング手法を提案し、従来のMDL法を改良した。

キーワード 統計形状モデル, 対応点, MDL法

Improvement of MDL Method by Adaptive Sampling on Spherical Parameter Space

Rui XU^a Xiangrong ZHOU^b Yasushi HIRANO^a Rie TACHIBANA^c

Shoji KIDO^a and Hiroshi FUJITA^b

^a Graduate School of Medicine, Yamaguchi University 2-16-1 Tokiwadai, Ube, Yamaguchi, 755-0097 Japan

^b Graduate School of Medicine, Gifu University 1-1 Yanagido, Gifu, 501-1194 Japan

^c Oshima National College of Maritime Technology 1091-1 Komatsu, Oshima, Yamaguchi, 742-2193, Japan

E-mail: xurui@yamaguchi-u.ac.jp

Abstract Statistical shape models (SSMs) is a very efficient method for medical image segmentation. An important problem of building SSMs is how to determine the corresponding points. Although minimal description length (MDL) was a good method to find corresponding points, it was suffered from the problem that the meshes constructed by the determined corresponding points were not precise to represent the original shapes. We tried to resolve this problem by an adaptive sampling method on the spherical parameter space in this paper.

Keyword Statistical Shape Models, Corresponding Points, Minimal Description Length (MDL)

1. Introduction

In order to reduce effects of noise in medical images, there had been more and more researches focused on including statistical information in practical problems. Statistical shape models (SSMs) was such a way to make use of statistical information of shapes as priors to increase the robustness of image processing algorithms. In recent years, lots of researchers had successfully applied SSMs in clinical segmentation problems and achieved promising results. For example, it was reported that the three best rated fully-automatic algorithms were based on SSMs in the 3D segmentation clinical contest held in the

MICCAI Workshop in 2007 [8].

According to our knowledge, several SSMs had been proposed, which were point distribution models (PDMs)[9], m-rep[10], SPHARMs[11,12], and so on. We focused on PDMs in this paper since it was the most widely used SSMs. Given a set of corresponding points of N training shapes, generalized procrustes alignment [13] was applied to eliminate the differences on translation, rotation and scaling of each shape. Then principal component analysis (PCA) was applied on these aligned points to calculate the base-functions and the statistical shape models can be represented by Eq. 1.

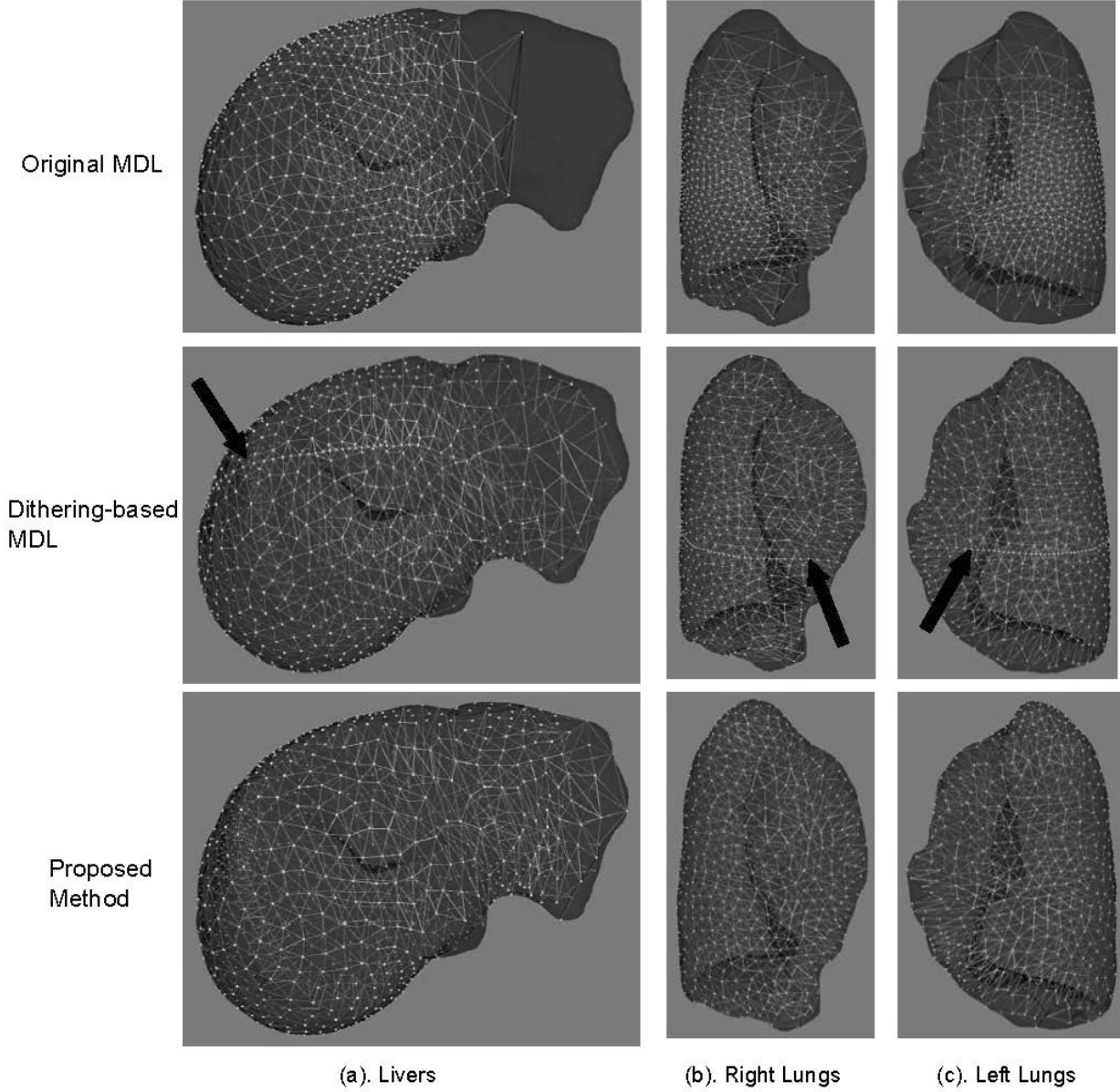


Figure 1. Corresponding points determined by the original MDL method [5], dithering-based MDL method [18] and the proposed method

$$\bar{\mathbf{s}} = \bar{\mathbf{s}} + \sum_{i=1}^{N-1} \alpha_i \mathbf{v}_i \quad (1)$$

where $\bar{\mathbf{s}}$ was the mean shape, \mathbf{v}_i was the base-functions and α_i is the parameters for the statistical shape models.

The main problem of SSMs construction was how to determine the corresponding points on each shape. At first, the determination of correspondence was usually carried manually to find landmarks. It was probable for simple 2D shapes, such as human faces, but obvious disadvantages rely on both of big burden of workflows and the inevitable

bias of different people. Especially for the complex 3D clinical data, manual determination of hundreds or thousands of landmarks are not practical. Therefore, lots of researches focused on automatic way to find corresponding points [1].

The determination of shape correspondence can be generalized as a registration problem. Many methods were proposed, such as surface matching based methods [14, 15], volume-based methods [16], and group-wise based methods [3,5,6,17]. A typical group-wise based method was proposed in [3], where a group of shapes were aligned with each other according to an information-based theory, called minimal description length (MDL), in order to get

the simplest description for the constructed statistical shape models. Although this method was efficient to obtain the corresponding points, its calculation was complex and expensive. This problem was resolved by [6], where a simpler version of MDL was proposed. In order to make the new version of MDL to converge faster, gradient descent based method was tried in [17] for 2D cases to replace the time-consuming Nelder-Mead optimization method. Followed the work in [17], gradient descent was applied to the 3D objects in [5] and the free source codes of this method was also given by [22].

Although it was showed that the MDL based method was efficient to automatically identify the corresponding points for 3D objects, a drawback was that the determined corresponding points were usually dense on a part of original surfaces while sparse on the rests. An example of the results was given by [5,22] was given in the first row of Fig. 1. It could be seen that the determined corresponding points were gathered on the bottom part of livers while there were almost no corresponding points on the top of livers. For lungs, the corresponding points were found mainly around the middle part and there were less points on the top and bottom. This problem caused that the meshes constructed by the determined corresponding points could not represent the original shapes very well. This non-accuracy brought bias into the statistical shape models. In [18], a remeshing technique [19] based on dithering [20] was applied to reconfigure sampling positions on the sphere parameter space in order to make the corresponding points to be uniformly spread on the original shape surfaces. According to [18], the surface of the unit sphere (in the parameter space) was separated into two half spherical parts. For each part, a disc-shaped control map was constructed which can reflect the distribution of vertices on the original shapes. In dense parts, the control map was set to be low-level values while for sparse parts it was set to be high-level values. For the inside parts of the control maps, dithering [20] was applied to find the sampling positions (black dots). For the boundary parts (the outer circle), a 1D dithering was applied in order to get the common sampling positions. Finally, the determined sampling positions were treated as vertices and 2D Delaunay triangles were firstly built separately on the two discs and then the two partial meshes were concatenated by the common sampling positions on the outer circles to generate a single mesh. Since there are no open source codes for [18], we implemented a version by ourselves. Since both of the

paper [18] and [19] were lack of the detailed descriptions on how to adjust the control maps in order to get a certain number of sampling positions, we implemented the work by our best guess. Unfortunately, we found the density of sampling positions on the concatenated part (outer circles for the two control maps) were usually denser than the rest parts in our implemented version. Examples were given in the second row of Fig. 1. Just as what the black arrows points to, a circle-shaped artifacts (the denser line) existed on both the livers and lungs. In order to correct this problem, we proposed a particle system based method to get the sampling positions on the sphere parameter space.

2. Proposed Method

MDL method could only be applied to genus-zero objects. Since a lot of organs obeyed this condition, the MDL method was widely used. Before the determination of corresponding points, the original shapes had to be firstly transformed onto a unit sphere. This procedure was usually called parameterization. Parameterization could be seen as a projection for each vertex of the original shapes from the original space onto the unit sphere in the parameter space. Therefore each shape had a counter-part of parameterized mesh on the unit sphere. MDL would drive these parameterized meshes sliding on the parameter space in order to align all shapes together. After the alignment, the same part of different shapes would be located on the same positions on the unit sphere. The vertices of the parameterized meshes would be gathered in some regions on the sphere while be sparse in other regions. If sampling positions were uniformly spread on the unit sphere, there would be less points in the dense regions while more points on the sparse regions. This is the reason why the work in [5] causes the under- and over-sampling problem on the original shapes.

In this paper, we proposed an adaptive sampling method to correct the sampling problem of the original MDL method. We hope to get more sampling points on the dense regions while get less points on the sparse regions. This was achieved by a carefully designed particle based system. Particle-based remeshing was proposed in [21] which was used to remesh surfaces of shapes. A set of particles was firstly put onto original iso-surfaces of shapes. Each particle had the repulsive forces push its surrounding particles away from itself. Nearest the distance was, much more forces it gave. Meanwhile, a weight term was also associated to each force term. The weights reflected geometrical information, such as curvature, for the positions where the pair of particles

were located. The forces for all particles determined an energy function for the particle system and each particle was slid along the iso-surface in order to minimize the total energy. Finally, these particles were treated as the vertices of the new mesh of the original shape.

Here, we adopted the idea of the particle-based system to find the optimal locations for the sampling on the unit sphere. A certain number of particles was placed on the surface of the unit sphere. The total energy of our particle based system was calculated by Eq. 2

$$E = \sum_i E_i = \sum_i \sum_{i \neq j} \omega_{ij} E_{ij} \quad (2)$$

where E_{ij} was the force term of a pair of particles and

ω_{ij} was the weight. For the force term, we adopted the original one proposed in [21], where the definition was given by Eq. 3

$$E_{ij} = \begin{cases} \cot\left(\frac{|\mathbf{r}_{ij}|}{\sigma} \cdot \frac{\pi}{2}\right) + \frac{|\mathbf{r}_{ij}|}{\sigma} \cdot \frac{\pi}{2} - \frac{\pi}{2} & |\mathbf{r}_{ij}| \leq \sigma \\ 0 & |\mathbf{r}_{ij}| > \sigma \end{cases} \quad (3)$$

where $|\mathbf{r}_{ij}|$ was the Euclidean distance of a pair of particles. σ was the parameter of the particle systems.

We designed the weight term which reflected the information about how the particles spread on the unit sphere. The definition of our proposed weight term was given by Eq. 4

$$\omega_{ij} = \frac{D(\mathbf{x}_i) + D(\mathbf{x}_j)}{2} \quad (4)$$

$$D(\mathbf{x}_i) = \begin{cases} a / (p(\mathbf{x}_i))^\gamma & p(\mathbf{x}_i) > b \\ a / b & p(\mathbf{x}_i) \leq b \end{cases}$$

where \mathbf{x}_i was the coordinate of where the i -th particle was located. $p(\mathbf{x}_i)$ gave the probability for vertices of parameterized shape meshes existed on the position of \mathbf{x}_i , and a , b , γ were the parameters of the particle-based system. Here we adopted the parzen-window method to estimate the probability density function for the vertices of parameterized shape meshes.

Gradient descent was used to minimize Eq. 2 to find the optimal sampling positions on the unit sphere.

Finally, these positions were treated as vertices and triangle meshes were built.

3. Experiments

Experiments were done on two kinds of data, 28 cases of livers and 17 cases of left and right lungs. The original MDL method [5], the dithering based MDL method [18] and the proposed method were applied on the two kinds of data to calculate the corresponding points. Then three different statistical shape models (SSMs) were built, and the generalization and specification experiments were done to evaluate the performances of the three SSMs. In both of the generalization and specification experiments, differences of two shapes was calculated by Eq. 5.

$$Dis(X, Y) = \frac{1}{2} \left(\frac{1}{N} \sum_{\mathbf{x} \in X} \min_{\mathbf{y} \in Y} d(\mathbf{x}, \mathbf{y}) + \frac{1}{M} \sum_{\mathbf{y} \in Y} \min_{\mathbf{x} \in X} d(\mathbf{x}, \mathbf{y}) \right) \quad (5)$$

where X and Y are the two sets of the vertices for two shapes. The number of vertices for the two sets were N and M respectively. $d(\mathbf{x}, \mathbf{y})$ was the Euclidean distance of

a pair of vertices of the two shapes.

Fig. 2 gave the results in the specification and generalization experiments. Both of the dithering-based and the proposed method were much better than the original MDL method. Although the dithering-based method was better than the original MDL, it was a little worse than the proposed method.

4. Conclusion

Although MDL was a good method for the determination of corresponding points of shapes [5], it suffered that problem that the determined corresponding points were not uniformly spread on the original shapes. Although there was a dithering-based method [18] to improve MDL method, we found it was suffered from the circle-shaped artifacts according to our implementation. In this paper, we proposed a particle-based method to resolve the problem of the original MDL method. Experiments were done by livers and lungs data. According to experimental results, it was showed that the proposed method was better than both of the original MDL method and a dithering-based MDL improved method.

Acknowledgement

This research was supported by a grand-in-aid for scientific research from the Ministry of Education, Culture, Sports, Science, and Technology, Japan, under the grand No. 21103008.

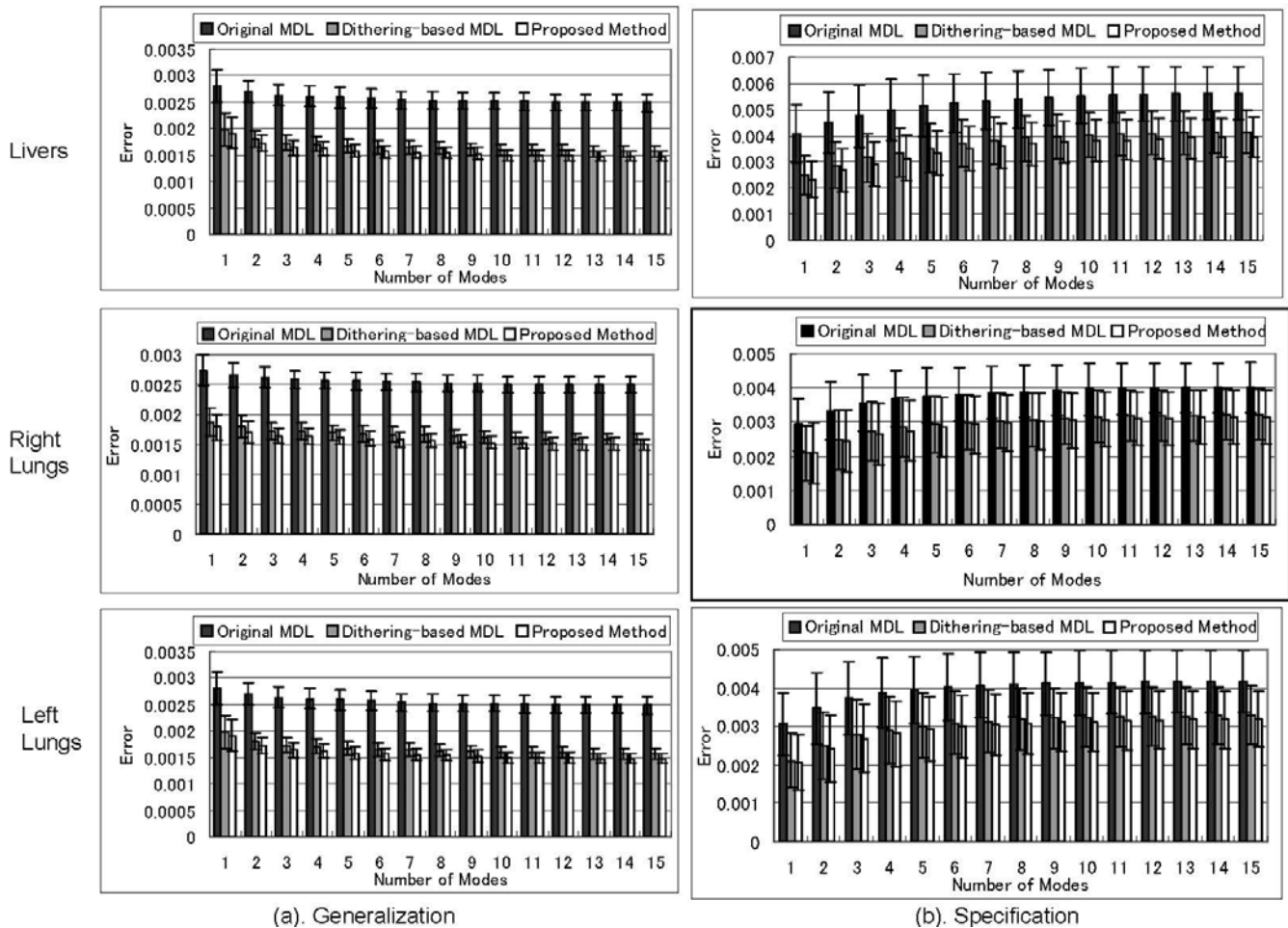


Figure 2. Experimental results of generalization and specification experiments

Reference

- [1] T. Heimann and H.P. Meinzer, Statistical shape models for 3D medical image segmentation: A review. *Medical Image Analysis*, Vol. 13, No. 4, pp.543-563, 2009
- [2] T. Heimann, *Statistical shape models for 3D medical image segmentation*, VDM Verlag Dr. Müller, 2008.
- [3] R.H. Davis, *Learning shape: optimal models for analyzing shape variability*. Phd thesis, University of Manchester, 2002.
- [4] M.A. Styner, J.A. Rajamani, et. al, Evaluation of 3D correspondence methods for model building, In proc IPMI, Vol. 2732 of LNCS, pp.63-75, 2003.
- [5] T. Heimann, et.al, 3D active shape models using gradient descent optimization of description length, In proc IPMI, Vol. 3565 of LNCS, pp.566-577, 2005.
- [6] H.H. Thodberg, Minimum description length shape and appearance models, In proc IPMI, volume 2732 of LNCS, pp.51-62, 2003
- [7] X. Gu, Y. Wang, et. al, Genus zero surface conformal mapping and its application to brain surface mapping, In proc IPMI, pp. 172-184, 2003.
- [8] T. Heimann, B. van Ginneken, et. al, Comparison and evaluation of methods for liver segmentation from CT datasets, *IEEE Trans on Medical Imaging*, Vol. 28, pp.1251-1265, 2009.
- [9] T. Cootes, C. Taylor, et. al, Active shape models -- their training and application, *Computer Vision and Image Understanding*, Vol. 61, No.1, pp.38-59, 1995.
- [10] S.M. Pizer, P.T. Fletcher, et.al, Deformable m-reps for 3D medical image segmentation, *Int J Comp Vis*, Vol. 55, no2, pp.85-106, 2003.
- [11] G. Székely, A. Kelemen, et.al, Segmentation of 2-D and 3-D objects from MRI volume data using constrained elastic deformations of flexible Fourier contour and surface models. *Medical Image Analysis*, Vol. 1, No.1, pp.19-34, 1996.
- [12] A. Kelemen, G. Székely, et.al, Elastic model-based segmentation of 3D neuroradiological datasets. *IEEE Trans. on Medical Imaging*, Vol. 18, No. 10, pp.828-839, 1999.
- [13] I.L. Dryden, K.V. Mardia, *Statistical Shape Analysis*. John Wiley & Sons. ISBN 0471958166 , 1998.
- [14] P.J. Besel and N.D. McKay, A method for registration of 3-D shapes. *IEEE Trans on PAMI*, Vol. 14, No. 2, pp.239-256, 1992.
- [15] H.L. Chui, A. Rangarajan, A New Algorithm for Non-Rigid Point Matching, in Proc CVPR, pp. 2044-2051, 2000.
- [16] R Xu, Y.W. Chen, et. al: Parzen-window based normalized mutual information for medical image registration, *IEICE Trans Information & Systems*, Vol. E91-D, No. 1, pp. 132-144, 2008
- [17] A. Ericsson, K Astrom, Minimizing the description

- length using steepest descent, In proc British Machine Vision Conference, pp. 93-102, 2003.
- [18] T. Heimann, Ivo Wolf, et. al, optimal landmark distributions for statistical shape model construction, Proc. SPIE Medical Imaging: Image Processing, vol. 6144, pp. 518-528, 2006.
- [19] P. Alliez, M. Meyer, et.al, Interactive geometry remeshing, ACM Transactions on Graphics, Vol. 21, No. 3, pp. 347-354, 2002.
- [20] V. Ostromoukhov, A simple and efficient error-diffusion algorithm, In Proc. SIGGRAPH, pp. 567-572, 2001.
- [21] M.D. Meyer, P. Georgel, and R.T. Whitaker, Robust particle systems for curvature dependent sampling of implicit surfaces, In Proc. of the International Conf. on Shape Modeling and Applications, pp. 124-133, 2005.
- [22] T. Heimann, I. Oguz, et. al., Implementing the automatic generation of 3D statistical shape models with ITK. In Proc MICCAI Open Science Workshop, 2006.