

Segmentation of the left ventricle in 4d-dSPECT data using free form deformation of super quadrics

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ABSTRACT

In dynamic SPECT (dSPECT) images, function of a particular organ may be analyzed by measuring the temporal change of the spatial distribution of a radioactive tracer. The organ-specific and location-specific time-activity curves (TAC) of the different heart regions (regions with normal blood circulation and with disturbed blood circulation) are helpful for the diagnosis of heart diseases. A problem of the derivation of the TACs is that the dSPECT images have a poor spatial and temporal resolution and the data is distorted because of noise effects, partial volume effects and scatter artifacts. Segmentation according to some homogeneity principle will deliver regions of similar functional behavior but the segmented regions do not directly point to anatomy. For our goal of anatomy-specific segmentation, information about anatomy is provided a-priori and it must be fitted to the data. For initialization the user has to place a super ellipsoid in the data set. The parameters of this super ellipsoid are obtained from the computed mean shape of six manually segmented left ventricles in test data sets. A closer fit to the high gradients of the boundaries of the heart wall is achieved using the free form deformation method. For evaluation segmentation results are compared with a manual segmentation. In all test images we could ascertain a good correspondence between the manual and automatic segmentation.

Keywords: dSPECT, Segmentation, Free Form Deformation

1. INTRODUCTION

Dynamic SPECT (dSPECT) is a novel technique in nuclear imaging. This technique can be used to obtain quantitative information about functional processes of the different organs in the human body. In our case the dSPECT data should be used for the analysis of the blood flow in the heart region for the support of the diagnosis of heart diseases. But the complexity of the visual analysis task increases if time-varying data is to be analyzed. In the field of the visual analysis of dSPECT data sets, the display of the time activity curves (TAC) is a good method. For the purpose of the derivation of the TACs for the different heart regions, the segmentation of the heart is necessary.

This segmentation is a problem because the data sets contain only functional information. But for diagnosis support we are interested in anatomical information. Therefore, the anatomical information must be derived a-priori. Then, in the following segmentation process this information can be fitted to the data.

For the purpose of shape-based segmentation different methods are described in literature. In medical image analysis, shape models can be used for instance in an active surface segmentation ¹, in active shape model segmentation ² and in active appearance segmentation ³. In our case the customary active surface segmentation has too many degrees of freedom for shape adaptation, and so the correct segmentation of hearts regions with perfusion defects is not guaranteed with this method. The other two segmentation methods require a large number of manual segmented data sets for statistical analysis. Because of the novelty of the dSPECT methods we cannot meet this requirement.

For the restriction of the degrees of freedom we use an implicit parametric shape description such as super-quadrics. With this approximation method we can describe the shape of the left ventricle of the heart with few parameters. The free form deformation is used for fitting the parametric model to the data. This procedure was already successful used for segmentation of the left ventricle in static SPECT data sets ⁴.

We begin the paper in section 2 with a short description of the image characteristics. Then we explain in section 3 the generation of the shape model and the free form deformation method. After that the use of these two parts for segmentation of the epicard and the endocard is presented. Section 4 describes experimental results of the segmentation. Finally, possible extensions of the method, and the future improvements are discussed.

2. DYNAMIC SPECT DATA

Over the last few years a small group of laboratories have begun investigations of the dynamic SPECT issues. It permits to obtain quantitative dynamic information about kinetic processes in the body from the data acquired using only a standard clinical acquisition protocol with standard equipment. The reconstruction of the data is based on a mathematical methodology for ill-posed inverse problems⁵.

The result of dSPECT reconstruction is a 4D data set, composed of a time-series of 3-dimensional images. A very important new feature of these images is that they contain, besides the standard information about the 3D spatial distribution of the radiotracer, additional temporal information about the dynamic changes of this tracer distribution. Using it in a routine medical practice can substantially improve the diagnostic power of SPECT, as these temporal changes clearly relate to normal or diseased organ functioning. At the moment the method has been tested for heart studies.

Dynamic studies of the heart perfusion use Teboroxime, a radiopharmaceutical, which has a fast and high uptake in the myocardium and an equally high but delayed uptake in the liver. In Figure 1 two examples of transaxial slices of dSPECT images of heart and liver region are depicted. The poor image resolution of the data sets is clearly visible. The data sets of 96x96 pixels in x- and y-direction have a image resolution of 4.67 mm. The data sets of 64x64 pixels have a resolution of 7.56 mm. Because of the small number of counts of every voxel their time activity curves may have some errors as a result from noise effects, reconstruction or scatter artifacts.

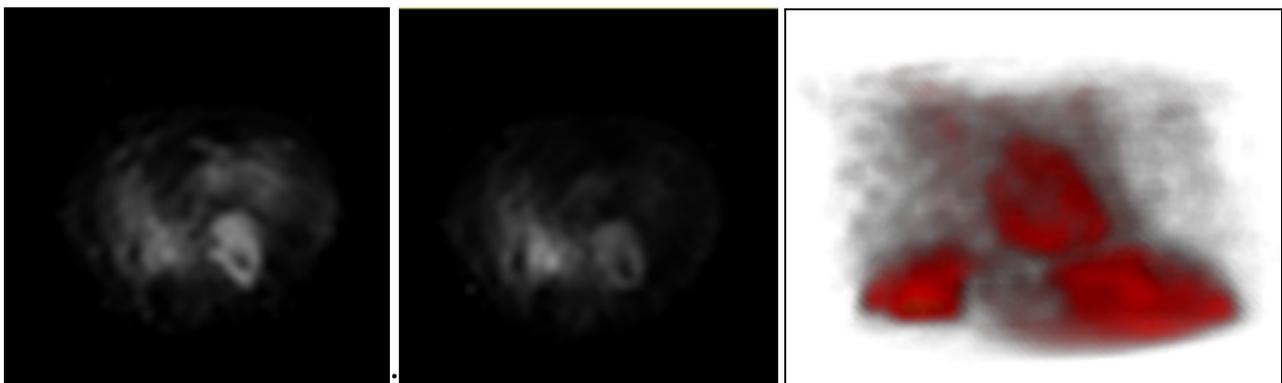


Fig. 1: Examples for the dSPECT data sets. Left: slice in the middle of the data set at the beginning of the time sequence, Center: the same slice four minutes later. It is clearly visible, that the activity in the liver region has increased while the activity in the left ventricle has decreased. Right: 3-D visualization of the mean activity values of the data set using volume rendering

For semi-automatic segmentation of the heart ventricles the reliability of the TACs needs to be improved. It is possible by increasing the number of counts used for the derivation of the curves. For this reason, we have integrated several voxels into small “segments” for which we compute an average curve. For segmentation we investigated three different image correction methods. The region merging method connects voxels based on a global homogeneity criterion. The multiresolution approach by means of pyramid linking uses a local homogeneity criterion. As a third method we investigated nonlinear anisotropic diffusion. Using this method, coherent regions are more homogenous and information on the region boundaries are in good condition.

Preliminary examinations have shown, that the data sets in the different time frames have a very large correlation. Therefore, we have used the Karhunen-Loeve transform for the reduction of this time correlation in the data sets. Tests have shown that the first four Eigen values contain about 99% of the time information⁶. For this reason, in all tested image enhancement approaches we use a combination of the first four coefficients of the Karhunen-Loeve transform of

the time activity curve of every voxel for computation of the homogeneity or diffusion criterion. All the three image enhancement methods deliver good results. The diffusions method was selected for pre-processing the data because of its low computation time. Based on the more reliable TACs the segmentation process can be carried out.

3. SEGMENTATION OF THE LEFT VENTRICLE

As dSPECT data sets show exclusively organ functions, only heart regions with an intact blood flow are visible. For diagnosis of infarcts, areas of perfusion defects need to be segmented as well. For an anatomy-specific segmentation, information about anatomy is provided in the segmentation approach. With the anatomical model the missing functional information can be completed. The developed segmentation method of the left ventricle should determine the position of the epicard as well as the position of the endocard. In the first segmentation step the external shape of the ventricle model is determined.

3.1 DERIVATION OF THE SHAPE MODEL

Dynamic SPECT images of the body consist of a four-dimensional sequence of more than 30 time frames. Preliminary investigations showed that there is a visible difference between the time behavior of different organs. This assumption can be used for segmentation of different organs. The gray values in the individual time frames of a pixel position can be used as a feature for the organ extraction in the segmentation process. The segmentation is carried out on the data of the first four values of the Karhunen-Loeve transform of the time data sets.

After the pre-processing step, a shape model of the left ventricle is obtained from manual segmentation. In six data sets a physician marked the object boundaries in all slices. Then, the center of gravity and the rotation around the z- axis for all six manual segmented heart objects are determined. With these values the individual objects are adjusted to each other. Afterwards, we determine the contour points on the individual surfaces for 30 regular distributed angles. The corresponding points can be used for computation of the mean position of the objects at a certain surface position. The mean shape model is then approximated by a super ellipsoid. Using a super ellipsoid has the advantage, that the shape is represented by only five parameters⁴. The surface of a super ellipsoid can be described with the following equation:

$$\left(\left(\left(\frac{x}{a_1} \right)^{\frac{2}{\varepsilon_2}} + \left(\frac{y}{a_2} \right)^{\frac{2}{\varepsilon_2}} \right)^{\frac{\varepsilon_2}{\varepsilon_1}} + \left(\frac{z}{a_3} \right)^{\frac{2}{\varepsilon_1}} \right)^{\frac{\varepsilon_1}{2}} = 1. \quad (1)$$

The parameters a_1 , a_2 and a_3 in this equation characterize the extension of the super ellipsoid in the x , y , and z direction. The two parameters ε_1 and ε_2 describe the shape along the two spherical components. The five parameters of the shape of the super ellipsoid and the six parameters for translation (t_x , t_y , t_z) and for rotation (r_x , r_y , r_z) are adapted in the next step on the mean shape model. For this reason we set the parameters ε_1 and ε_2 to 1. The values t_x , t_y and t_z correspond to the center of gravity of the mean shape and the rotation is determined with the matrix M of the second order moments of the mean shape points. The initial dimensions of the model are computed as

$$a_1^2 = \frac{3}{2}(\lambda_2 + \lambda_3 - \lambda_1), \quad a_2^2 = \frac{3}{2}(\lambda_1 + \lambda_3 - \lambda_2) \quad \text{and} \quad a_3^2 = \frac{3}{2}(\lambda_1 + \lambda_2 - \lambda_3), \quad (2)$$

with λ_1 , λ_2 and λ_3 as the Eigen values of the matrix M . The five parameters ε_1 , ε_2 , a_1 , a_2 and a_3 are changed such that the points of the super ellipsoid are positioned near the surface of the mean shape. This adaptation can be obtained using a multidimensional minimization of the following energy function

$$E = \sum_{i=1}^N \left[1 - \hat{F}(x_d, y_d, z_d, a_1, a_2, a_3, \varepsilon_1, \varepsilon_2, r_x, r_y, r_z) \right]^2, \quad (3)$$

with \hat{F} as the inside-outside function of the super ellipsoid after the transformation follow equation 1. This function has a value of 0 if all data points are located on the model surface. We use the Fletcher-Reeves algorithm⁷ For computation of minimization.

An example of a super ellipsoid is shown in figure 2 on the left. Only a limited number of shapes can be represented, which is the main disadvantage if we use super ellipsoids for shape description in medical images. Thus, the super ellipsoid approximation is deformed using the free form deformation method (figure 2 in the center) in order to better fit on the computed mean shape.

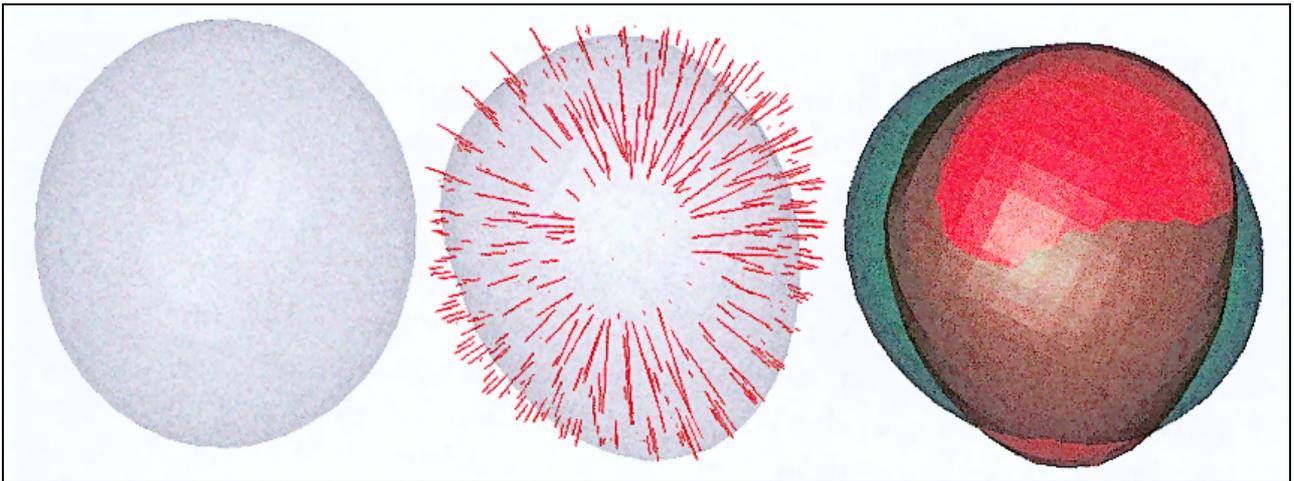


Fig. 2: left: super ellipsoid after mean shape approximation, Centre: shape model after FFD with displacement field, right: visualization of the modification from the super ellipsoid to the initial model.

3.2 FREE FORM DEFORMATION (FFD)

The free form deformation was used by Szeliski and Lavalée⁸ for the matching of 3D surfaces of anatomical structures. By this deformation method a super ellipsoid is included in a 3D box of control points. A translation of an individual control point of the box causes translations of the points of the embedded super ellipsoid. The deformation function, which links control and object points, can be defined by a trivariate Bernstein polynomial. This connection between the object and the control point positions can be written as

$$X = \sum_{i=0}^l \sum_{j=0}^m \sum_{k=0}^n C_l^i C_m^j C_n^k (1-s)^{l-i} s^i (1-t)^{m-j} t^j (1-u)^{n-k} u^k P_{ijk}, \quad (4)$$

with s, t and u as the parameters of the local coordinates of the super ellipsoid in the control point grid. Equation 4 can be written in matrix form as

$$X = BP, \quad (5)$$

where B is the deformation matrix, P is the matrix of the control points and X is the matrix of the super ellipsoid points. New positions of the control points, which minimize the distance between the points of the manually constructed model and the points of the super ellipsoid, are computed by minimization of the displacement field. This leads to the following least square problem:

$$\min_P \|BP - X\|^2 \equiv \min_{\delta P} \|B\delta P - \delta X\|^2 \quad (6)$$

This problem can be solved by singular value decomposition of the matrix B . Details are described in literature ⁹. Afterwards, new model point positions can be computed with help of the new control point coordinates using equation 4. The computation of the displacement field, the determination of the new control point positions and the deviation of the new model coordinates is repeated iteratively until a given similarity between deformed model and manually segmented object is reached. An advantage of the FFD method is, that the displacement parameters of few control points describe the deformation of the whole object.

The described approach with a combination of super ellipsoid and FFD is used for the smoothing of the shape representation. In the concrete case we eliminated 50 % of the singular values greater than 0 by computation of the singular value decomposition minimization by the least squares method. This guarantees the smoothness of the initial model.

3.3 SEGMENTATION OF THE EPICARD

In the approach for the segmentation of the epicard contour the anatomical model needs to be positioned in the data set near the object boundaries. For this purpose, the user marks the first and the last slice, which contain the left ventricle, and the maximum extension in x- and y- direction. Using these six input points the bounding box of the searched object is estimated. Then, the mean point of the initial model is positioned on the mean point of this box. For fitting the model to high gradient values it is enlarged by a scaling factor of 1.2. The enlargement ensures that all object points of the epicard are inside the model volume. This has the effect that we can assume a search direction towards the model mean point. As a result of the user interaction the shape model is already positioned near by the epicard boundary. Therefore, the maximum gradient values are searched only in a distance of 6 pixels from the model contour. With these new points the displacement field between model and contour candidates can be computed with FFD. The FFD was realized by an elimination of two thirds of the singular values in order to guarantee stiffness and to reduce the influence of falsely detected points. With this specification of the stiffness of the epicard surface it was possible to use the approach for segmentation of the patient data sets as well.

3.4 SEGMENTATION OF THE ENDOCARD

After epicard segmentation the procedure is repeated for endocard segmentation. In the first step the user must mark again the first and last slice of the appearance of the endocard. Based on this we can compute the coordinates of the ventricle mean points for all slices between these two slices. Then all contour points of the epicard in the different slices and the appropriate mean points are connected by a line. Along these lines we search for the maximum gradient values in order to determine positions of endocard contour candidates. These candidates are used in the next step for the deformation of a new initial model. This new super ellipsoid is generated using the parameters from the segmented epicard surface. The displacement field between the endocard contour candidates and the corresponding super ellipsoid points is computed by use of a third of the singular values in the FFD. Several segmented ventricle models are shown in Figure 3.

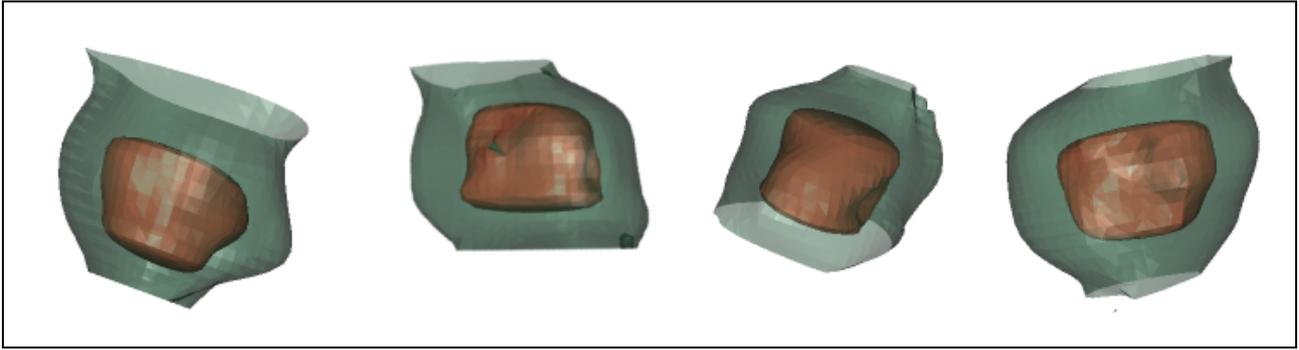


Fig. 3: Examples for segmented ventricle models in four different test data sets

4. RESULTS

For evaluation of the results of our segmentation method we compared them with manual segmentations. The manual segmentation was carried out by three different experts. Tests on six data sets have shown that our method of free form deformation of super ellipsoids enable a very good segmentation despite of the bad quality of the images. The segmentation error was in the same range as errors in manual segmentation. The mean deviation between corresponding points from the mean manually segmented and computer-segmented surfaces was one pixel for epicard well as for endocard segmentation.

Tests with simulated images from phantom data have shown equally good results because the number of used singular values can be varied in order to modify the stiffness. Stiffness modification was necessary in order to minimize the under-segmentation in heart areas with perfusion defects.

Only a small number of contour candidates can be determined due to the poor image resolution in both cases (endocard and epicard segmentation). In our tests, we found that the influence of falsely segmented contour candidates on the shape of the segmented surface increased with an increased number of iteration steps. Thus, the FFD computation may be stopped after one iteration step for model approximation on the candidate points.

We also investigated the influence of the initialization on the result. In these tests the maximum difference between the three different user inputs was three pixels. It had no influence on the segmentation results.

All algorithms were implemented in C⁺⁺. The tests were carried out on a 900 MHz Athlon PC. For the segmentation of a single data set the user needed about two to four minutes. The semiautomatic segmentation was faster as the manual segmentation which took approximately 30 minutes.

5. DISCUSSIONS AND FUTURE WORK

dSPECT is a novel technique for investigating time-varying behavior of anatomy. We presented a method for segmentation of the left ventricle in such images using a combination of temporal information about the dynamic changes of the tracer distribution in the organ and a priori anatomic knowledge.

We have shown that the integration of the user expectations in a segmentation approach as a model is practicable if the information in the data sets is insufficient. This model can be fitted to the data in order to solve the segmentation problem. It is difficult, however, to balance the knowledge from the model and the information from the data. In our case, we controlled the influence of the model by varying the number of singular values in the FFD.

The results will serve three purposes. Firstly, we will try to remove scatter artifacts from the heart. Secondly, anatomical information is fed back to the data reconstruction process in order to improve anatomy-based correction schemes. Thirdly, as the main part of our work, the analysis information provides additional information to the rendering system for improved perception and evaluation of dSPECT images.

REFERENCES

1. Fenster, S. D.: Training, Evaluation and Local Adaptation in Deformable Models, PhD. Thesis, Columbia University, Department of Computer Science, 2000.
2. Duta, N., Sonka, M.: Segmentation and Interpretation of MR Brain Images: An improved active shape model, IEEE Transactions on Medical Imaging, Vol.17, No.6, pp.1049–1067, 1998.
3. Cootes, T.F., Edwards, G., Taylor, C.J.: Comparing Active Shape Models with Active Appearance Models, Proc. British Machine Vision Conference, Vol. 1, pp. 173-182, 1999.
4. Bardinet, E., Cohen, L.D., Ayache, N.: Tracking and motion analysis of the left ventricle with deformable superquadrics. Medical Image Analysis, No. 2, pp: 129-149, 1996.
5. Celler, A., Farncombe, T., Bever, C., Noll, D., Maeght, J., Harrop, R., Lyster, D.: Performance of the dynamic single photon emission computed tomography (dSPECT) method for decreasing or increasing activity changes, Physics in Medicine and Biology, Vol. 45, pp. 3525-3544, 2000.
6. Toennies, K.D., Celler, A., Blinder, S., Möller, T., Harrop, R.: Scatter segmentation in dynamic SPECT images using principal component analysis, Proceedings of SPIE (Medical Imaging 2003), San Diego, Part I, pp. 507-516, 2003.
7. Ueberhuber, C.W.: Numerical Computation, Springer, Volume 2, Chapter 14, pp. 325-335, 1997.
8. Szeliski, R., Lavallée, S.: Matching 3-D anatomical surfaces with non-rigid deformations using octree-splines, Proc. of the IEEE Workshop on Biomedical Image Analysis, Seattle, pp. 144-153, 1994.
9. Bardinet, E., Cohen, L.D., Ayache, N.: Super quadrics and free-form deformations: a global model to fit and track 3D medical data. Proceedings of the Conference on Computer Vision, Virtual Reality and Robotics in Medicine (CVRMed'95), Lecture Notes in Computer Science, Nice, Springer Verlag, 1995.