# Fully automatic liver scan planning - slice and navigator positioning from stacked 2D localizer scans

M. Fenchel[1,2], S. Thesen[3], A. Schilling[4]

[1]Magnetic Resonance, Siemens Medical Solutions, Erlangen, Germany, [2]WSI, Eberhard-Karls-University, Tuebingen, Germany, [3]Siemens Medical Solutions, Erlangen, Germany, [4]WSI-GRIS, Eberhard-Karls-University, Tuebingen, Germany

**Introduction:**

In MR liver examinations, slice positioning can be a tedious task. This even increases when using navigator based multi-breathhold methods like [5], which have entered current clinical practise. Manual navigator positioning in 2D is especially error prone as the physician tends to forget to ensure a correct placement in 3D, resulting in bad image quality. We present a fast and fully automatic approach for liver slice and navigator position planning by registering a 3D statistical model of the liver to a set of stacked 2D localizer images. In contrast to other slice positioning methods, it is neither dependent on special scanning protocols like [3], nor on 3D input data like [4], but on standard localizers images, which are acquired in clinical practise anyway. The method can be easily adapted to other organs as well.

**Methods and Results:**

The images used were acquired using a standard 1.5 T clinical scanner, MAGNETOM Avanto, SIEMENS Erlangen. Our method consists of an offline process, the statistical model generation, which is done once in advance, and an online process, the localizer registration itself, which has to be performed every time.

Statistical Liver Model Generation:

A statistical liver model [1] is generated by segmenting image data from a pool of 10 volunteers. This model describes the abundant variability of shapes in human livers, while maintaining natural anatomical restrictions. These data sets were acquired by using a T1 weighted abdominal standard protocol (3D FLASH with FatSat, 128 slices, 192x156 matrix). We then segment one data set manually slice by slice. This data set is called the reference data set, the segmented data is called the reference liver. We register [2] all other data sets to the reference data set in a 5-way process. For the registration process we use gradient magnitude images of the data sets.

1.) We perform a rigid scaled registration with 8 degrees of freedom (scaling in axial direction is left out) on the gradient images according to the second moments to roughly align the torsos.
2.) We then register the data sets along the axis defining the axial direction with one degree of freedom. Now, the liver in the data set is located close to the reference liver
3.) If the registration is not good enough, we perform additional deformable thin-plate-spline registration based on landmarks which are set by hand.
4.) We then perform an affine registration with 12 degrees of freedom of the data sets to the reference liver, using a probability weighted affine transformation estimation.
5.) Finally, we perform a probability weighted deformable registration to the reference liver to obtain the final registration

For the statistical modelling process we need point to point correspondences. We therefore extract a discrete data structure, i.e. a polygonal mesh from our reference liver and simplify it to an adequate number of vertices. This polygonal mesh is called the reference mesh. The deformation field obtained from the 5 registration steps is used to warp the reference mesh and thus align it to the respective data set that has been registered to the reference data set. High frequency content of the deformation field is removed before by low-pass filtering, since we expect the deformation to be smooth and continuous.

We thus obtain for each point $p_i$ in the reference mesh a corresponding point $p_i'$ in the data set. These correspondences can be used to calculate a statistical model as in [1]. The model itself can be described as $x = \underline{x} + P \cdot b$, where $\underline{x}$ is the average model, P the matrix of the Eigenvalues of the covariance matrix and b the so called feature vector or the internal parameters of the model. We find that using 6 internal parameters is sufficient for describing more than 95% of the variation of our data sets.

Localizer Registration:

We register our model to a set of localizers from a patient study. We currently use a set of 6 localizers scanned with spoiled GRE, 3 of which are axial and 3 coronary. The localizer slices each have a thickness of 10 mm and a respective distance of 15 mm with a 256x128 matrix.

First, a rough estimation of the liver position is calculated using the second moments from the axial localizers similar to registration step 1 mentioned above. We then set up a correlation function, depending on 6+6 degrees of freedom, i.e. 3 space coordinates (x, y, z), 3 orientation angles ($\varphi$, $\theta$, $\psi$) and the feature vector (b) of the model with additional 6 parameters. The correlation function is sampled at the vertices of the model on the gradient magnitude of the localizer images.

We maximize this function to obtain the most probable shape, position and orientation of our model. See Fig 1 for an example of a registration. We discard the parameters found, if a criterion of confidence is not fulfilled. The position of the navigator ROI is easily obtained from the coordinates and the orientation of our model. Fig 2 shows the placement of slices, saturation bands and a navigator ROI (2D PACE method, see [5]) at the diaphragm using the result from the localizer registration process.

**Discussion:**

Using the current limited amount of data, the maximum inaccuracy of the localizer registration is at least better than 10mm. Accuracy can probably be improved by increasing the total number of localizer images used for the registration. However, this would increase the total scanning time needed. So a tradeoff is made between running time and accuracy. We found that 6 localizer images are enough for a robust registration under the given accuracy conditions. Increasing the number of internal parameters will produce only slightly better results, since most of the variation is already handled by the 6 internal parameters mentioned.

**Conclusion:**

We are able to determine the geometry and position of a patient's liver with a maximal inaccuracy that is sufficient for a good placement of the navigator ROI. Once the model has been generated, the method is fast: we are able to register our model to standard localizers and place slices, saturations bands and navigator ROIs. The execution of the online process is performed in an average time of approximately 1s, which is a significant gain in examination time and reliability compared to manual positioning of slices and navigator ROIs. Therefore this method seems to be a promising approach for automatic and semi-automatic scan planning in clinical practise. Furthermore it can be expected that follow-up studies will greatly benefit from this approach. Extending the method to other organs is straightforward and may also be applied for automation of post-processing functionality.

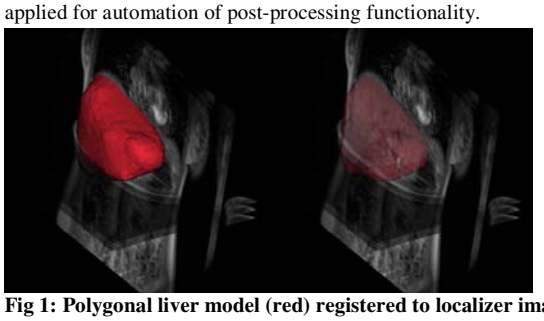

**Fig 1: Polygonal liver model (red) registered to localizer images**

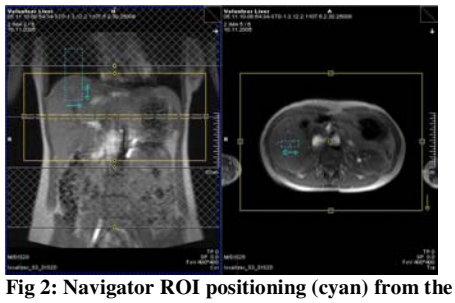

**Fig 2: Navigator ROI positioning (cyan) from the registration result**

**References:**

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