

Mark Holden¹, Nadeem Saeed², K. Kumar Changani², David Templeton², Derek L. G. Hill¹

¹Radiological Sciences, School of Medicine, King's College London, London, UK. ²GlaxoSmithKline, Frythe, Welwyn, Herts., UK.

Abstract

Quantitative measurements of anatomical change from serial MR images are useful for the evaluation of subject response to new drugs. Large numbers of images are needed to test whether a response is statistically significant, necessitating automated image analysis. Generally applicable automatic segmentation algorithms are not available so here we investigate using non-rigid registration to segment the liver of four repeat scans of three subjects using a technique known as segmentation propagation. We compare rat hepatic volume measurements to demonstrate the potential of such a technique in organs with registration complexities, such as the liver.

Introduction

- Serial MR imaging enables non-invasive monitoring of anatomical change
- Large numbers of subject images are needed to achieve statistical significance
- Segmentation approaches require manual intervention to be reliable
- Non-rigid registration could automatically measure anatomical change
- Liver can also deform because of: repositioning and intestinal activity

Subjects and Imaging

- Three Zucker rat livers scanned¹ following treatment at: -1, 1, 3, 8 and 12 weeks
- Free breathing (under isoflurane anaesthesia)
- Respiratory triggering using a plethysmograph
- Bruker 2T (Medspec S200) MR scanner
- 3D inversion recovery GRE sequence (scan time 15 mins)
- TI=600ms, TE=5.2ms, TR=25ms
- FOV = 7×7×7cm³ (128×128×96 matrix)
- 128×128×128 voxels (0.55×0.55×0.55mm)

Method

Liver contours were delineated in the baseline scans using semi-automatic segmentation and propagated to the repeats using non-rigid registration. To validate the propagations the repeats were also delineated using semi-automatic segmentation and the two sets of volume measurements compared.

Semi-automatic segmentation:

- Baselines: thresholding, contour following and interactive editing² to give B_s
- Repeats: rigid registration to baseline and manual editing to give A_s

Segmentation propagation:

The baseline scans (B) were registered to the repeats (A) using a rigid-body approx starting estimate, affine and B-spline registration algorithms. The resulting transformation was used to propagate the baseline segmented liver contours B_s into the space of the repeat scans.

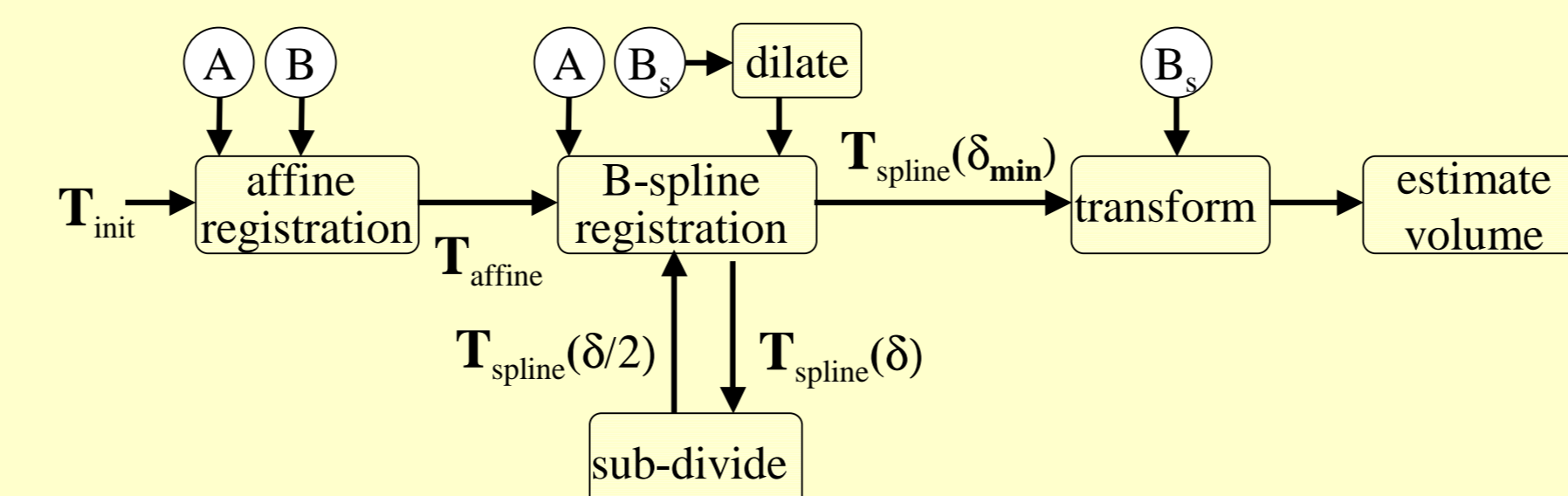
Affine registration:

- Determine T_{affine} (12 degrees of freedom: 6 rigid-body, 3 scale and 3 shears)
- Maximise normalised mutual information (NMI) similarity measure
- Hierarchical/isotropic search of transformation space for maximum similarity [3]

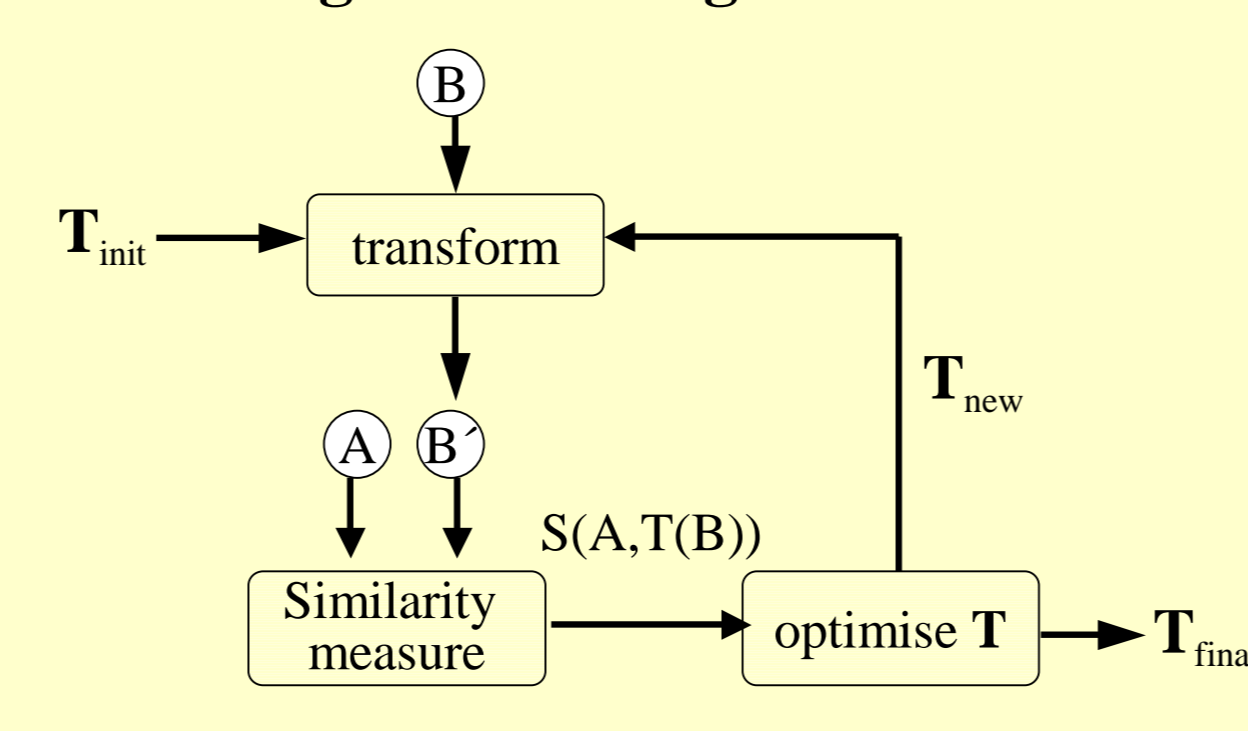
B-spline registration:

- Regularly spaced δ grid of control points Φ_{i,j,k} defined in target image
- Φ_{i,j,k} constrained to translate as a tensor product of B-Splines [4]
- T_{spline} defines a smooth C² continuous transformation between images
- Translate control points in direction of ∇S(A, B¹)
- Search for set of translations to maximise image similarity (NMI)
- Multi-grid search strategy using set of control point spacings δ = {20, 10, 5}mm to efficiently determine low and high spatial frequencies of the deformation.
- Fine grid δ_{min} registration performed on dilated ROI around organ using a coarse grid propagation of baseline segmentation B_s
- Target organ volume determined by integrating interpolated intensities of the propagated binary image.

Segmentation propagation: overall strategy



Registration algorithm



Similarity Measure: Normalised mutual information

$$NMI(A,B) = \frac{H(A)+H(B)}{H(A,B)}$$

$$H(A,B) = - \sum_{a \in A, b \in B} P(a,b) \log P(a,b)$$

B-spline transformation of control points

$$T_{spline}(x) = \sum_{l=0}^3 \sum_{m=0}^3 \sum_{n=0}^3 B_l(u) B_m(v) B_n(w) \Phi_{i+1,j+m,k+n}$$

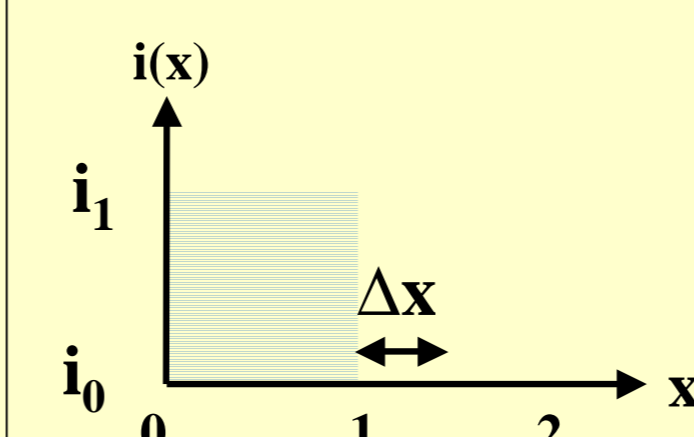
$$B_0(u) = (1-u)^3$$

$$B_1(u) = (3u^3 - 6u + 4)/6$$

$$B_2(u) = (-3u^3 + 3u^2 + 3u + 4)/6$$

$$B_3(u) = u^3/6$$

Trilinear transformation and volume estimation



$$i' = i_0 \times (1 - \Delta x) + i_1 \times \Delta x$$

$$\Delta x = (i_0 - i') / (i_1 - i_0) \quad (i_1=1000, i_0=0)$$

$$\Delta v = \frac{1}{i_1 - i_0} \sum i'$$

Results

Fig 1 shows a propagated segmentation derived from non-rigid registration and a manually segmented one for comparison.

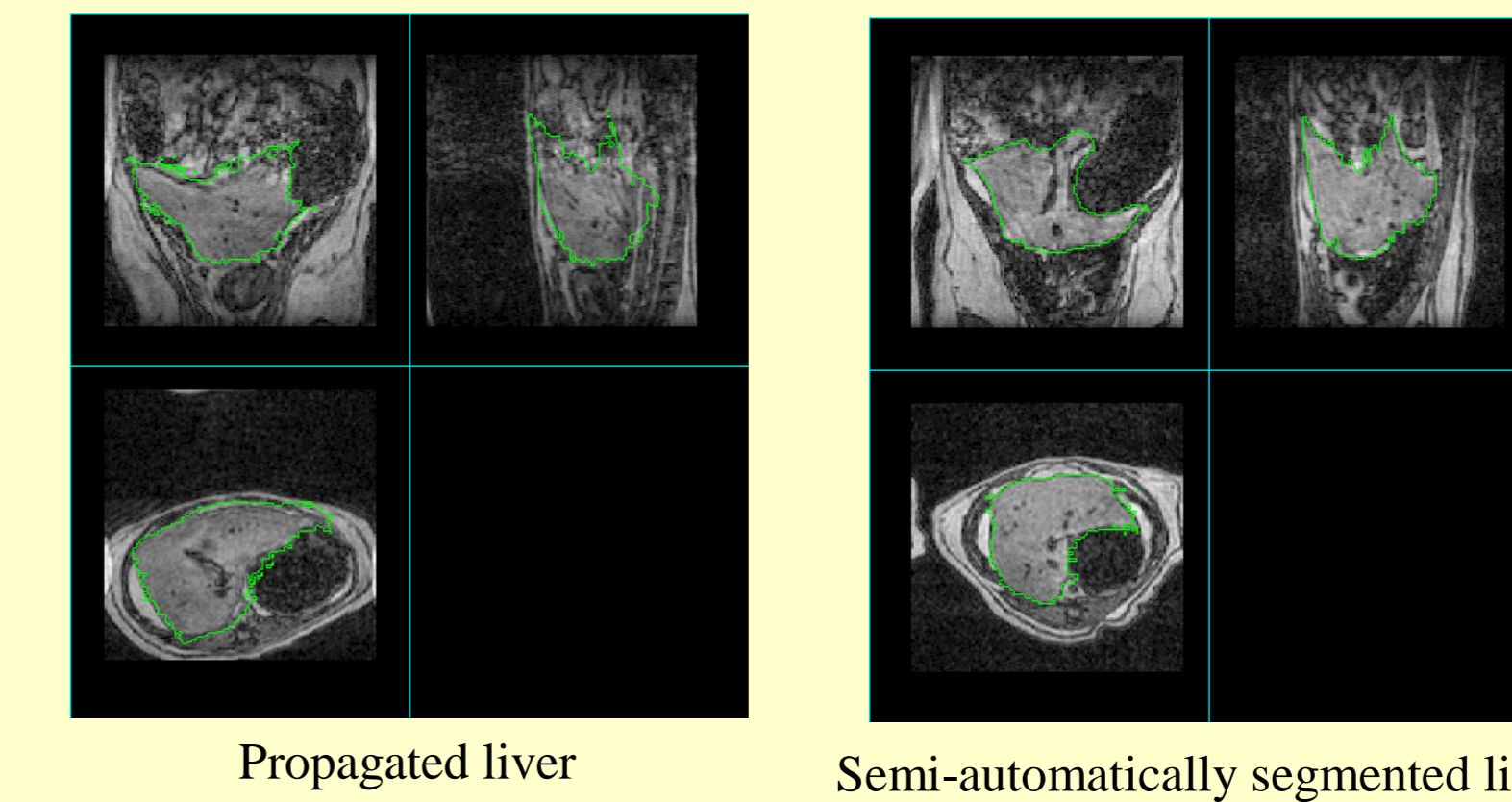


Fig 1: Comparison of automatically propagated and manually segmented liver.

Table 1 shows liver volume measurements (mm³) for all three subjects. The correlation coefficient (r) for the two sets of measurements, derived from non-rigid registration and semi-automatic segmentation, was 0.59 (n=12).

control	baseline	week 1	week 3	week 8	week 12
Non-Rigid	20821	24175	25267	30859	34720
segment	20821	18243	20249	22225	23269
treated	baseline	week 1	week 3	week 8	week 12
Non-Rigid	17575	19636	18733	39454	20976
segment	17574	15838	15644	17489	17261
treated	baseline	week 1	week 3	week 8	week 12
Non-Rigid	17333	18712	18814	25758	28773
segment	17331	16689	15947	16415	16551

Discussion

- This work demonstrates the potential of segmentation propagation for automatic quantification of liver volume change in response to drugs
- The differences between the propagated and semi-automatic segmentation are because of errors in segmentation and registration
- Registration error is thought to be related to the following:
 1. Low CNR between the liver and adjacent tissue
 2. Insufficient FOV leading to wraparound which confounds matching
 3. Large amounts of deformation due to repositioning

References

- [1] B Dawant et al. TMI 18(10) pp 909-916, 1999
- [2] M. Holden et al. MICCAI 2001, pp 49-56, 2001
- [3] C. Studholme et al. Med Phys 24(1) pp25-35 1997
- [4] D. Rueckert et al. TMI 18(8) pp 712-721, 1999

¹All experiments complied with the Animals (Scientific Procedures) Act 1986 UK.
²See ISMRM 2002 poster 2453 for further details.