# MULTIMODAL REGISTRATION OF NMR-VOLUMES AND HISTOLOGICAL CROSS-SECTIONS OF BARLEY GRAINS ON THE CELL BROADBAND ENGINE PROCESSOR

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Abstract: Representation of developmental gradients in biological structures requires visualization of storage compounds, metabolites or mRNA hybridization patterns in a 3D morphological framework. NMR imaging can generate such a 3D framework by non-invasive scanning of living structures. Histology provides the distribution of developmental markers as 2D cross-sections. Multimodal alignment tries to put such different image modalities into correspondence. Here we compare different methods for rigid registration of 3D NMR datasets and 2D cross-sections of developing barley grains. As metrics for similarity measurements mutual information, cross correlation and overlap index are used. In addition, different filters are applied to the images before the alignment. The algorithms are parallelized, partially vectorized and implemented on the Cell Broadband Engine processor in a Playstation® 3. Evaluation is done by a comparison of the results to a manually defined gold standard of a NMR dataset and a corresponding 2D cross-section of the same grain. The results show, that best alignment is achieved by application of mutual information on sobel-filtered images and, compared to the implementation on a standard single-core CPU, the computation is accelerated by a factor up to 1.95.

## 1 INTRODUCTION

Analysis of developmental processes in the growing barley grain gives insights into regulatory phenomena and helps for enhancing seed quality and breeding more robust and useful barley varieties. The analysis of developmental gradients requires stacks of 2D slices obtained by histological standard procedures at certain developmental stages. Putting these 2D slices into spatial correspondence enables the visualization of developmental gradients at this stage. For the correct determination of the spatial position of each slice we have generated 3D datasets of barley grains at different developmental stages by Nuclear Magnetic Resonance (NMR) imaging. The 3D datasets serve as spatial frameworks to register the 2D slices, which require the registration of multimodal data.

The registration of multimodal images, which are obtained from different imaging techniques, is one of the important applications in biological and medical image processing. Different imaging techniques show different aspects of anatomy or functional activity, so that optimal registration puts heterogeneous information into the same spatial framework. Clinical applications like comparing images of the human brain, e.g. obtained by NMR imaging and Positron Emission Tomography (PET) (Thevenanz and Unser, 2000) spurred the investigation of multimodal alignment algorithms.

For correct alignment the correspondence of both multimodal images has to be found. In case of rigid alignment, one image is held fixed and the floating image is translated and rotated. Automatic

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approaches determine the correct translation and rotation based on a similarity function, which measures the degree of correspondence between the fixed and the floating image. The similarity function can rely on differences in intensity like cross correlation (van den Elsen, 1994) or gradient information (Maintz, et al., 1996). In multimodal image alignment mutual information is mainly used as similarity measurement (Maes, et al., 2003; Pluim, et al., 2003). The combination of intensity gradients and mutual information is also used in medical image processing (Pluim, et al., 2000).

Implementations of alignment algorithms need usually much computation time, therefore ways for acceleration are searched. The upcoming of multi-core processors motivates the exploitation of inherent parallelisms in many algorithms dealing with images. The Cell Broadband Engine (CBE) Processor, developed by Sony, Toshiba and IBM, is a heterogeneous multicore-processor, consisting of one PowerPC Processor Element (PPE) and eight Synergistic Processor Elements (SPE). The SPE are optimized for calculations, whereas the PPE is more suitable for running operating systems. By running Linux on a Playstation® 3 console only six SPEs are available, but this system gives the inexpensive opportunity to unleash the power of an amazing state-of-the-art multi-core processor. We have implemented different 2D/3D multimodal alignment algorithms on the Playstation® 3 and on standard hardware and compared the computation times. The algorithms were tested by registration of a cross-section of a barley grain to a corresponding NMR volume and the alignment results were compared to a gold standard, which was obtained by manual alignment.

# 2 MATERIAL & METHODS

For this study a 3D NMR dataset of a whole barley grain at 7 days after flowering was obtained with a Bruker DMX 400 spectrometer (Bruker, Rheinstetten, Germany). The image resolution was 31 µm along the axial and 16 µm along the transverse directions. The dimension of the dataset was 256 x 175 x 512 voxels. The 2D cross-section was obtained by standard histological procedures and was digitized with an original dimension of 1600 x 1200 pixel. It was converted into grayvalues and scaled to meet the pixelsize of the NMR dataset. The backgrounds in both images were manually corrected.

## 2.1 Alternative Preprocessing

The reduction of noise was realized by application of a median filter with a filter radius of 2.0. Alternatively, the contrast was enhanced by histogram equalization. In case of the median-filtered images, optionally the gradient information was extracted to detect the contours of structures. For this task a sobel filter with a 5 x 5 mask was applied.

## 2.2 Similarity Functions

Most prominent in multimodal registration is the application of mutual information as similarity function. Mutual information measure the degree of dependence of a random variable to another by comparing the probability distributions. Given two probability distributions $p_T(t)$ and $p_F(f)$ and the joint probability $p_{TF}(t,f)$ of the target image $T$ and the floating image $F$, the normalized mutual information $NMI$ is defined as (Maes, et al., 2003):

$$NMI(T,F) = \sum_{t,f} p_{TF}(t,f) * \log\left(\frac{p_{TF}(t,f)}{p_T(t) * p_F(f)}\right) \quad (1)$$

If image $T$ and image $F$ are perfectly aligned, this function should give the highest signal.

The linear cross correlation coefficient $CC$ compares the similarity of the intensity distributions $g(t_i)$ and $g(f_i)$ between both images $T$ and $F$:

$$CC(T,F) = \frac{\sum_i g(t_i) * g(f_i)}{\sqrt{\sum_i g(t_i)^2} * \sqrt{\sum_i g(f_i)^2}} \quad (2)$$

The index $i$ denotes the position. The comparison of the gray value images should lead to bad results, because same structures in multimodal images tend to be visualized by different gray values. If the gradient information is used, contours are matched and should improve the results.

The last similarity function used in this paper is the overlap index $OI$, which describes the extent of the image overlap and therefore quantifies the geometric correspondence between both images:

$$OI(T,F) = \frac{2 * N_{TF}}{N_T + N_F} \quad (3)$$

$N_T$ and $N_F$ are the areas of the images $T$ and $F$ and $N_{TF}$ is the area of overlap. $N$ is simply the number of non-background pixels.

The 2D/3D registration procedure was composed by single 2D/2D alignments. At each single z-position in the NMR volume the best alignment was calculated by varying the translation parameters and the rotation angle in the xy-plane. This procedure was done successively for all slices in the NMR volume and the slice with the highest signal of the used similarity function gives the translation parameter in the z-direction. The search space was constrained in x- and y-direction from -30 to 30 pixel translation and from slice 100 to slice 300 in the NMR volume (translation in z-direction). The rotation angle in the xy-plane was constrained to -20° to 20°. Due to the noisy solution space (Pielot, et al., in preparation) all possible combinations of parameters were calculated.

On the Playstation® 3 the Cell-SDK 2.1 was used under Yellow Dog Linux 5.0. The implementations of the similarity functions were vectorized to exploit the SIMD architecture of the SPEs. For comparison, the same algorithms were implemented on a Opteron 850 SMP-System (2.4 GHz) with Linux 2.6.13 and gcc 4.2.0.

## 3 RESULTS

The NMR dataset is depicted in Fig. 1a as a volume rendering. The histological cross-section is shown in Fig. 1b and the same image after scaling and converting into grayvalues in Fig.1c.

The calculations were performed with the unprocessed images and, in case of using *NMI* and *CC* as similarity functions, with median-filtered, contrast-enhanced and sobel-filtered images. Application of *OI* as similarity functions on gradient or filtered images would not change the result due to thresholding. Table 1 shows the results of alignments. The quality $Q$ of alignment is evaluated by

$$Q = k_x e^{-a\Delta x} + k_y e^{-a\Delta y} + k_z e^{-a\Delta z} + k_\alpha e^{-a\Delta \alpha} \qquad (4)$$

with $k_{\{x;y;z;\alpha\}}=\{0,2;0,2;0,2;0,4)$ as weighting factors and a=0,2 as global factor. $\Delta x$, $\Delta y$, $\Delta z$ and $\Delta \alpha$ are the absolute differences between the found alignment parameters and the defined gold standard.

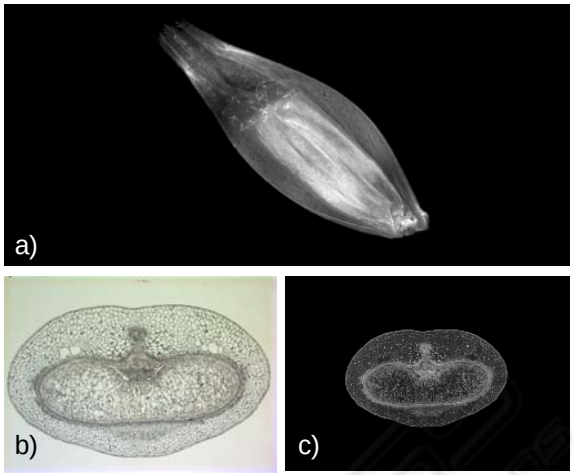


Figure 1: A volume rendering of the target NMR 3D dataset (a). The original histological 2D cross-section from the same grain is depicted in (b) and after converting into grayvalues and scaling in (c). The NMR dataset includes the complete grain (caryopsis + glumes), whereas the cross-section shows only the caryopsis.

Table 1: Found alignment parameters. The manual defined gold standard was: x=9 pixel, y=-5 pixel, z=slice 170 and α=2. The quality $Q$ was calculated with the differences of these parameters to the gold standard.

| Pre-processing | Similarity function | x | y | z | α | Q |
|---|---|---|---|---|---|---|
| - | NMI | 1 | 0 | 251 | 3 | 0,45 |
| median | NMI | 1 | 2 | 260 | 0 | 0,36 |
| contrast | NMI | 7 | -3 | 188 | 1 | 0,60 |
| median + sobel | NMI | 10 | -7 | 170 | 0 | 0,77 |
| - | CC | 12 | -3 | 100 | 2 | 0,64 |
| median | CC | 10 | -2 | 103 | 2 | 0,67 |
| contrast | CC | 4 | -30 | 100 | -19 | 0,08 |
| median + sobel | CC | 8 | -1 | 205 | 2 | 0,65 |
| - | OI | 7 | -1 | 203 | 1 | 0,55 |

It can be seen, that *NMI* in combination with gradient images achieved the highest quality value.

The computation times are depicted in Table 2. The simple parallelization and vectorization speeds up the computation time with a factor from 1.26 to 1.95.

Table 2: Computation times for the application of *NMI* as similarity function. Only the results for the unprocessed images are shown.

| Similarity function | Computation time CBE [s] | Computation time Opteron [s] | Speed up factor |
|---|---|---|---|
| NMI | 10,289 | 20,068 | 1.95 |
| CC | 9,963 | 12,518 | 1.26 |
| OI | 7,038 | 10,557 | 1.50 |

Fig. 2 shows the results after application of *NMI* as similarity function on gradient images (x=10 pixel, y=-7 pixel, z=slice 170 and α=0°). The position of the aligned cross-section (in red) is shown in Fig. 2a. Overlays of the aligned cross-section with the corresponding slice of the NMR dataset (slice 170) are depicted in Fig. 2b and c.

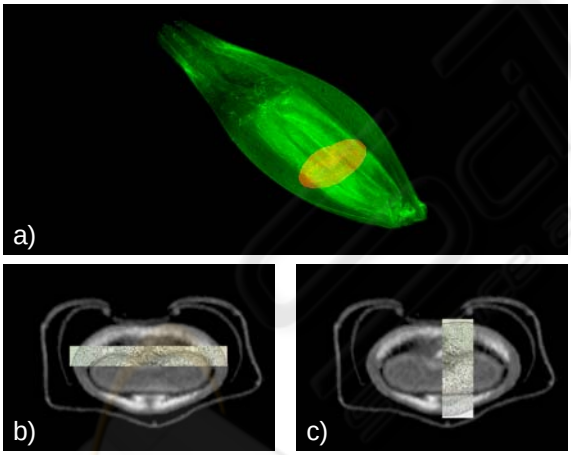


Figure 2: (a) shows a volume rendering of the NMR dataset (green) together with the aligned cross-section (red) after application of NMI on gradient images. Overlays of the NMR-slice 170 with the cross-section are shown in (b) and (c).

## 4 CONCLUSIONS

In this paper, we investigated different approaches for rigid multimodal alignment of 3D NMR image datasets and 2D histological cross-sections. The NMR dataset served as spatial framework and the histological cross-section was automatically aligned at an optimal position within this 3D dataset. The results were compared to a manually defined gold-standard. Best results were achieved by application of normalized mutual information to gradient images. This finding corresponds to results of other authors (Butz and Thiran, 2001; Haber and Modersitzki, 2004), but is shown here for the first time for non-medical images.

Simple parallelization of the algorithms for the CBE processor in a Playstation 3 leads to a speed up factor about 2, compared to a standard CPU.

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