# Reconstruction of liver blood vessel network spanning multiple ultrasound volumes using point cloud registration

Kaho Takahashi<sup>1†</sup>, Koki Tanaka<sup>1</sup>, Takeru Kurihara<sup>1</sup>, Yoshihiro Edamoto<sup>2</sup>, and Kohji Masuda<sup>1\*</sup>

(<sup>1</sup>Tokyo Univ. of Agriculture and Technology; <sup>2</sup>Secomedic Hospital)

## 1. Introduction

Drug delivery systems (DDS), which aim to deliver and concentrate drug to target area in human body, has a potential to reduce side effects. We have been developing a technique<sup>1,2</sup> to actively control microbubbles using acoustic radiation force in order to apply to DDS. Thus, we aim to reconstruct a shape of blood vessel network (BVN) to recognize treatment area in advance by processing ultrasound images or volumes. Since the size of ultrasound volume was limited, we developed a system to extend the area of BVNs by combining multiple BVN volumes individually extracted ultrasound volumes <sup>3)</sup>. Also, we developed a system to register the shape of BVNs between a preoperatively constructed ultrasound volume and an intraoperatively obtained ultrasound image<sup>4)</sup>.

However, since previous methods required adjustment manually, there was a limitation in the reliability in a shape of reconstructed BVNs. Therefore, this study attempts to realize an automatic and robust augmentation by introducing a method of point cloud registration (PCR) to register between multiple BVNs, which replaces the conventional connected components to dispersed point cloud. In this report, we present our initial attempt to extend the BVNs originated ultrasound volumes using PCR.

#### 2. Method

**Fig.1** shows an overview of PCR, which is a process of integrating a source point cloud into the coordinates of a target point cloud. In the rigid registration, the combination between nearest points was chosen to maintain the position relationship in each point cloud without a deformation, whereas the non-rigid registration takes a deformation into account. In this study, we adopted three PCR methods of Iterative Closest Point (ICP) <sup>5)</sup>, Random Sample Consensus (RANSAC) <sup>6)</sup>, and Coherent Point Drift (CPD) <sup>7)</sup>, where the former two methods are rigid registrations, and the latter one is a non-rigid registration.

The method of ICP calculates nearest neighbor points between the source and the target to update a simultaneous transformation matrix. The method of RANSAC is more robust method than ICP, where a hypothetical homogeneous transformation matrix is obtained considering an average distance between corresponding points less than a threshold. The method of CPD formulates a likelihood maximization of a probabilistic model, where a deformed source point cloud is assumed to be centroids of a Gaussian mixture model and the outlier points are not deformed.



Fig.1 Comparison of the process between rigid and nonrigid registrations.

First, the source and target volumes are transformed into the solid and hollow point clouds, which are indicated in **Fig.2** as a cross-section of blood vessel. **Fig.3** shows the flowchart of the proposed method. We performed the rigid registration by directly connecting between RANSAC and ICP with the solid point clouds of the source and target volumes to obtain the homogeneous transformation matrix and the Output A. Then, the homogeneous transformation matrix is utilized to the non-rigid registration with the hollow point clouds of the source and target volumes. Finally, CPD conducted to obtain Output B.



E-mail: <sup>†</sup>s240527w@st.go.tuat.ac.jp \*ultrason@cc.tuat.ac.jp



Fig.3 Flowchart of the proposed method.

### 3. Results

First, we produced an artificial blood vessel model (in silico) with Y-shape to simulate the proposed PCR. The spacing between the points was established to 0.5 mm. **Fig.4** shows the position relationships of source and target in the initial position, output A, and output B. The distance and the angle between the source and the target were set to 15 mm and 10 degree, respectively.



Fig. 4 Position relationships of source (blue) and target (red) of artificial blood vessel model: (a) initial position, (b) output A, and (c) output B.

We obtained multiple ultrasound volumes of healthy human liver (23 y.o., male) using an echography (EPIQ Elite, Philips Inc.) with a threedimensional probe (X6-1), where the conditions were B-mode gain of 60%, depth of 150 mm, and mechanical index of 1.0. While the ultrasound volumes were recorded, the global coordinates of the probe were acquired using an optical position sensor (Polaris, NDI Inc.). The three-dimensional shape of the BVN was extracted manually in this procedure. Since the voxel spacing in the original volume was (x, y, z) = (0.369, 0.316, 0.545) mm, we reduced the density in a hollow point cloud 10 times lower than a solid point cloud. **Fig.5** shows the position relationships as the similar combination to Fig.4.



Fig.5 Position relationships of source (blue) and target (red) BVNs of human liver (portal vein and hepatic vein) : (a) initial position, (b) output A, and (c) output B...

In both results, although the rigid registration performed so that the common structures in the source and the target matched, the position correspondence was insufficient. In contrast, the non-rigid registration deformed to minimize the differences between the source and target, where the effectiveness of the proposed method was confirmed. In the result of human liver, the deformation was limited to the points that were commonly contained in the source and target, without deforming the independently possessing points.

#### 4. Conclusions

In this study, we proposed a method of nonrigid PCR and verified the effectiveness by comparing with rigid PCR using an artificial model and BVNs of human liver. In both results, the source point cloud was properly registered to the target point cloud with a smooth extension. Since the proposed method does not require any manual work, we consider to expand these procedures to include machine learning.

#### References

- 1) T. Chikaarashi, et al: Jpn. J. Appl. Phys., 61, SG1071, 2022.
- 2) H. Ushimizu, et al: Jpn. J. Appl. Phys., 57, 07LF21, 2018.
- T. Katai, et al: Proc. IEEE Eng. Med. Biol. Conf., 5824-5827, 2019.
- 4) K. Masuda, et al: Current Med. Imaging, 19, 2023.
- 5) P. J. Besl, and N. D. McKay: IEEE Trans. Patt. Anal. and Machine Intel., 14, 2, 239-256, 1992.
- 6) M. A. Fischler and R. C. Bolles: Comm. Assoc. Comput. Machinery, 24, 6, 381-395, 1981.
- A. Myronenko, et al: Adv. Neural Info. Process. Sys. 19, 1009-1016, 2006.