



## Abstract

In this study, postimplant seed displacement errors were analyzed using a softassign point match algorithm. Seed locations in the postimplant CT image dataset were first matched with the seed positions in the treatment plan. A CT scan was taken 2.5 – 6 hours after implantation in four testing cases. The average 3D displacement error was  $0.34 \pm 0.16$  cm (mean  $\pm$  standard deviation of the displacement error), and the percentage of seeds within 0.5 cm discrepancy was 69%. The CT seed locations were matched also with the seed positions estimated using actual needle positions tracked intraoperatively using TRUS. The needle position was taken as the transverse 2D location of the seeds implanted along the needle. The axial seed locations were assigned as in plan. The average displacement error was  $0.31 \pm 0.17$  cm, and the percentage of seeds within 0.5 cm discrepancy was 77%. The seed positions in plan and those from estimation were then matched. The average displacement error was  $0.16 \pm 0.11$  cm, and the percentage of seeds within 0.5 cm discrepancy was 99%. This suggests that the seed displacement errors are dominated by the movement of the prostate itself, not by the needle insertion procedure.

## I. Introduction

To compare the seed locations in postimplant CT image dataset against the planned positions, we used a point match method based on the "robust point matching algorithm (RPM)" (Gold et al., 1995; Rangarajan et al., 1996). RPM simultaneously finds homologies (correspondences) and similarity transformation parameters (rotation, translation, and scale) between two sets of points. The effectiveness of the algorithm comes from two techniques: **SoftAssign** and **deterministic annealing**. It is considered robust in that it tolerates noise, and can automatically evaluate all evidence and reject outliers. Also, it possess ma strong ability to overcoming local minima and bad initializations. In our study, we used this algorithm to match planned seed positions to those localized on postimplant CT for 4 patients where the implantation and CT scan were separated by 2.5 – 6 hr. RPM resulted in optimal matching of two point sets so that meaningful, quantitative comparisons could be made directly.

## II. Methods

The problem of alignment was formulated as a mixed variable (binary and continuous) optimization problem: the binary variables are the point correspondences and the continuous variables are the spatial mapping parameters (rotation, translation, and scale). Correspondence is parameterized as a permutation. Parameterized in this manner, for any fixed value of the spatial mapping parameters, the correspondence problem is mapped into the linear assignment problem (Bertsekas and Tsitsiklis, 1989). The SoftAssign, a new technique that first arose in the neural computation literature (Kosowsky and Yuille, 1994), has been shown to find the optimum solution to the assignment problem when embedded in a deterministic annealing scheme. When the correspondence variables are frozen, a standard least-squares problem results that can be solved efficiently for the spatial mapping parameters. The RPM algorithm essentially iterates between solving for the spatial mapping and the correspondence variables at each setting of the temperature (in deterministic annealing). Of course, correspondence is never a permutation due to the presence of outliers. The SoftAssign within deterministic annealing performs outlier rejection in addition to assigning the point correspondences. (Rangarajan et al., 1997)

Assume  $X_i, i = 1, 2, \dots, N_1$ , and  $Y_j, j = 1, 2, \dots, N_2$ , denotes the points in two point sets.  $N_1$  and  $N_2$  are the numbers of points in the sets  $X$  and  $Y$ , respectively. The RPM algorithm minimizes the following objective function:

$$\min_{M, t, s} E(M, t, s) = \sum_{i=1}^{N_1} \sum_{j=1}^{N_2} M_{ij} |X_i - t - sR(Y_j)|^2 + \frac{\gamma}{2} (\log s)^2 - \sum_{i=1}^{N_1} \sum_{j=1}^{N_2} M_{ij} \quad (1)$$

$$\text{subject to } \sum_{j=1}^{N_2} M_{ij} = 1, \forall i \in \{1, \dots, N_1\}, \quad \sum_{i=1}^{N_1} M_{ij} = 1, \forall j \in \{1, \dots, N_2\}$$

$$\text{and } M_{ij} \in \{0, 1\}$$

Equation (1) describes an optimization problem from which the transformation parameters—rotation angle  $\theta$ , translation  $t$  and scale  $s$ —can be obtained by minimization. In Eq. (1),  $\gamma$  is a regularization parameter which controls the degree of departure of the scale parameter from unity. However, Eq. (1) also sets up an optimization problem on the point correspondences. A set of correspondence variables  $\{M_{ij}\}$ —the match matrix—has been defined such that:

$$M_{ij} = \begin{cases} 1 & \text{if point } X_i \text{ corresponds to point } Y_j; \\ 0 & \text{otherwise} \end{cases}$$

$$M_{i(N_2+1)} = \begin{cases} 1 & \text{if point } X_i \text{ is an outlier} \\ 0 & \text{otherwise} \end{cases}$$

$$M_{(N_1+1)j} = \begin{cases} 1 & \text{if point } Y_j \text{ is an outlier} \\ 0 & \text{otherwise} \end{cases}$$

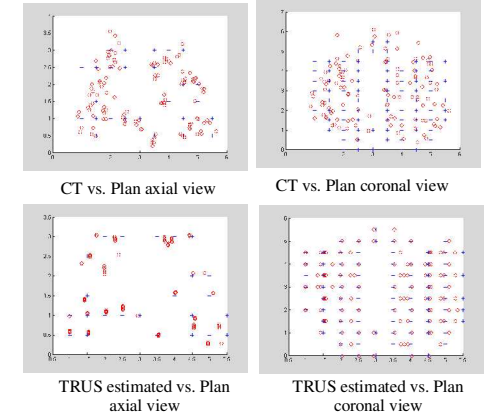
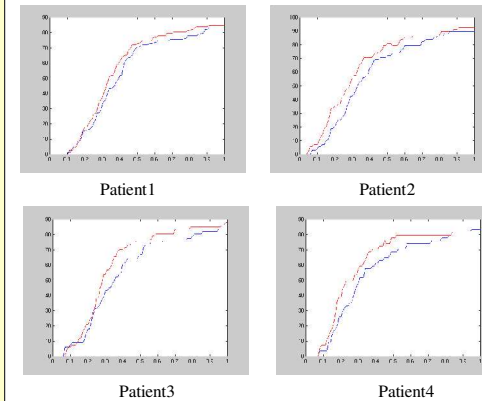
The variable  $M_{ij}$  is a correspondence variable which indicates when homologies have been found or outliers discarded. The above optimization problem in Eq. (1) contains two related optimization problems—one on the spatial mapping between the two point sets and the other on the point-to-point correspondences between the two point sets.

## III. Results

Table 1 shows the 3D displacement errors between different sets of seeds, Plan versus CT localized seeds, plan versus TRUS estimated seeds, and TRUS estimated versus CT localized seeds.

Table 1 3D displacement errors between seed sets of 4 patients

Patient #	Plan vs. CT	Estimated vs. CT	Estimated vs. Plan
#1	0.35 $\square$ 0.14	0.35 $\square$ 0.15	0.15 $\square$ 0.10
#2	0.34 $\square$ 0.18	0.28 $\square$ 0.17	0.15 $\square$ 0.11
#3	0.33 $\square$ 0.15	0.32 $\square$ 0.18	0.15 $\square$ 0.11
#4	0.34 $\square$ 0.18	0.29 $\square$ 0.18	0.17 $\square$ 0.11



Above Figure: shows the seeds localized in CT images (red circle, upper) and estimated in TRUS (lower) transformed to the planning space (seed positions in plan are represented using the blue cross)

Left Figure: shows the sigmoid curve plotting the percent of seeds that is within a series of discrepancies of the 4 patient, using the CT localized seed positions as the gold standard. The blue curve represents the planned seed set, and the red curve represents the TRUS estimated seed set.

## IV. Conclusions

The results shown in this study suggests that the seed displacement errors are caused primarily by the movement of the prostate itself during and after implantation, and not by the needle insertion procedure.

## V. References

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