Baseline Prevalence and Magnitude of Spatial Deviations in a Simulator from the Transrectal Ultrasound Prostate Biopsy Template

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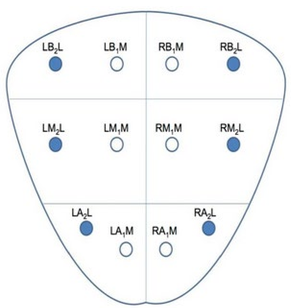
INTRODUCTION

- An ideal transrectal ultrasound prostate biopsy (TRUS PBx) would detect clinically significant prostate cancer, have a high negative predictive value and have good concordance with final pathology [1]
- Although there is an increased use of imaged guided techniques, systematic sampling of a 12-core template (incorporating apical and far-lateral cores) remains the standard in practice [1]



- During TRUS PBx, a mental model for the template is a set of 12 circles (2D representation of spheres construed as the recommended centers for the cylindrical biopsy cores) evenly distributed on a posterior-anterior view of the prostate.
- We set out to quantify the baseline (first attempt at sampling a 12-core set) prevalence and magnitude of deviation from the 12-circle template during simulated side-fire TRUS PBx by trainees and experienced urologic practitioners

Methods

- With IRB approval, 15 participants (12 residents, 3 faculty) performed a 12-core templated TRUS PBx using a mixed reality simulator: tracked TRUS probe (BK 8818), side-firing needle guide, tracked needle gun (Bard Max-Core MC1825).
- We measured the spatial deviation error (mm) of the actual core center from each of the 12 templated centers for each study participant. (Figure 1)
- The centers of the 12 target spheres are set in a plane parallel to, and 7 mm away, from the rectal surface of the prostate.

Templated Prostate Visualization

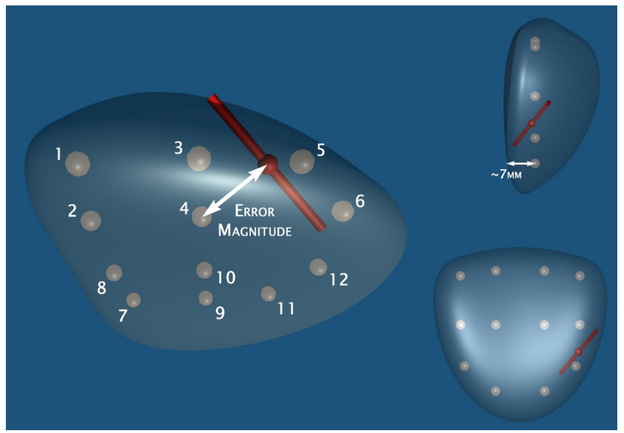


Figure 1. Error is shortest distance between the center of a core (red cylinder) and the center of the intended templated location (gray circles/spheres

RESULTS

- Mean baseline deviations (averaged over 12 cores) ranged from 6.5 to 24.5 mm (Table 1).
- Two-thirds (10/15) of urologist participants achieved a baseline error (averaged over 12 cores) of 11 mm or less.
- The distribution of urologists for different error thresholds (mm) was: ≤7:1; ≤8:5; ≤9:6; ≤10:9; ≤11:10, ≤12:11.

Baseline Side-Fire Point Accuracy

Table 1: Baseline Deviations Averaged Over 12 Cores

Subject	Deviation Mean ± SD (mm)	Deviation Range (mm)	Deviation Median (mm)
1	9 ± 4.7	3.5-16.7	7.7
2	9.4 ± 3	5.1-15	8.9
3	11.7 ± 6.7	3.9-25.3	9.65
4	9.6 ± 3.6	5.7-18.2	8.15
5	8 ± 3.6	3.4-15.1	7.35
6	24.5 ± 8.1	11-40.9	24.1
7	7.1 ± 4.5	1.3-17.9	5.8
8	6.5 ± 2.9	2.2-10.9	6.25
9	13.5 ± 9.3	3.7-35.5	8.8
10	19.1 ± 10.1	2-41.2	17.8
11	10.7 ± 3.8	5.8-18.2	11.25
12	9.1 ± 4	3.9-18.7	8.2
13	20.1 ± 6.3	12.1-30.7	21
14	7.1 ± 3.1	3.2-14.2	6.45
15	7.7 ± 4.8	2-18.2	6.45

DISCUSSION

- We have provided quantitative data about error prevalence and a means to readily measure and display error during templated TRUS PBx in a simulator.
- The baseline deviation in our study was high suggesting that the commonly used 12-circle mental/graphical 2D model may need reconsideration.
- The new TRUS PBx simulator may be helpful in developing and evaluating consensus guidelines about error thresholds and quantitatively comparing different templated TRUS PBx techniques.
- Future studies will aim to validate the TRUS PBx simulator, study effect of training sessions on decreasing deviations and look at clinical outcomes such as cancer detection rates or false negative results before and after training

Acknowledgements

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References

1. Taneja et al., AUA/Optimal Techniques of Prostate Biopsy and Specimen Handling. AUA White Paper. 2015.