Enhancing prostate cancer recurrence prediction using an atlas-based tumour control probability model

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Abstract:

Aim:
This study aimed to evaluate an atlas-based tumour control probability (TCP) model[1,2] for predicting prostate cancer (PCa) recurrence by integrating patient-specific primary radiotherapy and histopathology data. The goal was to investigate segment-wise adjustments to TCP model parameters to derive realistic TCP estimates and improve recurrence prediction.

Method:
Nine patients with available histopathology reports and primary radiotherapy dose-fractionation data were selected from an ethics-approved study (NCT03073278) on re-irradiation of locally recurrent prostate cancer. A population-based biological atlas[3], consisting of voxelised cell density and tumour probability models, was deformably registered to each patient's prostate and segmented based on individual histopathology. Radiosensitivity parameters, including a single PCa grade-independent α/β ratio, four Gleason Pattern (GP)-dependent α values, and nine Gleason Score (GS)-dependent α/β ratios, were derived from a separate cohort using numerical optimization[2]. The TCP model calculated overall TCP and

generated voxel-wise TCP maps. Three segment-wise parameter adjustment approaches (cell density only, with GP-dependent α, and with GS-dependent α/β) were compared to a baseline model without adjustments, with recurrent tumour contours overlaid on TCP maps to assess alignment with lower TCP regions.

Results:

The combination of segment-wise cell density with GS-dependent α/β adjustments demonstrated the strongest predictive performance (Figure1). All nine recurrent PCa patients showed a significant overall TCP reduction, and in seven patients, regions of low TCP corresponded with the relapsed gross tumour volume. Voxel-level histogram analysis and statistically significant volume-weighted TCP differences between tumour and non-tumour regions (Wilcoxon signed-rank test, $p = 0.003$) further supported this outcome. In contrast, adjustments based on GP-dependent α with cell density failed to effectively predict recurrence, while cell density alone provided only moderate improvement.

Conclusion:

The atlas-based TCP model, incorporating patient-specific histopathology, showed potential to enable personalized, biologically-based dose prescriptions.

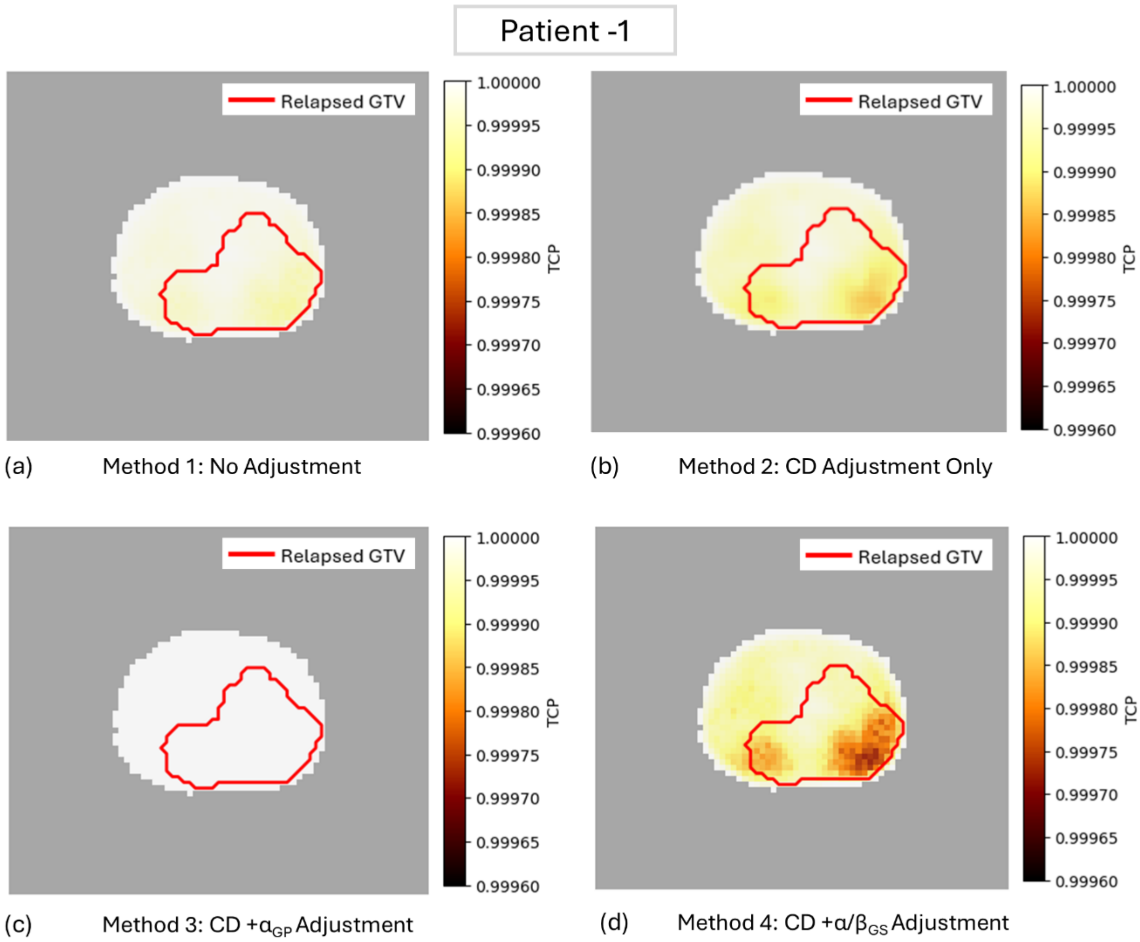

Figure 1: Axial TCP maps for Patient-1 using four methods: (a) No parameter adjustment, (b) Cell density adjustment only, (c) Cell density + GP-dependent α adjustment, and (d) Cell density + GS-dependent α/β adjustment. Warmer regions indicate lower TCP, with the red contour outlining the relapsed Gross Tumor Volume (GTV).

References:

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