

Gaussian Process Regression of HDR Prostate Biopsy Dose for Improved Modelling of Localization-Induced Uncertainty

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ABSTRACT

Purpose: To estimate spatially correlated HDR prostate biopsy dose profiles under localization uncertainty using Gaussian process regression (GPR).

Methods: Twenty-seven biopsy cores were propagated through a Monte Carlo localization framework. Per-voxel MC median dose was used as the GPR target, with voxel-specific MC variance included as heteroscedastic observation noise. Biopsy-specific semivariograms were fit with Matérn covariance models, and model behaviour was evaluated using kernel sensitivity, residual diagnostics, Bland-Altman analysis, and blocked cross-validation.

Results: The selected Matérn 3/2 model preserved along-core dose-profile structure while reducing posterior SD relative to independent voxelwise MC uncertainty. Across the cohort, mean posterior SD reduction was 58.2%, with blocked-CV RMSE = 1.99 Gy and MAE = 1.58 Gy.

Conclusions: GPR converts independent voxelwise MC dose summaries into covariance-informed posterior dose profiles, providing more stable biopsy-scale dosimetric context for future dose-response and assay-linked analyses.

References

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INTRODUCTION

- HDR prostate biopsies sample tissue within steep, spatially varying dose fields.
- Monte Carlo localization propagates biopsy-position uncertainty into voxelwise dose distributions.
- Independent voxelwise summaries ignore axial spatial correlation along the biopsy core.
- GPR provides a natural framework for modelling the latent along-core dose profile as a correlated random field.

Objective: Estimate covariance-informed posterior dose uncertainty along HDR prostate biopsy cores using GPR, and test whether uncertainty reduction is stable under model diagnostics and held-out validation.

METHODS

Patient cohort and input data

- 27 HDR prostate biopsies with Monte Carlo localization trials.
- Dose sampled along voxelized biopsy cores in the prostate reference frame.
- Per-voxel MC median dose used as a robust target statistic.

Spatial correlation model

- Empirical semivariograms quantified dose dissimilarity versus axial separation.
- Matérn covariance models estimated biopsy-specific axial coherence length, partial sill, and nugget variance.

- Selected baseline: Matérn $\nu = 3/2$.

GPR inference

- Ordinary-mean GPR was applied to centered along-core dose targets.
- Voxel-specific MC variance entered as heteroscedastic observation noise.
- Posterior mean and posterior SD were computed along each biopsy core.

Model checks

- Kernel sensitivity: exponential, Matérn 3/2, Matérn 5/2, and RBF.
- Residual diagnostics: standardized residual centering and spread.
- Blocked CV: contiguous held-out core segments tested out-of-sample prediction.

DISCUSSION

- Independent MC summaries quantify localization uncertainty but ignore spatial continuity along the biopsy core.
- GPR reframes biopsy dose as a latent spatial profile with covariance-informed posterior uncertainty.
- SD reduction is interpreted as covariance-informed uncertainty contraction, supported by kernel sensitivity, residual diagnostics, and blocked CV.
- The resulting profiles provide stable biopsy-scale dosimetry descriptors for downstream dose-response and assay-contextualization studies.

RESULTS

Key findings

- Dose uncertainty along HDR prostate biopsy cores is spatially structured, not purely voxel-independent.
- GPR reduced posterior SD by approximately 58% while preserving along-core dose-profile structure.
- Kernel sensitivity, residual diagnostics, and blocked CV supported model stability and held-out prediction.

Figure 1. Representative semivariogram-derived GPR dose profiles. Empirical semivariograms estimate biopsy-specific axial covariance, while GPR preserves along-core dose structure and reduces independent voxelwise MC uncertainty.

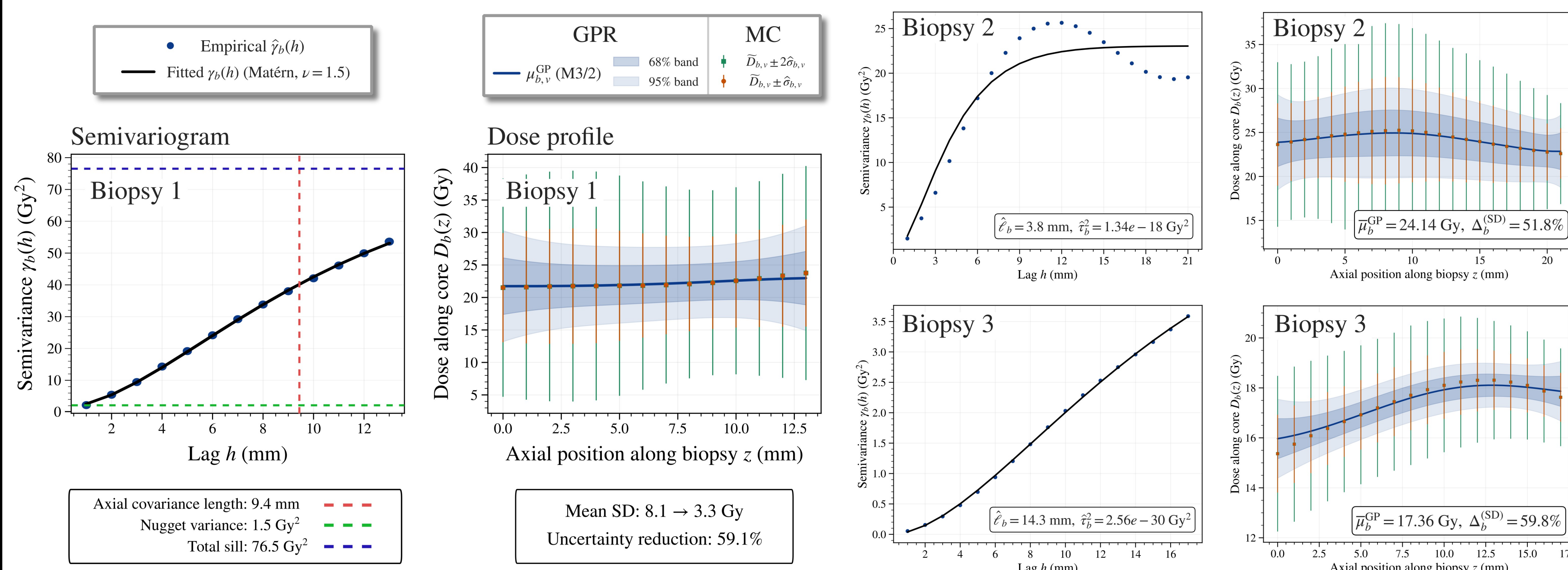


Figure 2. Cohort-level posterior SD reduction. Bland-Altman analysis summarizes proportional reduction in GPR posterior SD relative to independent voxelwise MC SD; table reports model and validation metrics.

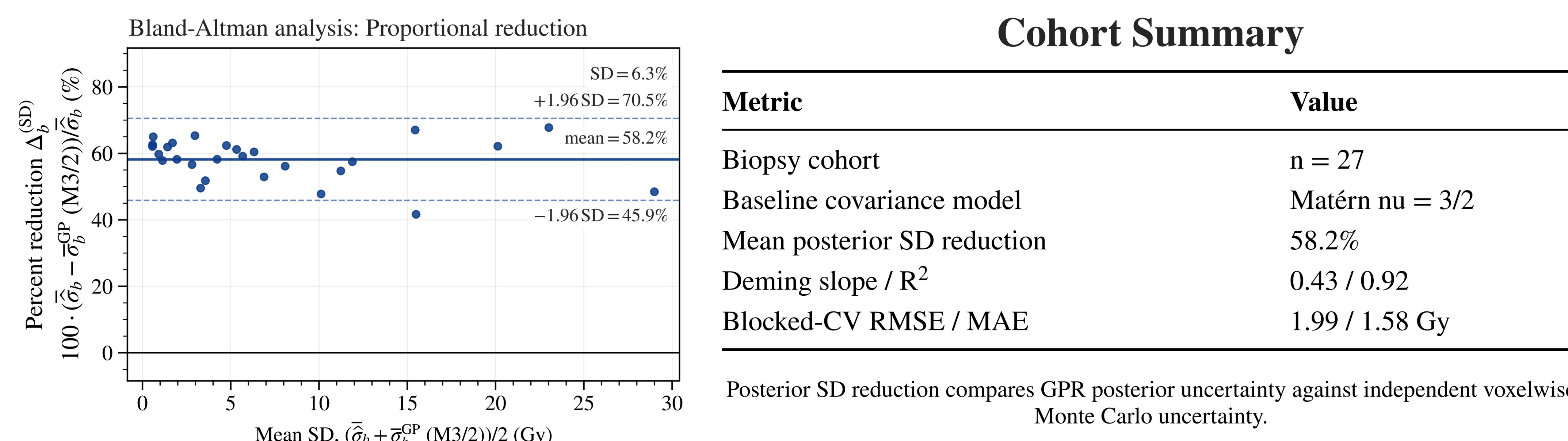


Figure 3. Model diagnostics. Kernel sensitivity assessed dependence on covariance choice; residual diagnostics evaluated calibration of posterior uncertainty; blocked cross-validation tested held-out prediction on contiguous biopsy-core segments.

