

PERSONALIZED COMPUTATIONAL FORECASTING OF PROSTATE CANCER GROWTH DURING ACTIVE SURVEILLANCE

Guillermo Lorenzo¹, Jon S. Heiselman², Michael A. Liss³, Michael I. Miga⁴, Hector Gomez⁵, Thomas E. Yankeelov⁶, Thomas J. R. Hughes⁷, and Alessandro Realì⁸

¹University of Pavia, via Ferrata 3, 27100 Pavia, Italy, Email: guillermo.lorenzo@unipv.it

²Vanderbilt University, 5824 Stevenson Center, Nashville, TN 37232, USA, Email: jon.s.heiselman@vanderbilt.edu

³University of Texas Health San Antonio, 7703 Floyd Curl Drive, San Antonio, TX 78229-3900, USA,
Email: Liss@uthscsa.edu

⁴Vanderbilt University, 5824 Stevenson Center, Nashville, TN 37232, USA, Email: michael.i.miga@vanderbilt.edu

⁵Purdue University, 585 Purdue Mall, West Lafayette, IN 47907-2088, USA, Email: hectorgomez@purdue.edu

⁶The University of Texas at Austin, 201 E 24th St, Austin, TX 78712-1229, USA,
Email: thomas.yankeelov@utexas.edu

⁷The University of Texas at Austin, 201 E 24th St, Austin, TX 78712-1229, USA, Email: hughes@oden.utexas.edu

⁸University of Pavia, via Ferrata 3, 27100 Pavia, Italy, Email: alessandro.reali@unipv.it

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Active surveillance (AS) is a feasible management option for low to intermediate-risk prostate cancer (PCa), which represents almost 70% of newly-diagnosed cases. During AS, patients have their tumor monitored *via* multiparametric magnetic resonance imaging (mpMRI), serum prostate-specific antigen (PSA, an ubiquitous blood biomarker of PCa), and biopsies [1]. If any of these data reveal tumor progression towards an increased clinical risk, the patient is prescribed a curative treatment. However, clinical decision-making in AS is usually guided by population-based protocols that do not account for the unique, heterogenous nature of each patient's tumor. This limitation complicates the personalization of monitoring plans and the early detection of tumor progression, which constitute two unresolved problems in AS. To address these issues, we propose to forecast PCa growth using personalized simulations of an mpMRI-informed mechanistic model.

We describe PCa growth *via* the dynamics of tumor cell density with a diffusion operator, representing tumor cell mobility, and a logistic reaction term, which accounts for tumor cell proliferation [2]. The prostate anatomy is segmented on T2-weighted MRI data, while we delineate PCa and estimate tumor cell density using standard apparent diffusion coefficient (ADC) maps from diffusion-weighted MRI data [1,2]. The model is initialized with data from a first mpMRI scan. A second mpMRI scan allows for the identification of patient-specific model parameters by using a nonlinear least-squares method, which aims at reducing the mismatch between ADC and model estimates of tumor cell density [2]. For validation, we further compare these two estimates of tumor cell density at a third mpMRI scan date. We use isogeometric analysis to perform computer simulations of our model [1,2]. To facilitate modelling, the mpMRI datasets from each patient are co-registered with a biomechanical elastic method that aligns the prostate segmentations [3].

Our preliminary results on a cohort of seven patients show a median concordance correlation coefficient (CCC) and Dice score (DSC) of 0.79 and 0.52, respectively, for the spatial fit of tumor cell density during calibration. For model validation, the corresponding median CCC and DSC are 0.65 and 0.46, respectively. Thus, while further improvement and testing in larger cohorts are required, we believe that our results are promising for the potential use of our methods to personalize AS protocols and predict tumor progression.

REFERENCES

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