Personalized Biopsy Schedules Based on Risk of Gleason Upgrading for Low-Risk Prostate Cancer Active Surveillance Patients*

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Abstract

`Objective`: To develop a model and methodology for predicting the risk of Gleason *upgrading* in prostate cancer active surveillance (AS) patients, and using the predicted risks to create risk-based *personalized* biopsy schedules as an alternative to one-size-fits-all schedules (e.g., annually). Furthermore,

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to assist patients and doctors in making shared decisions of biopsy schedules, by providing them quantitative estimates of the *burden* and *benefit* of opting for personalized versus any other schedule in AS. Last, to externally validate our model and implement it along with personalized schedules in a ready to use web-application.

`Materials and Methods`: We used longitudinal prostate-specific antigen (PSA) measurements, timing and results of previous biopsies, and age at baseline from the world's largest AS study, Prostate Cancer Research International Active Surveillance or PRIAS (7813 patients, 1134 experienced upgrading). We fitted a Bayesian joint model for time-to-event and longitudinal data to the PRIAS dataset. We then externally validated our model in the largest six AS cohorts of the Movember Foundation's Global Action Plan (GAP3) database ($> 20,000$ patients, 27 centers worldwide), covering nearly 73% of all GAP3 patients. We used the predicted upgrading-risks from the validated models to schedule biopsies whenever a patient's risk of upgrading was above a certain threshold. To assist patients in choice of this threshold to compare the resulting schedule with currently practiced schedules, we provided them the timing and the total number of biopsies (burden) planned, and the predicted time delay in detecting upgrading (shorter is better) for each schedule.

`Results`: The cause-specific cumulative upgrading-risk at year five of follow-up was 35% in PRIAS, and at most 50% in GAP3 cohorts. In the PRIAS based model, PSA velocity was a stronger predictor of upgrading

(Hazard Ratio: 2.47, 95%CI: 1.93–2.99) than PSA value (Hazard Ratio: 0.99, 95%CI: 0.89–1.11). Our model had a moderate area under the receiver operating characteristic curve (0.6–0.7) in validation cohorts. The prediction error was moderate (0.1–0.2) in GAP3 cohorts where the impact of PSA value and velocity on upgrading-risk was similar to PRIAS, but large (0.2–0.3) otherwise. Our model required recalibration of baseline upgrading-risk in validation cohorts. We used predicted upgrading-risk from the validated model to create personalized biopsy schedules for real AS patients and implemented them in a web-application (`http://tiny.cc/biopsy`).

`Conclusions`: We successfully developed and validated a model for predicting upgrading-risk, and providing risk-based personalized biopsy decisions, in prostate cancer AS. Personalized prostate biopsies are a novel alternative to fixed one-size-fits-all schedules that may help to reduce unnecessary prostate biopsies while maintaining cancer control. The model and schedules made available via a web-application enable shared decision making of biopsy schedules by comparing fixed and personalized schedules on total biopsies and expected time delay in detecting upgrading.

Keywords: Active Surveillance, Biopsies, Personalized Medicine, Prostate Cancer, Shared Decision Making

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1. Introduction

Patients with low- and very low-risk screening-detected localized prostate cancer are usually recommended active surveillance (AS) instead of immediate radical treatment [1]. In AS, cancer progression is routinely monitored

via prostate-specific antigen (PSA), digital rectal examination (DRE), repeat biopsies, and recently magnetic resonance imaging (MRI). Among these, the strongest indicator of cancer-related outcomes is the biopsy Gleason grade group [2]. When it increases from group 1 (Gleason 3+3) to 2 (Gleason 3+4) or higher, it is called *upgrading* [3]. Upgrading is a key endpoint in AS upon which patients are commonly advised curative treatment [4].

In AS, biopsies are always conducted with a time gap between them. Consequently, upgrading is always detected with a time delay (Figure 1) that cannot be measured directly. For detecting upgrading timely, many patients are prescribed fixed and frequent biopsies, most often annually [5]. Such one-size-fits-all schedules lead to unnecessary biopsies in slow/non-progressing patients. Biopsies are invasive, may be painful, and are prone to medical complications such as bleeding and septicemia[6]. Thus, biopsy burden and patient non-compliance to frequent biopsies [7] have raised concerns regarding the optimal biopsy schedule [8, 9] in AS.

Apart from the confirmatory biopsy at year one of AS [7], opinions and practice regarding the timing of remaining biopsies lack a consensus [10]. Some support periodical one-size-fits-all biopsy schedules instead of schedules based on clinical data and MRI results [11, 5]. Others suggest infrequent periodical schedules (e.g., biennially) [8, 12]. In contrast, many AS programs utilize patients' observed PSA, DRE, previous biopsy Gleason grade, and lately, MRI results to decide biopsies [13, 4, 10]. However, each of these approaches has limitations. For example, one-size-fits-all schedules can lead to many unnecessary biopsies because of differences in baseline *upgrading-risk* across cohorts [8]. Whereas, since observed data has measurement error

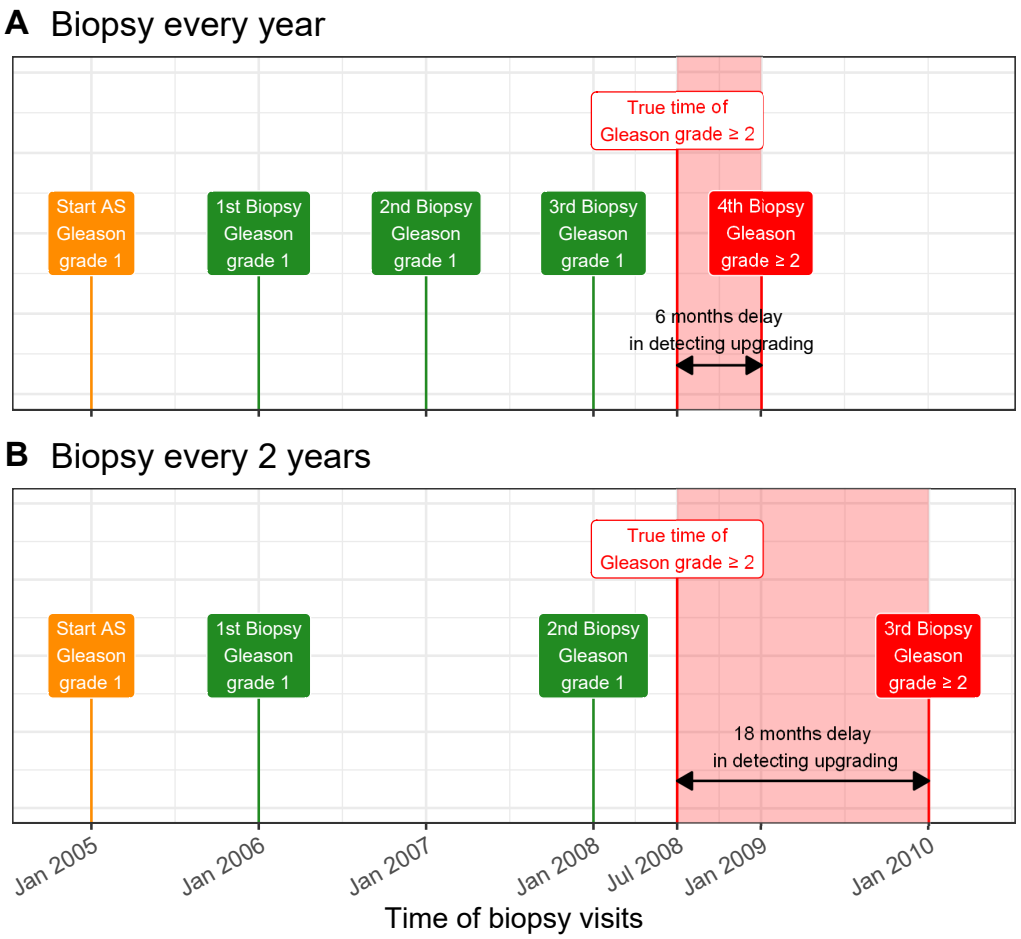

Figure 1: **Trade-off between the timing and number of biopsies (burden) and time delay in detecting Gleason upgrading (shorter is better):** The true time of Gleason upgrading (increase in Gleason grade group from group 1 to 2 or higher) for the patient in this figure is July 2008. When biopsies are scheduled annually (**Panel A**), upgrading is detected in January 2009 with a time delay of six months, and a total of four biopsies are scheduled. When biopsies are scheduled biennially (**Panel B**), upgrading is detected in January 2010 with a time delay of 18 months, and a total of three biopsies are scheduled. Since biopsies are conducted periodically, the time of upgrading is observed as an interval. For example, between Jan 2008–Jan 2009 in **Panel A** and between Jan 2008–Jan 2010 in **Panel B**. The phrase 'Gleason grade group' is shortened to 'Gleason grade' for brevity.

(e.g., PSA fluctuations), a flaw of using it directly is that it may lead to poor decisions. Also, typically such decisions rely only on the latest data point and ignore previous repeated measurements. A novel alternative that counters these drawbacks is first processing patient data via a statistical model, and subsequently using model predicted upgrading-risks to create *personalized* biopsy schedules [10] (Figure 2). While, upgrading-risk calculators are not new [14, 15, 16, 17], not all are personalized either. Besides, they do not specify how risk predictions can be exploited to create a schedule.

The work is motivated by the problem of scheduling biopsies in AS, and our goal is two-fold. First, we want to assist practitioners in using clinical data in biopsy decisions in a statistically sound manner. To this end, we plan to develop a robust, generalizable statistical model that provides reliable individual upgrading-risk in AS. Subsequently, we will employ these predictions to derive risk-based personalized biopsy schedules. Our second goal is to enable shared decision making of a biopsy schedule. We intend to achieve this by allowing patients and doctors to compare the *burden* and *benefit* (Figure 1) of opting for personalized schedules versus periodical schedules versus schedules based on clinical data. Specifically, we propose timing and number of planned biopsies (more/frequent are burdensome), and the expected time delay in detecting upgrading (shorter is beneficial) for any given schedule. In this whole process, we want to capture the maximum possible information from the available data. Thus, we will exploit all repeated measurements of patients, previous biopsy results, baseline characteristics, and keep our model flexible to accommodate novel biomarkers in the future. To fit this model, we will use data of the world's largest AS study, Prostate Cancer

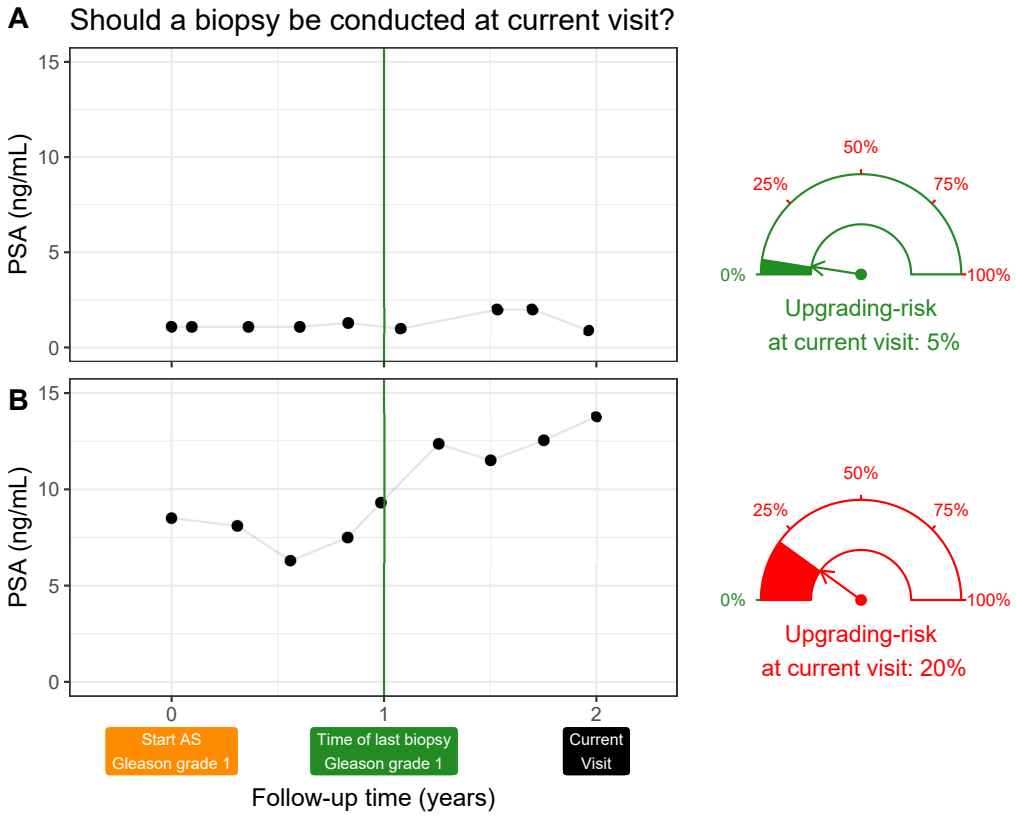

Figure 2: **Motivation for personalized upgrading-risk based biopsy decisions**: To combine patients' complete longitudinal data and results from previous biopsies into estimates for risk of Gleason upgrading and using these estimates to schedule biopsies. For example, Patient A (**Panel A**) and B (**Panel B**) had their latest biopsy at year one of follow-up (green vertical line). Patient A's prostate-specific antigen (PSA) profile remained stable until his current visit at year two, whereas patient B's profile has shown a rise. Consequently, patient B's upgrading-risk at the current visit (year two) is higher than that of patient A. This makes patient B a more suitable candidate for biopsy than Patient A. Risk estimates in this figure are only illustrative.

Research International Active Surveillance (PRIAS). To evaluate our model, we will externally validate it in the largest six AS cohorts from the Movember Foundation's Global Action Plan (GAP3) database [18]. Last, we aim to implement the validated model and methodology in a web-application.

2. Patients and Methods

2.1. Study Cohort

For developing a statistical model to predict upgrading-risk, we used the world's largest AS dataset, Prostate Cancer International Active Surveillance or PRIAS [4], dated April 2019 (Table 1). In PRIAS, biopsies were scheduled at year one, four, seven, ten, and additional yearly biopsies were scheduled when PSA doubling time was between zero and ten years. We selected all 7813 patients who had Gleason grade group 1 at inclusion in AS. Our primary event of interest is an increase in this Gleason grade group observed upon repeat biopsy, called *upgrading* (1134 patients). Upgrading is a trigger for treatment advice in PRIAS. Also, 2250 patients were provided treatment based on their PSA, the number of biopsy cores with cancer, or anxiety/other reasons. However, our reasons for focusing solely on upgrading are that upgrading is strongly associated with cancer-related outcomes, and other treatment triggers vary between cohorts [10].

For externally validating our model's predictions, we selected the following largest (by the number of repeated measurements) six cohorts from Movember Foundation's GAP3 database [18] version 3.1, covering nearly 73% of the GAP3 patients: the University of Toronto AS (Toronto), Johns Hopkins AS (Hopkins), Memorial Sloan Kettering Cancer Center AS (MSKCC),

King's College London AS (KCL), Michigan Urological Surgery Improvement Collaborative AS (MUSIC), and University of California San Francisco AS (UCSF, version 3.2). Only patients with a Gleason grade group 1 at the time of inclusion in these cohorts were selected. Summary statistics are presented in Supplementary A.2.

Choice of predictors:. In our model, we utilized all repeated PSA measurements, timing and previous biopsy Gleason grade, and age at inclusion in AS. Other predictors such as prostate volume, MRI results may also be important. While MRI is already used for targeting biopsies, but currently, there are arguments both for and against its use in deciding the time of biopsies [13, 11, 19]. MRI is still a recent addition in most AS protocols, and thus, repeated MRI data is very sparsely available in both PRIAS and GAP3 databases to make a stable prediction model. Prostate volume data is also sparsely available, especially in validation cohorts. Based on these reasons, we did not include them in our model. However, the model we propose next is extendable to include MRI and other novel biomarkers in the future.a

2.2. Statistical Model

Modeling an AS dataset such as PRIAS, posed certain challenges. First, PSA was measured longitudinally, and over follow-ups, it did not always increase linearly. Also, PSA was available only until a patient observed upgrading. Hence, we need to accommodate the within-patient correlation for PSA, the association between the Gleason grades and PSA profiles of a patient, and handle missing PSA measurements after a patient experienced upgrading. Second, since the PRIAS biopsy schedule uses PSA, a patient's observed

Table 1: **Summary of the PRIAS dataset as of April 2019**. The primary event of interest is upgrading, that is, increase in Gleason grade group from group 1 [2] to 2 or higher. IQR: interquartile range, PSA: prostate-specific antigen. Study protocol URL: `https://www.prias-project.org`

Characteristic	**Value**
Total centers	> 100
Total patients	7813
Upgrading (primary event)	1134
Treatment	2250
Watchful waiting	334
Loss to follow-up	249
Death (unrelated to prostate cancer)	95
Death (related to prostate cancer)	2
Median age at diagnosis (years)	66 (IQR: 61–71)
Median maximum follow-up per patient (years)	1.8 (IQR: 0.9–4.0)
Total PSA measurements	67578
Median number of PSA measurements per patient	6 (IQR: 4–12)
Median PSA value (ng/mL)	5.7 (IQR: 4.1–7.7)
Total biopsies	15686
Median number of biopsies per patient	2 (IQR: 1–2)

time of upgrading also depends on their PSA. That is, while estimating the effect of PSA on the upgrading-risk, we have to adjust for the effect of PSA on the observed times of upgrading. Third, many patients obtained treatment and watchful waiting. Since we considered events other than upgrading as censoring, the model needs to account for patients' reasons for treatment or watchful waiting (e.g., age, treatment based on observed data). A model that handles these challenges in a statistically sound manner is the joint model for time-to-event and longitudinal data [20, 14, 21].

Our joint model consisted of two sub-models. Namely, a linear mixed-effects sub-model [22] for longitudinally measured PSA (log-transformed), and a relative-risk sub-model (similar to the Cox model) for the interval-censored time of upgrading. Patient age was used in both sub-models. Whereas, results and timing of the previous negative biopsies were used only in the risk sub-model (Panel C, Figure 3). To account for PSA fluctuations [23], we assumed t-distributed measurement errors for PSA. The correlation between PSA measurements of a patient was established using patient-specific random-effects. We fitted a unique curve to the PSA measurements of each patient (Panel A, Figure 3). Subsequently, we calculated the mathematical derivative of the patient's fitted PSA profile (Equation 2, Supplementary A), to obtain his follow-up time specific instantaneous PSA velocity (Panel B, Figure 3). This instantaneous velocity is a stronger predictor of upgrading than the widely used average PSA velocity [24]. We modeled the impact of PSA on upgrading-risk by employing fitted PSA value and instantaneous velocity as predictors in the risk sub-model. However, to adjust these effects for the PSA dependent PRIAS biopsy schedule, we used

a full likelihood method for parameter estimation. This approach also accommodates watchful waiting and treatment protocols that are also based on patient data. Specifically, the parameters of our two sub-models were estimated jointly under the Bayesian paradigm (Supplementary A) using the R package **JMbayes** [25].

2.3. Risk Prediction and Model Validation

Our model provides predictions for upgrading-risk over the entire future follow-up period of a patient (Panel C, Figure 3). However, we recommend using predictions after year one. This is because most AS programs recommend a confirmatory biopsy at year one, especially to detect patients who may be misdiagnosed as low-grade at inclusion in AS. The model also automatically updates risk-predictions over follow-up as more patient data becomes available (Figure 5, Supplementary B). We validated our model internally in the PRIAS cohort, and externally in the largest six GAP3 database cohorts. We employed calibration plots [26, 27] and follow-up *time-dependent* mean absolute risk prediction error or MAPE [28] to graphically and quantitatively evaluate our model's risk prediction accuracy, respectively. We assessed our model's ability to discriminate between patients who experience/do not experience upgrading via the time-dependent area under the receiver operating characteristic curve or AUC [28].

The aforementioned *time-dependent* AUC and MAPE [28] are temporal extensions of their standard versions [27] in a longitudinal setting. Specifically, at every six months of follow-up, we calculated a unique AUC and MAPE for predicting upgrading-risk in the subsequent one year (Supplementary B.1). For emulating a realistic situation, we calculated the AUC and

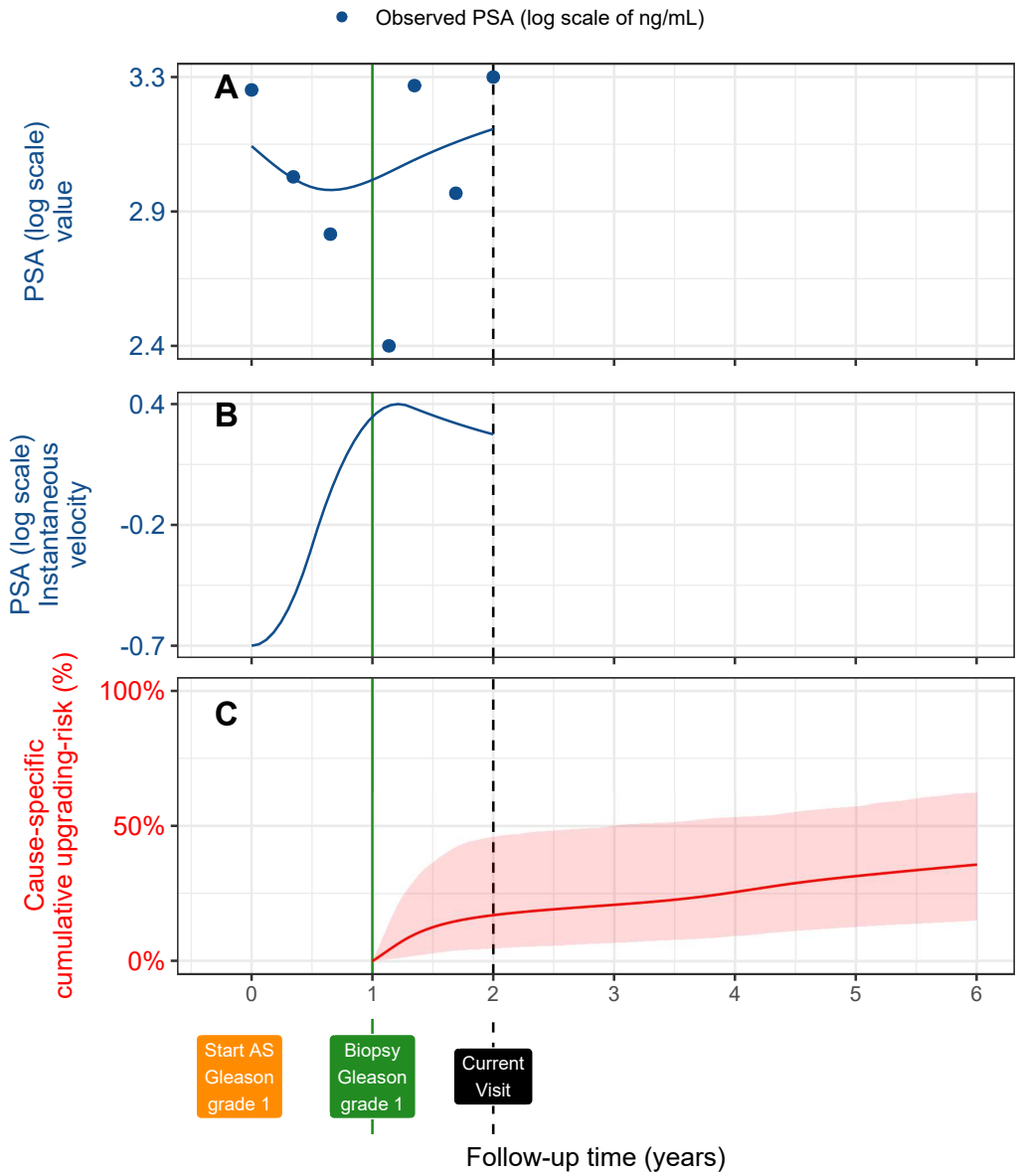

Figure 3: **Illustration of the joint model on a real PRIAS patient**. **Panel A:** Observed PSA (blue dots) and fitted PSA (solid blue line), log-transformed from ng/mL. **Panel B:** Estimated instantaneous velocity of PSA (log-transformed). **Panel C**: Predicted cause-specific cumulative upgrading-risk (95% credible interval shaded). Upgrading is defined as an increase in the Gleason grade group from group 1 [2] to 2 or higher. This upgrading-risk is calculated starting from the time of the latest negative biopsy (vertical green line at year one of follow-up). The joint model estimated it by combining the fitted PSA (log scale) value and instantaneous velocity, and time of the latest negative biopsy. Black dashed line at year two denotes the time of current visit.

MAPE at each follow-up using only the validation data available until that follow-up. Last, to resolve any potential model miscalibration in validation cohorts, we aimed to recalibrate our model's baseline hazard of upgrading (Supplementary B.1), individually for each cohort.

3. Results

The cause-specific cumulative upgrading-risk at year five of follow-up was 35% in PRIAS and at most 50% in validation cohorts (Panel B, Figure 4). In the fitted PRIAS model, the adjusted hazard ratio (aHR) of upgrading for an increase in patient age from 61 to 71 years (25-th to 75-th percentile) was 1.45 (95%CI: 1.30–1.63). For an increase in fitted PSA value from 2.36 to 3.07 (25-th to 75-th percentile, log scale), the aHR was 0.99 (95%CI: 0.89–1.11). The strongest predictor of upgrading-risk was instantaneous PSA velocity, with an increase from -0.09 to 0.31 (25-th to 75-th percentile), giving an aHR of 2.47 (95%CI: 1.93–2.99). The aHR for PSA value and velocity was different in each GAP3 cohort (Supplementary Table 8).

The time-dependent AUC, calibration plot, and time-dependent MAPE of our model are shown in Figure 4, and Supplementary Figure 8. In all cohorts, time-dependent AUC was moderate (0.6 to 0.7) over the whole follow-up period. Time-dependent MAPE was moderate (0.1 to 0.2) in those cohorts where the impact of PSA on upgrading-risk was similar to PRIAS (e.g., Hopkins cohort, Supplementary Table 8), and large (0.2 to 0.3) otherwise. Our model was miscalibrated for validation cohorts (Panel B, Figure 4). Recalibrating the baseline hazard of upgrading in validation cohorts resolved this issue (Supplementary Figure 6). We compared risk predictions from the

recalibrated models, with predictions from separately fitted cohort-specific joint models (Supplementary Figure 7). The difference in predictions was lowest in the Johns Hopkins cohort (impact of PSA on upgrading-risk similar to PRIAS). Comprehensive results are in Supplementary A.2 and B.

3.1. Personalized Biopsy Schedules

We employed the PRIAS based fitted model to create personalized biopsy schedules for real PRIAS patients. Particularly, first using the model and patient's observed data, we predicted his cumulative upgrading-risk (Figure 5) on all of his future follow-up visits (biannually in PRIAS). Subsequently, we planned biopsies on those future visits where his conditional cumulative upgrading-risk was more than a certain threshold (see Supplementary C for mathematical details). The choice of this threshold dictates the timing of biopsies in a risk-based personalized schedule. For example, personalized schedules based on 5% and 10% risk thresholds are shown in Figure 5, and in Supplementary Figure 10–12.

To facilitate the choice of a risk-threshold, and for comparing the consequences of opting for a risk-based schedule versus any other schedule (e.g., annual, PRIAS), we predict expected time delay in detecting upgrading if a schedule is followed. This delay can be predicted for any schedule. For example, in Panel C of Figure 5, the annual schedule has the least expected delay. In contrast, a personalized schedule based on a 10% risk threshold has a slightly larger expected delay, but it also schedules much fewer biopsies. An important aspect of this delay is that it is personalized as well. This is because it is estimated using all available clinical data of the patient (see Supplementary C). That is, even if two different patients are prescribed the

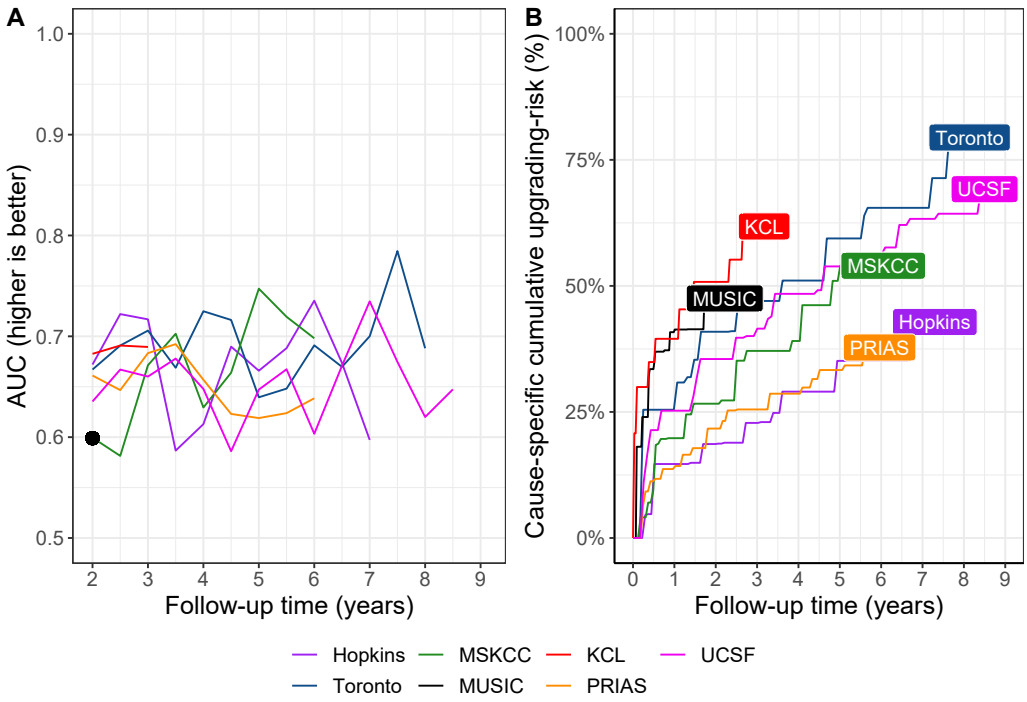

Figure 4: **Model Validation Results**. **Panel A**: time-dependent area under the receiver operating characteristic curve or AUC (measure of discrimination). **Panel B**: calibration-at-large indicates model miscalibration. This is because solid lines depicting the non-parameteric estimate of the cause-specific cumulative upgrading-risk [29], and dashed lines showing the average cause-specific cumulative upgrading-risk obtained using the joint model fitted to the PRIAS dataset, are not overlapping. Recalibrating the baseline hazard of upgrading resolved this issue (Supplementary Figure 6). Full names of Cohorts are *PRIAS*: Prostate Cancer International Active Surveillance, *Toronto*: University of Toronto Active Surveillance, *Hopkins*: Johns Hopkins Active Surveillance, *MSKCC*: Memorial Sloan Kettering Cancer Center Active Surveillance, *KCL*: King's College London Active Surveillance, *MUSIC*: Michigan Urological Surgery Improvement Collaborative Active Surveillance, *UCSF*: University of California San Francisco AS.

same biopsy schedule, their expected delays will be different. While the timing and the total number of planned biopsies denote the burden of a schedule, a shorter expected time delay in detecting upgrading can be a benefit. These two, along with other measures such as a patient's comorbidities, anxiety, etc., can help to make an informed decision of biopsy.

3.2. Web-Application

We implemented the PRIAS based model and recalibrated models for GAP3 cohorts, and personalized schedules in a user-friendly web-application `https://emcbiostatistics.shinyapps.io/prias_biopsy_recommender/`. This application also works on mobile devices. Patient data can be entered in Microsoft Excel format. The maximum follow-up time up to which predictions can be obtained depends on each cohort (Supplementary Table 9). The web-application supports personalized, annual, and PRIAS schedules. For personalized schedules, users can control the choice of risk-threshold and compare the risk-based schedule's timing of biopsies, and expected time delay in detecting upgrading, with annual and PRIAS schedule before making a decision.

4. Discussion

We successfully developed and externally validated a statistical model for predicting upgrading-risk [3] in prostate cancer AS, and providing risk-based personalized biopsy decisions. Our work has four novel features over earlier risk calculators [14, 15]. First, our model was fitted to the world's largest AS dataset PRIAS and externally validated in the largest six cohorts of the Movember Foundation's GAP3 database [18]. Second, the model predicts a

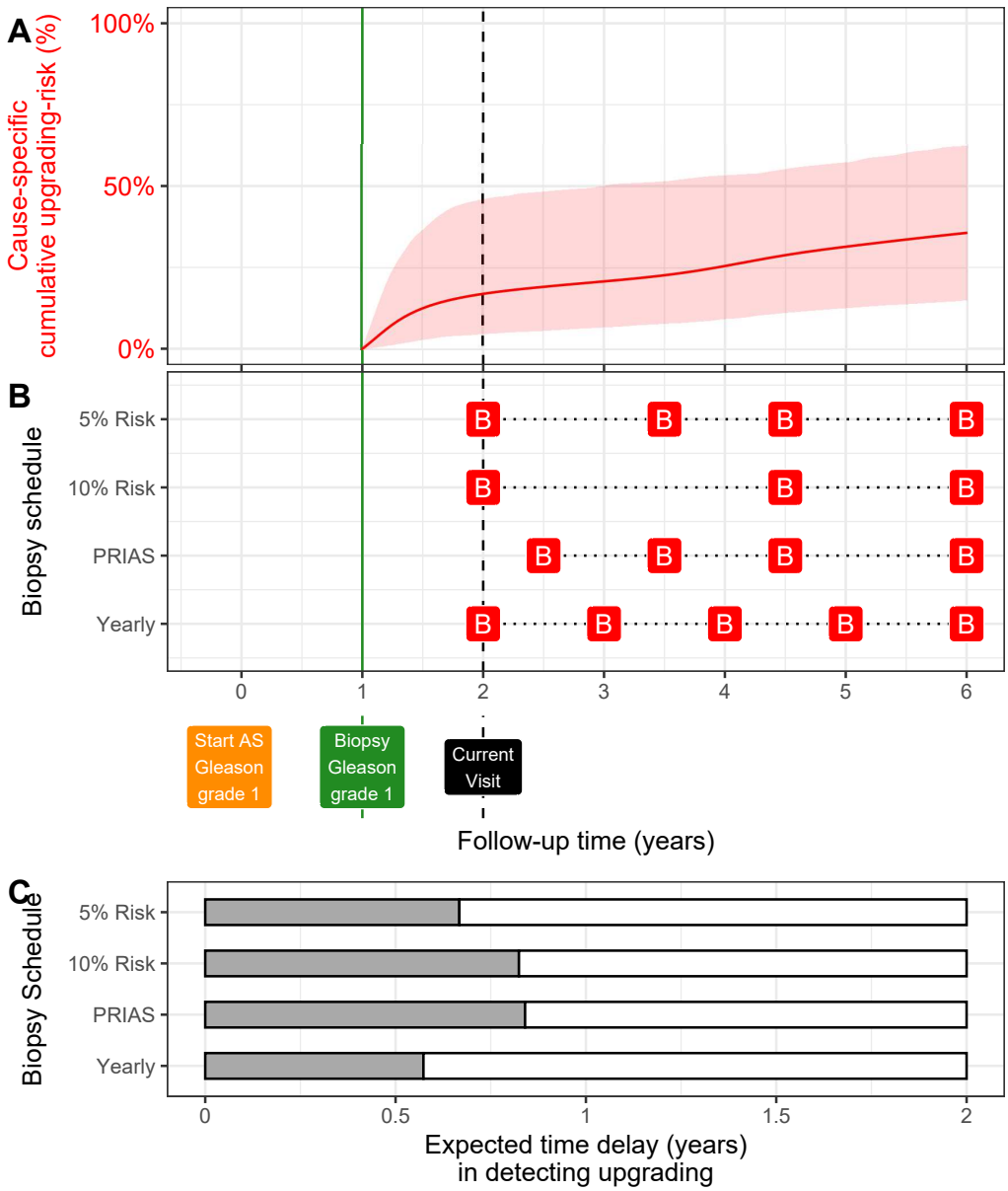

Figure 5: **Illustration of personalized and fixed schedules of biopsies for patient from Figure 3**. **Panel A:** Predicted cumulative upgrading-risk (95% credible interval shaded). **Panel B:** Different biopsy schedules with a red 'B' indicating a future biopsy. Risk: 5% and Risk: 10% are personalized schedules in which a biopsy is planned whenever the conditional cause-specific cumulative upgrading-risk is above 5% or 10% risk, respectively. Green vertical line at year one is the time of the latest negative biopsy. Black dashed line at year two denotes the time of the current visit. **Panel C:** Expected time delay in detecting upgrading (years) if patient progresses before year six. A compulsory biopsy was scheduled at year six (maximum biopsy scheduling time in PRIAS, Supplementary C) in all schedules for a meaningful comparison between them.

patient's current and future upgrading-risk in a personalized manner. Third, using the predicted risks, we created personalized biopsy schedules and also calculated the expected time delay in detecting upgrading (less is beneficial) if that schedule was followed. Thus, patients/doctors can compare schedules before making a choice. Fourth, we implemented our methodology in a user-friendly web-application (`https://emcbiostatistics.shinyapps.io/prias_biopsy_recommender/`) for both PRIAS and validated cohorts.

Our model and methods can be useful for numerous patients from PRIAS and validated GAP3 cohorts. The model utilizes all repeated PSA measurements, results of previous biopsies, and baseline characteristics of a patient. Although we could not include MRI and PSA volume because of sparsely available data in both PRIAS and GAP3 databases, our model is extendable to include them in the near future. The current discrimination ability of our model, exhibited by the *time-dependent* AUC, was between 0.6 and 0.7 over-follow. While this is moderate, it is also so because unlike the standard AUC [27] the time-dependent AUC is more conservative as it utilizes only the validation data available until the time at which it is calculated. The same holds for the time-dependent MAPE (mean absolute prediction error), although it varied much more between cohorts than AUC. In cohorts where the effect size for the impact of PSA value and velocity on upgrading-risk was similar to that for PRIAS (e.g., Hopkins cohort), MAPE was moderate. Otherwise, MAPE was large (e.g., KCL and MUSIC cohorts). We required recalibration of our model's baseline hazard of upgrading for all validation cohorts. The PRIAS and validation cohorts cover nearly 73% of all GAP3 patients.

The clinical implications of our work are as follows. First, the cause-specific cumulative upgrading-risk at year five of follow-up was at most 50% in all cohorts (Panel B, Figure 4). That is, many patients may not require some of the biopsies planned in the first five years of AS. Given the non-compliance and burden of frequent biopsies [7], the availability of our methodology as a web-application may encourage patients/doctors to consider upgrading-risk based personalized schedules instead. An additional advantage of personalized schedules is that they update as more patient data becomes available over follow-up. We have shown via a simulation study [30] that personalized schedules plan, on average, six fewer biopsies compared to annual schedule and two fewer biopsies than the PRIAS schedule in slow/non-progressing AS patients, while maintaining almost the same time delay in detecting upgrading as PRIAS schedule. Personalized schedules with different risk thresholds indeed have different performance. In this regard, to assist patients/doctors in choosing between fixed schedules and personalized schedules based on different risk thresholds, the web-application provides a patient-specific estimate of the expected time delay in detecting upgrading, for both personalized and fixed schedules. We hope that this will objectively address patient apprehensions regarding adverse outcomes in AS. Last, we note that our web-application should only be used to schedule biopsies after the first compulsory confirmatory biopsy at year one of follow-up.

This work has certain limitations. Predictions for upgrading-risk and personalized schedules are available only for a currently limited, cohort-specific, follow-up period (Supplementary Table 9). This problem can be mitigated by refitting the model with new follow-up data in the future. Recently, some

cohorts started utilizing MRI to explore the possibility of targeting visible lesions by biopsy. Presently, the GAP3 database has limited MRI follow-up data available. As more such data becomes available, the current model can be extended to include MRI based predictors. We scheduled biopsies using cause-specific cumulative upgrading-risk, which ignores competing events such as treatment based on the number of positive biopsy cores. Employing a competing-risk model may lead to improved personalized schedules. Upgrading is susceptible to inter-observer variation too. Models which account for this variation [14, 31] will be interesting to investigate further. Even with an enhanced risk prediction model, the methodology for personalized scheduling and calculation of expected time delay (Supplementary C) need not change. Last, our web-application only allows uploading patient data in Microsoft Excel format. Connecting it with patient databases can improve usability. However, a validated upgrading-risk calculator and risk-based biopsy schedules implemented in a web-application is a significant first step towards more informed biopsy decisions in AS.

5. Conclusions

We successfully developed a statistical model and methodology for predicting upgrading-risk, and providing risk-based personalized biopsy decisions, in prostate cancer AS. We externally validated our model, covering nearly 73% patients from the Movember Foundations' GAP3 database. The model made available via a user-friendly web-application (`https://emcbiostatistics.shinyapps.io/prias_biopsy_recommender/`) enables shared decision making of biopsy schedules by comparing fixed and personalized

schedules on total biopsies and expected time delay in detecting upgrading. Novel biomarkers and MRI data can be added as predictors in the model to improve predictions in the future. Recalibration of baseline upgrading-risk is advised for cohorts not validated in this work.

Author Contributions

Anirudh Tomer had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

Study concept and design: Tomer, Nieboer, Roobol, Bjartell, and Rizopoulos

Acquisition of data: Tomer, Nieboer, and Roobol

Analysis and interpretation of data: Tomer, Nieboer, and Rizopoulos

Drafting of the manuscript: Tomer, and Rizopoulos

Critical revision of the manuscript for important intellectual content: Tomer, Nieboer, Roobol, Bjartell, Steyerberg, and Rizopoulos

Statistical analyses: Tomer, Nieboer, Steyerberg, and Rizopoulos

Obtaining funding: Roobol, Steyerberg, and Rizopoulos

Administrative, technical or material support: Nieboer

Supervision: Roobol, and Rizopoulos

Other: none

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Appendix A. Members of The Movember Foundation's Global Action Plan Prostate Cancer Active Surveillance (GAP3) consortium

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