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A Ready To Use Web-Application Providing a Personalized Biopsy Schedule for Men With Low-Risk PCa Under Active Surveillance

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Abstract:	Background: Prostate cancer active surveillance (AS) patients undergo repeat biopsies. Active treatment is advised when biopsy Gleason grade group >= 2 (upgrading). Many patients never experience upgrading, yet undergo biopsies frequently. Personalized biopsy decisions based on upgrading-risk may reduce patient burden. Objective: Develop a risk prediction model and web-application to assist patients/doctors in personalized biopsy decisions. Design, Setting, and Participants: Model development: world's largest AS study PRIAS, 7813 patients, 1134 experienced upgrading; External validation: largest six cohorts of Movember Foundation's GAP3 database (>20,000 patients, 27 centers worldwide); Data: repeat prostate-specific antigen (PSA) and biopsy Gleason grade group. Outcome Measurements, and Statistical Analysis: A Bayesian joint model fitted to PRIAS dataset. This model was validated in GAP3 cohorts using risk prediction error, calibration, area under ROC (AUC). Model and personalized biopsy schedules based on predicted risks were implemented in a web-application. Results and Limitations: Cause-specific cumulative upgrading-risk at year five of follow-up: 35% in PRIAS, at most 50% in GAP3 cohorts. PRIAS based model: PSA velocity was 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). Validation: Moderate AUC (0.55 - 0.75) in PRIAS and GAP3 cohorts. Moderate prediction error (0.1 - 0.3) in GAP3 cohorts where impact of PSA value and velocity on upgrading-risk was similar to PRIAS, but large (0.3 - 0.45) otherwise. Recalibration of baseline risk required for external cohorts. Conclusions: We successfully developed and validated a model for predicting upgrading-risk, and providing risk-based personalized biopsy decisions, in prostate cancer AS. The model made available via a web-application enables shared decision making of biopsy schedules by comparing fixed and personalized schedules on total biopsies and expected time delay in detecting upgrading. Patient Summary: Personalized prostate biopsies are a novel alternative to fixed one-size-fits-all schedules. The underlying statistical models are made available through a user-friendly web-application and may help to reduce unnecessary prostate biopsies while maintaining cancer control.
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A Ready To Use Web-Application Providing a Personalized Biopsy Schedule for Men With Low-Risk PCa Under Active Surveillance*

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Abstract

Background: Prostate cancer active surveillance (AS) patients undergo repeat biopsies. Active treatment is advised when biopsy Gleason grade group ≥ 2 (*upgrading*). Many patients never experience upgrading, yet undergo biopsies frequently. Personalized biopsy decisions based on upgrading-risk may

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reduce patient burden.

`Objective`: Develop a risk prediction model and web-application to assist patients/doctors in personalized biopsy decisions.

`Design, Setting, and Participants`: Model development: world's largest AS study PRIAS, 7813 patients, 1134 experienced upgrading; External validation: largest six cohorts of Movember Foundation's GAP3 database ($> 20,000$ patients, 27 centers worldwide); Data: repeat prostate-specific antigen (PSA) and biopsy Gleason grade group.

`Outcome Measurements, and Statistical Analysis`: A Bayesian joint model fitted to PRIAS dataset. This model was validated in GAP3 cohorts using risk prediction error, calibration, area under ROC (AUC). Model and personalized biopsy schedules based on predicted risks were implemented in a web-application.

`Results and Limitations`: Cause-specific cumulative upgrading-risk at year five of follow-up: 35% in PRIAS, at most 50% in GAP3 cohorts. PRIAS based model: PSA velocity was 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). Validation: Moderate AUC (0.55–0.75) in PRIAS and GAP3 cohorts. Moderate prediction error (0.1–0.3) in GAP3 cohorts where impact of PSA value and velocity on upgrading-risk was similar to PRIAS, but large (0.3–0.45) otherwise. Recalibration of baseline risk required for external cohorts.

`Conclusions`: We successfully developed and validated a model for predicting upgrading-risk, and providing risk-based personalized biopsy decisions, in prostate cancer AS. The model made available via a web-application enables shared decision making of biopsy schedules by comparing fixed and personalized schedules on total biopsies and expected time delay in detecting upgrading.

`Patient Summary`: Personalized prostate biopsies are a novel alternative to fixed one-size-fits-all schedules. The underlying statistical models are made available through a user-friendly web-application and may help to reduce unnecessary prostate biopsies while maintaining cancer control.
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, and repeat biopsies. 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, called *upgrading* [3], patients are commonly advised curative treatment [4].

Usually, AS protocols schedule biopsies periodically. Consequently, up-

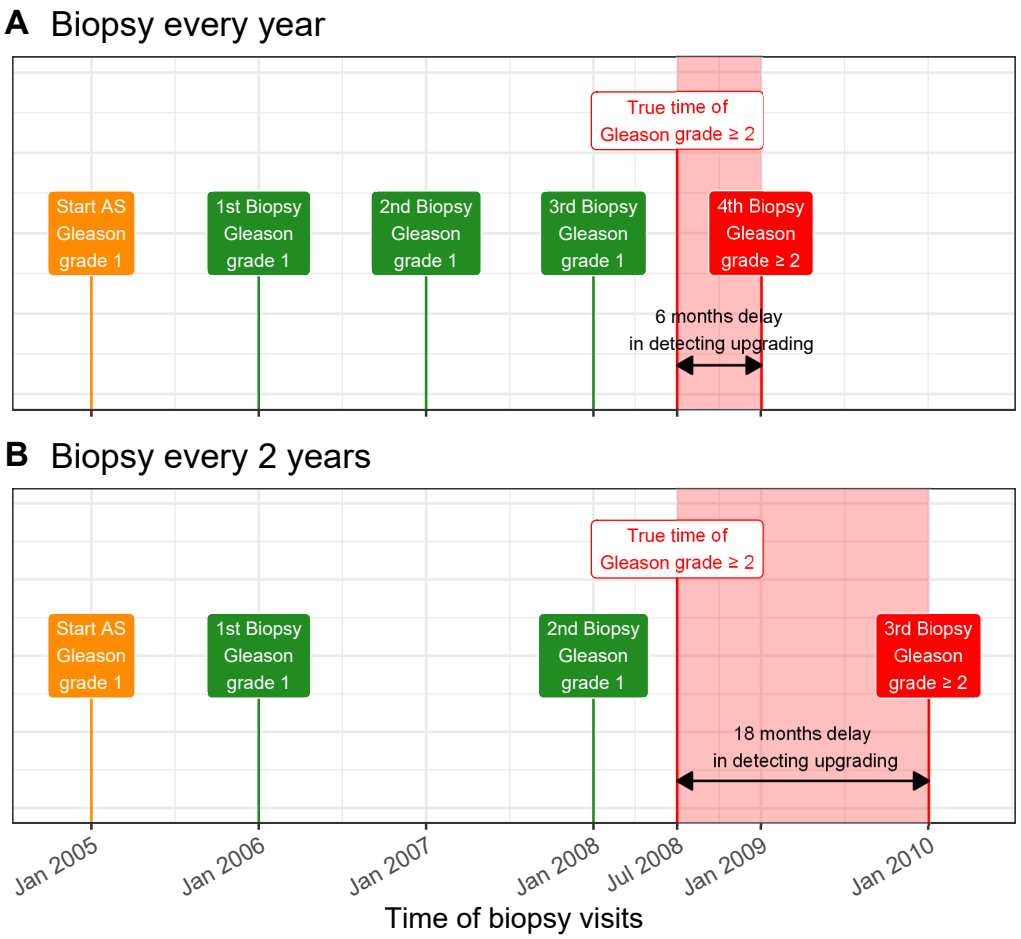

Figure 1: **Trade-off between the number of biopsies and time delay in detecting upgrading (Increase in Gleason grade group from 1 to 2 or higher):** The true time of upgrading for the patient in this figure is July 2008. When biopsies are scheduled annually (**Panel A**), upgrading is detected in January 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.

grading is always detected with a time delay (Figure 1). For detecting upgrading timely, many AS programs schedule fixed and frequent biopsies (e.g., annually) for all patients [5, 6]. However, this leads 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[7]. Biopsy burden and patient non-compliance to frequent biopsies [8] have raised concerns regarding the optimal biopsy schedule [9, 10]. In this regard, in some cohorts, magnetic resonance imaging (MRI) is employed for targeted biopsies and to study its value for tumor monitoring. Although, due to currently limited AS data, MRI's value is not clear. Others have proposed the option of scheduling biopsies infrequently (e.g., biennially) [9, 11]. However, due to differences in baseline upgrading-risk across cohorts [9], fixed biopsy schemes can still lead to many unnecessary biopsies. A promising alternative to fixed schedules are personalized biopsy schedules based on the patient-specific upgrading-risk (Figure 2).

The first challenge in creating personalized biopsy schedules is developing a statistical model to consolidate accumulated patient data (e.g., PSA, previous biopsy results) into predictions for upgrading-risk. Existing upgrading-risk [12, 13] calculators use only the latest PSA measurement of a patient. Comparatively, more information is captured by considering all repeatedly measured PSA, previous biopsy results, and baseline characteristics of a patient. To this end, a suitable model is the joint model for time-to-event and longitudinal data [14, 15, 16]. A joint model predicts upgrading-risk in a personalized manner. However, a subsequent challenge is translating predicted risks into clinical decisions. For example, a 10% upgrading-risk can

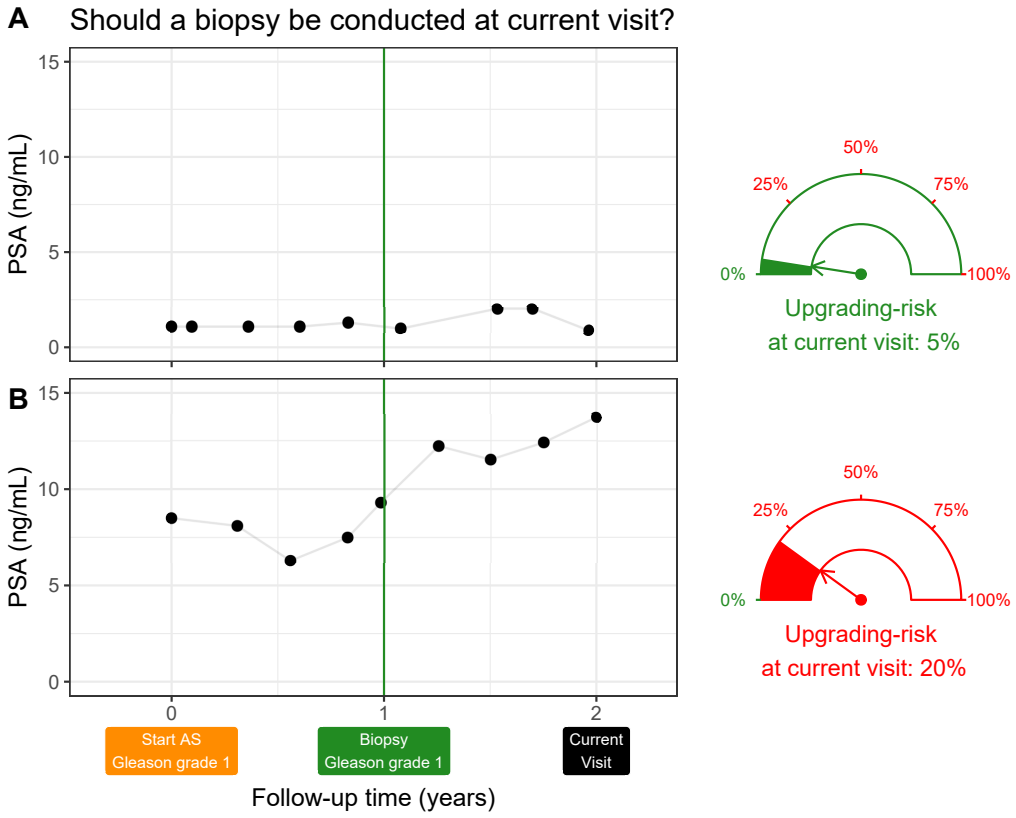

Figure 2: **Motivation for personalized upgrading-risk based decisions of biopsy**: Patient A (**Panel A**) and B (**Panel B**) had their latest biopsy at year one of follow-up (green vertical line). Patient A's prostate-specific antigen (PSA) profile remained stable until his current visit at year two, 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.

be perceived high/low depending upon the patient's age. Patients may also weigh risks of upgrading with the potential *consequences* of another biopsy. Two such relevant consequences (Figure 1) are the timing and the total number of planned biopsies (burden), and the time delay in detecting upgrading (smaller is beneficial). The relative importance of these consequences can vary between the patients, and also within a patient over the follow-up period.

The goal of this work is two-fold. First, to develop a robust, generalizable model that gives reliable estimates for individual upgrading-risk in AS. Second, to utilize the predicted upgrading-risks to create personalized biopsy schedules. To facilitate shared decision making of biopsy schedules, we also intend to provide quantitative estimates of the aforementioned *consequences* of opting for a personalized versus the standard fixed schedule. For developing our model, we will use the world's largest AS dataset PRIAS. Subsequently, we want to externally validate our model in the largest six AS cohorts from the Movember Foundation's GAP3 database [17]. Last, we intend to implement our 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, PSA was measured quarterly for the first two years of follow-up and semiannually thereafter. Biopsies were scheduled at year one, four, seven, and ten of follow-up. Addi-

tional 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 the time of inclusion in PRIAS. 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, number of biopsy cores with cancer, or anxiety/other reasons. Our reasons for focusing solely on upgrading are, namely, upgrading is strongly associated with cancer-related outcomes, and other treatment triggers vary between cohorts [5].

For model validation, we selected the following largest (by number of repeated measurements) six cohorts from Movember Foundation's GAP3 database version 3.1 [17]: University of California San Francisco AS (UCSF, version 3.2), University of Toronto AS (Toronto), Johns Hopkins AS (Hopkins), Memorial Sloan Kettering Cancer Center AS (MSKCC), King's College London AS (KCL), and Michigan Urological Surgery Improvement Collaborative AS (MUSIC). 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.

2.2. Statistical Model

For developing an upgrading-risk prediction model, the data we utilized from the PRIAS cohort was patient age at inclusion in AS, longitudinally measured PSA, timing of repeat biopsies and Gleason grades, and observed time of upgrading. Analysis of this data required modeling the within-patient correlation for PSA, the association between the Gleason grades and PSA

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)

profiles of a patient, and handling missing PSA measurements after a patient experienced upgrading. In such situations, a commonly used model is the joint model for time-to-event and longitudinal data [14, 15, 16].

Our joint model consisted of two sub-models. First, a linear mixed sub-model [18] for longitudinally measured PSA (log-transformed). Second, a relative-risk sub-model (similar to the Cox model) for obtaining the cause-specific upgrading-risk. We included patient age in both sub-models. In the PSA sub-model, 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 [19]. We modeled the impact of PSA on upgrading-risk by employing fitted PSA value and instantaneous velocity as predictors in the risk sub-model. Also, we included the time of the latest negative biopsy in the risk sub-model (Panel C, Figure 3). The parameters of the two sub-models were estimated jointly (Supplementary A) using the R package **JMbayes** [20].

2.3. Risk Prediction and Model Validation

Our model provides predictions for upgrading-risk over the entire future follow-up period of a patient. Predictions also automatically update over follow-up as more patient data becomes available (Figure 5, Supplementary B). We validated our PRIAS based model internally in the PRIAS cohort, and externally in the largest six GAP3 database cohorts. We employed calibration plots [21, 22] and follow-up *time-dependent* mean absolute

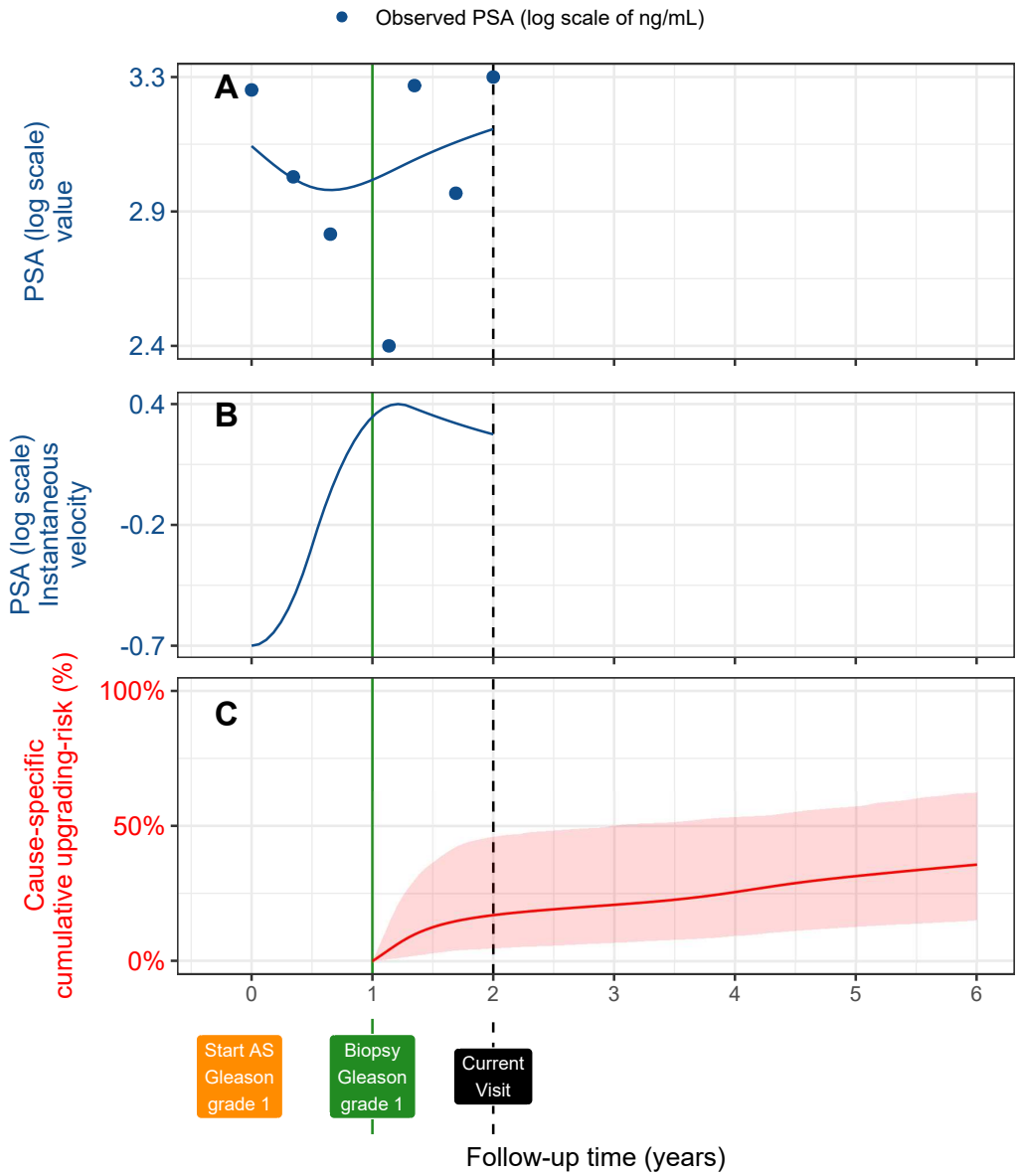

Figure 3: **Illustration of the joint model on a real PRIAS patient**. **Panel A:** Observed PSA (blue dots) and fitted PSA (solid blue line), log-transformed from ng/mL. **Panel B:** Estimated instantaneous velocity of PSA (log-transformed). **Panel C**: Predicted cause-specific cumulative upgrading-risk (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.

risk prediction error or MAPE [23] 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 [23].

The aforementioned *time-dependent* AUC and MAPE [23] are temporal extensions of their standard versions [22] 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 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). Hence, many patients do not require all biopsies planned in the first five years of AS. 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 varied between GAP3 cohorts (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 (0.55 to 0.75) over the whole follow-up period. Time-dependent MAPE was large (0.3 to 0.45) in those cohorts where the impact of PSA on upgrading-risk was different from PRIAS (e.g., MUSIC cohort, Supplementary Table 8), and moderate (0.1 to 0.3) otherwise. In all cohorts, the MAPE decreased rapidly after year one of follow-up. 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 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. Specifically, 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 (Supplementary Figure 9). Example personalized schedules based on 5% and 10% risk thresholds are shown in Figure 5, and in Supplementary Figure 10–12. For both personal-

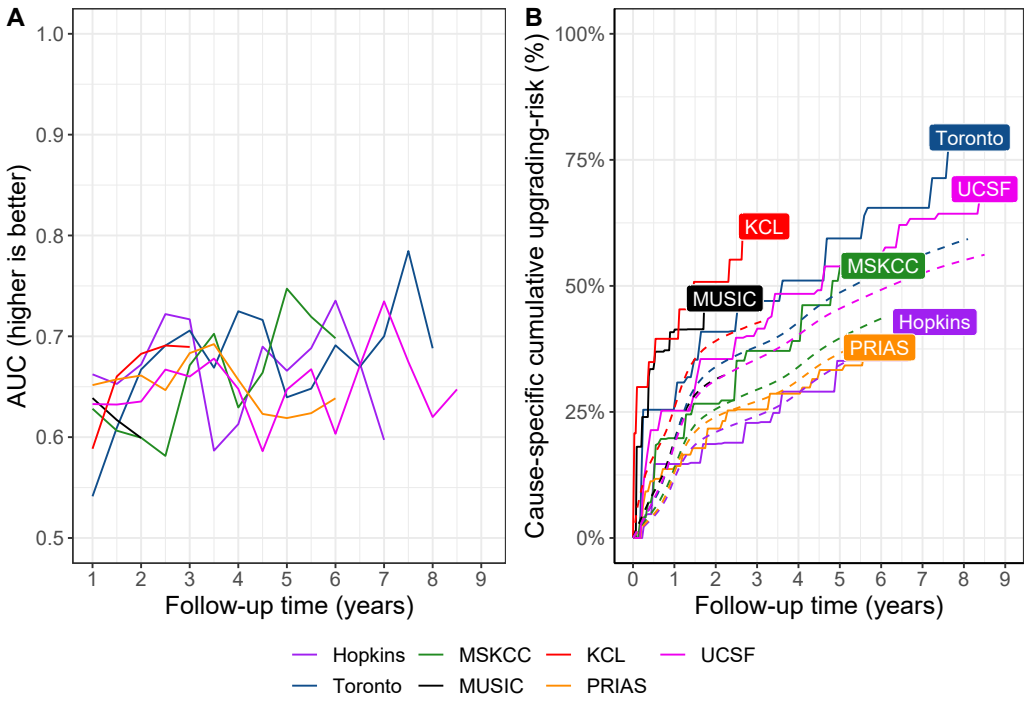

Figure 4: **Model Validation Results**. **Panel A**: time-dependent area under the receiver operating characteristic curve or AUC (measure of discrimination). **Panel B**: calibration-at-large indicates model miscalibration. This is because solid lines depicting the non-parameteric estimate of the cause-specific cumulative upgrading-risk [24], 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.

ized and fixed schedules, we estimated the expected time delay in detecting upgrading if the patient progresses before the time of the last planned biopsy (Panel C, Figure 5). This delay is also personalized (Supplementary C.1). That is, even if two different patients are prescribed the same biopsy schedule, their expected delays will depend on their individual upgrading-risk profiles. Patients/doctors can utilize the expected delay and schedule of biopsies as criteria to compare fixed, and different risk-based personalized schedules.

3.2. Web-Application

We implemented our model and personalized schedules in a user-friendly web-application `https://emcbiostatistics.shinyapps.io/prias_biopsy_recommender/`. Currently, the web-application supports PRIAS and the six validation cohorts. Patient data can be entered manually and in Microsoft Excel format. Predictions for upgrading-risk are available for a currently limited, cohort-specific, follow-up period (Supplementary Table 9). The web-application visualizes the timing of biopsies, and expected time delay in detecting upgrading, for personalized schedules based on 5%, 10%, and 15% risk threshold; annual biopsies; biennial biopsies; and PRIAS schedule.

4. Discussion

We successfully developed and externally validated a 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 [15, 25]. 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 [17]. Second, the model predicts a

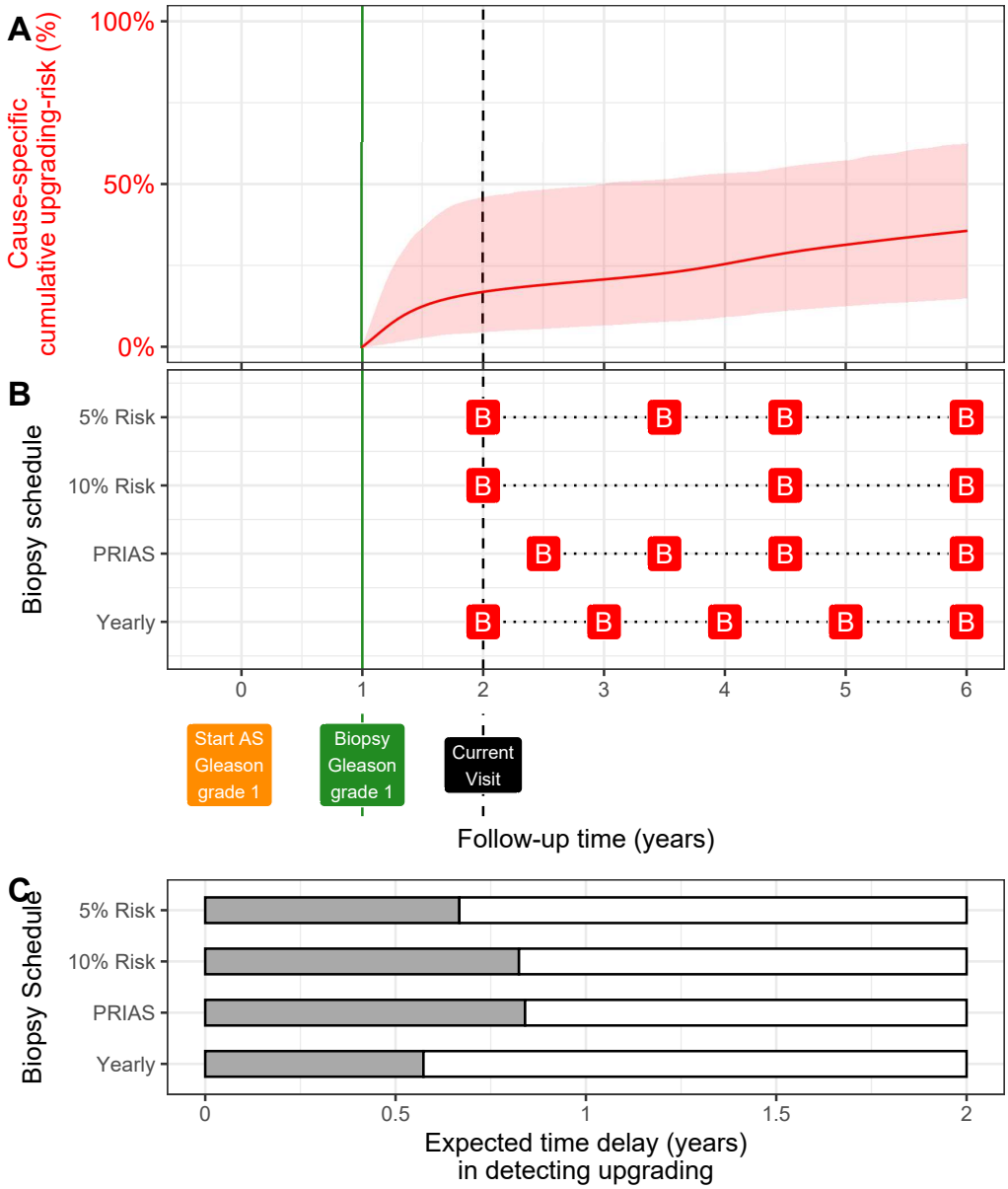

Figure 5: **Illustration of personalized and fixed schedules of biopsies for patient from Figure 3**. **Panel A:** Predicted cumulative upgrading-risk (95% credible interval shaded). **Panel B:** Different biopsy schedules with a red 'B' indicating a future biopsy. Risk: 5% and Risk: 10% are personalized 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 is useful for numerous patients from PRIAS and validated cohorts. The discrimination ability of our model, exhibited by the *time-dependent* AUC, was moderate (0.55–0.75). This is possible because, unlike the standard AUC [22], the time-dependent AUC 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, MAPE 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). In all cohorts, MAPE decreased rapidly after year one of follow-up. A plausible reason is that at year one, the validation data also contains those patients who may have been misclassified as Gleason grade group 1 at the time of inclusion in AS. This issue can be obviated by scheduling a compulsory biopsy at year one for all patients (current PRIAS recommendation). Last, we required recalibration of our model's baseline hazard of upgrading for all validation cohorts.

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 all biopsies planned in the first five years of AS. Given the non-compliance and burden of frequent biopsies [8], 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 [26] that personalized schedules may reduce, on average, six biopsies compared to annual schedule and two biopsies compared to 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.

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 [15, 27] will be interesting to investigate further. However, even with an enhanced risk prediction model, the methodology for personalized scheduling and calculation of expected time delay (Supplementary C) need not change.

5. Conclusions

We successfully developed and externally validated a model for predicting upgrading-risk, and providing risk-based personalized biopsy decisions, in prostate cancer AS. 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 external cohorts.

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 Foundations Global Action Plan Prostate Cancer Active Surveillance (GAP3) consortium

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Supplementary File containing full results, and extra figures referred in the main manuscript begins here onwards.

Supplementary Materials for "A Ready To Use Web-Application Providing a Personalized Biopsy Schedule for Men With Low-Risk PCa Under Active Surveillance"

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Appendix A. A Joint Model for the Longitudinal PSA, and Time to Gleason Upgrading

Let T_i^* denote the true time of upgrading (increase in biopsy Gleason grade group from 1 to 2 or higher) for the i-th patient included in PRIAS. Since biopsies are conducted periodically, T_i^* is observed with interval censoring $l_i < T_i^* \leq r_i$. When upgrading is observed for the patient at his latest

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biopsy time r_i, then l_i denotes the time of the second latest biopsy. Otherwise, l_i denotes the time of the latest biopsy and $r_i = \infty$. Let $\boldsymbol{y}_i$ denote his observed PSA longitudinal measurements. The observed data of all n patients is denoted by $\mathcal{A}_n = \{l_i, r_i, \boldsymbol{y}_i; i = 1, \ldots, n\}$.

In our joint model, the patient-specific PSA measurements over time are modeled using a linear mixed effects sub-model. It is given by (see Panel A, Figure 1):

$$\begin{aligned} \log_2\big\{y_i(t)+1\big\} &= m_i(t) + \varepsilon_i(t), \\ m_i(t) &= \beta_0 + b_{0i} + \sum_{k=1}^{4}(\beta_k + b_{ki})B_k\Big(\frac{t-2}{2}, \frac{\mathcal{K}-2}{2}\Big) + \beta_5 \text{age}_i, \end{aligned} \tag{1}$$

where, $m_i(t)$ denotes the measurement error free value of $\log_2(\text{PSA}+1)$ transformed [2, 3] measurements at time t. We model it non-linearly over time using B-splines [4]. To this end, our B-spline basis function $B_k\{(t-2)/2, (\mathcal{K}-2)/2\}$ has three internal knots at $\mathcal{K} = \{0.5, 1.3, 3\}$ years, which are the three quartiles of the observed follow-up times. The boundary knots of the spline are at 0 and 6.3 years (95-th percentile of the observed follow-up times). We mean centered (mean 2 years) and standardized (standard deviation 2 years) the follow-up time t and the knots of the B-spline $\mathcal{K}$ during parameter estimation for better convergence. The fixed effect parameters are denoted by $\{\beta_0, \ldots, \beta_5\}$, and $\{b_{0i}, \ldots, b_{4i}\}$ are the patient specific random effects. The random effects follow a multivariate normal distribution with mean zero and variance-covariance matrix $\boldsymbol{W}$. The error $\varepsilon_i(t)$ is assumed to be t-distributed with three degrees of freedom (see Appendix B.1) and scale σ, and is independent of the random effects.

To model the impact of PSA measurements on the risk of upgrading, our joint model uses a relative risk sub-model. More specifically, the hazard of upgrading denoted as $h_i(t)$, and the cumulative-risk of upgrading denoted as $R_i(t)$, at a time t are (see Panel C, Figure 1):

$$\begin{aligned} h_i(t) &= h_0(t)\exp\Big(\gamma \text{age}_i + \alpha_1 m_i(t) + \alpha_2 \frac{\mathrm{d}m_i(t)}{\mathrm{d}t}\Big), \\ R_i(t) &= \exp\Big\{-\int_0^t h_i(s)\mathrm{d}s\Big\}, \end{aligned} \tag{2}$$

where, γ is the parameter for the effect of age. The impact of PSA on the hazard of upgrading is modeled in two ways, namely the impact of the error

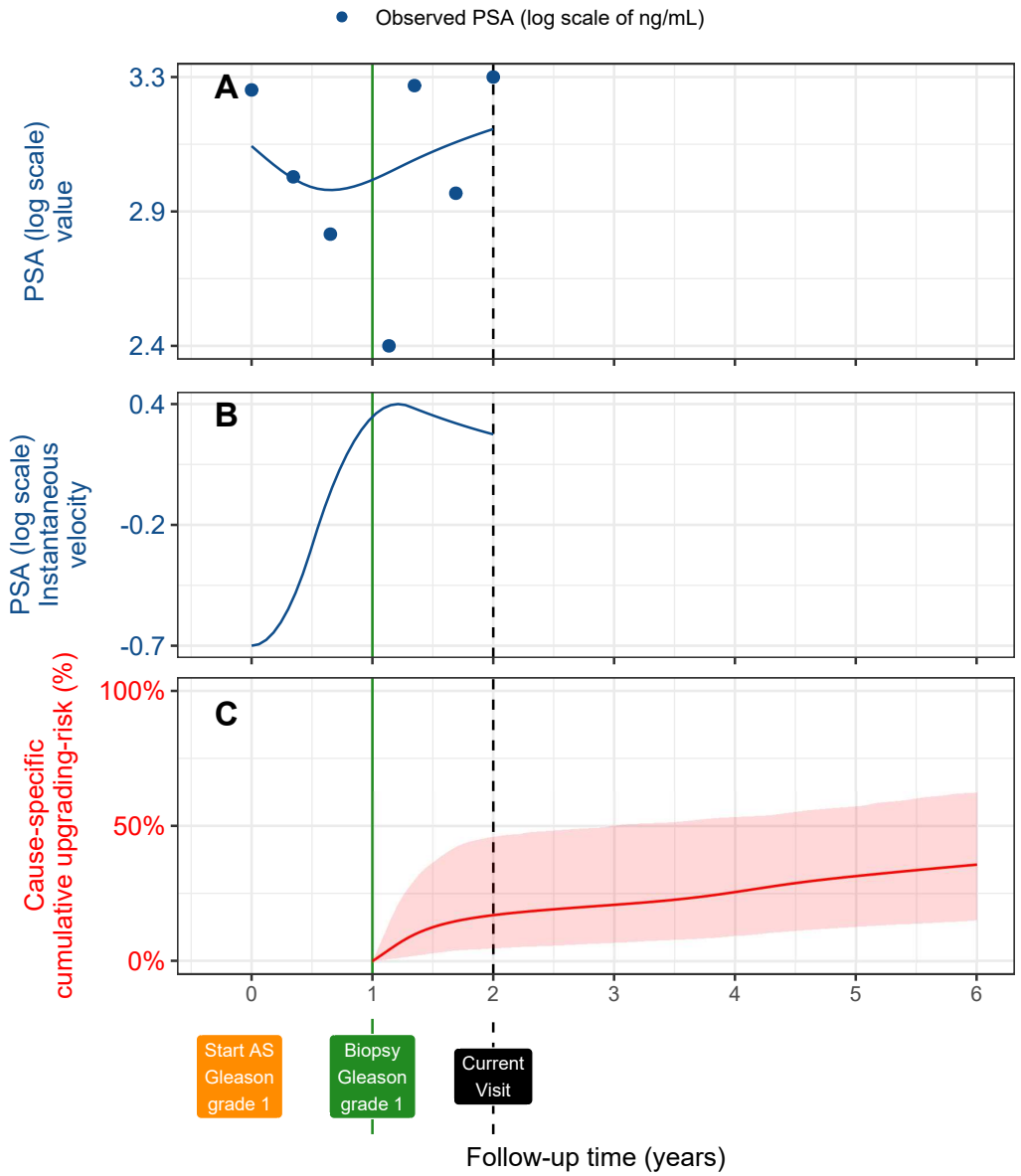

Figure 1: **Illustration of the joint model on a real PRIAS dataset patient**. **Panel A:** Observed (blue dots) and fitted PSA (solid blue line) measurements, log-transformed. **Panel B:** Estimated instantaneous velocity of PSA (log-transformed). **Panel C**: Predicted cumulative-risk of upgrading (95% credible interval shaded). Upgrading is defined as an increase in Gleason grade group [1] from grade group 1 to 2 or higher. This risk of upgrading is available starting from the time of the latest negative biopsy (vertical green line at year 1 of follow-up). The joint model estimated it by combining the fitted PSA value and velocity (both on the log scale of PSA) and time of the latest negative biopsy. Black dashed line at year 4 denotes the time of current visit.

free underlying PSA value $m_i(t)$ (see Panel A, Figure 1), and the impact of the underlying PSA velocity $\mathrm{d}m_i(t)/\mathrm{d}t$ (see Panel B, Figure 1). The corresponding parameters are α_1 and α_2, respectively. Lastly, $h_0(t)$ is the baseline hazard at time t, and is modeled flexibly using P-splines [5]. More specifically:

$$\log h_0(t) = \gamma_{h_0,0} + \sum_{q=1}^{Q} \gamma_{h_0,q} B_q(t, \boldsymbol{v}),$$

where $B_q(t, \boldsymbol{v})$ denotes the q-th basis function of a B-spline with knots $\boldsymbol{v} = v_1, \ldots, v_Q$ and vector of spline coefficients γ_{h_0}. To avoid choosing the number and position of knots in the spline, a relatively high number of knots (e.g., 15 to 20) are chosen and the corresponding B-spline regression coefficients γ_{h_0} are penalized using a differences penalty [5].

We estimate the parameters of the joint model using Markov chain Monte Carlo (MCMC) methods under the Bayesian framework. Let $\boldsymbol{\theta}$ denote the vector of all of the parameters of the joint model. The joint model postulates that given the random effects, the time of upgrading, and the PSA measurements taken over time are all mutually independent. Under this assumption the posterior distribution of the parameters is given by:

$$\begin{aligned} p(\boldsymbol{\theta}, \boldsymbol{b} \mid \mathcal{A}_n) &\propto \prod_{i=1}^{n} p(l_i, r_i, \boldsymbol{y}_i, \mid \boldsymbol{b}_i, \boldsymbol{\theta}) p(\boldsymbol{b}_i \mid \boldsymbol{\theta}) p(\boldsymbol{\theta}) \\ &\propto \prod_{i=1}^{n} p(l_i, r_i \mid \boldsymbol{b}_i, \boldsymbol{\theta}) p(\boldsymbol{y}_i \mid \boldsymbol{b}_i, \boldsymbol{\theta}) p(\boldsymbol{b}_i \mid \boldsymbol{\theta}) p(\boldsymbol{\theta}), \\ p(\boldsymbol{b}_i \mid \boldsymbol{\theta}) &= \frac{1}{\sqrt{(2\pi)^q \det(\boldsymbol{W})}} \exp\Big\{ -\frac{1}{2} (\boldsymbol{b}_i^T \boldsymbol{W}^{-1} \boldsymbol{b}_i) \Big\}, \end{aligned}$$

where, the likelihood contribution of the PSA outcome, conditional on the random effects is:

$$p(\boldsymbol{y}_i \mid \boldsymbol{b}_i, \boldsymbol{\theta}) = \frac{1}{\left(\sqrt{2\pi\sigma^2}\right)^{n_i}} \exp\Big\{ -\frac{\sum_{j=1}^{n_i} (y_{ij} - m_{ij})^2}{2\sigma^2} \Big\},$$

where n_i is the number of PSA measurements of the i-th patient. The likelihood contribution of the time of upgrading outcome is given by:

$$p(l_i, r_i \mid \boldsymbol{b}_i, \boldsymbol{\theta}) = \exp\Big\{ -\int_0^{l_i} h_i(s) \mathrm{d}s \Big\} - \exp\Big\{ -\int_0^{r_i} h_i(s) \mathrm{d}s \Big\}. \qquad (3)$$

The integrals in (3) do not have a closed-form solution, and therefore we use a 15-point Gauss-Kronrod quadrature rule to approximate them.

We use independent normal priors with zero mean and variance 100 for the fixed effects $\{\beta_0, \ldots, \beta_5\}$, and inverse Gamma prior with shape and rate both equal to 0.01 for the parameter σ^2. For the variance-covariance matrix $\boldsymbol{W}$ of the random effects, we take inverse Wishart prior with an identity scale matrix and degrees of freedom equal to 5 (number of random effects). For the relative risk model's parameter γ and the association parameters α_1, α_2, we use independent normal priors with zero mean and variance 100.

Appendix A.1. Assumption of t-distributed (df=3) Error Terms

With regards to the choice of the distribution for the error term ε for the PSA measurements (see Equation 1), we attempted fitting multiple joint models differing in error distribution, namely t-distribution with three, and four degrees of freedom, and a normal distribution for the error term. However, the model assumption for the error term was best met by the model with t-distribution having three degrees of freedom. The quantile-quantile plot of subject-specific residuals for the corresponding model in Panel A of Figure 2, shows that the assumption of t-distributed (df=3) errors is reasonably met by the fitted model.

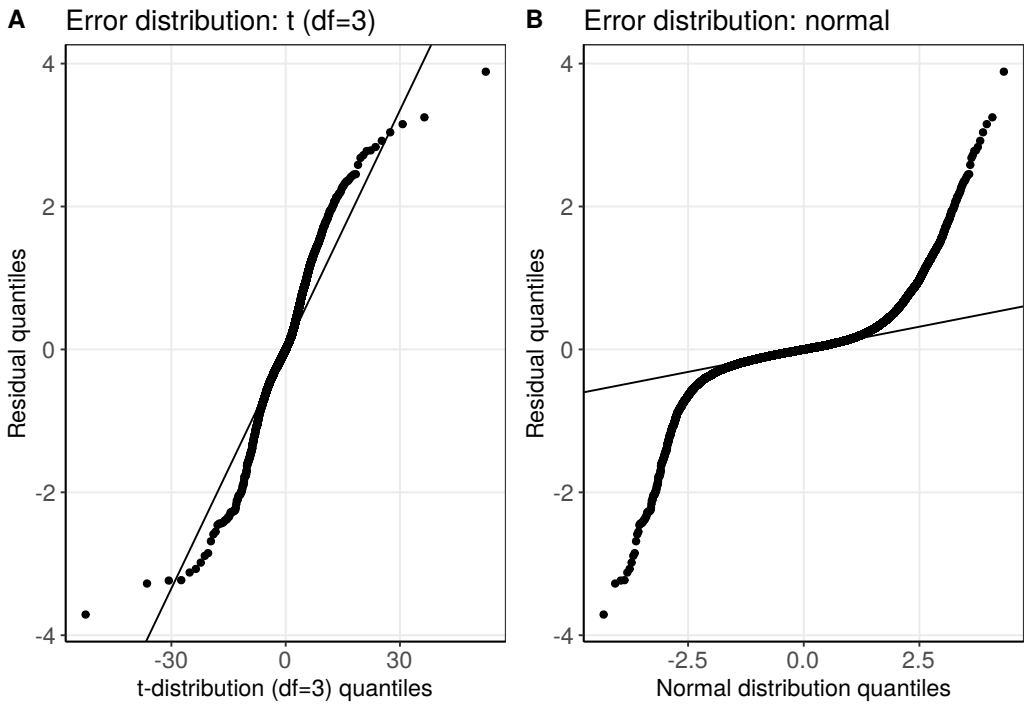

Figure 2: **Quantile-quantile plot** of subject-specific PSA residuals from two different joint models fitted to the PRIAS dataset. **Panel A**: model assuming a t-distribution (df=3) for the error term ε (see Equation 1). **Panel B**: model assuming a normal distribution for the error term ε. We selected the model with t-distributed error terms.

Appendix A.2. Results

Characteristics of the six validation cohorts from the GAP3 database [6] are shown in Table 1, Table 2, and Table 3. The cause-specific cumulative upgrading-risk in these cohorts is shown in Figure 3.

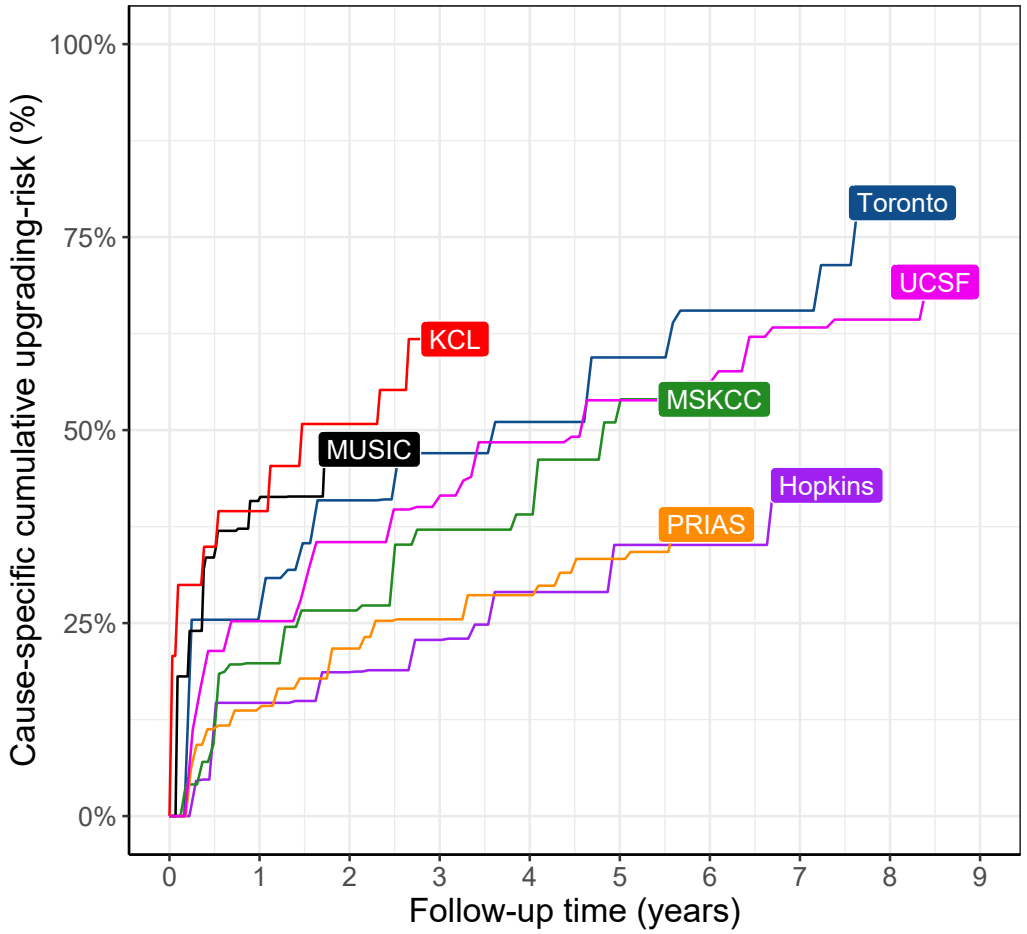

Figure 3: **Nonparametric estimate [7] of the cause-specific cumulative upgrading-risk** in the world's largest AS cohort PRIAS, and largest six AS cohorts from the GAP3 database [6]. Abbreviations are *Hopkins*: Johns Hopkins Active Surveillance, *PRIAS*: Prostate Cancer International Active Surveillance, *Toronto*: University of Toronto Active Surveillance, *MSKCC*: Memorial Sloan Kettering Cancer Center Active Surveillance, *KCL*: King's College London Active Surveillance, *MUSIC*: Michigan Urological Surgery Improvement Collaborative AS, *UCSF*: University of California San Francisco Active Surveillance.

Table 1: **Summary of the Hopkins and Toronto validation cohorts from the GAP3 database [6]**. The primary event of interest is upgrading, that is, increase in Gleason grade group from group 1 to 2 or higher. #PSA: number of PSA, #biopsies: number of biopsies, IQR: interquartile range, PSA: prostate-specific antigen. Full names of cohorts are *Hopkins*: Johns Hopkins Active Surveillance, *Toronto*: University of Toronto Active Surveillance

Characteristic	**Hopkins**	**Toronto**
Total patients	1392	1046
Upgrading (primary event)	260	359
Median age (years)	62 (IQR: 66–69)	67 (IQR: 60–72)
Median maximum follow-up per patient (years)	3 (IQR: 1.3–5.8)	4.5 (IQR: 1.9–8.4)
Total PSA measurements	11126	13984
Median #PSA per patient	6 (IQR: 4–11)	12 (IQR: 7–19)
Median PSA (ng/mL)	4.7 (IQR: 2.9–6.7)	6 (IQR: 3.7–9.0)
Total biopsies	1926	909
Median #biopsies per patient	1 (IQR: 1–2)	1 (IQR: 1–2)

Table 2: **Summary of the MSKCC and UCSF validation cohorts from the GAP3 database [6]**. The primary event of interest is upgrading, that is, increase in Gleason grade group from group 1 to 2 or higher. #PSA: number of PSA, #biopsies: number of biopsies, IQR: interquartile range, PSA: prostate-specific antigen. Full names of cohorts are *MSKCC*: Memorial Sloan Kettering Cancer Center Active Surveillance, *UCSF*: University of California San Francisco Active Surveillance.

Characteristic	**MSKCC**	**UCSF**
Total patients	894	1397
Upgrading (primary event)	242	547
Median age (years)	63 (IQR: 57–68)	63 (IQR: 57–68)
Median maximum follow-up per patient (years)	5.3 (IQR: 1.8–8.3)	3.6 (IQR: 1.5–7.2)
Total PSA measurements	10704	16093
Median #PSA per patient	11 (IQR: 5–17)	8 (IQR: 4–16)
Median PSA (ng/mL)	4.7 (IQR: 2.8–7.1)	5.0 (IQR: 3.4–7.2)
Total biopsies	1102	3512
Median #biopsies per patient	1 (IQR: 1–2)	2 (IQR: 2–3)

Table 3: **Summary of the MUSIC and KCL validation cohorts from the GAP3 database [6]**. The primary event of interest is upgrading, that is, increase in Gleason grade group from group 1 to 2 or higher. #PSA: number of PSA, #biopsies: number of biopsies, IQR: interquartile range, PSA: prostate-specific antigen. Full names of cohorts are *KCL*: King's College London Active Surveillance, *MUSIC*: Michigan Urological Surgery Improvement Collaborative AS.

Characteristic	**MUSIC**	**KCL**
Total patients	2743	616
Upgrading (primary event)	385	198
Median age (years)	65 (IQR: 60–71)	63 (IQR: 58–68)
Median maximum follow-up per patient (years)	1.2 (IQR: 0.6–2.2)	2.4 (IQR: 1.3–3.8)
Total PSA measurements	12087	2987
Median #PSA per patient	4 (IQR: 2–6)	4 (IQR: 2–6)
Median PSA (ng/mL)	5.1 (IQR: 3.4–7.1)	6 (IQR: 4–9)
Total biopsies	1032	484
Median #biopsies per patient	1 (IQR: 1–1)	1 (IQR: 1–1)

Table 4: **Estimated variance-covariance matrix $\boldsymbol{W}$** of the random effects $\boldsymbol{b} = (b_0, b_1, b_2, b_3, b_4)$ from the joint model fitted to the PRIAS dataset. The variances of the random effects are highlighted along the diagonal of the variance-covariance matrix.

Random Effects	b_0	b_1	b_2	b_3	b_4
b_0	**0.229**	0.030	0.023	0.073	0.007
b_1	0.030	**0.149**	0.098	0.171	0.085
b_2	0.023	0.098	**0.276**	0.335	0.236
b_3	0.073	0.171	0.335	**0.560**	0.359
b_4	0.007	0.085	0.236	0.359	**0.351**

The joint model was fitted using the R package **JMbayes** [8]. This package utilizes the Bayesian methodology to estimate model parameters. The corresponding posterior parameter estimates are shown in Table 5 (longitudinal sub-model for PSA outcome) and Table 6 (relative risk sub-model). The parameter estimates for the variance-covariance matrix $\boldsymbol{W}$ from the longitudinal sub-model for PSA are shown in the following Table 4:

For the PSA mixed effects sub-model parameter estimates (see Equation 1), in Table 5 we can see that the age of the patient trivially affects the baseline $\log_2(\text{PSA} + 1)$ measurement. Since the longitudinal evolution of $\log_2(\text{PSA} + 1)$ measurements is modeled with non-linear terms, the interpretation of the coefficients corresponding to time is not straightforward. In lieu of the interpretation, in Figure 4 we present plots of observed versus fitted

Table 5: **Parameters of the longitudinal sub-model**: Estimated mean and 95% credible interval for parameters in Equation (1).

Variable	Mean	Std. Dev	2.5%	97.5%	P
Intercept	2.129	0.060	2.009	2.244	<0.001
Age	0.008	0.001	0.007	0.010	<0.001
Spline: [0.0, 0.5] years	0.063	0.007	0.051	0.075	<0.001
Spline: [0.5, 1.3] years	0.196	0.010	0.177	0.217	<0.001
Spline: [1.3, 3.0] years	0.244	0.014	0.217	0.272	<0.001
Spline: [3.0, 6.3] years	0.382	0.014	0.356	0.410	<0.001
σ	0.139	0.001	0.138	0.140	

Table 6: **Parameters of the relative risk sub-model**: Estimated mean and 95% credible interval for the parameters in Equation (2).

Variable	Mean	Std. Dev	2.5%	97.5%	P
Age	0.037	0.006	0.025	0.049	<0.001
Fitted $\log_2(\text{PSA}+1)$ value	-0.012	0.076	-0.164	0.135	0.856
Fitted $\log_2(\text{PSA}+1)$ velocity	2.266	0.299	1.613	2.767	<0.001

PSA profiles for nine randomly selected patients.

For the relative risk sub-model (see Equation 2), the parameter estimates in Table 6 show that $\log_2(\text{PSA}+1)$ velocity and age of the patient were significantly associated with the hazard of upgrading.

It is important to note that since age, and $\log_2(\text{PSA}+1)$ value and velocity are all measured on different scales, a comparison between the corresponding parameter estimates is not easy. To this end, in Table 7, we present the hazard ratio of upgrading, for an increase in the aforementioned variables from their 25-th to the 75-th percentile. For example, an increase in fitted $\log_2(\text{PSA}+1)$ velocity from -0.085 to 0.308 (fitted 25-th and 75-th percentiles) corresponds to a hazard ratio of 2.433. The interpretation of the rest is similar.

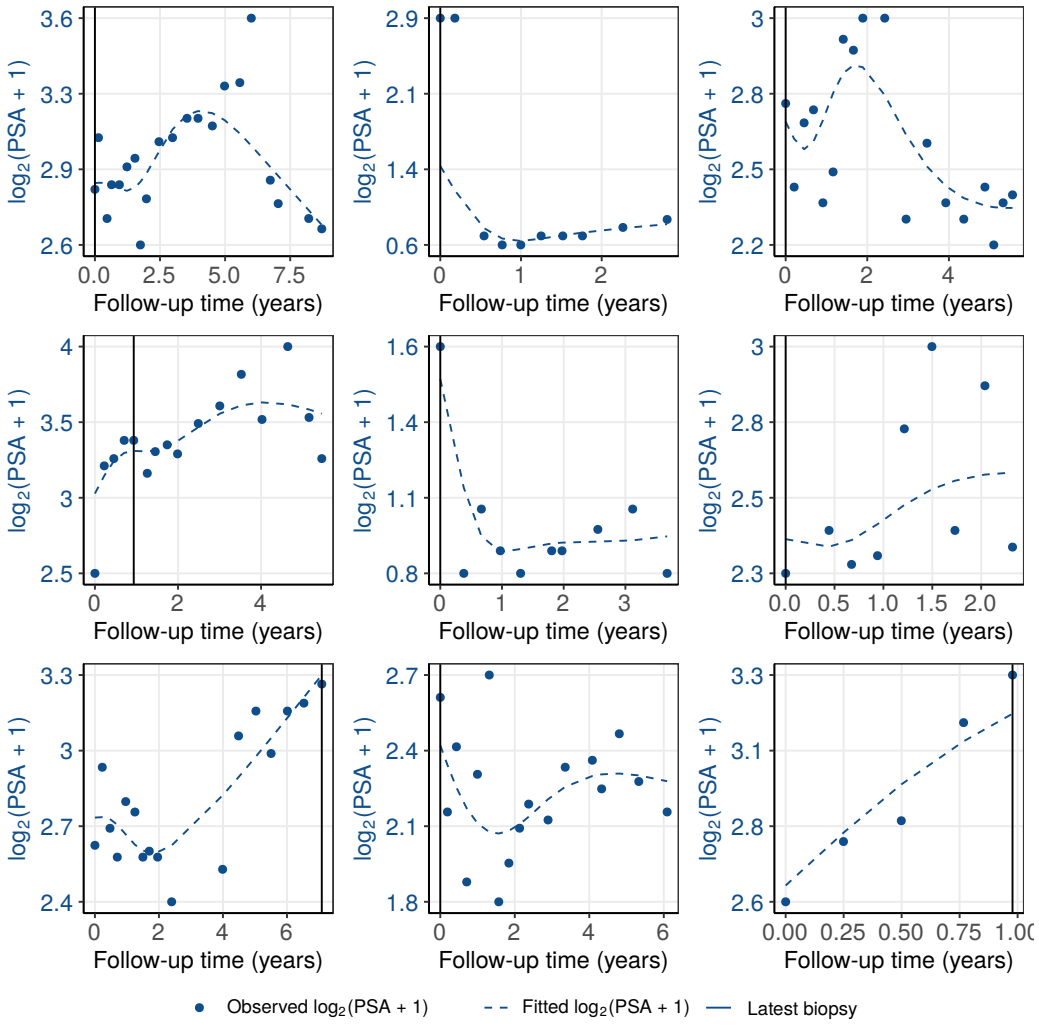

Figure 4: **Fitted versus observed** $\log_2(\mathbf{PSA}+1)$ **profiles** for nine randomly selected PRIAS patients. The fitted profiles utilize information from the observed PSA measurements, and time of the latest biopsy.

Table 7: **Hazard ratio and 95% credible interval (CI) for upgrading**: Variables are on different scale and hence we compare an increase in the variables of relative risk sub-model from their 25-th percentile (P_{25}) to their 75-th percentile (P_{75}). Except for age, quartiles for all other variables are based on their fitted values obtained from the joint model fitted to the PRIAS dataset.

Variable	P_{25}	P_{75}	Hazard ratio [95% CI]
Age	61	71	1.455 [1.285, 1.631]
Fitted $\log_2(\text{PSA}+1)$ value	2.360	3.078	0.991 [0.889, 1.102]
Fitted $\log_2(\text{PSA}+1)$ velocity	-0.085	0.308	2.433 [1.883, 2.962]

Table 8: **Parameters of the relative risk sub-model in validation cohorts**. We fitted separate joint models for each of the six GAP3 validation cohorts as well. The specification of these joint models was same as that of the model for PRIAS. Two important predictors in the relative-risk sub-model, namely, the $\log_2(\text{PSA}+1)$ value and velocity have different impact on upgrading-risk across the cohorts. Table shows the mean estimate of these parameters with 95% credible interval in brackets. Strongest average effect of $\log_2(\text{PSA}+1)$ velocity is in PRIAS cohort, whereas the weakest is in MUSIC cohort. The strongest average effect of $\log_2(\text{PSA}+1)$ value is in the Toronto cohort whereas the weakest is in PRIAS cohort. Full names of cohorts are *Hopkins*: Johns Hopkins Active Surveillance, *PRIAS*: Prostate Cancer International Active Surveillance, *Toronto*: University of Toronto Active Surveillance, *MSKCC*: Memorial Sloan Kettering Cancer Center Active Surveillance, *KCL*: King's College London Active Surveillance, *MUSIC*: Michigan Urological Surgery Improvement Collaborative AS, *UCSF*: University of California San Francisco Active Surveillance.

Cohort	Fitted $\log_2(\text{PSA}+1)$ value	Fitted $\log_2(\text{PSA}+1)$ velocity
PRIAS	-0.012 [-0.164, 0.135]	2.266 [1.613, 2.767]
Hopkins	0.061 [-0.323, 0.329]	1.839 [0.761, 4.378]
MSKCC	0.336 [0.081, 0.583]	1.122 [0.421, 1.980]
Toronto	0.572 [0.347, 0.794]	0.943 [0.464, 1.554]
UCSF	0.498 [0.326, 0.673]	0.812 [0.280, 1.383]
MUSIC	0.441 [0.092, 0.767]	0.029 [-0.552, 0.512]
KCL	0.194 [-0.104, 0.540]	0.840 [-0.087, 1.665]

Appendix B. Risk Predictions for Upgrading

Let us assume a new patient j, for whom we need to estimate the upgrading-risk. Let his current follow-up visit time be v, latest time of biopsy be t, observed vector PSA measurements be $\mathcal{Y}_j(v)$. The combined information from the observed data about the time of upgrading, is given by the following posterior predictive distribution $g(T_j^*)$ of his time T_j^* of upgrading:

$$\begin{aligned} g(T_j^*) &= p\big\{T_j^* \mid T_j^* > t, \mathcal{Y}_j(v), \mathcal{A}_n\big\} \\ &= \int\int p\big(T_j^* \mid T_j^* > t, \boldsymbol{b}_j, \boldsymbol{\theta}\big) p\big\{\boldsymbol{b}_j \mid T_j^* > t, \mathcal{Y}_j(v), \boldsymbol{\theta}\big\} p\big(\boldsymbol{\theta} \mid \mathcal{A}_n\big) \mathrm{d}\boldsymbol{b}_j \mathrm{d}\boldsymbol{\theta}. \end{aligned}$$

The distribution $g(T_j^*)$ depends not only depends on the observed data of the patient $T_j^* > t, \mathcal{Y}_j(v)$, but also depends on the information from the PRIAS dataset $\mathcal{A}_n$. To this the the posterior distribution of random effects $\boldsymbol{b}_j$ and posterior distribution of the vector of all parameters $\boldsymbol{\theta}$ are utilized, respectively. The distribution $g(T_j^*)$ can be estimated as detailed in Rizopoulos et al. [9]. Since, many prostate cancer patients may not obtain upgrading in the current follow-up period of PRIAS, $g(T_j^*)$ can only be estimated for a currently limited follow-up period.

The cause-specific cumulative upgrading-risk can be derived from $g(T_j^*)$ as given in [9]. It is given by:

$$R_j(u \mid t, v) = \Pr\big\{T_j^* > u \mid T_j^* > t, \mathcal{Y}_j(v), \mathcal{A}_n\big\}, \quad u \geq t. \tag{4}$$

The personalized risk profile of the patient (see Panel C, Figure 5) updates as more data is gathered over follow-up visits.

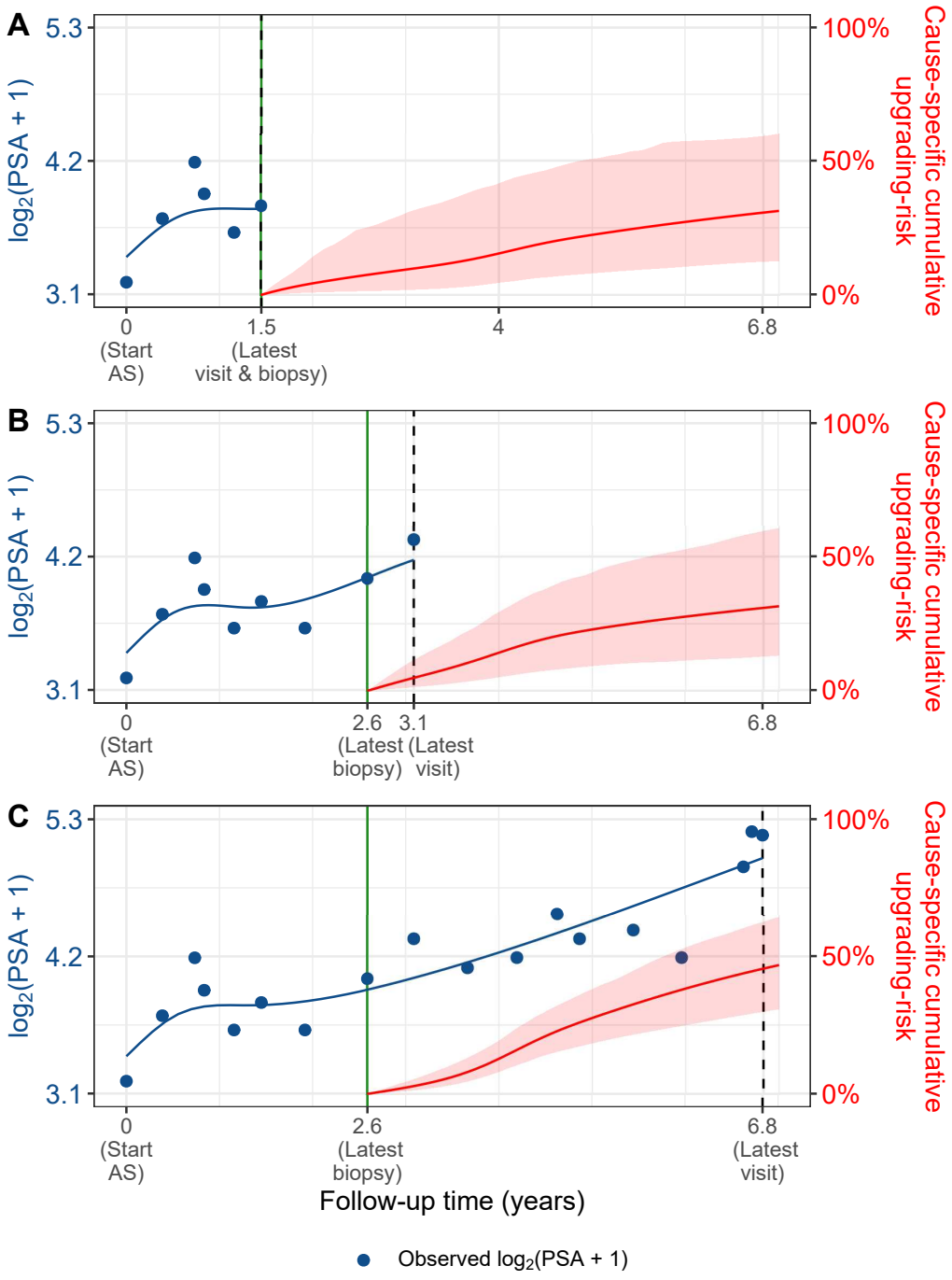

Figure 5: **Cause-specific cumulative upgrading-risk changing dynamically over follow-up** as more patient data is gathered. The three **Panels A,B and C:** are ordered by the time of the latest visit (dashed vertical black line) of a new patient. At each of the latest follow-up visits, we combine the accumulated PSA measurements (shown in blue), and latest time of negative biopsy (solid vertical green line) to obtain the updated cumulative-risk profile (shown in red) of the patient.

Appendix B.1. Validation of Risk Predictions

We wanted to check the usefulness of our model for not only the PRIAS patients but also for patients from other cohorts. To this end, we validated our model in the PRIAS dataset (internal validation) and the largest six cohorts from the GAP3 database [6]. These are the University of Toronto AS (Toronto), Johns Hopkins AS (Hopkins), Memorial Sloan Kettering Cancer Center AS (MSKCC), University of California San Francisco Active Surveillance (UCSF), King's College London AS (KCL), Michigan Urological Surgery Improvement Collaborative AS (MUSIC).

Calibration-in-the-large We first assessed calibration-in-the-large [10] of our model in the aforementioned cohorts. To this end, we used our model to predict the cause-specific cumulative upgrading-risk for each patient, given their PSA measurements and biopsy results. We then averaged the resulting profiles of cause-specific cumulative upgrading-risk. Subsequently, we compared the averaged cumulative-risk profile with a non-parametric estimate [7] of the cause-specific cumulative upgrading-risk in each of the cohorts. The results are shown in Panel A of Figure 6. We can see that our model is miscalibrated in external cohorts, although it is fine in the Hopkins cohort. To improve our model's calibration in all cohorts, we recalibrated the baseline hazard of the joint model fitted to the PRIAS dataset, individually for each of the cohorts except the Hopkins cohort. More specifically, given the data of an external cohort $\mathcal{A}^c$, where c denotes the cohort, the recalibrated parameters $\boldsymbol{\gamma}_{h_0}^c$ (Appendix A) of the log baseline hazard are given by:

$$p(\boldsymbol{\gamma}_{h_0}^c \mid \mathcal{A}^c, \boldsymbol{b^c}, \boldsymbol{\theta}) \propto \prod_{i=1}^{n^c} p(l_i^c, r_i^c \mid \boldsymbol{b_i^c}, \boldsymbol{\theta}) p(\boldsymbol{\gamma}_{h_0}^c) \tag{5}$$

where n^c are the number of patients in the c-th cohort, and $\boldsymbol{\theta}$ is the vector of all parameters of the joint model fitted to the PRIAS dataset. The interval in which upgrading is observed for the i-th patient is given by l_i^c, r_i^c, with $r_i^c = \infty$ for right-censored patients. The symbol $\boldsymbol{b_i^c}$ denotes patient-specific random effects (Appendix A) in the c-th cohort. The random effects are obtained using the joint model fitted to the PRIAS dataset before recalibration. We re-evaluated the calibration-in-the-large of our model after the recalibration of the baseline hazard individually for each cohort. The improved calibration-in-the-large is shown in Panel B of Figure 6.

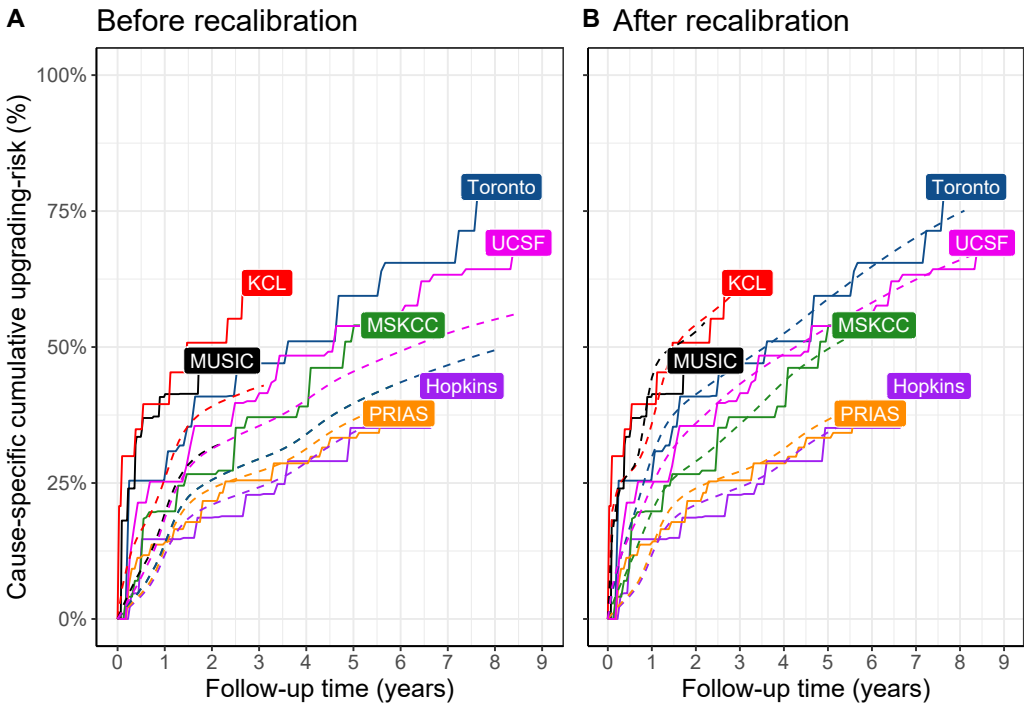

Figure 6: **Calibration-in-the-large of our model:**. In **Panel A** we can see that our model is not well calibrated for use in KCL, MUSIC, Toronto and MSKCC. In **Panel B** we can see that calibration of model predictions improved in KCL, MUSIC, Toronto and MSKCC cohorts after recalibrating our model. Recalibration was not necessary for Hopkins cohort. 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 Active Surveillance.

Recalibrated PRIAS Model Versus Individual Joint Models For Each Cohort We wanted to check if our recalibrated PRIAS model performed as good as a new joint model that could be fitted to the external cohorts. To this end, we predicted cause-specific cumulative upgrading-risk for each patient from each cohort using two sets of models, namely the recalibrated PRIAS model for each cohort, and a new joint model fitted to each cohort. The difference in predicted cause-specific cumulative upgrading-risk from these models is shown in Figure 7. We can see that the difference is smaller in those cohorts in which the effects of $\log_2(\text{PSA} + 1)$ value and velocity were similar to that of PRIAS (Table 8). For example, the Hopkins cohort had parameter estimates similar to that of PRIAS, and consequently, the difference in predicted risks for this cohort is smallest. The opposite of this phenomenon holds for the MUSIC and KCL cohorts.

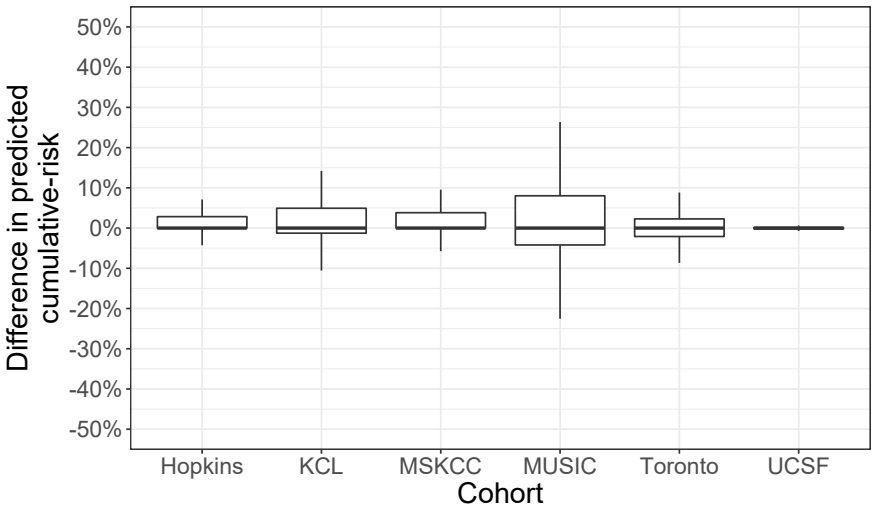

Figure 7: **Comparison of predictions from recalibrated PRIAS model with individual joint models fitted to external cohorts:** On Y-axis we show the difference between predicted cause-specific cumulative upgrading-risk for individual patients using two models, namely the recalibrated PRIAS model for each cohort, and individual joint model fitted to each cohort. The figure shows that the difference is smaller in those cohorts in which the effects of $\log_2(\text{PSA} + 1)$ value and velocity were similar to that of PRIAS (Table 8). 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 Active Surveillance.

Validation of Dynamic Cumulative-Risk Predictions As shown in Figure 5, the cumulative-risk predictions from the joint model are dynamic in nature. That is, they update as more data becomes available over time. Consequently, the discrimination and prediction error of the joint model also depend on the available data. We assessed these two measures dynamically in the PRIAS cohort (interval validation) and in the largest six external cohorts that are part of the GAP3 database. For discrimination, we utilized the time-varying area under the receiver operating characteristic curve or time-varying AUC [9]. For time-varying prediction error, we assessed the mean absolute prediction error or MAPE [9]. The AUC indicates how well the model discriminates between patients who experience upgrading, and those do not. The MAPE indicates how accurately the model predicts upgrading. Both AUC and MAPE are restricted to $[0, 1]$. However, it is preferred that AUC > 0.5 because an AUC ≤ 0.5 indicates that the model performs worse than random discrimination. Ideally, MAPE should be 0.

We calculate AUC and MAPE in a time-dependent manner. More specifically, given the time of latest biopsy t, and history of PSA measurements up to time v, we calculate AUC and MAPE for a medically relevant time frame $(t, v]$, within which the occurrence of upgrading is of interest. In the case of prostate cancer, at any point in time v, it is of interest to identify patients who may have experienced upgrading in the last one year $(v - 1, v]$. That is, we set $t = v - 1$. We then calculate AUC and MAPE at a gap of every six months (follow-up schedule of PRIAS). That is, $v \epsilon \{1, 1.5, \ldots\}$ years. To obtain reliable estimates of AUC and MAPE, in each cohort, we restrict v to a maximum time point $v_{\max}$, such that there are at least ten patients who experience upgrading after $v_{\max}$. This maximum time point $v_{\max}$ differs between cohorts, and is given in Table 9.

The results for estimates of AUC and MAPE are summarized in Figure 8, and in Table 10 to Table 16. Results are based on the recalibrated PRIAS model for the GAP3 cohorts. The results show that AUC remains more or less constant in all cohorts as more data becomes available for patients. The AUC obtains a moderate value, roughly between 0.5 and 0.7 for all cohorts. On the other hand, MAPE reduces by a big margin after year one of follow-up. This could be because of two reasons. Firstly, MAPE at year one is based only on four PSA measurements gathered in the first year of follow-up, whereas after year one number of PSA measurements increases. Secondly, patients in year one consist of two sub-populations, namely patients with a correct Gleason grade group 1 at the time of inclusion in AS, and patients

Table 9: **Maximum follow-up period up to which we can reliably predict upgrading-risk**. In each cohort, this time point is chosen such that there are at least 10 patients who experience upgrading after this time point. 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 Active Surveillance.

Cohort	Maximum Prediction Time (years)
PRIAS	6
KCL	3
MUSIC	2
Toronto	8
MSKCC	6
Hopkins	7
UCSF	8.5

who probably had Gleason grade group 2 at inclusion but were misclassified by the urologist as Gleason grade group 1 patients. To remedy this problem, a biopsy for all patients at year one is commonly recommended in all AS programs [11].

Table 10: **Internal validation of predictions of upgrading in PRIAS cohort**. The area under the receiver operating characteristic curve or AUC (measure of discrimination) and mean absolute prediction error or MAPE are calculated over the follow-up period at a gap of 6 months. In addition bootstrapped 95% confidence intervals (CI) are also presented.

Follow-up period (years)	AUC (95% CI)	MAPE (95%CI)
0.0 to 1.0	0.652 [0.611, 0.690]	0.220 [0.214, 0.227]
0.5 to 1.5	0.657 [0.641, 0.673]	0.260 [0.254, 0.265]
1.0 to 2.0	0.661 [0.647, 0.678]	0.187 [0.183, 0.191]
1.5 to 2.5	0.647 [0.596, 0.688]	0.129 [0.122, 0.140]
2.0 to 3.0	0.683 [0.642, 0.723]	0.135 [0.125, 0.146]
2.5 to 3.5	0.692 [0.632, 0.748]	0.118 [0.111, 0.128]
3.0 to 4.0	0.657 [0.603, 0.709]	0.086 [0.080, 0.092]
3.5 to 4.5	0.623 [0.582, 0.660]	0.111 [0.105, 0.116]
4.0 to 5.0	0.619 [0.582, 0.654]	0.126 [0.118, 0.131]
4.5 to 5.5	0.624 [0.537, 0.711]	0.119 [0.103, 0.135]
5.0 to 6.0	0.639 [0.582, 0.696]	0.121 [0.103, 0.138]

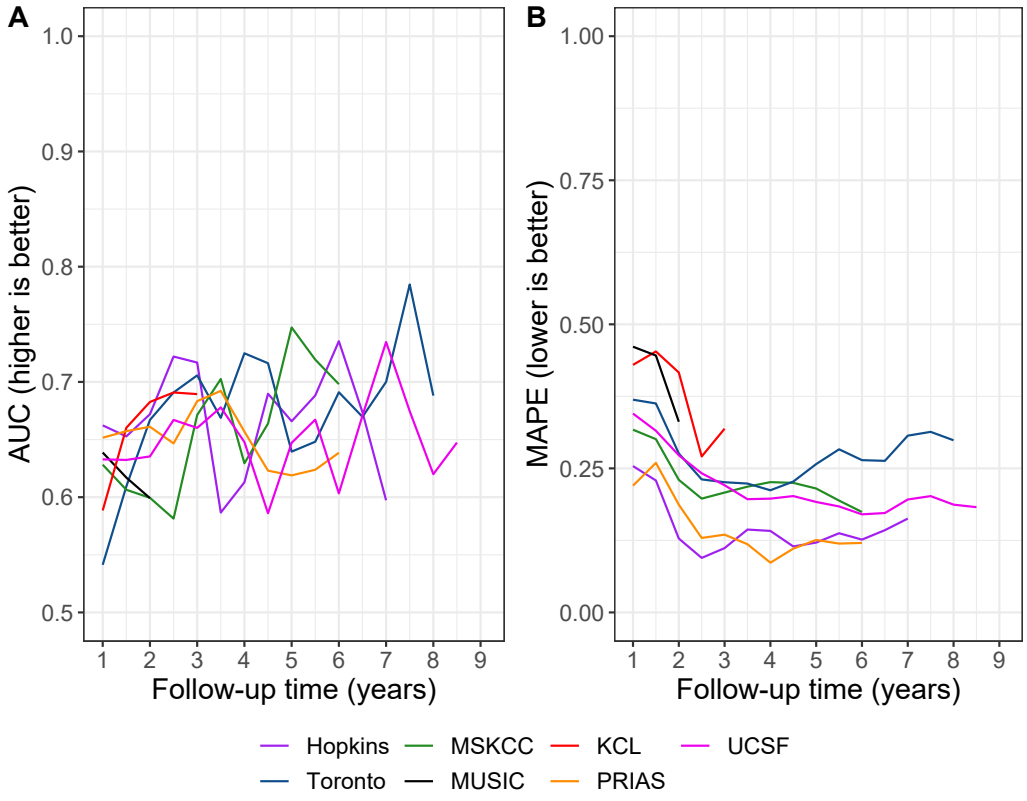

Figure 8: **Validation of dynamic predictions of cause-specific cumulative upgrading-risk**. In **Panel A** we can see that the time dependent area under the receiver operating characteristic curve or AUC (measure of discrimination) is above 0.5 in PRIAS (internal validation), and in Toronto, Hopkins, MSKCC, KCL, and MUSIC AS cohorts (external validation). In **Panel B** we can see that the time dependent root mean squared prediction error or MAPE is similar for PRIAS and Hopkins cohorts. The bootstrapped 95% confidence interval for these estimates are presented in Table 10 to Table 15. 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 Active Surveillance.

Table 11: **External validation of predictions of upgrading in University of Toronto Active Surveillance cohort**. The area under the receiver operating characteristic curve or AUC (measure of discrimination) and mean absolute prediction error or MAPE are calculated over the follow-up period at a gap of 6 months. In addition bootstrapped 95% confidence intervals (CI) are also presented.

Follow-up period (years)	AUC (95% CI)	MAPE (95%CI)
0.0 to 1.0	0.541 [0.470, 0.621]	0.369 [0.352, 0.381]
0.5 to 1.5	0.609 [0.547, 0.661]	0.363 [0.348, 0.376]
1.0 to 2.0	0.667 [0.634, 0.712]	0.276 [0.259, 0.296]
1.5 to 2.5	0.691 [0.651, 0.730]	0.231 [0.205, 0.254]
2.0 to 3.0	0.706 [0.637, 0.762]	0.226 [0.196, 0.260]
2.5 to 3.5	0.669 [0.586, 0.741]	0.224 [0.195, 0.258]
3.0 to 4.0	0.725 [0.649, 0.806]	0.212 [0.184, 0.238]
3.5 to 4.5	0.716 [0.642, 0.793]	0.227 [0.206, 0.258]
4.0 to 5.0	0.640 [0.579, 0.717]	0.257 [0.222, 0.312]
4.5 to 5.5	0.648 [0.579, 0.740]	0.283 [0.247, 0.326]
5.0 to 6.0	0.691 [0.608, 0.793]	0.264 [0.232, 0.302]
5.5 to 6.5	0.670 [0.543, 0.776]	0.263 [0.227, 0.307]
6.0 to 7.0	0.700 [0.544, 0.851]	0.307 [0.258, 0.363]
6.5 to 7.5	0.785 [0.640, 0.866]	0.313 [0.272, 0.360]
7.0 to 8.0	0.688 [0.532, 0.786]	0.299 [0.249, 0.361]

Table 12: **External validation of predictions of upgrading in University of California San Francisco Active Surveillance cohort**. The area under the receiver operating characteristic curve or AUC (measure of discrimination) and mean absolute prediction error or MAPE are calculated over the follow-up period at a gap of 6 months. In addition bootstrapped 95% confidence intervals (CI) are also presented.

Follow-up period (years)	AUC (95% CI)	MAPE (95%CI)
0.0 to 1.0	0.633 [0.585, 0.674]	0.345 [0.337, 0.357]
0.5 to 1.5	0.632 [0.599, 0.673]	0.315 [0.308, 0.323]
1.0 to 2.0	0.635 [0.595, 0.677]	0.273 [0.266, 0.281]
1.5 to 2.5	0.667 [0.628, 0.715]	0.241 [0.224, 0.259]
2.0 to 3.0	0.660 [0.600, 0.713]	0.221 [0.205, 0.238]
2.5 to 3.5	0.678 [0.614, 0.757]	0.197 [0.175, 0.214]
3.0 to 4.0	0.648 [0.574, 0.707]	0.197 [0.179, 0.221]
3.5 to 4.5	0.586 [0.525, 0.638]	0.202 [0.180, 0.229]
4.0 to 5.0	0.647 [0.590, 0.754]	0.192 [0.168, 0.217]
4.5 to 5.5	0.667 [0.582, 0.773]	0.184 [0.159, 0.220]
5.0 to 6.0	0.603 [0.496, 0.696]	0.170 [0.144, 0.207]
5.5 to 6.5	0.671 [0.576, 0.786]	0.173 [0.145, 0.202]
6.0 to 7.0	0.735 [0.663, 0.794]	0.196 [0.166, 0.219]
6.5 to 7.5	0.675 [0.565, 0.769]	0.202 [0.168, 0.231]
7.0 to 8.0	0.620 [0.518, 0.740]	0.187 [0.144, 0.217]
7.5 to 8.5	0.647 [0.538, 0.787]	0.183 [0.146, 0.222]

Table 13: **External validation of predictions of upgrading in Johns Hopkins Active Surveillance cohort**. The area under the receiver operating characteristic curve or AUC (measure of discrimination) and mean absolute prediction error or MAPE are calculated over the follow-up period at a gap of 6 months. In addition bootstrapped 95% confidence intervals (CI) are also presented.

Follow-up period (years)	AUC (95% CI)	MAPE (95%CI)
0.0 to 1.0	0.662 [0.586, 0.715]	0.254 [0.245, 0.265]
0.5 to 1.5	0.653 [0.603, 0.707]	0.229 [0.219, 0.240]
1.0 to 2.0	0.672 [0.604, 0.744]	0.128 [0.115, 0.141]
1.5 to 2.5	0.722 [0.652, 0.792]	0.095 [0.081, 0.111]
2.0 to 3.0	0.717 [0.638, 0.777]	0.112 [0.100, 0.123]
2.5 to 3.5	0.587 [0.493, 0.704]	0.144 [0.129, 0.154]
3.0 to 4.0	0.613 [0.486, 0.742]	0.141 [0.126, 0.156]
3.5 to 4.5	0.690 [0.594, 0.783]	0.115 [0.100, 0.133]
4.0 to 5.0	0.666 [0.572, 0.754]	0.121 [0.104, 0.147]
4.5 to 5.5	0.688 [0.519, 0.779]	0.137 [0.119, 0.161]
5.0 to 6.0	0.735 [0.676, 0.820]	0.126 [0.102, 0.152]
5.5 to 6.5	0.674 [0.581, 0.765]	0.143 [0.121, 0.172]
6.0 to 7.0	0.597 [0.472, 0.712]	0.163 [0.126, 0.195]

Table 14: **External validation of predictions of upgrading in Memorial Sloan Kettering Cancer Center Active Surveillance cohort**. The area under the receiver operating characteristic curve or AUC (measure of discrimination) and mean absolute prediction error or MAPE are calculated over the follow-up period at a gap of 6 months. In addition bootstrapped 95% confidence intervals (CI) are also presented.

Follow-up period (years)	AUC (95% CI)	MAPE (95%CI)
0.0 to 1.0	0.628 [0.577, 0.688]	0.317 [0.316, 0.318]
0.5 to 1.5	0.606 [0.532, 0.657]	0.301 [0.290, 0.311]
1.0 to 2.0	0.599 [0.518, 0.671]	0.230 [0.207, 0.256]
1.5 to 2.5	0.581 [0.504, 0.663]	0.198 [0.168, 0.235]
2.0 to 3.0	0.671 [0.599, 0.741]	0.208 [0.182, 0.232]
2.5 to 3.5	0.703 [0.610, 0.777]	0.218 [0.197, 0.246]
3.0 to 4.0	0.629 [0.499, 0.706]	0.226 [0.194, 0.259]
3.5 to 4.5	0.664 [0.589, 0.756]	0.225 [0.199, 0.262]
4.0 to 5.0	0.747 [0.642, 0.841]	0.215 [0.188, 0.247]
4.5 to 5.5	0.719 [0.597, 0.852]	0.194 [0.165, 0.232]
5.0 to 6.0	0.698 [0.565, 0.792]	0.174 [0.136, 0.227]

Table 15: **External validation of predictions of upgrading in King's College London Active Surveillance cohort**. The area under the receiver operating characteristic curve or AUC (measure of discrimination) and mean absolute prediction error or MAPE are calculated over the follow-up period at a gap of 6 months. In addition bootstrapped 95% confidence intervals (CI) are also presented.

Follow-up period (years)	AUC (95% CI)	MAPE (95%CI)
0.0 to 1.0	0.589 [0.514, 0.653]	0.430 [0.407, 0.450]
0.5 to 1.5	0.660 [0.550, 0.742]	0.453 [0.431, 0.474]
1.0 to 2.0	0.683 [0.604, 0.753]	0.416 [0.396, 0.445]
1.5 to 2.5	0.691 [0.621, 0.766]	0.271 [0.246, 0.297]
2.0 to 3.0	0.689 [0.616, 0.785]	0.319 [0.282, 0.344]

Table 16: **External validation of predictions of upgrading in Michigan Urological Surgery Improvement Collaborative Active Surveillance cohort**. The area under the receiver operating characteristic curve or AUC (measure of discrimination) and mean absolute prediction error or MAPE are calculated over the follow-up period at a gap of 6 months. In addition bootstrapped 95% confidence intervals (CI) are also presented.

Follow-up period (years)	AUC (95% CI)	MAPE (95%CI)
0.0 to 1.0	0.639 [0.607, 0.672]	0.461 [0.450, 0.469]
0.5 to 1.5	0.617 [0.588, 0.652]	0.446 [0.441, 0.453]
1.0 to 2.0	0.599 [0.553, 0.632]	0.331 [0.317, 0.348]

Appendix C. Personalized Biopsies Based on Cause-Specific Cumulative Upgrading-Risk

Consider some real patients from the PRIAS database shown in Figure 10– 12. In line with the protocols of most AS cohorts [12], we first schedule a compulsory biopsy at year one of follow-up. This promises early detection of Gleason upgrade for patients misdiagnosed as low-grade cancer patients or patients who chose AS despite having a higher grade at diagnosis. We also maintain a recommended minimum gap of one year between consecutive biopsies [11]. That is, we intend to develop a personalized schedule of biopsies for these patients starting from the second year. The added benefit of planning biopsies year two onwards is that due to the longitudinal measurements accumulated over two years, and year one biopsy results, we are able to make reasonably accurate predictions of the cause-specific cumulative upgrading-risk.

Using the joint model fitted to the PRIAS dataset, we first obtain a patient's cause-specific cumulative upgrading-risk over the entire future follow-up period (see 4), given their accumulated two year clinical data. Typically biopsies may be decided on the same visit on which PSA is measured. Let $U = u_1, \ldots, u_L$ represent a schedule of such visits (e.g., every six months in prostate cancer for PSA measurement), where $u_1 = v$ is also the time of the current visit, and u_L is the horizon up to which we intend to plan biopsies. Depending upon how much training/validation data is available, this horizon differs between cohorts (Table 17). First, we make L successive decisions for conducting biopsies on each of the L future visit times $u_l \in U$. Specifically, we decide to conduct a biopsy at time u_l if the conditional cumulative-risk of upgrading at u_l is larger than a certain risk threshold $0 \leq \kappa \leq 1$ (e.g., $\kappa = 12\%$ risk as shown in Figure 9). If a biopsy gets planned at time u_l, then the successive biopsy decision at time u_{l+1} is made using an updated cumulative-risk profile. This updated cumulative-risk profile accounts for the possibility that upgrading may occur after time $u_l < T_j^*$. The biopsy decisions on each future visit time u_l are defined as:

$$Q_j^{\kappa}(u_l \mid t_l, v) = I\big\{R_j(u_l \mid t_l, v) \geq \kappa\big\},$$

$$t_l = \left\{ \begin{array}{lll} t, & \text{if} & l = 1 \\ t_{l-1}, & \text{if} & Q_j^{\kappa}(u_{l-1} \mid t_{l-1}, v) = 0, l \geq 2 \\ u_{l-1}, & \text{if} & Q_j^{\kappa}(u_{l-1} \mid t_{l-1}, v) = 1, l \geq 2 \end{array} \right\}.$$

The cumulative-risk $R_j(u_l \mid t_l, v)$ at future visit time u_l utilizes the time t_l

as the time of the last conducted biopsy on which upgrading may not be observed. However, the contribution of the observed longitudinal data $\mathcal{Y}_j(v)$ in the risk function remains the same over all time points in U. The biopsy decision at time u_l is denoted by $Q_j^\kappa(u_l \mid t_l, v)$. Via the indicator function $I(\cdot)$ it obtains a value 1 (or 0) when a biopsy is to be conducted (or not conducted) at time u_l. The subset of future time points in U on which a biopsy is to be performed results into a personalized schedule of planned future biopsies, given by:

$$S_j^\kappa(U \mid t, v) = \big\{u_l \in U \mid Q_j^\kappa(u_l \mid t_l, v) = 1\big\}. \tag{6}$$

The personalized schedule in (6) is updated as more patient data becomes available over subsequent follow-up visits.

Appendix C.1. Expected Time Delay in Detecting Upgrading

The schedule $S_j^\kappa(U \mid t, v)$ manifests a personalized biopsy plan for the j-the patient. However, the time delay in detecting upgrading that may subsequently be observed depends on the true time of upgrading T_j^* of the patient. Since two different patients with the same timing of biopsies will expect different time delays, we estimate it in a patient-specific manner as well. Although, this calculation is not limited to personalized schedules only, but can be done for any schedule S of biopsies with N time points $S = \{s_n \mid n = 1, \ldots, N\}$.

For each of the N planned biopsies there exist N possible time intervals $s_{n-1} < T_j^* \leq s_n$ in which upgrading may be observed. Correspondingly, there are N possible time delays in detecting upgrading $s_n - T_j^*$. Given a schedule S, the true time delay in detecting upgrading D_j that the patient will experience can be defined as:

$$D_j(S \mid t) = \left\{ \begin{array}{ll} s_1 - T_j^*, & \text{if} \quad t < T_j^* \leq s_1 \\ \ldots & \\ s_N - T_j^*, & \text{if} \quad s_{N-1} < T_j^* \leq s_N \end{array} \right\}. \tag{7}$$

The time delay is cannot be defined for the scenario in which the patient obtains upgrading after the time of the last biopsy in the schedule $T_j^* > s_N$. Hence, this delay should be interpreted as the delay that will be observed if the patient will experience upgrading before time of the last planned biopsy at $T_j^* \leq s_N$. To estimate the expected value of $D_j(\cdot)$ in a patient-specific manner, we exploit the personalized cumulative-risk profile of the patient

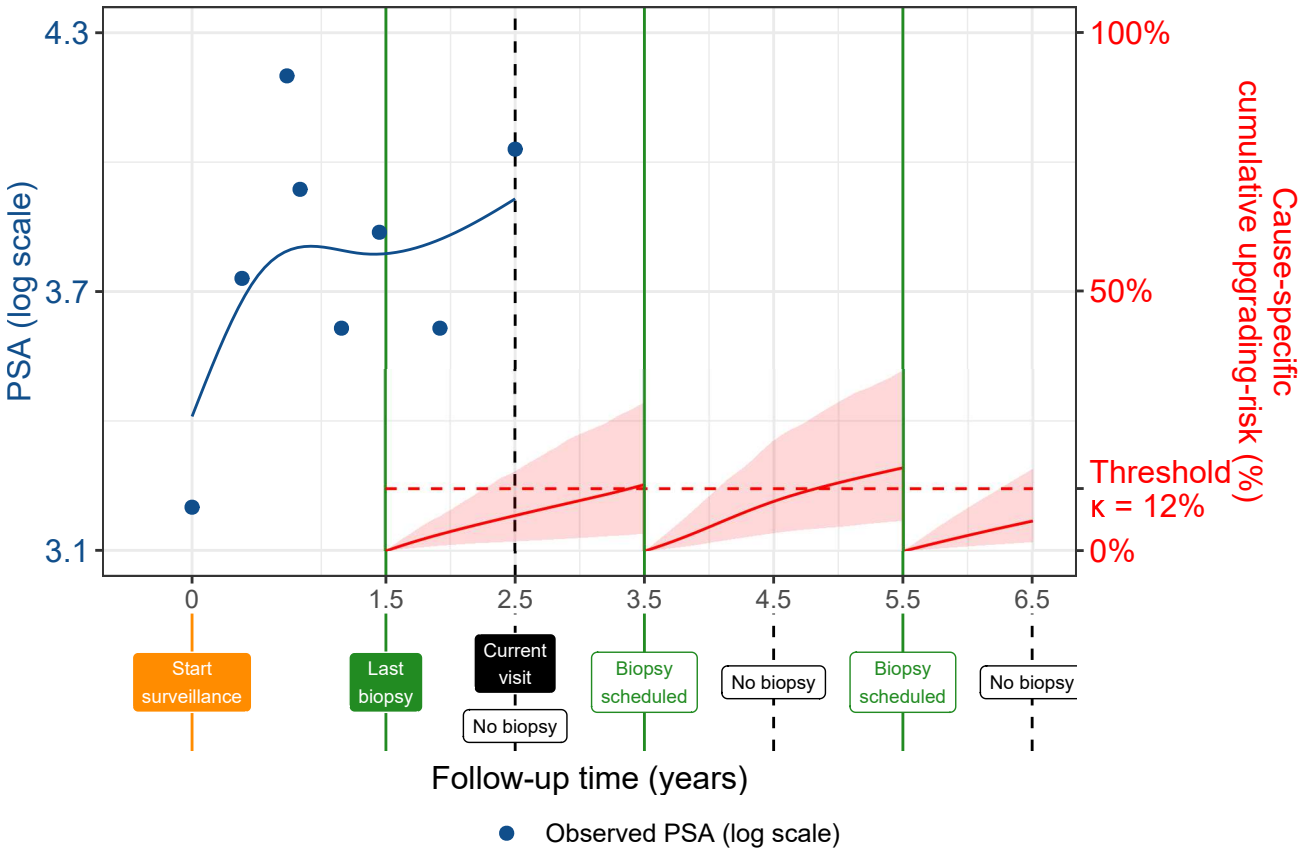

Figure 9: **Illustration of Personalized Biopsy Decisions Using Patient-specific Conditional Cumulative Upgrading-risk**. The last biopsy on which upgrading was not observed was conducted at $t = 1.5$ years. The current visit time of the patient is $v = 2.5$ years. Decisions for biopsy need to be made at a gap of every one year starting from the current visit until a horizon of 6.5 years. That is, $U = \{2.5, 3.5, 4.5, 5.5, 6.5\}$ years. Based on an example risk threshold of 12% ($\kappa = 0.12$) the future biopsy decisions at time points in U lead to a personalized schedule $S_j^{\kappa^*}(U \mid t = 1.5, v = 2.5) = \{3.5, 5.5\}$ years. The conditional cumulative-risk profiles $R_j(u_l \mid t_l, v)$ employed in (Appendix C) are shown with red line (confidence interval shaded). It is called 'conditional' because, for example, the second biopsy at future time 5.5 years, is scheduled after accounting for the possibility that upgrading (true time T_j^*) may not have occurred until the time of the previously scheduled biopsy at time $T_j^* > 3.5$ years. All values are illustrative.

defined in (4). Specifically, the expected time delay $E\{D_j(\cdot)\}$ can be calculated as the weighted sum of N possible time delays defined in (7). The n-th weight is equal to the probability of the patient obtaining upgrading in the n-th interval $s_{n-1} < T_j^* \leq s_n$.

$$E\Big\{D_j(S \mid t)\Big\} = \sum_{n=1}^{N} \Big\{s_n - E(T_j^* \mid s_{n-1}, s_n, v)\Big\} \times \Pr\Big\{s_{n-1} < T_j^* \leq s_n \mid T_j^* \leq s_N, \mathcal{Y}_j(v), \mathcal{A}_n\Big\}, \quad s_0 = t$$

$$E(T_j^* \mid s_{n-1}, s_n, v) = s_{n-1} + \int_{s_{n-1}}^{s_n} \Pr\Big\{T_j^* \geq u \mid s_{n-1} < T_j^* \leq s_n, \mathcal{Y}_j(v), \mathcal{A}_n\Big\} \mathrm{d}u,$$

where $E(T_j^* \mid s_{n-1}, s_n, v)$ denotes the conditional expected time of upgrading for the scenario $s_{n-1} < T_j^* \leq s_n$, and is calculated as the area under the corresponding survival curve.

The personalized expected time delay in detecting upgrading has the advantage that it is updated over follow-up as more patient data become available. Since it can be calculated for any schedule, patients and doctors can utilize it along with the plan of biopsies to compare schedules before making a decision. Although, in order to have a fair comparison of time delays between different schedules for the same patient, a compulsory biopsy at a common horizon time point should be planned in all schedules.

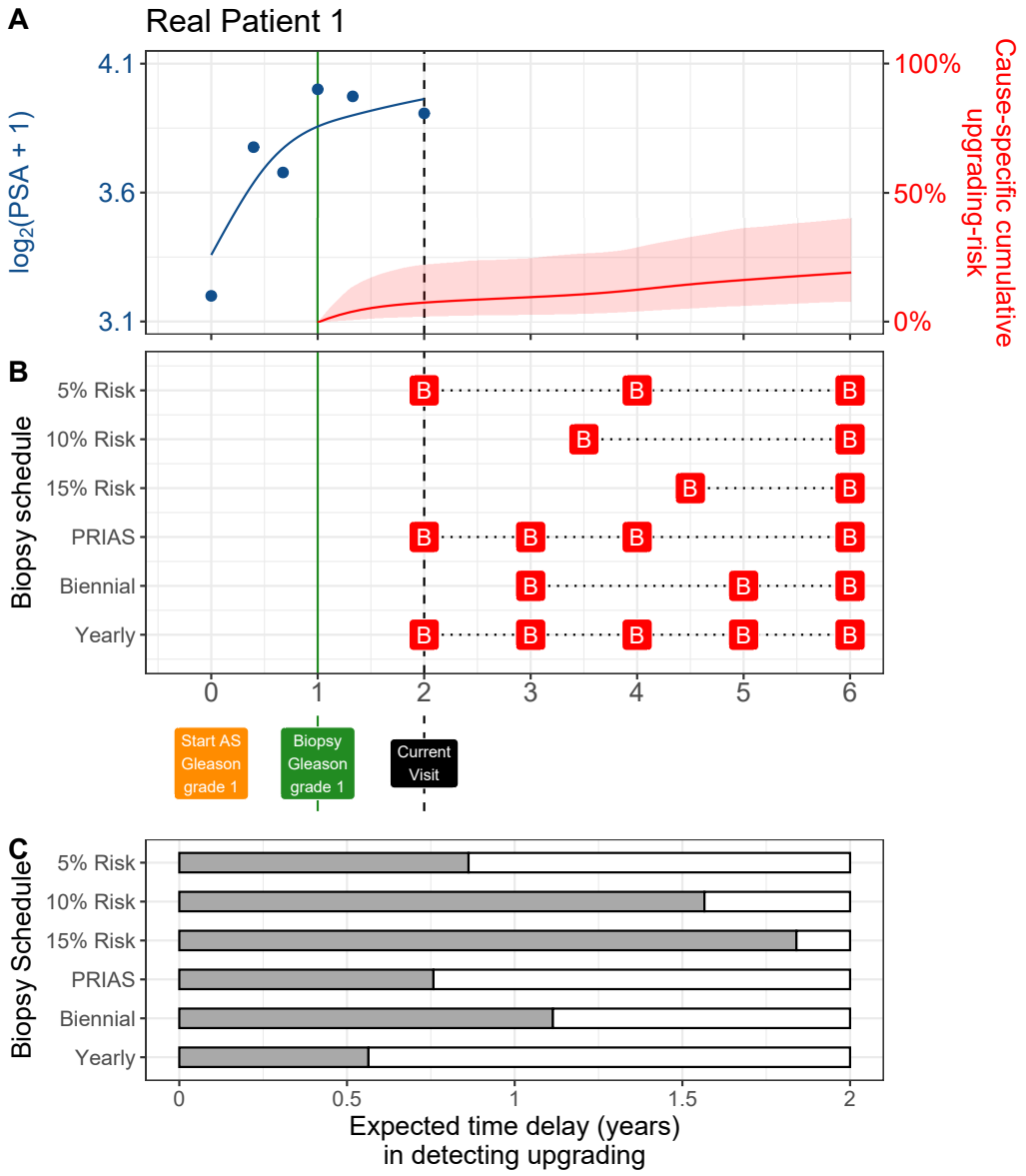

Figure 10: **Personalized and fixed schedules of biopsies for patient 1**. **Panel A:** shows the observed and fitted $\log_2(\text{PSA} + 1)$ measurements (Equation 1), and the dynamic cause-specific cumulative upgrading-risk (see Appendix B) over follow-up period. **Panel B** shows the personalized and fixed schedules of biopsies with a 'B' indicating times of biopsies. **Panel C** various schedules are compared in terms of the 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, Table 17) in all schedules for a meaningful comparison between them.

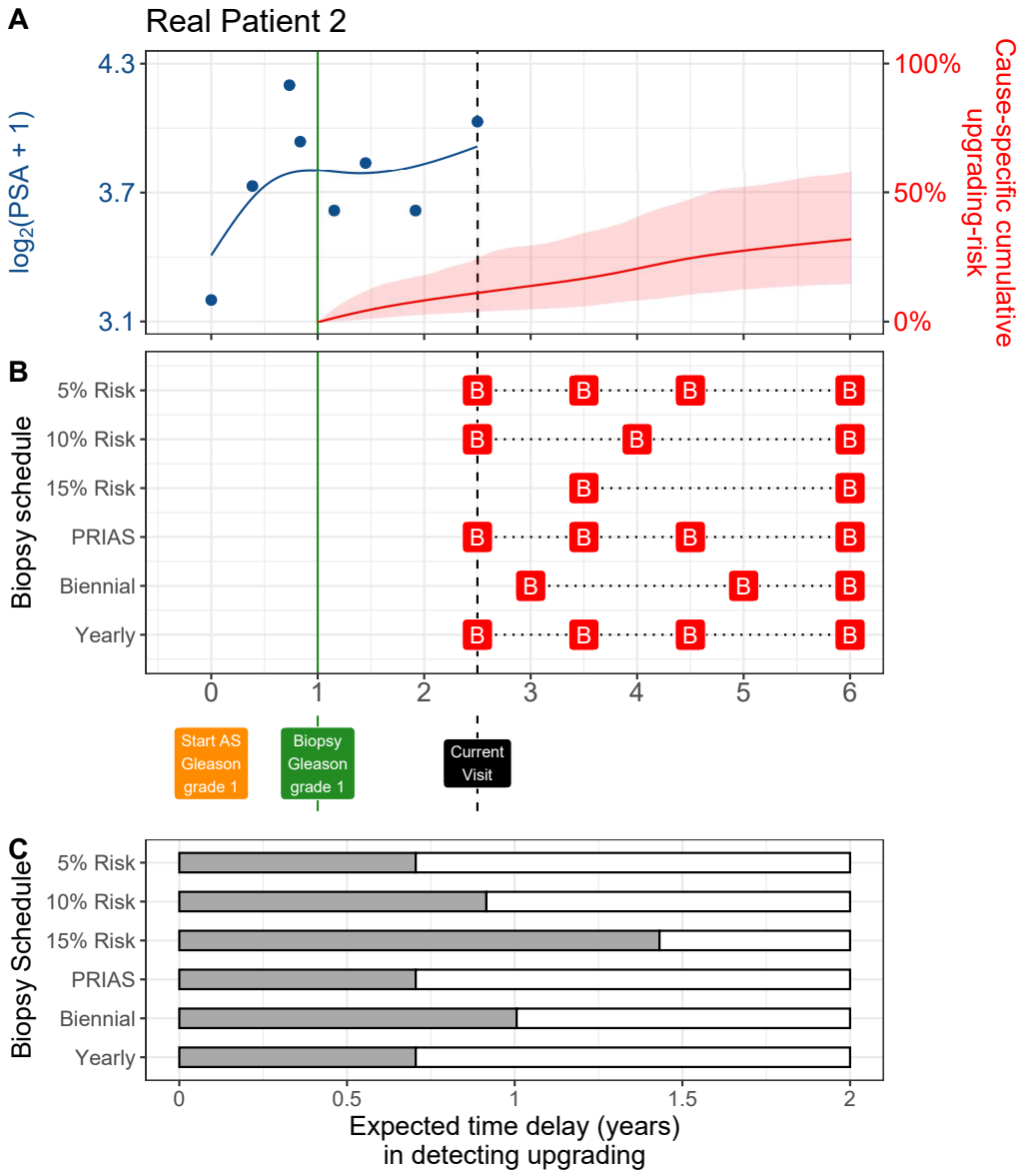

Figure 11: **Personalized and fixed schedules of biopsies for patient 2**. **Panel A:** shows the observed and fitted $\log_2(\text{PSA} + 1)$ measurements (Equation 1), and the dynamic cause-specific cumulative upgrading-risk (see Appendix B) over follow-up period. **Panel B** shows the personalized and fixed schedules of biopsies with a 'B' indicating times of biopsies. **Panel C** various schedules are compared in terms of the 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, Table 17) in all schedules for a meaningful comparison between them.

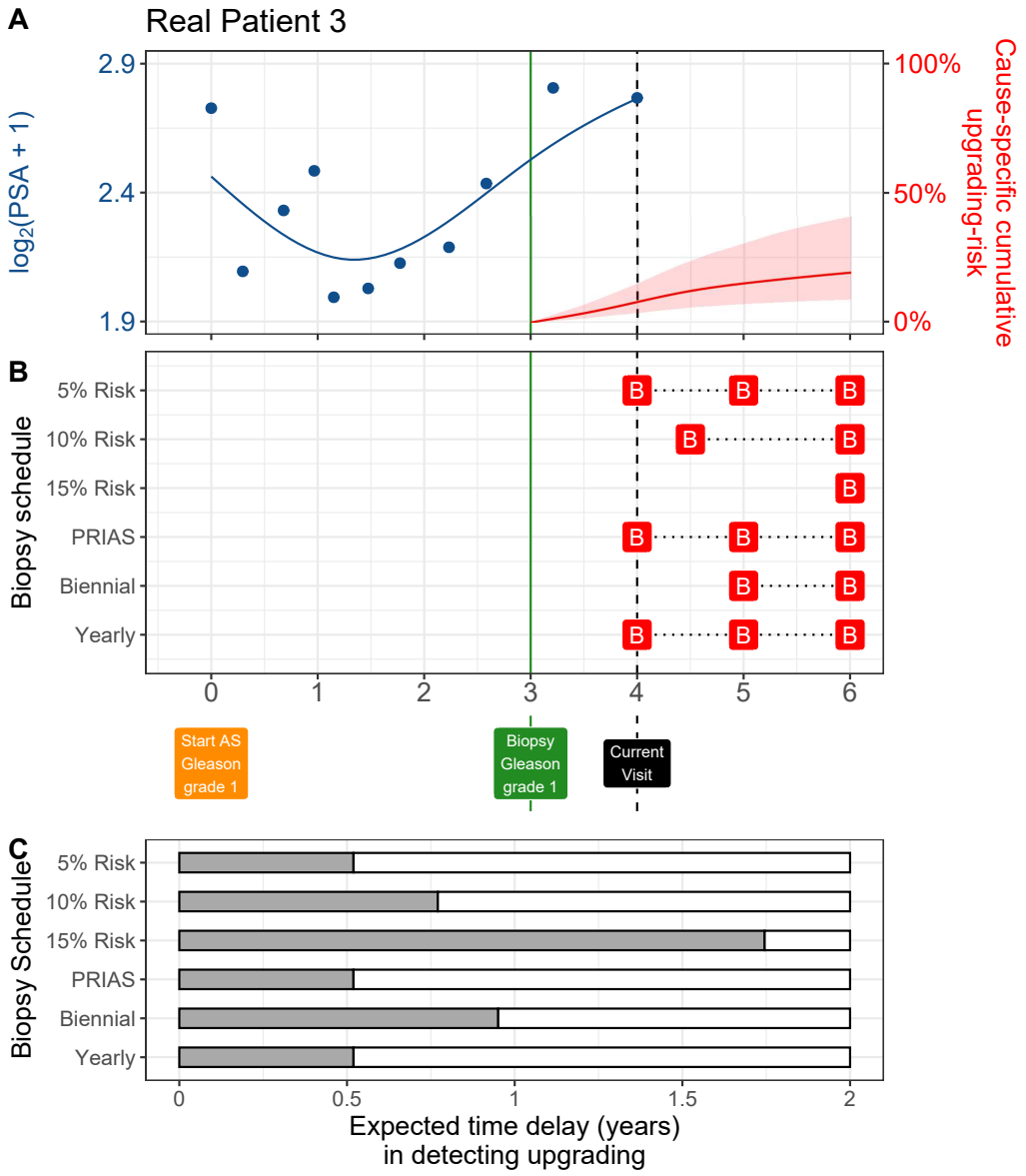

Figure 12: **Personalized and fixed schedules of biopsies for patient 3**. **Panel A:** shows the observed and fitted $\log_2(\text{PSA}+1)$ measurements (Equation 1), and the dynamic cause-specific cumulative upgrading-risk (see Appendix B) over follow-up period. **Panel B** shows the personalized and fixed schedules of biopsies with a 'B' indicating times of biopsies. **Panel C** various schedules are compared in terms of the 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, Table 17) in all schedules for a meaningful comparison between them.

Table 17: **Maximum follow-up period up to which we can reliably make personalized schedules**. In each cohort, this time point is chosen such that there are at least 10 patients who experience upgrading after this time point. 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 Active Surveillance.

Cohort	Maximum Personalized Schedule Time (years)
PRIAS	6
KCL	3
MUSIC	2
Toronto	8
MSKCC	6
Hopkins	7
UCSF	8.5

Appendix D. Web-Application for Practical Use of Personalized Schedule of Biopsies

We implemented our methodology in a web-application to assist patients and doctors in better decision making. It works on desktop as well as mobile devices. The cohorts that are currently supported in this web-application are PRIAS and the largest six cohorts from the GAP3 database [6]. These are 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 Active Surveillance (UCSF). The web application is hosted at `https://emcbiostatistics.shinyapps.io/prias_biopsy_recommender/`.

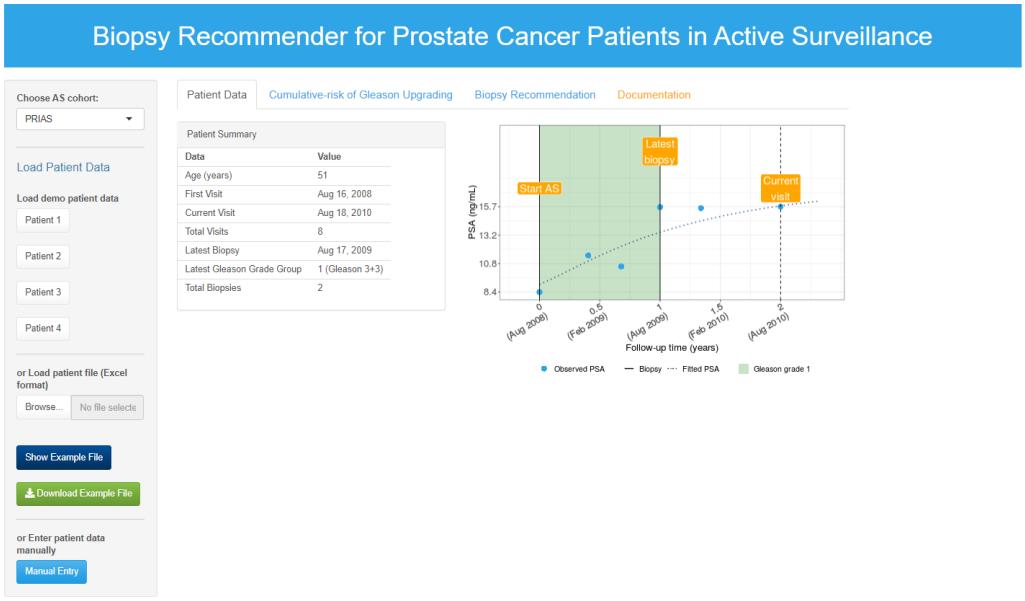

Figure 13: Landing page of the web-application. Panel on the left allows users to load patient data and panel on the right provides information. Patient data can be entered manually, or via Excel files. In addition, demo patient data is already uploaded to assist users in understanding the web-application.

Appendix E. Source Code

The R code for fitting the joint model to the PRIAS dataset, is at `https://github.com/anirudhtomer/prias/tree/master/src/clinical_gap3`. We refer to this location as 'R_HOME' in the rest of this document.

Appendix E.1. Fitting the Joint Model to the PRIAS dataset

Accessing the dataset: The PRIAS dataset is not openly accessible. However, access to the database can be requested via the contact links at `https://www.prias-project.org`.

Formatting the dataset: This dataset, however, is in the so-called wide format and also requires the removal of incorrect entries. This can be done via the R script `R_HOME/dataset_cleaning.R`. This will lead to two R objects, namely 'prias_final.id' and 'prias_long_final'. The 'prias_final.id' object contains information about the time of upgrading for PRIAS patients. The 'prias_long_final' object contains longitudinal PSA measurements, the time of biopsies and results of biopsies.

Fitting the joint model: We use a joint model for time-to-event and longitudinal data to model the evolution of PSA measurements over time, and to simultaneously model their association with the risk of upgrading. The R package we use for this purpose is called **JMbayes** (https://cran.r-project.org/web/packages/JMbayes/JMbayes.pdf). The API we use, however, is currently not hosted on CRAN, and can be found here: `https://github.com/anirudhtomer/JMbayes`. The joint model can be fitted via the script `R_HOME/analysis.R`. It takes roughly 6 hours to run on an Intel Core-i5 machine with four cores and 8GB of RAM.

The graphs presented in the main manuscript, and the supplementary material can be generated by the scripts in `R_HOME/plots/`.

Appendix E.2. Validation of Predictions of Upgrading

Validations can be done using the scripts `R_HOME/validation/auc_brier/auc_calculator.R`, and `R_HOME/validation/auc_brier/gof_calculator.R`. For external validation access to GAP3 database is required.

Appendix E.3. Creating Personalized Schedules of Biopsies

Once a joint model is fitted to the PRIAS dataset, personalized schedules of biopsies based on the risk of upgrading for new patients can be developed as shown in the script `R_HOME/plots/demo_schedule_supplementary.R` or directly using the script `https://raw.githubusercontent.com/anirudhtomer/prias/master/src/lastpaper/pers_schedule_api.R`.

Appendix E.4. Source Code for Web Application

Source code for the shiny web application which provides biopsy schedules for patients can be found at `R_HOME/shinyapp`

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_ critical revision of the manuscript for important intellectual content	Tomer, Nieboer, Roobol, Bjartell, Steyerberg, Rizopoulos
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_ other (specify)	none

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☐ Design and conduct of the study
☒ Collection of the data
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☐ Analysis
☐ Interpretation of the data
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☐ Approval of the manuscript

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Acknowledgment Statement

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Take Home Message

Personalized prostate biopsies are a novel alternative to fixed one-size-fits-all schedules. The underlying statistical models are made available through a user-friendly web-application and may help to reduce unnecessary prostate biopsies while maintaining cancer control.