Personalized Risk Based Shared Decision Making Framework for Biopsies in Prostate Cancer Active Surveillance[☆]

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Abstract

`Background`: Low-risk prostate cancer patients enrolled in active surveillance undergo repeat biopsies. Treatment is provided upon detection of biopsy Gleason upgrade.

`Objective`: Reduce the number of biopsies for patients who do not need them

`Design, Setting, and Participants`: adadadad

`Outcome Measurements, and Statistical Analysis`: adadadad

`Results and Limitations`: adadadad

`Conclusions`: adadadad

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`Patient Summary`: adadadad

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

1. Introduction

Patients with low- and very low-risk screening-detected localized prostate cancer (PCa) are usually advised active surveillance (AS) instead of immediate radical treatment [1]. In AS, PCa progression is routinely monitored via prostate-specific antigen (PSA), digital rectal examination, and the Gleason score from repeat prostate biopsies. Among these, the Gleason score is the strongest indicator of cancer related outcomes. Thus, patients are commonly advised curative treatment upon detecting a Gleason score > 6 (referred to as reclassification hereafter) [2].

Since biopsies are scheduled intermittently, reclassification is always detected with a delay. The smaller this delay is, the larger is the window of opportunity for curative treatment. To this end, majority of the AS programs worldwide, schedule biopsies every 12-24 months for all patients [3, 4]. Such fixed and frequent biopsies may benefit a small proportion of men with a high risk of reclassification. However, for many of the *slow progressing* patients (see Figure 1) frequent biopsies are redundant . Biopsies are also invasive, painful and prone to medical complications. The unnecessary burden of biopsies, and patient non-compliance [5] to frequent biopsies, has raised questions about the optimal time interval between subsequent biopsies [6, 7].

The simplest solution to frequent biopsies is reducing the frequency of biopsies for all patients. However, simulation studies have suggested that reducing the frequency beyond 24 months may not leave sufficient window of opportunity for curative treatment [6]. Although, even with a gap of 24 months, up to five unnecessary biopsies over ten years of follow-up may still be scheduled for *slow progressing* patients. A promising alternative to such

fixed decision of biopsies are the risk based decisions of biopsies. Consider for instance the two patients shown in Figure 2. Both patients had their latest biopsy at year one of follow-up and are now scheduled for a biopsy after a 24 month gap at year three. The PSA profile of patient A is stable and the PSA profile of patient B is rising. The cumulative risk of reclassification of patient B at year three is also higher than patient A's. Consequently, at year three he is a more suitable candidate for biopsy than patient A.

The first challenge in such a risk based approach is the consolidation of observed patient data (e.g., PSA, previous biopsy results) into estimates of the risk of reclassification (Figure 2). To this end, previous studies have employed joint models for time-to-event and longitudinal data [9, 10, 11]. A subsequent challenge however, is to translate these risk estimates into clinical decisions. For example, a 10% risk can be perceived as high/low depending upon the patient's age. Patients may also weigh the risk of reclassification with the potential consequences of another biopsy. Two such consequences are the delay in detection of reclassification (smaller is beneficial), and the total burden of biopsies. These consequences vary between the patients, and also over the follow-up period for the same patient.

The goal of this work is to assist patients and doctors in making better decisions of biopsies than fixed and frequent biopsies. We intend to achieve this by providing patient- and visit specific risks of reclassification. To further facilitate shared decision making, we also provide estimates of the delay in detection of reclassification and the total burden of biopsies. To this end, we fit a prediction (joint) model to the world's largest AS dataset, PRIAS [2]. We then validate the predictions in multiple external cohorts that are

part of the GAP3 database. Lastly, we implement risk based schedules as a web-application, and demonstrate them with real patient data.

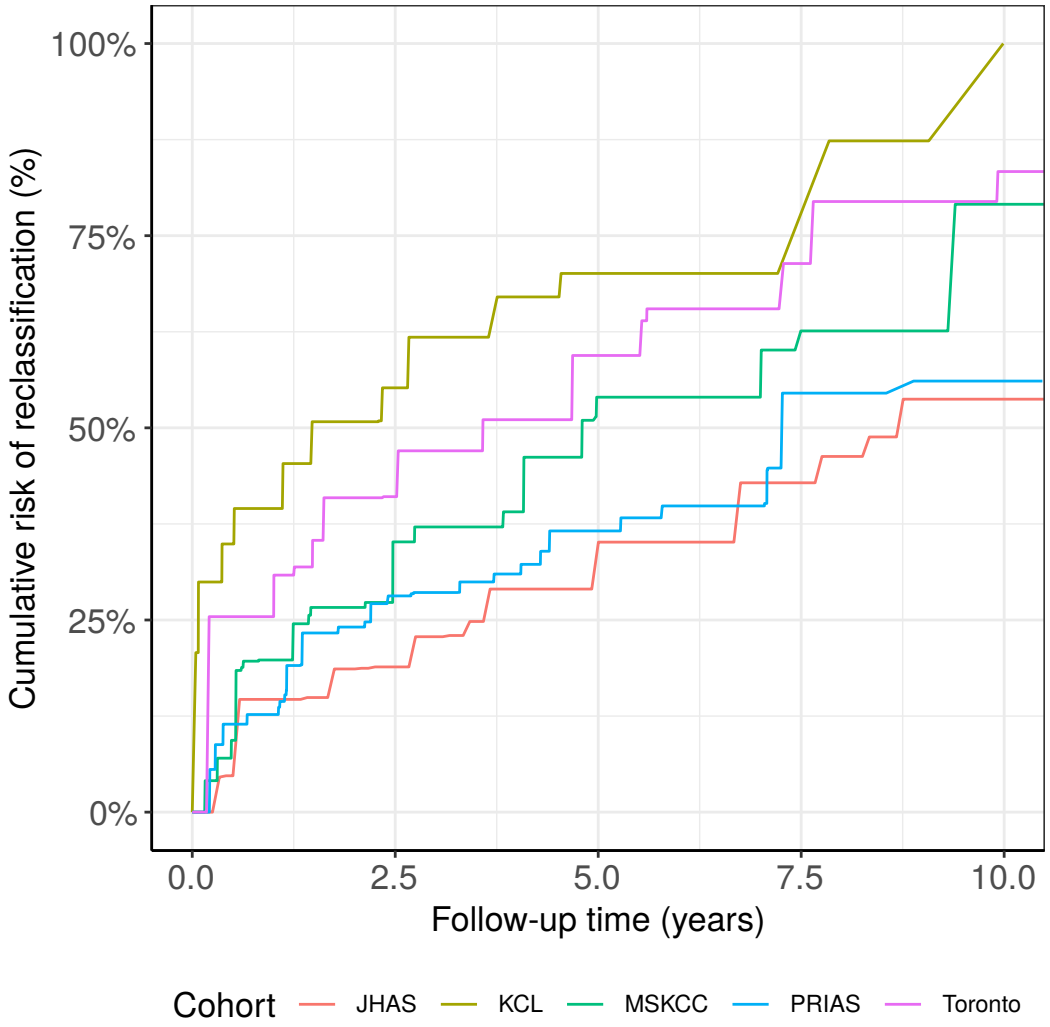

Figure 1: **Active surveillance cancer patients are often *slow progressing***. Graph shows estimated cumulative risk of having a Gleason score > 6 in five of the largest AS studies that are part of the GAP3 database [8]. In all cohorts except KCL, roughly 50% patients may not require any biopsy in first five years. In the world's largest AS cohort PRIAS and in JHAS, roughly 50% patients may not require any biopsy in the first ten years. **Legend**: *JHAS*: 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

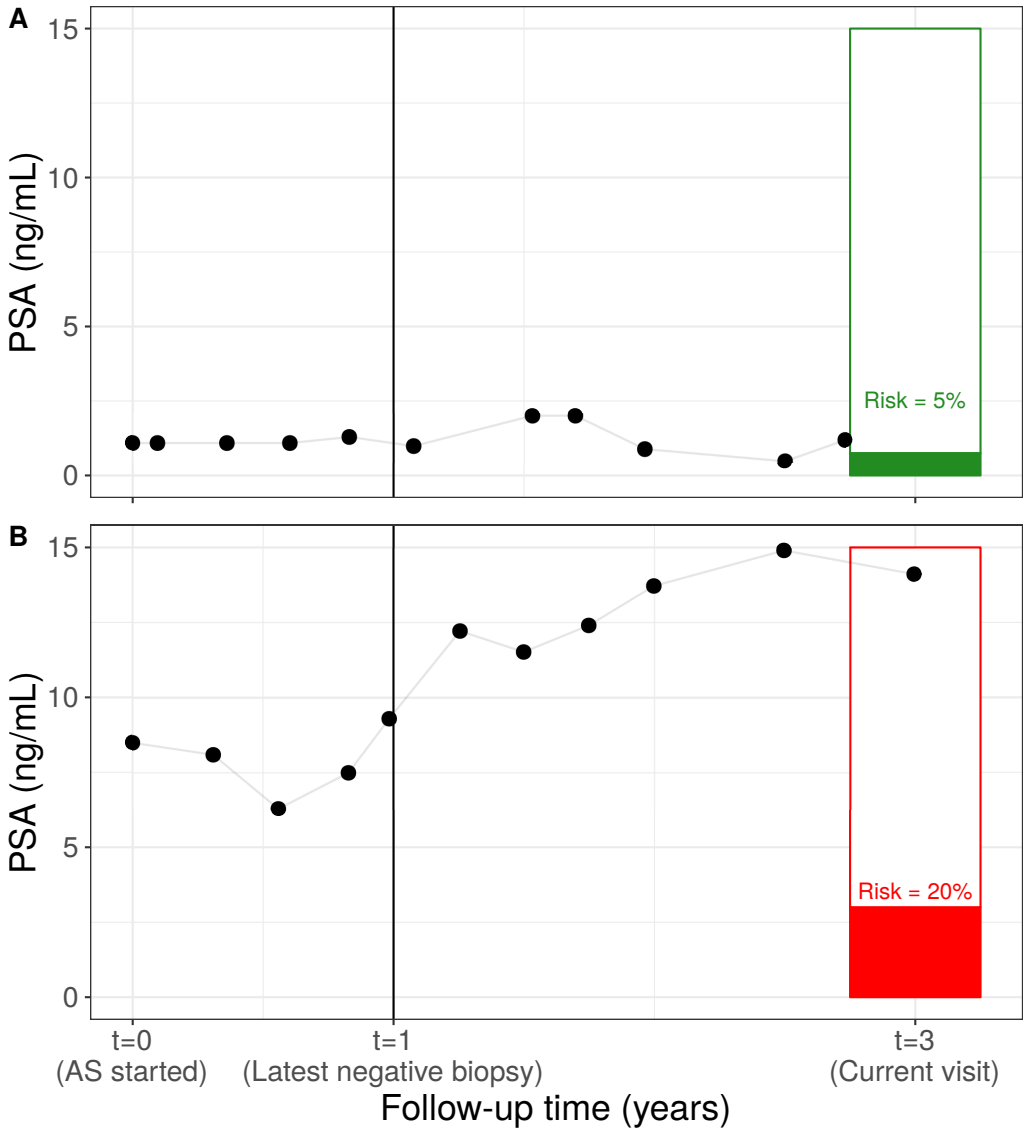

Figure 2: **Motivation for risk based decisions of biopsy**: Patient A and B had their latest biopsy at year one of follow-up. Patient A's prostate-specific antigen (PSA) profile remained stable until the current visit time at year three. Consequently, his cumulative risk of reclassification at year three is 5%. On the other hand patient B's PSA profile has shown a rise since the latest biopsy, and his cumulative risk of reclassification is also 20%. Patient B is a better candidate for biopsy than Patient A.

2. Patients and Methods

2.1. Study Cohort

Prostate Cancer International Active Surveillance (PRIAS) is an ongoing prospective cohort study of men with low- and very-low risk PCa diagnoses [2]. More than 100 medical centers from 17 countries worldwide contribute in PRIAS `www.prias-project.org`. We use the data collected between December 2006 (beginning of PRIAS study) and May 2019. The follow-up protocol scheduled PSA measurements (ng/mL) every three months for the first two years and every six months thereafter. Repeat biopsies were scheduled after one, four, seven, and ten years. Additional yearly biopsies were scheduled for patients having PSA doubling time between three and ten years. Reclassification (Gleason > 6) was observed in 866 patients, and ... were provided treatment (see Table 1). Treatment in absence of reclassification may have been advised on the basis of PSA, number of biopsy cores with cancer, or anxiety. However, we focus only on Gleason reclassification because of its strong association with cancer related outcomes. Due to the periodical nature of biopsies, the time of reclassification was only known as a time interval in which it occurred.

Table 1: **Patient characteristics for the PRIAS dataset**. The primary event of interest is disease reclassification. IQR: interquartile range, PSA: prostate-specific antigen.

Characteristic	Value
Total patients	5270
Disease reclassification (primary event)	866
Loss to follow-up (anxiety or unknown)	685
Patient removal on the basis of protocol	464
Death (unrelated to prostate cancer)	61
Death (related to prostate cancer)	2
Median age at diagnosis (years)	70 (IQR: 65–75)
Median follow-up period per patient (years)	1.9 (IQR: 1.0–3.8)
Total PSA measurements	46015
Median number of PSA measurements per patient	7 (IQR: 7–12)
Median PSA value (ng/mL)	5.6 (IQR: 4.0–7.5)
Total biopsies	11042
Median number of biopsies per patient	2 (IQR: 1–3)

2.2. Statistical Methods

The goal of the statistical analysis of the PRIAS data was to develop a model for predicting the time of reclassification. To this end, for each patient we have the information about his age at the start of AS, all observed PSA measurements, and the history of biopsies. Since PRIAS data is longitudinal in nature, the PSA measurements of a patient are correlated. PSA can be higher when measured closer to the time of reclassification. An additional complication is that such higher values are also often missing once a patient obtains reclassification. The vice versa, that is, reclassification is more likely when PSA increases is also plausible. A commonly used statistical method to model such complex correlation between a longitudinal outcome (PSA) and a time-to-event (reclassification) outcome is the joint model for time-to-event and longitudinal data [11, 9, 10].

A joint model exploits patient-specific random effects (similar to random effects of a linear mixed effects model) to act as a common source of correlation between various outcomes (see Figure 3). These random effects manifest the unobservable patient-specific state of PCa. The joint model has separate sub-models for PSA and time of reclassification. However, both models utilize these random effects as covariates in the model. We used a linear mixed effects model for $\log_2\{\text{PSA} + 1\}$ transformed measurements, and a relative risk model (similar to cox model) for time of reclassification. The mixed effects model for PSA uses random effects to non-linearly model the evolution of PSA over time in a patient-specific manner. Simultaneously, in the relative risk model we establish the correlation between time of reclassification and PSA. This is achieved by using fitted $\log_2\{\text{PSA} + 1\}$ value and velocity as

time dependent covariates, that is, random effects are used indirectly. Unlike observed $\log_2\{\text{PSA} + 1\}$ values, the fitted values are free of measurement errors. The $\log_2\{\text{PSA} + 1\}$ velocity is not modeled separately, but is rather mathematically derived as the rate of change of fitted $\log_2\{\text{PSA} + 1\}$ value over time. Since fitted $\log_2\{\text{PSA} + 1\}$ profiles are modeled non-linearly, the corresponding velocity is also allowed to change over follow-up.

The various parameters of the two sub-models estimated jointly using the R **JMbayes** [12]. This package utilizes the Bayesian methodology to estimate model parameters. The parameters and 95% credible intervals are presented in Table.. of Appendix.

2.3. Assessment of Predictions

We assessed the goodness of fit of our model using both in-sample and out-of-sample predictions of reclassification. For out-of-sample predictions we utilized the five largest AS cohorts that constitute the GAP3 database [8]. We measured the accuracy of these predictions via two commonly used measures, namely the root mean squared prediction error (RMSPE) and the area under the receiver operating characteristic curve (AUC). Both of these measures take a value between zero and one. The RMSPE represents the difference between the true reclassification status of a patient, and the predicted risk of reclassification. Ideally the RMSPE should be zero. The AUC indicates if the model is able to discriminate between patients who obtain reclassification and those do not obtain it. Ideally it should be equal to one. In practice it should not be less than 0.5 (AUC of random discrimination). Since PRIAS is a longitudinal study, we compute these measures in a time dependent manner, at a gap of every one year until xx years of follow-up (95% quantile

of observed reclassification times).

2.4. Estimate Risk of Reclassification and Consequences of Biopsies

Consider a new patient with a certain history of biopsies, and PSA measurements. Using the joint model fitted to the PRIAS dataset, we first obtain his cumulative risk of reclassification over the entire follow-up period.

In order to subsequently apply a cumulative risk based rule for the decision of biopsy requires a maximum risk threshold as an input. That is, a biopsy decision

We also provide an estimate of the number and time of biopsies that may be conducted, and the corresponding estimate of delay in detection of time of reclassification. Simultaneously, the patient is provided estimate of the number of time of biopsies with fixed schedule of biopsies. This allows patients to weigh harms and benefits of each strategy. We also implement this in a web-based risk calculator.

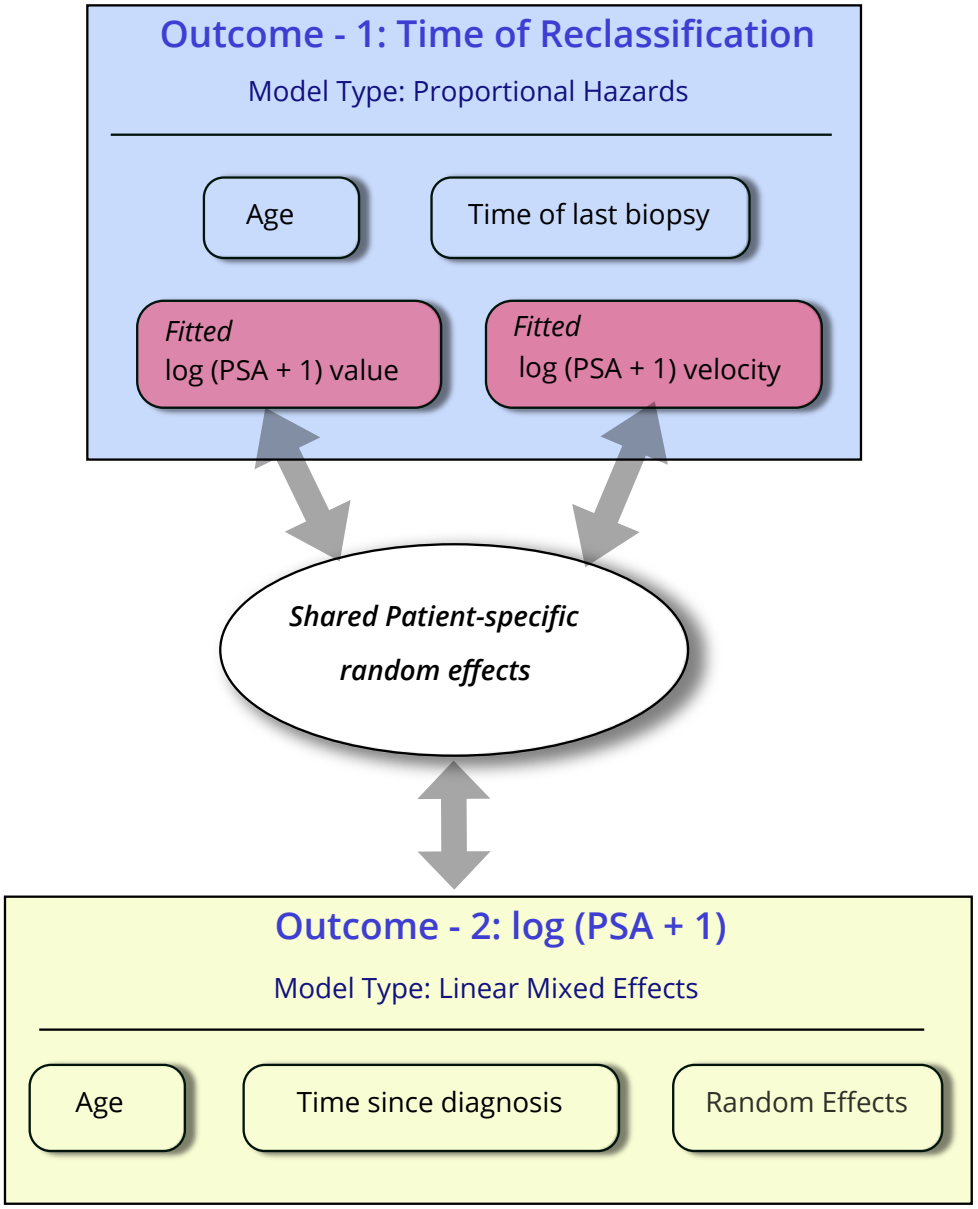

Figure 3: **Diagram of the joint model**: Per patient we observe the $\log_2\{\text{PSA} + 1\}$ transformed PSA, and the results of biopsies. We combine information from these observations to estimate the time of disease reclassification. To this end, we use a linear mixed effects model for $\log_2\{\text{PSA} + 1\}$ measurements, and proportional hazards model for time of disease reclassification. The time of disease reclassification depends on patient age, time of latest negative biopsy and underlying trend of PSA. To account for the correlation between PSA measurements and time of reclassification, the two models share patient-specific random effects in their model equations.

135 *2.5. Model Assessment*

136 We evaluated the accuracy of our predictios

3. Results

4. Discussion

Resources are more for only serious patients, better decisions like in the case of prostatectomy patients....so personalized approch can lead to better decisions overall as well

Such a shared random effect structure allows easy addition of more disease progression indicators (e.g., MRI information) when they are available in future. Furthermore, this structure also allows the follow-up schedule for outcomes/biopsies to depend on the observed values of each other. This is especially important because yearly biopsies in the PRIAS program are scheduled on the basis of the observed PSA doubling time of a patient.

5. Conclusions

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Here are two sample references:.

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