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Title	Predicting recurrence-free survival in prostate cancer following surgical intervention
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Publication date	2022-03-01
Original Citation	O'Donnell, A., Moghaddam, S., Cronin, M. and Wolsztynski, E. (2022) 'Predicting Recurrence-Free Survival in Prostate Cancer Following Surgical Intervention', IACR 5oth Annual Conference, Irish Association for Cancer Research Early Career Researcher Symposium Cork, Ireland, 30 Mar-01 Apr.
Type of publication	Conference item
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Download date	2026-11-17 12:11:26
Item downloaded from	https://hdl.handle.net/10468/14072

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Predicting Recurrence-Free Survival in Prostate Cancer Following Prostatectomy

Prostate cancer is among the most common cancers for men globally, accounting for 13% of cancer diagnoses in the male population each year. Radical prostatectomy (RP) fails in 20-40% of patients, who subsequently develop biochemical recurrence (BCR). Determining factors that influence time-to-BCR is vital for patient treatment decision-making. This study aims to identify clinically useful variables, including genetic attributes, with strong predictive ability in determining BCR-free survival.

The dataset used for this analysis contained 198 patients with BCR-free time information, 140 of which also had mRNA data. Two predictive modelling approaches were implemented, the traditional Cox regression and a newer machine learning technique, random survival forest (RSF). Models were built to investigate important variables in predicting BCR-free survival from both pre-RP and post-RP perspectives.

Models that included mRNA data performed better than those with clinical variables only (Cross-validated C-index: 0.76 vs. 0.71; 95% Confidence Interval: (0.010, 0.011)). Post-operative prediction outperformed pre-operative performance (0.80 vs 0.73; (-0.14, -0.01)). Excluding mRNA variables, no statistically significant difference was found between Cox models and RSF. When including mRNA variables, the Cox models outperformed RSF (CV C-index: 0.74 vs. 0.63; 95% CI: (0.04, 0.19)), and univariate Cox feature selection was preferable over correlation-based filtering (0.72 vs 0.64; (-0.16, -0.01)).

The results indicated that including mRNA information can further improve prediction of BCR. This work includes a discussion on the clinical usefulness of such models in a practical setting, including relative to routine predictive nomograms.