

Big-RT: Big Data Analysis to Identify Combinatorial Predictors of Radiotherapy Toxicity for Personalised Treatment in Prostate Cancer Patients

Sebastian Pölsterl, Anna Wilkins, Sarah Gulliford, James Campbell, Carmen Rodriguez-Gonzalvez, Sheng Yu, Veronica Garcia-Perez, Claire Griffin, Judith Bliss, John Yarnold, Uwe Oelfke, David Dearnaley, Emma Hall, Bissan Al-Lazikani, Navita Somaiah

Background

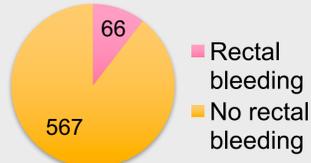
- ~ 2/3 of cancer patients will receive radiotherapy (RT).
- Up to 20% experience **long-term RT-induced toxicity**.
- **Problem:** no stratification by risk of side effects, which limits the ability to personalise treatment.
- **Challenge:** The pathogenesis of RT-induced toxicity is complex and multi-factorial, yet most **prior work focused on isolated data types** and standard statistical techniques, with limited success.

Aim

To identify **multi-parametric predictors of late RT-induced rectal bleeding** by developing novel machine learning techniques that **fully integrate** clinical, dosimetric, and genetic data from the CHHiP prostate RT-fractionation trial (CRUK/06/016)^{1,2}.

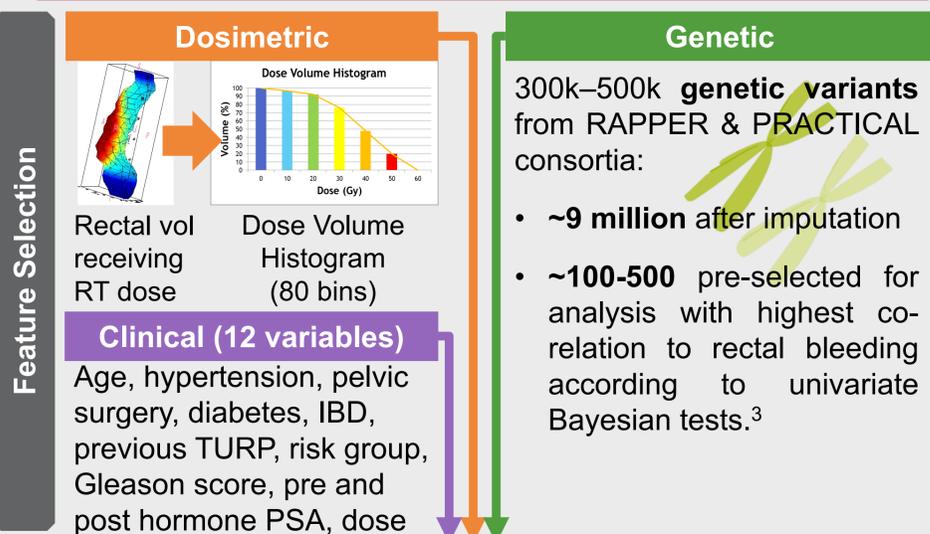
Data

- **3,212** patients recruited → **721** have all data types.
- 88 patients excluded if rectal bleeding information is missing for >3 time points and/or had haemorrhoids and/or rectal bleeding prior to radiotherapy.
- **633** patients eligible for analysis.
- Rectal bleeding defined as having grade ≥ 2[‡] @t ≥ 12 months.



‡: Moderate rectal bleeding (simple out-patient management)

Methods



Integrative Modelling

- Evaluated >1300 models including Multilayer Perceptron, in-house hybrid functional-scalar⁴, Naïve Bayes, Gradient Boosting, and Support Vector Machine.
- Introduced Bayesian optimisation⁵ to select the final model.
- Performed 10-fold cross validation.

Results

Fig 1. *Top:* Median (AUROC) performance scores for models using clinical, genetic and dosimetric factors. Black lines indicate the range of scores for our 10-fold cross validation. *Bottom:* Results using subsets of the data and **Naïve Bayes, our best performing model**. **The strongest predictions are achieved by jointly analysing all data types.**

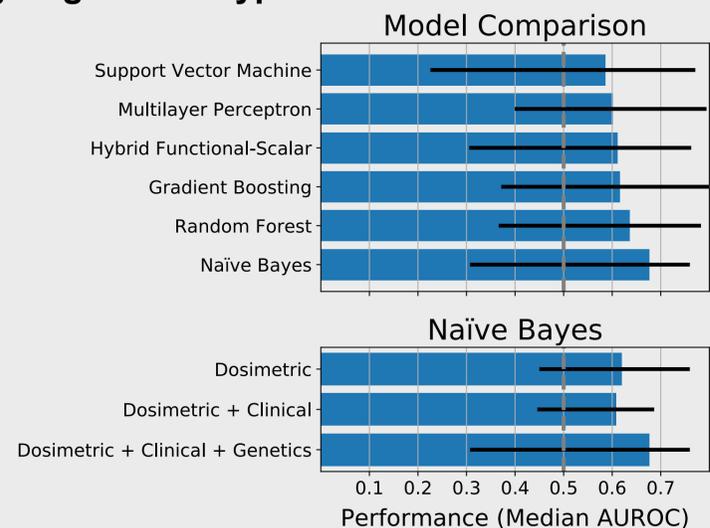
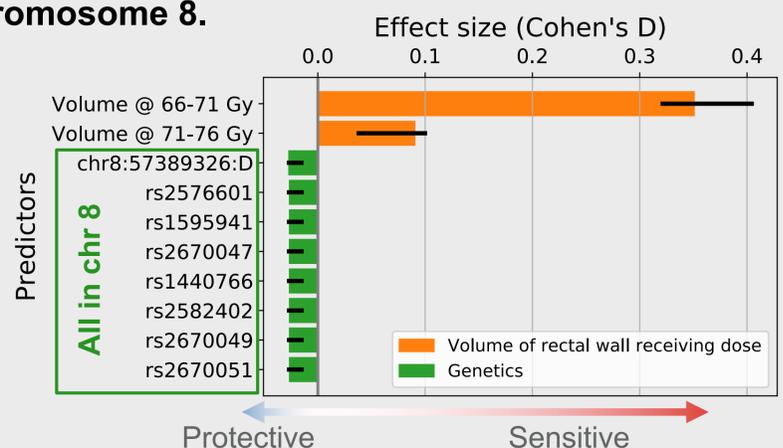


Fig 2. Strength of association to late RT-induced rectal bleeding for our top 10 predictors for the Naïve Bayes model using all data types. Genetic features shown were selected in at least 9 out of 10 folds. **Higher risk of rectal bleeding was associated with an increase in rectal volume receiving 66-76Gy, whilst lower risk was linked to genetic variants in a region of chromosome 8.**



Conclusions

- Identified novel combinatorial markers predictive of RT-induced rectal bleeding.
- Markers must be validated on independent dataset.
- Techniques developed here could be applied to other tumour types treated with radiotherapy.

References

1. Dearnaley et al. Lancet Oncol 2016; 17: 1047–60.
2. Wilkins et al. Lancet Oncol 2015; 16: 1605–16.
3. Marchini et al. Nature Genet 2007; 39: 906–913.
4. Ramsay and Silverman. Functional Data Analysis. Springer, 2005.
5. Shahriari et al. Proc IEEE. 2016 Jan;104(1):148–75.