Development of integrated Clinical Support Decision Dashboard of South African Prostate Cancer Patients: Genomic Integrity Layer

INTRO-Why Tumour Heterogeneity Matters

- Prostate cancer outcomes often more aggressive in South African populations.
- Tumour heterogeneity reflects:
  - ✓ genomic instability
  - ✓ evolutionary complexity
  - ✓ treatment resistance potential
- Existing genomic workflows are difficult for clinicians to interpret.
- **Gap:** Need for an interpretable clinical decision-support system.

OBJECTIVE

Develop an interactive Streamlit-based dashboard integrating:

- ✓ genomic analytics
- ✓ dimensionality reduction (NMF)
- ✓ machine learning (XGBoost Regression)
- ✓ visual analytics

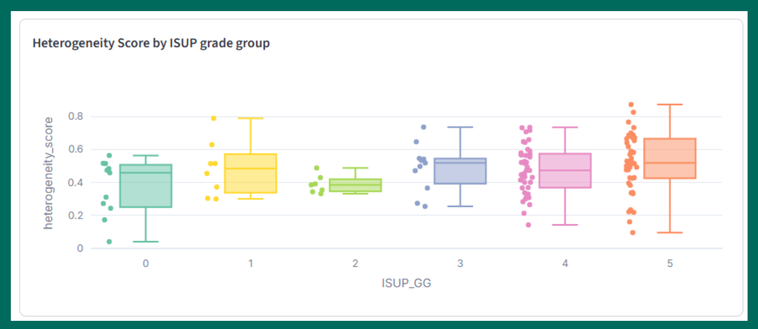
To support interpretable tumour heterogeneity analysis in South African prostate cancer patients.

METHODS

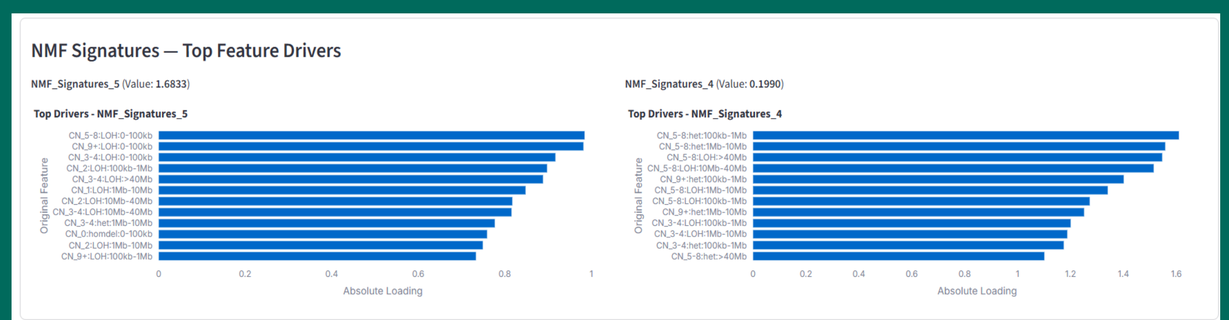
Clinical + Genomic Data → Feature Engineering → **NMF** Dimensionality Reduction → **XGBoost** Regression Model Best Predictive Power → Interactive Streamlit **Dashboard**

MAIN FINDINGS

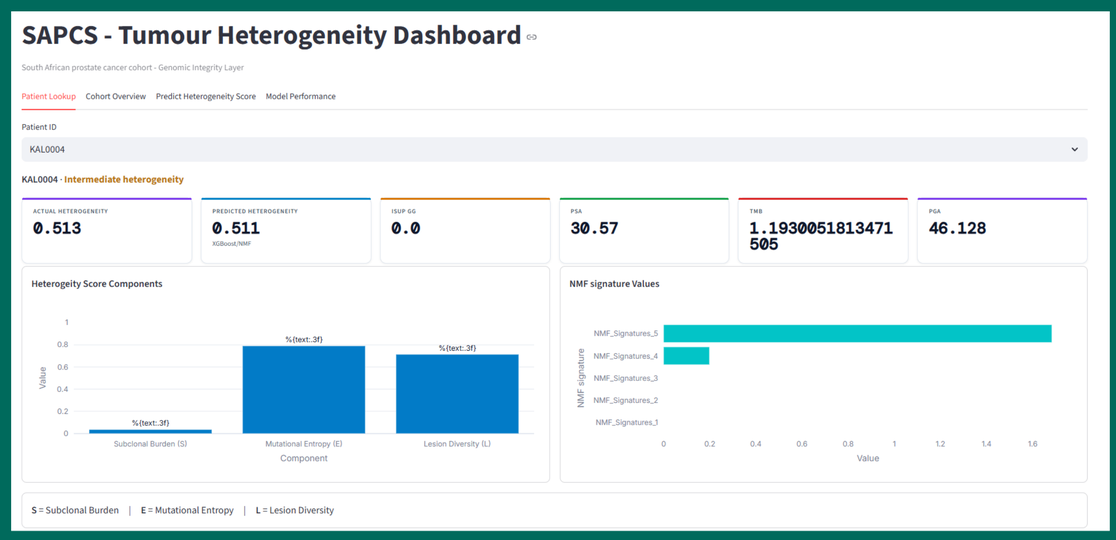
1. Higher heterogeneity scores were observed in **advanced ISUP grade groups**



2. NMF signatures improved interpretability of genomic mutation patterns



3. The **dashboard enabled clinician-centred exploration** of complex genomic data

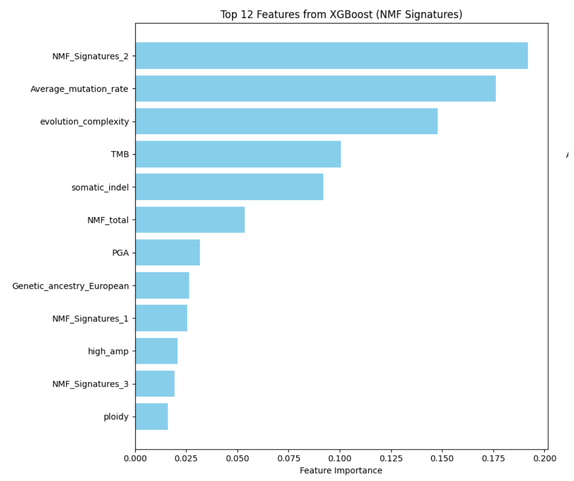


4. XGBoost provided **effective prediction of tumour heterogeneity** using structured genomic features

RESULTS

- Model Performance

METRIC	Value
TEST R^2-Hold-out set	0.698
RMSE-Error magnitude	0.075
MAE-Absolute error	0.060
CV R^2- Cross validation	0.670
TOTAL SAMPLES-Total Sample	123
FEATURES-Encoded inputs	29



DISCUSSION-Clinical relevance

- Supports exploratory risk stratification
- Enables interpretable genomic analysis
- Improves accessibility of precision oncology analytics
- Supports clinician-centred decision-making workflows

AMMO BAR

Key Variables

TMB(Tumour Mutational Burden)

Represents the total number of mutations within the tumour genome. High TMB =increased genomic instability and tumour evolution.

PGA (Percent Genome Altered)

Measures the proportion of the genome affected by copy number alterations. Higher PGA values = higher genomic instability.

Lesion diversity

Diversity across tumour lesions or regions, to quantify spatial heterogeneity

Mutational entropy

Reflects mutation pattern diversity and complexity

Chromothripsis

Indicates the presence of chromothripsis, a genomic rearrangement event associated with aggressive tumour behaviour and genomic instability.

Subclonal burden

. Proportion of mutations originating from subclonal tumour populations. Higher values = increased tumour evolutionary diversity.

Limitations

- Prototype system
- No external validation yet
- Limited cohort size
- Not a treatment recommendation system
- Requires clinical validation

Ndaedzo Makgatho (u25739906) , Simamkele Mtsengu (u17042845) , MIT 808

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

Department of Computer Science

Faculty of Engineering, Built Environment and Information Technology

Fakulteit Ingenieurswese, Bou-omgewing en Inligtingtegnologie / Lefapha la Boetšenere, Tikologo ya Kago le Theknolotši ya Tshedimošo

Capstone Project - MIT 808

Course Coordinators:
Dr. Vukosi Marivate (vukosi.marivate@cs.up.ac.za)
Abiodun Modupe (abiodun.modupe@cs.up.ac.za)

Scan me