A Machine Learning Approach for Identifying Breast Cancer Recurrence Events in Population-based Claims Data

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Introduction

- Cancer recurrence is an important outcome for measuring illness burden and treatment efficacy, however cancer recurrence is not explicitly documented in US cancer registries[1].
- Studies show promising results in inferring cancer recurrence from claims data, but primarily on small or single-institution studies.
- We developed a supervised machine learning framework to identify the occurrence and the timing of the second breast cancer events (SBCE) using registry and medical claims data at population level.

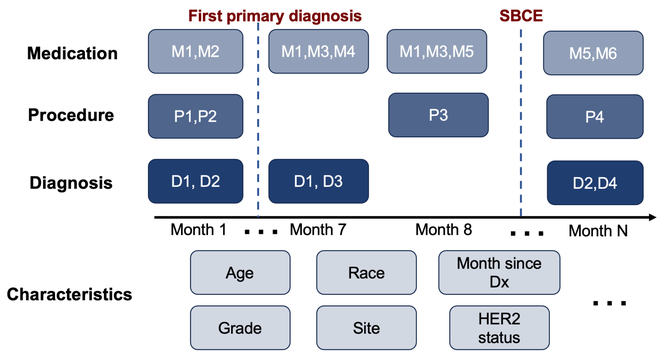
Data

- This study includes **18239** adult female patients diagnosed with first primary, stages I,II,III, local or regional breast cancer between 2004 and 2015 in Kentucky.
- Data are collected from Kentucky Cancer Registry (KCR) linked with Medicaid and Medicare claims. The SBCE rates were **7.25%** in the study cohort.
- **SBCE definition**:
  1) Recurrence of the first primary breast cancer **or**
  2) Diagnosis of the second primary breast cancer **or**
  3) Death caused by the first primary breast cancer
- **Features**:
  - **22** patients' characteristics (e.g., age, etc.) and first primary breast cancer characteristics (e.g., tumor size, etc.)
  - **29811** ICD9/10 diagnosis codes
  - **17718** ICD9/10 and HCPCS procedures codes
  - **41271** NDC and AHFS drug codes

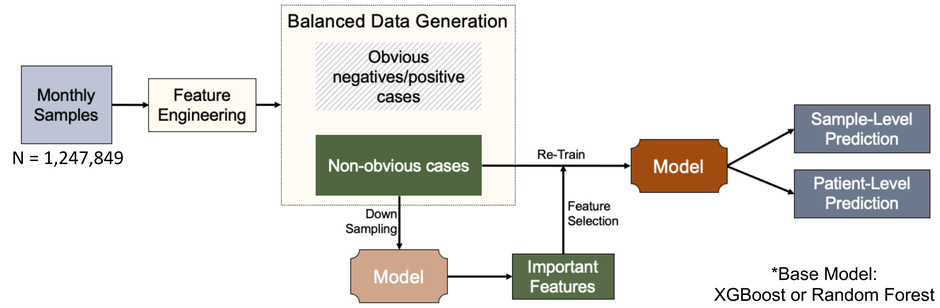
Abbreviation :
ICD: The International Classification of Disease
HCPCS: Healthcare Common Procedure Coding System
NDC: The National Drug Code
AHFS: American Hospital Formulary Service Pharmacologic-Therapeutic Classification System

Methods

Patient Data



Overall Framework



Results

Table 1. Patient-level prediction performance on test data

Threshold	Accuracy	Sensitivity	Specificity	*Difference
0.1	0.85	0.77	0.86	-6.0 ± 17.1
0.2	0.87	0.72	0.88	-5.1 ± 15.5
0.3	0.88	0.69	0.90	-5.0 ± 15.7
0.4	0.89	0.68	0.91	-4.7 ± 15.4
0.5	0.90	0.66	0.92	-3.8 ± 17.3
0.6	0.90	0.63	0.93	-3.1 ± 17.7
0.7	0.91	0.61	0.93	-2.5 ± 18.5
0.8	0.91	0.56	0.94	-1.4 ± 19.3
0.9	0.92	0.50	0.96	0.9 ± 19.2

*Raw difference (mean ± SD) between the predicted and observed time of SBCE
** ROCAUC is 0.93 at sample-level prediction

For more information, please contact Lucas J. Liu at jliu6@fredhutch.org

Results, cont.

Figure 1. Example of Prediction Trajectory

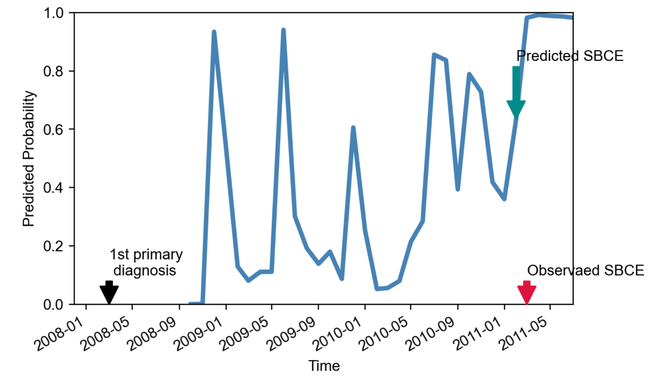
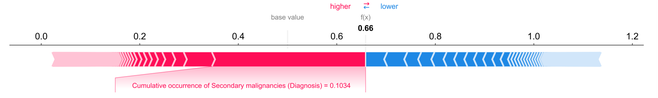


Figure 2. Individual SHAP[2] Interpretation



- Cumulative occurrence of diagnosis secondary malignancies contributes the most to the prediction

Conclusions

- Our machine learning framework identified SBCE using claims data with high ROCAUC, accuracy, and specificity at the population level.
- It is important to validate this framework in other populations' datasets for further confirmation of its effectiveness.

Acknowledgements

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References

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2. Lundberg SM, Lee S-I: A unified approach to interpreting model predictions. Advances in neural information processing systems 30, 2017