

Comparison of Sybil with Brock and PLCOm2012 Models among Screening Participants with Positive and Negative Baseline Screens

Rafael Meza

BC Cancer Research Institute
Canada

Co-authors

Rafael Meza^{1,2}, Clinton Durney¹, Yoonseo Mok¹, Sukhinder Atkar-Khattra¹, Renzo Phellan Aro³, Matthew T. Warkentin⁴, Martin Tammemagi⁵, Renelle Myers¹, Rayjean J. Hung³ & Stephen Lam^{1,6}

1. Department of Integrative Oncology, British Columbia Cancer Research Institute, Vancouver, BC, Canada
2. School of Population and Public Health, University of British Columbia, Vancouver, BC, Canada
3. Lunenfeld-Tanenbaum Research Institute, Sinai Health, Toronto, ON, Canada
4. Department of Oncology, Cumming School of Medicine, University of Calgary, Calgary, AB, Canada
5. Brock University, St. Catharines, ON, Canada
6. Department of Medicine, University of British Columbia, Vancouver, BC, Canada

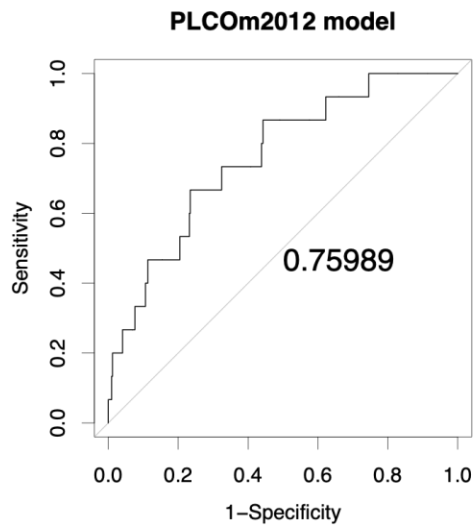
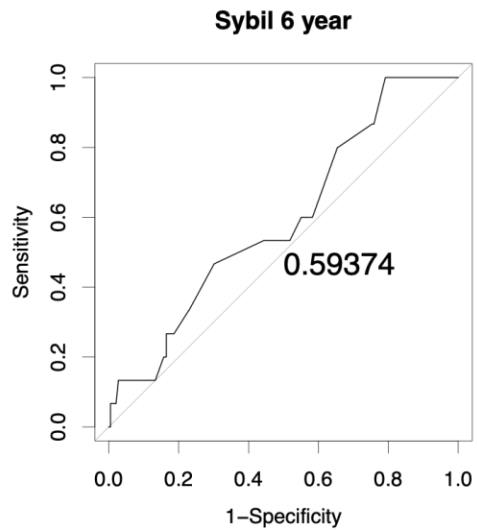
Background

- There is growing interest in using artificial intelligence (AI) decision-support tools to enhance lung cancer risk prediction
- Sybil is a deep learning model developed to predict future lung cancer risk for up to six years from a single low-dose computed tomography (LDCT) to personalize lung cancer screening
- The ability to **accurately stratify screen participants with lower risk who can have their next screening or surveillance CT in 2 to 6 years** has significant implications for health care resource utilization, radiation exposure and costs
- To pave the way for clinical adoption of AI tools, their effectiveness must be compared with existing risk tools, ensuring they meet the high standards required for patient care

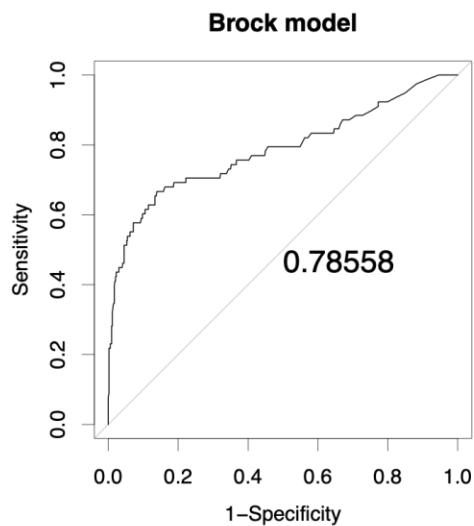
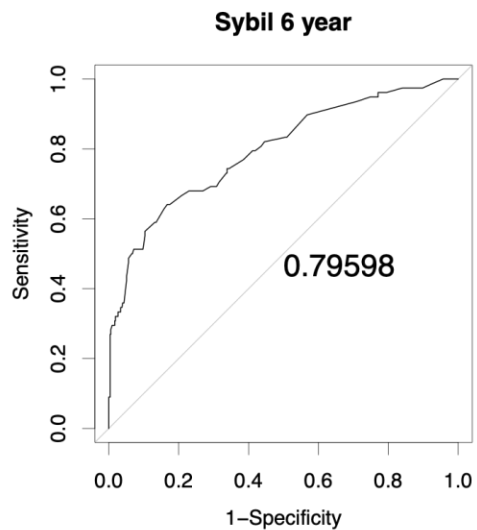
Study Goal and Methods

- Evaluate the performance of Sybil versus the International Lung Screening Trial (ILST) protocol, which is based on the Brock lung nodule risk prediction model
- Baseline LDCTs from the ILST Vancouver (N=2121) and the Pan-Canadian Early Detection of Lung Cancer Study (PanCan, N=2192) were analyzed with Sybil
- Sybil 6-year risk was compared with the *PLCOm2012* lung cancer risk prediction model for individuals with no nodules or with nodules with <1.5% Brock lung cancer probability (**termed here as negative screens; *Very Low Risk PanCan Cat1***)
- We also compared Sybil 6-year risk versus the “*Brock model*” in participants with lung nodules with lung cancer probability greater than 1.5%
 - “Brock model” individual risk = maximum of Brock nodule risk among all nodules found in a CT scan
- Model performance was assessed with the area under (AUC) ROC curve

ILST individuals without nodules or with nodules with cancer prob<1.5%



ILST individuals with nodules with cancer prob>=1.5%



- ILST-Vancouver participants
- For individuals with *negative screens* (having no nodule with Brock probability < 1.5%), PLCOm2012 had better risk prediction than Sybil
- Similar risk prediction between Sybil and the “Brock model” for those with positive screens (having at least one nodule with Brock probability >1.5%)
- Similar results when using the PanCan cohort

Summary of Results

- **Among patients with negative screens**, PLCOm2012 performed better with AUCs of 0.760 in ILST versus 0.590 for Sybil
- The “Brock model” and Sybil had similar performance in **patients with lung nodules with malignancy risk >1.5%**. Brock AUC of 0.786 vs Sybil AUC of 0.796
- Similar results were obtained when the comparisons were performed using the PanCan cohort
 - Negative screens: PLCOm2012 model with AUC of 0.633; Sybil with AUC of 0.560
 - Positive screens (>1.5% risk): “Brock model” with AUC of 0.753; Sybil with AUC of 0.743
- **The performance of Sybil for individuals with negative screens improved after recalibration with additional smoking covariates (similar AUC as PLCOm2012)**

Conclusions and Discussion

- AI tools have the potential to enhance lung cancer risk prediction
- However, their performance needs to be compared with existing lung cancer risk prediction tools using cohorts with adequate follow-up and known outcomes before prospective evaluation in clinical settings
- In this study, Sybil performed similarly to the "Brock model" for individuals with nodules with more than 1.5% lung cancer risk, but PLCOm2012 had better performance for individuals with no nodules or with only low-risk nodules
 - Limitation: larger samples of patients with low risk are needed to have enough cases to better validate models
- More research is needed to identify the right way to incorporate Sybil and other AI tools into the lung cancer screening process

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