Predictive Model for Mortality Risk Stratification Using Laboratory Biomarkers in Singaporeans

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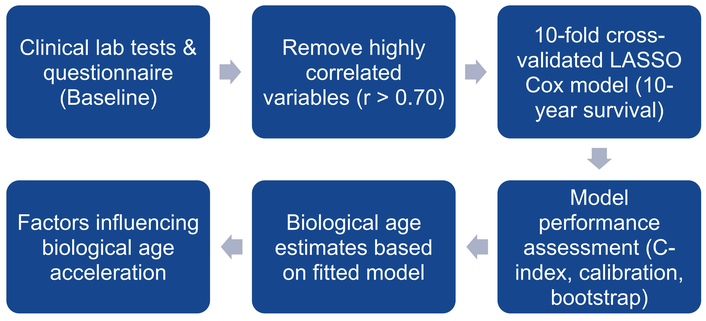
BACKGROUND

- Existing clinical tools relying on subjective or aggregate scores may miss early signs of high mortality risk.
- Here, we showed that routine lab tests offer an untapped, low-cost opportunity to build an evidence-based model for earlier and more accurate risk prediction.
- Using Singaporean cohort data (2003-2020; median follow-up years 11.4) and validation in a U.S. cohort, our model provides robust, generalizable long-term health risk prediction.

METHODS

- Singapore Longitudinal Ageing Studies (SLAS-1 and SLAS-2; NCT03405675)



RESULTS

- The Lasso Cox model achieved strong predictive accuracy (C-index: 0.63) with good calibration and minimal overfitting.
- Core predictors included age, gender, glucose fasting, albumin, creatinine, red blood cell, basophils, monocytes and polymorphs/neutrophils.
- Model performance was replicated in NHANES (C-index: 0.72), demonstrating cross-population generalizability.

DISCUSSION

- This model can be used to monitor health status, enhance screening accuracy, and serve as a universal measure applicable across diverse populations.

We developed a **model** that uses **common blood test results and clinical data** to predict and classify mortality risk, helping to **identify high-risk individuals earlier** and more **accurately**.

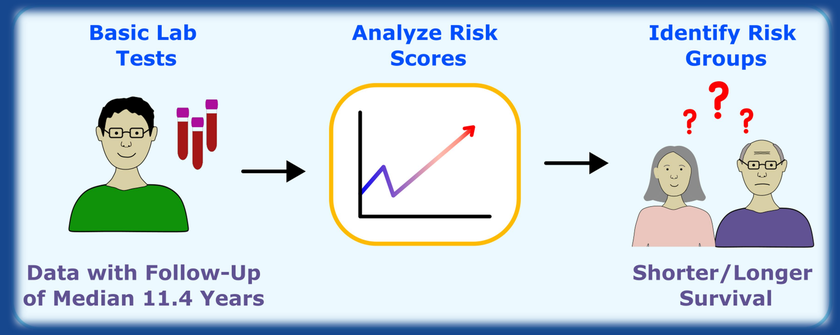


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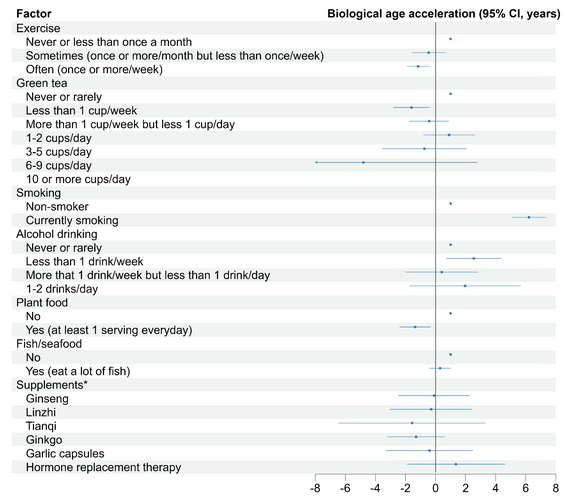
Table 1. Baseline characteristics of the SLAS cohort.

Number of participants included	5409
Number of events	1145
Follow-up (years, median [IQR])	11.4 (9.0-15.4)
Age (years, mean [SD])	66.2 (7.7)
Gender (male, %)	1987 (36.7)
Glucose fasting (mmol/L, median [IQR])	4.9 (4.6-5.5)
Albumin (g/L, median [IQR])	42 (40-44)
Creatinine (umol/L, median [IQR])	70 (59-86)
Red blood cell (10^12/L, median [IQR])	4.51 (4.23-4.83)
Basophils (10^9/L, median [IQR])	0.05 (0.13-0.12)
Monocytes (10^9/L, median [IQR])	0.39 (0.31-0.49)
Polymorphs/neutrophils (10^9/L, median [IQR])	3.13 (2.49-3.93)

Figure 1. Factors influencing biological age acceleration.



Biological age acceleration was calculated as the residuals from regressing biological age on chronological age.
*Often/Very often/Always vs. Never or Rarely and Occasionally (less than once/month)

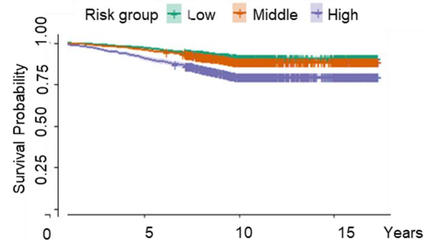


Figure 2. Survival curve by tertiles of the risk scores (low-, middle-, high-risk) from the Cox model for 10-year all-cause mortality.

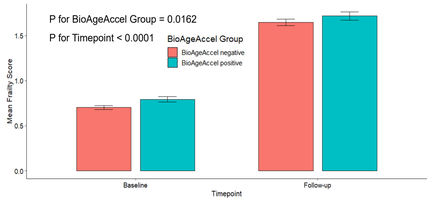


Figure 3. Frailty scores differed significantly between the two timepoints (baseline and follow-up) and between the BioAgeAccel-positive and –negative groups (P < 0.0001 and P = 0.0162, respectively).
Positive value indicates that an individual's biological age exceeds expected value; negative value indicates that biological aging is slower than expected. Baseline: Year 2008-2012; Follow-up: Year 2014-2017.

BioAgeAccel = Biological Age Acceleration

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