Appendix 1 (as submitted by the authors): Details regarding prognostic index creation and assessment

We then used the methods described by Sullivan et al[1] to modify the regression model into a prognostic index to predict 5-year survival. This time point was chosen because it was close to the median observation time of the cohort. The number of points assigned to each covariate in the regression model equaled its coefficient divided by the parameter estimate for the categorical variable with the smallest absolute value, rounded to the nearest whole number. Continuous variables were categorized using deciles. Overlapping categories or those with the same point value were combined.
Each person's final index score was then calculated by summing up the points for each factor that applied to that person. The 5-year survival estimate for each possible score was calculated as $1 - So(t)^{\exp(B*P - \sum_{i=1}^{q} B_i \overline{X_i})}$ where: *So(t)* was the 5-year survival estimate for a patient group with a mean value for all covariates in the model; B is the smallest parameter estimate in the model; *P* is the point total; *q* is the total number of covariates in the model; B_i is the parameter estimate for covariate *i*; and $\overline{X_i}$ is the mean value of covariate *i*.

To measure discrimination of the index, we grouped prognostic index scores in the derivation group together so their Kaplan–Meier survival estimate significantly differed from that in all other index score groups at the $p = 0.01$ level by the Log-Rank statistic. We then used the validation group to determine if survival estimates between these index score groups remained significant. We also measured discrimination using the concordance probability.[2] This measures, for all possible patient pairs, the proportion of times that the person with the greater predicted survival actually lived longer than the other person.

To measure calibration of the index, we compared the model-based expected and observed 5-year patient survival in the validation group at each prognostic index score. Within each index score, expected and observed death rates were deemed similar if the 95% confidence interval around the observed death rate (calculated as the number of deaths divided by total observation time) included the expected death rate. 95% confidence intervals for observed mortality rates were calculated using exact methods.[3] We also compared mortality rates in the derivation and validation groups using 83% confidence intervals since point estimates whose 83% confidence intervals that do not overlap differ significantly at an a-error of 0.05.[4]

References

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Appendix to: van Walraven C, Austin PC, Knoll G. Predicting potential survival benefit of renal transplantation in patients with chronic kidney disease. *CMAJ* 2010. DOI:10.1503/cmaj.091661.