

Identifying myocardial infarction risk factors in the Wisconsin Longitudinal Survey

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Abstract

Introduction

Coronary artery disease (CAD) is a leading cause of death in the United States and much of North America and Europe. In 2011, one American died of CAD every 40 seconds, on average, and 155,000 of those deaths were people aged less than 65 years.¹ One manifestation of CAD is a myocardial infarction (MI), which is also called a “heart attack”. A MI results from a clot in a coronary artery that diminishes blood flow to the heart muscle, or myocardium. If blood flow disruption persists for a sufficiently long time, the muscle may die, or infarct. The irreparable dead heart muscle diminishes the overall ability of the heart to pump blood. Severe MIs may lead to a patient’s death.

Epidemiologists have identified modifiable and non-modifiable risk factors that contribute to CAD risk. Smoking is among the strongest modifiable risk factors, and is thought to elevate CAD risk by triggering elevations in inflammatory molecules in the bloodstream. _____

What is mechanism for smoking causing CAD?

. Diabetes mellitus and hypertension (systolic or diastolic) are typically considered non-modifiable risk factors, although their contribution to CAD risk may be reduced in patients who undertake dramatic lifestyle interventions, such as exercise programs and diet with weight loss. Non-modifiable risk factors include age, a family history of CAD and presence of certain genetic variants

what are other known risk factors?

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Our collaborators at the Wisconsin Longitudinal Study (WLS) have undertaken an investigation on a subset of WLS participants with the goal of identifying CAD risk factors in the WLS study population. The ultimate goal of this project is to develop an intervention program to reduce CAD morbidity and mortality in Wisconsin. The investigators would like to extend such an intervention program to Wisconsin residents who are not WLS subjects. Our goal in this report is to identify risk factors for MI among WLS participants.

¹Mozaffarian et al., “Executive Summary.”

Study design

The Wisconsin Longitudinal Study (WLS) is a long-term study of a random sample of 10,317 men and women who graduated from Wisconsin high schools in 1957. According to the WLS website “WLS provides an opportunity to study the life course, intergenerational transfers and relationships, family functioning, physical and mental health and well-being, and morbidity and mortality from late adolescence through 2011.”²

need more info on WLS?

Our collaborators collected data from the original respondents or their parents in 1957, 1964, 1975, 1992, 2004, and 2011; from a selected sibling in 1977, 1994, 2005, and 2011; from the spouse of the original respondent in 2004; from the spouse of the selected sibling in 2006; and from widow(er)s of the graduates and siblings in 2006.

Data description

Our collaborators shared with us a data set that contains records for 19095 individuals (including original subjects and siblings) with 310 variables per subject. 9363 subjects responded (with yes or no) to the 2011 question of whether they had ever had a heart attack.

Exploratory data analyses

Since our WLS data included 310 variables, we won't provide summaries for all of them in this document. Instead, we focus our exploratory analyses on our response variables (HAC2011, HAC2004, HACinc, doc2011, doc2004, docinc) and covariates that other researchers have identified as associated with coronary artery disease.

Age is known, from epidemiologic studies, to be a strong risk factor for CAD, with older individuals having an elevated CAD risk.

what to explore for categorical data? Only the proportion in each category????

Statistical modeling

We used statistical modeling to try to identify covariates that associated with six distinct outcomes: 1) HAC2004, 2) HAC2011, 3) DOC2004, 4) DOC2011, 5) new self-reported heart attacks (from 2004 to 2011) and 6) new heart attack per doctor's report (from 2004 to 2011). For a subject to qualify as a “new” self-reported heart attack, they must have responded “No” in 2004 and “Yes” in 2011. Analogous definition applies for “new” doctor-reported heart attack.

We found that HAC2004 had 11534 non-missing responders (with 665 responding “Yes” and 10869 responding “No”). Counts for other variables are provided in Appendix A.

Statistical modeling with Framingham study predictors

We identified those variables in the WLS that closely match those in the Framingham study³ (Table ??). It's important to note that the Framingham study used survival analysis methods, including Cox

²“Wisconsin Longitudinal Study”.

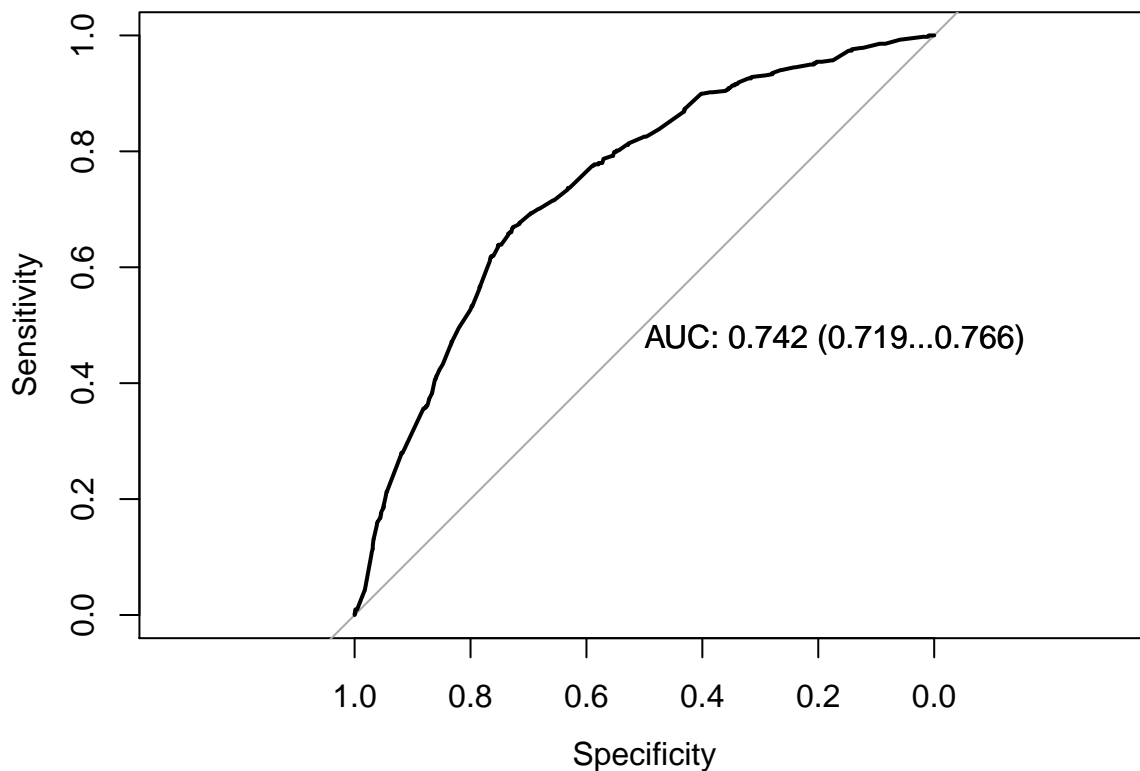
³D'Agostino et al., “General Cardiovascular Risk Profile for Use in Primary Care the Framingham Heart Study.”

Framingham study variable	WLS Variable
Sex	Sex
Quantitative total cholesterol	highchol2011 or highchol2004
Quantitative HDL cholesterol	None
Smoking	Columns 61 to 87 aim to quantify smoking
Diabetes	diabetes2004, diabetes2011, diabdiag2004, diabdiag2011
Age	Age
Systolic BP	highbp2004, highbp2011*
Treated for high blood pressure	None

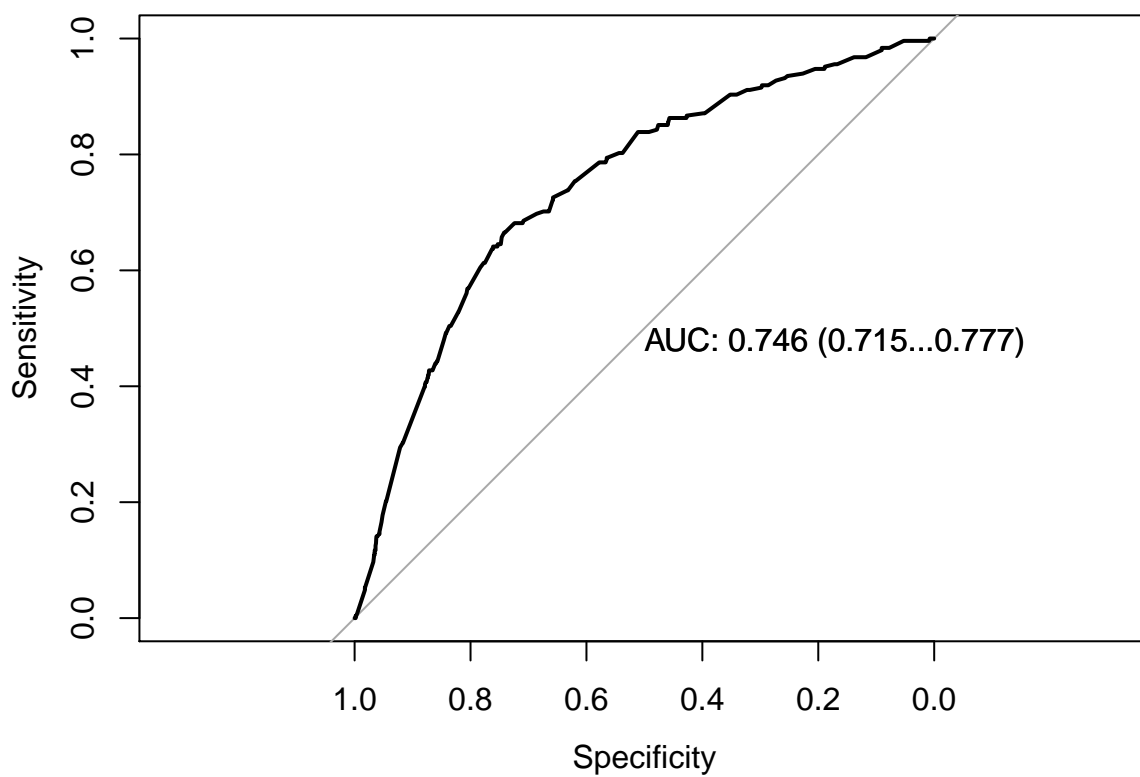
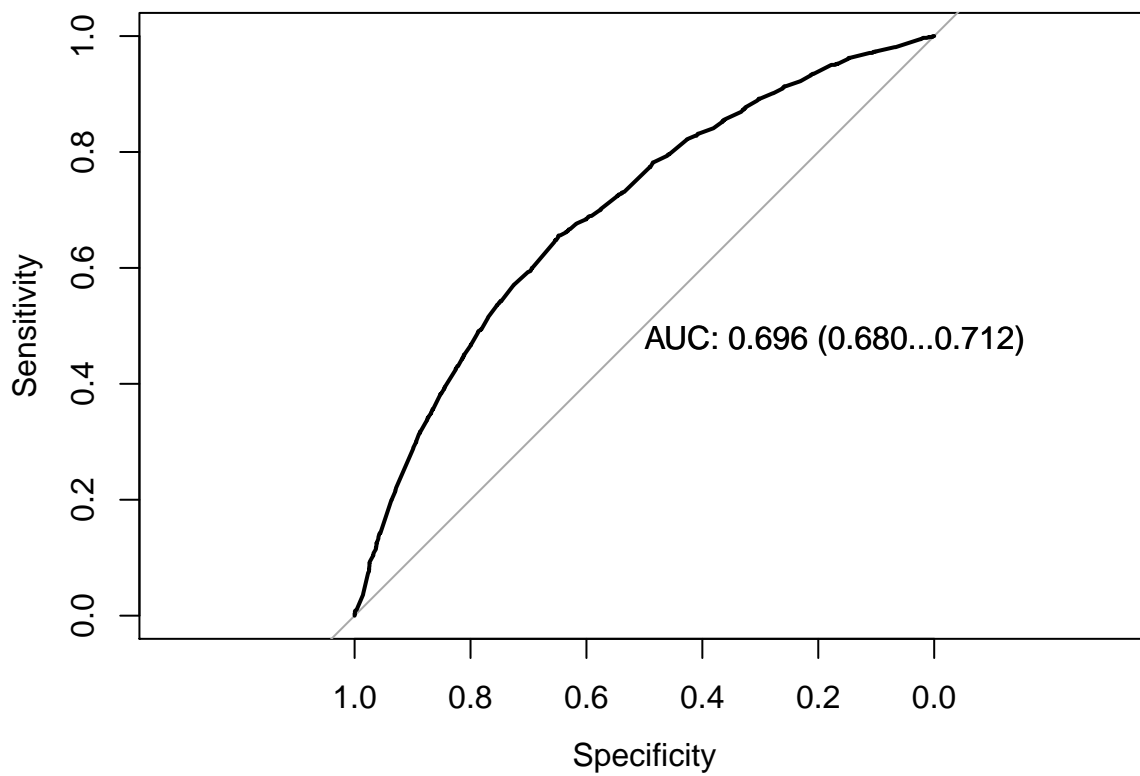
Table 1: Framingham study variables and their closest analogs in WLS. (* SBP not available, so we used reported "high BP".)

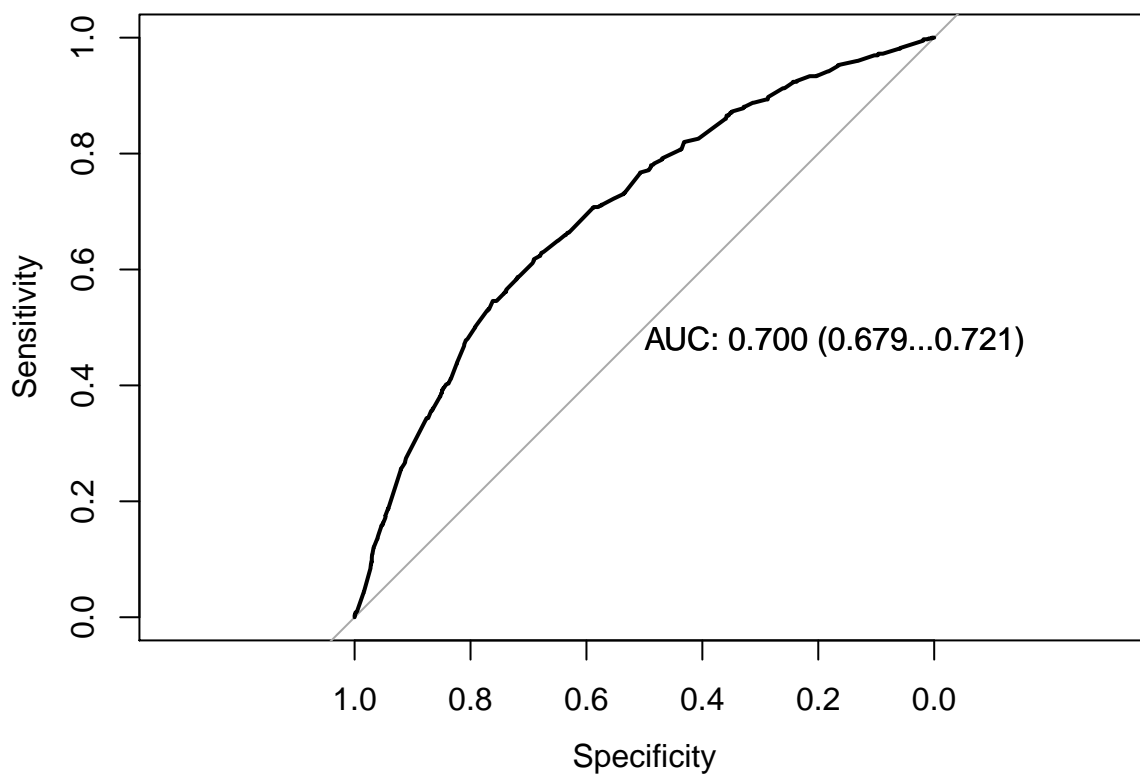
proportional hazards regression, to identify risk factors for a cardiovascular event. Thus, their study design, analysis, and purpose differ from ours.

Because the risk factors from the Framingham study have strong effect sizes, are easily interpreted, and widely used by both physicians and public health scientists, we decided to perform logistic regression analyses with solely those WLS variables that most closely matched the Framingham variables. We analyzed each of the 6 outcomes of interest. For each outcome variable, we fitted a logistic regression model using the entire data set (omitting those subjects with missing data). We then transformed the fitted logit values to probabilities before plotting a receiver operating characteristic (ROC) curve for each model, in which we use the fitted probabilities to examine the trade-off between specificity and sensitivity. We also calculated the area under the curve (AUC) for each ROC curve.⁴

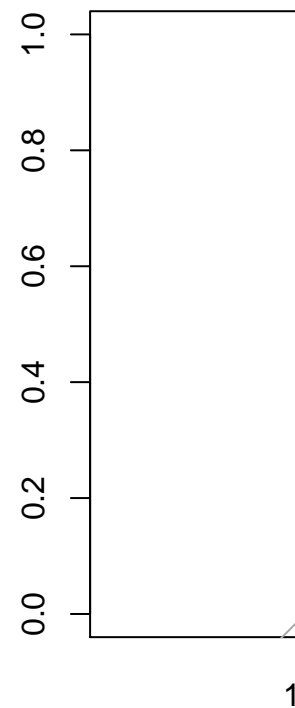
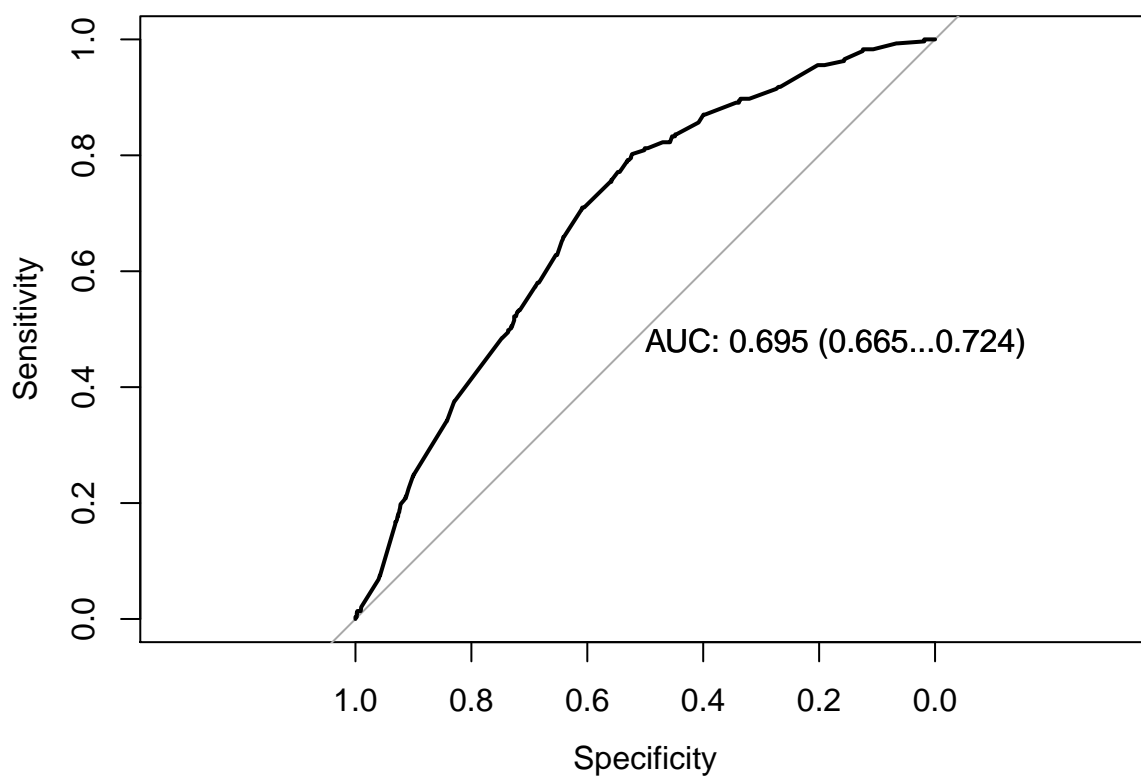


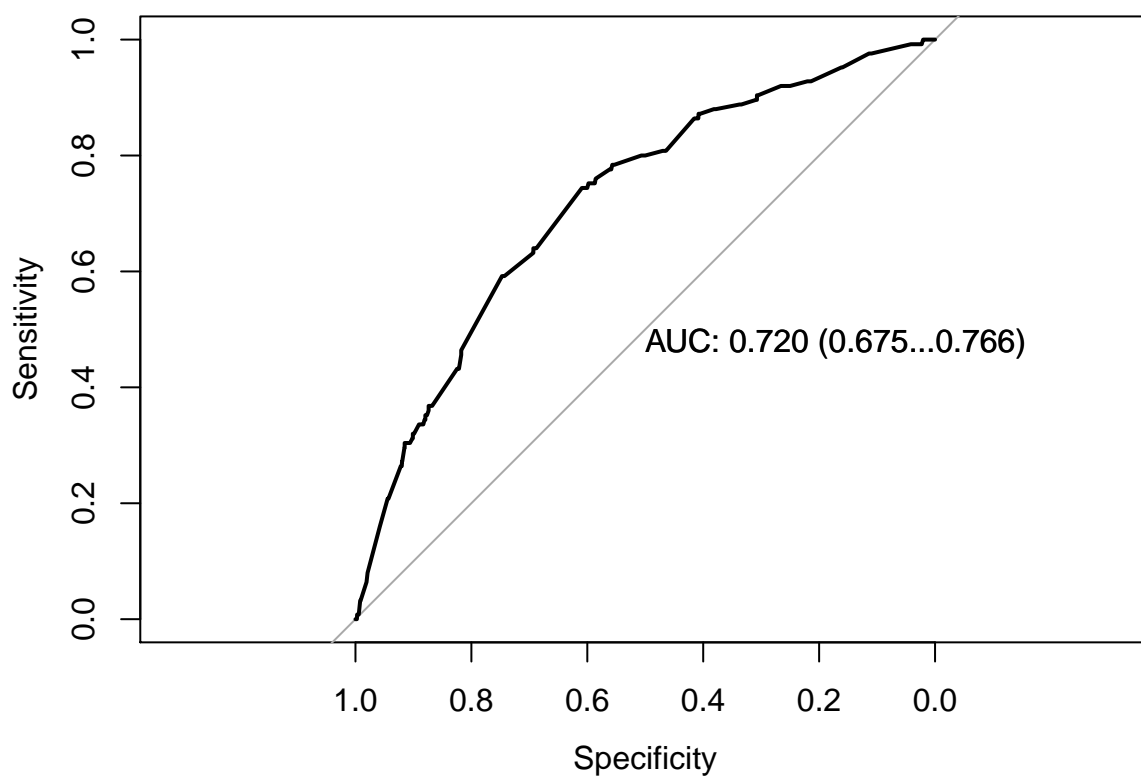
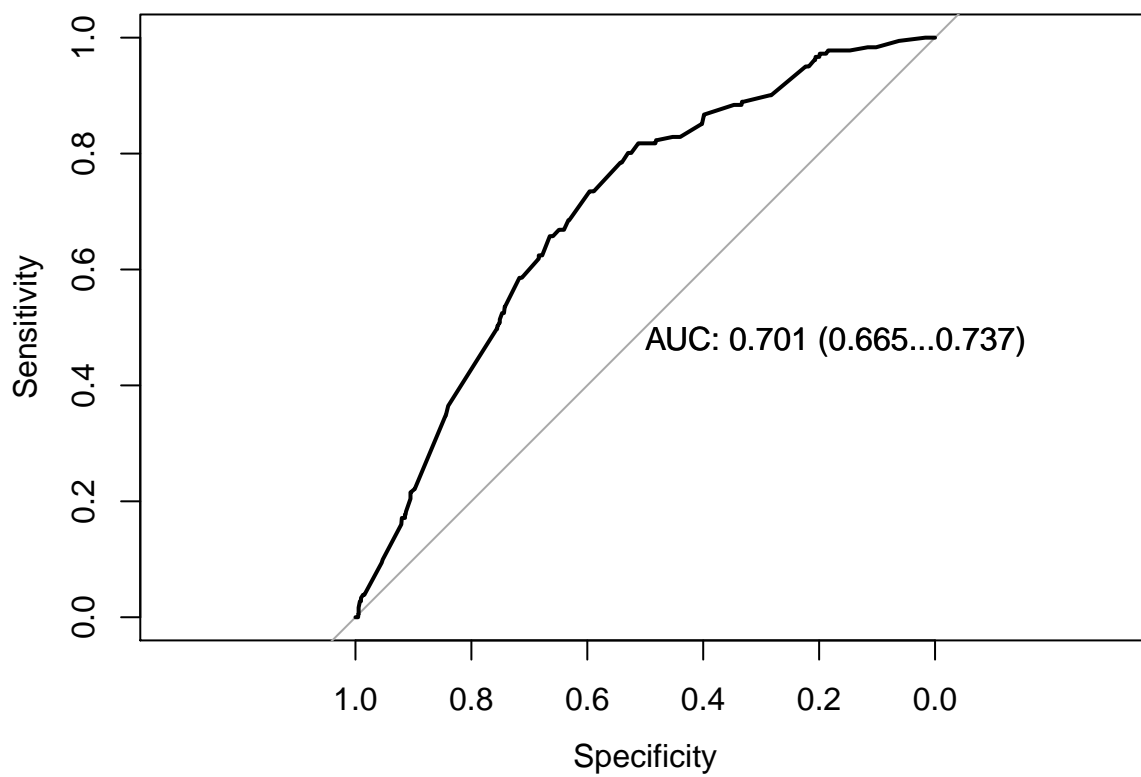
⁴Robin et al., "pROC."

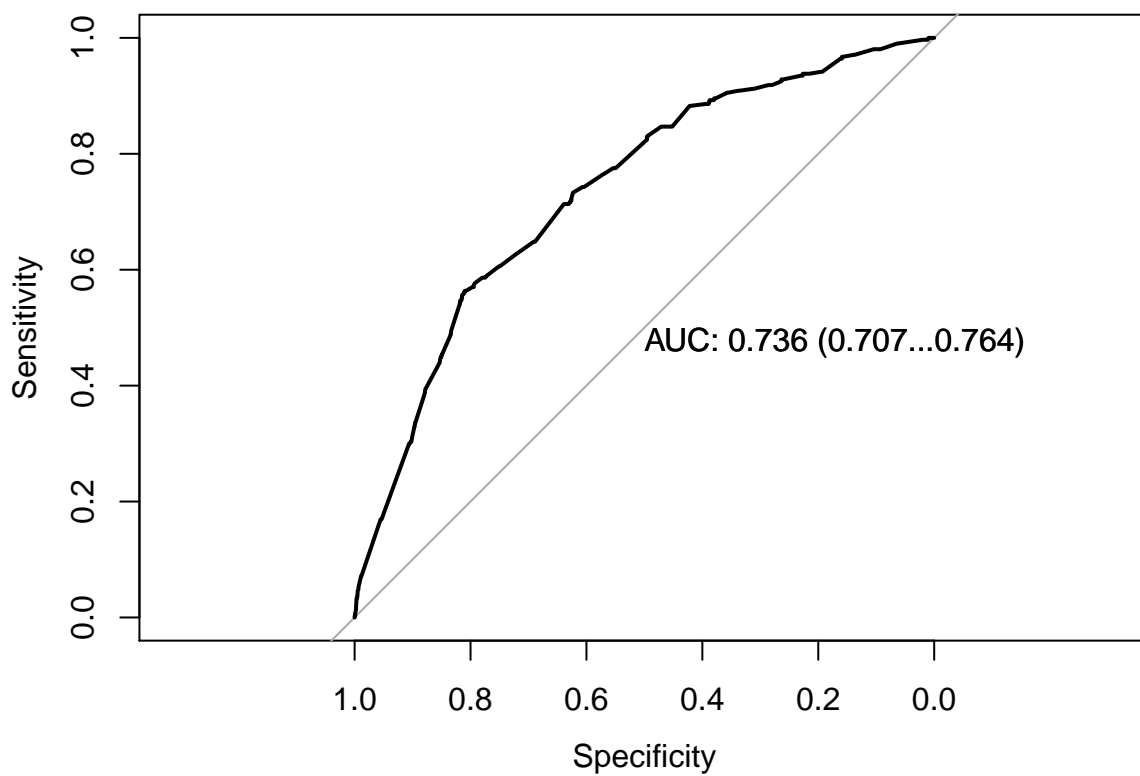
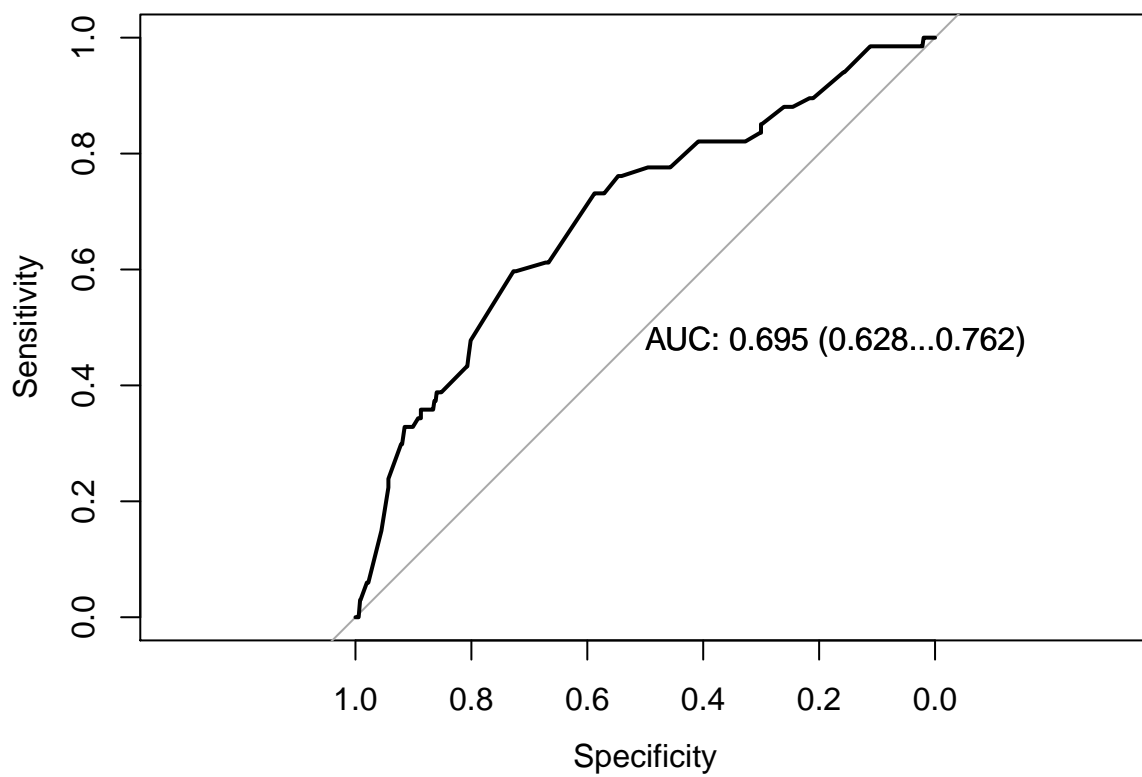




Subgroup-specific modeling







Results

Discussion

Future directions

Given the relatively low cost of acquiring genomics data, one possible future direction is to acquire genomics data for a subset of study subjects. For example, SNP genotype data from each subject may enable us to further discriminate those subjects that are at high risk for a CAD event. Such knowledge may be translated into the proposed intervention program, for example, by promoting healthy diet and physical activity among those at greatest risk.

Appendix A: Supplementary materials

Appendix B: Questions for client

Appendix C: Computing code

Appendix D: Additional note

Throughout this report, we tried to adhere to the style suggested by Leek⁵. We used the R statistical environment for all calculations⁶.

References

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⁵*The Elements of Data Analytic Style*.

⁶R Core Team, *R*.