Using Support Vector Machines to Predict Health Conditions

Introduction

This research uses support vector machines (SVMs) to predict whether someone has had diabetes or cancer based on health variables. The data is from the IPUMS Health Survey [1]. It contains variables about the respondents' demographics, health habits, and whether they have had 5 different health conditions. I used the following models and predictors:

- An SVM with a linear kernel to predict diabetes presence based on BMI, weight, and age
- An SVM with a polynomial kernel to predict diabetes presence based on BMI, work hours, age, and height
- An SVM with a radial kernel to predict cancer presence based on the variables above and the days used alcohol yearly.

Theoretical Background

A support vector classifier (SVC) separates classes by fitting a linear boundary between them and maximizing the margin. The margin is the distance between the boundary and the closest points, or the support vectors. Some points can be misclassified or in the margin.

The equations that formulate an SVC are as follows:
$\max_{\beta_0,\beta_1,\ldots,\beta_p,\epsilon_0,\ldots,\epsilon_n,M} M$ subject to:

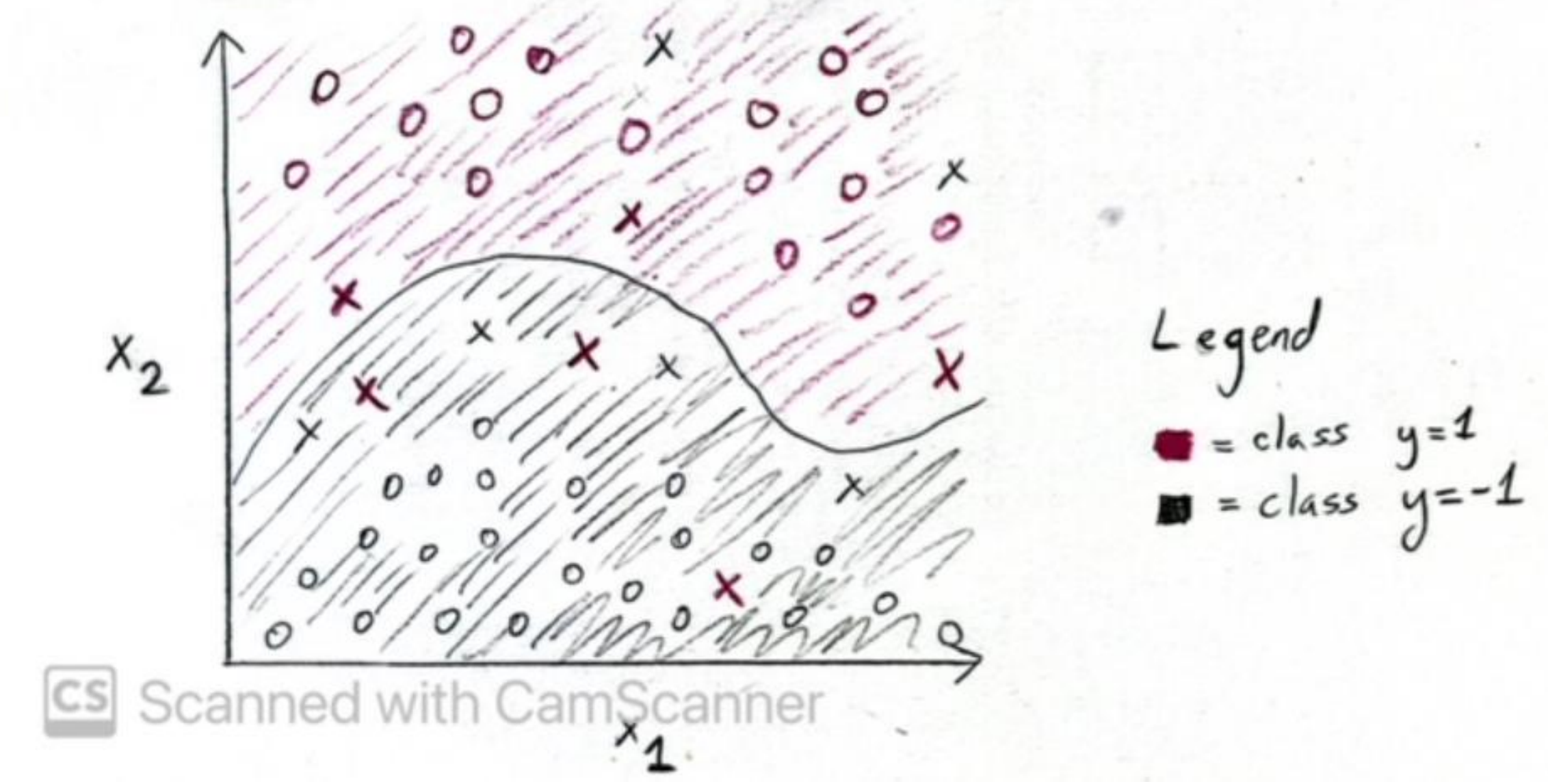
$\sum_{j=1}^{p} \beta_j^2 = 1$ (1)
$y_i(\beta_0 + \beta_1 X_1 + \cdots + \beta_p X_p) \geq M(1 - \epsilon_i)$ (2)
$\epsilon_i \geq 0, \sum_{i=1}^{n} \epsilon_i \leq C$ (3)

M is the margin size, and ϵ_i is the distance of a data point from the correct side of the margin. (2) allows some points to be on the wrong side, but, in (3), the tuning parameter C constrains how many points and how far away they can be.

SVMs can create nonlinear decision boundaries by combining SVCs with kernels. Kernels transform the data to a higher dimension, where it is now linearly separable.

A decision boundary with a kernel K is $f(x) = \beta_0 + \sum_{i \in \delta} \alpha_i K(x, x_i)$, where δ are the support vectors. A linear kernel is equivalent to an SVC. A polynomial kernel has the form $K(x_i, x_{i'}) = \left(1 + \sum_{j=1}^{p} x_{ij} x_{i'j}\right)^d$. It creates polynomial relationships between points, allowing curved boundaries. *d* is the polynomial degree, a tuning parameter. Another nonlinear kernel is the radial kernel: $K(x_i, x_{i'}) = \exp\left(-\gamma \sum_{j=1}^{p} (x_{ij} - x_{i'j})^2\right)$. Gamma, a positive constant, is a tuning parameter.

The plot below shows an SVM with a nonlinear kernel. The points and the regions are color-coded by the classes. All the points above the decision boundary are classified as y = 1, and all the points below it are classified as y = -1. The x's are support vectors, while the round points are not support vectors. Notice that some points are on the wrong side of the decision boundary, but most are classified correctly.



Methodology

To pre-process the data, I selected the relevant variables, I dropped the rows where the survey response was "Unknown". I recoded the class labels to strings, and I performed standardization. A huge problem was class imbalance. About 93% of the respondents have never had diabetes or cancer, and only about 7% have. Also, the classes were completely overlapped with no boundary. To mitigate the class imbalance, I used cost-sensitive SVMs. Cost-sensitive SVMs weight C differently for each class. Assigning a larger weight to the minority class forces minority points to be classified correctly.

I used 2-fold cross-validation for hyperparameter tuning. During cross-validation, I maximized the F1 score. Accuracy is misleading for imbalanced classes, and F1 score is a better metric because it balances both precision and recall.

For the linear kernel, I tried cost values of 0.01, 0.1, 1, and 10. The best was 1. For the polynomial kernel, I tried the same cost values, I degrees of 2, 3, and 4, and I tried coef0 values of 0, 1, and 2. The best model had cost = 10, degree = 2, and coef0 = 0. For the radial kernel, I tried the same cost values and gamma = 0.5, 1, and 2. To evaluate the models, I used the overall training and test accuracy, the training and test accuracy for each class, and ROC curves.

Discussion

Overall, age, BMI, and weight highly impacted diabetes predictions. Older people, people with a higher BMI, and people with a higher weight were more likely to have diabetes. It makes sense that older people are at risk because of the changes that come with aging, such as the immune system weakening.

Limitations were class imbalance and class overlap. The overlap was so severe that the minority class data points were located right in the middle of the majority class ones. So, a true, reasonable decision boundary doesn't exist. Also, the classes were so imbalanced that, even with cost-sensitive SVMs, the models had a lower accuracy for the minority class than the majority one.

An extension is to use neighborhood-based undersampling [2] as a data preprocessing step, to address both the imbalance and the overlap. This technique removes majority data points from the overlapping region while also minimizing information loss.

There is a clear correlation between age and diabetes, regardless of other health variables. That means more people are at risk of diabetes. So, I suggest that policymakers require insurance companies to cover insulin, making insulin easier to obtain for people with diabetes.

Conclusion

The findings about BMI and weight have many implications. They could be maliciously used to stigmatize and put down people who are overweight or have a higher body size. However, using BMI to determine if someone is "healthy" can be misleading [3]. Firstly, BMI was originally developed by studying a population of only white men, so BMI may not have accurate results for people of all ethnicities and genders. Secondly, BMI should be used along with other metrics, like blood pressure, cholesterol, and glucose levels, to get an accurate picture of someone's health. Hopefully, these findings about BMI could motivate medical researchers to find better metrics for someone's health status than BMI. Aside from requiring insurance companies to cover insulin, people could use the findings about age and diabetes to store emergency insulin in establishments where older people commonly spend time.

References

[1] Lynn A. Blewett, Julia A. Rivera Drew, Miriam L. King, Kari C.W. Williams, Daniel Backman, Annie Chen, and Stephanie Richards. IPUMS Health Surveys: National Health Interview Survey, Version 7.4 [dataset]. Minneapolis, MN: IPUMS, 2024. https://doi.org/10.18128/D070.V7.4. Links to an external site.http://www.nhis.ipums.org.

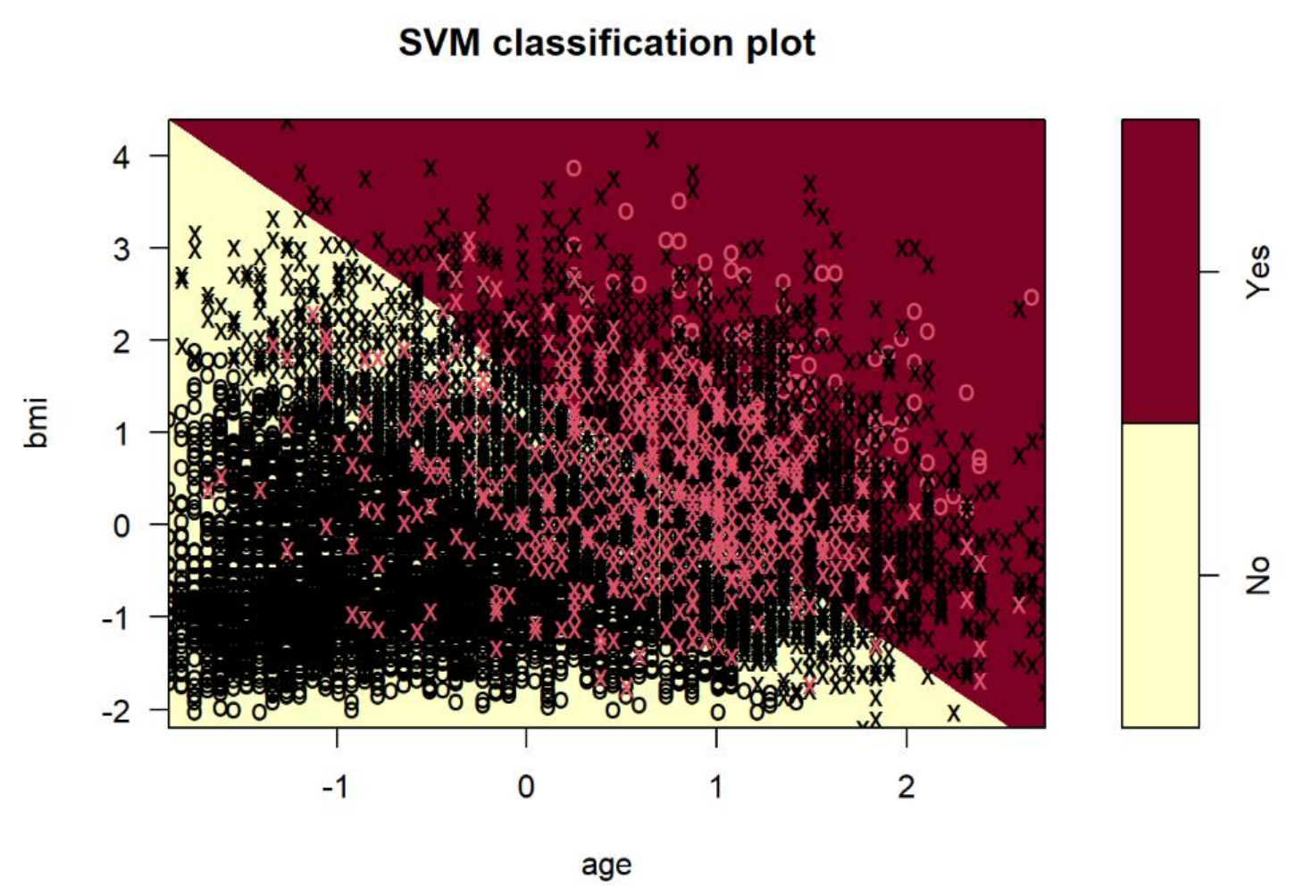
[2] Vuttipittayamongkol, Pattaramon, and Eyad Elyan. "Neighbourhood-based undersampling approach for handling imbalanced and overlapped data." *Information Sciences* 509 (2020): 47-70.

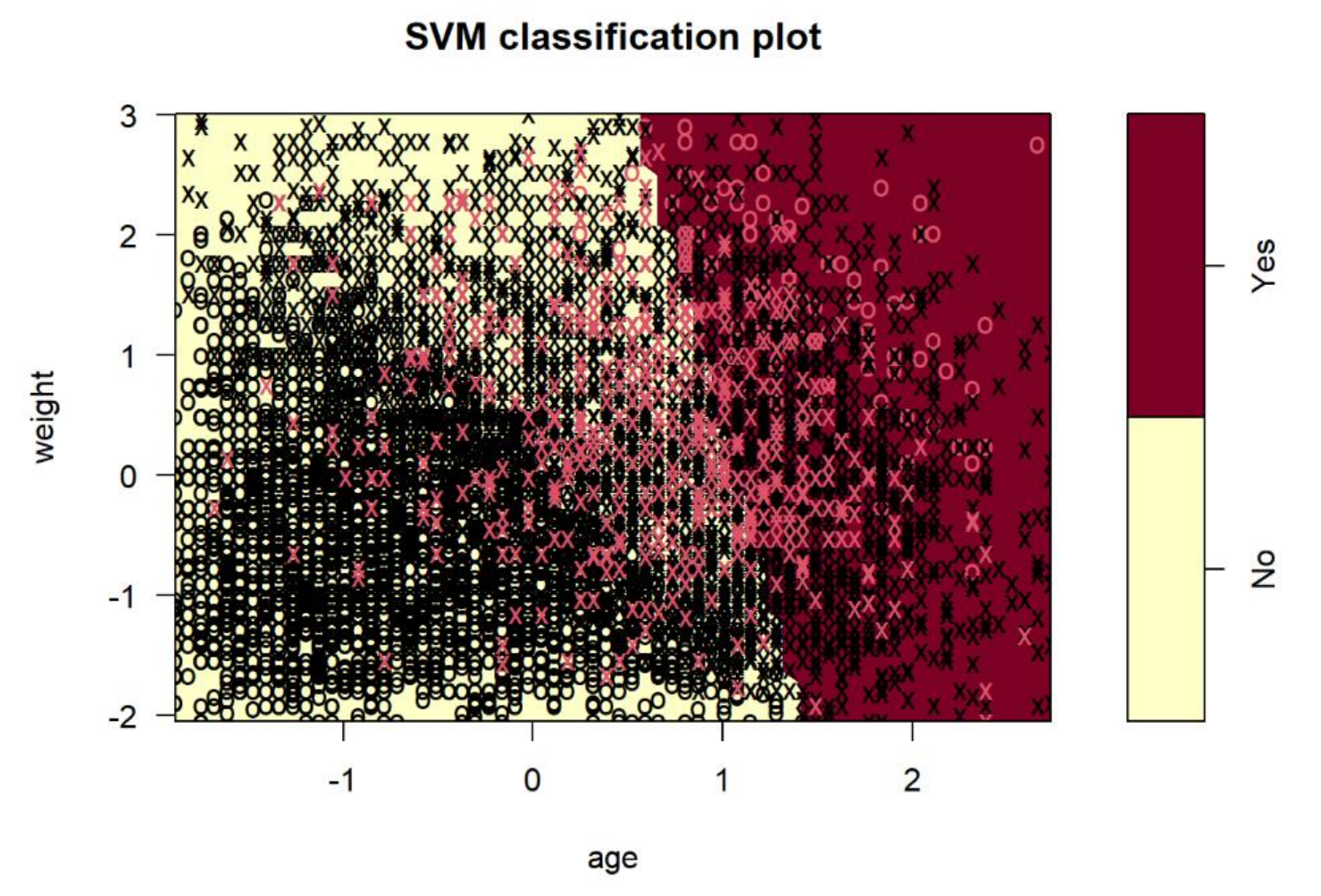
[3] Katella, Kathy. "Why You Shouldn't Rely on BMI Alone." *Yale Medicine*, 4 Aug. 2023, www.yalemedicine.org/news/why-you-shouldnt-rely-on-bmi-alone.

Results

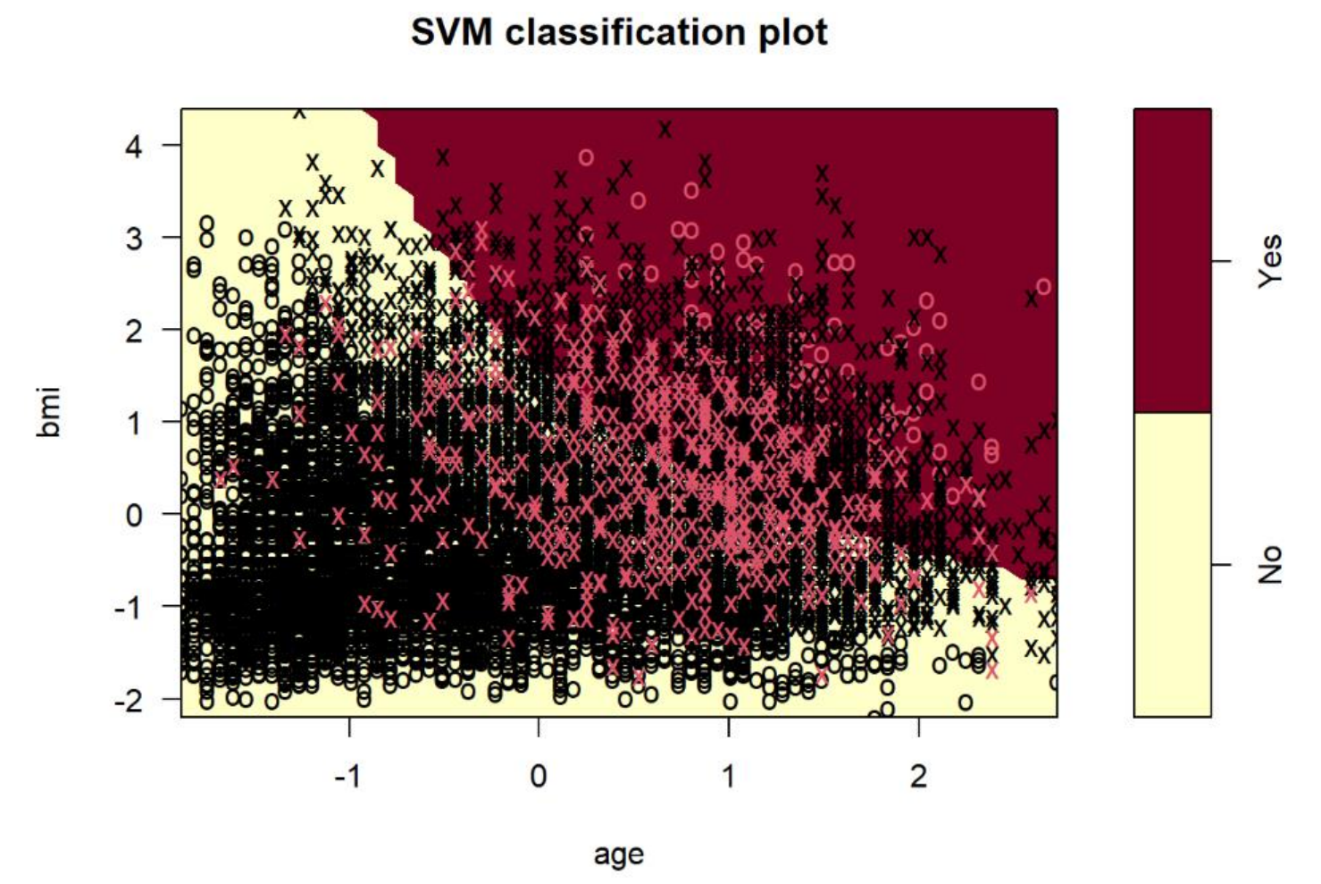
While there were many predictors, one pattern was consistent: older people and people with a high BMI were predicted as having diabetes. Also, the linear model predicted people with a higher weight as more likely to have diabetes.

The following plots are from the linear model:

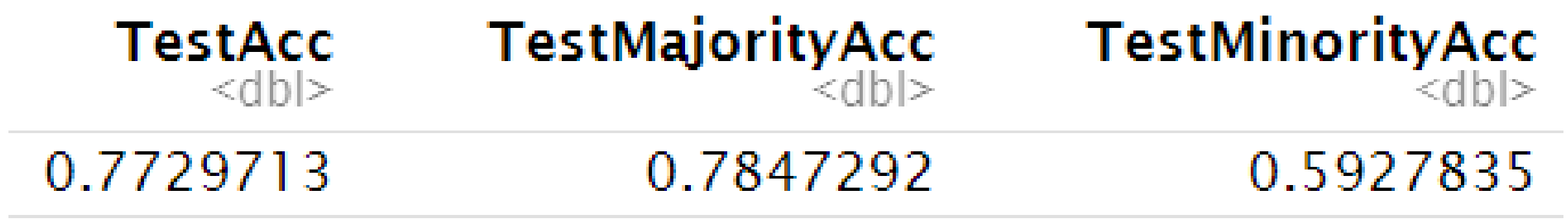




The plot below is from the nonlinear model for diabetes:

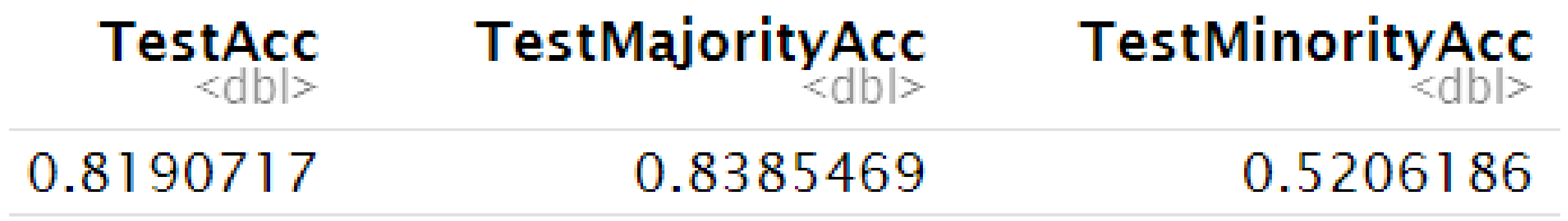


The linear model is better than the polynomial one for predicting people who *do* have diabetes, while the polynomial one is better for predicting people who *don't*.



TestAcc <dbl>	TestMajorityAcc <dbl>	TestMinorityAcc <dbl>
0.7729713	0.7847292	0.5927835

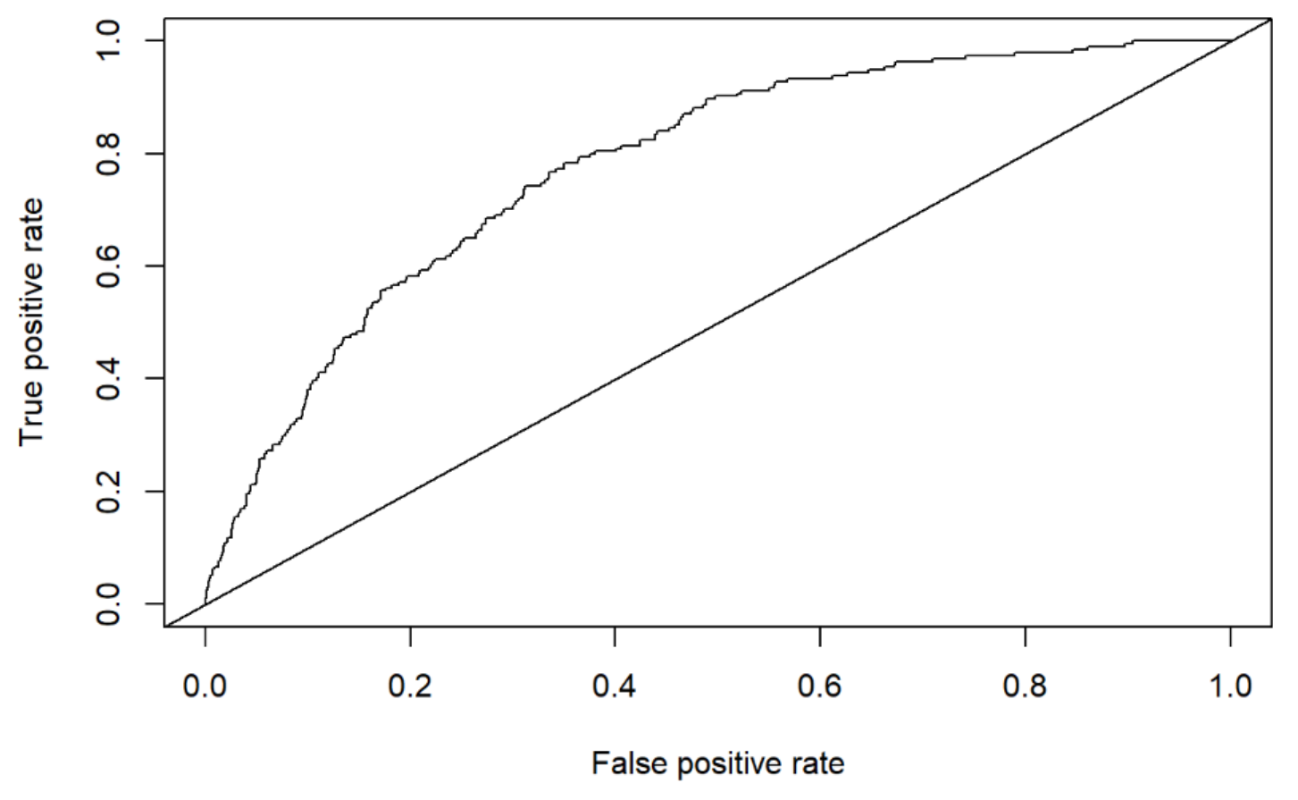
SVM with a linear kernel



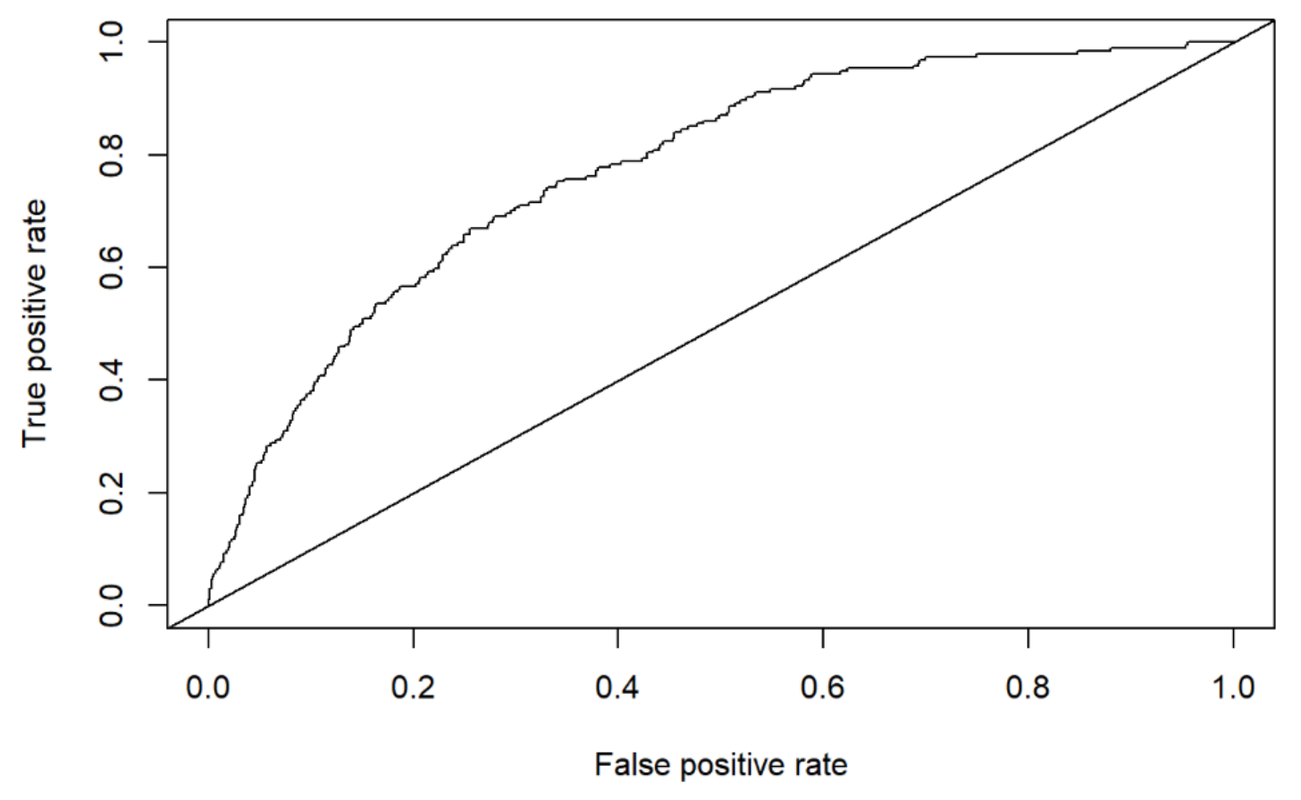
TestAcc <dbl>	TestMajorityAcc <dbl>	TestMinorityAcc <dbl>
0.8190717	0.8385469	0.5206186

SVM with a polynomial kernel

Both models perform relatively well, given the severe class imbalance and the trade-off between predicting both classes accurately. The ROC curves below show that both models perform better than random guessing.



Linear kernel



Polynomial kernel