

An Investigation of Demographic and Behavioral Factors of Autism Screening Tests

The Repos - Jeffrey Bohrer, Alexandra Green, Anna Zhang, Kevin Lee

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I. Introduction

Autism Spectrum Disorder (ASD) is a highly prevalent condition with nearly 2.2% of adults affected by ASD, and growing awareness has led to an uptick in diagnoses, particularly in adults who went undiagnosed early in life (Hirota 2023). However, ASD screening tests for all age groups currently contain significant inaccuracies. For example, the most widely used toddler screening test, CHAT-R/FAs, was found to produce false negatives in 25% of cases; the most commonly used adult autism screening test – the Autism-Spectrum Quotient (AQ) – was found to have limited predictive value in certain populations (Aishworiya 2023; Curnow 2023). Thus, it is critical to identify stronger predictors and explore underlying relationships for more accurate tests to predict ASD in adults.

In this study, we will focus on identifying the features that most greatly affect the probability of being encouraged to pursue a diagnosis within a questionnaire created by Prof. Fadi Thabtah of the Manukau Institute of Technology. The data was sourced from users of his app, ASDTests, which screens its users for potential indicators of autism using a ten-question survey (Faizunnabi 2024; Thabtah 2017). The data set contains nine demographic characteristics – ranging from age to history of neonatal jaundice – along with the binary answers to the ten behavioral questions of this survey. An individual of 383 years old was observed as a clear data entry error, so we restricted age to under 120 years old to remove implausible ages. We relabeled the features representing questions in the data set with their actual wording for interpretability, in addition to representing “Yes” as a 1 and “No” as a 0 for their values.

Because ASD is difficult to identify and can significantly impair an individual’s quality of life, understanding the relationship between demographics, behaviors, and their association with autism could encourage individuals to seek the diagnosis they may need, which then enables access to the necessary resources for support. Accordingly, our research question is: what characteristics of an individual are most closely associated with a high score on this screening test?

i. Univariate EDA

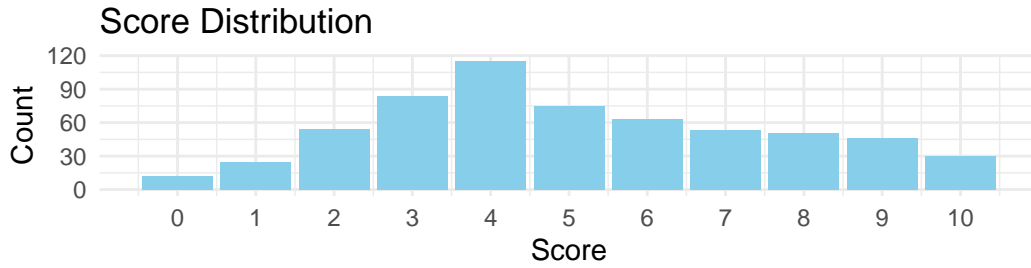


Figure 1: Distribution of total scores across dataset

The final score of individuals ranges from 0 to 10 for each of the 10 behavioral questions. The mean score is 5.084, and the median is 5, which are relatively high considering that scores above 6 warrant further diagnostic evaluation. However, as suspecting a diagnosis is a reason for taking the test to begin with, these are reasonable reflections of the test-taking population. We also observe that roughly 29.6% of subjects are encouraged to seek a diagnosis due to a score higher than 6; the IQR is 4 points, as most subjects have a score between 3 and 7 points inclusive. In the context of the data, such a spread is reasonable, as no outliers exist.

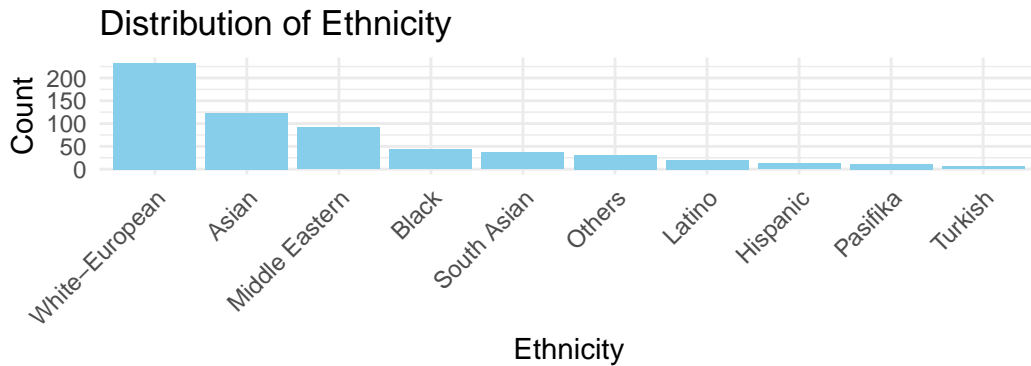


Figure 2: Distribution of ethnicities across dataset

White-Europeans comprised the most common ethnicity of our respondents, with over 200 observations in our data set, while the Asian and Middle Eastern populations have over 100 and slightly below 100 observations, respectively. All other ethnicities have fewer than 50 observations in our data set, suggesting it may be more difficult to draw conclusions about those groups. We will later observe the differing score distributions as categorized by ethnicity to better understand the relationship between score and ethnicity.

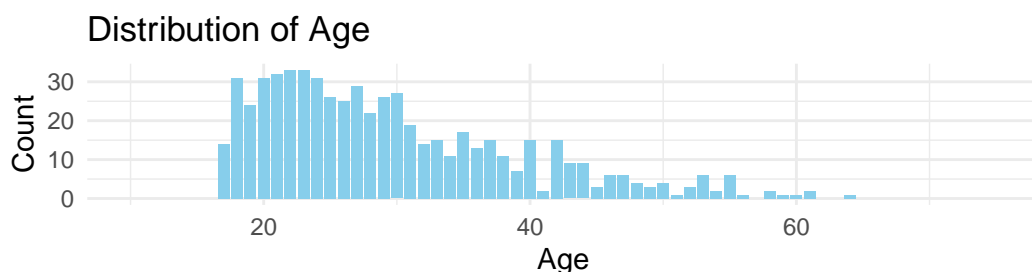


Figure 3: Age distribution across dataset

The distribution of ages possesses a strong right-skewness, with a mean age of 29.63 and a median age of 27. There is a clear peak in the age distribution roughly around the early to mid-20s. The ages range from a minimum of 17 to a maximum of 64 years old. The IQR is 13 years, which is a fairly small spread given the range of ages, as the majority of test-takers are under 30 years old.

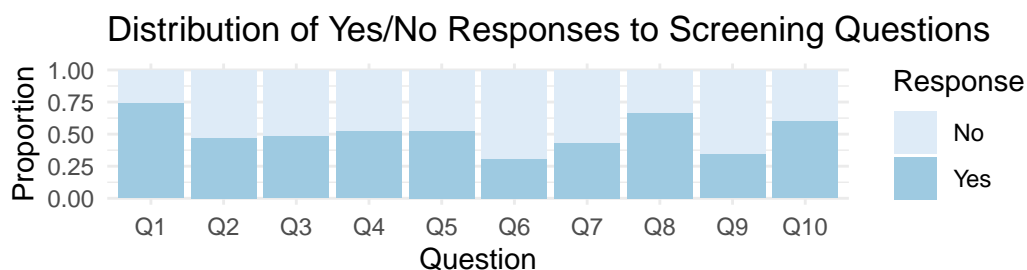


Figure 4: Distribution of Y/N responses for Q1-10 (question details found in appendix).

The two questions with the highest proportion of “Yes” responses were Q1 and Q8, suggesting that these behaviors are relatively common among respondents. On the other hand, Q6 and Q9 had noticeably lower “Yes” responses, potentially indicating difficulties in such areas. Other questions, however, had roughly even proportions of “Yes” and “No” responses.

ii. Bivariate EDA

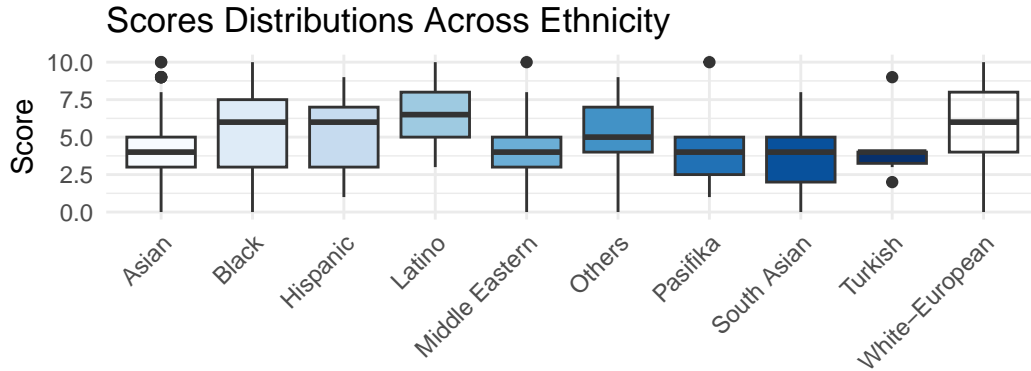


Figure 5: Score distribution across ethnicities

Here we present several graphs displaying bivariate relationships. With our first set of box plots, we find further evidence for our previous suspicion that test score distributions differ by ethnicity. Although most ethnicities have a median within the range of roughly 3 to 6, some ethnicities, like the White-European, Black, and Hispanic populations, demonstrate a greater spread through their larger IQRs, while the Turkish, Middle Eastern, and Asian populations are much more concentrated around their medians.

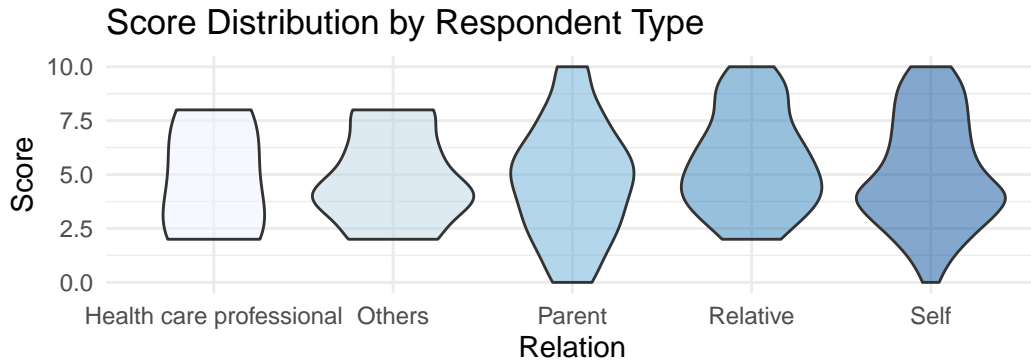


Figure 6: Distribution of scores by respondent type

Interestingly, we can observe how the relationship between the test taker and the subject appears to lead to differing distributions of test scores. When it is filled out by a relative or health care professional for example, the observed test score is 2 or greater, while in the case of the test taker being the subject or the parent of the subject, some still received a score of 0.

We wonder if this could reflect how personal biases or relationships affect truthfulness during the test.

We choose to continue to investigate how our demographic data may impact the odds of being encouraged to seek a formal diagnosis as observed by a high score on this screening test. Though we cannot definitively answer whether it is due to social or cultural perceptions of autism within and surrounding these subgroups or true differences in rates of its presence, it is worth identifying whether over- or under-diagnosis for certain populations is more probable.

II. Methodology

i. Choosing Predictors

We aim to use predictors to determine the probability of obtaining a high score on the screening test. Firstly, a drop-in-deviance test between a logistic null model without predictor variables and only an intercept, and a logistic model with a single predictor was systematically conducted across ethnicity, gender, presence of neonatal jaundice, and relationship to the subject as a means of assessing which predictors provide a statistically significant improvement in model fit against this null condition. Additionally, we also tested the interaction effects of these demographics; we note that we did not explore potential interactions with jaundice as a neonatal condition unlikely to have any relationship with the other variables. Additionally, we did not test ethnicity and relation's interaction effect due to the high number of levels for both (10 and 5, respectively), so the distribution of observations across these subgroups severely limits our sample sizes across coefficients. These tests were done to gain information on the relationship between demographic data and test scores. The hypothesis for this test can be observed below, where $\beta_{predictor}$ represents the coefficient for a single associated predictor variable (also noted for the case of a single-level variable):

$$H_0 : \beta_{predictor} = 0$$

$$H_a : \beta_{predictor} \neq 0$$

The formulas for the models compared are the following:

$$\text{Null: } \log\left(\frac{\hat{\pi}}{1 - \hat{\pi}}\right) = \beta_0$$

$$\text{Alternative: } \log\left(\frac{\hat{\pi}}{1 - \hat{\pi}}\right) = \beta_0 + \beta_{predictor}x_{predictor}$$

Similarly, for our interaction effects, where x_1, x_2 are the predictors for which we test the interaction effect, again using the example of single-level variables:

$$H_0 : \beta_{12} = 0$$

$$H_a : \beta_{12} \neq 0$$

$$\text{Null: } \log\left(\frac{\hat{\pi}}{1-\hat{\pi}}\right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2$$

$$\text{Alternative: } \log\left(\frac{\hat{\pi}}{1-\hat{\pi}}\right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12}(x_1 * x_2)$$

The following table summarizes these results.

Table 1: Non-obvious predictors drop-in-deviance test results

	Deviance	G statistic (respect to null)	p-value
Null	738.699	NA	NA
Ethnicity	645.118	93.581	0
Relation	737.478	1.221	0.875
Age	728.342	10.357	0.001
Gender	734.117	4.582	0.032
Jaundice	729.426	9.273	0.002
GenderRelation	731.886	0.973	0.914
GenderEthnicity	637.567	5.053	0.83
GenderAge	724.316	0.031	0.86
RelationAge	716.49	9.925	0.042
EthnicityAge	638.937	5.864	0.753

The results show that the demographics that may prove statistically significant for our future model are ethnicity, gender, age, and, quite surprisingly, neonatal jaundice, when compared to a null model, as the p-values are either below 0.05. Additionally, we acknowledge potential interactions between relationship to the subject and age – but as relationship to the test subject on its own appears largely insignificant as a predictor, we choose to neglect this interaction effect in our modeling to minimize complexity. We retain the potentially statistically significant predictors for our final model.

We now check our model conditions for these tests. We note that in using our statistically significant predictors later, they are all categorical and thus, do not need to assess linearity between log-odds and our predictors for the logistic regression model. We also note that presumably all of the observations of this test are independent due to no apparent spatial or temporal correlations. However, the model condition at risk is randomness, as our population is primarily those who already suspect autism. This does limit the generalization of our model to the overall population, especially as taking the screening test is voluntary, which leads to a clear response bias. However, pertaining to the population of individuals seeking screening tests, we will assume randomness within this group, and again use this primarily as an investigation of the nature of this questionnaire and associations between demographics and scores. We note an additional limitation that certain subgroups (e.g., the Pasifika ethnic group) possess small sample sizes with less than 30 observations. We further investigate the

correlation between answers to questions below, as a means of assessing if the test has any pitfalls regarding multicollinearity:

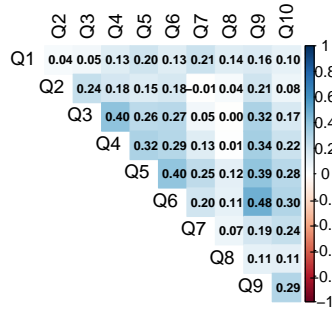


Figure 7: Correlation between AQ10 questions

Unexpectedly, only a few questions have moderate correlations with one another when typically we would expect many behaviors to be grouped together and more correlated (e.g., social behaviors). The highest correlation is between questions 6 and 9, which are the questions about multitasking and liking to collect information, respectively – a rather surprising pairing. Accordingly, principal component analysis was used to determine the question clusters that explain the highest variance to gain further understanding of the nature of the variety of questions in the screening test (Szczęsna, 2022; finnstats, 2021).

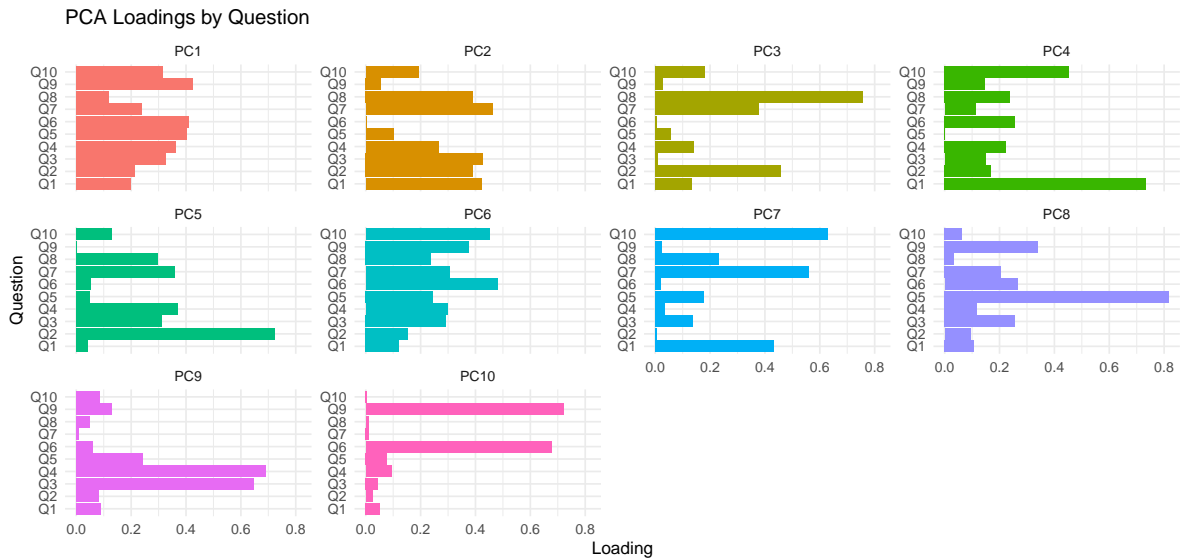


Figure 8: Principal component analysis Q1-10 as a means of choosing questions that best explain the variance in the response

We can observe that Q3, Q5, and Q6 have high correlation to Q4, Q6, and Q9, respectively. Beyond these three, the questions that also observe notable loading for principal components (i.e. the parameters that explain the most variance) are Q10, Q8, Q4, Q2, and Q1 (i.e finding it hard to figure out others intentions, ease of going back to work when interrupted, focus on whole picture, difficulty to understand characters in stories, and picking up on small sounds). In general, it seems that some questions form categories that are highly correlated to explain the different subsets of behaviors in autism. However, since the answer to each question might directly be added to the final result if the answer is TRUE, we decide to focus on examining the predictive power of the demographic data on the likelihood of autism.

ii. Fitting the Model

To identify correlations between demographic data and the odds of a high test score, two models will be fitted and compared by a drop-in-deviance test: (a) a null model fitted only to an intercept, and (b) an alternative model that accounts for our chosen demographic predictors.

$$\text{Null: } \log\left(\frac{\hat{\pi}}{1 - \hat{\pi}}\right) = \beta_0$$

$$\text{Alternative: } \log\left(\frac{\hat{\pi}}{1 - \hat{\pi}}\right) = \beta_0 + \beta_{ethnicity}X_{ethnicity} + \beta_{gender}X_{gender} + \beta_{jaundice}X_{jaundice} + \beta_{age}X_{age}$$

And the hypotheses for the test will be the following:

$$H_0 : \beta_{ethnicity} = \beta_{gender} = \beta_{jaundice} = \beta_{age} = 0$$

$$H_a : \text{at least one of } \beta_{ethnicity}, \beta_{gender}, \beta_{jaundice}, \beta_{age} \neq 0$$

This is to assess whether the chosen demographic predictors significantly improve model fit and our predictions of the odds of obtaining a high score on the test, and consequently, being encouraged to pursue an ASD diagnosis. We include AIC and BIC for further comparison. We note that we reasonably assume no multicollinearity between demographic information.

Table 2: Alternative and null model comparison in terms of deviance, AIC, and BIC

Model	Residual_Deviance	Df	AIC	BIC
Null Model	738.70	607	740.70	745.11
Alternative Model	638.12	595	664.12	721.46

Based on the output, we observe that the alternative model (i.e. the one with demographic information) performs better exhibiting lower deviance, AIC, but also surprisingly BIC, which more harshly penalizes its higher complexity.

Table 3: Drop-in-deviance test result for alternative and null models

Test	G_stat	df	p_value
Drop-in-deviance (Chi-sq)	100.5752	12	0

The drop-in-deviance tests corroborates that these results are statistically significant; we reject the null hypothesis since the p-value is much less than 0.05. Hence, the alternative model will be further assessed as a means of understanding how demographic data impacts the odds of a positive screening test.

III. Results

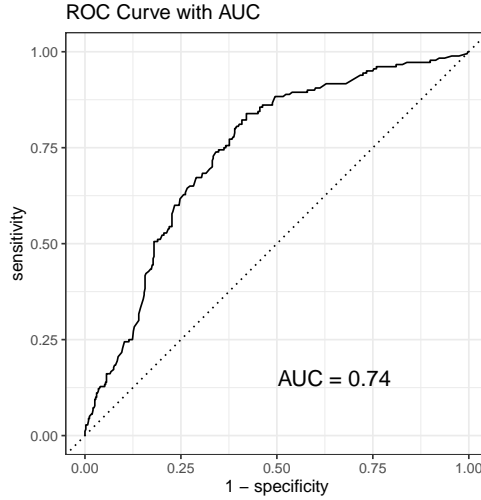
Table 4: Output for alternative model

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	-0.194	0.362	-0.534	0.593	-0.904	0.519
ethnicityAsian	-1.682	0.305	-5.511	0.000	-2.310	-1.107
ethnicityBlack	-0.150	0.340	-0.442	0.659	-0.828	0.512
ethnicityHispanic	-0.191	0.593	-0.322	0.747	-1.425	0.952
ethnicityLatino	0.147	0.475	0.310	0.757	-0.796	1.090
ethnicityMiddle Eastern	-2.161	0.399	-5.409	0.000	-3.016	-1.432
ethnicityOthers	-0.689	0.422	-1.634	0.102	-1.562	0.109
ethnicityPasifika	-2.114	1.061	-1.992	0.046	-5.036	-0.425
ethnicitySouth Asian	-2.173	0.623	-3.489	0.000	-3.625	-1.098
ethnicityTurkish	-1.322	1.107	-1.194	0.233	-4.287	0.533
genderm	-0.293	0.195	-1.497	0.134	-0.677	0.090
age	0.003	0.010	0.353	0.724	-0.016	0.023
jundiceyes	0.628	0.307	2.050	0.040	0.026	1.233

We note that age, gender, and many ethnic groups possess p-values greater than 0.05. Among statistically significant demographic predictors, subjects who identify as Asian, Middle Eastern, or South Asian appear significantly less likely to be categorized as high probability for ASD with expected odds ratios (ORs) of approximately 0.186, 0.115, and 0.114 respectively, compared to the baseline category of White-European, holding all else constant. This leads us to wonder if these subgroups are more prone to under-diagnosis or others to over-diagnosis. The Pasifika population also has a notable odds ratio, but is once again a small group of less than 30 individuals and proves more difficult to generalize.

In individuals with a history of neonatal jaundice, we expect the odds of a positive screening test to multiply by a factor of 1.87 compared to those without, holding all else constant. In practice, this could suggest that individuals with neonatal jaundice should be screened for ASD

at a higher rate than their counterparts, as we note it seems unlikely for these individuals to experience bias in their screening and diagnoses since the effects of neonatal jaundice are nearly imperceptible as adults. For that reason, we do not suspect over-diagnosis for this group.



The area under the curve is 0.74, which means that the model, although not a terrible fit, is likely insufficient to explain the variation in the odds of a high score on its own. However, as a model fitted entirely to demographic data that we would expect to be independent of one's screening result, this is a notable result.

IV. Discussion + Conclusion

Our model uses demographic data such as ethnicity, gender, age, and neonatal jaundice to predict the likelihood of a positive screening test for ASD, for this given screening test examining a variety of behaviors and attitudes. Despite a low to moderate AUC value of 0.74, the classification power of the model is notable given the nature of its predictors. For our model conditions, as previously noted, the randomness of our sample is unlikely, which limits the conclusions of our model and its significance. This limitation is in addition to the small sample sizes of certain tested populations, like the Pasifika ethnic group. Still, this assessment could serve as an argument to pursue further research on the subject of the relationship between particular ethnic subgroups and their rates of over- or under-diagnosis, and how neonatal jaundice impacts the risk of developing ASD. This is especially true given that the odds of a positive test appear notably higher for individuals that identify as White, Black, and Hispanic – which could either indicate over-diagnosis of these groups or under-diagnosis of others in the test-taking population. Presence of neonatal jaundice could also potentially serve as an additional reason to screen and test individuals. Thus, broader comparisons on the impact of these demographics would be insightful. Further work on exploring these relationships, in addition to how particular subsets of behaviors may inflate the significance of these demographic predictors, could provide a strong framework for understanding the current state of ASD diagnostics in our healthcare system.

V. References

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VI. Additional Materials

In Figure 5, the distribution of Y/N responses for Q1-10 is illustrated. Here are the details of the 10 behavioral questions (also shown in the data dictionary).

Q1, noticing small sounds;

Q2, finding it difficult to work out character intentions;

Q3, finding it easy to read between lines;

Q4, big picture-oriented;

Q5, can tell if someone listening to me is bored;

Q6, can multitask;

Q7, can tell feelings from faces;

Q8, can go back to work when interrupted;

Q9, enjoy collecting info on categories;

Q10, find it difficult to work out people’s intentions.

One thing to note is that while we renamed the ten variables to more descriptive names in our dataset for clarity, we decided to use the Q1–Q10 labels in the visualization for simplicity and cleaner presentation.

In the methodology section, we first performed five drop-in-deviance tests for each of the demographic predictor. In table 1, a summary of the results of the five tests is presented. We would like to show the full output of each test here.

Table 5: Drop-in-deviance test for ethnicity

term	df.residual	residual.deviance	df	deviance	p.value
highProb ~ 1	607	738.699	NA	NA	NA
highProb ~ ethnicity	598	645.118	9	93.581	0

Table 6: Drop-in-deviance test for relation

term	df.residual	residual.deviance	df	deviance	p.value
highProb ~ 1	607	738.699	NA	NA	NA
highProb ~ relation	603	737.478	4	1.221	0.875

Table 7: Drop-in-deviance test for age

term	df.residual	residual.deviance	df	deviance	p.value
highProb ~ 1	607	738.699	NA	NA	NA
highProb ~ age	606	728.342	1	10.357	0.001

Table 8: Drop-in-deviance test for gender

term	df.residual	residual.deviance	df	deviance	p.value
highProb ~ 1	607	738.699	NA	NA	NA
highProb ~ gender	606	734.117	1	4.582	0.032

Table 9: Drop-in-deviance test for jaundice

term	df.residual	residual.deviance	df	deviance	p.value
highProb ~ 1	607	738.699	NA	NA	NA
highProb ~ jundice	606	729.426	1	9.273	0.002