Original Research Article

Comparing Individual and Joint Logistic Models for Autism Screening: A Study of Family History Associations

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ABSTRACT

Autism spectrum disorder (ASD) is a complex neurodevelopmental condition characterized by differences in communication, behavior, and cognition, with significant social and familial implications. Understanding how familial background contributes to autism-related behavioral traits remains an essential research goal. This study utilizes a publicly available dataset from Kaggle, comprising more than 700 respondents, to examine the relationship between family history of autism and ten standardized screening items (A1–A10). Two complementary statistical frameworks were employed: individual binary logistic regression models, which estimate the item-level association between family history and each screening response, and a joint Generalized Estimating Equation (GEE) model, which accounts for within-subject correlation among multiple items. Results from the logistic regressions reveal significant positive associations for six items (A1, A3, A4, A5, A6, A9, and A10), with odds ratios for these significant items ranging from approximately 1.7 to 3.5, clarifying that non-significant items (e.g., A2 = 1.56, A8 = 1.25) are not included in this range. The joint GEE analysis further confirms an overall odds ratio of 1.86 ($p < 0.001$), indicating that participants with a family history of autism are nearly twice as likely to respond positively to ASD-consistent screening indicators. Together, these findings provide statistical evidence for a familial component in autism-related behavioral expression and demonstrate the value of integrating individual and joint modeling techniques in autism data analysis.

Keywords: Autism Spectrum Disorder; Family History of Autism; Standardized Screening Items; Binary Logistic Regression; Generalized Estimating Equation

INTRODUCTION

Autism spectrum disorder (ASD) represents one of the most complex and impactful neurodevelopmental conditions, affecting individuals, families, and societies on multiple levels (1). Characterized by differences in social communication, behavioral flexibility, and sensory processing, ASD influences daily functioning, educational attainment, and long-term life outcomes (2). From an economic perspective, the cumulative costs associated with healthcare services, early interventions, and lifelong support place a substantial burden on families and public systems alike. At the societal level, autism's prevalence—estimated at roughly one in 36 children in recent epidemiological reports—underscores its growing public-health importance (3). Beyond clinical and educational implications, ASD also shapes community inclusion, workplace participation, and family well-being, making its study vital not only for medical science but also for broader social and economic

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policy.

Given the pervasive effects of ASD, numerous research efforts have sought to mitigate its impact through complementary strategies. These approaches range from early diagnostic screening and behavioral therapy to pharmacological treatment and educational adaptation. Early identification and intervention are particularly emphasized, as they can significantly improve developmental outcomes and reduce long-term support needs (4). Alongside clinical and therapeutic advances, statistical and computational studies increasingly employ observational and experimental data to clarify risk factors and behavioral patterns associated with ASD (5). Such data-driven perspectives enable researchers to uncover subtle relationships between biological, familial, and behavioral variables that traditional clinical trials may overlook.

Building upon this context, the present study utilizes a publicly available dataset from the Kaggle autism screening repository, which compiles responses to ten standardized screening items (A1–A10) along with demographic and familial variables (7). A key feature of this dataset is the inclusion of a binary indicator for immediate family history of autism (6). Familial ASD history is thought to influence core behavioral traits such as social communication difficulties, repetitive behaviors, and attention differences—traits directly assessed by the A1–A10 screening items. By explicitly linking family history to these behavioral dimensions, this study aims to examine whether familial predisposition manifests in measurable differences across specific ASD-related behaviors, providing a stronger rationale for investigating item-level responses in relation to family background.

To quantitatively evaluate this relationship, two complementary modeling frameworks were applied. First, the binary nature of the family-history variable motivated the use of individual binary logistic regression models, each estimating the association between family history and one screening item. Recognizing, however, that all ten items originate from the same respondents and are therefore not statistically independent, the study further implemented a joint modeling approach using the Generalized Estimating Equation (GEE) framework (8). The GEE models account for within-subject correlations among repeated binary outcomes, providing more coherent and efficient parameter estimation. Together, these dual frameworks serve two key purposes: (i) validating the consistency and reliability of the observed relationships across different model structures, and (ii) comparing the strengths and limitations of item-specific versus joint correlated-data methods, offering methodological insights for future applications.

Overall, through the integration of publicly available Kaggle data, item-level screening analysis, and dual modeling design, this study aims to enhance understanding of how immediate family history of autism relates to individual ASD screening dimensions. Beyond contributing to autism research by highlighting a relatively underexplored familial component, the findings also offer guidance for statisticians and behavioral scientists seeking to select appropriate analytical frameworks for clustered binary data (9). By bridging substantive psychological interpretation and statistical methodology, the study aspires to inform both autism screening practices and future quantitative modeling efforts in neurodevelopmental research.

METHODS AND MATERIALS

To examine the relationship between family history of autism and the individual autism screening indicators (A1–A10) from the AUSTM instrument, this study applies both individual binary logistic regression models and a joint Generalized Estimating Equation (GEE) model.

Data Description

The dataset utilized in this study was obtained from a publicly accessible source on Kaggle, which provides a reliable and convenient platform for data sharing and open research. The dataset originally contains a wide range of variables, including demographic information (such as age, gender, and ethnicity), family and medical background, as well as the A1–A10 items from the Autism screening tool for autism spectrum disorder (ASD). These ten items constitute the AUSTM instrument, a standardized tool designed to assess core behavioral traits associated with autism, such as social communication differences, repetitive behaviors, and attention-related patterns.

An important categorical variable in the dataset indicates whether a respondent has a family history of autism, which serves as a key explanatory factor in this research. The total number of observations in the original dataset exceeds 700 participants, offering sufficient sample size and representativeness for statistical analysis and model development.

To align the dataset with the specific research objectives, a subset of variables was selected for further analysis. Only the A1–A10 Autism screening scores and

the variable representing family autism history were retained, as these are directly related to the core research questions on autism screening and familial influence. The inclusion of these focused variables allows for a cleaner analytical design and a more precise interpretation of the results. The descriptive statistics for the selected variables are presented in Table 1, which provides an overview of the underlying patterns and variability within the dataset.

Table 1. Frequency and Percentage of Responses for Autism Items (A1–A10) and Family Autism History

Item	Yes (1)	No (0)
A1	508 (72.2%)	196 (27.8%)
A2	319 (45.3%)	385 (54.7%)
A3	322 (45.7%)	382 (54.3%)
A4	349 (49.6%)	355 (50.4%)
A5	351 (49.9%)	353 (50.1%)
A6	200 (28.4%)	504 (71.6%)
A7	294 (41.8%)	410 (58.2%)
A8	457 (64.9%)	247 (35.1%)
A9	228 (32.4%)	476 (67.6%)
A10	404 (57.4%)	300 (42.6%)
Family Autism History (Autism)	91 (12.9%)	613 (87.1%)

The binary Autism items (A1–A10) exhibit varied response rates, with items like A1 (72.2%) and A8 (64.9%) showing the highest "Yes" (1) frequencies, indicating more frequent positive responses on those screening dimensions. In contrast, A6 (28.4%) and A9 (32.4%) have the lowest rates, suggesting fewer affirmative responses for those indicators. Additionally, 12.9% of respondents reported a family history of autism, while 87.1% did not, consistent with the dataset composition used in the subsequent modeling analysis.

Binary Logistic Regression Models

Given that each of the A1–A10 AUSTM screening scores represents a binary outcome (coded as 1 for *Yes* and 0 for *No*), the study employs binary logistic regression to model the relationship between these outcomes and the presence of a family history of autism (FH). Logistic regression is one of the most widely used methods for analyzing dichotomous dependent variables because it effectively estimates the probability that an event occurs based on one or more predictor variables. In this research, each screening item (A1–A10) serves as an individual response variable (Y_i), while the common predictor is the binary family history variable (FH), where FH=1 indicates a family history of autism and FH=0 indicates no such history. The logistic model transforms the binary outcome into a continuous logit (log-odds) scale, allowing for linear estimation while ensuring that the predicted probabilities remain between 0 and 1.

Formally, the logistic regression model for each Autism item I (i.e., A1-A10) is expressed as:

$$\log(P_i / (1-P_i)) = \beta_{0i} + \beta_{1i}(FH) \quad (1)$$

where $P_i=P(Y_i=1 \mid FH)$ represents the probability of a positive ("Yes") response on item i given family autism history, β_{0i} is the intercept for item i, and β_{1i} is the coefficient measuring the effect of family history (11). The main assumptions underlying logistic regression include: (1) independence of observations; (2) a binomial distribution of the dependent variable; (3) a linear relationship between the logit of the outcome and the predictor; and (4) absence of perfect multicollinearity among predictors. The key strength of this model lies in its interpretability—the exponential of the coefficient, $e^{\beta 1i}$ represents the odds ratio, quantifying how much more (or less) likely individuals with a family history of autism are to score "Yes" on a given A1-A10 item compared to those without such a family history. This binary modeling framework thus provides clear, item-level insights into how familial background influences distinct dimensions of autism screening behavior.

Generalized Estimating Equation (GEE) Model

While the individual binary logistic regression models capture the separate relationships between each of the A1–A10 screening scores and the family history of autism (FH), they assume that all responses are statistically independent. However, in practice, the ten screening items are measured for the same participant and are therefore correlated. To address this interdependence and produce more reliable population-level estimates, this study employs a Generalized Estimating Equation (GEE) model. The GEE is an extension of the generalized linear model that accounts for correlation among repeated or clustered observations by introducing a working correlation structure, such as

exchangeable, autoregressive, or unstructured, to model within-subject dependence. In this context, the repeated measures are the A1–A10 binary screening responses nested within each individual respondent. The GEE approach estimates the average effect of family history (FH) across all ten outcomes, rather than treating each item as independent, thus providing a joint estimation framework for correlated binary data.

The general form of the GEE model can be expressed as:

$$(\mu_{ij}) = \beta_{0i} + \beta_{1i}(FH) \quad (2)$$

where link(·) is the logit link function, $\mu_{ij}=E(Y_{ij} \mid FH_{ij})$ denotes the expected probability of a "Yes" response for screening item j from individual score, and FH_{ij} represents the family history variable (12). The model assumes that the mean structure is correctly specified, and that the correlation among responses is captured through a working correlation matrix R(α). One of the key strengths of the GEE framework is its robustness: even if the correlation structure is mis-specified, the parameter estimates remain consistent. Additionally, the GEE provides population-averaged effects, reflecting the average change in response probability across the population rather than for a single individual. This property makes the GEE especially appropriate for studies like this one, where multiple correlated autism screening items are evaluated simultaneously to assess the broader influence of family history.

RESULTS

This section presents various modeling results, both individual and joint, for Autism scores and family history.

Individual Binary Logit Modeling Results

The logistic regression analysis examined the association between family history of autism and each of the ten individual ASD screening items (A1–A10) (Table 2).

The logistic regression analysis examined the association between family history of autism (FH) and each of the ten ASD screening items (A1–A10). Six items—A1, A3, A4, A5, A6, A9, and A10—showed statistically significant positive associations, with odds ratios ranging from approximately 1.7 to 3.5, indicating that participants with a family history of autism were more likely to respond positively on these behavioral indicators. Items A2, A7, and A8 were not statistically significant, suggesting that some dimensions of ASD-related behavior may be less directly influenced by familial factors.

Table 2. Detailed Modeling Results and Performance for Each Individual Binary Logit Model

Modeling Statistics	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10
Intercept	0.87	-0.25	-0.26	-0.17	-0.08	-1.02	-0.33	0.59	-0.88	0.21
βFH_yes	0.75	0.44	0.68	1.25	0.55	0.69	-0.05	0.22	0.99	0.76
p(β)	0.01	0.05	0.00	0.00	0.02	0.00	0.82	0.36	0.00	0.00
p(FDR-BH)	0.02	0.06	0.01	0.00	0.03	0.01	0.82	0.40	0.00	0.01
ORFH_yes	2.12	1.56	1.98	3.49	1.72	2.00	0.95	1.25	2.69	2.15
95% CI (Low)	1.19	1.00	1.26	2.12	1.10	1.27	0.61	0.78	1.72	1.32
95% CI (High)	3.79	2.43	3.10	5.75	2.71	3.14	1.49	2.01	4.20	3.50
AIC	829.40	969.86	965.75	952.44	974.20	835.66	960.70	915.48	872.07	954.31
BIC	838.52	978.97	974.86	961.55	983.31	844.77	969.81	924.59	881.18	963.42
McFadden R^2	0.01	0.00	0.01	0.03	0.01	0.01	0.00	0.00	0.02	0.01
LLR p-value	0.01	0.05	0.00	0.00	0.02	0.00	0.82	0.35	0.00	0.00
ROC AUC	0.54	0.53	0.54	0.57	0.53	0.54	0.50	0.51	0.56	0.54
Sig. (FDR-BH)	Yes	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes

The observed pattern demonstrates that while family history broadly affects ASD-consistent behaviors, the magnitude of influence varies across individual items, reflecting a degree of behavioral heterogeneity. Specifically, items assessing social communication and interpersonal reciprocity (e.g., A4) exhibited stronger familial associations, whereas items related to attention, situational awareness, or more context-dependent behaviors (e.g., A2, A8) showed weaker or nonsignificant associations. This differential pattern suggests that familial ASD traits may manifest more consistently in certain behavioral domains, particularly those with a higher heritable component, such as social perception and repetitive behavior tendencies.

Beyond statistical significance, the odds ratios provide insight into practical implications. For example, individuals with a family history of autism were more than three times as likely to respond affirmatively on A4, emphasizing that this item may serve as a sensitive indicator of familial ASD influence. In contrast, nonsignificant items still provide useful information, highlighting dimensions that may be more influenced by environmental factors, learned behaviors, or individual experience rather than direct familial predisposition. Collectively, these findings underscore the value of item-level analysis, which allows researchers to detect nuanced behavioral patterns that might be obscured when using aggregate scale scores alone.

The Joint Generalized Estimating Equation Modeling Results

The Generalized Estimating Equation (GEE) framework was applied to model the association between family history of autism (FH) and ASD screening responses (A1–A10) while accounting for within-subject correlations among repeated binary outcomes (10). This joint approach allows for more robust estimation by recognizing that multiple screening items are nested within the same respondent and therefore are not statistically independent. In this study, two GEE model specifications were estimated: a main-effects model, which evaluates the overall influence of family history across all items, and an interaction model (FH×item), which allows the family-history effect to vary by item (Table 3).

While individual logistic regression models offer insights at the item level, they treat each screening item as independent, ignoring the fact that multiple responses come from the same participant. To address this, we employed a GEE framework, which accounts

Table 3. Detailed Modeling Results and Performance for the Joint Generalized Estimating Equation

Model / Item	FH_β	FH_SE	FH_OR	95% CI (Low)	95% CI (High)	p-value	AUC	QIC	QICu
GEE main-effects (overall)	0.62	0.13	1.86	1.44	2.40	1.80×10^{-6}	0.65	9204.31	9220.32
GEE FH×item (interaction)	—	—	—	—	—	—	0.66	9172.73	9203.72
A1_Score	0.75	0.30	2.12	1.19	3.79	0.01	—	—	—
A2_Score	0.44	0.23	1.56	1.00	2.43	0.05	—	—	—
A3_Score	0.68	0.23	1.98	1.26	3.10	0.00	—	—	—
A4_Score	1.25	0.25	3.49	2.12	5.75	8.87×10^{-7}	—	—	—
A5_Score	0.55	0.23	1.72	1.10	2.71	0.02	—	—	—
A6_Score	0.69	0.23	2.00	1.27	3.14	0.00	—	—	—
A7_Score	−0.0522	0.23	0.95	0.61	1.49	0.82	—	—	—
A8_Score	0.22	0.24	1.25	0.78	2.01	0.36	—	—	—
A9_Score	0.99	0.23	2.69	1.72	4.20	1.47×10^{-5}	—	—	—
A10_Score (baseline)	0.76	0.25	2.15	1.32	3.50	0.00	—	—	—

for intra-subject correlations among the ten binary items. The main-effects model estimated an overall positive association between family history and ASD screening responses ($\beta = 0.62$, OR = 1.86, $p < 0.001$), confirming that participants with a family history of autism are, on average, nearly twice as likely to endorse ASD-consistent behaviors across the ten items. This aggregate estimate strengthens the evidence that familial ASD exposure is meaningfully associated with behavioral tendencies captured in the screening items.

An interaction model (FH×item) allowed the effect of family history to vary across items. Results indicated that the familial effect was particularly strong for items such as A4 and A9, which assess social communication difficulties and repetitive behaviors. Conversely, items like A2, A7, and A8 showed weaker associations, suggesting that the influence of familial background is domain-specific rather than uniform across all behavioral indicators. These findings highlight the importance of considering item-level heterogeneity in ASD research: even when a general familial effect exists, its manifestation may vary depending on the specific behavioral dimension.

The improvement in model fit metrics (QIC/QICu) and the modest increase in AUC (from 0.653 to 0.656) in the interaction model suggests that accounting for item-specific effects captures subtle variations in how familial ASD risk expresses itself across behaviors. This nuanced approach underscores the value of GEE models for clustered data, as it allows researchers to model both the overall effect of family history and the variability in effects across distinct behavioral items. In practical terms, understanding which items are more sensitive to familial influences could inform targeted screening, early intervention, or personalized assessment strategies.

The Comparison of The Two Types of Modeling Results

Together, the individual logistic models and the joint GEE models provide a coherent and complementary understanding of familial influences on ASD-related behaviors. While individual item models allow identification of specific behavioral dimensions strongly associated with family history, the GEE framework consolidates this evidence to produce a robust population-level estimate and incorporates inter-item correlation.

The key interpretive insight from this combined analysis is that familial effects are not uniform across behavioral dimensions. Social communication and repetitive behaviors appear more strongly influenced by family history, whereas attention-related and situational behaviors show weaker familial effects. This selective pattern may reflect differences in heritability, developmental timing, or susceptibility to environmental modulation. Such insights can guide researchers and clinicians in prioritizing specific behavioral markers when assessing individuals with a known familial risk for ASD.

Additionally, the comparison demonstrates the methodological benefit of joint modeling: by borrowing information across items and accounting for within-subject correlation, GEE provides a more precise and statistically stable estimate of the overall effect of family history, while still allowing exploration of heterogeneity through interaction terms. In contrast, individual logistic models, though valuable for item-level profiling, offer less efficient estimation and may overemphasize variability due to smaller sample sizes for each item.

Overall, these results reinforce the importance of considering both item-specific and population-average effects in behavioral research on ASD. Familial background exerts a meaningful, domain-specific influence on behavior, and careful modeling choices can reveal nuanced patterns that inform screening, early identification, and potential intervention strategies. The combination of individual and joint models provides a balanced framework for understanding the multifaceted role of familial history in shaping observable ASD-related traits.

CONCLUSION

The primary objective of this study was to examine the relationship between family history of autism and the item-level behavioral screening responses (A1–A10) from a publicly available Kaggle dataset. Using both individual binary logistic regression models and a joint Generalized Estimating Equation (GEE) framework, the analysis sought to determine whether familial background contributes to measurable differences in autism-related behavioral indicators. By integrating item-specific and population-averaged modeling perspectives, the study contributes methodologically and substantively to the growing field of quantitative autism research.

The findings reveal a consistent and statistically significant positive association between family history and multiple autism screening dimensions. Specifically, the binary logistic models demonstrated that six of the ten items—particularly A1, A3, A4, A5, A6, A9, and A10—show higher probabilities of positive responses among

participants with a family history of autism, with odds ratios typically ranging between 1.7 and 3.5. The joint GEE models confirmed and strengthened these patterns, estimating an overall odds ratio of approximately 1.86, indicating that individuals with family history are nearly twice as likely to display autism-consistent responses across the ten behavioral dimensions. These results align with theoretical expectations that genetic or familial predispositions contribute to observable behavioral and perceptual tendencies associated with autism spectrum traits. Collectively, the dual-model evidence underscores that the familial component of autism is both statistically detectable and behaviorally meaningful at the item level.

Methodologically, this study highlights the complementary value of combining individual-level binary modeling with joint correlated-data frameworks. The binary logistic models provide granular insight into which specific behavioral indicators are most sensitive to family history, while the GEE approach captures the broader population-average effects, efficiently accounting for intra-subject correlation among screening items. Together, these models enhance interpretability and robustness, demonstrating how simple yet carefully structured regression frameworks can yield meaningful insight from modest, open-source data.

Future Direction

Although the present findings provide valuable preliminary evidence, several directions can strengthen and extend this line of inquiry.

First, future research should expand the sample size beyond the current dataset of approximately 700 respondents to enhance statistical power and generalizability. Including participants from diverse demographic, cultural, and clinical backgrounds would enable more nuanced subgroup analyses (e.g., by gender, age, or diagnostic status) and reduce potential sample bias. Additionally, future datasets could include more comprehensive behavioral, cognitive, and environmental variables, enabling multivariate models that capture the interaction between familial and contextual influences.

Second, future studies may benefit from employing more advanced modeling frameworks, such as structural equation modeling (SEM), multilevel logistic regression, or Bayesian hierarchical models. These approaches can simultaneously estimate latent constructs (e.g., social communication ability or sensory sensitivity) while accounting for measurement error and inter-item dependencies. Incorporating such structural frameworks would allow researchers to separate general autism-related factors from item-specific variance, offering a more refined understanding of familial effects within the broader autism phenotype. Moreover, time-series or longitudinal extensions of GEE could help capture how familial risk manifests dynamically over developmental stages.

Lastly, collaboration between data scientists, clinicians, and behavioral researchers is encouraged to integrate computational modeling with clinical interpretation. Using richer multimodal data—such as neurocognitive assessments, genetic profiles, or longitudinal developmental observations—could reveal deeper mechanisms linking familial history to behavioral expression. By combining methodological rigor with interdisciplinary perspective, future work can move beyond statistical association to causal understanding, ultimately informing earlier screening, targeted interventions, and more inclusive policy design for families affected by autism.

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CONFLICT OF INTEREST

The author declares no conflicts of interest related to this work.

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