

Genetic Test Ordering After Chatbot-Based Versus Standard Pre-Test Genetic Counseling: Findings from the BRIDGE Trial

Asma Binte Afzal¹

Accepted

May 10, 2026

Published Online

May 17, 2026

Affiliations

¹School of Public Health,
Indiana University
Bloomington

Correspondence

asbafzal@iu.edu

Abstract

Background. Genetic counseling and testing can identify individuals at elevated hereditary cancer risk, but access remains uneven. Digital delivery may improve reach, yet disparities in engagement and uptake may persist.

Purpose. This secondary analysis of the Broadening the Reach, Impact, and Delivery of Genetic Services (BRIDGE) randomized controlled trial examined whether chatbot-based versus standard-of-care pretest genetic counseling was associated with genetic test ordering and whether associations differed by race/ethnicity or preferred language.

Methods. De-identified participant-level data from 3,073 adults randomized across two United States health systems were analyzed. Test ordering was measured using electronic health record data. Firth logistic regression estimated associations while addressing sparse outcomes and quasi-complete separation in some engagement groups.

Results. In engagement-adjusted models, chatbot assignment was associated with lower odds of ordering genetic tests than standard-of-care counseling. Across both pathways, progression to a test-request stage was the strongest correlate of ordering. No clear evidence indicated that modality associations differed by race/ethnicity or preferred language, although smaller subgroup estimates were imprecise.

Conclusion. Digital counseling may expand access, but access alone may not ensure completion of clinically meaningful care. Implementation should pair digital delivery with supports that help patients move from information exposure to action.

Keywords: genetic counseling; chatbot; BRIDGE trial; genetic test ordering; Firth logistic regression

Introduction

Advances in genetic testing have created important opportunities to identify individuals at elevated risk for hereditary cancers and to support earlier, more personalized care. At the same time, access to cancer genetic services remains uneven, particularly for populations affected by social, structural, and geographic barriers [1,2]. This makes access to genetic counseling not only a clinical issue but also a service-delivery and health-equity issue, especially when eligible individuals do not move far enough through the pathway to receive testing.

Digital tools such as chatbots have emerged as potential scalable alternatives to traditional pre-test

counseling models. Existing studies suggest that automated or chatbot-based counseling can be acceptable, usable, and efficient in some settings and may increase the reach of cancer genetic services [3–5]. Related work on alternative and remote delivery models has also shown that expanding access does not automatically yield equivalent participation or completion across settings, which makes downstream implementation outcomes especially important to evaluate [6–8]. However, available evidence also suggests that digital delivery alone does not eliminate disparities in uptake or follow-through. More broadly, telehealth-based genetic counseling has shown outcomes often comparable to in-person delivery across multiple domains, although diverse

populations remain underrepresented in much of the evidence base [9]. Also, hereditary cancer testing remains underused despite its clinical and preventive relevance, and barriers extend beyond patient education alone to include structural, neighborhood, and workflow-related factors [10,11]. In addition, a recent systematic review and meta-analysis concluded that chatbot-based tools may help reduce barriers to genetic cancer risk assessment and counseling, but comparative-effectiveness data and evidence on equitable access and follow-through remain limited [12,13]. Prior findings from the Broadening the Reach, Impact, and Delivery of Genetic Services (BRIDGE) also reported subgroup differences in service uptake, including disparities by race, rurality, and social vulnerability, even when access pathways were expanded [1–3]. These challenges are also relevant beyond cancer genetics, as many health systems are seeking ways to expand specialist services while maintaining equitable follow-through.

The BRIDGE randomized controlled trial compared chatbot-based pre-test genetic counseling with standard-of-care counseling across two United States (U.S.) health systems, the University of Utah Health system and New York University (NYU) Langone Health [1,3,14]. Prior BRIDGE publications showed that chatbot and standard-of-care delivery models were comparable for broader cancer genetic service outcomes, while also highlighting important differences in utilization and engagement across subgroups [2,3]. These studies established the relevance of scalable delivery models, but they left open a more specific implementation question: within this pathway, what predicts whether eligible participants actually proceed to genetic test ordering, and does that process differ across counseling modalities and participant groups?

The present study addresses that gap. Rather than retesting overall trial equivalence, this secondary analysis focuses specifically on genetic test ordering as a proximal implementation outcome and examines its relationship to counseling modality, pathway engagement, and equity-relevant characteristics. This framing adds to the existing BRIDGE literature by shifting attention from overall service completion to the mechanisms of follow-through within each pathway, which may be more informative for health systems considering whether and how to scale automated counseling tools [2,3].

This study examined two questions. First, was counseling modality associated with genetic test ordering? Second, did that association vary by race/ethnicity, preferred language, or clinical context? Exploratory arm-stratified models were also used to examine whether pathway engagement was associated with ordering within each

counseling modality.

Methods

Study design, data source, and analytic sample

This secondary analysis used de-identified participant-level data from the BRIDGE randomized controlled trial, archived through the Inter-university Consortium for Political and Social Research (ICPSR Study No. 39256) [14]. The parent trial enrolled 3,073 adults between 2020 and 2023 across two U.S. health systems, University of Utah Health and NYU Langone Health. Eligible participants met National Comprehensive Cancer Network (NCCN) criteria for cancer genetic counseling and were randomized to chatbot-based or standard-of-care (SOC) pre-test genetic counseling [2,3].

A complete-case analysis was used in this secondary analysis. Observations missing the dependent variable or key independent variables were excluded, yielding an analytic sample of 3,063 participants. Because the dataset was publicly available and de-identified, this study did not involve recruiting new participants or direct contact with participants.

Outcome, exposure, and covariates

The primary outcome was genetic test ordering, defined as whether a participant had a documented genetic test order in the electronic health record. This variable was coded as binary, with 1 indicating that a test was ordered and 0 indicating that it was not.

The primary exposure was a randomized assignment to counseling, coded as chatbot-based versus SOC counseling. Several other variables were selected to represent participant characteristics, care context, and pathway progression. These included race/ethnicity, preferred language, gender, age group, residence, study site, primary care provider (PCP) status, and algorithm-defined risk criteria (AlgoMet). Two pathway-specific composite variables were also included to summarize participants' progress after randomization within each counseling pathway. These measures were not treated as baseline characteristics; rather, they were used as pathway descriptors to show how far participants progressed before or around the point at which test ordering could occur.

In the chatbot arm, Chatbot Engagement was categorized as No Engagement, Unknown, Read Only, Pretest Only, and Pretest + Requested. In the SOC arm, genetic counseling (GC) status was categorized as Unknown, No Engagement, Scheduled, and Scheduled +

Requested. The highest categories in each pathway included a documented request step and therefore occurred late in the pathway, temporally close to the ordering outcome. For that reason, these composite variables summarize progression toward ordering rather than independent upstream predictors, and categories that included a documented request were expected to be closely linked to the outcome by design.

Reference categories and variable coding

All variables, whether text-based or categorical, were recoded into analysis-ready binary or grouped-categorical forms before modeling. The original ordering field was converted into a numeric binary outcome. PCP status and algorithm-defined eligibility criteria were recoded into binary variables. Initially, Age was summarized descriptively using the original dataset groupings and then collapsed for regression modeling to improve interpretability and cell stability. Categorical predictors were represented using reference-cell coding for regression analyses.

To improve interpretability, the lowest-engagement category was used as the reference group for pathway progression variables. For example, for both Chatbot Engagement and GC Status, No Engagement served as the reference category (Table 1). For race/ethnicity, White was used as the reference category because it was the largest

racial/ethnic group in the analytic dataset, which supported more stable estimation and clearer comparison across smaller groups. This was an analytic convention selected for model stability and interpretability rather than a normative standard. In the case of language, non-English served as the reference category, so the English-language coefficient reflected comparison with non-English speakers. Variable definitions, coding decisions, and reference categories are summarized in Table 1.

Descriptive and unadjusted analyses

Descriptive statistics were calculated to summarize the analytic sample and major study variables. Frequency distributions were used to describe the dependent variable, counseling assignment, pathway engagement variables, and participant characteristics.

Chi-square tests were then used to evaluate unadjusted associations between genetic test ordering and candidate predictors. Because counseling assignment was randomized and pathway engagement variables occurred later in care, the unadjusted assignment-ordering association is presented separately from the engagement-adjusted multivariable models.

Table 1. Variable coding with reference categories

Variable/ Construct	Role	Coding	Reference
Genetic test ordering	Outcome	0 = No, 1 = Yes	—
Counseling assignment	Exposure	Chatbot, SOC	SOC
Chatbot engagement	Pathway variable	No Engagement, Read Only, Pretest Only, Pretest + Requested, Unknown	No Engagement
GC status	Pathway variable	No Engagement, Scheduled, Scheduled + Requested, Unknown	No Engagement
Race/ethnicity	Covariate / modifier	White, Black, Latine, Other, Missing	White
Preferred language	Covariate / modifier	English, non-English	non-English
Gender	Covariate	Female, Male	Female
Age group	Covariate	25-44, 45-60, Other	Other
Residence	Covariate	Urban, Rural	Urban
Study site	Covariate / interaction	Utah, NYU	Utah
PCP status	Covariate / interaction	No PCP, Has PCP	No PCP
Algorithm-defined criteria	Covariate / interaction	One criterion, Multiple criteria	One criterion

*SOC = standard of care; PCP = primary care provider; NCCN = National Comprehensive Cancer Network; NYU = New York University Langone Health; Genetic Counseling = GC. Composite pathway variables were included to capture participant progression after randomization within each counseling pathway; categories that include a documented request represent late-stage pathway behavior rather than baseline characteristics. Full operational definitions and detailed coding decisions are provided in Supplementary Table S1.

Multivariable modeling strategy

Multivariable logistic regression models were estimated using Firth penalized likelihood because some subgroups were small and some cells were sparse, which could otherwise lead to unstable estimates [15–17]. This method was appropriate because some engagement categories were strongly associated with genetic test ordering, which can produce unstable estimates under ordinary logistic regression. All models were estimated in SAS (Statistical Analysis System) using PROC LOGISTIC with the FIRTH option, and exponentiated coefficients are reported as odds ratios with 95% confidence intervals.

Model building followed a prespecified sequence aligned with the study aims. The fixed-effect and interaction models included counseling assignment, participant characteristics, contextual factors, and the pathway composite variables. These full-sample models were intended to describe conditional associations between assignment, pathway progression, and genetic test ordering. They were not interpreted as total intent-to-treat effects of randomized assignment, because Chatbot Engagement and GC Status occurred after randomization and could function as mediators or pathway descriptors. Conditioning on these post-randomization variables changes the estimand and may also introduce collider bias.

Let $Y_i = 1$ if participant i had a genetic test ordered and $Y_i = 0$ otherwise. Let $p_i = P[Y_i = 1]$. All models used the logit link:

$$\text{logit}[p_i] = \log \left(\frac{p_i}{1 - p_i} \right)$$

Model building followed a prespecified sequence aligned with the study aims.

Model 1: Fixed-effect model

The first model estimated the conditional association between counseling assignment and genetic test ordering after adjustment for participant characteristics, contextual factors, and pathway engagement variables:

$$\text{logit}[p_i] = \beta_0 + \beta_1 \text{Chatbot}_i + \sum_{k=1}^K \beta_k X_{ki}$$

where Chatbot_i indicates assignment to chatbot-based counseling and X_{ki} denotes the set of prespecified covariates.

Model 2: Interaction-effect model

The second model tested whether the conditional association between counseling assignment and genetic test ordering differed by PCP status, algorithm-defined risk criteria, and study site:

$$\begin{aligned} \text{logit}[p_i] = & \beta_0 + \beta_1 \text{Chatbot}_i + \beta_2 \text{HasPCP}_i + \beta_3 \text{AlgoMet}_i + \\ & \beta_4 \text{Site}_i + \beta_5 [\text{Chatbot}_i \times \text{HasPCP}_i] + \beta_6 [\text{Chatbot}_i \times \text{AlgoMet}_i] \\ & + \beta_7 [\text{Chatbot}_i \times \text{Site}_i] + \sum_{k=1}^K \beta_k X_{ki} \end{aligned}$$

In this model, the main chatbot coefficient represents the chatbot-versus-SOC association within the reference stratum.

Model 3: Chatbot-arm model

The third model was estimated only among participants assigned to chatbot-based counseling and examined whether Chatbot Engagement predicted genetic test ordering within that subgroup:

$$\text{logit}[p_i] = \alpha_0 + \sum_{k=1}^K \alpha_k X_{ki} + \sum_{m=1}^M \lambda_m \text{ChatbotEngagement}_{im}$$

Model 4: SOC-arm model

The fourth model was estimated only among participants assigned to SOC counseling and examined whether GC Status predicted genetic test ordering within that subgroup:

$$\text{logit}[p_i] = \alpha_0 + \sum_{k=1}^K \alpha_k X_{ki} + \sum_{m=1}^M \lambda_m \text{GCStatus}_{im}$$

Reduced and demographic models

In addition to the four primary Firth logistic regression models, a reduced model was estimated to provide a more parsimonious summary of predictors while retaining counseling assignment as the primary exposure. A separate demographic model was also estimated to assess whether demographic and equity-related variables remain associated with genetic test ordering when interactions between condition assignment and race/ethnicity or language were examined.

Model evaluation and comparative fit

Because residual and influence diagnostics are less informative under penalized likelihood estimation, model evaluation emphasized comparative fit and interpretability rather than conventional residual-based diagnostics [15–17]. All model fits were compared using the Akaike information criterion (AIC), $-2 \log$ -likelihood, the Schwarz criterion/Bayesian information criterion (SC/BIC), and the likelihood ratio chi-

square statistic.

These indices were used to compare the relative explanatory performance of the fixed-effect, interaction-effect, chatbot-arm, and SOC-arm models, as well as the reduced and demographic models. The interaction model was treated as the strongest full-sample model for interpretation because it showed the best comparative fit among the full models, whereas the chatbot-arm and SOC-arm models were interpreted as within-arm models rather than directly generalizable full-sample models. In the supplementary document, forest plots and diagnostic plots referenced in the manuscript are provided to support transparency, model interpretation, and diagnostic evaluation.

Results

The association of counseling arms with genetic test ordering was examined, as well as whether this association varied across clinical/contextual factors and equity-related characteristics. Results are presented in the sequential order: descriptive sample characteristics, unadjusted associations, multivariable Firth logistic regression results, and a comparison of model fit.

Sample characteristics

The complete case analytic dataset included 3,063 participants. Participants were nearly evenly distributed across counseling arms, with 1,551 (50.64%) assigned to the chatbot arm and 1,512 (49.36%) assigned to the SOC arm.

Genetic testing was ordered for 508 participants (16.59%), whereas 2,555 (83.41%) did not have a documented genetic test order. The analytic sample was predominantly female (72.74%), White (68.27%), and English-speaking (98.73%). Most participants resided in urban areas (96.38%), and representation across study sites was relatively balanced, with 1,624 participants (53.02%) from NYU and 1,439 (46.98%) from Utah. Most participants had a primary care provider (76.85%) and met only one NCCN eligibility criterion (93.47%).

Pathway engagement differed across the two service models. In the chatbot pathway, 36.96% of participants were classified as No Engagement, 20.18% as Read Only, 4.96% as Pretest Only, and 6.92% as Pretest + Requested; 30.98% were categorized as Unknown. In the SOC pathway, 39.11% were classified as No Engagement, 3.40% as Scheduled, and 6.86% as Scheduled + Requested, while 50.64% were categorized as Unknown. Overall, these descriptive findings suggest that in both pathways, many participants did not progress to the highest action-oriented stages before test ordering.

Table 2. Frequency distribution of key variables in the BRIDGE dataset

Variable	Category	Frequency	Percent
CONDITION_ASSIGNED	Chatbot	1551	50.64
	SOC	1512	49.36
CHATBOT_	No Engagement	1132	36.96
	Unknown	949	30.98
	Read Only	618	20.18
	Pretest + Requested	212	6.92
	Pretest Only	152	4.96
GC_STATUS4	Unknown	1551	50.64
	No Engagement	1198	39.11
	Scheduled + Requested	210	6.86
	Scheduled	104	3.40
	ORDERED_NUM	Ordered = No (0)	2555
	Ordered = Yes (1)	508	16.59
Gender	Gender (0 = Female)	2228	72.74
	Gender (1 = Male)	828	27.03
RACE	White	2091	68.27
	Latine	317	10.35
	Black	203	6.63
	Other	130	4.24
AGE_GROUP	25-39	1210	39.50
	40-49	884	28.86
	50-60	811	26.48
	Other	158	5.16
LANGUAGE	English	3024	98.73
	non-English	39	1.27
RESIDENCE	Urban	2952	96.38
	Rural	111	3.62
STUDY_SITE	NYU	1624	53.02
	Utah	1439	46.98
has_pcp	Has PCP (1 = Yes)	2354	76.85
	Has PCP (0 = No)	708	23.11
algo_mult	One NCCN Criteria (0 = one)	2863	93.47
	Multiple NCCN Criteria (1 = Multiple)	200	6.53

Unadjusted associations with genetic test ordering

Chi-square analyses were used to assess unadjusted associations between candidate predictors and genetic test ordering. Among all the variables, five were significantly associated with the outcome at the bivariate level: counseling assignment ($p = 0.0185$), Chatbot Engagement ($p < .0001$), GC Status ($p < .0001$), PCP status ($p = 0.0016$), and the study site ($p = 0.0004$).

These findings indicate that both the intervention arm and the degree of pathway engagement were associated with participants' proceeding to genetic testing before multivariable adjustment. Because these bivariate comparisons do not condition on post-randomization engagement variables, they are distinct from the conditional models reported below.

Table 3. Significant chi-square associations with genetic test ordering

Interaction terms	Statistic	DF	Prob
CONDITION_ASSIGNED * ORDERED_NUM	Chi-Square	1	0.0185
CHATBOT_ENGAGEMENT * ORDERED_NUM	Chi-Square	4	< .0001
GC_STATUS4 * ORDERED_NUM	Chi-Square	3	< .0001
has_pcp_clean * ORDERED_NUM	Chi-Square	1	0.0016

Multivariable Firth logistic regression analysis

Firth logistic regression models were used in a multivariable analysis to examine whether counseling arm, pathway engagement, and participant- or contextual-level factors were associated with genetic test ordering. Table 4 reports odds ratios with 95% confidence intervals.

In the fixed-effect model (Table 4), assignment to the chatbot arm was associated with significantly lower odds, measured through odds ratios (OR), of ordering a genetic test compared with SOC (OR = 0.291, 95% CI, 0.18-0.48). In both pathways, the highest engagement categories, which included a documented request step, showed extremely large odds ratios because they were structurally close to the outcome. By contrast, lower chatbot engagement categories were associated with lower odds of ordering, including Read Only (OR, 0.06; 95% CI, 0.01-0.29) and Unknown (OR, 0.006; 95% CI, <0.001-0.09). Participants with a PCP also had higher odds of ordering (OR, 2.83; 95% CI, 1.51-5.32).

In the interaction-effect model, two interaction terms were statistically significant: Condition Assigned × Study Site (OR, 0.09; 95% CI, 0.03-0.30) and Condition Assigned × AlgoMult (OR, 4.95; 95% CI, 1.00-24.48). However, the Condition Assigned × Has PCP interaction was not statistically

significant. These findings suggest that the conditional association between counseling modality and ordering differed across study sites and by whether participants met one versus multiple NCCN criteria.

In the chatbot-arm model, Pretest + Requested was again associated with a very large odds ratio, reflecting its late-stage proximity to the outcome. Read Only remained negatively associated with ordering (OR, 0.06; 95% CI, 0.01-0.25). Within the chatbot arm, meeting multiple NCCN criteria was positively associated with ordering (OR, 4.97; 95% CI, 1.62-15.20), whereas receiving care at NYU rather than Utah was associated with lower odds of ordering (OR, 0.10; 95% CI, 0.03-0.30). In the SOC-arm model, Scheduled + Requested was again associated with a very large odds ratio because it included a documented request step. Having a PCP (OR, 2.23; 95% CI, 1.05-4.73) and male gender (OR, 1.71; 95% CI, 1.03-2.83) were associated with higher odds of ordering.

In the reduced model, the main counseling-assignment finding was preserved (OR, 0.29; 95% CI, 0.17-0.48). In the demographic model, the main effect of chatbot assignment was not statistically significant, and none of the interaction terms between counseling assignment and race/ethnicity or preferred language were statistically significant. Overall, the most consistent finding across models was that progression to a documented request stage within either counseling arm was most closely associated with ordering; these very large estimates reflect pathway structure and should not be interpreted as independent or directly comparable effect sizes.

Comparative model fit

Comparative model fit statistics are presented in Table 5. Among the full-sample models, the interaction model showed the strongest overall fit, with the lowest AIC (564.4) and lowest -2 Log L (518.4). The fixed-effect model also demonstrated good fit (AIC = 582.6; -2 Log L = 542.6). The reduced model was more parsimonious but showed a slightly poorer fit (AIC = 592.7; -2 Log L = 572.7), indicating a slight loss of explanatory power relative to the fuller models. The chatbot-arm and SOC-arm models both showed strong fit within their respective subgroups but were interpreted only within their arms and were not treated as directly comparable to the full-sample models because they were estimated on different denominators. The demographic model showed fit comparable to the full model but had a higher SC/BIC, suggesting less favorable performance after accounting for model complexity. Taken together, these statistics support the use of the interaction model as the primary full-sample model for interpretation, while the arm-specific models provide complementary within-pathway insights.

Table 4. Firth logistic regression models predicting genetic test ordering, OR (95% CI)

Effect	Fixed-effect model	Interaction-effect model	Chatbot-arm model	SOC-arm model	Reduced model	Demographic model
Condition assigned Chatbot vs SOC	0.29 (0.18–0.48) ^{***}	0.98 (0.29–3.31)	–	–	0.28 (0.17–0.48) ^{***}	0.67 (0.04–11.5)
GC status Scheduled vs No Engagement	5.58 (0.13–243.7)	5.97(0.14–257.9)	–	0.09 (0.006–1.27)	5.66 (0.11–284.9)	5.72 (0.14–240.6)
GC status Scheduled + Requested vs No Engagement	>999.999 (22.36–44729.58) ^{***}	>999.999 (22.66–44128.73) ^{***}	–	>999.999 (79.61–12560.48) [*]	>999.999 (20.08–49811.16) ^{***}	>999.999 (69.69–14348.41) ^{***}
Chatbot engagement Pretest + Requested vs No Engagement	>999.999 (63.79–15677.57) ^{***}	>999.999 (58.48–17099.67) ^{***}	>999.999 (65.71–15217.39) ^{***}	–	>999.999 (60.88–16426.22) ^{***}	>999.999 (69.69–14348.41) ^{***}
Chatbot engagement Pretest Only vs No Engagement	0.09 (0.006–1.33)	0.09 (0.006–1.28)	0.07 (0.005–1.00)	–	0.08 (0.005–1.31) ^{***}	0.09 (0.006–1.24) ^{***}
Chatbot engagement Read Only vs No Engagement	0.06 (0.01–0.29) ^{***}	0.06 (0.01–0.29) ^{***}	0.06 (0.01–0.25) ^{***}	–	0.06 (0.01–0.30) ^{***}	0.06 (0.01–0.28) ^{***}
Chatbot engagement Unknown vs No Engagement	0.006 (<0.001–0.09) ^{***}	0.006 (<0.001–0.09) ^{***}	0.43 (0.02–10.0)	–	0.005 (<0.001–0.08) ^{***}	0.006 (<0.001–0.08) ^{***}
Has PCP clean 1 vs 0	2.83 (1.51–5.32) ^{**}	2.83 (1.51–5.30) ^{**}	2.67 (0.96–7.42)	2.23 (1.05–4.73) [*]	3.12 (1.66–5.87) ^{***}	2.87 (1.54–5.37) ^{***}
Gender 1 vs 0	1.47 (0.92–2.33)	1.47 (0.92–2.33)	1.12 (0.44–2.84)	1.71 (1.03–2.83) [*]	0.74 (0.48–1.16)	1.45 (0.91–2.30)
Algo_mult 1 vs 0	1.44 (0.64–3.24)	1.44 (0.64–3.23)	4.97 (1.62–15.2) ^{**}	0.89 (0.30–2.63)	–	1.42 (0.63–3.17)
Race Black vs White	1.24 (0.48–3.18)	1.24 (0.48–3.17)	4.17 (0.92–19.0)	0.85 (0.27–2.64)	–	0.99 (0.43–2.29)
Race Latine vs White	1.20 (0.59–2.43)	1.20 (0.59–2.43)	1.03 (0.27–3.96)	1.35 (0.60–3.05)	–	1.19 (0.58–2.46)
Race Other vs White	1.69 (0.60–4.71)	1.69 (0.60–4.70)	0.79 (0.04–14.1)	1.69 (0.61–4.68)	–	2.39 (1.48–3.86)
Study site NYU vs Utah	0.62 (0.38–1.00)	0.62 (0.39–1.00)	0.10 (0.03–0.30) ^{***}	1.33 (0.76–2.32)	–	0.64 (0.29–1.42)
Age group 25–44 vs Other	0.55 (0.25–1.21)	0.55 (0.25–1.21)	1.48 (0.25–8.68)	0.45 (0.20–1.02)	–	0.52 (0.22–1.23)
Age group 45–60 vs Other	0.61 (0.26–1.44)	0.61 (0.26–1.43)	0.86 (0.13–5.79)	0.49 (0.20–1.19)	–	0.58 (0.08–4.19)
Language English vs non-English	0.41 (0.10–1.76)	0.41 (0.10–1.76)	0.25 (0.03–2.28)	0.62 (0.10–3.66)	–	–
Residence Rural vs Urban	1.03 (0.28–3.84)	1.03 (0.28–3.81)	2.06 (0.54–7.85)	0.22 (0.01–4.26)	–	1.02 (0.28–3.78)
CONDITION_ASSIGNED × STUDY SITE	–	0.09 (0.03–0.30) ^{***}	–	–	–	–
CONDITION_ASSIGNED × has_pcp	–	0.62 (0.17–2.24)	–	–	–	–
CONDITION_ASSIGNED × algo_mult	–	4.95 (1.00–24.5) [*]	–	–	–	–
CONDITION × Black	–	–	–	–	–	1.50 (0.25–8.89)
CONDITION × Latine	–	–	–	–	–	0.85 (0.19–3.85)
CONDITION × Other	–	–	–	–	–	0.39 (0.02–8.05)
CONDITION × English	–	–	–	–	–	0.16 (0.010–2.71)

Exponentiated odds ratios are reported as OR (95% CI). Confidence intervals are Wald intervals. For very large request-stage estimates, the displayed odds ratio was truncated at >999.999 in the exported output, so the confidence bounds were derived from the reported odds ratio and log-scale standard error. These very large estimates should be interpreted as evidence of strong pathway dependence rather than as precise effect sizes. * p < .05, ** p < .01, *** p < .001, p = “.” indicates moderate significance.

Table 5. Summary comparison of model fit statistics across Firth logistic regression models

Model	AIC	SC (BIC)	-2 Log L	LR χ^2	Fit Summary
Fixed Effect	582.6	703.0	542.6	2128.4	Good fit and strong explanatory power
Interaction	564.4	702.9	518.4	2144.6	Best overall fit (lowest AIC and -2 Log L)
Chatbot Arm	186.0	276.9	152.1	1111.8	Best fit within subgroup; not generalizable
SOC Arm	485.6	565.4	455.6	925.1	Strong within-arm model
Reduced Model	592.7	653.0	572.7	2139.9	Parsimonious but slightly poorer fit
Demographic Model	588.8	739.4	538.8	2124.1	Comparable fit to full model, but higher SC

Interpretation of extreme odds ratio

Several odds ratios were reported as greater than 999.999. These values occurred because some pathway engagement categories, particularly those involving a documented test request, were nearly deterministic for genetic test ordering. Even with Firth penalized likelihood, categories that almost fully predict the outcome can yield extremely large exponentiated odds ratios and very wide or uninformative confidence bounds. These estimates, therefore, indicate strong pathway dependence and close structural proximity to the outcome rather than precise, independently interpretable effect sizes.

Forest plots (Fig S1-S3) and diagnostic plots (Fig S4-S5) referenced in the manuscript are provided in the supplementary material to support transparency, model interpretation, and the diagnostic evaluation of the regression analyses.

Discussion

This secondary analysis found that genetic test ordering differed by counseling modality in engagement-adjusted models, with lower odds of ordering among participants assigned to chatbot-based counseling than among those assigned to standard-of-care counseling. These estimates should be interpreted as conditional pathway-dependent associations rather than total causal effects of randomized assignment, because the models included post-randomization engagement variables. At the same time, the strongest associations with ordering in both arms were observed among participants who progressed to the highest engagement categories involving a documented

test request. Taken together, these findings suggest that the key implementation challenge is not simply whether digital counseling can deliver information, but whether it can support participants in moving from information exposure to a concrete action within the care pathway [18–25]. This interpretation also has broader global-health relevance. In high-income settings, technology-enabled genetic service models may improve convenience, reduce travel burden, and expand reach, but the evidence base has often underrepresented diverse populations and has not consistently addressed equitable follow-through [9,12]. In lower-resource settings, digital tools may help extend limited genetics capacity, but equitable implementation is also likely to depend on workforce availability, referral pathways, affordability, and culturally appropriate delivery systems [10,26].

This interpretation adds a more focused perspective to the existing BRIDGE literature. Earlier BRIDGE publications showed that alternative delivery models for cancer genetic services could broaden access and that chatbot-based versus standard-of-care pathways could produce comparable uptake for broader service outcomes, while also revealing disparities related to race, rurality, and social vulnerability [1–3]. The present analysis adds to that literature by focusing specifically on genetic test ordering as a proximal behavioral and implementation outcome. In this sense, the current paper is less about whether chatbot delivery is broadly acceptable and more about where pathway progression appears to strengthen or weaken across delivery models.

These findings indicate that expanding access alone may not be enough to produce equitable uptake of genetic services. Earlier BRIDGE-related work showed lower utilization among socially vulnerable participants, and other chatbot-based studies have also shown that acceptability and usability do not automatically translate into uniform follow-through across all groups [2,4,5]. In this study, participants who only read information or completed pre-test content without reaching the action stage had much lower predicted likelihoods of ordering a test, whereas those who reached a documented request stage showed near-deterministic ordering. This pattern indicates that the largest drop-off may occur not at the point of eligibility, but between receiving counseling content and taking the next concrete step.

No clear evidence was found that the association between counseling modality and ordering differed by race/ethnicity or preferred language. However, that finding should be interpreted cautiously. The analytic sample was overwhelmingly English-speaking and estimates for smaller racial/ethnic and non-English subgroups were imprecise. As a result, the lack of statistically significant interaction terms should not be taken to mean that equity concerns have been resolved. Instead, these findings are likely to reflect limited

power to detect some subgroup differences and reinforce the need for future studies with more diverse populations and multilingual settings [2]. That need is reinforced by recent work showing that neighborhood disadvantage and underserved clinical contexts continue to shape who reaches and completes cancer genetic services, even when eligibility can be identified through scalable screening approaches [11,27].

Differences across clinical settings were also apparent. The significant interaction terms for study site and algorithm-defined risk criteria indicate that the relationship between counseling modality and ordering was not identical across settings or risk strata. This matters for implementation because digital counseling tools operate within real clinical systems that differ in workflow, referral patterns, navigation support, and local practice environments. This interpretation is supported by studies showing that workflow design, risk-assessment strategy, and integration of genetics services into primary care or specialty pathways can substantially affect whether patients move from identification to completed testing [8,28]. For example, a well-resourced academic cancer center with embedded genetic counselors, streamlined electronic referrals, and on-site sample collection may support faster progression from counseling to test ordering than a safety-net, rural, or resource-constrained system that relies on fewer genetics personnel, external referrals, or home-based sample return. As a result, a model that appears effective in one clinical system may not produce the same level of follow-through in another [29,30].

The extreme odds ratios observed in the highest engagement categories should also be interpreted with caution. These estimates occurred because participants in some engagement groups were almost certain to order a test, leading to quasi-complete separation. Firth penalized likelihood regression was an appropriate method for this setting because it reduces small-sample bias and improves numerical stability under separation, but it does not force such estimates into narrow finite bounds when prediction is nearly deterministic [15–17]. For that reason, these extreme odds ratios are more informative as an indication of strong pathway dependence than as precise effect-size estimates.

Implications for practice and implementation

These findings have practical implications for cancer genetics programs and health systems considering digital counseling pathways. Automated counseling tools should not be evaluated solely on reach, satisfaction, or information delivery. They should also be assessed according to whether participants move through key action steps, including test requests and test ordering. The findings here suggest that digital models may benefit from added supports such as follow-up prompts, navigation assistance, or rapid transition

to human counseling when participants stall before the action stage. This interpretation is consistent with earlier BRIDGE work showing that service uptake remains socially patterned even when alternative delivery models are introduced [1–3].

The study also contributes to the literature on artificial intelligence-enabled and chatbot-enabled service delivery by showing that behavioral progression within the care pathway may be more informative than assignment alone. Studies by Siglen et al. (2023) and Al-Hilli et al. (2023) support the feasibility and acceptability of chatbot or artificial intelligence-based counseling approaches, but the present results suggest that implementation success should also be judged by whether these approaches produce meaningful follow-through in practice. This interpretation is also consistent with broader service-delivery research showing that alternative counseling models can achieve comparable knowledge or satisfaction outcomes while still facing challenges in testing completion and downstream implementation, particularly in underserved populations [9,31]. Remote and digital models can expand reach, but outcomes still vary according to workflow design, patient population, and the level of implementation support built into the pathway [6,7,32]. In addition, interventions designed to improve uptake of cancer-related genomic services in Latino communities remain limited, reinforcing the importance of evaluating digital counseling not only for feasibility, but also for equitable completion across diverse populations [33]. For this reason, the current findings may be useful to programs interested in scaling digital genetic services while maintaining attention to equity and completion. These findings may also be relevant to other areas of healthcare where digital tools are used to extend access to specialist services, because the main challenge is often not initial contact but whether patients move far enough through the pathway to complete the next meaningful step.

Future directions

Future research should evaluate whether navigation-enhanced or hybrid counseling models improve follow-through among participants who start but do not complete the pathway to test ordering. Future studies may also benefit from implementation-science frameworks that distinguish reach from adoption, completion, and sustainability, because these dimensions are especially relevant when digital genetics services are introduced across diverse health-system contexts [34]. Additional research is also required in more diverse and multilingual populations to determine whether digital counseling models perform similarly across social and linguistic contexts. These next steps would help clarify whether scalable digital counseling can improve not only access, but also equitable completion of recommended clinical pathways.

Conclusion

In this BRIDGE trial secondary analysis, genetic test ordering differed across counseling modalities in models adjusted for covariates and engagement measures, with lower odds of ordering in the chatbot arm than in the standard-of-care counseling arm. These estimates should be interpreted as conditional, pathway-dependent associations rather than total effects of randomized assignment. The magnitude of this conditional association varied by clinical and contextual factors, specifically study site and algorithm-defined risk criteria, but no evidence of effect modification by race/ethnicity or preferred language was detected. Across both modalities, engagement progression, particularly reaching a documented test-request stage, was most closely associated with test ordering.

Overall, these outcomes suggest that scalable digital counseling models may improve access to cancer genetic services, but access alone is not sufficient to ensure follow-through. For health systems seeking to expand equitable delivery of genetic services, the more important question may be not only whether patients are reached, but whether the care pathway supports them in moving from information exposure to meaningful action. This message may also extend beyond cancer genetics to other settings in which digital tools are used to expand access to specialist care.

Limitations

Several limitations should be acknowledged. First, quasi-complete separation in engagement strata (particularly the test-request categories) produced extremely large odds ratios; these reflect pathway structure and sparse subgroup counts rather than precise effect sizes. Second, the analytic dataset was derived via complete-case analysis, and the “Unknown” engagement categories may capture heterogeneous reasons for missingness, which can influence estimates. Third, engagement variables are downstream of randomization; therefore, models including engagement composites should be interpreted as explanatory associations conditional on pathway behavior rather than as total randomized effects. These models may reflect mediation and may also be influenced by structural dependence or collider bias. Finally, estimates for non-English speakers and smaller racial/ethnic subgroups were imprecise due to limited counts, which reduced power to detect moderation by race/ethnicity or language.

Acknowledgements

I acknowledge the Inter-university Consortium for Political and Social Research (ICPSR) for providing access to the publicly available BRIDGE study dataset (ICPSR 39256). The original study was supported by the National Cancer Institute of the U.S. National Institutes of Health under grant number U01CA232826. The author is also grateful to the study investigators for making this important dataset accessible for secondary analysis.

Declarations

Ethical approval declarations

This study used publicly available de-identified secondary data from the BRIDGE Study (ICPSR 39256), which was approved and archived by the Inter-university Consortium for Political and Social Research (ICPSR). As no identifiable personal information was used and the data were previously collected with informed consent, separate IRB (Institutional Review Board) approval for this analysis was not required under Indiana University guidelines.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or non-profit sectors.

Conflict of interest

The author declares no conflict of interest.

Data availability

The dataset analyzed in this study, “Broadening the Reach, Impact, and Delivery of Genetic Services (BRIDGE): Chatbot or Standard of Care Trial for Genetic Cancer Counseling, New York and Utah, 2020-2023,” is publicly available via ICPSR (Study No. 39256): <https://doi.org/10.3886/ICPSR39256.v1>.

Code availability

Code used for data processing and statistical analysis is available from the corresponding author upon reasonable request.

References

- Kaphingst KA, Kohlmann W, Chambers RL, Goodman MS, Bradshaw R, Chan PA, et al. Comparing models of delivery for cancer genetics services among patients receiving primary care who meet criteria for genetic evaluation in two healthcare systems: BRIDGE randomized controlled trial. *BMC Health Serv Res*. 2021 Dec 1;21[1].
- Bather JR, Goodman MS, Harris A, Del Fiol G, Hess R, Wetter DW, et al. Social vulnerability and genetic service utilization among unaffected BRIDGE trial patients with inherited cancer susceptibility. *BMC Cancer* [Internet]. 2025 Dec 1 [cited 2025 May 4];25[1]:180. Available from: <https://bmccancer.biomedcentral.com/articles/10.1186/s12885-025-13495-4>
- Kaphingst KA, Kohlmann WK, Lorenz Chambers R, Bather JR, Goodman MS, Bradshaw RL, et al. Uptake of Cancer Genetic Services for Chatbot vs Standard-of-Care Delivery Models: The BRIDGE Randomized Clinical Trial. *JAMA Netw open* [Internet]. 2024 Sep 9 [cited 2025 May 4];7[9]:e2432143. Available from: <https://pubmed.ncbi.nlm.nih.gov/39250153/>
- Al-Hilli Z, Noss R, Dickard J, Wei W, Chichura A, Wu V, et al. A Randomized Trial Comparing the Effectiveness of Pre-test Genetic Counseling Using an Artificial Intelligence Automated Chatbot and Traditional In-person Genetic Counseling in Women Newly Diagnosed with Breast Cancer. *Ann Surg Oncol* [Internet]. 2023 Oct 1 [cited 2025 May 4];30[10]:5990–6. Available from: <https://link.springer.com/article/10.1245/s10434-023-13888-4>
- Siglen E, Vetti HH, Augestad M, Steen VM, Lunde Å, Bjorvatn C. Evaluation of the Rosa Chatbot Providing Genetic Information to Patients at Risk of Hereditary Breast and Ovarian Cancer: Qualitative Interview Study. *J Med Internet Res*. 2023;25[1]:1–12.
- Buchanan AH, Datta SK, Skinner CS, Hollowell GP, Beresford HF, Freeland T, et al. Randomized Trial of Telegenetics vs. In-Person Cancer Genetic Counseling: Cost, Patient Satisfaction and Attendance. *J Genet Couns* [Internet]. 2015 Dec 1 [cited 2026 Mar 26];24[6]:961–70. Available from: <https://pubmed.ncbi.nlm.nih.gov/25833335/>
- Rodriguez NJ, Furniss CS, Yurgelun MB, Ukaegbu C, Constantinou PE, Fortes I, et al. A Randomized Trial of Two Remote Health Care Delivery Models on the Uptake of Genetic Testing and Impact on Patient-Reported Psychological Outcomes in Families With Pancreatic Cancer: The Genetic Education, Risk Assessment, and Testing [GENERATE] Study. *Gastroenterology* [Internet]. 2024 May 1 [cited 2026 Mar 26];166[5]:872–885.e2. Available from: <https://pubmed.ncbi.nlm.nih.gov/38320723/>
- Wang C, Lu H, Bowen DJ, Xuan Z. Implementing digital systems to facilitate genetic testing for hereditary cancer syndromes: An observational study of 4 clinical workflows. *Genet Med* [Internet]. 2023 May 1 [cited 2026 Mar 26];25[5]. Available from: <https://pubmed.ncbi.nlm.nih.gov/36906849/>
- Danylchuk NR, Cook L, Shane-Carson KP, Cacioppo CN, Hardy MW, Nusbaum R, et al. Telehealth for genetic counseling: A systematic evidence review. *J Genet Couns* [Internet]. 2021 Oct 1 [cited 2026 Mar 26];30[5]:1361–78. Available from: <https://onlinelibrary.wiley.com/doi/full/10.1002/jgc4.1481>
- Pederson HJ, Narod SA. Commentary: Why is genetic testing underutilized worldwide? The case for hereditary breast cancer. *BJC reports* [Internet]. 2024 Oct 1 [cited 2026 Mar 26];2[1]. Available from: <https://pubmed.ncbi.nlm.nih.gov/39516714/>
- Bather JR, Goodman MS, Kaphingst KA. Neighborhood Disadvantage and Genetic Testing Use Among a Nationally Representative Sample of US Adults. *J Prim Care Community Health* [Internet]. 2025 Jan 1 [cited 2026 Mar 26];16. Available from: <https://pubmed.ncbi.nlm.nih.gov/40413740/>
- Webster EM, Ahsan MD, Perez L, Levi SR, Thomas C, Christos P, et al. Chatbot Artificial Intelligence for Genetic Cancer Risk Assessment and Counseling: A Systematic Review and Meta-Analysis. *JCO Clin cancer informatics* [Internet]. 2023 Sep [cited 2026 Mar 26];7[7]. Available from: <https://pubmed.ncbi.nlm.nih.gov/37934933/>
- Culver JO, Bertsch NL, Kurz RN, Cheng LL, Pritzlaff M, Rao SK, et al. Systematic evidence review and meta-analysis of outcomes associated with cancer genetic counseling. *Genet Med* [Internet]. 2024 Jan 1 [cited 2026 Mar 26];26[1]. Available from: <https://pubmed.ncbi.nlm.nih.gov/37688462/>
- aphingst KA. ICPSR. 2025 [cited 2025 Jul 18]. Broadening the Reach, Impact, and Delivery of Genetic Services [BRIDGE] Chatbot or Standard of Care Trial for Genetic Cancer Counseling, New York and Utah, 2020-2023. Available from: <https://www.icpsr.umich.edu/web/ICPSR/studies/39256>
- Devika S, Jeyaseelan L, Sebastian G. Analysis of sparse data in logistic regression in medical research: A newer approach. *J Postgrad Med* [Internet]. 2016 Jan 1 [cited 2025 May 4];62[1]:26. Available from: <https://pmc.ncbi.nlm.nih.gov/articles/PMC4944325/>
- Firth D. Bias Reduction of Maximum Likelihood Estimates Author [s]: David Firth Published by : Oxford University Press on behalf of Biometrika Trust Stable URL : <http://www.jstor.org/stable/2336755> REFERENCES Linked references are available on J. Biometrika Trust. 1993;80[1]:27–38.
- Heinze G, Schemper M. A solution to the problem of separation in logistic regression. *Stat Med*. 2002 Aug 30;21[16]:2409–19.
- Zidaru T, Morrow EM, Stockley R. Ensuring patient and public involvement in the transition to AI-assisted mental health care: A systematic scoping review and agenda for design justice. *Health Expect* [Internet]. 2021 Aug 1 [cited 2026 Apr 12];24[4]:1072. Available from: <https://pmc.ncbi.nlm.nih.gov/articles/PMC8369091/>
- Thieme A, Hanratty M, Lyons M, Palacios J, Marques RF, Morrison C, et al. Designing Human-centered AI for Mental Health: Developing Clinically Relevant Applications for Online CBT Treatment. *ACM Trans Comput Interact* [Internet]. 2023 Apr 1 [cited 2026 Apr 12];30[2]:27.

Available from: <https://dl.acm.org/doi/10.1145/3564752>

20. 20. Ames HMR, Glenton C, Lewin S, Tamrat T, Akama E, Leon N. Clients' perceptions and experiences of targeted digital communication accessible via mobile devices for reproductive, maternal, newborn, child, and adolescent health: a qualitative evidence synthesis. *Cochrane database Syst Rev* [Internet]. 2019 Oct 14 [cited 2026 Apr 12];10[10]. Available from: <https://pubmed.ncbi.nlm.nih.gov/31608981/>
21. 21. Evans-Lacko S, Jarrett M, McCrone P, Thornicroft G. Facilitators and barriers to implementing clinical care pathways. *BMC Health Serv Res* [Internet]. 2010 [cited 2026 Apr 12];10. Available from: <https://pubmed.ncbi.nlm.nih.gov/20584273/>
22. 22. McLeod J, Estcourt CS, MacDonald J, Gibbs J, Woode Owusu M, Mapp F, et al. Opening the digital doorway to sexual healthcare: Recommendations from a behaviour change wheel analysis of barriers and facilitators to seeking online sexual health information and support among underserved populations. *PLoS One* [Internet]. 2025 Jan 1 [cited 2026 Apr 12];20[1]. Available from: <https://pubmed.ncbi.nlm.nih.gov/39775372/>
23. 23. Bucci S, Berry N, Morris R, Berry K, Haddock G, Lewis S, et al. "They Are Not Hard-to-Reach Clients. We Have Just Got Hard-to-Reach Services." Staff Views of Digital Health Tools in Specialist Mental Health Services. *Front psychiatry* [Internet]. 2019 [cited 2026 Apr 12];10[MAY]. Available from: <https://pubmed.ncbi.nlm.nih.gov/31133906/>
24. 24. Graham AK, Lattie EG, Powell BJ, Lyon AR, Smith JD, Schueller SM, et al. Implementation strategies for digital mental health interventions in health care settings. *Am Psychol* [Internet]. 2020 [cited 2026 Apr 12];75[8]:1080–92. Available from: <https://pubmed.ncbi.nlm.nih.gov/33252946/>
25. 25. Kaihlaniemi J, Liljamo P, Rajala M, Kaakinen P, Oikarinen A. Health care Professionals' experiences of counselling competence in digital care pathways – A descriptive qualitative study. *Nurs Open* [Internet]. 2023 Jul 1 [cited 2026 Apr 12];10[7]:4773–85. Available from: <https://onlinelibrary.wiley.com/doi/full/10.1002/nop2.1729>
26. 26. Rungta A, Kapoor A, Redkar G, Kapoor AR, Mishra BK, Gupta A, et al. Implementing genetics clinic for hereditary cancer in resource-constrained settings: a narrative review. *J Community Genet* [Internet]. 2026 Feb 1 [cited 2026 Mar 26];17[1]:14-. Available from: <https://link.springer.com/article/10.1007/s12687-025-00849-5>
27. 27. Kizub D, Bluebond R, Green S, Duckworth J, Shanker S, Vara A, et al. Improving genetics equity: identifying women eligible for genetic care services using mammography clinics in underserved areas as screening hubs. *Oncologist* [Internet]. 2025 Jul 1 [cited 2026 Mar 26];30[7]. Available from: <https://pubmed.ncbi.nlm.nih.gov/40613751/>
28. 28. Pan V, Berman N, Bauer S, Bell M, Borle K, Carrion P, et al. The case for integrating genetic counselors into primary care: A paradigm shift for our profession. *J Genet Couns* [Internet]. 2025 Jun 1 [cited 2026 Mar 26];34[3]. Available from: <https://pubmed.ncbi.nlm.nih.gov/40349148/>
29. 29. Dubsy P, Jackisch C, Im SA, Hunt KK, Li CF, Unger S, et al. BRCA genetic testing and counseling in breast cancer: how do we meet our patients' needs? *NPJ breast cancer* [Internet]. 2024 Dec 1 [cited 2026 Mar 26];10[1]. Available from: <https://pubmed.ncbi.nlm.nih.gov/39237557/>
30. 30. Espinoza-Moya ME, Guertin JR, Floret A, Dorval M, Lapointe J, Chiquette J, et al. Mapping inter-professional collaboration in oncogenetics: Results from a scoping review. *Crit Rev Oncol Hematol* [Internet]. 2024 Jul 1 [cited 2026 Mar 26];199. Available from: <https://pubmed.ncbi.nlm.nih.gov/38729319/>
31. 31. Lahiri S, Mersch J, Zimmerman J, Mauer Hall C, Moriarty K, Gemmell A, et al. Randomized control trial comparing genetic counseling service delivery models in an underserved population. *J Genet Couns* [Internet]. 2025 Apr 1 [cited 2026 Mar 26];34[2]:e1975. Available from: <https://onlinelibrary.wiley.com/doi/full/10.1002/jgc4.1975>
32. 32. Bednar EM, Nitecki R, Krause KJ, Rauh-Hain JA. Interventions to improve delivery of cancer genetics services in the United States: A scoping review. *Genet Med* [Internet]. 2022 Jun 1 [cited 2026 Mar 26];24[6]:1176–86. Available from: <https://pubmed.ncbi.nlm.nih.gov/35389342/>
33. 33. Ramirez Leon D, Martinez D, Rivera Rivera J, Fuzzell L, Vadaparampil S, Rogers H, et al. Assessing interventions promoting the uptake of cancer-related genomic services within the Latino community: A scoping review using the RE-AIM framework. *Cancer Med* [Internet]. 2024 Jul 1 [cited 2026 Mar 26];13[13]:e7440. Available from: <https://pmc.ncbi.nlm.nih.gov/articles/PMC11237879/>
34. 34. Kulchak Rahm A, Cragun D. A guide to utilizing implementation science for genetic counseling. *J Genet Couns* [Internet]. 2025 Jun 1 [cited 2026 Mar 26];34[3]. Available from: <https://pubmed.ncbi.nlm.nih.gov/40305162/>

AI Statement

The author declares that AI was used in line with the MJGH AI policy. The author used Grammarly for checking grammar and ChatGPT for editing language, refining words, and condensing text to meet the journal requirements. All AI-assisted content was reviewed, revised, and verified by the author.