Assessing Baseline Variables as Potential Moderators of the Behavioral Treatment Effects on End-of-treatment (EOT) Abstinence

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Abstract

Background: Smoking cessation among individuals with Major Depressive Disorder (MDD) presents unique challenges, including heightened nicotine dependence and withdrawal severity. Prior research has shown that pharmacotherapy (varenicline) and behavioral activation can improve abstinence rates; however, the role of baseline demographic, psychological, and clinical variables as moderators of treatment outcomes remains underexplored.

Objective: This study aims to assess baseline characteristics as potential moderators of behavioral and pharmacological treatment effects on end-of-treatment (EOT) smoking abstinence. Specifically, it evaluates how these variables influence treatment efficacy, including interaction effects between treatment type and participant characteristics.

Methods: Using data from a 2×2 factorial, randomized, placebo-controlled trial with 300 adult smokers (current or past MDD), multiple imputation was applied to address missing data (21.67% missing). Logistic and Lasso regression models were used to identify significant predictors and their interactions, followed by a comparative analysis of model performance based on Area Under the Curve (AUC) metrics. Key predictors included FTCD scores, readiness to quit, and demographic factors such as race/ethnicity.

Results: Several key baseline variables emerged as significant moderators of smoking abstinence. Higher Nicotine Metabolite Ratio (NMR) was associated with increased odds of abstinence (OR = 2.453, 95% CI: 1.187-5.046), potentially moderating the effectiveness of pharmacological treatments. Lower readiness to quit drastically reduced abstinence odds (OR = 0.038, 95% CI: 0.001-0.878), highlighting the need for motivational enhancement strategies for less-ready individuals. Race/ethnicity was a significant factor, with Non-Hispanic White individuals showing substantially higher odds of abstinence (OR = 5.82, 95% CI: 2.497-14.597), possibly due to socioeconomic and healthcare access disparities. Other moderators included menthol use (OR = 2.169, 95% CI: 1.335-3.565), cigarettes per day (cpd_ps) (OR = 0.921, 95% CI: 0.884-0.959), income level (OR = 0.491, 95% CI: 0.274-0.861), and age (OR = 1.034, 95% CI: 1.013-1.056, p = 0.0011). Logistic regression outperformed Lasso in predictive accuracy (AUC: training = 0.964; testing = 1), identifying robust predictors and interactions.

Conclusion: Baseline characteristics significantly moderated treatment effects on smoking cessation, with pharmacotherapy and demographic variables playing pivotal roles. Logistic regression outperformed Lasso in predictive accuracy, emphasizing the value of including interaction terms in modeling efforts. These findings underscore the importance of personalized interventions for enhancing smoking cessation outcomes among individuals with MDD.

Introduction

Mental health disorders are among the most common health conditions associated with tobacco dependence. Studies have shown that smokers with depression find smoking more pleasurable and are more dependent on nicotine, leading to more severe withdrawal symptoms than smokers without major depressive disorder (MDD). "Smokers with depression are more likely to smoke heavily, perceive smoking as more pleasureable than other traditionally rewarding activities, show greater dependence and experience more severe withdrawal than smokers without MDD (Hitsman, Papandonatos, et al., 1711). Dr. George Papandonatos, from Brown University's highly regarded Biostatistics Department, investigated smoking cessation outcomes in adults diagnosed with MDD.

The motivation behind this study stems from the need to address to bacco dependence in individuals with major depressive disorder (MDD). Due to high prevalence of smoking among people with MDD, more than 30% of individuals with depression are daily smokers. Smokers that has depression, tend to smoke more heavily and frequently, which causes a greater dependence. To evaluate the impact of to bacco dependence on individuals with MDD, this study was conducted in research clinics at Northwestern University (Chicago, IL) and the University of Pennsylvania (Philadelphia, PA). Recruitment for this study was conducted between 06/01/2015 and 03/13/2020. This study employed a randomized, placebo-controlled, 2x2 factorial design to compare behavioral activation for smoking cessation (BASC) against standard behavioral treatment (ST), with an additional comparison of varenicline versus placebo. This study included 300 adult smokers with either current or past MDD.

Findings indicated that BASC did not surpass standard behavioral treatment in effectiveness, regardless of concurrent varenicline therapy. It also indicate that individuals with MDD tend to smoke more heavily, exhibit greater nicotine dependence, and endure more severe withdrawal symptoms than individuals without MDD. Studies have found strong evidence that the varenicline treatment improved short and long term abstinence rates compared to placebo among racially and socioeconomically diverse groups with varied motivations and psychiatric presentations (Hitsman, Papandonatos, et al., 1722). While varenicline has proven effective in supporting smoking cessation, addressing the psychological aspects of smoking behavior, particularly those linked to depression, may further enhance cessation rates among adults with MDD.

In this analysis, we will focus on three primary aims. The first aim is to assess baseline characteristics as potential moderators of the effects of behavioral treatment on end-of-treatment (EOT) abstinence. The second aim is to investigate whether baseline predictors of abstinence vary depending on the type of behavioral intervention and pharmacotherapy administered. The third aim is to identify which baseline variables (e.g., demographic, psychological, and clinical factors) have the strongest influence on abstinence outcomes. We hypothesize that certain baseline characteristics like (race, income, educ) will significantly interact with treatment type, influencing the likelihood of smoking cessation.

Methods

Missingness

The raw data used for this analysis consisted of 300 rows and 25 columns. To begin this analysis, I got the sum of missing values from the dataset by columns. From this analysis, it was observed that the variables Income, FTCD Score at Baseline, Cigarette Reward Value at Baseline, Anhedonia, Nicotine Metabolism Ratio, Exclusive Mentholated Cigarette User, and Baseline Readiness to Quit Smoking contained missing data. The missing data were examined using the naniar package in R to determine the percentage missing and available in the data. Following this procedure, there is a percentage of 21.67% of missing data. The missing percentage goes as follows: Income(1%), FTCD Score at Baseline (.33%), Cigarette Reward Value at Baseline (6%), Anhedonia (1%), Nicotine Metabolism Ratio (7%), Exclusive Mentholated Cigarette User(.67%), and Baseline Readiness to Quit Smoking (5.67%). To further quantify the extent of missingness, the naniar package in R was employed to calculate the percentage of missing and available data. The missing data represent only .9% of the dataset, while 99.1% of the data remains well-represented. Therefore, these

Missing Data Summary for Smoking Sessation

Variables	Missing Values	Percentage Missing (%)
Income	3	1.00
FTCD Score at Baseline	1	0.33
Cigarette Reward Value at Baseline	18	6.00
Anhedonia	3	1.00
Nicotine Metabolism Ratio	21	7.00
Exclusive Mentholated Cigarette User	2	0.67
Baseline Readiness to Quit Smoking	17	5.67
Total	65	21.67

missing data properties led to the implementation imputation.

Pre-processing

The initial exploratory analysis was conducted to identify patterns and relationships among key variables. During preprocessing, it was observed that there are treatment groups in the dataset, but the paper discussed a 2 by 2 factorial design to compare behavioral activation for smoking cessation (BASC) against standard behavioral treatment (ST). The four treatment groups that we will be exploring consists of BASC + Varenicline ST + Placebo, BASC + Placebo and ST + Varenicline. Due to limited number of participants in education levels, Grade School, Some High School, and High School were combined to High School or Less to make it more balance to other education levels in the data.

Multiple Imputations

Multiple Imputation is a statistical process in the mice package that handles missing data by creating several datasets that fills in missing values. In the case here, we will implement 5 imputations for more accurate analyses by accounting for the uncertainty around the missing data, compared to single imputation methods that replace missing values with a single estimate. Each imputed dataset is then arrange into long format using the complete long function treating each as if it were the real, complete data. The statistical model we will be anticipating throughout this process is Logistic and Lasso regression. Following these results, we will examine summary statitiscs like the p-values, odd ratios, and beta estimates to examine the best potential moderators for abstinence for smokers that experience MDD.

EDA (Exploratory Data Analysis)

To investigate the relationships between categorical variables, we utilized barplots to examine significant associations between baseline characteristics, such as income and education levels, and abstinence outcomes. This approach involves comparing observed frequencies across different categories to determine if the differences are statistically significant or likely due to chance. By assessing the independence of two categorical variables, we aim to identify patterns, relationships, and potential associations between risk factors and abstinence.

Barplots were used to visually evaluate these relationships, highlighting interactions between two categorical variables. Patterns in bar heights or proportions provided insights into how one variable influences or interacts with another. Additionally, density plots were included to observe data concentration, with peaks indicating areas of high frequency. Overlaying these density plots allowed for a comparative analysis of differences in distributions, further revealing potential trends or differences in the data.

Test Train Splits on models

In our logistic and lasso models, we will implement a test, train, split process with 70% on the trained data and 30% on the test data.

Logistic

The logistic regression model doesn't use a penalty term and it's objective is to model the probability of a binary outcome Pr(Y=1|X) OR Pr(Y=0|X). Logistic regression uses the MLE (Maximum Likelihood Estimate) of the observed data without imposing any regularization on the coefficients. Logistic regression finds the coefficients that best predict the outcome (abstinence in this case) based on the given predictors by maximizing the likelihood (or minimizing the negative log-likelihood).

To refine the model, variables with statistical significance ($\alpha \le 0.05$) will be selected and observed for their summary statistics of p-values, beta coefficients, confidence intervals, and odd ratios. This step enables the identification of potential moderating factors that may influence abstinence outcomes among participants which provide insights into key predictors.

Lasso

In the lasso regression model, we use the l_1 penalty rather than the l_2 , where we take the absolute value of the β rather than the squaring them. The l_1 penalty has the effect of forcing some of the coefficients to be exactly equal to zero. Lasso performs variable selection and models are easier to interpret that produces sparse models due to all the zeroes represented inside of the model. After observing our β coefficients, we observe the non-zero coefficients in both our main effects model and interaction term model. Following the test, train , split, we will implement the process of crossvalidation and using the respective lasso mechanics. We will pool the results using Rubin's Rules find the odd ratios, means, confidence intervals and other statistical attributes. Then we observe the non-zero coefficients to represent the predictor variables that have the most impact on our model and on the prediction of abstinence.

Comparison Analysis (Area Under the Curve (AUC))

Following the regression model analysis, we will evaluate and compare the performance of the logistic and LASSO regression models. This comparison aims to assess each model's predictive accuracy, interpretability, and ability to identify significant predictors of abstinence. We'll compare models using AUC on both training and testing data to assess generalization and discrimination between abstinent and non-abstinent outcomes. Higher AUC indicates better performance.

Summary Statistics Table

This table provides a detailed breakdown of baseline characteristics for participants in four treatment groups: BASC + Placebo, BASC + Varenicline, ST + Placebo, and ST + Varenicline. Demographically, there is a high representation of Black participants, ranging from 45% in the BASC + Varenicline group to 59% in the ST + Placebo group. Non-Hispanic White participants make up a smaller proportion, ranging from 31% in the ST + Varenicline group to 41% in the BASC + Varenicline group. Hispanic participants account for less than 8% in all groups, with the lowest representation (4%) in BASC + Varenicline. Regarding sex, females are slightly more represented across all groups, with percentages ranging from 53% to 57%. These demographic trends highlight a study population where Black participants and females are highly represented, potentially reflecting disparities in smoking prevalence or recruitment efforts targeting underserved populations.

Socioeconomic factors also provide important context for understanding the challenges these participants may face in smoking cessation. A significant proportion of participants report annual incomes below \$20,000, ranging from 36% in BASC + Varenicline and ST + Varenicline to 38% in ST + Placebo. In contrast, those with incomes above \$75,000 are minimally represented, accounting for only 9-16% across groups. Educational attainment reveals that a large percentage of participants (30-39%) have attended some college or technical

school, while a smaller subset (25-35%) are college graduates. This socioeconomic profile indicates that the study population includes a high proportion of individuals from lower-income and mid-level educational backgrounds, groups often at higher risk for smoking persistence and less likely to access cessation resources. These demographic and socioeconomic factors are critical in interpreting treatment effects, as they may influence both baseline smoking behaviors and responsiveness to cessation interventions.

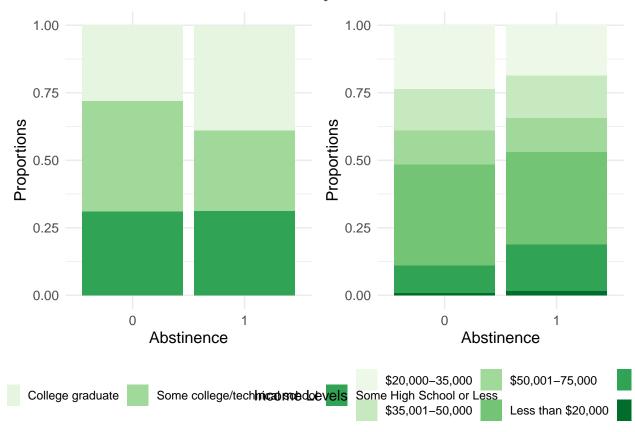
Characteristic	N = 68	BASC + Varenicline N = 83	ST + Placebo N = 68	ST + Vareniclino N = 81
Age	54 (42, 61)	53 (40, 60)	51 (45, 58)	52 (41, 59)
Sex				
Female	38 (56%)	44 (53%)	39 (57%)	44 (54%)
Male	30 (44%)	39 (47%)	29 (43%)	37 (46%)
Non-Hispanic White	24 (35%)	34 (41%)	22 (32%)	25 (31%)
Black	37 (54%)	37 (45%)	40 (59%)	43 (53%)
Hispanic	5 (7.4%)	4 (4.8%)	4 (5.9%)	5 (6.2%)
Income				
\$20,000-35,000	16 (24%)	17 (20%)	14 (21%)	21 (26%)
\$35,001–50,000	8 (12%)	13 (16%)	14 (21%)	11 (14%)
\$50,001–75,000	12 (18%)	12 (14%)	8 (12%)	6 (7.4%)
Less than \$20,000	25 (37%)	30 (36%)	26 (38%)	29 (36%)
More than \$75,000	6 (8.8%)	10 (12%)	6 (8.8%)	13 (16%)
Unknown	1 (1.5%)	1 (1.2%)	0 (0%)	1 (1.2%)
Education Level				
College graduate	19 (28%)	29 (35%)	17 (25%)	26 (32%)
Some college/technical school	22 (32%)	32 (39%)	38 (56%)	24 (30%)
Some High School or Less	27 (40%)	22 (27%)	13 (19%)	31 (38%)
FTCD Score	5.00 (4.00, 7.00)	5.00 (4.00, 7.00)	6.00 (4.00, 7.00)	5.00 (4.00, 7.00
Unknown	0	0	1	0
FTCD Score (5 mins)	32 (47%)	33 (40%)	35 (51%)	38 (47%)
BDI Score	18 (9, 27)	18 (10, 25)	18 (12, 25)	18 (11, 27)
Cigarettes per day	15 (10, 20)	15 (10, 20)	13 (10, 20)	15 (10, 20)
Craving Total	7.0 (5.0, 10.0)	8.0 (4.5, 10.0)	7.0 (4.5, 9.0)	7.0 (5.0, 9.0)
Unknown	1	3	8	6
Hedonic Sum (Negative)	21 (10, 31)	20 (9, 32)	14 (9, 27)	20 (9, 35)
Hedonic Sum (Positive)	23 (14, 34)	17 (11, 31)	25 (12, 38)	21 (13, 34)
Shaps Score	0.00 (0.00, 3.00)	1.00 (0.00, 4.00)	1.00 (0.00, 5.00)	1.00 (0.00, 3.00
Unknown	2	0	1	0
Other Diagnoses	35 (51%)	30 (36%)	28 (41%)	40 (49%)
Antidepressant Medication	28 (41%)	24 (29%)	15 (22%)	15 (19%)
Current Major Depression Episode	32 (47%)	40 (48%)	31 (46%)	44 (54%)
Nicotine Metabolism Ratio	0.32 (0.23, 0.46)	0.33 (0.22, 0.50)	0.32 (0.20, 0.43)	
Unknown	7	3	2	9
Only Menthol	40 (59%)	48 (59%)	43 (64%)	47 (58%)
Unknown	0	1	1	0
Readiness to Quit		· ·	'	
3	1 (1.6%)	0 (0%)	0 (0%)	0 (0%)
4	2 (3.1%)	2 (2.6%)	1 (1.6%)	0 (0%)
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5	6 (9.4%)	11 (14%)	9 (14%)	9 (12%)
7	18 (28%)	22 (28%)	14 (22%)	29 (38%)
7	16 (25%)	21 (27%)	16 (25%)	18 (23%)
8	17 (27%)	20 (26%)	19 (30%)	18 (23%)
9	2 (3.1%)	1 (1.3%)	2 (3.1%)	2 (2.6%)
10	2 (3.1%)	1 (1.3%)	3 (4.7%)	1 (1.3%)
Unknown	4	5	4	4

Exploratory Data Analysis

In the Baseline Characteristics of Abstinence Status by Socioecomonic Levels ,the stacked bar plot offers a clear visual depiction of the association between education and income levels based on abstinence status. The plot indicates that individuals with higher education levels, such as "College Graduate," appear more prevalent among the abstinent group compared to the non-abstinent group, while those with "Some High School or Less" education are more represented in the non-abstinent group. This suggests a potential positive relationship between higher education levels and the likelihood of abstinence.

The proportions of individuals in each income bracket appear relatively consistent between the abstinent and non-abstinent groups, with no clear dominance of any specific income level in either group. However, a slight trend may suggest higher proportions of abstinent individuals in middle to higher income brackets (e.g., "\$35,001-\$75,000"), whereas lower income categories (e.g., "Less than \$20,000") appear more prominent in the non-abstinent group. Through further analysis, it would be interesting to see if income and education levels may be potential moderators for abstinence.

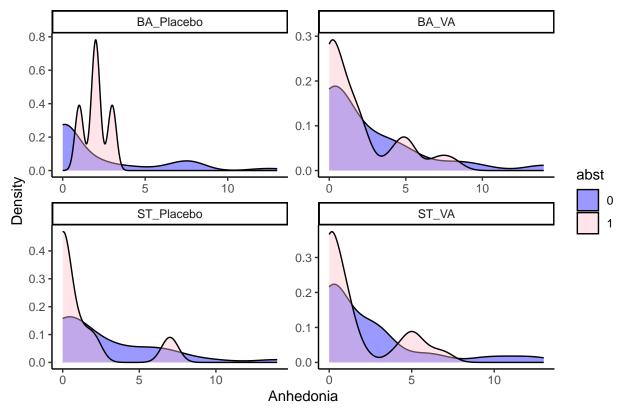
Baseline Characteristics of Abstinence Status by Socioecomonic Levels



Anhedonia is the inability to feel pleasure, experience joy, or pleasure. Anhedonia is a common symtom of depression and mental health disorders. Based off the observations Baseline Characteristics of Abstinence Status with Continous Variables plot, the BA_Placebo group exhibit lower anhedonia scores in the abstinent group (blue) compared to non-abstinent individuals (red), with the density peaks concentrated at lower values. This is similarly reflected in the BA_VA group, where the abstinent participants also tend to have lower anhedonia scores, though the distributions for the two groups overlap more. The ST_Placebo group, a similar trend is observed, where abstinent individuals have a higher density at lower anhedonia scores, suggesting less severe anhedonia among those who are abstinent. The ST_VA group, demonstrated a consisted distribution towards lower anhedonia scores in the abstinent group compared to their non-abstinent counterparts. These plot offers interesting insights due to the overlapping different treatment groups which contributes to lower anhedonia scores are associated with higher likelihoods of abstinence, regardless of the

treatment group.

Baseline Characteristics of Abstinence Status with Continuous Variables



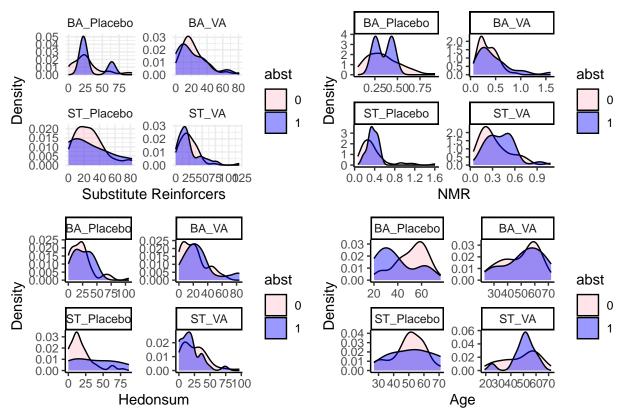
For substitute reinforcers, abstinent individuals (blue) consistently exhibit a higher density at lower scores compared to non-abstinent individuals, particularly in the BA_VA and ST_VA groups. This suggests that individuals who rely less on substitute reinforcers may have a greater likelihood of abstinence, potentially due to a higher capacity for intrinsic motivation in these groups.

Regarding NMR, there is noticeable variation across the treatment groups. In the BA_Placebo and ST_Placebo groups, abstinent individuals tend to cluster around moderate to high NMR values, indicating a potential metabolic or physiological influence on treatment efficacy. However, in the BA_VA and ST_VA groups, the distributions are more similar, suggesting that NMR may have a weaker predictive value in these settings.

For Hedonic capacity, the BA_Placebo and ST_Placebo groups show higher densities for abstinent individuals at moderate hedonic scores, while non-abstinent participants are more evenly distributed across the range. This indicates that hedonic capacity may be a key moderator for predicting abstinence, as individuals with moderate to high capacity for experiencing pleasure may respond better to treatment.

In terms of Age, the relationship with abstinence varies by treatment group. In the BA_Placebo group, abstinent individuals are skewed toward younger ages, while the ST_Placebo group shows a more balanced distribution. In the BA_VA and ST_VA groups, older participants appear more likely to be abstinent, suggesting age may interact with the type of intervention to influence outcomes.

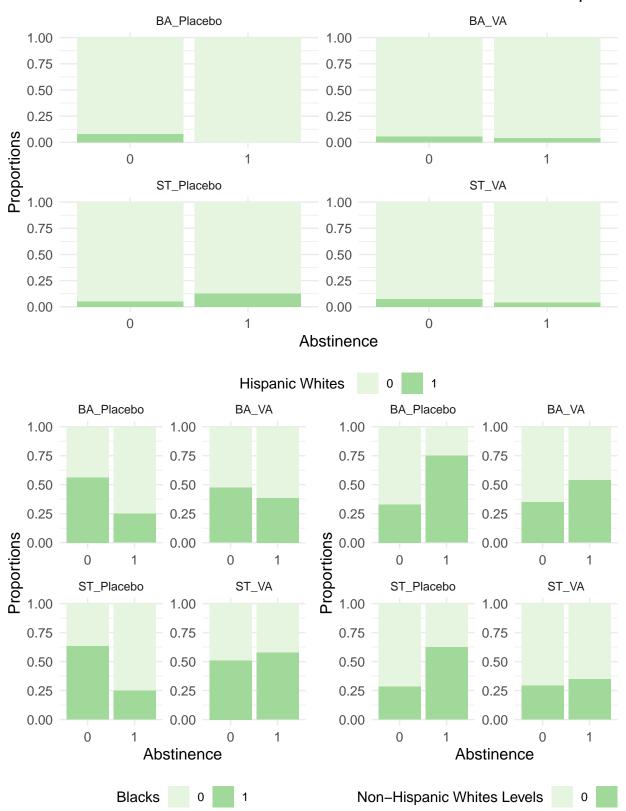




According to Baseline Characteristics of Abstinence Status in Racial Groups, the proportion of abstinent individuals appears slightly lower compared to non-abstinent individuals in the Black group, suggesting a potential disparity in abstinence rates. For Non-Hispanic Whites, the proportions of abstinent and non-abstinent individuals appear relatively balanced, indicating no strong visual difference in abstinence outcomes for this group. In contrast, the Hispanic White group shows a much smaller representation of abstinent individuals compared to non-abstinent individuals, suggesting that this group may face unique barriers to achieving abstinence.

These patterns highlight potential racial disparities in abstinence outcomes, with Black and Hispanic White individuals appearing less likely to achieve abstinence compared to Non-Hispanic Whites. This may be bias, because the racial groups were highly sampled in the data compared to Non-Hispanic Whites.

Baseline Characteristics of Abstinence Status in Racial Groups



Correlation Plot

According to the Correlation to Smoking Cessation Plot, the highest postive correlation presented is the ftcd_score with cpd_ps of (.53) which may introduce multicollinearity in our regression models. The rest of the plot indicates weaker associations which are more ideal for our regression. Depression Score (bdi score w00) demonstrates a notable positive correlation with shaps score pq1 (0.39), which might indicate that higher depression levels are associated with anhedonia or reduced pleasure response (as measured by the SHAPS score). Negative correlations with several variables like age ps and hedonsum n pq1 (-0.34), indicating that higher depression scores might be associated with specific clinical or psychological profiles. Anhedonia (shaps score pq1) offers a positive correlation with bdi score w00 (depression score, 0.39), highlighting an association between depressive symptoms and anhedonia. Negative correlations with abstinence-related measures (hedonsum n pq1, -0.26), which could indicate that anhedonia is negatively associated with behaviors linked to smoking cessation. Craving (crv_total_pq1) illustrates a moderate positive correlation with shaps score pq1 (0.27), potentially indicating that craving and anhedonia are related. High craving scores might represent a barrier to smoking cessation, as they indicate higher dependence and difficulty abstaining.NMR (Nicotinic Metabolism Rate) indicate aminor correlation with other variables, suggesting it may not be as directly related to the psychological measures shown here but could independently influence cessation outcomes by affecting nicotine processing and addiction levels.

Abstinence from smoking may be more challenging for individuals with higher craving levels, depressive symptoms, and anhedonia. The strong relationships between these psychological variables indicate a potential cumulative effect, where individuals facing multiple psychological challenges might experience a higher barrier to achieving and maintaining abstinence.

This matrix provides valuable insights into the psychological and demographic factors that may need to be addressed to improve smoking cessation success, highlighting the importance of targeting depressive symptoms, managing craving, and enhancing motivation in cessation interventions.

Correlation of Smoking Cessation -0.030.01 0.02 -0.01-0.141 NMR 0.15 -0.01-0.040.18 0.39 0.14 -0.270.27 -0.26-0.08-0.04shaps_score_pq1 -0.010.09 -0.08-0.080.04 -0.181 -0.08-0.14hedonsum_y_pq1 -0.28-0.34-0.12-0.26-0.180.04 1 -0.26-0.01hedonsum_n_pq1 Variables 0.2 0.04 -0.10.28 0.15 1 -0.260.27 0.02 crv_total_pq1 0.1 0.53 0.02 0.2 -0.12-0.080.14 0.01 cpd_ps 1 -0.08-0.240.13 0.02 0.15 -0.340.39 -0.03bdi_score_w00 0.13 1 0.13 0.28 0.09 -0.010.53 -0.280.18 ftcd_score 0.13 -0.240.1 -0.10.04 -0.01-0.270.15 age_ps Variables Correlation -1.0 -0.5 0.0 0.5

Logistic Main Effects

Several key variables emerge as potential moderators for abstinence, influencing how other factors or interventions impact cessation outcomes. One significant moderator is the **Nicotine Metabolite Ratio** (**NMR**), which reflects an individual's metabolic capacity to process nicotine. With an odds ratio of 2.453 (95% CI: 1.187–5.046), higher NMR values are associated with increased odds of abstinence. This suggests that NMR could moderate the effectiveness of pharmacological treatments, such as nicotine replacement therapy, as faster metabolizers may require higher doses or alternative strategies to achieve success.

Another critical factor is **readiness to quit**. Individuals with lower readiness to quit (readiness9) have drastically reduced odds of abstinence, with an odds ratio of 0.038 (95% CI: 0.001–0.878). Readiness may moderate the relationship between treatment intensity and outcomes, where higher readiness levels may enhance the effectiveness of behavioral interventions, while lower readiness levels might necessitate motivational enhancement strategies. Similarly, **race/ethnicity** plays a significant role, with Non-Hispanic White (NHW1) individuals showing an odds ratio of 5.82 (95% CI: 2.497–14.597), indicating much higher odds of abstinence compared to other racial/ethnic groups. Race could moderate the impact of socioeconomic factors, such as income and access to culturally tailored healthcare resources, which may affect treatment outcomes.

Other moderators include menthol use and cigarettes per day (cpd_ps). Individuals who exclusively smoke menthol products have 116.9% higher odds of abstinence (odds ratio: 2.169, 95% CI: 1.335–3.565), potentially reflecting unique behavioral or physiological patterns in menthol smokers. This could moderate the effectiveness of treatment modalities, as menthol smokers may respond differently to pharmacological or behavioral interventions. On the other hand, higher cigarette consumption significantly reduces abstinence odds, with an odds ratio of 0.921 (95% CI: 0.884–0.959). Cigarette consumption may moderate the relationship between treatment type and cessation outcomes, where heavier smokers likely require more intensive or combined therapy approaches.

Socioeconomic factors, such as **income level (inc2)**, also show a significant moderating effect. Individuals in lower income brackets are 50.9% less likely to achieve abstinence (odds ratio: 0.491, 95% CI: 0.274–0.861), indicating that affordability and accessibility of resources could moderate cessation success. **Age (age_ps)** is another important moderator, with older individuals showing higher odds of abstinence (odds ratio: 1.034, 95% CI: 1.013–1.056, p-value:0.00111). Age may moderate the effectiveness of interventions, as younger individuals might require different or more intensive strategies compared to older adults, who may be more motivated by health concerns or long-term smoking behavior patterns.

In summary, variables such as NMR, readiness to quit, race/ethnicity, menthol use, cigarettes per day, income level, and age are critical moderators that influence the effectiveness of treatments and the likelihood of abstinence. Understanding and addressing these moderators can guide tailored, individualized interventions, ultimately improving cessation outcomes for diverse populations.

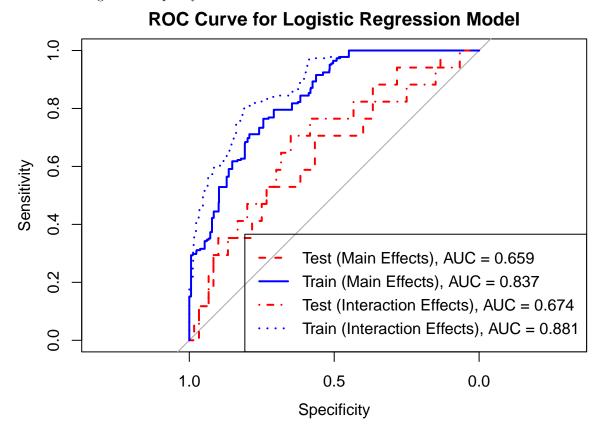
#Logistic Interaction Results Positive predictors include **age** (OR: 1.03), **Non-Hispanic White** (NHW) race (OR: 5.82), and **menthol use** (OR: 2.17), all significantly increasing the odds of abstinence. In contrast, negative predictors such as **cigarettes per day** (OR: 0.92), **low income levels** (e.g., inc2: OR: 0.49), and **current major depression** (OR: 0.66) significantly reduce the odds. Notably, **readiness to quit** is a critical factor, where lower readiness levels (readiness9: OR: 0.04) drastically decrease abstinence likelihood.

10.2838379	3.245743547 10.2838379	5.91997 0.00000 5.68172908	0.00000	5.91997	0.29346	1.73726	Var1
0.8620887	0.364560624	0.56281421	0.00874	-2.62222 0.00874	0.21921	-0.57481	sex_ps2
0.8781230	0.001021493	0.03779048	0.04649	-1.99094	1.64530	-3.27570	readiness9
3.5653320	1.334872735	2.16913248	3.09447 0.00197	3.09447	0.25023	0.77433	Only.Menthol1
5.0457181	1.186540044	2.45317212	2.44034 0.01467	2.44034	0.36773	0.89738	NMR
14.5965742	2.496757092	5.82000635	0.00008	3.93340	0.44778	1.76130	NHW1
0.8600788	0.273563876	0.49019013	0.01446	-2.44572 0.01446	0.29151	-0.71296	inc2
0.9587546	0.884188515	0.92141492	0.00007	-3.96780 0.00007	0.02063	-0.08184	cpd_ps
0.5365057	0.097605331	0.23679232	0.00084	-3.33966	0.43135	-1.44057	BA1
1.0557966	1.013784799	1.03429919	0.00111	3.26154 0.00111	0.01034	0.03372	age_ps
Upper Conf.	Estimate Std. Error z value Pvalue Odds Ratios Lower Conf. Upper Conf.	Odds Ratios	Pvalue	z value	Std. Error	Estimate	Variable

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Var1	readiness9	Only.Menthol1	NHW1	mde_curr1	inc4	inc2	crv_total_pq1	cpd_ps	BA1	age_ps	Variable
2.23885	-3.51694	0.85021	1.75800	-0.73720	-0.97457	-1.03869	-0.07802	-0.11507	-1.39716	0.05721	Estimate
0.26203	1.70093	0.33973	0.65575	0.29216	0.42630	0.31014	0.03590	0.05048	0.42812	0.02578	Std. Error
8.54442	-2.06766	2.50260	2.68089	-2.52326	-2.28611	-3.34916	-2.17343	-2.27949	-3.26346	2.21956	z value
0.00000	0.03867	0.01233	0.00734	0.01163	0.02225	0.00081	0.02975	0.02264	0.00110	0.02645	Pvalue
5.68172908	0.03779048	2.16913248	5.82000635	0.65973224	0.52150065	0.49019013	0.99741471	0.92141492	0.23679232	1.03429919	Odds Ratios
5.7062888765	0.0007221262	1.2069551958	1.6796287603	0.2678539287	0.1600182669	0.1900225325	0.8613717262	0.8069043096	0.1048287398	1.0073187162	Lower Conf.
15.9763840	0.7141533	4.5882301	22.6375553	0.8436322	0.8547352	0.6429069	0.9918186	0.9839622	0.5645902	1.1146117	Upper Conf.

Area Under Curve

ROC Curve for Logistic Regression Model plot compares the predictive performance of logistic regression models with main effects and interaction effects on both training and test datasets. The interaction effects model demonstrates slightly better performance than the main effects model, with higher AUC values for both training (0.881 vs. 0.837) and test datasets (0.674 vs. 0.659). However, the gap between training and test AUC values for both models highlights a decline in predictive accuracy when applied to unseen data, indicating potential overfitting, particularly for the interaction effects model. The training ROC curves for both models (solid blue for main effects and dotted blue for interaction effects) fit the data well, but the sharper drop-off in performance on the test curves (red dashed and red dot-dash) suggests that these models generalize less effectively. This disparity reinforces the need to balance model complexity, as adding interaction terms may capture relationships in the training data at the expense of broader applicability. While the interaction effects model slightly improves predictions, the main effects model may offer comparable performance with greater simplicity.



Lasso Main Effects Model

Interpretation of the Lasso Model

The Lasso regression model identified significant predictor variables influencing abstinence status with both main effects and odds ratios that provide meaningful insights into the relationships. Variables such as **Nicotine Metabolite Ratio (NMR)** (OR = 1.09), which reflects an individual's ability to metabolize nicotine, were associated with higher odds of abstinence, suggesting that individuals with faster nicotine metabolism might benefit more from pharmacological treatments. Similarly, **menthol smoking status** (**Only.Menthol1**) was associated with increased odds of abstinence (OR = 1.06), possibly due to behavioral or physiological characteristics specific to menthol smokers that make them more responsive to certain interventions. Sociodemographic factors, including **income levels** (e.g., inc2: OR = 0.91, inc5: OR = 0.91, inc5: OR = 0.91

1.00), had varied effects, indicating that financial stability and access to resources are critical moderators of treatment success. Moreover, race/ethnicity (e.g., NHW1: OR = 1.20, Hisp1: OR = 1.03), reflecting the role of cultural, socioeconomic, and systemic disparities in shaping cessation outcomes.

Behavioral and psychological variables further underscore the complexity of smoking cessation interventions. Readiness to quit emerged as a significant predictor, with lower readiness levels (e.g., readiness4: OR = 0.74, readiness9: OR = 0.82) associated with reduced odds of abstinence, highlighting the need for motivational enhancement strategies for individuals in these stages. Variables such as current depressive episodes (mde_curr1: OR = 0.95) and use of antidepressant medication (antidepmed1: OR = 1.03) further emphasized the interaction of mental health with smoking cessation outcomes. Lastly, education levels (e.g., edu4: OR = 0.48) and cigarette consumption (cpd_ps: OR = 0.99) were inversely related to abstinence, suggesting that tailored interventions targeting heavy smokers and those with limited educational opportunities could be essential for improving cessation rates. These findings collectively underscore the need for individualized approaches that integrate sociodemographic, behavioral, and mental health factors for effective smoking cessation interventions.

Variable	Coefficient	Odds_Ratio
Var1	0.1963241115	1.2169213
BA1	-0.0617443960	0.9401232
age_ps	0.0030070519	1.0030116
sex_ps2	-0.0437059135	0.9572354
NHW1	0.1795789498	1.1967134
Black1	0.0370573431	1.0377525
Hisp1	0.0253552300	1.0256794
inc2	-0.0952689647	0.9091284
inc3	-0.0492222622	0.9519695
inc4	-0.0834304770	0.9199550
edu2	-0.6699831563	0.5117172
edu3	-0.7116073213	0.4908546
edu4	-0.7250695338	0.4842909
edu5	-0.6737517135	0.5097924
ftcd_score	-0.0243890796	0.9759059
ftcd.5.mins1	0.0365625459	1.0372392
bdi_score_w00	0.0009785729	1.0009791
cpd_ps	-0.0043346447	0.9956747
crv_total_pq1	-0.0005169362	0.9994832
hedonsum_n_pq1	-0.0003202853	0.9996798
hedonsum_y_pq1	0.0006423462	1.0006426
shaps_score_pq1	-0.0035341547	0.9964721
otherdiag1	-0.0418391279	0.9590240
antidepmed1	0.0282303314	1.0286326
mde_curr1	-0.0526112558	0.9487488
NMR	0.0938947450	1.0984441
Only.Menthol1	0.0617780267	1.0637262
readiness4	-0.3005134288	0.7404380
readiness5	0.0129826545	1.0130673
readiness6	-0.1041613249	0.9010799
readiness7	0.0369034199	1.0375928
readiness8	-0.1276852819	0.8801303
readiness9	-0.1932869156	0.8242455
readiness10	-0.1384063057	0.8707448
treatment_groupsST_VA	0.0338250561	1.0344036

Interaction Lasso Model

The Lasso regression analysis identified several potential moderators of abstinence, reflecting diverse demographic, behavioral, and clinical factors that influence cessation outcomes. Notably, interaction terms such as BA1:inc2 (OR = 1.14) and antidepmed1:treatment_groupsBA_VA (OR = 1.14) suggest that socioeconomic status and antidepressant use may significantly interact with behavioral activation and treatment assignment to impact abstinence rates. Behavioral readiness, measured through variables like readiness5 interacting with depression status (mde_curr1:readiness5, OR = 1.13) and treatment group (readiness5:treatment_groupsBA_VA, OR = 1.13), emerged as critical moderators, highlighting the importance of psychological preparedness in determining the effectiveness of both pharmacological and behavioral interventions. Additionally, demographic factors such as race/ethnicity (e.g., NHW1:edu4, OR = 1.13) and menthol smoking status (e.g., NHW1:Only.Menthol1, OR = 1.12) appear to play a role

Table is in Supplementary Materials

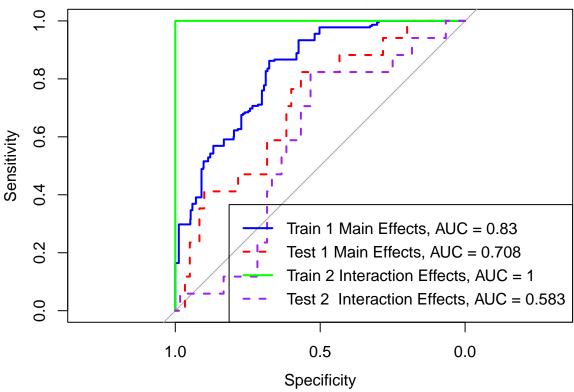
AUC CURVE for Lasso Models

The ROC curves provide a comparative evaluation of the Lasso regression model's predictive performance across different datasets and interaction effects. The Train 1 Main Effects curve (blue) shows strong predictive performance, with an AUC of 0.83, indicating a well-calibrated model for the training set. However, the corresponding Test 1 Main Effects curve (red, AUC = 0.708) demonstrates some degree of performance drop-off, suggesting potential overfitting to the training data or challenges in generalizing to the test set.

For the interaction effects, the Train 2 Interaction Effects curve (green, AUC=1) indicates a perfect separation of classes in the training set, likely reflecting a high degree of model complexity or overfitting to the specific interaction terms. Conversely, the Test 2 Interaction Effects curve (purple, AUC=0.583) shows diminished performance on the test set, suggesting that the interaction terms might not generalize well and could be overparameterized or poorly estimated.

Overall, while the main effects model demonstrates reasonable generalizability (train-test AUC difference of ~ 0.12), the interaction effects model likely introduces overfitting, as evidenced by the stark disparity in training and test performance.





Comparative Analysis

In comparing logistic regression models to Lasso (Least Absolute Shrinkage and Selection Operator) models, we find distinct advantages in each approach regarding predictor selection and model performance. Logistic regression models, especially those with main and interaction effects, provide insights into significant predictors with interpretable coefficients, making it easier to understand the direct impact of variables on smoking cessation. However, logistic models can be sensitive to multicollinearity and may include non-contributing predictors.

Lasso models, on the other hand, are effective at handling multicollinearity and automatically selecting the most relevant predictors by applying a penalty to reduce less important coefficients to zero. This feature makes Lasso ideal for variable selection, often resulting in a more parsimonious model focused on predictors with the strongest associations to the outcome. If the Lasso model excludes non-contributing or weak predictors that logistic regression retained, this indicates Lasso's utility in identifying the most critical predictors for smoking cessation.

Limitations

The study was conducted in a research clinic at Northwestern University (Chicago, Illinois) and University of Pennsylvania (Philadelphia, Pennsylvania). While the study mentions that the overal therapist competence was rated very good, but it may raise potential concerns because of the therapist level of education. The students from University of Pennsylvania has their Bachelor's degree while Northwestern University students has their Master's. This a potential limitation because the quality of education, knowledge, and expertise may be compromise which will influence results.

In logistic regression, models are sensitive to multicollinearity, which occurs when predictor variables are highly correlated. Introducing interaction terms to capture the combined effects of risk factors can amplify this issue, as seen in some of our results. The appearance of high multicollinearity in certain tables may indicate

overfitting, where the model captures noise instead of meaningful patterns. Overfitting not only complicates interpretation but also undermines the model's generalizability to new data. Addressing multicollinearity and considering techniques like regularization may help to mitigate these risks and improve the model's reliability.

For small sample sizes, logistic regression may outperform lasso because lasso can be prone to overfitting with limited data. Lasso's feature selection might end up removing too many predictors, reducing the model's ability to generalize well. In the case here, we have 300 participants in this dataset which is a indication of a small sample which causes the logistic to outperform lasso. logistic regression uses all available information, which can be an advantage when data is scarce. Lastly, predictors in logistic are highly correlated and need to be considered together which can impact the multicollinearity.

Logistic regression are sensitive to multicollimearity and most of the interact terms are highly correlated. This complicates things and causes overfitting. Lasso regressions uses a penalty term which implements more constraints. Because of it's constraints, we can observe the non-zero β coefficients to and identify predictor variables for model selection.

One of the key limitations observed with the Lasso regression model is its susceptibility to **data leakage** and **overfitting**, particularly when the model complexity increases or interaction terms are introduced. Data leakage occurs when information from the test set or future data inadvertently influences the training process, leading to overly optimistic performance metrics during model development. This leakage can bias the estimated coefficients and inflate the apparent predictive accuracy of the model, as seen in the perfect separation (AUC = 1) for the **Train 2 Interaction Effects** curve. While this might indicate a highly predictive model in training, the corresponding test set performance (AUC = 0.583) reveals substantial degradation, underscoring the lack of generalizability and the potential for spurious relationships in the data.

Additionally, overfitting emerges as a prominent limitation of Lasso when the model captures noise or overly specific patterns in the training data. This is particularly evident in the stark discrepancy between the training and test set AUC values for the interaction effects model, suggesting that the additional complexity introduced by interaction terms does not translate to better real-world performance. Overfitting not only undermines the robustness of the model but can also bias the coefficient estimates, leading to misinterpretation of predictor importance and compromised inference. These issues emphasize the importance of rigorous validation procedures, careful feature selection, and mechanisms to mitigate data leakage, such as proper train-test splits, cross-validation, and ensuring that imputation or scaling processes are confined strictly to the training data. Without addressing these limitations, the reliability of Lasso model estimates can be significantly compromised.

Conclusion

In conclusion, the logistic performed better according to the area under the curve models due to it's target estimates of AUC and not alot of data leakage in our models. In the lasso models, the AUC are more moderate compare. When predictors are highly correlated, Lasso may arbitrarily select one variable from a correlated set and set others to zero, potentially missing relevant information and leading to suboptimal performance. In the case here, t. Lasso remove those correlated variable and keep the one's that are more important as a nonzero. Logistic regression keeps all correlated variables, which can sometimes capture the overall signal better when correlations are essential to the model's interpretation. Factors like NMR, readiness to quit, race/ethnicity, menthol use, cigarettes per day, income level, and age are critical moderators that influence the effectiveness of treatments and the likelihood of abstinence.

References

Hitsman B, Papandonatos GD, Gollan JK, Huffman MD, Niaura R, Mohr DC, Veluz-Wilkins AK, Lubitz SF, Hole A, Leone FT, Khan SS, Fox EN, Bauer AM, Wileyto EP, Bastian J, Schnoll RA. Efficacy and safety of combination behavioral activation for smoking cessation and varenicline for treating tobacco dependence among individuals with current or past major depressive disorder: A 2×2 factorial, randomized, placebocontrolled trial. Addiction. 2023 Sep;118(9):1710-1725. doi: 10.1111/add.16209. Epub 2023 May 3. Erratum in: Addiction. 2024 Sep;119(9):1669. doi: 10.1111/add.16609. PMID: 37069490.

Supplementary Materials

	-4.144018e-02	inc3	0.9594067
	4.065996e-02	shaps_score_pq1:readiness7	1.0414979
	-4.019463e-02	Var1:Only.Menthol1	0.9606025
	-4.011894e-02 3.997340e-02	otherdiag1	0.9606752
	-3.958669e-02	Black1:readiness7 readiness9	1.0407831 0.9611866
	3.946074e-02	Black1:treatment_groupsST_Placebo	1.0402497
103	-3.927609e-02	BA1:readiness4	0.9614852
337	3.870995e-02	inc5:mde_curr1	1.0394689
	-3.864365e-02	inc3:otherdiag1	0.9620935
	-3.841813e-02	Var1:inc2	0.9623105
	-3.821582e-02	inc4	0.9625052
	-3.710541e-02 3.703220e-02	shaps_score_pq1:treatment_groupsBA_VA NHW1:readiness4	0.9635746 1.0377264
	-3.672510e-02	BA1:sex_ps2	0.9639411
	-3.561019e-02	inc2	0.9650164
52	3.537222e-02	Var1:edu4	1.0360053
423	-3.529737e-02	edu3:antidepmed1	0.9653183
	3.501472e-02	inc5:readiness6	1.0356350
	3.500110e-02	ftcd.5.mins1	1.0356208
	3.478548e-02	BA1:Black1	1.0353976
	-3.469420e-02 3.451364e-02	Var1:NHW1 ftcd.5.mins1:readiness7	0.9659007 1.0351162
	-3.433152e-02	Var1:inc3	0.9662511
	-3.236629e-02	inc4:ftcd.5.mins1	0.9681519
50	-3.225057e-02	Var1:edu2	0.9682639
87	-3.217310e-02	BA1:edu3	0.9683389
	3.119173e-02	edu4:ftcd.5.mins1	1.0316833
	3.117328e-02	otherdiag1:antidepmed1	1.0316643
	3.073254e-02	edu3:ftcd.5.mins1	1.0312097
	-3.068088e-02 -3.046779e-02	ftcd_score:treatment_groupsBA_VA	0.9697850
	-3.046779e-02	shaps_score_pq1:treatment_groupsST_VA inc2:Only.Menthol1	0.9699917
	-2.992877e-02	Var1:sex_ps2	0.9705147
148	2.945693e-02	sex_ps2:NHW1	1.0298951
31	-2.898138e-02	readiness5	0.9714346
346	2.890208e-02	inc2:readiness4	1.0293238
	2.804910e-02	sex_ps2:Only.Menthol1	1.0284462
	2.799559e-02	Hisp1:Only.Menthol1	1.0283912
	-2.791671e-02 2.761532e-02	BA1:edu4 ftcd_score:Only.Menthol1	0.9724694 1.0280002
	-2.681021e-02	BA1:Only.Menthol1	0.9735460
	-2.673049e-02	sex_ps2	0.9736236
	-2.667583e-02	NHW1:antidepmed1	0.9736768
105	2.666636e-02	BA1:readiness6	1.0270251
	2.592155e-02	edu2:treatment_groupsBA_VA	1.0262604
	-2.572611e-02	edu5:otherdiag1	0.9746020
	2.516614e-02	sex_ps2:antidepmed1	1.0254855
	-2.484870e-02 2.475563e-02	inc5 BA1:treatment_groupsBA_VA	0.9754575 1.0250646
	2.475563e-02 2.434814e-02	Var1:treatment_groupsST_VA	1.0250646
	-2.424942e-02	edu3:readiness4	0.9760422
	2.379892e-02	Var1:ftcd.5.mins1	1.0240844
415	2.358531e-02	edu3:shaps_score_pq1	1.0238656
	2.337514e-02	shaps_score_pq1:antidepmed1	1.0236505
	2.297496e-02	edu2:shaps_score_pq1	1.0232409
	-2.296784e-02	NHW1:inc4	0.9772939
	2.285670e-02 -2.254351e-02	otherdiag1:readiness8	1.0231199 0.9777087
	-2.254351e-02 -2.250250e-02	inc5:treatment_groupsBA_VA Var1:shaps_score_pq1	0.9777087
	2.183303e-02	readiness6	1.0220731
81	2.181754e-02	BA1:Hisp1	1.0220573
	-2.174718e-02	Var1:readiness9	0.9784876
	2.168834e-02	BA1:shaps_score_pq1	1.0219252
	-2.159195e-02	Only.Menthol1:treatment_groupsBA_VA	0.9786395
	-2.109819e-02 -2.067182e-02	inc3:cpd_ps inc3:shaps_score_pq1	0.9791228
	2.059626e-02	antidepmed1	1.0208098
	1.971221e-02	ftcd_score:NMR	1.0208098
	1.883712e-02	inc4:shaps_score_pq1	1.0190157
611	-1.860867e-02	shaps_score_pq1:otherdiag1	0.9815634
	1.825807e-02	Hisp1:readiness5	1.0184258
	-1.817693e-02	edu5:shaps_score_pq1	0.9819873
	-1.803245e-02	ftcd_score:antidepmed1	0.9821292
	1.787130e-02 1.628342e-02	ftcd.5.mins1:crv_total_pq1 Var1:readiness7	1.0180319
	-1.613096e-02	ftcd_score:ftcd.5.mins1	0.9839984
	1.581552e-02	inc4:bdi_score_w00	1.0159413
	1.565681e-02	edu2:cpd_ps	1.0157800
192	-1.552678e-02	NHW1:ftcd_score	0.9845931
	1.549789e-02	inc5:cpd_ps	1.0156186
	1.515760e-02	inc5:crv_total_pq1	1.0152731
	-1.513291e-02	inc4:crv_total_pq1	0.9849810
	-1.482428e-02 1.449902e-02	edu4:treatment_groupsBA_VA edu3:mde_curr1	0.9852851 1.0146046
721	02026-02	23	1.01-100-10

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Code Appendix

```
knitr::opts_chunk$set(warning = FALSE,
                      message = FALSE,
                      echo = FALSE,
                      fig.align = "center")
library(readr)
library(tidyverse)
library(dplyr)
library(ggplot2)
library(MASS)
library(tidyr)
library(kableExtra)
library(knitr)
library(GGally)
library(naniar)
library(visdat)
library(gtsummary)
library(gt)
library(mice)
library(corrplot)
library(reshape2)
library(ggwordcloud)
library(magick)
library(glmnet)
library(caret)
library(car)
library(broom)
library(gridExtra)
library(pROC)
library(broom)
library(cowplot)
# Path to your image
fig_path2 <- "/Users/diahminhawkins/Documents/GitHub/Project2/SmokePicture.png"
# Load the image using magick
img2<- image_read(fig_path2)</pre>
# Convert image to raster for use in ggplot
img_raster2<- as.raster(img2)</pre>
# Example data
words <- c("Smoking Cessation", "Depression", "MDD", "Readiness", "FTCD",</pre>
           "Menthol", "Antidepressant", "Gender", "Carbon Monoxide", "BDI",
           "Duration", "Waking up Smoking", "Psychiatric Diagnosis", "Black", "Hispanic", "Non-white His
         "Anhedonia", "Complimentary Reinforcers", "Substitute Reinforcers",
         "Cigarette Reward", "Varenicline", "Behavioral Activations", "Pharmacotherapy", "Psychotherapy"
frequencies <- c(1, 18, 1, 16, 14, 55, 5, 1, 4, 42, 3, 14, 14, 18, 16, 4,7,9,10,22, 55, 36, 40,55)
```

Table 1: Smoking Cessation Data Description

Variables	Type	Description
id	Numeric	Participants id number
abst	Categorical	Smoking Abstinence
Var	Categorical	Varenicline (Pharma- cotherapy)
BA	Categorical	Behavioral Activation (Pyschother- apy)
age_ps	Numeric	Age at phone interview
sex_ps	Categorical	Sex at interview
NHW	Categorical	Non- Hispanic White Indicator
Black	Categorical	Black Indicator
Hisp	Categorical	Hispanic Indicator
inc	Categorical	Income Levels (Low to High)
edu	Categorical	Education Levels (Low to High.
ftcd_score	Numeric	FTCD score at Baseline
ftcd.5.mins	Categorical	Smoking within 5 minutes of waking up
bdi_score_w00	Numeric	BDI score at baseline
cpd_ps	Numeric	Cigarettes per day at baseline phone interview
crv_total_pq1	Numeric	Cigarette reward value at baseline
hedonsum_n_pq1	Numeric	Pleasurable events scale at baseline- substitute reinforcers
hedonsum_y_pq1	Numeric 25	Pleasureable events scale at baseline- complemen-

tary

```
new_frame <- data.frame(words, frequencies)</pre>
# Generate the word cloud on top of the image background
ggplot(new frame, aes(label = words, size = frequencies)) +
  # Add the image background
  annotation_raster(img_raster2, xmin = -Inf, xmax = Inf, ymin = -Inf, ymax = Inf) +
  # Generate the word cloud
  geom_text_wordcloud(aes(color = frequencies)) +
  scale_size_area(max_size = 10) +
  # Customize the colors of the words
  scale_color_gradient(low = "white", high = "black") +
  # Remove axis titles and labels since we want the word cloud only
  theme_void()
#Load the data in
project2<- read_csv("project2.csv")</pre>
#Check for missing data
#project2%>% vis_dat()
#vis_miss(project2)
#project2%>% glimpse()
#Get all the missing data from each column
Missing_Data<- sapply(project2, function(x) sum(is.na(x)))</pre>
# Convert to dataframe
Missing_Data_df <- data.frame(ColumnName = names(Missing_Data), `Missing Data` = Missing_Data)
# Set names for the dataframe columns if necessary
names(Missing_Data_df) <- c("Variables", "Missing Data")</pre>
# Calculate the total number of rows in the dataset
total_rows <- nrow(project2)</pre>
#Create Missing Data Summary
missing_data_summary <-Missing_Data_df %>%
  filter(Variables %in% c('ftcd_score', 'inc', 'crv_total_pq1', 'shaps_score_pq1',
                          'NMR', 'Only.Menthol', 'readiness')) %>%
    mutate(Percent_Missing = (`Missing Data` / total_rows) * 100) %>%
  dplyr::select(Variables, `Missing Data`, Percent_Missing)%>%
  mutate(Variables = case_when(
   Variables == "ftcd_score" ~ "FTCD Score at Baseline",
     Variables == "inc" ~ "Income",
   Variables == "crv_total_pq1" ~ "Cigarette Reward Value at Baseline",
   Variables == "shaps_score_pq1" ~ "Anhedonia",
   Variables == "NMR" ~ "Nicotine Metabolism Ratio",
   Variables == "Only.Menthol" ~ "Exclusive Mentholated Cigarette User",
   Variables == "readiness" ~ "Baseline Readiness to Quit Smoking"))
```

```
# Obtain the total missing data and the percentage or missing data
total_missing <- sum(missing_data_summary$`Missing Data`)</pre>
percent missing total <- (total missing / total rows) * 100
#Create row to combine with the summart table
total row <- data.frame(</pre>
   Variables = "Total",
   `Missing Data` = total_missing,
 Percent_Missing =percent_missing_total
#Both data frames have identical column names
names(total_row) <- names(missing_data_summary)</pre>
# Bind the summary table and the total row
missing_data_summary <- rbind(missing_data_summary, total_row)</pre>
# Convert to a gtsummary table
missing_data_summary %>%
    gt() %>%
    tab_header(
        title = "Missing Data Summary for Smoking Sessation"
    ) %>%
    cols label(
        Variables = "Variables",
        `Missing Data` = "Missing Values",
        Percent_Missing = "Percentage Missing (%)"
    ) %>%
    fmt_number(
        columns = vars(Percent_Missing),
        decimals = 2  # Format percentage to two decimal places
    )
#Create variable table dataframe with description of the Marathon Dat
Variables_description<- data_frame(</pre>
    Variables= c("id", "abst", "Var", "BA", "age_ps",
                                "sex_ps", "NHW", "Black",
                                "Hisp", "inc", "edu",
                                "ftcd_score", "ftcd.5.mins", "bdi_score_w00", "cpd_ps",
                                "crv_total_pq1", "hedonsum_n_pq1", "hedonsum_y_pq1", "shaps_score_pq1", "otherdiag",
                                "antidepmed", "mde_curr", "NMR", "Only.Menthol", "readiness"),
    Type= c("Numeric", "Categorical", "Categorical", "Categorical", "Numeric",
                     "Categorical", "Categorical", "Categorical", "Categorical",
                     "Categorical", "Numeric", "Categorical", "Numeric", "Nu
                     "Categorical", "Categorical", "Numeric", "Categorical", "Numeric"),
    Description = c("Participants id number",
                                    "Smoking Abstinence",
                                    "Varenicline (Pharmacotherapy)",
                                    "Behavioral Activation (Pyschotherapy)",
```

```
"Age at phone interview",
                 "Sex at interview",
                 "Non-Hispanic White Indicator",
                 "Black Indicator ",
                 "Hispanic Indicator",
                 "Income Levels (Low to High)",
                 "Education Levels (Low to High.",
                 "FTCD score at Baseline",
                 "Smoking within 5 minutes of waking up ",
                 "BDI score at baseline",
                 "Cigarettes per day at baseline phone interview",
                 "Cigarette reward value at baseline",
                 "Pleasurable events scale at baseline- substitute reinforcers",
                 "Pleasureable events scale at baseline- complementary reinforcers",
                 "Anhedonia",
                 "Other lifetime DSM-5 diagnosis",
                 "Taking antidepressant medication at baseline",
                 "Current vs. Past MDD",
                 "Nicotine Metabolism Cigarette User",
                 "Exclsuive Mentholated Cigarette User",
                 "Baseline readiness to quit smoking"
)
# Create the table with kable and customize with kableExtra
table_summary<- kable(Variables_description, "latex", booktabs = TRUE, caption = "Smoking Cessation Dat
  kable_styling(latex_options = c("striped", "scale_down")) %>%
  column_spec(1, width = "3cm") %>%
  column_spec(2, width = "2cm") %>%
  column_spec(3, width = "2cm") %>%
  column_spec(4, width = "8cm")
# Load the PNG file
table_image <- image_read("adjustedtable2.png")</pre>
# Display the image in RStudio's Viewer or an external window
table_image
# define treatment categories
project2_treatments <- project2 %>%
  mutate(
   treatment_groups = case_when(
      Var == 1 & BA == 1 ~ "BASC + Varenicline",
```

```
Var == 0 & BA == 1 ~ "BASC + Placebo",
      Var == 1 & BA == 0 ~ "ST + Varenicline",
      Var == 0 & BA == 0 ~ "ST + Placebo"
   )
 )
# Combine education levels
project2_treatments <- project2_treatments %>%
  mutate(edu = as.character(edu))%>%
 mutate(edu = case_when(
   edu %in% c( "2", "3") ~ "1",
   TRUE ~ edu # Keep other values as they are
 ))
# recode income, education, and sex levels
project2_treatments <- project2_treatments %>%
  mutate(
   inc= case_when(
     inc == 1 ~ "Less than $20,000",
      inc == 2 \sim "$20,000-35,000",
     inc == 3 \sim "$35,001-50,000",
     inc == 4 \sim "$50,001-75,000",
     inc == 5 \sim "More than $75,000",
     TRUE ~ "Unknown"
   ),
   edu = case_when(
      edu == 1 ~ "Some High School or Less",
      edu == 4 ~ "Some college/technical school",
      edu == 5 ~ "College graduate",
     TRUE ~ "Unknown"
   ),
   sex_ps = case_when(
      sex_ps == 1 ~ "Male",
      sex_ps == 2 ~ "Female",
     TRUE ~ "Unknown")
 )
#Define Treatment Groups
project2_table <- project2 %>%
 mutate(treatment_groups = case_when(
   Var == 1 & BA == 1 ~ "BA_VA",
   Var == 0 & BA == 0 ~ "ST_Placebo",
   Var == 0 & BA == 1 ~ "BA_Placebo",
   Var == 1 & BA == 0 ~ "ST_VA"
  ))
```

```
#Change variables into factor and continous variables
factor_vars <- c("abst","Var","BA","sex_ps", "NHW",</pre>
                 "Black", "Hisp", "inc", "edu", "readiness",
                 "ftcd.5.mins", "otherdiag", "antidepmed", "mde curr",
                 "Only.Menthol", "treatment_groups")
#Mutate variables as factors
project2 table<- project2 table%>%
  mutate(across(all_of(factor_vars), as.factor))
#Mutate variables as factors
project2_treatments<- project2_treatments%>%
  mutate(across(all_of(factor_vars), as.factor))
# Create a stacked bar plot
income_plot<-ggplot(project2_treatments, aes(x = abst, fill = inc)) +</pre>
  geom_bar(position = "fill") + # Use position = "fill" for proportions
 labs(
   x =  "Abstinence",
   y = "Proportions",
   fill = "Income Levels"
  scale_fill_brewer(palette = "Set4") + # Apply a Brewer palette
  theme minimal() +
 theme(
   plot.title = element_text(hjust = 0.5, size = 14),
   axis.text = element_text(size = 10),
   axis.title = element_text(size = 12),
   legend.position = "bottom"
  )
# Create a stacked bar plot
education_plot<-ggplot(project2_treatments, aes(x = abst, fill = edu)) +
  geom_bar(position = "fill") + # Use position = "fill" for proportions
  labs(
   x = "Abstinence",
   y = "Proportions",
   fill = "Education Levels"
  ) +
  scale_fill_brewer(palette = "Set4") + # Apply a Brewer palette
  theme minimal() +
  theme(
   plot.title = element_text(hjust = 0.5, size = 14),
   axis.text = element_text(size = 10),
   axis.title = element_text(size = 12),
   legend.position = "bottom"
```

```
# Combine plots with cowplot
demo_plot <- plot_grid(</pre>
  education_plot, income_plot,
  ncol = 2, # Two columns
 align = "hv", # Align both horizontally and vertically
  label_size = 14 # Increase label size
)
demo_plot
# Hedonsum Complementary Rewards
hedonsum_y_pq_plot <- ggplot(project2_table, aes(x = hedonsum_y_pq1, fill = abst)) +
  geom_density(alpha = 0.4) +
  facet_wrap(~treatment_groups, scales = "free") +
  theme_minimal() +
  labs(
   x = "Substitute Reinforcers",
   y = "Density"
  scale_fill_manual(values = c("0" = "pink", "1" = "blue"), name = "abst")
 # Nicotine Metabolism Ratio
nmr_plot <- ggplot(project2_table, aes(x = NMR, fill = abst)) +
  geom_density(alpha = 0.4) +
  facet_wrap(~treatment_groups, scales = "free") +
  theme_classic() +
  labs(
   x = "NMR",
   y = "Density"
  ) +
  scale_fill_manual(values = c("0" = "pink", "1" = "blue"), name = "abst")
# Hedonsum Substitute Reinforcers
hedonsum_N_plot<-ggplot(project2_table, aes(x = hedonsum_n_pq1 , fill = abst)) +
  geom density(alpha = 0.4) +
  facet_wrap(~treatment_groups, scales = "free")+
  theme_classic()+
  labs(
       x = "Hedonsum"
       y = "Density")+
  scale_fill_manual(values = c("0" = "pink", "1" = "blue"), name = "abst")
age_plot<-ggplot(project2_table, aes(x =age_ps , fill = abst)) +</pre>
  geom_density(alpha = 0.4) +
  facet_wrap(~treatment_groups, scales = "free")+
  theme_classic()+
  labs(
```

```
x = "Age",
       y = "Density")+
  scale fill manual(values = c("0" = "pink", "1" = "blue"), name = "abst")
anhedonia_plot <- ggplot(project2_table, aes(x = shaps_score_pq1, fill = abst)) +
  geom_density(alpha = 0.4) +
  facet_wrap(~treatment_groups, scales = "free") +
 theme_classic() +
 labs(
   title = "Baseline Characteristics of Abstinence Status with Continuous Variables",
   x = "Anhedonia",
   y = "Density"
  ) +
  scale_fill_manual(values = c("1" = "pink", "0" = "blue"), name = "abst")
anhedonia plot
grid.arrange(
 hedonsum_y_pq_plot, nmr_plot, hedonsum_N_plot, age_plot,
 ncol = 2,
 nrow = 2,
 top= "Baseline Characteristics of Abstinence Status with Continous Variables"
# Create a stacked bar plot
NHW_plot<-ggplot(project2_table, aes(x = abst, fill = NHW)) +</pre>
  geom_bar(position = "fill") + # Use position = "fill" for proportions
  facet_wrap(~treatment_groups, scales = "free")+
 labs(
   x = "Abstinence",
   y = "Proportions",
   fill = "Non-Hispanic Whites Levels"
  ) +
  scale_fill_brewer(palette = "Set4") + # Apply a Brewer palette
  theme_minimal() +
  theme(
   axis.text = element_text(size = 10),
   axis.title = element_text(size = 12),
   legend.position = "bottom"
```

```
# Create a stacked bar plot
Hisp_plot \leftarrow ggplot(project2\_table, aes(x = abst, fill = Hisp)) +
  geom_bar(position = "fill") + # Use position = "fill" for proportions
  facet_wrap(~treatment_groups, scales = "free")+
 labs(title = "Baseline Characteristics of Abstinence Status in Racial Groups",
    x = "Abstinence",
   y = "Proportions",
   fill = "Hispanic Whites "
  ) +
  scale_fill_brewer(palette = "Set4") + # Apply a Brewer palette
  theme minimal() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 14),
    axis.text = element_text(size = 10),
   axis.title = element_text(size = 12),
    legend.position = "bottom"
  )
# Create a stacked bar plot
Black_plot \leftarrow ggplot(project2\_table, aes(x = abst, fill = Black)) +
  geom_bar(position = "fill") + # Use position = "fill" for proportions
 facet_wrap(~treatment_groups, scales = "free")+
 labs(
   x = "Abstinence",
   y = "Proportions",
   fill = "Blacks"
  scale_fill_brewer(palette = "Set4") + # Apply a Brewer palette
  theme_minimal() +
  theme(
   plot.title = element_text(hjust = 0.5, size = 14),
    axis.text = element_text(size = 10),
   axis.title = element_text(size = 12),
   legend.position = "bottom"
  )
Hisp_plot
# Combine plots with cowplot
combined_plot <- plot_grid(</pre>
 Black_plot, NHW_plot,
 ncol = 2, # Two columns
 align = "hv", # Align both horizontally and vertically
  label_size = 14  # Increase label size
```

```
)
combined plot
# Find the variables in project2 that are not in factor_vars
continous_vars <- setdiff(names(project2), factor_vars)</pre>
project2 <- project2 %>%
  mutate(across(all_of(continous_vars), as.numeric))
# Select only numeric columns for the correlation plot
numeric_data <- project2 %>% select(all_of(continous_vars))%>%
dplyr::select(-c(id))
# Calculate the correlation matrix
cor_matrix <- cor(numeric_data, use = "complete.obs")</pre>
# Melt the correlation matrix for ggplot2
cor_data2 <- melt(cor_matrix)</pre>
#Cessation Smoking correlation plot
cessation_smoking_plot2<-ggplot(data = cor_data2, aes(x = Var1, y = Var2, fill = value)) +</pre>
  geom_tile(color = "white") +
  geom_text(aes(label = round(value, 2)), color = "black", size = 4) +
  scale_fill_gradient2(low = "hotpink", high = "royalblue", mid = "white",
                        midpoint = 0, limit = c(-1, 1), space = "Lab",
                        name = "Correlation") +
  labs(title = "Correlation of Smoking Cessation",
       x= "Variables",
       y= "Variables") +
  theme_minimal(base_family = "Times") +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1),
        legend.position = "bottom",
        plot.title = element_text(hjust = 0.5, size= 20))
cessation_smoking_plot2
set.seed(222)
#project2_table<- project2_table%>%
  #dplyr::select(-id,)
trainIndex <- createDataPartition(project2_table$abst, p = 0.7, list = FALSE)
  train_data <- project2_table[trainIndex, ]</pre>
  test_data <- project2_table[-trainIndex, ]</pre>
```

```
# Data Imputation for Logistic Modeling
imputed_data <- mice(train_data, m = 5, method = 'pmm', maxit = 10, seed = 222, print=FALSE)</pre>
stacked data primary <- complete(imputed data, action = "long", include = FALSE)
stacked_data_primary<-stacked_data_primary%>%
  dplyr::select(-.id, -.imp)
# Fit the logistic regression model with
main_effects <- glm(abst ~ ., family = binomial(link = "logit"), data = stacked_data_primary)</pre>
# Fit the logistic model with interaction terms on Training Data
  interaction_effects <- glm(abst ~ Var + BA + age_ps + sex_ps + NHW + Black + Hisp +</pre>
                              inc + edu + ftcd_score + ftcd.5.mins + bdi_score_w00 + cpd_ps +
                              crv_total_pq1 + hedonsum_n_pq1 + hedonsum_y_pq1 + shaps_score_pq1 +
                              otherdiag + antidepmed + mde_curr + NMR + Only.Menthol + readiness +
                              sex_ps * Black + sex_ps * NHW + Black * Only.Menthol+ Hisp *
                              Only.Menthol +NHW * edu + Black * edu+ ftcd_score*age_ps + ftcd_score *
                                BA*NMR,
                              family =binomial(link = "logit"), data=stacked_data_primary)
#Make table for Main Effects
data_frame2<- round(summary(main_effects)$coefficients,5)</pre>
# Make into dataframs
data_frame2<-as.data.frame(data_frame2)</pre>
# Convert row names to a column in the dataframe
data_frame2$Variable <- rownames(data_frame2)</pre>
# Rearrange the columns to make "Variable" the first column
data_frame2 <- data_frame2[, c("Variable", colnames(data_frame2)[-ncol(data_frame2)])]</pre>
# Compute odds ratios
odds_ratios <- exp(coef(main_effects, na.rm=TRUE))</pre>
# Make odd ratios into dataframe
yea<-as.data.frame(odds ratios)</pre>
# Create row names for odd ratios
yea$Variable<- rownames(yea)</pre>
# Rearrange the columns to make "Variable" the first column
yea <- yea[, c("Variable", colnames(yea)[-ncol(yea)])]</pre>
#Removes NAs in odd ratios
yea<- yea[!is.na(yea$odds_ratios), ]</pre>
# Compute confidence intervals for the coefficients
conf_intervals <- exp(confint(main_effects))</pre>
# Make confidence intervals into a dataframe
```

```
conf_intervals_<-as.data.frame(conf_intervals)</pre>
# A
conf_intervals_$Variable<- rownames(conf_intervals_)</pre>
# Rearrange the columns to make "Variable" the first column
 conf_intervals_<- conf_intervals_[, c("Variable", colnames(conf_intervals_)[-ncol(conf_intervals_)])]</pre>
 # Remove rows where treatment_groups are "ST_Placebo" or "ST_VA"
conf_intervals_ <- conf_intervals_[!(conf_intervals_$Variable %in% c("treatment_groupsST_Placebo", "t.
combined_df <- merge(merge(data_frame2, yea, by = "Variable"), conf_intervals_, by = "Variable")
combined_df<-combined_df%>%
  group_by(Variable)%>%
 filter(Pr(>|z|) < 0.05) \%>\%
 rename(`Lower Conf.` = `2.5 %`,
         `Upper Conf.`= `97.5 %`,
         `Pvalue`= `Pr(>|z|)`,
    `Odds Ratios` = `odds_ratios`)
combined_df<- combined_df[!(combined_df$Variable %in% c("id")), ]</pre>
# Format numerical columns for LaTeX (e.g., Odds Ratios, Confidence Intervals)
table2<-combined_df %>%
  kbl(caption = "Logistic Model:Significant Predictor Variables for Main Effects Data",
      booktabs = TRUE, escape = FALSE, align = "c") %>%
  kable_styling(full_width = FALSE, latex_options = c('hold_position'))
# Path to your image
fig_path4<- "~/Documents/GitHub/PDA Final Project Portfolio/table2.png"</pre>
# Load the image using magick
img4<- image_read(fig_path4)</pre>
rotated_image <- image_rotate(img4, 90)</pre>
rotated_image
#Make table for Main Effects
data_frame3<- round(summary(interaction_effects)$coefficients,5)</pre>
# Make into dataframs
```

```
data_frame3<-as.data.frame(data_frame3)</pre>
# Convert row names to a column in the dataframe
data_frame3$Variable <- rownames(data_frame3)</pre>
# Rearrange the columns to make "Variable" the first column
data_frame3<- data_frame3[, c("Variable", colnames(data_frame3)[-ncol(data_frame3)])]
# Compute odds ratios
odds_ratios2 <- exp(coef(interaction_effects, na.rm=TRUE))</pre>
# Make odd ratios into dataframe
yea1<-as.data.frame(odds_ratios2)</pre>
# Create row names for odd ratios
yea1$Variable<- rownames(yea1)</pre>
# Rearrange the columns to make "Variable" the first column
yea1 <- yea1[, c("Variable", colnames(yea1)[-ncol(yea1)])]</pre>
#Removes NAs in odd ratios
yea1<- yea1[!is.na(yea1$odds_ratios), ]</pre>
# Compute confidence intervals for the coefficients
conf_intervals2<- exp(confint(interaction_effects))</pre>
# Make confidence intervals into a dataframe
conf_intervals_2<-as.data.frame(conf_intervals2)</pre>
conf_intervals_2$Variable<- rownames(conf_intervals_2)</pre>
# Rearrange the columns to make "Variable" the first column
conf_intervals_2<- conf_intervals_2[, c("Variable", colnames(conf_intervals_2)[-ncol(conf_intervals_2)]
 # Remove rows where treatment_groups are "ST_Placebo" or "ST_VA"
 conf_intervals_2 <- conf_intervals_2[!(conf_intervals_2$Variable %in% c("NHW1:edu5", "Black1:edu2", "
combined_df2<- merge(merge(data_frame3, yea, by = "Variable"), conf_intervals_2, by = "Variable")
combined_df2 <- combined_df2 %>%
  group_by(Variable) %>%
 filter(`Pr(>|z|)` < 0.05) %>%
  rename(`Lower Conf.` = `2.5 %`,
         `Upper Conf.`= `97.5 %`,
         `Pvalue`= `Pr(>|z|)`,
          `Odds Ratios` = `odds_ratios` # Rename column for readability
  )
combined_df2<- combined_df2[!(combined_df2$Variable %in% c("id")), ]</pre>
```

```
table0<-combined_df2 %>%
  kbl(caption = "Logistic Model:Significant Predictor Variables for Training Data with Interaction Term
      booktabs = TRUE, escape = FALSE, align = "c") %>%
  kable_styling(full_width = FALSE, latex_options = c('hold_position'))
# Path to your image
fig_path3 <- "~/Documents/GitHub/PDA Final Project Portfolio/Table0.png"</pre>
# Load the image using magick
img3<- image_read(fig_path3)</pre>
rotated_image2 <- image_rotate(img3, 90)</pre>
rotated_image2
# Predict probabilities on test data
predicted_probs <- predict(main_effects, newdata = test_data, type = "response")</pre>
predict_probs_2<- predict(main_effects, newdata = stacked_data_primary, type = "response")</pre>
predicted_probs3 <- predict(interaction_effects, newdata = test_data, type = "response")</pre>
predict_probs_4<- predict(interaction_effects, newdata = stacked_data_primary, type = "response")</pre>
# Calculate ROC
roc_curve <- roc(test_data$abst, predicted_probs)</pre>
roc_curve2<- roc(stacked_data_primary$abst, predict_probs_2)</pre>
roc_curve3 <- roc(test_data$abst, predicted_probs3)</pre>
roc_curve4<- roc(stacked_data_primary$abst, predict_probs_4)</pre>
#Calculate AUC
auc_value <- auc(roc_curve)</pre>
auc_value2<-auc(roc_curve2)</pre>
auc_value3 <- auc(roc_curve3)</pre>
auc_value4<-auc(roc_curve4)</pre>
plot(roc_curve, col = "red", lty = 2, main = "ROC Curve for Logistic Regression Model", lwd = 2)
lines(roc_curve2, col = "blue", lty = 1, lwd = 2) # Main Effects Training
lines(roc_curve3, col = "red", lty = 4, lwd = 2) # Interaction Effects Test
lines(roc_curve4, col = "blue", lty = 3, lwd = 2) # Interaction Effects Training
# Add a legend
legend("bottomright",
       legend = c(
         paste("Test (Main Effects), AUC =", round(auc_value, 3)),
         paste("Train (Main Effects), AUC =", round(auc_value2, 3)),
         paste("Test (Interaction Effects), AUC =", round(auc_value3, 3)),
         paste("Train (Interaction Effects), AUC =", round(auc_value4, 3))
```

```
col = c("red", "blue", "red", "blue"),
       lty = c(2, 1, 4, 3),
       lwd = 2)
# Define the formula for Lasso
formula \leftarrow abst \sim . # This includes all variables in the dataset for prediction
# Set up parameters
set.seed(222)
stacked_data_primary<-stacked_data_primary%>%
  dplyr::select(-id)
test_data<-test_data%>%
   dplyr::select(-id)
stacked_data_primary <- stacked_data_primary[complete.cases(stacked_data_primary), ]</pre>
test_data <- test_data[complete.cases(test_data), ]</pre>
# Model matrix for training and test sets
 X_train <- model.matrix(formula, data = stacked_data_primary)[, -1] # Remove intercept column
 Y_train <- stacked_data_primary$abst</pre>
 X_test <- model.matrix(formula, data = test_data)[, -1] # Remove intercept column</pre>
  Y_test <- test_data$abst
  BA_position <- which(colnames(X_train) == "BA")
  penalty_factors <- rep(1, ncol(X_train))</pre>
 penalty_factors[BA_position] <- 0</pre>
 Y_train <- as.numeric(as.character(stacked_data_primary$abst))</pre>
 Y_test <- as.numeric(as.character(test_data$abst))</pre>
cv_lasso <- cv.glmnet(X_train, Y_train, alpha = 1, penalty.factor = penalty_factors, family= "binomial"</pre>
  # Use lambda.min for final model
best_lambda <- cv_lasso$lambda.min
lasso_model <- glmnet(X_train, Y_train, alpha = 1, penalty_factor = penalty_factors,lambda = best_lamb</pre>
  lasso_train_predictions <- predict(lasso_model, newx = X_train, s=best_lambda,type = "response")
  lasso_test_predictions <- predict(lasso_model, newx = X_test, s=best_lambda, type = "response")
  \# Calculate ROC and AUC for training and test data
  roc_train <- roc(Y_train, lasso_train_predictions)</pre>
  auc_train <- auc(roc_train)</pre>
 roc_test <- roc(Y_test,as.numeric(lasso_test_predictions))</pre>
```

```
auc_test <- auc(roc_test)</pre>
# Extract coefficients for the best lambda
lasso_coefficients <- coef(lasso_model, s = best_lambda)</pre>
# Convert to a readable data frame
lasso_coefficients_df <- as.data.frame(as.matrix(lasso_coefficients))</pre>
colnames(lasso_coefficients_df) <- "Coefficient"</pre>
lasso_coefficients_df$Variable <- rownames(lasso_coefficients_df)</pre>
rownames(lasso_coefficients_df) <- NULL</pre>
# Calculate Odds Ratios (OR)
lasso_coefficients_df$Odds_Ratio <- exp(lasso_coefficients_df$Coefficient)</pre>
# Reorder columns: Variable first, Coefficient second, then Odds_Ratio
lasso_coefficients_df <- lasso_coefficients_df[, c("Variable", "Coefficient", "Odds_Ratio")]</pre>
# Filter for nonzero coefficients
lasso coefficients df <- lasso coefficients df [lasso coefficients df $Coefficient != 0, ]
lasso_coefficients_df <- lasso_coefficients_df %>%
  filter(!(Variable %in% c("(Intercept)", "id")))
kable_lasso_table3<-lasso_coefficients_df %>%
  kbl(caption = "Lasso Model:Significant Predictor Variables for with Main Effects",
      booktabs = TRUE, escape = FALSE, align = "c") %>%
  kable_styling(full_width = FALSE, latex_options = c('hold_position'))
# Path to your image
fig_path_lasso <- "~/Documents/GitHub/PDA Final Project Portfolio/kable_lasso_table_3.png"
# Load the image using magick
img_lasso<- image_read(fig_path_lasso)</pre>
img_lasso
# Define the formula for Lasso
formula2 <- abst ~ .^2 # This includes all variables in the dataset for prediction
# Set up parameters
set.seed(222)
stacked_data_primary <- stacked_data_primary[complete.cases(stacked_data_primary), ]</pre>
```

```
test_data <- test_data[complete.cases(test_data), ]</pre>
# Model matrix for training and test sets
  X_train2 <- model.matrix(formula2, data = stacked_data_primary)[, -1] # Remove intercept column</pre>
  Y_train2 <- stacked_data_primary$abst</pre>
  X_test2 <- model.matrix(formula2, data = test_data)[, -1] # Remove intercept column
  Y_test2 <- test_data$abst
  BA_position2 <- which(colnames(X_train2) == "BA")
  penalty_factors2 <- rep(1, ncol(X_train2))</pre>
  penalty_factors2[BA_position2] <- 0</pre>
  Y_train2 <- as.numeric(as.character(stacked_data_primary$abst))</pre>
  Y_test2 <- as.numeric(as.character(test_data$abst))</pre>
cv_lasso2 <- cv.glmnet(X_train2, Y_train2, alpha = 1, penalty.factor = penalty_factors2, family= "binom")</pre>
  # Use lambda.min for final model
best_lambda2 <- cv_lasso2$lambda.min</pre>
 lasso_model2 <- glmnet(X_train2, Y_train2, alpha = 1, penalty.factor = penalty_factors2,lambda = best_</pre>
  lasso_train_predictions2 <- predict(lasso_model2, newx = X_train2, s=best_lambda2,type = "response")</pre>
  lasso_test_predictions2 <- predict(lasso_model2, newx = X_test2, s=best_lambda2, type = "response")</pre>
  # Calculate ROC and AUC for training and test data
  roc_train2 <- roc(Y_train2, lasso_train_predictions2)</pre>
  auc_train2 <- auc(roc_train2)</pre>
  roc_test2 <- roc(Y_test2,as.numeric(lasso_test_predictions2))</pre>
  auc_test2 <- auc(roc_test2)</pre>
#stacked_data_primary <- stacked_data_primary[complete.cases(stacked_data_primary), ]</pre>
#test_data <- test_data[complete.cases(test_data), ]</pre>
#length(test_data)
#dim(stacked_data_primary)
#head(stacked_data_primary)
#names(stacked_data_primary)
#stacked_data_primary<-stacked_data_primary_%>%
 # select(-id)
# Extract non-zero coefficients from the Lasso model
lasso_coefficients2 <- coef(lasso_model2, s = best_lambda2)</pre>
# Convert to a data frame
```

```
lasso_summary <- as.data.frame(as.matrix(lasso_coefficients2))</pre>
colnames(lasso_summary) <- "Coefficient"</pre>
lasso_summary$Variable <- rownames(lasso_summary)</pre>
rownames(lasso_summary) <- NULL</pre>
# Calculate odds ratios (OR)
lasso_summary$Odds_Ratio <- exp(lasso_summary$Coefficient)</pre>
# Filter for non-zero coefficients
lasso_summary_filtered <- lasso_summary[lasso_summary$Coefficient != 0 & lasso_summary$Variable != "(In
# Sort by the absolute value of the coefficient
lasso_summary_filtered <- lasso_summary_filtered[order(-abs(lasso_summary_filtered$Coefficient)), ]</pre>
# Create a summary statistics table with kable
kable_lasso_summary <- lasso_summary_filtered %>%
  kable(caption = "Summary Statistics: Lasso Model (Non-Zero Coefficients and Odds Ratios)",
        col.names = c("Variable", "Coefficient", "Odds Ratio")) %>%
  kable_styling(full_width = FALSE, font_size = 12)
# Calculate ROC and AUC for training and test data
roc_train <- roc(Y_train, lasso_train_predictions)</pre>
auc_train <- auc(roc_train)</pre>
roc_train2 <- roc(Y_train2, lasso_train_predictions2)</pre>
auc_train2 <- auc(roc_train2)</pre>
roc_test <- roc(Y_test, as.numeric(lasso_test_predictions))</pre>
auc_test <- auc(roc_test)</pre>
roc_test2 <- roc(Y_test2, as.numeric(lasso_test_predictions2))</pre>
auc_test2 <- auc(roc_test2)</pre>
# Plot ROC curve for the first training data
plot(roc_train, col = "blue", lty = 1, main = "ROC Curve for Lasso Regression Model", lwd = 2, xlim = c
# Add ROC curves for test data and second training/test sets
lines(roc_test, col = "red", lty = 2, lwd = 2)
lines(roc_train2, col = "green", lty = 1, lwd = 2)
lines(roc_test2, col = "purple", lty = 2, lwd = 2)
# Add a legend
legend(
 "bottomright",
```

```
legend = c(
   paste("Train 1 Main Effects, AUC =", round(auc_train, 3)),
   paste("Test 1 Main Effects, AUC =", round(auc_test, 3)),
   paste("Train 2 Interaction Effects, AUC =", round(auc_train2, 3)),
   paste("Test 2 Interaction Effects, AUC =", round(auc_test2, 3))
),
   col = c("blue", "red", "green", "purple"),
   lty = c(1, 2, 1, 2),
   lwd = 2
)

#kable_lasso_summary
# Path to your image

fig_path5 <- "-/Documents/GitHub/PDA Final Project Portfolio/table_lasso_interractions.png"
# Load the image using magick
img5 <- image_read(fig_path5)

img5
table_summary</pre>
```