P9185 Project 1: Protocol of a Phase II MATIK Trial

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Contents

I. Introduction

II. Methods

Notation:

$$k : \text{subject}, k = 1, ..., 180$$
$$j : \text{sequence}, j = 0, 1, 2$$
$$i : \text{period}, i = 1, 2, 3$$
$$h : \text{week}, h = 1, 2, 3, 4$$
$$\pi : \text{period effect}$$
$$\tau : \text{treatment effect}$$
$$\alpha : \text{grouped treatment effects}$$
$$\beta : \text{demographic effects}$$
$$\lambda : \text{sequence/carryover effect}$$
$$\gamma : \text{week effect}$$
$$b : \text{subject-specific intercepts}$$
$$\mu : \text{fixed-effect intercept}$$
$$\varepsilon : \text{residual error}$$

III. Results

3.1 Primary Objective 1

Proportion of Adverse Events per period
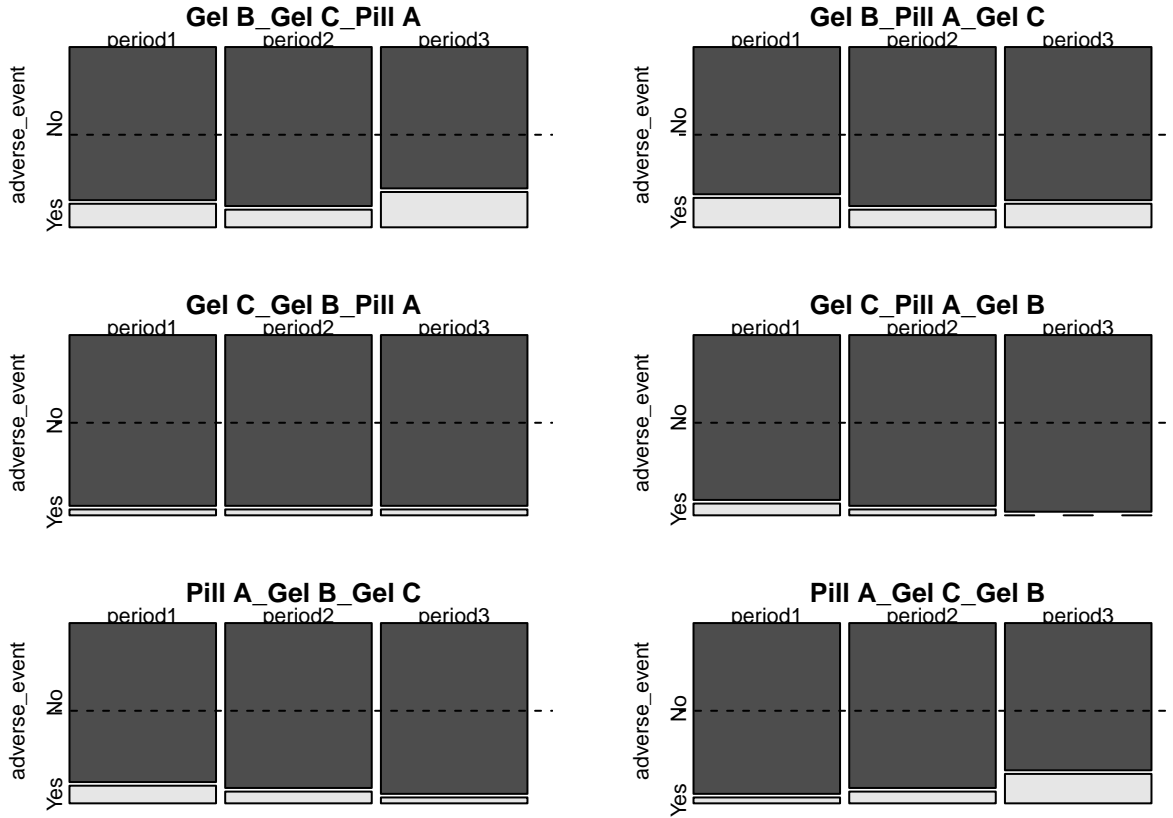
Patient Distribution: 30 people in per treatment sequence Initial Observation: Most patients do not face adverse events over the course of 4 weeks in each of the consecutive periods.

add demographic data

demographic summary

Table 1: Distributional Summary of Predictor variables in the Study

Characteristic	period1			period2			period3		
	No N = 164	**Yes** N = 16	**p-value**	**No** N = 168	**Yes** N = 12	**p-value**	**No** N = 163	**Yes** N = 17	**p-value**
age	31 (25, 37)	42 (40, 44)	<0.001	32 (25, 38)	40 (37, 44)	<0.001	32 (25, 38)	38 (32, 42)	0.012

[1] Median (Q1, Q3)

[2] Wilcoxon rank sum test

GLMM

Model Selection

Characteristic	OR	95% CI	p-value
(Intercept)	0.00	0.00, 0.00	**<0.001**
Treatment			
Pill A	—	—	
Gel B	1.20	0.55, 2.64	0.6
Gel C	0.84	0.37, 1.92	0.7
Period			
period1	—	—	
period2	0.71	0.31, 1.64	0.4
period3	1.13	0.52, 2.46	0.8
Treatment Sequence			
ABC or BAC	—	—	
CAB or ACB	0.61	0.23, 1.62	0.3
BCA or CBA	0.84	0.35, 2.02	0.7
age	1.19	1.11, 1.27	**<0.001**
gender			
Female	—	—	
Male	0.90	0.43, 1.89	0.8
race			
black	—	—	
others	1.55	0.61, 3.95	0.4
white	1.74	0.65, 4.68	0.3

Abbreviations: CI = Confidence Interval, OR = Odds Ratio

Table 2: LRT Between Model w/ and w/o Interaction Between Tx and Period

term	npar	AIC	BIC	logLik	deviance	statistic	df	p.value
glmm2	12	278.67	330.17	-127.34	254.67	NA	NA	NA
glmm1	16	281.34	350.01	-124.67	249.34	5.33	4	0.25

Table 3: LRT Between Model w/ and w/o Race, Gender and Carryover Effect

term	npar	AIC	BIC	logLik	deviance	statistic	df	p.value
glmm3	7	271.25	301.29	-128.62	257.25	NA	NA	NA
glmm2	12	278.67	330.17	-127.34	254.67	2.57	5	0.77

Characteristic	OR	95% CI	p-value
(Intercept)	0.00	0.00, 0.00	**<0.001**
Treatment			
Pill A	—	—	
Gel B	1.18	0.54, 2.58	0.7
Gel C	0.85	0.37, 1.94	0.7
Period			
period1	—	—	
period2	0.72	0.31, 1.65	0.4
period3	1.11	0.51, 2.40	0.8
age	1.19	1.12, 1.27	**<0.001**

Abbreviations: CI = Confidence Interval, OR = Odds Ratio

Model Result (with Carryover Effect)

Final Model Result (without Carryover Effect)

Notation:

$$\widehat{logit}(P(AE_{ijk} = 1)) = b_k + \mu + \tau_i + \pi_j + \beta a_k,$$
$$i = 1, 2, 3, \ j = 1, 2, 3, \ k = (1, 2, \dots, 180),$$
$$b_k \sim N(0, \sigma^2{}_b)$$
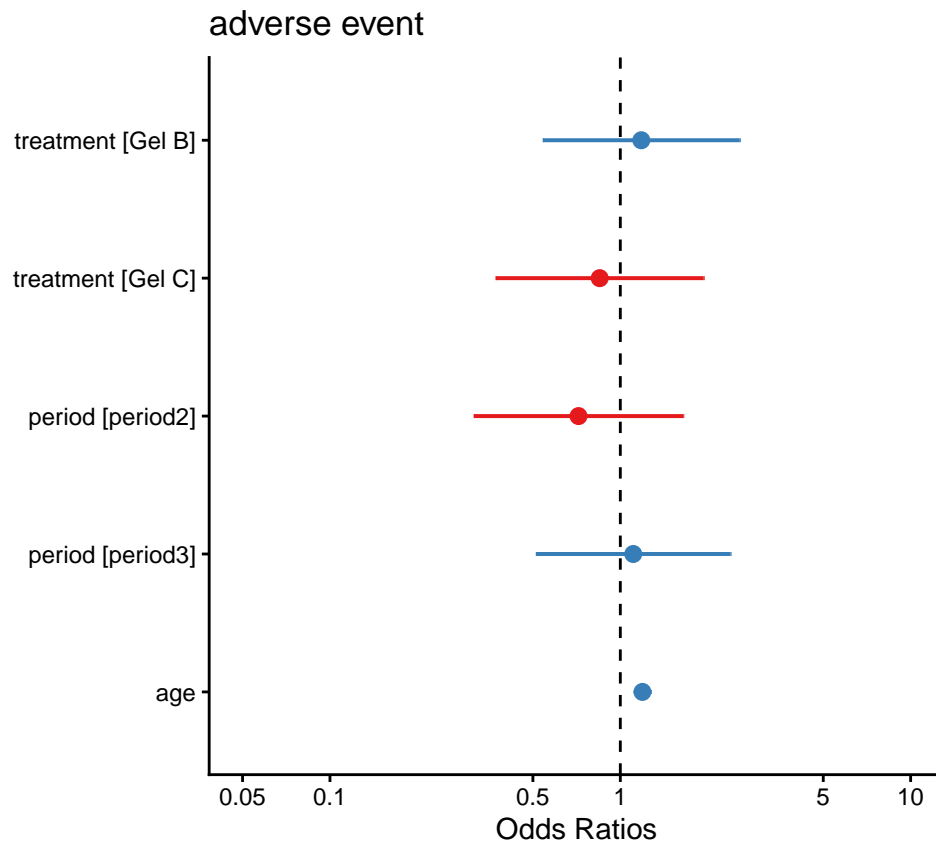
AE Prediction

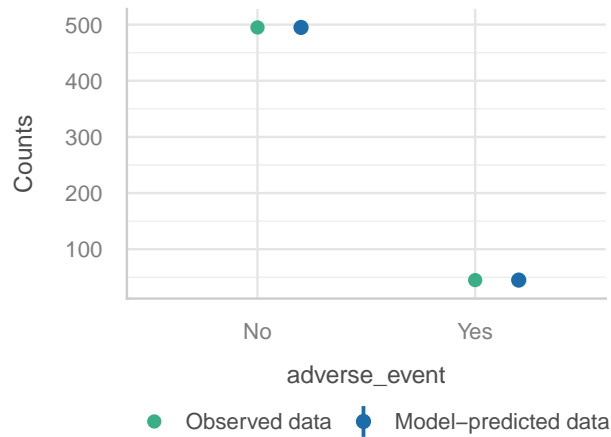## Distribution of OR for Adverse Events
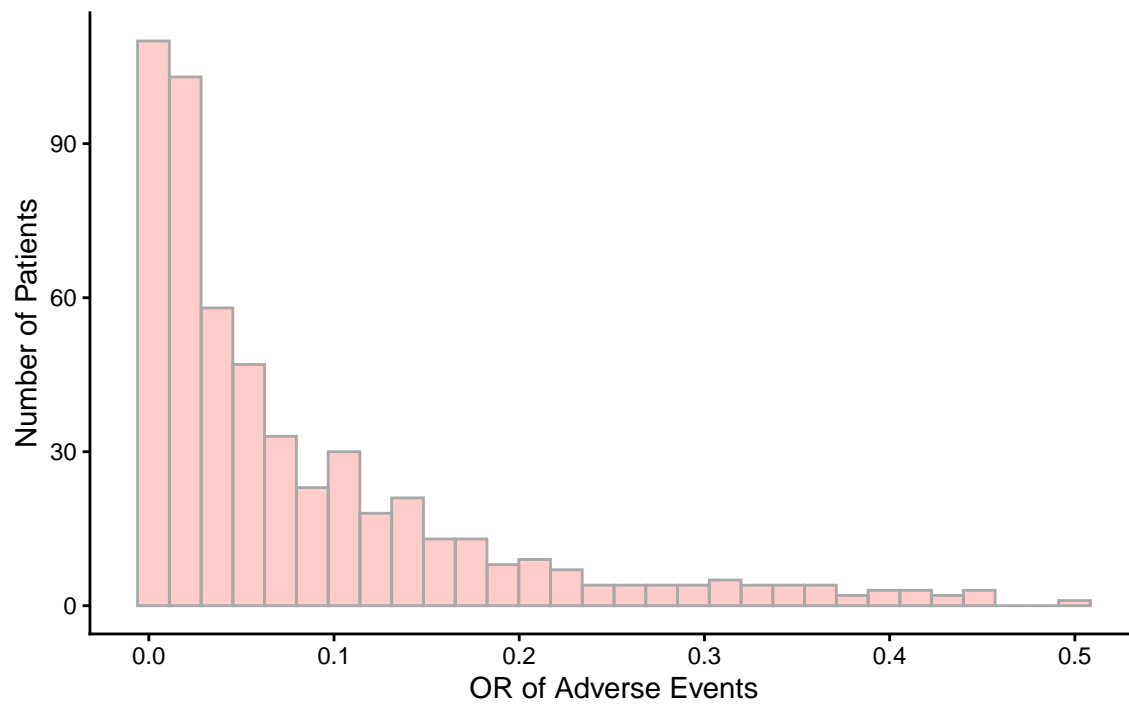
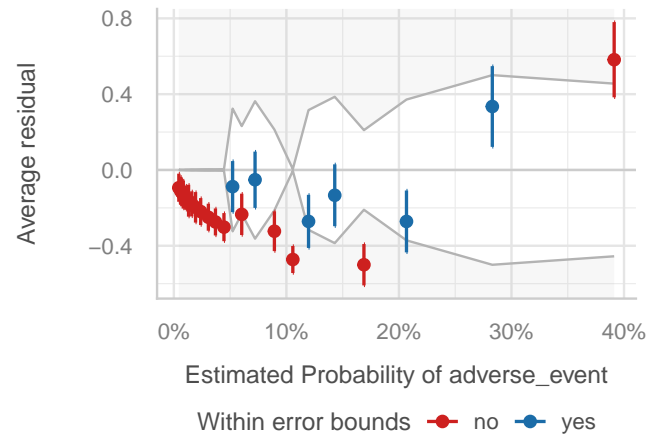## Predicted probabilities of adverse event
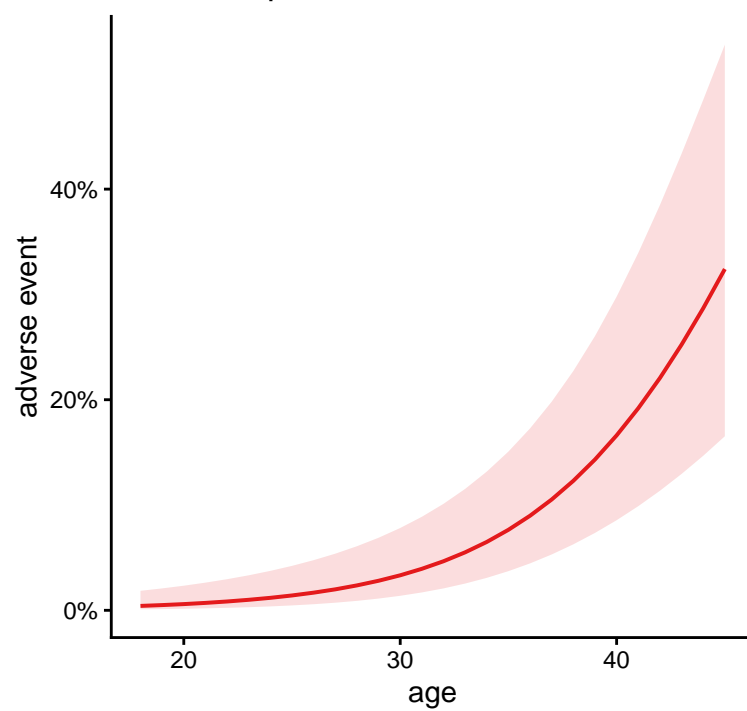
Model Diagnostics

Posterior Predictive Check

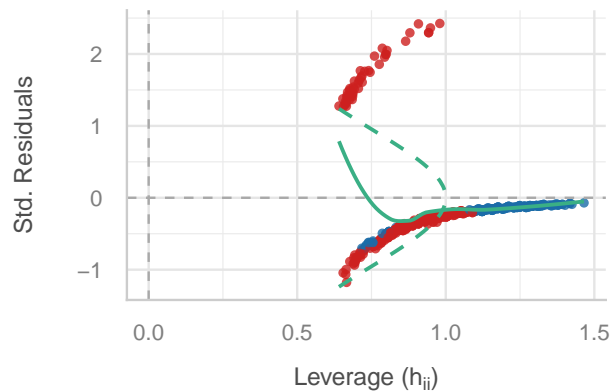Model–predicted intervals should include observed data points
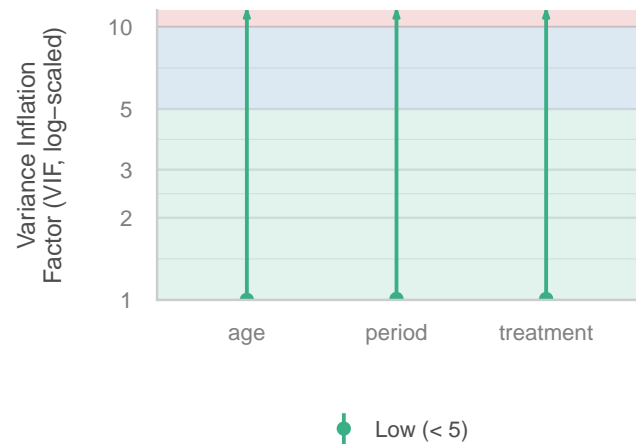
Binned Residuals

Points should be within error bounds

Influential Observations

Points should be inside the contour lines
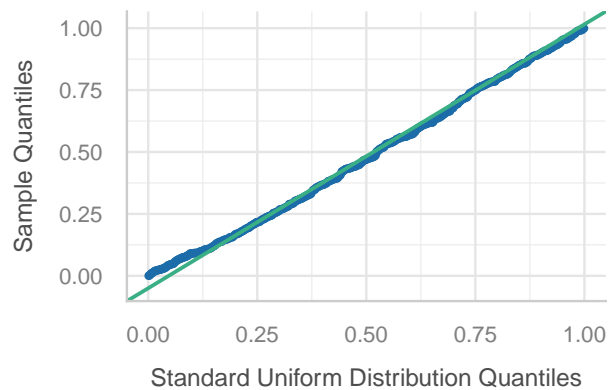
Collinearity
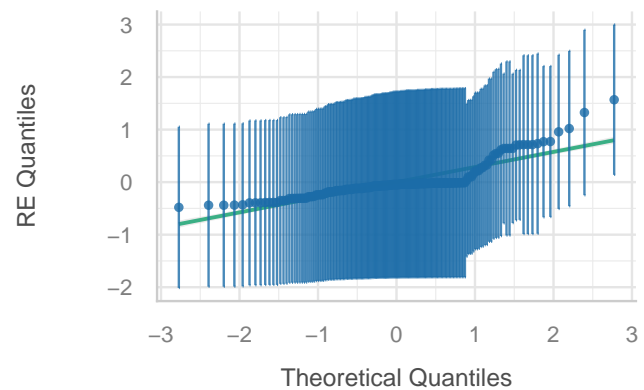
High collinearity (VIF) may inflate parameter uncertainty

Distribution of Quantile Residuals

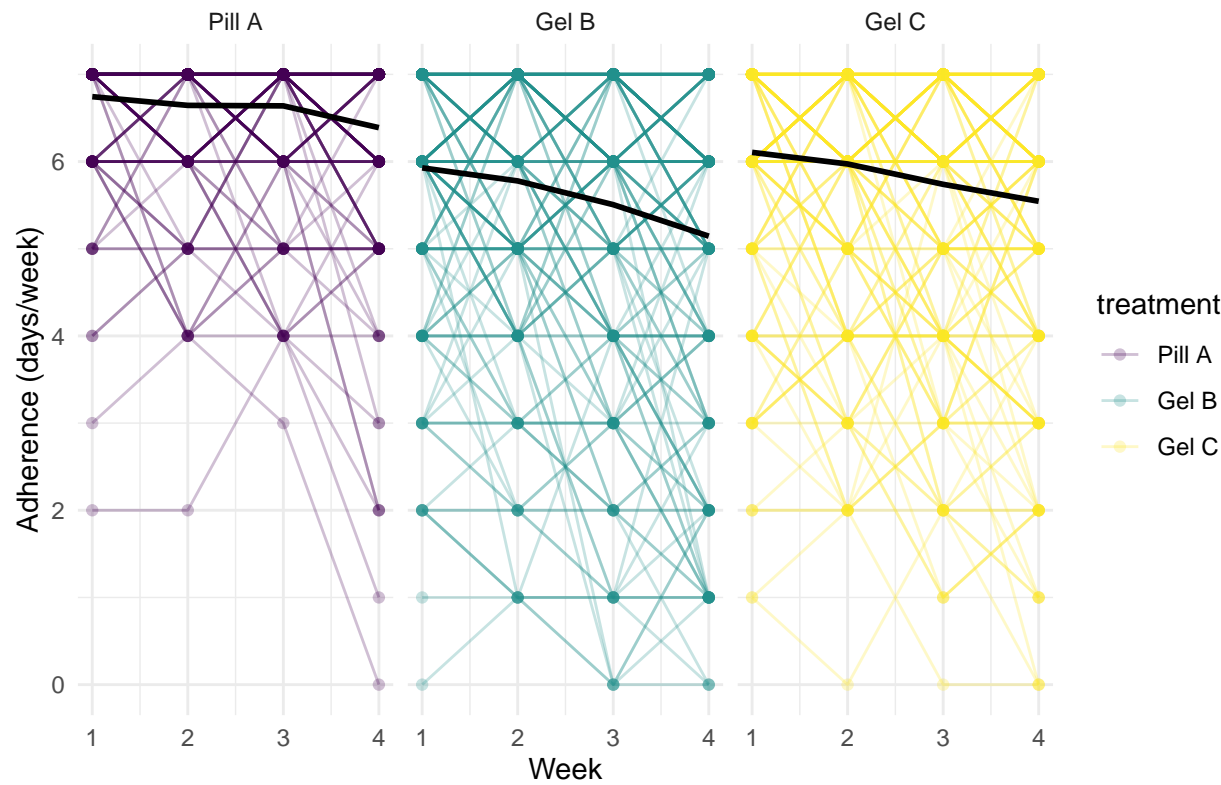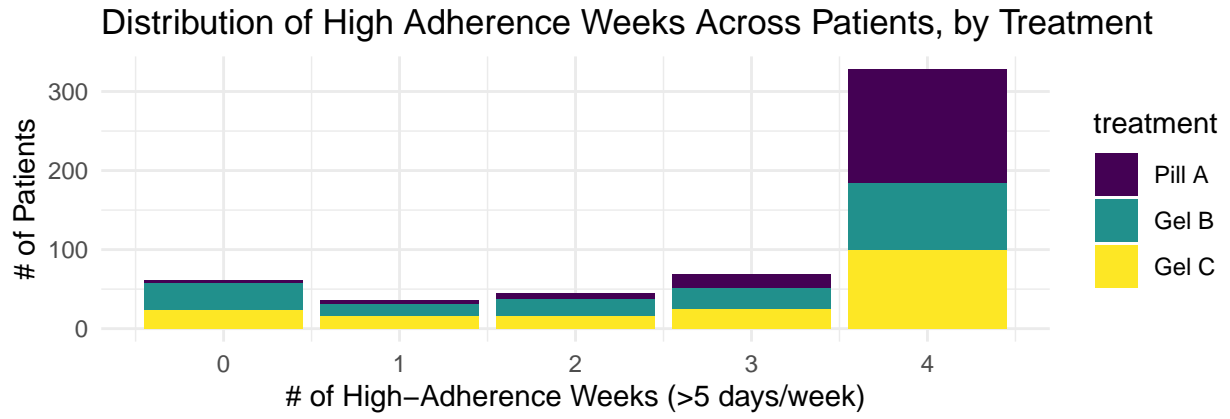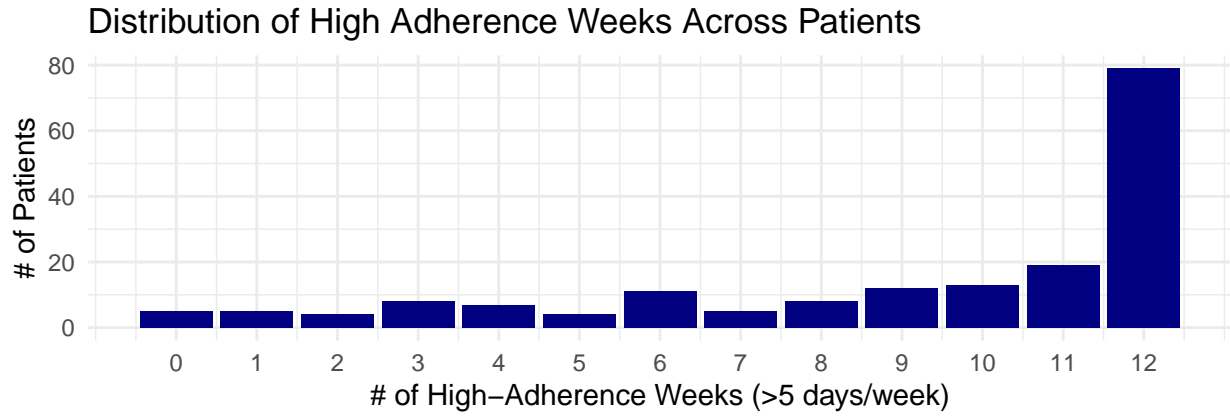Dots should fall along the line

Normality of Random Effects (ptid)

Dots should be plotted along the line

3.2 Primary Objective 2

Individual Patient Adherence Over Time, by Treatment

Distribution of High Adherence Weeks Across Patients

Distribution of High Adherence Weeks Across Patients, by Treatment

Model

$$

$$
Y_{hik} \sim \text{Binomial}\big(n = 7, p_{hik}\big), \tag{1}
$$

$$
\text{logit}(p_{hik}) = \mu + b_k + \pi_i + \tau_i + \lambda_j + \gamma * h, \tag{2}
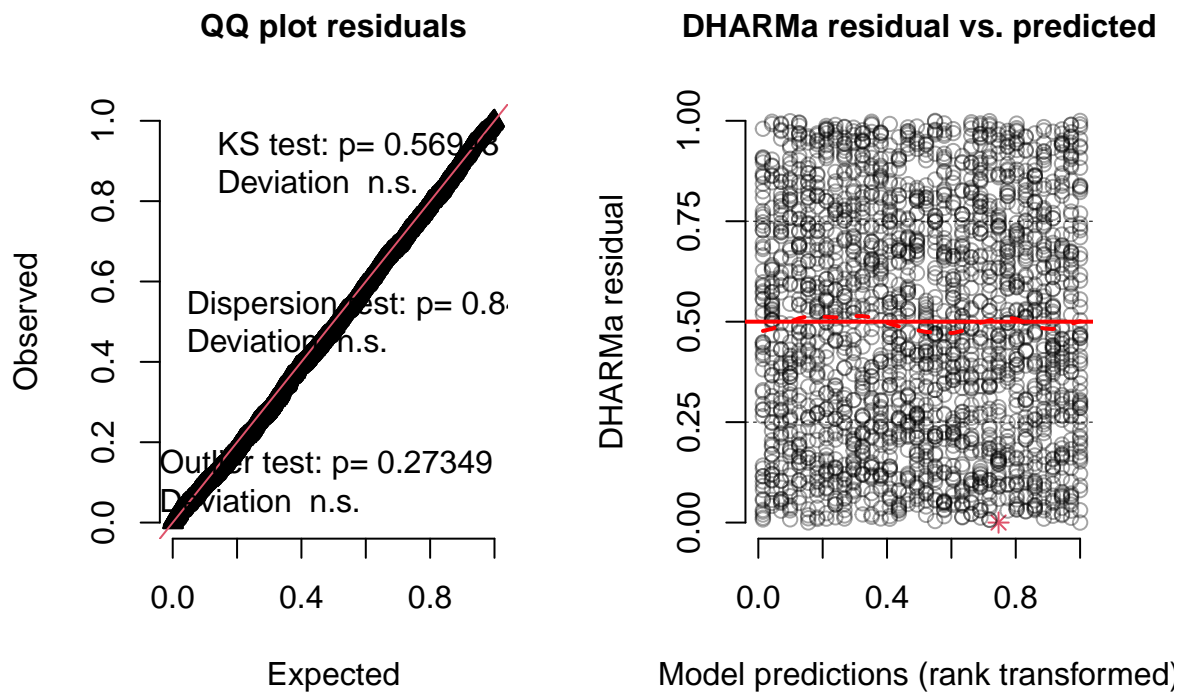$$

$$
b_k \sim \mathcal{N}(0, \sigma_b^2) \tag{3}
$$

$$

Table 4: **GLMM Results of Treatment on Adherence**

Characteristic	OR	95% CI	p-value
Treatment			
Pill A	—	—	
Gel B	0.14	0.12, 0.17	**<0.001**
Gel C	0.21	0.17, 0.24	**<0.001**
Week	0.73	0.69, 0.76	**<0.001**
Period			
1	—	—	
2	1.15	1.00, 1.32	0.051
3	1.05	0.92, 1.20	0.5

Abbreviations: CI = Confidence Interval, OR = Odds Ratio

DHARMa residual

QQ plot residuals

KS test: p= 0.569
Deviation n.s.

Dispersion test: p= 0.8
Deviation n.s.

Outlier test: p= 0.27349
Deviation n.s.

Observed

Expected

DHARMa residual vs. predicted

DHARMa residual

Model predictions (rank transformed)

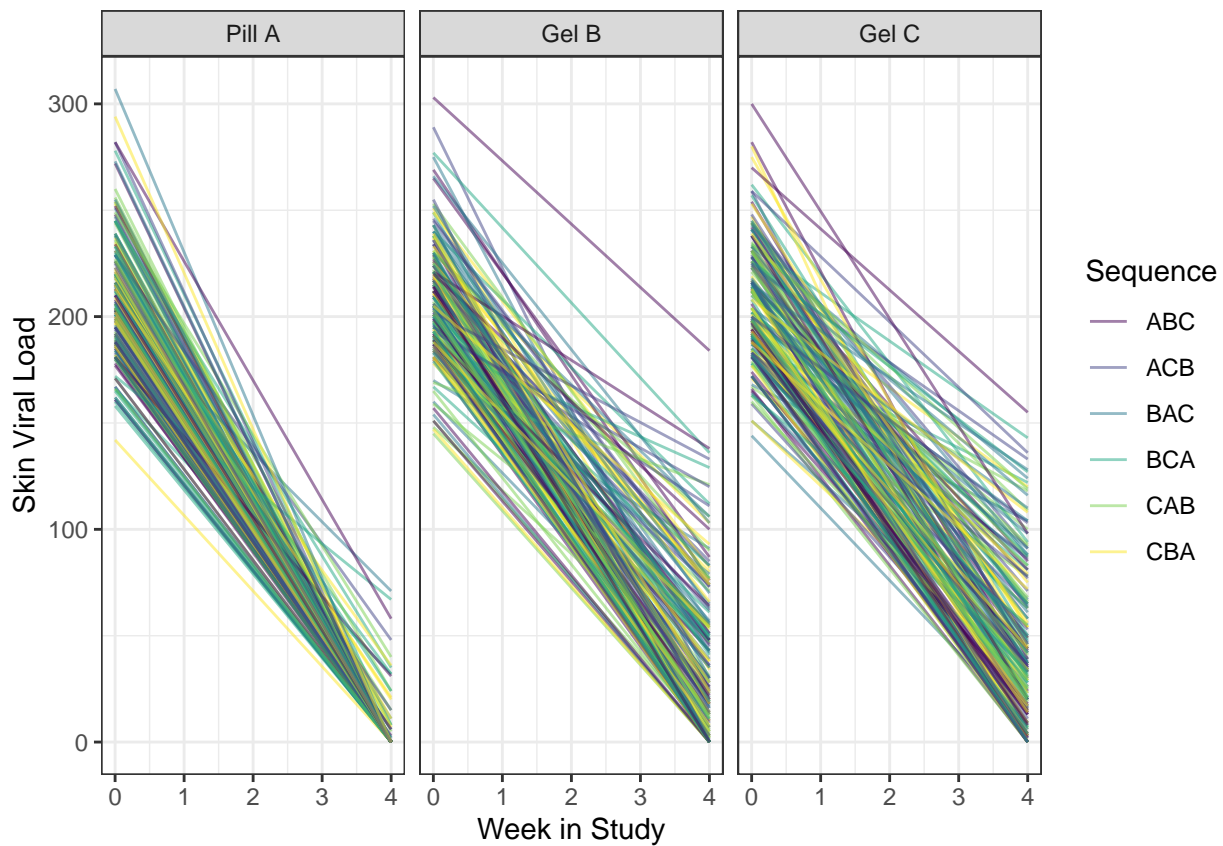## 3.3 Secondary Objective 1

EDA: Blood VL
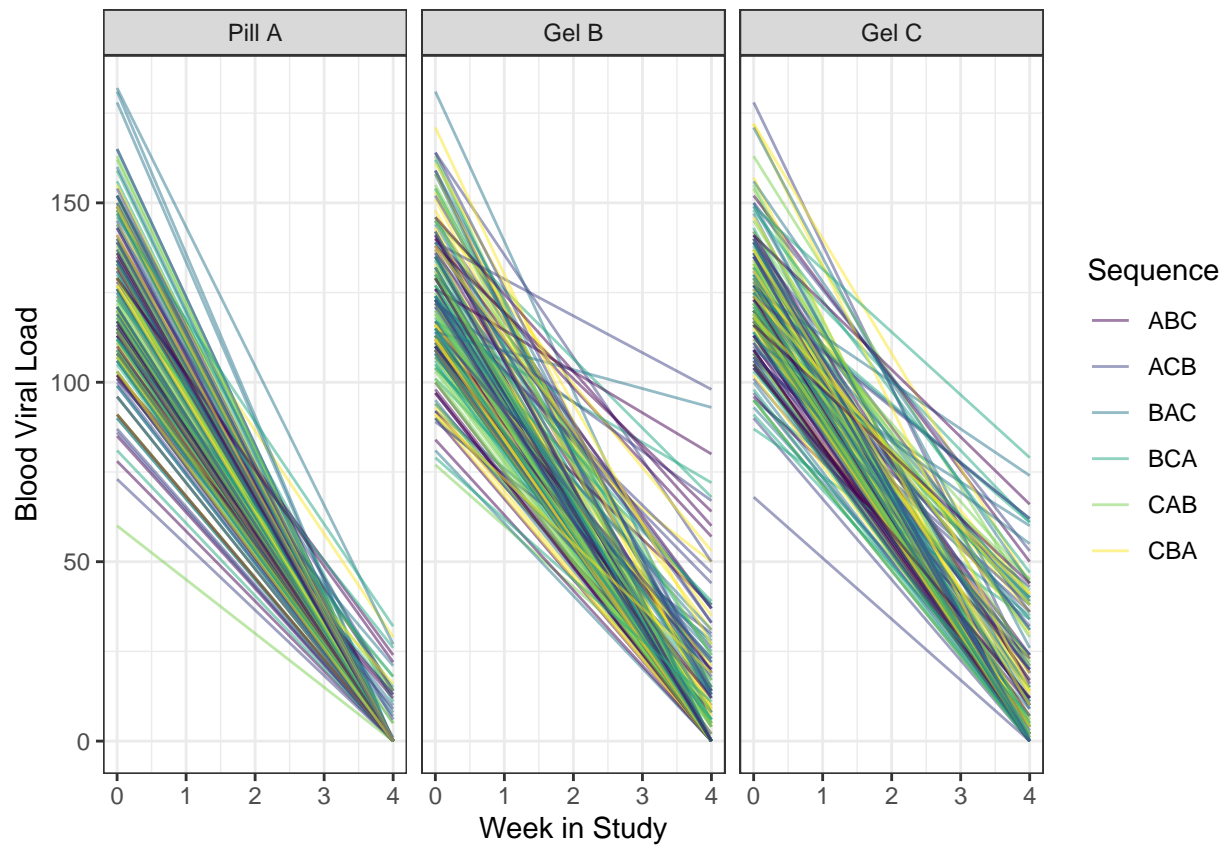
EDA: Skin VL

Table 5: Linear mixed-effects model results examining change in blood and skin viral loads (baseline minus end of period) by treatment group, adverse event status, study period, and baseline viral load. Results show beta coefficients, 95% confidence intervals, and p-values for each predictor.
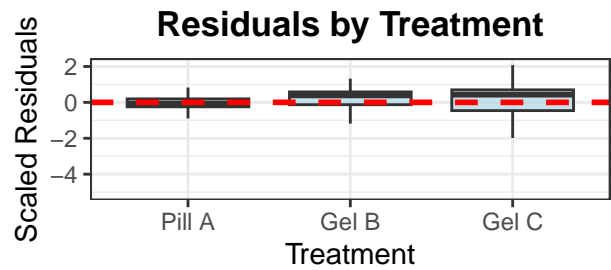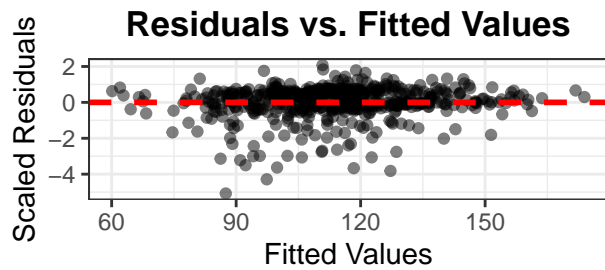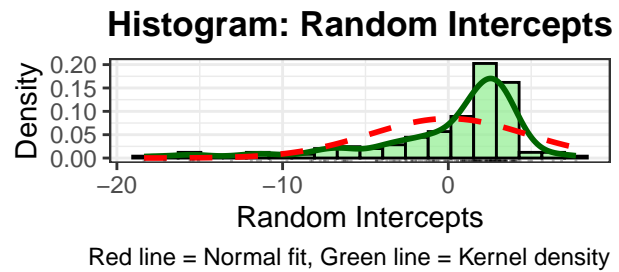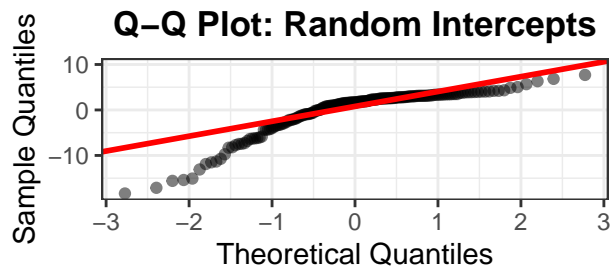
Comparison	Blood Viral Load			Skin Viral Load		
	Beta	95% CI	p-value	Beta	95% CI	p-value
Intercept	14.6	6.2, 23.1	**<0.001**	45.0	25.9, 64.0	**<0.001**
Treatment						
Gel B vs Pill A	-9.8	-12.5, -7.0	**<0.001**	-31.7	-36.9, -26.5	**<0.001**
Gel C vs Pill A	-12.1	-14.8, -9.4	**<0.001**	-41.5	-46.7, -36.3	**<0.001**
Adverse Event						
Adverse Event	-21.0	-25.6, -16.5	**<0.001**	-44.8	-53.5, -36.1	**<0.001**
Period						
Period 2 vs Period 1	-1.4	-4.1, 1.3	0.3	-1.0	-6.2, 4.3	0.7
Period 3 vs Period 1	-1.5	-4.2, 1.2	0.3	0.4	-4.8, 5.7	0.9
Baseline Blood VL	0.9	0.8, 1.0	**<0.001**			
Baseline Skin VL				0.8	0.7, 0.9	**<0.001**

Abbreviation: CI = Confidence Interval

Safety   Mixed Models

Model Diagnostics: Blood VL

Q–Q Plot: Scaled Residuals

Histogram: Scaled Residuals

Red line = Normal(0,1), Blue line = Kernel density

Q–Q Plot: Random Intercepts

Histogram: Random Intercepts

Red line = Normal fit, Green line = Kernel density

Residuals vs. Fitted Values
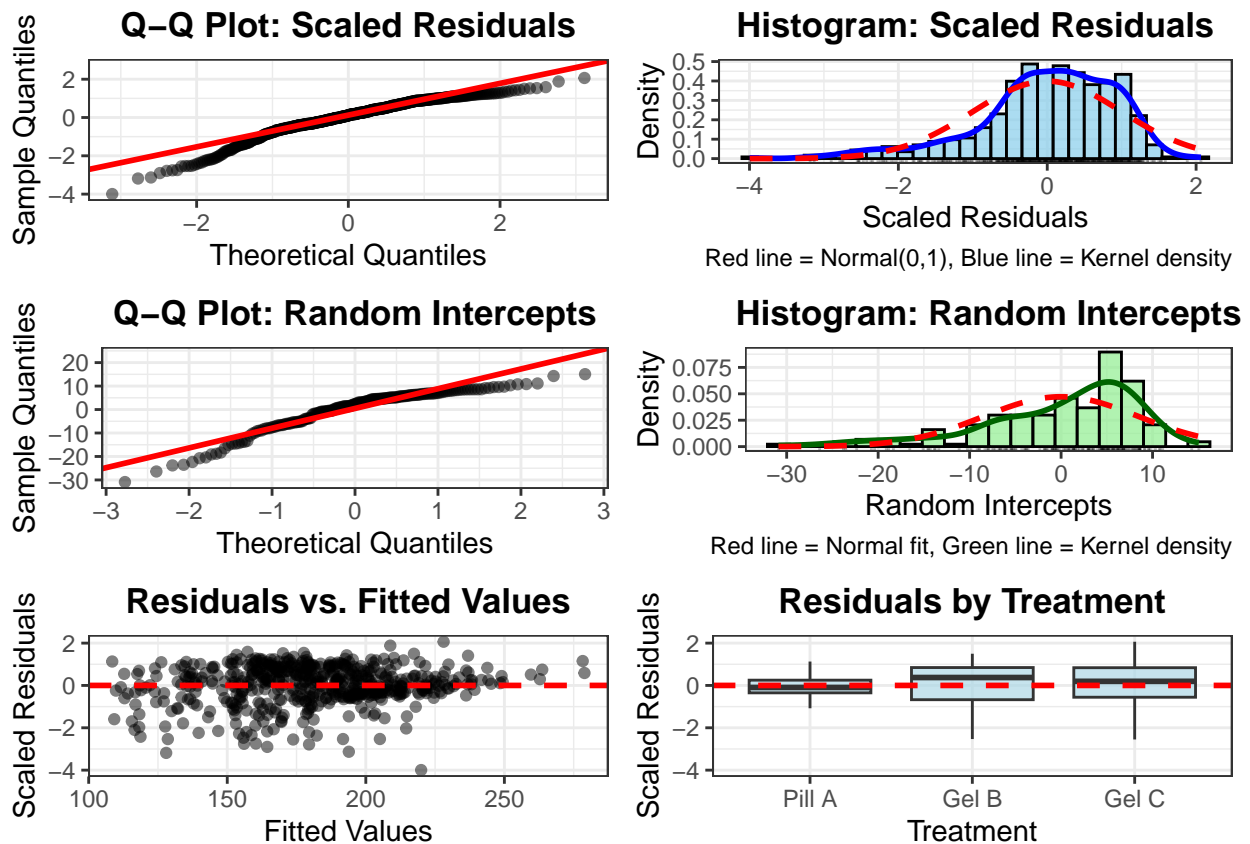
Residuals by Treatment
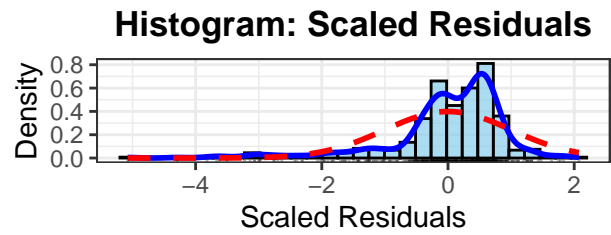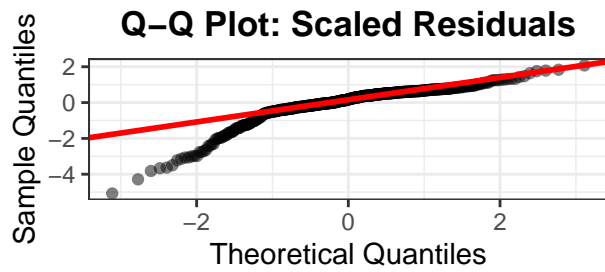
Model Diagnostics: Skin VL

Table 6: Linear mixed-effects model results examining change in blood and skin viral loads (baseline minus end of period) by treatment group, adverse event status, study period, and baseline viral load. Results show beta coefficients, 95% confidence intervals, and p-values for each predictor.
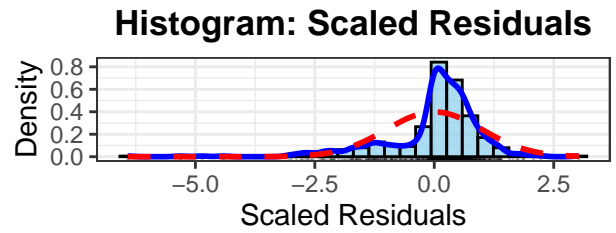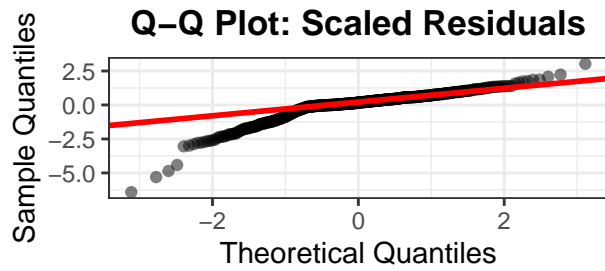
Comparison	Blood Viral Load			Skin Viral Load		
	Beta	**95% CI**	**p-value**	**Beta**	**95% CI**	**p-value**
Intercept	-31.8	-43.1, -20.5	**<0.001**	-45.7	-71.4, -20.1	**<0.001**
Treatment						
Gel B vs Pill A	-4.4	-7.5, -1.3	**0.005**	-22.0	-27.9, -16.1	**<0.001**
Gel C vs Pill A	-7.7	-10.7, -4.7	**<0.001**	-33.2	-39.0, -27.5	**<0.001**
Additional Day of Adherence	1.4	1.1, 1.6	**<0.001**	2.5	2.0, 3.0	**<0.001**
Period						
Period 2 vs Period 1	-1.2	-4.1, 1.7	0.4	-0.8	-6.4, 4.7	0.8
Period 3 vs Period 1	-1.6	-4.5, 1.3	0.3	0.1	-5.5, 5.7	>0.9
Baseline Blood VL	1.0	0.9, 1.0	**<0.001**			
Baseline Skin VL				0.9	0.8, 1.0	**<0.001**

Abbreviation: CI = Confidence Interval

Q–Q Plot: Scaled Residuals

Histogram: Scaled Residuals

Red line = Normal(0,1), Blue line = Kernel density

Q–Q Plot: Random Intercepts

Histogram: Random Intercepts

Red line = Normal fit, Green line = Kernel density

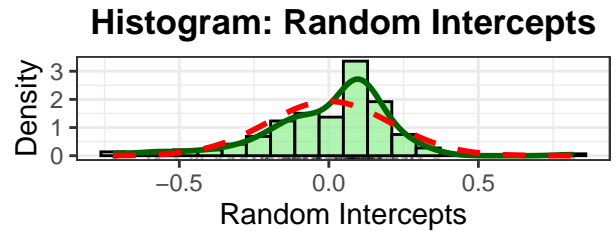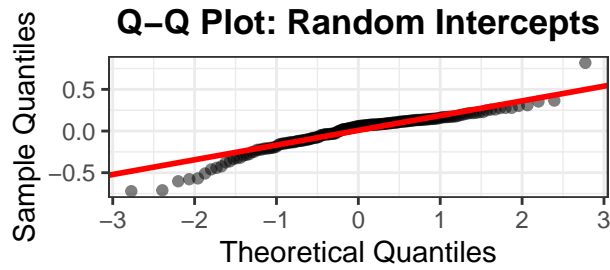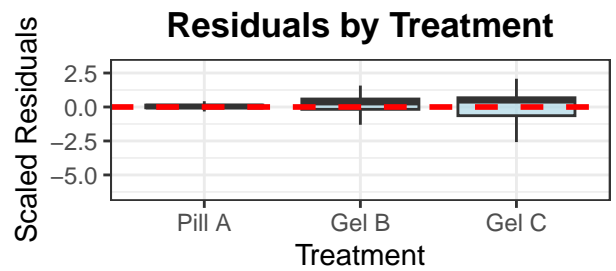**Residuals vs. Fitted Values**

Residuals by Treatment
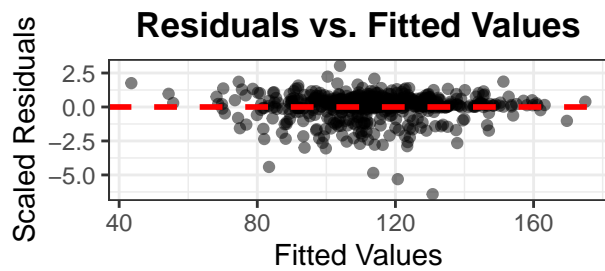
Adherence   Mixed Models

Model Diagnostics: Blood VL

Q–Q Plot: Scaled Residuals

Histogram: Scaled Residuals

Red line = Normal(0,1), Blue line = Kernel density

Q–Q Plot: Random Intercepts

Histogram: Random Intercepts

Red line = Normal fit, Green line = Kernel density

Residuals vs. Fitted Values

Residuals by Treatment

Model Diagnostics: Skin VL

Q–Q Plot: Scaled Residuals

Histogram: Scaled Residuals

Red line = Normal(0,1), Blue line = Kernel density

Q–Q Plot: Random Intercepts

Histogram: Random Intercepts

Red line = Normal fit, Green line = Kernel density

Residuals vs. Fitted Values

Residuals by Treatment

3.4 Secondary Objective 2

Adherence vs Age by Product

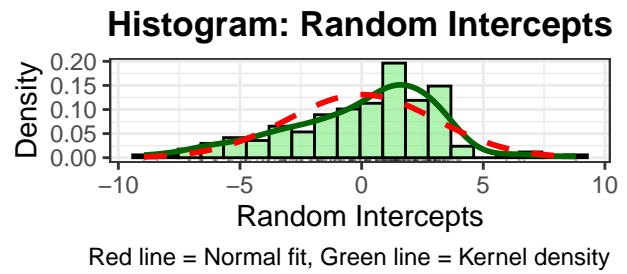## Adherence vs Age by Regimen
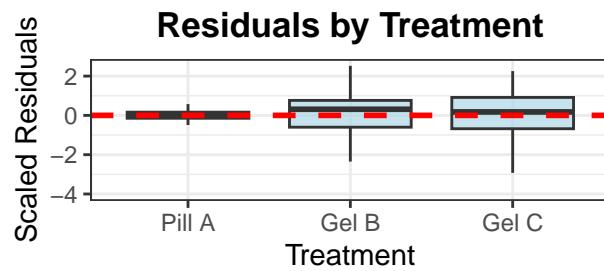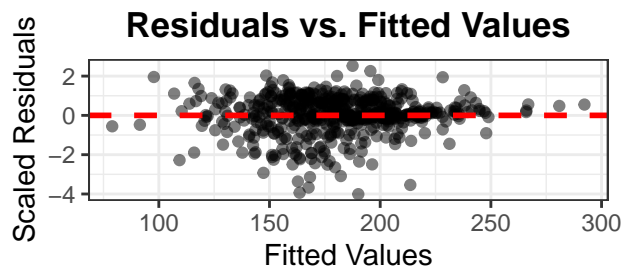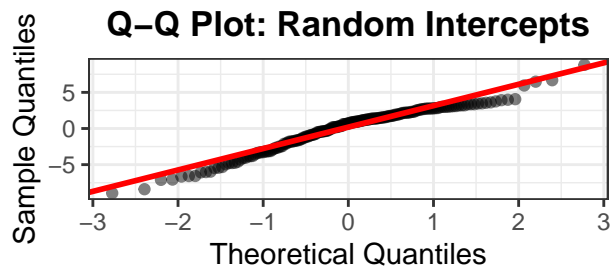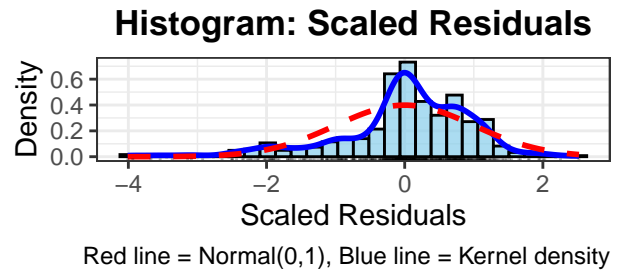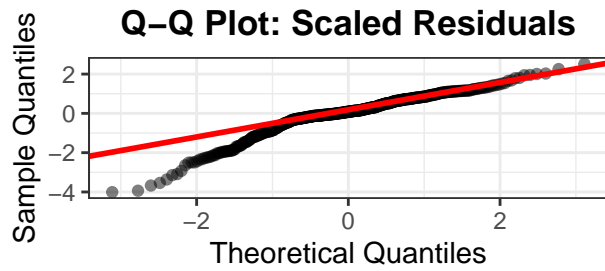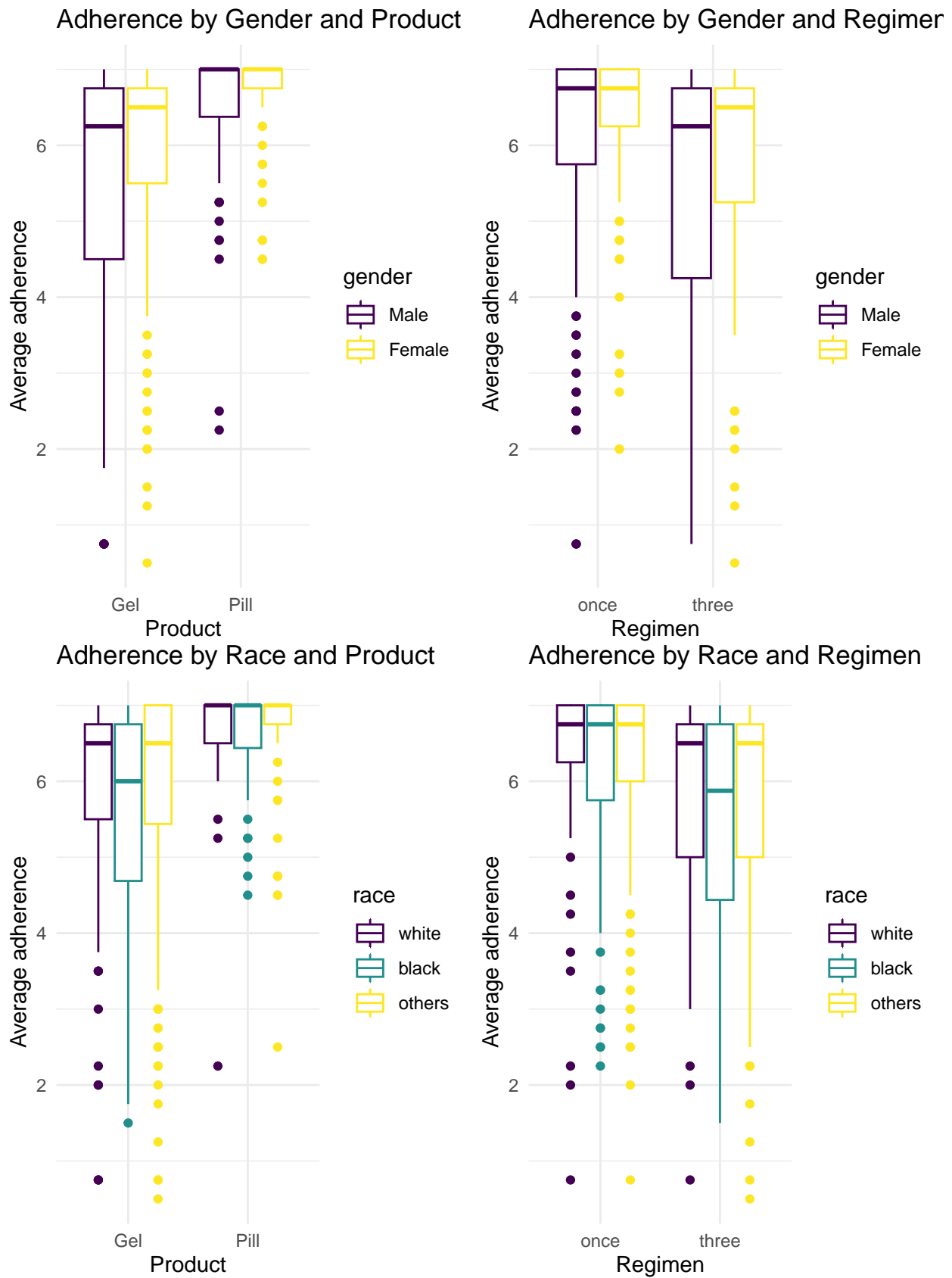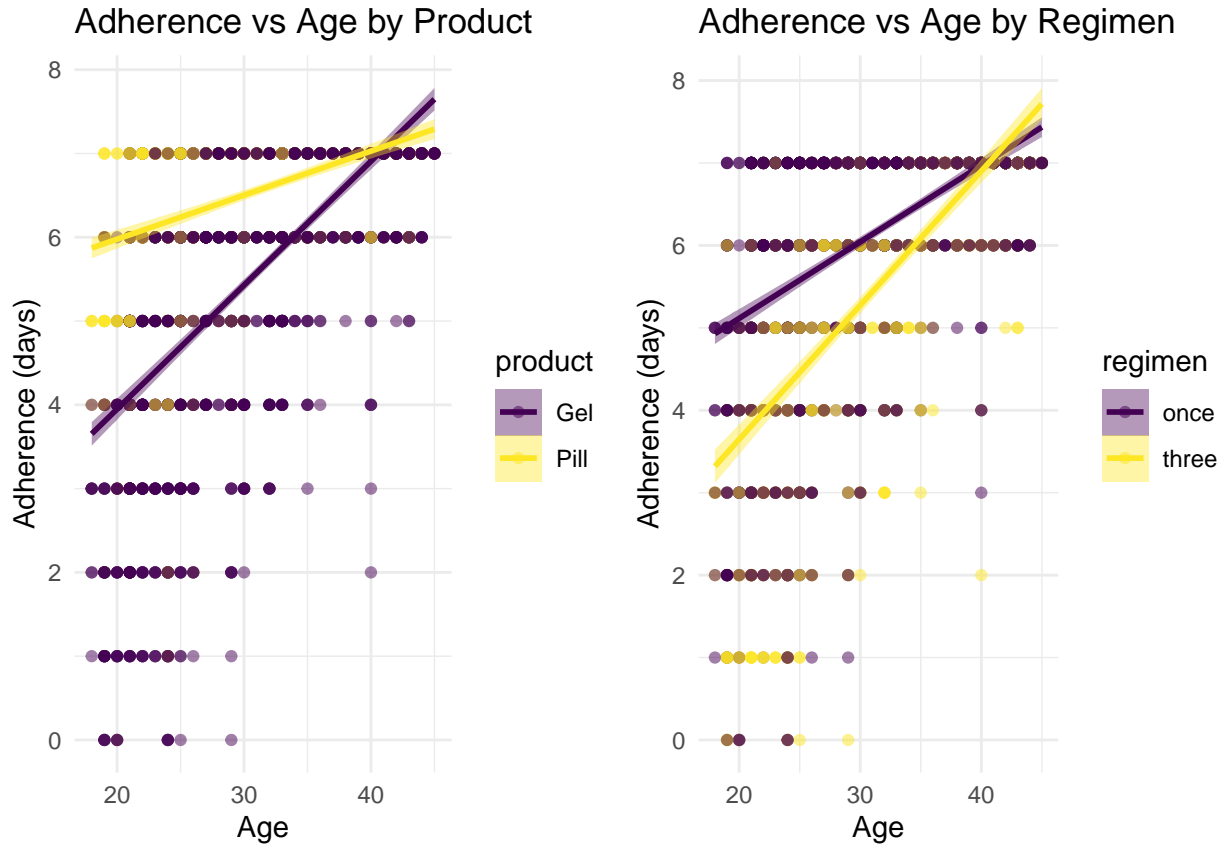
Model

$$

$$
\begin{align}
Y_{hik} &\sim \text{Binomial}\big(n = 7, p_{hik}\big), \tag{4}\\
\text{logit}(p_{hik}) &= \mu + b_k + \pi_i + \lambda_j + \gamma * h + \beta_d * d_k + \beta_r * regimen + \beta_p * product \tag{5}\\
&\quad + \beta_{dr} * d_k * regimen + \beta_{dp} * d_k * product \tag{6}\\
b_k &\sim \mathcal{N}(0, \sigma_b^2) \tag{7}
\end{align}
$$

$$

DHARMa residual

QQ plot residuals

DHARMa residual vs. predicted

KS test: p= 0.287
Deviation n.s.

Dispersion test: p= 0.81
Deviation n.s.

Outlier test: p= 0.33232
Deviation n.s.

Observed

Expected

DHARMa residual

Model predictions (rank transformed)
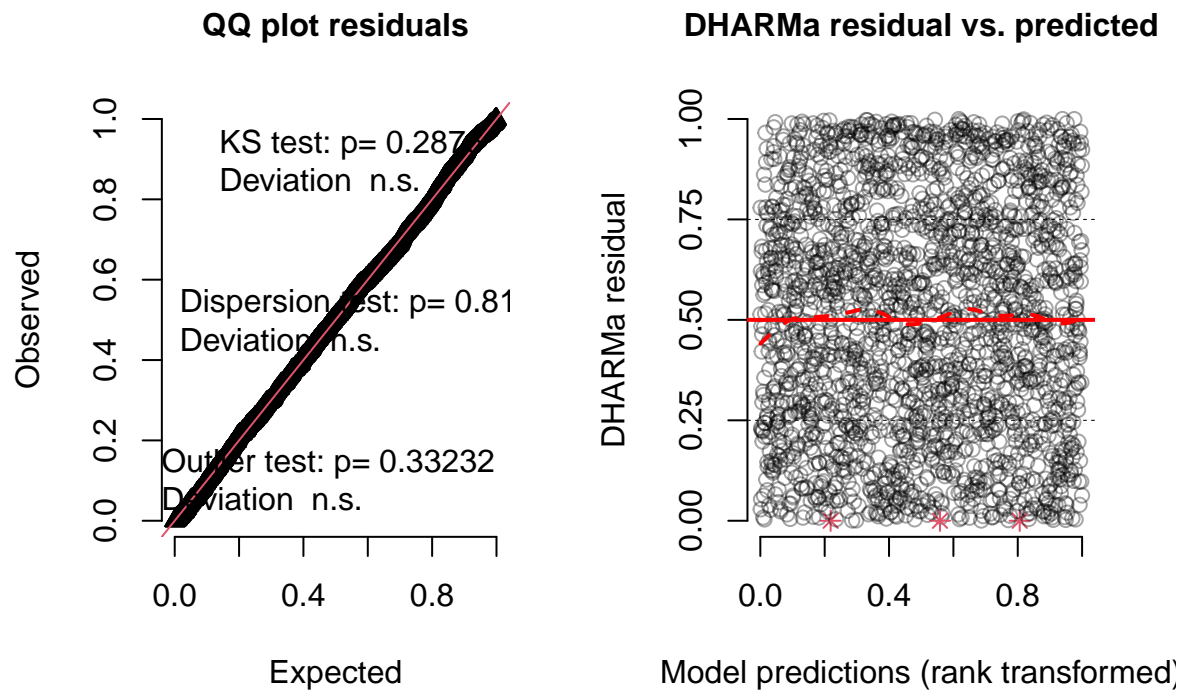
IV. Discussion

V. Conclusion

VI. Appendix

Table 7: **Interaction Results of Demographic Variables on Adherence**

Characteristic	OR	95% CI	p-value
Age	1.21	1.18, 1.24	**<0.001**
Product			
Gel	—	—	
Pill	4.35	2.98, 6.35	**<0.001**
Gender			
Male	—	—	
Female	1.36	0.95, 1.95	0.10
Race			
white	—	—	
black	1.02	0.65, 1.60	>0.9
others	0.97	0.62, 1.53	0.9
Regimen			
once	—	—	
three	0.76	0.58, 1.00	**0.050**
Period			
1	—	—	
2	1.14	0.99, 1.32	0.073
3	1.03	0.89, 1.18	0.7
Week	0.73	0.69, 0.76	**<0.001**
Age * Product			
Age * Pill	1.00	0.97, 1.03	>0.9
Product * Gender			
Pill * Female	1.00	0.71, 1.40	>0.9
Product * Race			
Pill * black	1.23	0.81, 1.86	0.3
Pill * others	1.05	0.69, 1.61	0.8
Age * Regimen			
Age * three	1.02	1.00, 1.04	0.074
Gender * Regimen			
Female * three	0.89	0.69, 1.15	0.4
Race * Regimen			
black * three	1.14	0.84, 1.56	0.4
others * three	1.02	0.74, 1.41	0.9

Abbreviations: CI = Confidence Interval, OR = Odds Ratio

Table 8: **Main Effect Results of Demographic Variables on Adherence**

Characteristic	OR	95% CI	p-value
Age	1.22	1.19, 1.25	**<0.001**
Gender			
Male	—	—	
Female	1.29	0.92, 1.80	0.14
Race			
white	—	—	
black	1.11	0.73, 1.69	0.6
others	0.99	0.65, 1.50	>0.9
Regimen			
once	—	—	
three	0.71	0.63, 0.80	**<0.001**
Product			
Gel	—	—	
Pill	4.84	4.12, 5.70	**<0.001**
Period			
1	—	—	
2	1.14	0.99, 1.32	0.065
3	1.04	0.91, 1.20	0.6
Week	0.73	0.69, 0.76	**<0.001**

Abbreviations: CI = Confidence Interval, OR = Odds Ratio