

Antibody Response Induced by HIV Glycoprotein Vaccines and T-cell Suppression Treatments in Rhesus Macaques

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1 Introduction

The current report describes multivariate and longitudinal data analyses done on a dataset from an HIV study, in which researchers administered HIV glycoprotein vaccines and immuno-suppression treatments to 20 rhesus macaques and measured antibody characteristics. This project aimed to determine whether the vaccine's efficacy, reflected by the variable `Binding`, was improved by vaccine injections and immuno-suppression treatments.

1.1 About the Study

A dominant vaccine development strategy is to induce neutralizing antibodies by immunizing humans with the virus' glycoproteins. HIV vaccines that adopted this strategy mostly failed, because HIV is an RNA virus, which mutates rapidly to escape the inhibition of neutralizing antibodies. By the time the human body generates neutralizing antibodies against the glycoproteins of some HIV strains, the RNA virus has already mutated. Thus, the existing antibody fails to recognize, bind with, and neutralize the HIV virus.

One possible solution is to increase the number of potential neutralizing antibodies that will cycle in the body by releasing a variety of them after glycoprotein immunization, which could be achieved by suppressing regulatory T (Treg) cells. Treg cells prevent autoimmune diseases and suppress allergic reactions by inhibiting adaptive antibody immune response in the germinal center. Theoretically, this adaptive response lowers the effectiveness of vaccines. Researchers hypothesize that suppressing Treg cells could improve the efficacy of immunization.

During the study, 20 rhesus macaques were given glycoprotein immunization at three time points (`Time_Point` 1, 2, 3) and supplemental antibody doses, as well as one of three treatments (two experimental regulatory T-cell suppression treatments as Drug 1 and 2 and one control as Drug 3). Blood samples were collected two weeks after vaccine dosing, and various numbers of antibodies, limited by assay yield, were isolated from the samples.

As one of the authors for four publications from the study, Kan Luo provided the dataset, which can be found [here](#). Now we turn to our research questions, after which the Methods section includes exploratory data analyses, multivariate data analyses, and longitudinal data analyses. The statistical results are included in the Methods section and summarized in the Results section. We discuss

implications and limitations in the Discussions and some final thoughts in the Conclusions.

1.2 Research questions

The current project focused on understanding whether the number of vaccine injections (Time_Point) and the different Treg inhibitor treatments (Drug) caused changes in the antibody characteristics and if the changes were related to the immune responses against HIV virus. Our research questions are:

RQ1: Did time points and drugs have effects on the mutation frequency (HMuFreq and LMuFreq) and the amino acid count in the third complementarity determining region (H_CDR3 and L_CDR3)?

RQ2: How did the binding strength of the antibodies (Binding or logBinding) develop in response to the number of vaccine dosages (Time_Point) and immuno-suppression treatments (Drug)?

2 Methods

This section first provides an overview and summaries of the dataset and then uses multivariate and longitudinal data analyses to answer the research questions.

2.1 Data Summaries

2.1.1 An Overview of Antibodies by Time Points and Drug Types

Section 7.1 contains a list of variables with brief descriptions. Note that each antibody contains two sets of heavy chains and light chains, all of which form a Y-shape immunoglobulin. Thus many of the variables start with H or L, indicating the chain from which the information comes. Some variables have missing numbers. We chose to let R functions ignore missing values to keep as much data as possible.

A total of 2465 antibodies, from 20 rhesus macaques, were collected at four different time points (0, 1, 2, 3) and each macaque was given one of three drugs (1 and 2 were immuno-suppressing drugs and 3 was a mock control). Figure 1 shows the histograms of antibody counts, and Table 1 shows the antibody counts in different combinations of drugs and time points.

2.1.2 Outlier Detection

We included five response variables for the project: H_CDR3, HMuFreq, L_CDR3, LMuFreq, and Binding. As shown in Figure 2, one data point of L_CDR3 seems an outlier. The summary statistics of standardized L_CDR3 in Table 2 show that a maximum value of 30, which is quite unusual. Figure 3 shows the Mahalanobis distances and Z scores of L_CDR3, and the same data point again appears to be an apparent outlier. The value for L_CDR3, 47, is quite unlikely. Since we were unable to reexamine the original data, we removed the data point.

2.1.3 Response Variables

Our five response variables were H_CDR3, HMuFreq, L_CDR3, LMuFreq, and Binding. Figure 4 shows H_CDR3's approximately normal distributions with the center around 13 at different time points. Figure 5 shows the distributions of H_CDR3 with respect to treatments at different time points, which are again approximately normal. With L_CDR3, Figure 6 and Figure 7 show approximately normal distribution, centered around 9, and with a longer right tail. The Q-Q plots in Figure 8 show that H_CDR3 and L_CDR3 are both approximately normal.

HMufreq and LMufreq were calculated by dividing H_Substitution by H_VBase for heavy chains and L_Substitution by L_VBase light chains. These two variables represent the degree to which the antibodies mutate. A higher mutation rate usually indicates better virus neutralization. Figure 9 and Figure 10 show that HMuFreq and LMuFreq are both approximately normal, each with a long right tail. The Q-Q plots in Figure 11 confirm the approximate normality of HMuFreq and LMuFreq.

Next, a histogram of Binding with respect to treatment at different time points and a Q-Q plot are shown in Figure 12 and Figure 13, both of which reveal that Binding is not normally distributed. Since the dataset has a large sample size ($n = 2464$, smallest group = 54), we can apply the Central Limit Theorem and assume normality. However, since many data points have the value 0 for Binding, linear models for longitudinal analyses might lead to negative values. To avoid this problem, we transformed Binding to $\log(\text{Binding} + 1)$ and called it logBinding. The Q-Q plot of logBinding is shown in Figure 14. Lastly, Figure 15 shows that none of the response variables are highly correlated.

2.2 Multivariate Data Analysis

To answer **RQ1** (Did time points and drugs have effects on the mutation frequency (HMuFreq and LMuFreq) and the amino acid count in the third complementarity determining region (H_CDR3 and L_CDR3)?), we tested whether predictors Time_Point and Drug had effects on four of our five response variables: H_CDR3, HMuFreq, L_CDR3, and LMuFreq. We excluded Binding from this section, because it has unequal variances across time points, which violated the equal variance assumption of MANOVA. Our concerns about the equal variance-covariance matrices assumption will be addressed in the Discussions. We used the `manova` function in base R for the MANOVA test and the `emmeans` package for pairwise comparisons^[7].

The assumption of independence requires a brief discussion here. A human antibody is formed heavy chains and light chains. A heavy chain has about 51 V-gene segments, 25 D-gene segments, and 6 J-gene segment. A light chain has about 71 V-gene segments and 9 J-gene segments^[5]. Any heavy chain V-D-J combination and light chain V-J combinations can randomly happen in germinal centers. Considering the frequent mutations and other factors, each individual can have over **10 billion** different antibodies. Thus, we followed the convention of vaccine studies and viewed each antibody as independent for multivariate data analyses. For longitudinal data analyses, since general linear and linear mixed models allow measurements from the same observational unit to correlate over time, we used different correlation structures to find a best model. This implies that the antibodies from the same macaque can be correlated.

2.2.1 MANOVA

Since we wanted to compare more than two populations, we used MANOVA to test for effects. We checked that the normality assumption was met due to large sample size ($n = 2464$). We performed the test with the formula $(\mathbf{H_CDR3, HMuFreq, L_CDR3, LMuFreq})^T \sim \mathbf{Time_Point} + \mathbf{Drug}$ and the null hypothesis that the means of the different populations (of Time_Point and Drug) were equal.

The output in Section 7.2 shows that both main effects of Time_Point and Drug have very small p-values (Time_Point: $F = 9.82$, $p \sim 0.0$; Drug: $F = 7.08$, $p \sim 0.0$). Thus we rejected the null hypothesis and concluded that both main effects were significant to the antibodies' four traits,

H_CDR3, HMuFreq, L_CDR3, and LMuFreq. To further understand the main effects, we proceeded to do pairwise comparisons.

2.2.2 Pairwise Comparisons

Table 3 summarizes the pairwise comparison results (see Sections 7.3, 7.4). We found heavy chains more sensitive than light chains to the immunization and drug treatments. Heavy-chain variables, H_CDR3 and HMuFreq, developed significant differences on both Time_Point and Drug, while only LMuFreq had significant differences over time.

More specifically, H_CDR3 at time point 3 is significantly higher than that at time points 1 and 2, but not time point 0, which is the baseline. This is because most baseline antibodies are not HIV-envelope specific antibodies but instead are present for other immunogens and accumulate longer H_CDR3. After the subject received HIV envelope immunogen, HIV specific antibodies became dominant and H_CDR3 grew longer over time. The macaques that received drug 1 had significantly longer H_CDR3 than those received drug 2, but this difference was not observed in other pairwise comparisons. Similarly, HMuFreq was sensitive to changes of time points and drugs; drugs 1 and 2 increased HMuFreq significantly compared to the control group.

2.3 Longitudinal Analysis

We used longitudinal data analyses to answer our **RQ2** (How did the binding strength of the antibodies (Binding or logBinding) develop in response to the number of vaccine dosages (Time_Point) and immuno-suppression treatments (Drug)?), including general linear models and linear mixed models. We used the `gls` and `lme` functions from the `nlme` package^[8].

2.3.1 One Covariate: Time Point

As shown in Figure 16 and Figure 17, the mean trend by test subject is not linear across all time points. Figure 18 and Figure 19 show that the different time points have different variances. Thus we used piecewise linear models and set variances as unequal over time. We first considered a

model with time point as the only covariate:

$$Y_{ij} = \beta_0 + \beta_1 Time_{ij} + e_{ij}$$

We then turned the model into a piecewise linear model and designated different intercepts and slopes for the line segments. The model includes three indicator variables: $S1, S2, S3$, where

$$S1 = \begin{cases} 1 & \text{if } 0 \leq \text{time point} < 1 \\ 0 & \text{otherwise} \end{cases}$$

$$S2 = \begin{cases} 1 & \text{if } 1 \leq \text{time point} < 2 \\ 0 & \text{otherwise} \end{cases}$$

$$S3 = \begin{cases} 1 & \text{if time point} \geq 2 \\ 0 & \text{otherwise} \end{cases}$$

The new model is

$$Y_{ij} = S1(\beta_0 + \beta_1 Time_{ij}) + S2(\beta_2 + \beta_3 Time_{ij}) + S3(\beta_4 + \beta_5 Time_{ij}) + e_{ij}$$

The trend should be continuous at time points 1 and 2. Our first complete model (`fit.gls`) is

$$Y_{ij} = \beta_0(S1 + 2S2 - S2Time_{ij}) + \beta_1(S1Time_{ij} + 2S2 - S2Time_{ij}) +$$

$$\beta_4(-S2 + S2Time_{ij} + S3) + \beta_5(-2S2 + 2S2Time_{ij} + S3Time_{ij}) + e_{ij}$$

where

$$\mathbf{e}_i \sim N(0, \sigma^2 I)$$

As mentioned earlier, we transformed `Binding` into `logBinding` with the formula

$$\log Binding = \log(Binding + 1).$$

We first used them as response variables in the above formula in two models (`fit.gls1` and `fit.gls2`, respectively) to find the better response variable. As seen in Table 4, the model using `logBinding` as the response variable has much lower AIC and BIC values. We decided to use `logBinding` as the response variable and build on this model (`glsl.fit2`). For the rest of the report, Y_{ij} denotes `logBinding`. Note that some plots below still use `Binding` in the y-axis, for which we had to plug the fitted values of `logBinding` into the exponential function to find `Binding`.

The model can also be written as

$$Y_{ij} = S1(\beta_0) + S1Time_{ij}(\beta_1) + S2(2\beta_0 + 2\beta_1 - \beta_4 - 2\beta_5) + S2Time_{ij}(-\beta_0 - \beta_1 + \beta_4 + 2\beta_5) \\ + S3(\beta_4) + S3Time_{ij}(\beta_5) + e_{ij}$$

We ran the model and plugged in coefficients to find the intercepts and slopes for all three segments of the mean trend:

- S1 = 1: $Binding = \exp(-0.0921720 + 0.1090234 * time) - 1$
- S2 = 1: $Binding = \exp(-0.109483 + 0.1263344 * time) - 1$
- S3 = 1: $Binding = \exp(0.3573358 - 0.1070750 * time) - 1$

Figure 20 shows the two segments S1 and S2 have very similar slopes. So we could refit the model with only two line segments between time points 0 and 2 and between time points 2 and 3. We called them S4 and S5. The next model is therefore

$$Y_{ij} = S4(\beta_0 + \beta_1 Time_{ij}) + S5(\beta_2 + \beta_3 Time_{ij}) + e_{ij}$$

where

$$S4 = \begin{cases} 1 & \text{if time point} < 2 \\ 0 & \text{otherwise} \end{cases}$$

$$S5 = \begin{cases} 1 & \text{if time point} \geq 2 \\ 0 & \text{otherwise} \end{cases}$$

Again, the trend should be continuous at time point 2. Our second complete model (`fit.gls3`) is then

$$Y_{ij} = \beta_1(-2S4 + S4Time_{ij}) + \beta_2(S4 + S5) + \beta_3(2S4 + S5Time_{ij}) + e_{ij}$$

where

$$\mathbf{e}_i \sim N(0, \sigma^2 I)$$

The model could also be written as

$$Y_{ij} = S4(-2\beta_1 + \beta_2 + 2\beta_3) + S4Time_{ij}(\beta_1) + S5(\beta_2) + S5Time_{ij}(\beta_3) + e_{ij}$$

After the model was constructed, we used the coefficients to find the mean trends for S4 and S5:

- S4 = 1: Binding = $\exp(-0.2146491 + 0.2448519 * time) - 1$
- S5 = 1: Binding = $\exp(0.26937508 + 0.00194581 * time) - 1$

As shown in Figure 21, one linear line connects time points 0 and 2 and another connects time points 2 and 3. The two lines are continuous. A comparison of AIC And BIC of these two models, shown in Table 5, indicates that the first model (`fit.gls2`) is a better model.

2.3.2 Adding Random Effects

Next we checked whether adding random effects could improve our model (`fit.gls2`). We assumed that random effects existed in the intercept and slope. Our linear mixed model is then:

$$Y_{ij} = \beta_0(S1 + 2S2 - S2Time_{ij}) + \beta_1(S1Time_{ij} + 2S2 - S2Time_{ij}) + \beta_4(-S2 + S2Time_{ij} + S3) + \beta_5(-2S2 + 2S2Time_{ij} + S3Time_{ij}) + b_{0i} + b_{1i}Time_{ij} + e_{ij}$$

where

$$\mathbf{b}_i \sim N\left(0, \mathbf{D} = \begin{bmatrix} D_{11} & D_{12} \\ & D_{22} \end{bmatrix}\right)$$

and

$$\mathbf{e}_i \sim N(0, \sigma^2 I)$$

We fit two models with random effects: `fit.a1` assumes random intercept and slope for time point, compound symmetric correlation structure, and unequal variances over time; and `fit.a2` assumes random intercept and slope for time point, exponential correlation structure, and unequal variances over time. As shown in Table 6, the model `fit.a2` has the lowest AIC and BIC, so it is the best model. We checked residuals for three models: `fit.gls2`, `fit.a1`, `fit.a2`, as shown in Figure 22. All three Q-Q plots show approximate normality.

2.3.3 Inference about β

Note the meanform for our three models are:

$$\begin{aligned} E(Y_{ij}) = & S1(\beta_0) + S1Time_{ij}(\beta_1) + S2(2\beta_0 + 2\beta_1 - \beta_4 - 2\beta_5) + S2Time_{ij}(-\beta_0 - \beta_1 + \beta_4 + 2\beta_5) \\ & + S3(\beta_4) + S3Time_{ij}(\beta_5) \end{aligned}$$

We would like to know if the slopes between time points 0 and 1, 1 and 2, and 2 and 3 equal zero, which means

$$H_0 : \beta_1 = 0, -\beta_0 - \beta_1 + \beta_4 + 2\beta_5 = 0, \beta_5 = 0$$

Thus, we performed three tests:

$$\mathbf{L}_1 \beta = 0$$

where $\mathbf{L}_1 = (0, 1, 0, 0)$ and $\beta = (\beta_0, \beta_1, \beta_4, \beta_5)^T$

$$\mathbf{L}_2 \beta = 0$$

where $\mathbf{L}_2 = (-1, -1, 1, 2)$ and $\beta = (\beta_0, \beta_1, \beta_4, \beta_5)^T$

$$\mathbf{L}_3 \beta = 0$$

where $\mathbf{L}_3 = (0, 0, 0, 1)$ and $\boldsymbol{\beta} = (\beta_0, \beta_1, \beta_4, \beta_5)^T$

As shown in Table 7, all three slopes have very small p-values (S1 = 1: F = 58.54, p ~ 0.0; S2 = 1: F = 137.96, P ~ 0.0; S3 = 1: F = 56.69, P ~ 0.0), which means the rates of change for logBinding in all three segments are significant. As shown in Figure 20, binding rates increase in S1 and S2 and decrease in S3. The use of logBinding as Y_{ij} made interpretation more difficult, but, with the very small p-values of β about logBinding and the directions of slopes for Binding, we could tentatively conclude that time point 2, when the monkeys had received two vaccines, had the highest binding rates, while the third vaccine injection at time point 3 failed to increase binding rates.

2.3.4 Two Covariates: Time Point and Drug

Next we added Drug as a covariate to the model `glms.a2` to see if it had effects on logBinding. We used two indicator variables: D2 and D3, where

$$D2 = \begin{cases} 1 & \text{if Drug} = 2 \\ 0 & \text{otherwise} \end{cases}$$

$$D3 = \begin{cases} 1 & \text{if Drug} = 3 \\ 0 & \text{otherwise} \end{cases}$$

Building on the model `glms.a2` and assuming that the random effects were the same for each drug, our model (`fit.a3`) with the extra covariate Drug is:

$$\begin{aligned} Y_{ij} = & \beta_0(S1 + 2S2 - S2Time_{ij}) + \beta_1(S1Time_{ij} + 2S2 - S2Time_{ij}) + \\ & \beta_2(-S2 + S2Time_{ij} + S3) + \beta_3(-2S2 + 2S2Time_{ij} + S3Time_{ij}) + \\ & \beta_4D2(S1 + 2S2 - S2Time_{ij}) + \beta_5D2(S1Time_{ij} + 2S2 - S2Time_{ij}) + \\ & \beta_6D2(-S2 + S2Time_{ij} + S3) + \beta_7D2(-2S2 + 2S2Time_{ij} + S3Time_{ij}) + \\ & \beta_8D3(S1 + 2S2 - S2Time_{ij}) + \beta_9D3(S1Time_{ij} + 2S2 - S2Time_{ij}) + \\ & \beta_{10}D3(-S2 + S2Time_{ij} + S3) + \beta_{11}D3(-2S2 + 2S2Time_{ij} + S3Time_{ij}) + \end{aligned}$$

$$b_{0i} + b_{1i}Time_{ij} + e_{ij}$$

where

$$\mathbf{b}_i \sim N\left(0, \mathbf{D} = \begin{bmatrix} D_{11} & D_{12} \\ & D_{22} \end{bmatrix}\right)$$

and

$$\mathbf{e}_i \sim N(0, \sigma^2 I)$$

Table 8 shows that the model with drug as the second covariate has the lowest AIC but not the lowest BIC. Considering the added complexity of the current model and the slight improvement with respect to AIC, we selected `fit.a2` as our best model. Next we made inference about β to find whether the drugs had different effects. To see whether Drug 1 and Drug 2 had different effects, we performed a hypothesis test on $H_0 : \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$ by testing

$$\mathbf{L}_4 \beta = 0$$

where

$$\mathbf{L}_4 = \begin{bmatrix} 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

and $\beta = (\beta_0, \beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \beta_6, \beta_7, \beta_8, \beta_9, \beta_{10}, \beta_{11})^T$

To see whether Drug 1 and Drug 3 had different effects, we performed a hypothesis test on $H_0 : \beta_8 = \beta_9 = \beta_{10} = \beta_{11} = 0$ by testing

$$\mathbf{L}_5 \beta = 0$$

where

$$\mathbf{L}_5 = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

and $\beta = (\beta_0, \beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \beta_6, \beta_7, \beta_8, \beta_9, \beta_{10}, \beta_{11})^T$

To see whether Drug 2 and Drug 3 had different effects, we performed a hypothesis test on $H_0 : \beta_4 = \beta_8, \beta_5 = \beta_9, \beta_6 = \beta_{10}, \beta_7 = \beta_{11}$ by testing

$$\mathbf{L}_6\beta = 0$$

where

$$\mathbf{L}_6 = \begin{bmatrix} 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 \end{bmatrix}$$

and $\beta = (\beta_0, \beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \beta_6, \beta_7, \beta_8, \beta_9, \beta_{10}, \beta_{11})^T$

As shown in Table 9 and Table 11, the p-values are smaller than 0.05. We rejected the null hypothesis and concluded that drugs 1 and 2 ($F = 2.48$, $p = 0.042$) and drugs 2 and 3 ($F = 5.25$, $p = 0.0003$) had different effects on logbinding rates. Table 10, on the other hand, shows a p-value slightly greater than 0.05, suggesting that drugs 1 and 3 ($F = 2.11$, $p = 0.077$) did not have different effects on logbinding rates.

3 Results

For multivariate analyses, we performed a MANOVA test on the main effects of Time_Point and Drug on the response variable vector $(H_CDR3, HMuFreq, L_CDR3, LMuFreq)^T$. We found that both main factors had very small p-values (Time_Point: $F = 9.82$, $p \sim 0.0$; Drug: $F = 7.08$, $p \sim 0.0$), indicating significant effects. We also performed pairwise comparisons to see where the effects were. As shown in Table 3, the main effect of Time_Point is significant among responses including H_CDR3, HMuFreq and LMuFreq, while the main effect of Drug is mostly on heavy-chain variables.

For longitudinal analyses, we found that the transformed variable logBinding was a better option and the linear mixed model fit.a2 had the lowest BIC:

$$Y_{ij} = \beta_0(S1 + 2S2 - S2Time_{ij}) + \beta_1(S1Time_{ij} + 2S2 - S2Time_{ij}) +$$

$$\beta_4(-S2 + S2Time_{ij} + S3) + \beta_5(-2S2 + 2S2Time_{ij} + S3Time_{ij}) + b_{0i} + b_{1i}Time_{ij} + e_{ij}$$

where

$$\mathbf{b}_i \sim N\left(0, \mathbf{D} = \begin{bmatrix} D_{11} & D_{12} \\ & D_{22} \end{bmatrix}\right)$$

and

$$\mathbf{e}_i \sim N(0, \sigma^2 I)$$

We performed F-tests to make inference about β for the three line segments. We rejected the hypothesis that the slopes of all three line segments were zero (S1 = 1: F = 58.54, p ~ 0.0; S2 = 1: F = 137.96, P ~ 0.0; S3 = 1: F = 56.69, P ~ 0.0). We then added Drug as another covariate to the above model and made inference about β . The comparison between three drug groups was done with three F-tests. The p-values for the tests between drugs 1 and 2 (F = 2.48, p = 0.042) and between drugs 2 and 3 (F = 5.25, p = 0.0003) were smaller than 0.05, while the p-value for the test between drugs 1 and 3 (F = 2.11, p = 0.077) were slightly greater than 0.05. Thus We rejected the null hypotheses that effects of drugs 1 and 2 as well as 2 and 3 were equal but failed to reject the null hypotheses that the effects of drugs 1 and 3 were equal.

4 Discussion

4.1 Limitations

4.1.1 Independence of Antibodies

In our multivariate analyses, we followed the common method of treating antibodies (rows in our data) as independent of each other. In our longitudinal analyses, the models allow measurements from the same observational unit (macaque) to correlate over time. It would be beneficial to formally test whether the antibodies were correlated or independent, but it would require more biological knowledge and the investigation would go beyond the scope of the current report. This remains an interesting topic that could be explored.

4.1.2 Equal Variance-covariance Matrices Assumption for MANOVA

For multivariate data analyses, the use of MANOVA was restricted by the assumptions of equal variance-covariance matrices among different populations. We ran the Fligner-Killeen Test of Homogeneity of Variances on all the four response variables H_CDR3, HMuFreq, L_CDR3, and LMuFreq. As shown in Section 7.5, most of the p-values are very small, meaning the null hypothesis of equal variance is rejected. In most cases, H_CDR3 and HMuFreq did not meet the equal variance-covariance matrices assumption.

Comparisons of the variance-covariance matrix of the response variables in different groups using element-wise division also reveals that the variance-covariance matrices might be unequal. For example, as shown in Table 12, the ratio between variance-covariance matrices of Drug 2 and Drug 3 has values as large as 26. Furthermore, the sample sizes of each populations, as shown in Table 1, are unequal. Thus, the results of the MANOVA test should be viewed with caution.

4.1.3 Longitudinal Models

For longitudinal data analyses, we did not try out more combinations of models. For example, we only tried two correlation structures (compound symmetry and exponential); other structures might have achieved better results. When we added drug as another covariate, we did not go back to test which correlation structure performed better and whether the piecewise model should include two or three line segments. Further, we did not assume different random effects for different line segments. These additional steps could lead to better models.

5 Conclusions

In our project, we performed multivariate data analyses and longitudinal data analyses to understand whether time points and drugs had effects on characteristics of antibodies and enhanced the efficacy of HIV vaccines. Our statistical analyses provided answers to our two research questions.

We performed a MANOVA test to answer our first research question, “Did time points and drugs have effects on the mutation frequency (HMuFreq and LMuFreq) and the amino acid count in the third complementarity determining region (H_CDR3 and L_CDR3)?” and found significant main

effects for time points and drugs. Light-chain variables tended to be less responsive to vaccine immunization and drug treatment. The macaques treated with drug 1 on average had longer H_CDR3 than those treated with drug 2, and the opposite was true for HMuFreq.

To answer our second research question, “How did the binding strength of the antibodies (Binding or logBinding) develop in response to the number of vaccine dosages (Time_Point) and immuno-suppression treatments (Drug)?”, we constructed longitudinal models. We found the model with the transformed response variable logBinding, three line segments, random effects of intercept and slope of time point, exponential correlation structure, and unequal variances over time performed best. F-tests for inference about β revealed that time point 2 had the highest logBinding value, suggesting that two HIV glycoprotein vaccines induced the strongest antibody response. We also found that adding drug as a covariate did not greatly improve the model and drug 2 appeared to have different effects from drug 1 and the mock control.

To date, no HIV vaccines have been found effective in creating immunity against the HIV virus. Our analyses showed that HIV glycoprotein immunization did increase binding rates but did not determine if the change was enough. The second type of Treg inhibitor treatments might be worth further examination. We hope that, even if the results did not reveal a direct solution, more analyses could find promising directions for future research.

6 References

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7 Appendix

7.1 List of Variables

- **Monkey_id**: The identity of monkey
- **Treatment (Drug)**: The 7 treatments in the dataset are coded into 3 drugs to simplify the data. Drug 1 and 2 are two different kinds of Treg inhibitor treatments, and drug 3 is the mock control.
- **Time_Point**: 0 represents before immunization; 1 represents 2 weeks post 1st immunization; 2 represents 2 weeks post 2nd immunization; and 3 represents 2 weeks post 3rd immunization, respectively.
- **Isotype**: There are 5 kinds of immunoglobulin isotypes: IgG, IgA, IgM, IgE, IgD. The two most important kinds are IgG and IgM. IgM occurs in the acute stage of infection and plays a role in the primary response. The secondary response IgG appears later in serum with higher binding affinity and neutralizing potentials against toxins and virus. IgA is mostly found in mucosal tissues such as Nasal mucosa. Non-dominant IgD and IgE are typically lower than 1% in blood.
- **H_ID** and **L_ID**: heavy chain and light chain IDs for the particular observation
- **H_VBase**: the number of nucleotide of the heavy chain variable region
- **H_Substitutions**: the number of relative nucleotide mutations in heavy chains
- **HMufreq**: calculated by $H_Substitutions / H_VBase$
- **H_CDR3**: the number of amino acid of a heavy chain's third complementarity determining region
- **L_VBase**: the number of nucleotide of a light chain's variable region
- **L_Substitutions**: the number of relative nucleotide mutations in the light chain
- **LMufreq**: calculated by $L_Substitutions / L_VBase$
- **L_CDR3**: the number of amino acid of a light chain's third complementarity determining region. **H_CDR3** and **L_CDR3** indicates the length of the third complementarity-determining region on the variable heavy chain and light chain. The longer they are, the more potential there is to produce diverse antibodies.
- **Binding**: affinity of antibodies against a selected HIV glycoprotein. Binding indicates the

rate of neutralizing, meaning how much the antibodies bind with the virus and thus make the virus ineffective. Larger values indicate stronger binding.

7.2 Output for the MANOVA Test

```
##              Df    Wilks approx F num Df den Df      Pr(>F)
## tp              3 0.95348    9.8224      12 6487.7 < 2.2e-16 ***
## drug            2 0.97728    7.0843       8 4904.0 2.375e-09 ***
## Residuals 2455
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.3 Pairwise comparisons by Time Point

```
## [1] "H_CDR3 pairwise CI's"
## contrast estimate SE df lower.CL upper.CL
## 0 - 1 0.489 0.231 2457 -0.223 1.202
## 0 - 2 0.194 0.237 2457 -0.535 0.923
## 0 - 3 -0.608 0.271 2457 -1.442 0.226
## 1 - 2 -0.295 0.159 2457 -0.784 0.194
## 1 - 3 -1.097 0.206 2457 -1.732 -0.462
## 2 - 3 -0.802 0.212 2457 -1.455 -0.148
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.997916666666667
## [1] "HMuFreq pairwise CI's"
## contrast estimate SE df lower.CL upper.CL
## 0 - 1 0.00870 0.00288 2457 -0.000188 0.0176
## 0 - 2 0.01872 0.00295 2457 0.009629 0.0278
## 0 - 3 0.02356 0.00338 2457 0.013153 0.0340
## 1 - 2 0.01002 0.00198 2457 0.003926 0.0161
## 1 - 3 0.01486 0.00257 2457 0.006938 0.0228
## 2 - 3 0.00484 0.00265 2457 -0.003316 0.0130
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.997916666666667
## [1] "L_CDR3 pairwise CI's"
## contrast estimate SE df lower.CL upper.CL
## 0 - 1 -0.0169 0.0652 2457 -0.218 0.184
## 0 - 2 -0.0287 0.0667 2457 -0.234 0.177
```

```

## 0 - 3      -0.0034 0.0764 2457   -0.239    0.232
## 1 - 2      -0.0117 0.0447 2457   -0.150    0.126
## 1 - 3       0.0135 0.0581 2457   -0.166    0.193
## 2 - 3       0.0253 0.0598 2457   -0.159    0.210
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.997916666666667
## [1] "LMuFreq pairwise CI's"
## contrast estimate      SE   df  lower.CL upper.CL
## 0 - 1      0.00853 0.00369 2457 -0.002847  0.0199
## 0 - 2      0.01465 0.00378 2457  0.003004  0.0263
## 0 - 3      0.01889 0.00432 2457  0.005567  0.0322
## 1 - 2      0.00611 0.00253 2457 -0.001694  0.0139
## 1 - 3      0.01036 0.00329 2457  0.000213  0.0205
## 2 - 3      0.00424 0.00339 2457 -0.006196  0.0147
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.997916666666667

```

7.4 Pairwise Comparisons by Drug

```
## [1] "H_CDR3 pairwise CI's"
## contrast estimate SE df lower.CL upper.CL
## 1 - 2 0.4907 0.160 2458 0.0316 0.950
## 1 - 3 0.4438 0.175 2458 -0.0589 0.946
## 2 - 3 -0.0469 0.171 2458 -0.5372 0.444
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.995833333333333
## [1] "HMuFreq pairwise CI's"
## contrast estimate SE df lower.CL upper.CL
## 1 - 2 -0.006 0.00199 2458 -0.01172 -0.000285
## 1 - 3 0.011 0.00218 2458 0.00476 0.017279
## 2 - 3 0.017 0.00213 2458 0.01091 0.023127
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.995833333333333
## [1] "L_CDR3 pairwise CI's"
## contrast estimate SE df lower.CL upper.CL
## 1 - 2 0.0451 0.0450 2458 -0.0839 0.174
## 1 - 3 0.1018 0.0492 2458 -0.0394 0.243
## 2 - 3 0.0567 0.0480 2458 -0.0810 0.194
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.995833333333333
## [1] "LMuFreq pairwise CI's"
```

```
## contrast estimate SE df lower.CL upper.CL
## 1 - 2 -0.000176 0.00256 2458 -0.00752 0.00717
## 1 - 3 0.002320 0.00280 2458 -0.00572 0.01036
## 2 - 3 0.002496 0.00273 2458 -0.00535 0.01034
##
## Results are averaged over the levels of: rep.meas
## Note: contrasts are still on the [.: scale
## Confidence level used: 0.995833333333333
```


7.5 Fligner-Killeen Test of Homogeneity of Variances

```
##
## Fligner-Killeen test of homogeneity of variances
##
## data:  H_CDR3 by Time_Point
## Fligner-Killeen:med chi-squared = 18.036, df = 3, p-value = 0.0004323

##
## Fligner-Killeen test of homogeneity of variances
##
## data:  HMuFreq by Time_Point
## Fligner-Killeen:med chi-squared = 50.662, df = 3, p-value = 5.775e-11

##
## Fligner-Killeen test of homogeneity of variances
##
## data:  L_CDR3 by Time_Point
## Fligner-Killeen:med chi-squared = 0.56825, df = 3, p-value = 0.9037

##
## Fligner-Killeen test of homogeneity of variances
##
## data:  LMuFreq by Time_Point
## Fligner-Killeen:med chi-squared = 16.585, df = 3, p-value = 0.0008601

##
## Fligner-Killeen test of homogeneity of variances
##
## data:  H_CDR3 by Drug
## Fligner-Killeen:med chi-squared = 13.463, df = 2, p-value = 0.001193

##
```

```

## Fligner-Killeen test of homogeneity of variances
##
## data:  HMuFreq by Drug
## Fligner-Killeen:med chi-squared = 48.86, df = 2, p-value = 2.456e-11

##
## Fligner-Killeen test of homogeneity of variances
##
## data:  L_CDR3 by Drug
## Fligner-Killeen:med chi-squared = 2.4113, df = 2, p-value = 0.2995

##
## Fligner-Killeen test of homogeneity of variances
##
## data:  LMuFreq by Drug
## Fligner-Killeen:med chi-squared = 0.17372, df = 2, p-value = 0.9168

```

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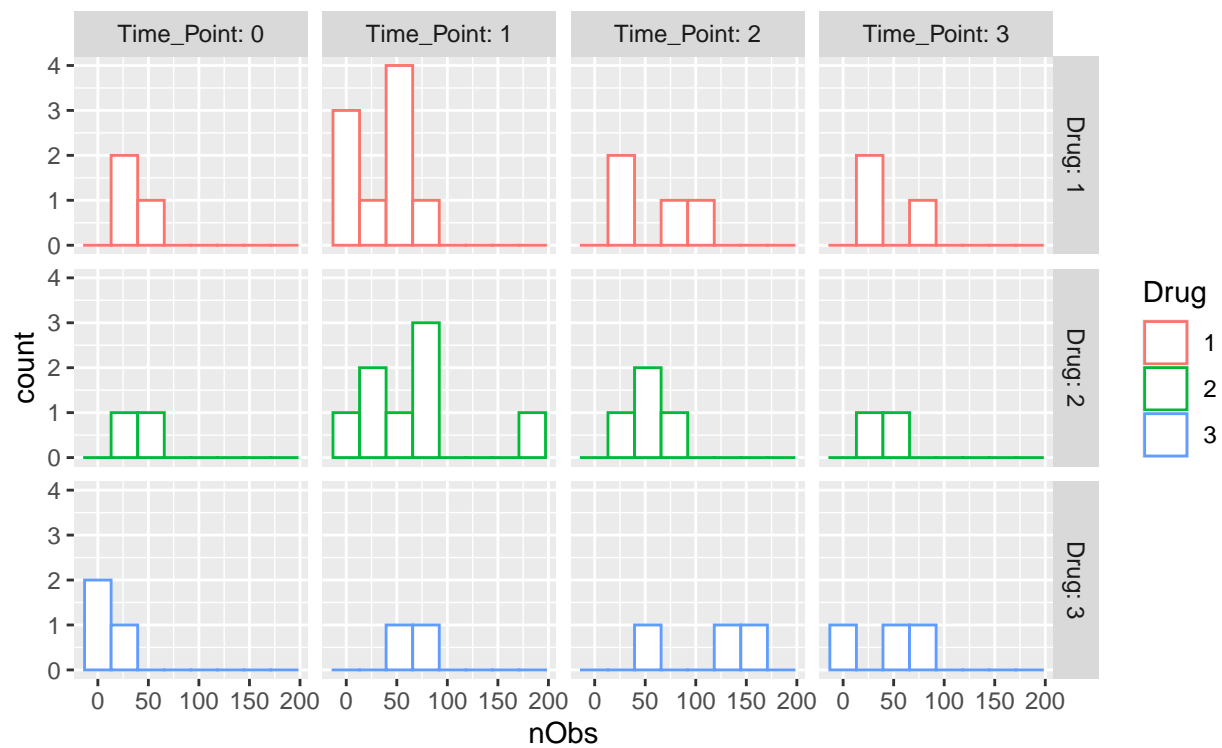


Figure 1: Histograms of Antibodies

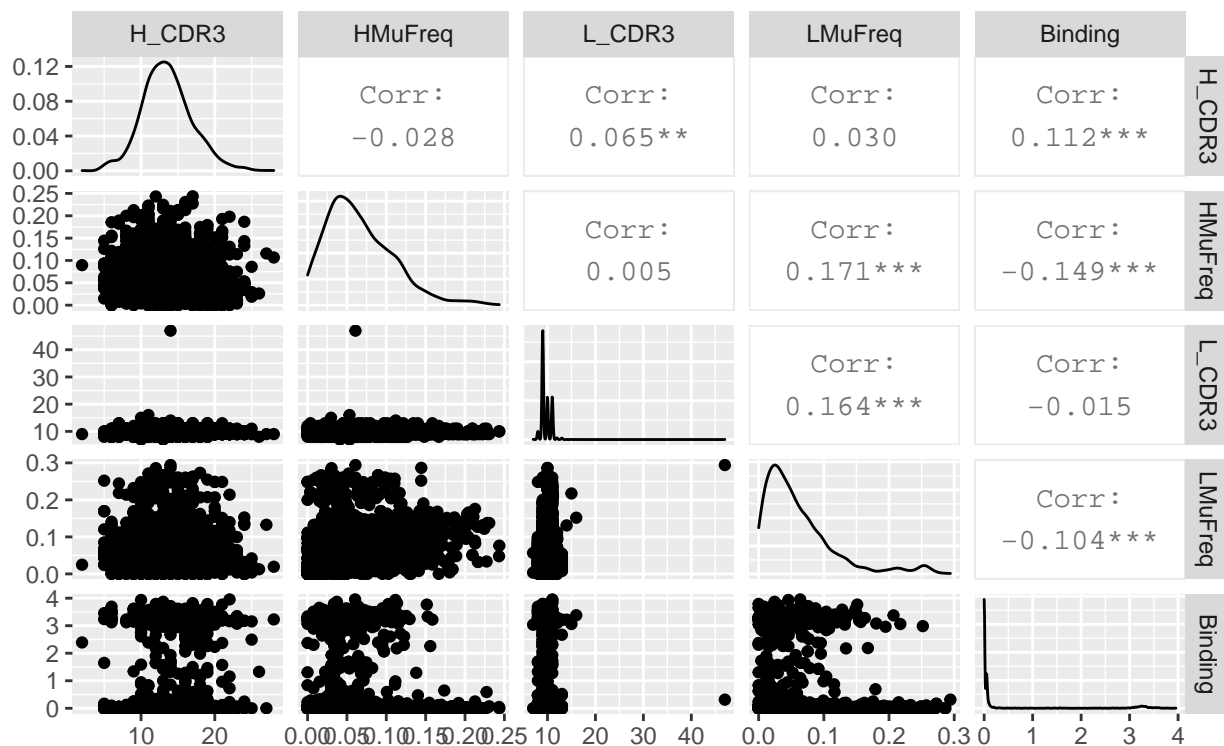


Figure 2: Scatterplot Matrix of Response Variables

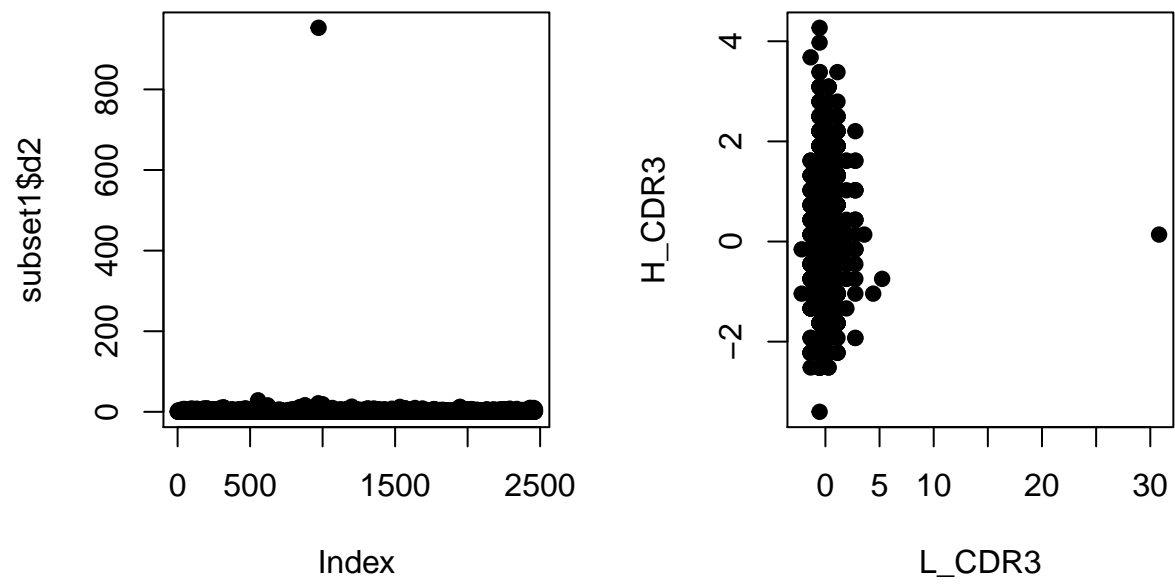


Figure 3: Mahalanobis Distances and Z Scores

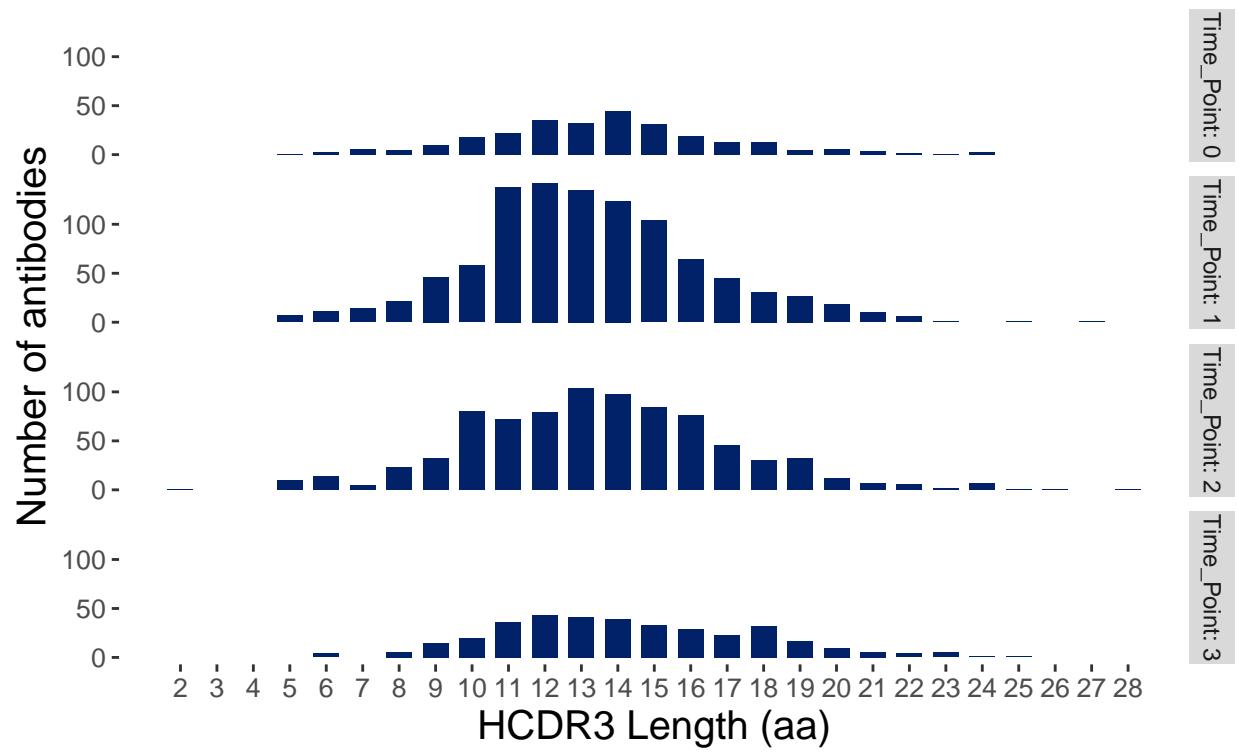


Figure 4: Histogram H_CDR3 by Time Point

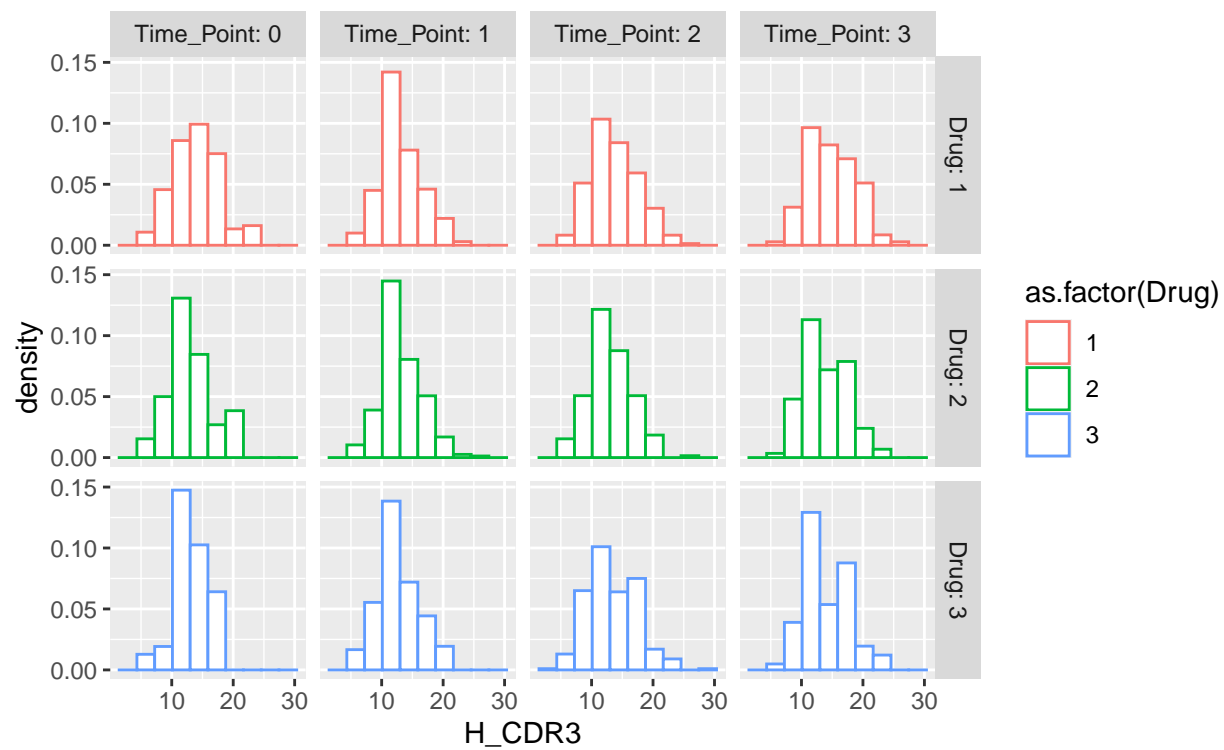


Figure 5: Histograms of H_CDR3 by Drug and Time Point

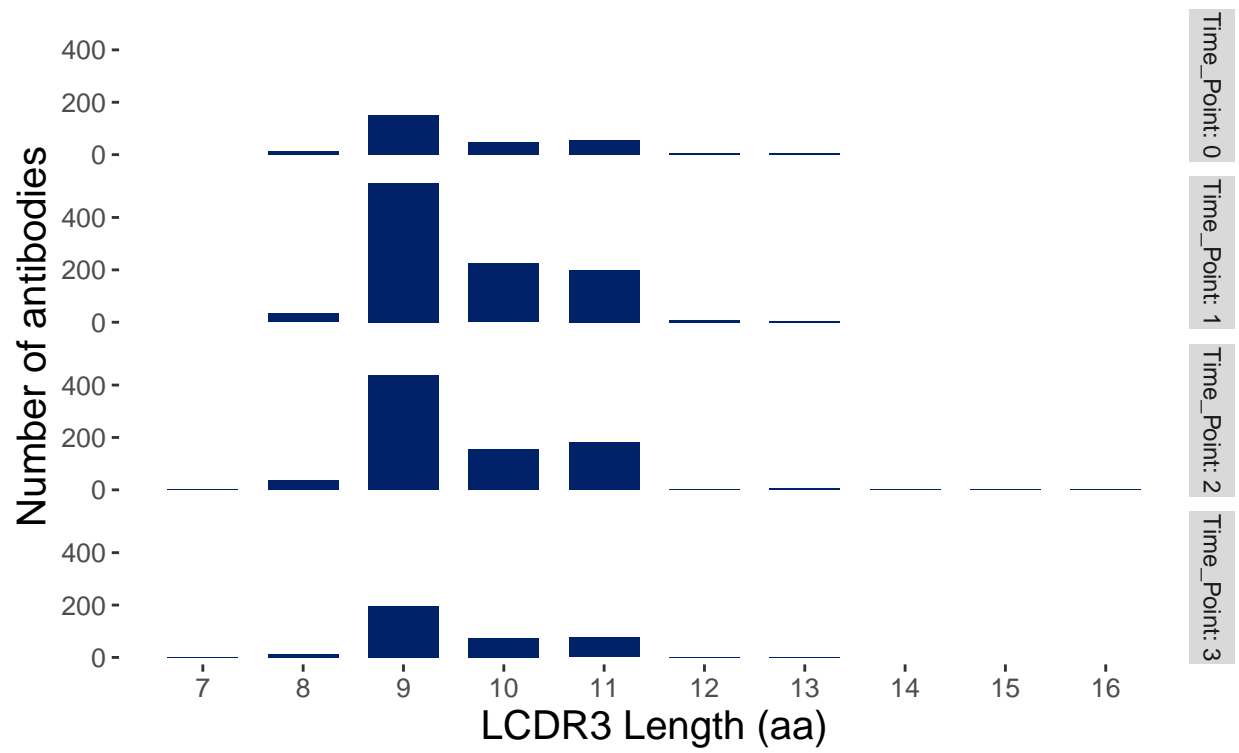


Figure 6: Histogram L_CDR3 by Time Point

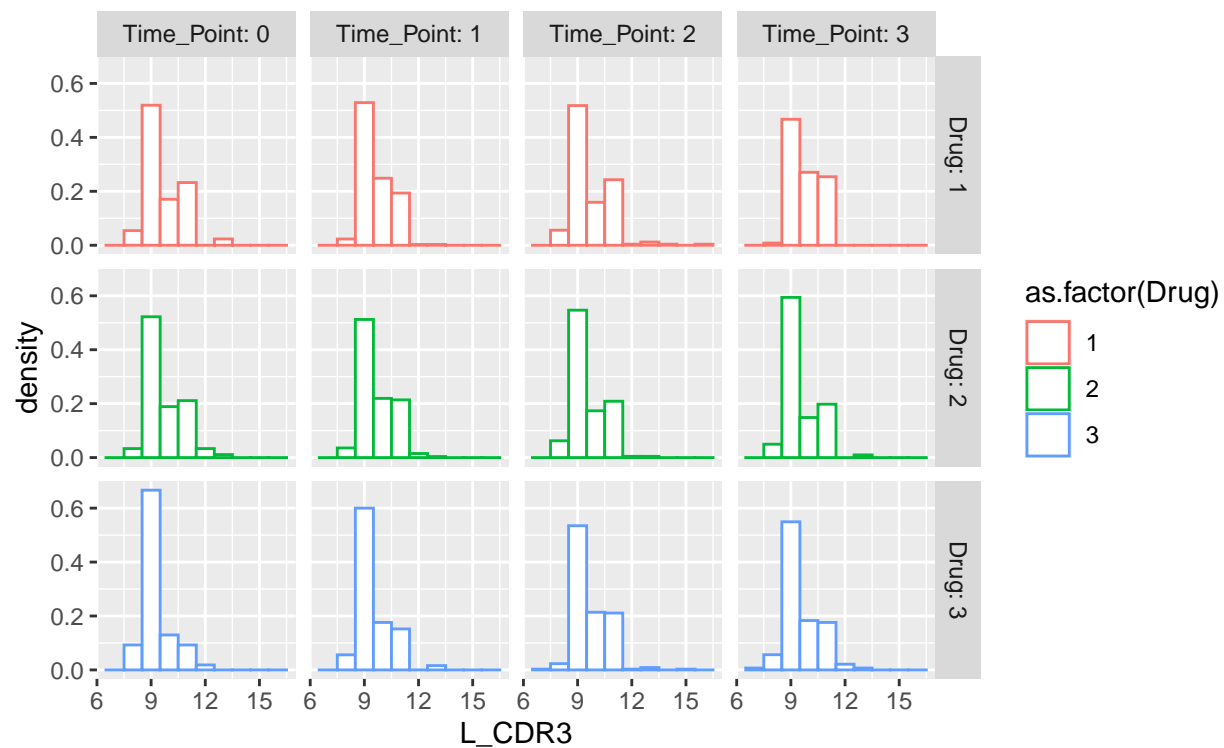


Figure 7: Histograms of L_CDR3 by Drug and Time Point

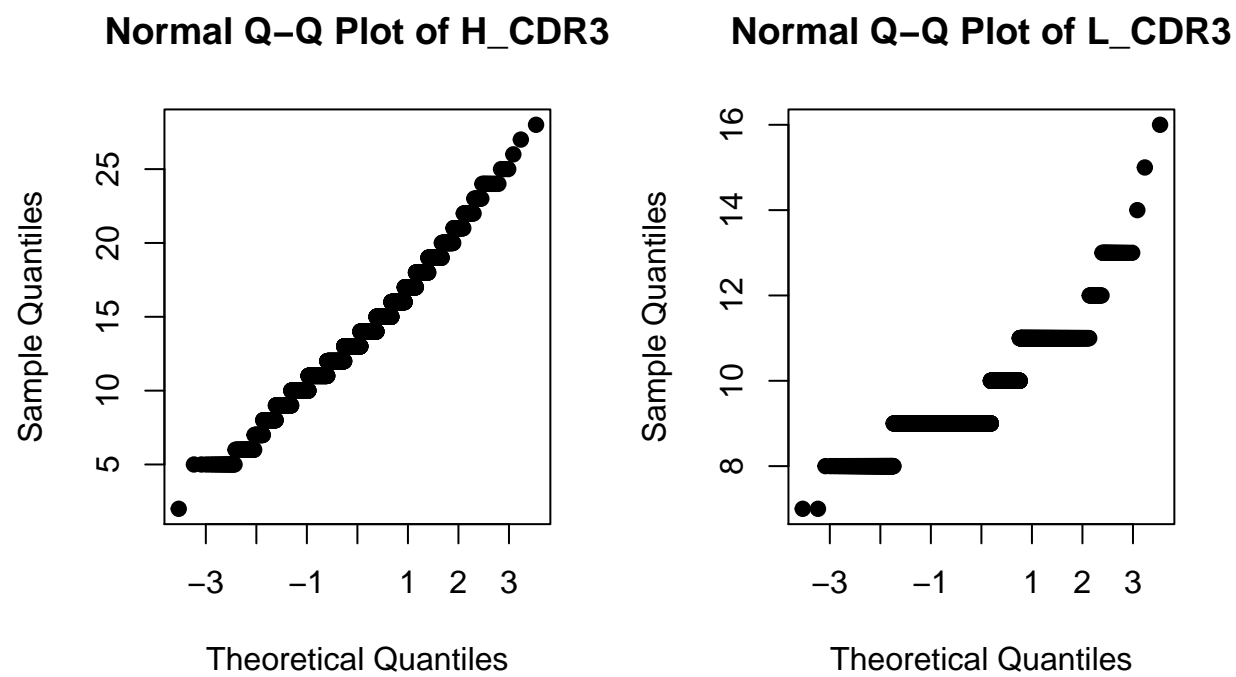


Figure 8: Q-Q Plots of H_CDR3 and L_CDR3

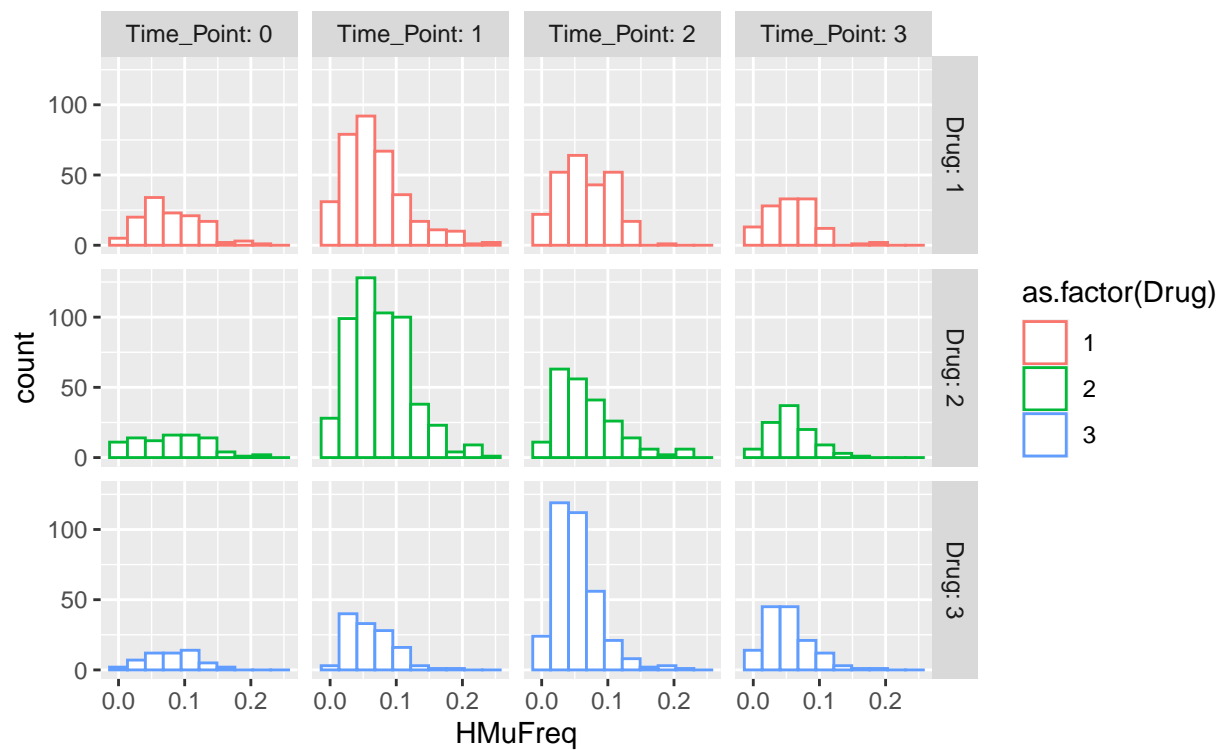


Figure 9: Histograms of HMuFreq by Drug and Time Point

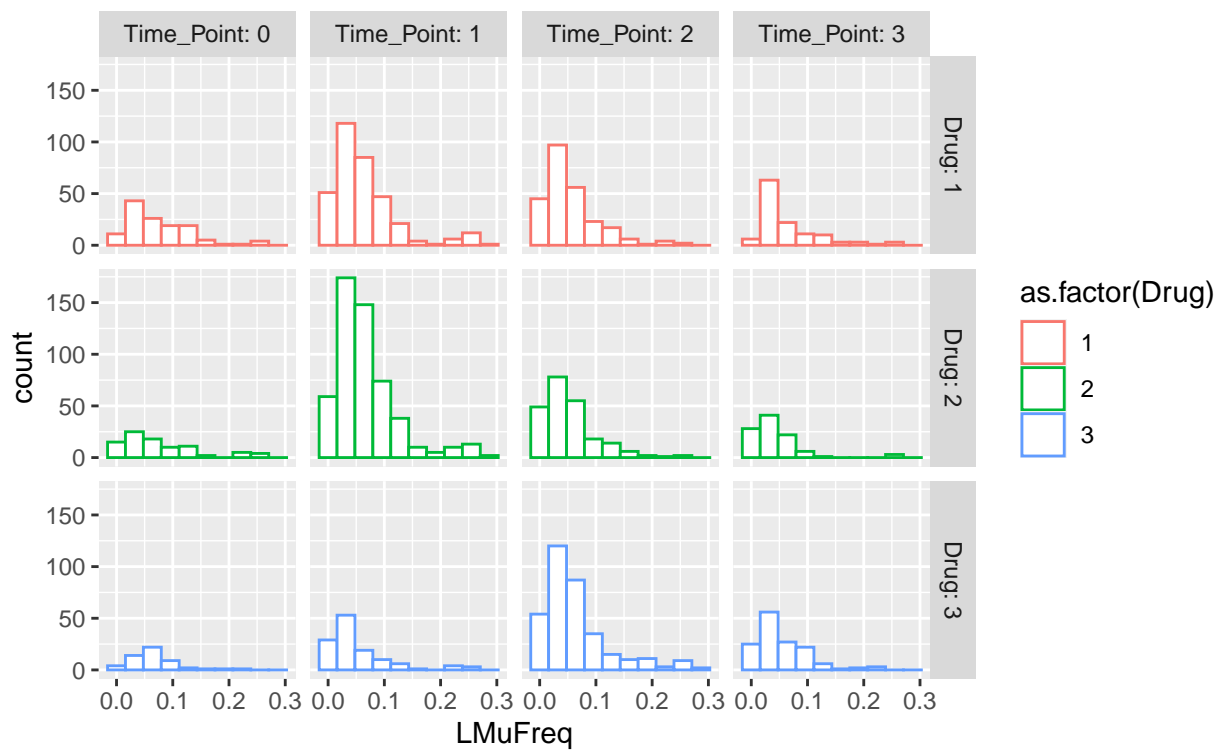


Figure 10: Histograms of LMuFreq by Drug and Time Point

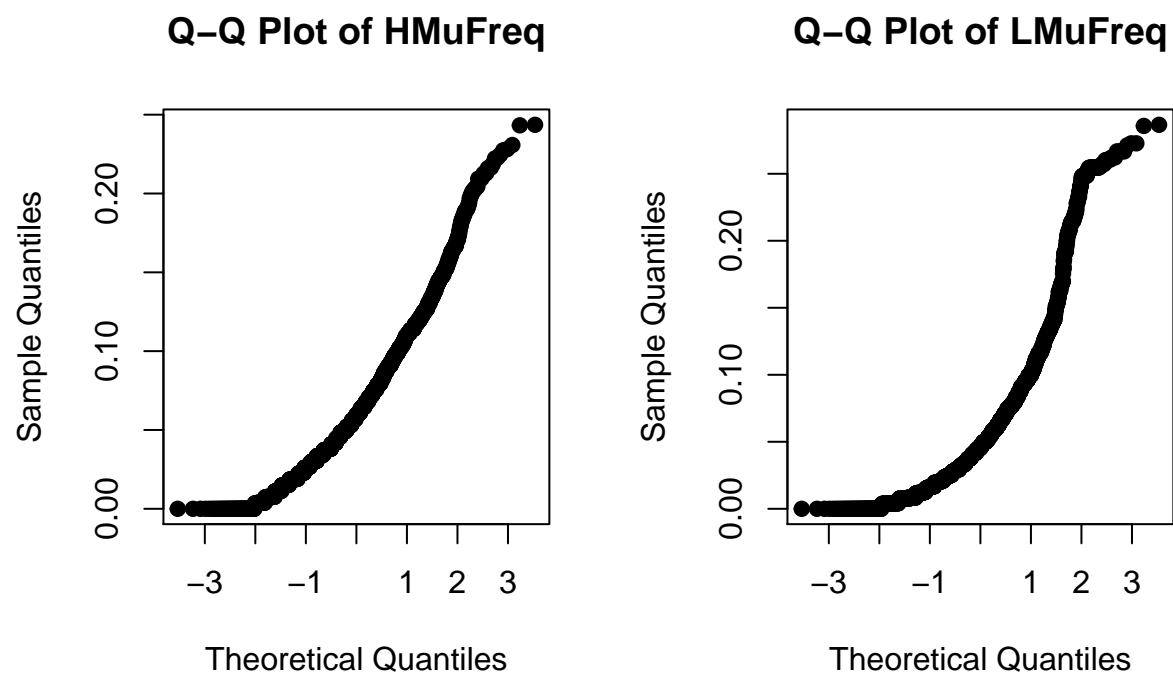


Figure 11: Q-Q Plot of HMuFreq and LMuFreq

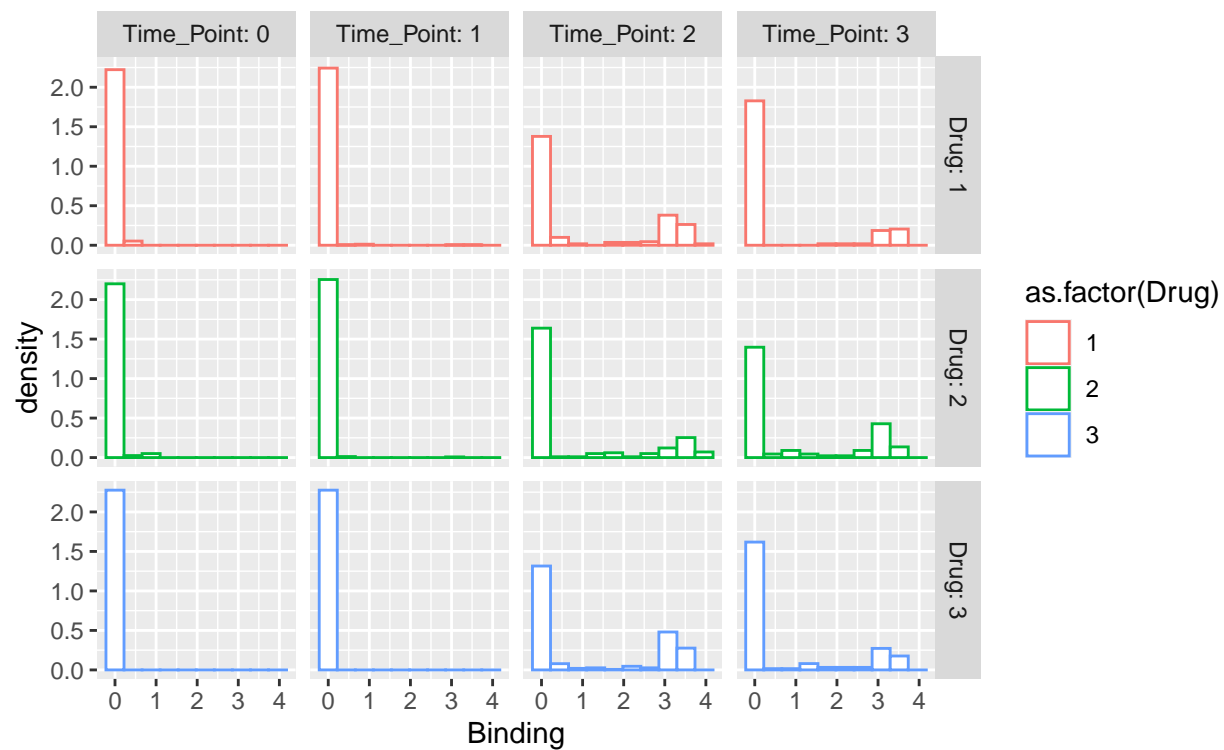


Figure 12: Histograms of Binding Strength by Drug and Time Point

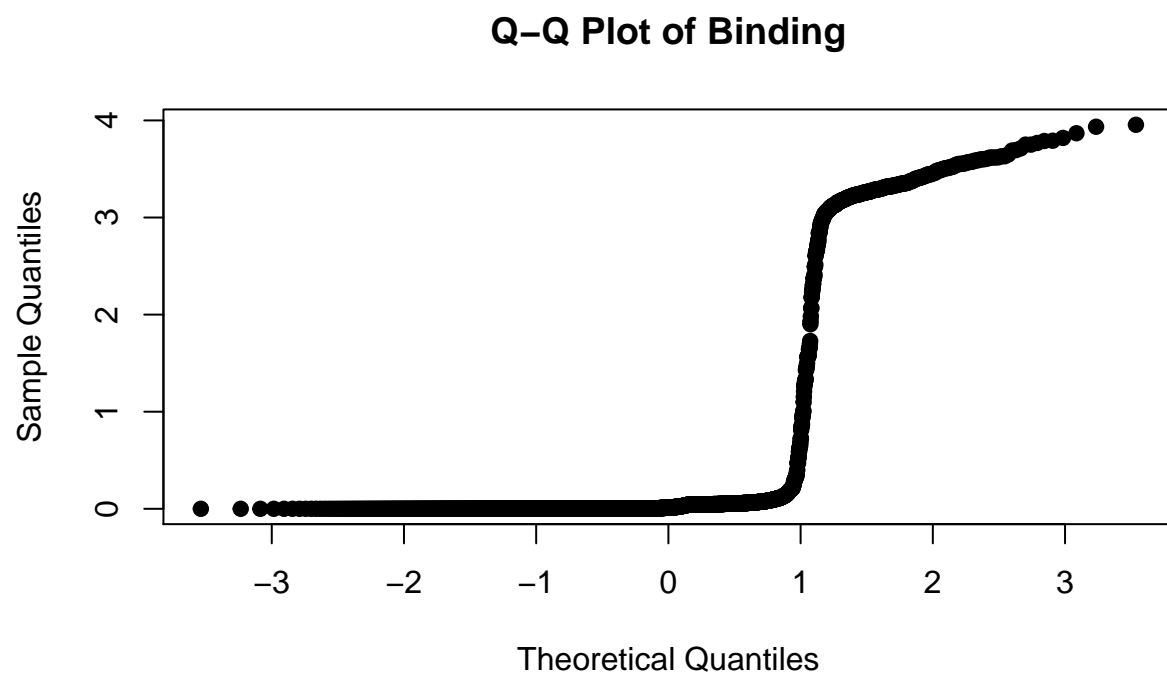


Figure 13: Q-Q Plot of Binding

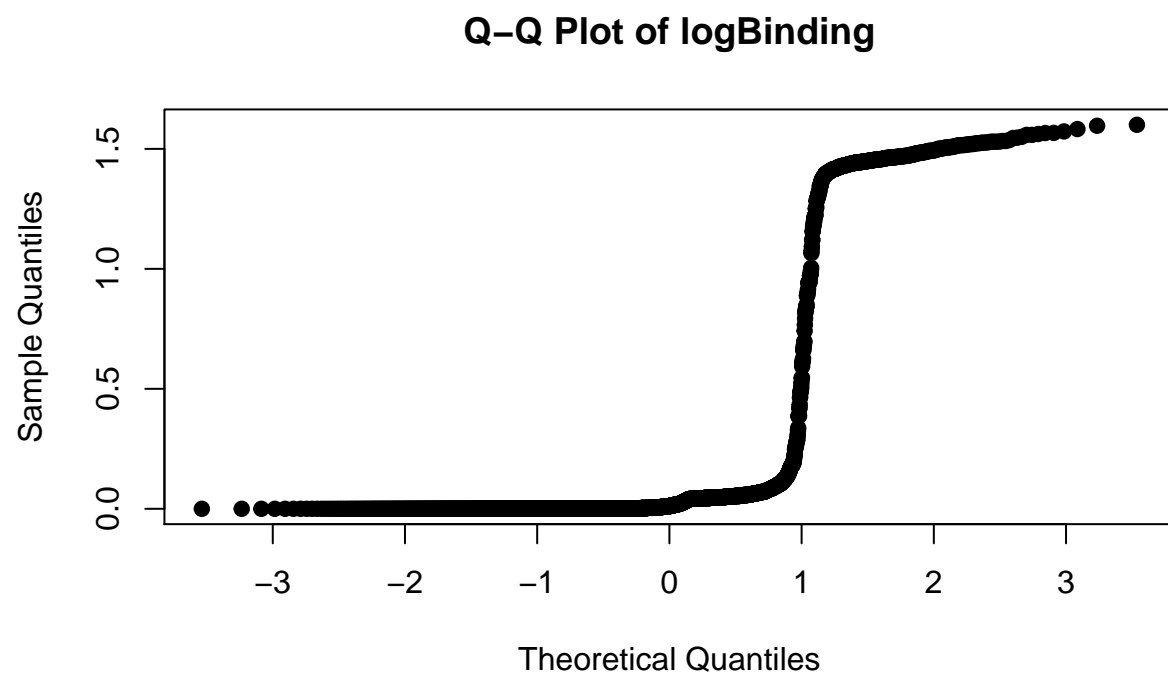


Figure 14: Q-Q plot of logBinding

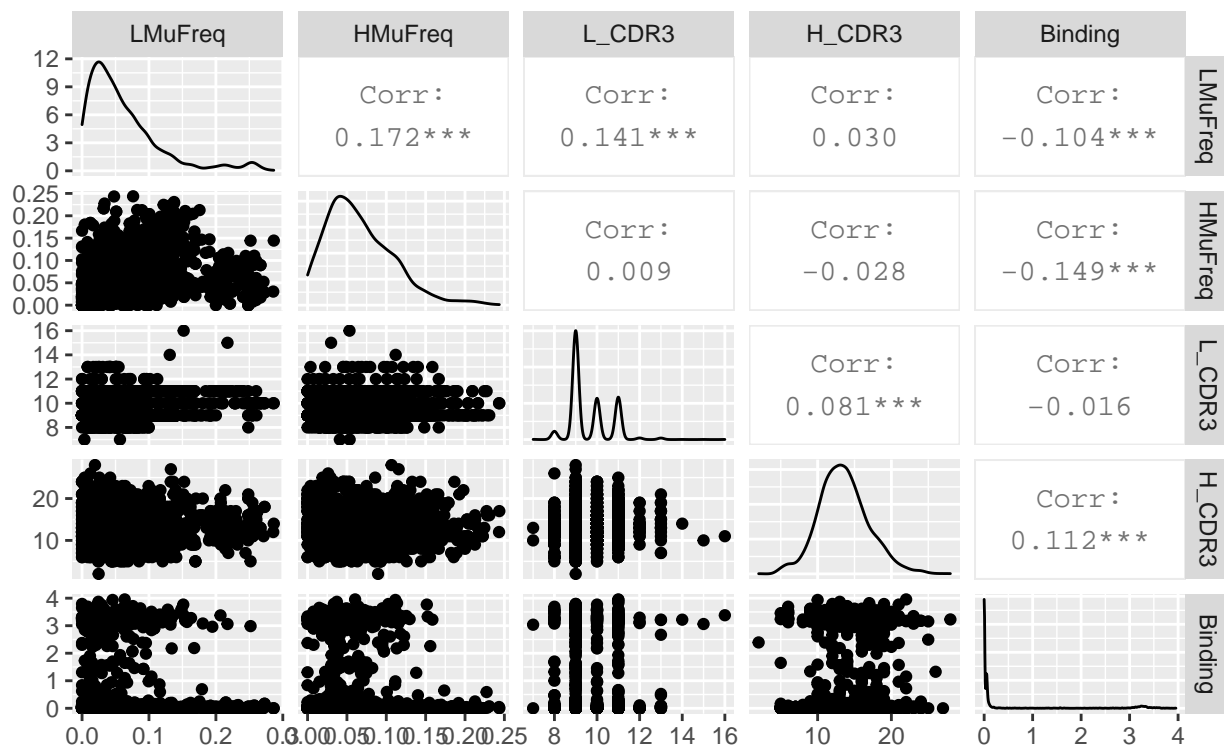


Figure 15: Scatterplot Matrix of Response Variables without Outlier

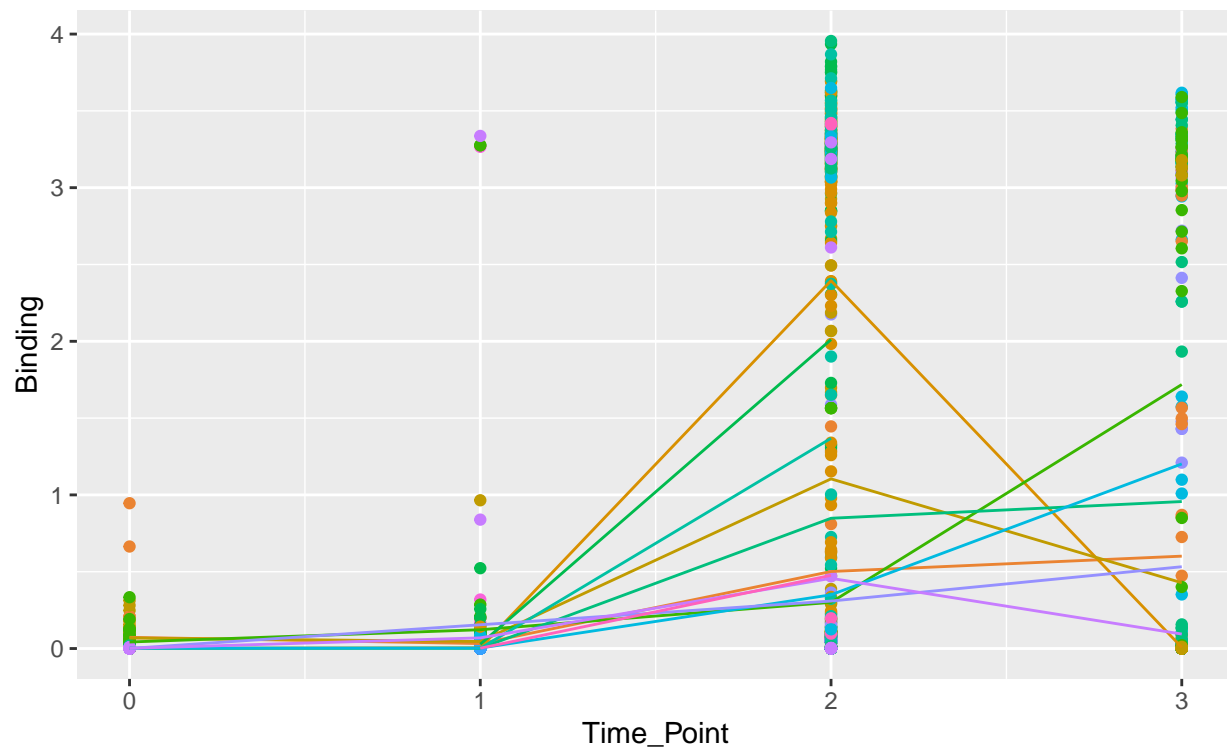


Figure 16: Mean Trends for Binding over Time by Macaque

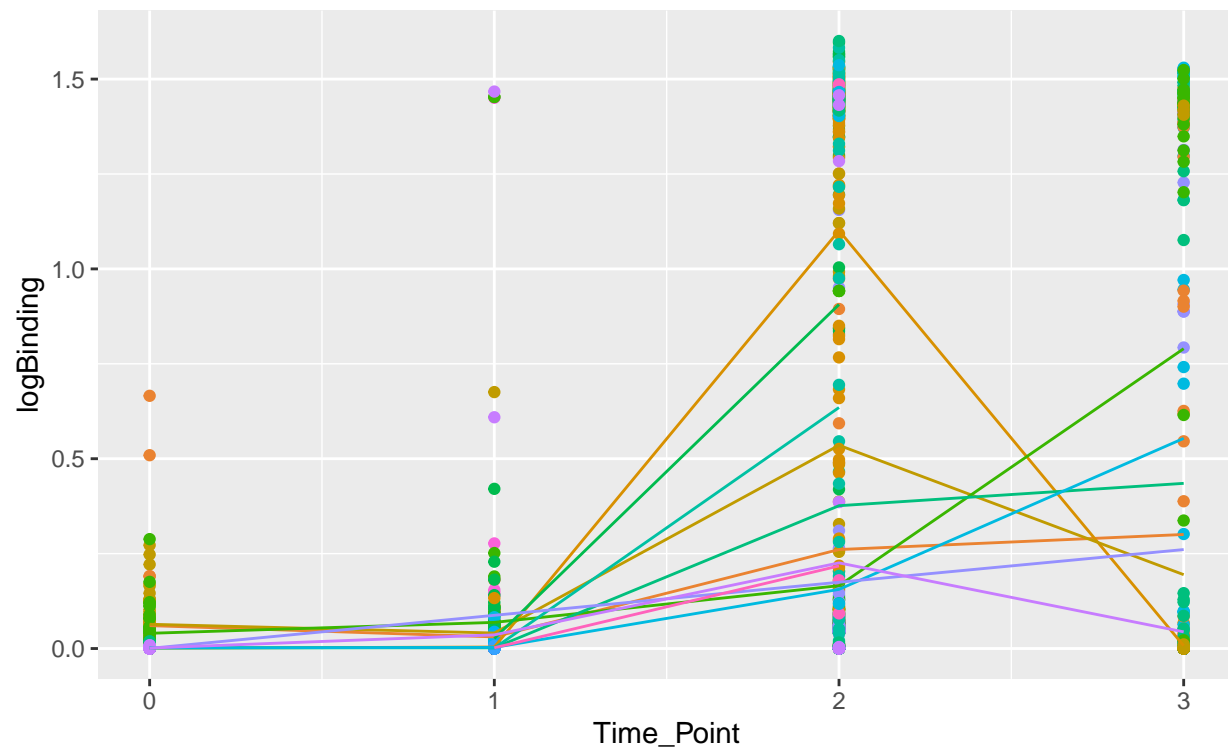


Figure 17: Mean Trends for logBinding over Time by Macaque

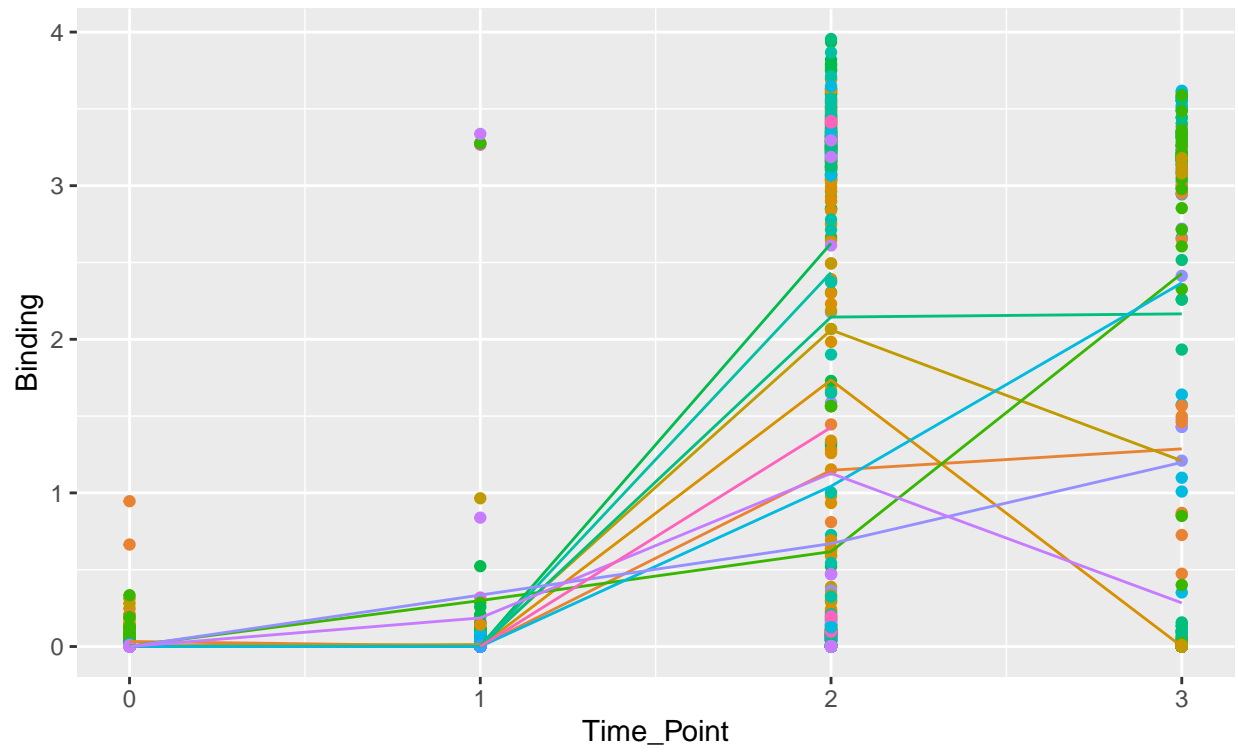


Figure 18: Variance Trends for Binding over Time by Macaque

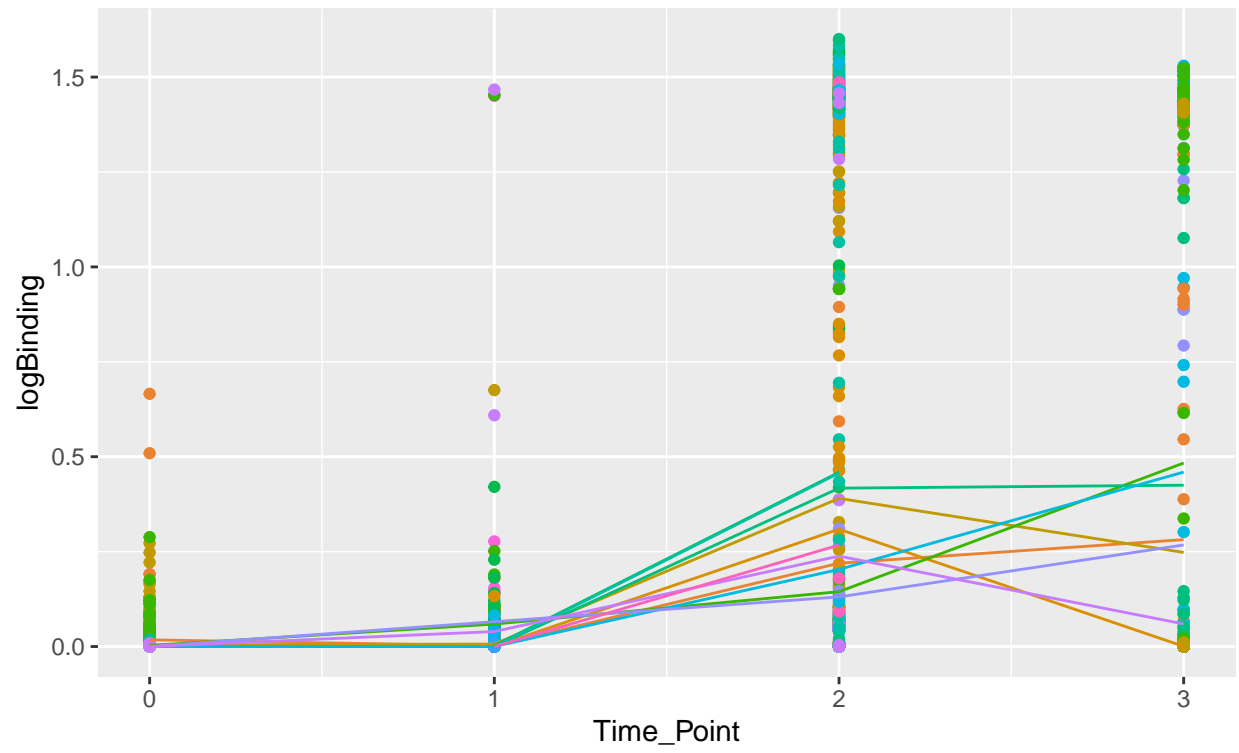


Figure 19: Variance Trends for logBinding over Time by Macaque

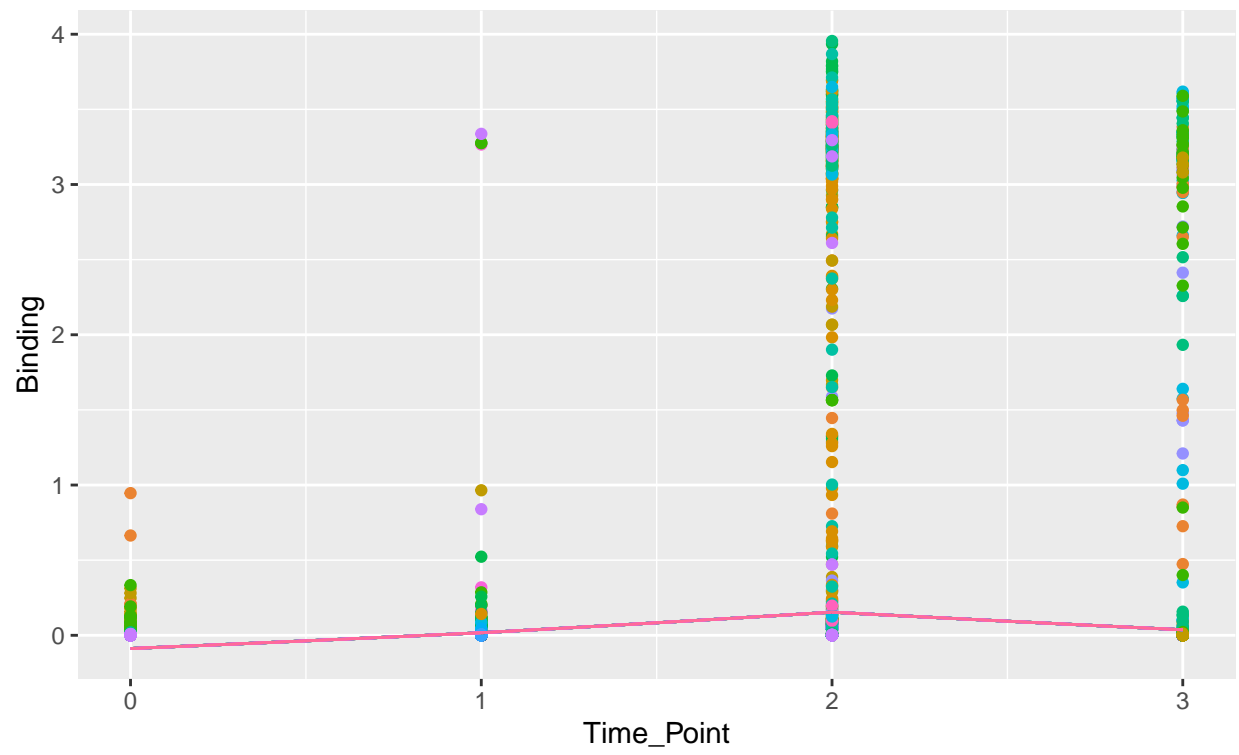


Figure 20: Piecewise Linear Function—Three Segments

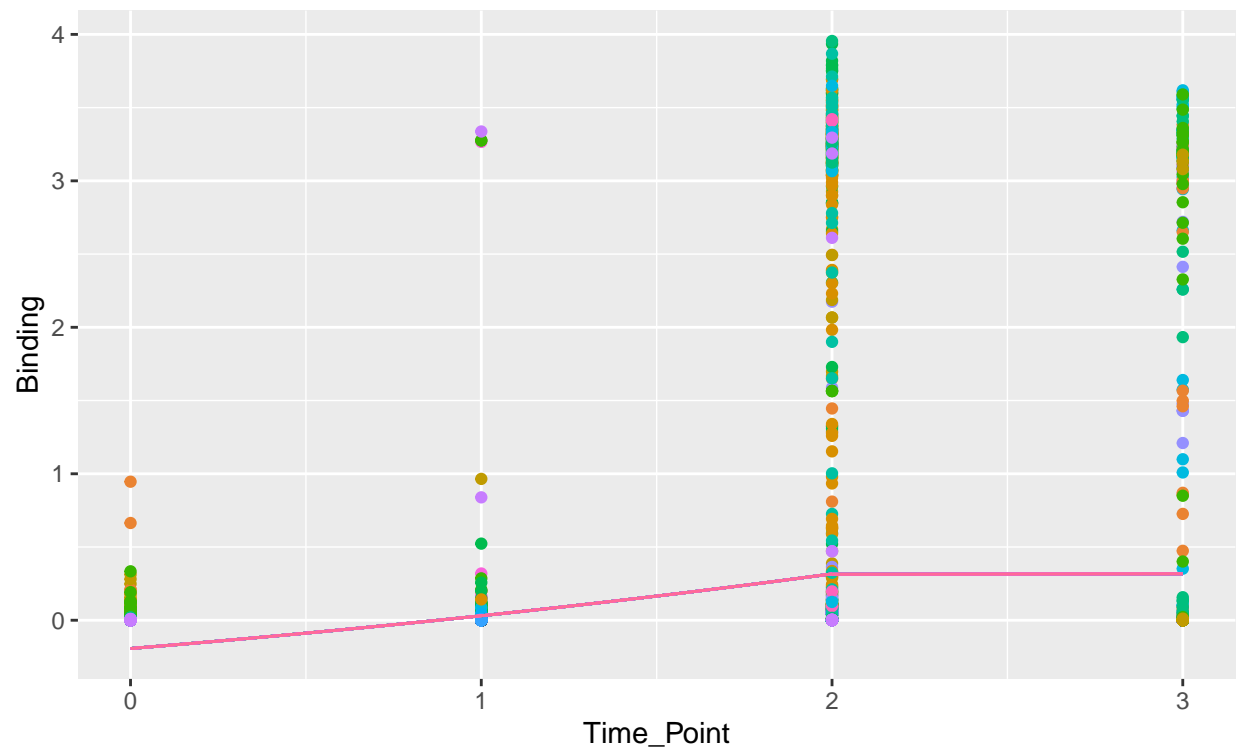


Figure 21: Piecewise Linear Function—Two Segments

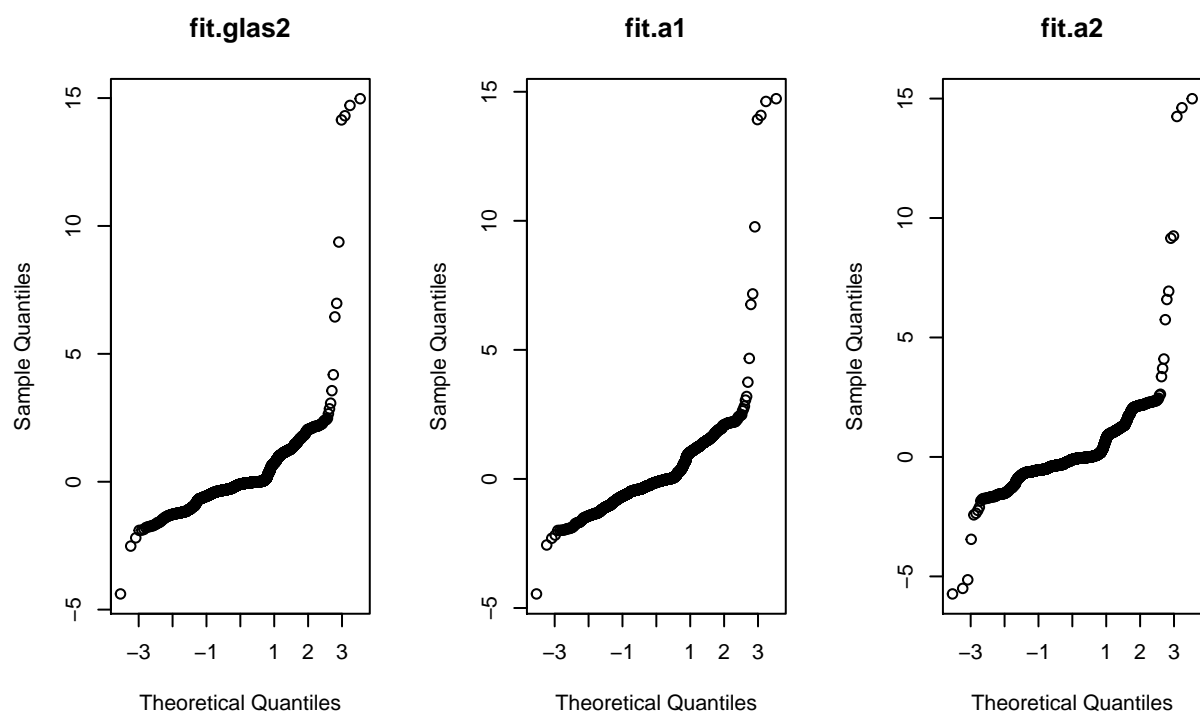


Figure 22: Q-Q Plots of Normalized Residuals

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Table 1: Frequency Table of Drug and Time Point

	0	1	2	3
1	129	346	251	122
2	90	533	225	101
3	54	125	347	142

Table 2: Summaries of Standardized LCDR3

Summaries
Min. :-2.1860
1st Qu.: -0.5361
Median :-0.5361
Mean : 0.0000
3rd Qu.: 0.2888
Max. :30.8110

Table 3: Significant Pairs by Time Point and Drug

	Time_Point	Drug
H_CDR3	$3 > 1, 3 > 2$	$1 > 2$
HMufreq	$0 > 2, 0 > 3, 1 > 2, 1 > 3$	$2 > 1 > 3$
L_CDR3	none	none
LMufreq	$0 > 2, 0 > 3, 1 > 3$	none

Table 4: AIC and BIC Comparison for Binding and logBinding

	df	AIC	df.1	BIC
fit.gls1	9	3293.6959	9	3345.9818
fit.gls2	9	-317.1771	9	-264.8913

Table 5: AIC and BIC Comparison between Two and Three Segments

	df	AIC	df.1	BIC
fit.gls2	9	-317.1771	9	-264.8913
fit.gls3	8	-310.8418	8	-264.3654

Table 6: AIC and BIC Comparison among GLS and LME Models

	df	AIC	df.1	BIC
fit.gls2	9	-317.1771	9	-264.8913
fit.a1	12	-407.9577	12	-338.2432
fit.a2	12	-591.4157	12	-521.7012

Table 7: Inference about S1, S2, and S3 Slopes

numDF	denDF	F.value	p.value
1	2441	58.83591	0
1	2441	137.96033	0
1	2441	56.69165	0

Table 8: AIC and BIC Comparison among GLS and LME Models with Time Point and Drug

	df	AIC	df.1	BIC
fit.gls2	9	-317.1771	9	-264.8913
fit.a1	12	-407.9577	12	-338.2432
fit.a2	12	-591.4157	12	-521.7012
fit.a3	20	-599.1739	20	-482.9831

Table 9: H_0 : drug 1 = drug 2

Fstat	p_value
2.483881	0.0418059

Table 10: H_0 : drug 1 = drug 3

Fstat	p_value
2.111719	0.0768574

Table 11: H_0 : drug 2 = drug 3

Fstat	p_value
5.251142	0.0003279

Table 12: Variance-covariance Matrices Comparison of Drug 2 and 3

	H_CDR3	HMufreq	L_CDR3	LMufreq
H_CDR3	0.8233467	0.0940387	1.7311285	-8.1369695
HMufreq	0.0940387	1.6459865	-1.2232736	26.2072877
L_CDR3	1.7311285	-1.2232736	0.9656927	0.7827240
LMufreq	-8.1369695	26.2072877	0.7827240	0.9973451