

Project 2

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```

1 library(mlmRev)                ## LOADING OF THE NECESSARY PACKAGES ##
2 library(tidyverse)
3 library(MASS)
4 library(lme4)
5 library(ggplot2)
6 library(performance)
7 library(DHARMA)
8 library(dotwhisker)
9 library(coefplot)
10 library(bbmle)
11 library(brglm2)
12 library(brms)
13 library(arm)
14 library(lmtest)
15 library(boot)
16 library(effects)
17 library(sjPlot)
18 library(AER)
19 library(pscl)
20 library(patchwork)

```

Question 1: Analysis of Contraception Data from the Package `mlmRev`

Loading the Contraception data and creating a new column called “use_num”. Essentially, the new column is the column use a binary as factor

```

1 # Load data
2 data("Contraception", package = "mlmRev")
3
4 # Creation of a new column called "u"
5 Contraception <- transform(
6   Contraception,
7   use_num = as.numeric(use)-1
8 )
9 head(Contraception,10)

```

	woman	district	use	livch	age	urban	use_num
1	1	1	N	3+	18.4400	Y	0
2	2	1	N	0	-5.5599	Y	0

3	3	1	N	2	1.4400	Y	0
4	4	1	N	3+	8.4400	Y	0
5	5	1	N	0	-13.5590	Y	0
6	6	1	N	0	-11.5600	Y	0
7	7	1	N	3+	18.4400	Y	0
8	8	1	N	3+	-3.5599	Y	0
9	9	1	N	1	-5.5599	Y	0
10	10	1	N	3+	1.4400	Y	0

1 `##?mlmRev::Contraception ## Data Description`

a. Data Analysis Description

This dataset originates from the 1988 Bangladesh Fertility Survey and includes a sub-sample of 1,934 women distributed across 60 districts.

According to Harrell's guidelines [Harrell], the optimal number of predictor variables in a logistic regression model should not exceed $\frac{m}{15}$, where m represents the limiting sample size, defined as $m = \text{nrow}(\text{Contraception})$. Given the current sample size, this criterion allows for the inclusion of the full number of predictor variables in the model.

Furthermore, it is essential to establish a threshold for assessing the significance of predictor variables. In this analysis, a threshold of 5% for the variable age and 10% for the other predictors will be employed. Specifically, if a unit change in any predictor variable results a change greater than 5% or 10%, respectively in the response variable, this effect will be considered statistically significant. (I decided to use different thresholds in every predictor because the units are different and my sense telling me that it is not the same one year of change and an additional kid for example)

My approach involves a basic logistic regression model, which utilizes the binomial family and a logit link function. This model is appropriate given the binary nature of the response variable, `use_num`, where a value of 1 indicates the use of contraception and 0 indicates non-use.

Predictors:

1. Centered Age of Women (age):

The first predictor is the centered age of women. Based on intuitive reasoning, it is hypothesized that the relationship between women's age and contraception use resembles an inverted U-shape. This suggests that both younger and older women are likely to use contraception less frequently than middle-aged women, making age a relevant predictor in the model.

2. Number of Living Children (livch):

The second predictor is the number of living children. It is posited that as individuals find a permanent partner, they tend to use contraception less frequently. Therefore, the presence of children is expected to correlate with contraception usage, making this a reasonable predictor to include in the model.

3. Type of Residence (urban):

The third and final predictor is the type of residence, categorized as urban or rural. Contraception use is strongly correlated with various socio-economic factors. For instance, urban areas that are wealthier tend to have higher levels of education. It is generally observed that individuals with higher educational attainment are more likely to use contraception. Thus, the type of residence is anticipated to be a significant predictor of contraception use.

I decide not to include the district at the first model because I can save a lot of degrees of freedom by using only the type of residence. However, I may lose some important information and eventually, the model's fit is not good enough

If the first model is inadequate to fit the dataset properly, a second approach would possibly involve a two-level main effect logistic regression model by including a random intercept for each district. This model will capture the variability at the district level, providing more accurate estimates if there are significant differences in contraceptive use between districts. It is widely known that it is especially useful for hierarchical data structures. The model will utilize the binomial family and a logit link function (I am gonna use this model if the overall fit of the first one is not good).

b. Data Visualization

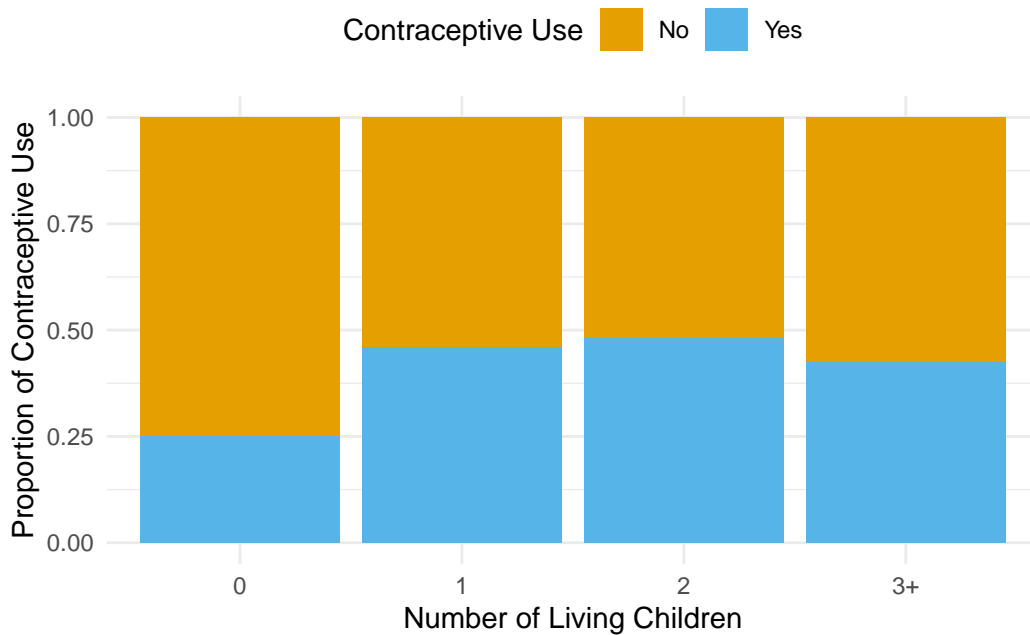
The visualizations include bar plots and histograms that elucidate the relationships between contraceptive use, number of living children, urban or rural residence, district, and the age of women.

```
1 # Function to create bar plots for contraceptive use by a given categorical variable
2 create_bar_plot <- function(data, x_var, x_label) {
3   ggplot(data, aes(x = .data[[x_var]], fill = factor(use_num))) +
4     geom_bar(position = "fill") +
5     labs(x = x_label,
6          y = "Proportion of Contraceptive Use",
7          fill = "Contraceptive Use") +
8     theme_minimal() +
9     scale_fill_manual(values = c("0" = "#E69F00", "1" = "#56B4E9"),
10                      labels = c("No", "Yes")) +
11     theme(legend.position = "top")
```

```

12 }
13
14 ## CONTRACEPTION VS LIVING CHILDREN BAR PLOT
15 create_bar_plot(Contraception, "livch", "Number of Living Children")

```



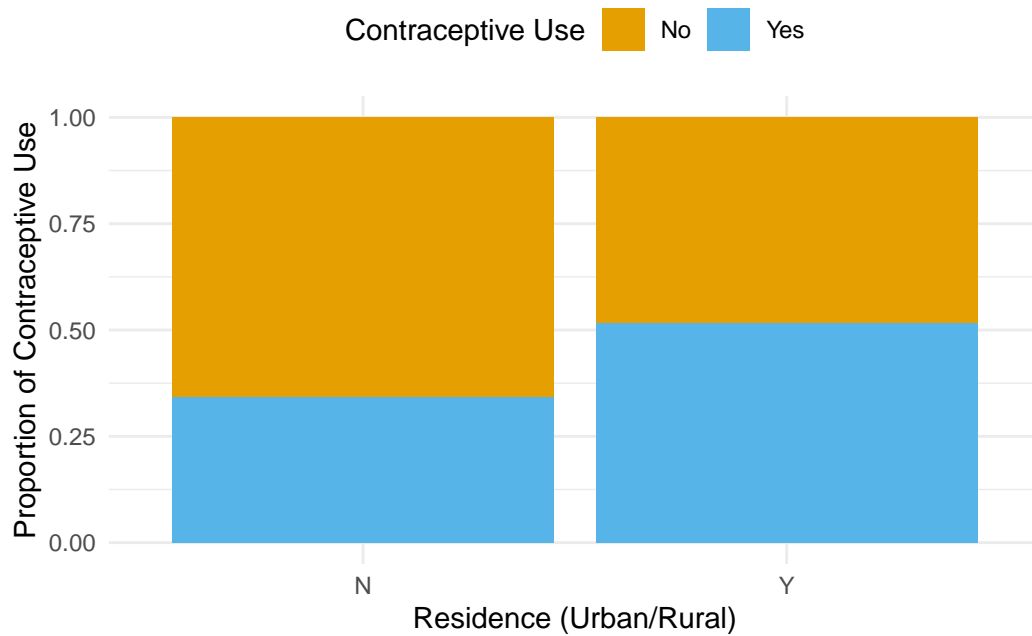
i) Proportion of Contraceptive Use by Number of Living Children

The bar plot depicting the proportion of contraceptive use by the number of living children reveals a clear trend. As the number of living children increases, there is a noticeable variation in the proportion of women using contraception. Specifically, women with fewer children are less likely to use contraception compared to those with more children. This suggests that family size may influence contraceptive decisions, indicating a potential focus area for family planning programs.

```

1 ## CONTRACEPTION VS URBAN BAR PLOT
2 create_bar_plot(Contraception, "urban", "Residence (Urban/Rural)")

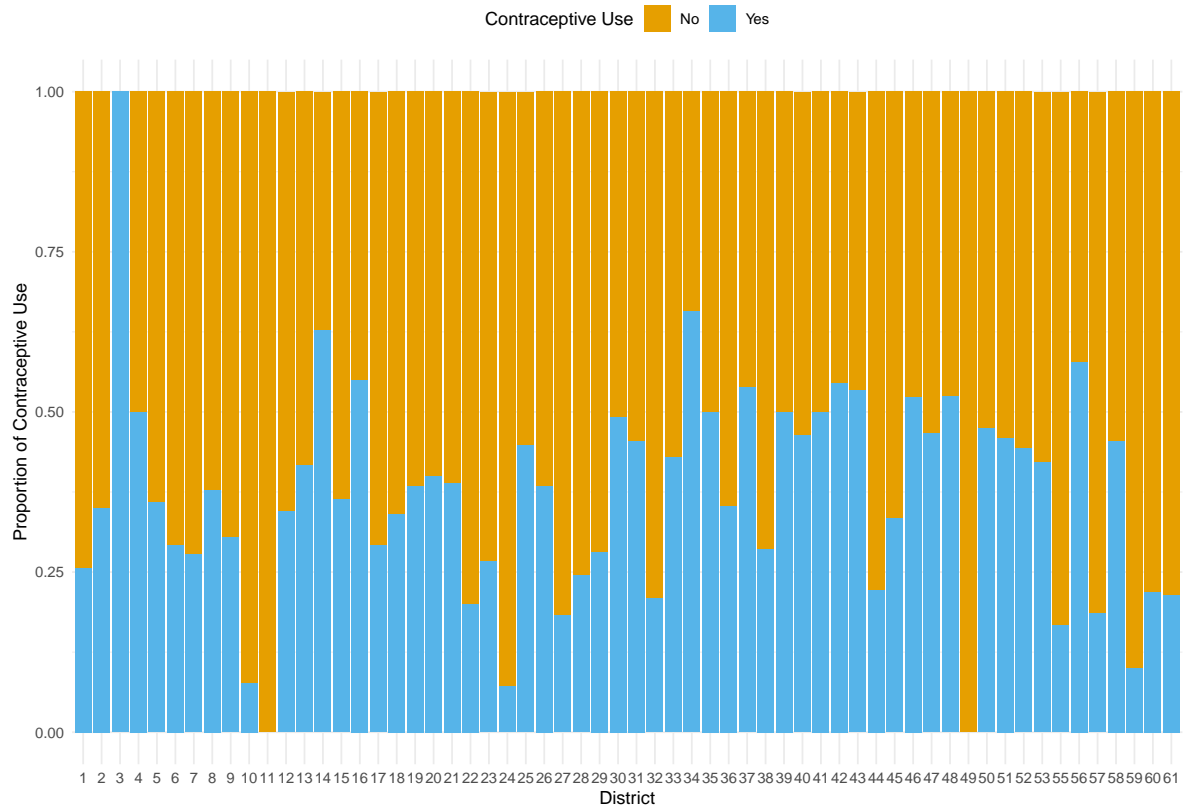
```



ii) Proportion of Contraceptive Use by Urban or Rural Residence

The second bar plot compares contraceptive use between women residing in urban and rural areas. The results show that women living in urban areas have a higher proportion of contraceptive use compared to their rural counterparts.

```
1 ## CONTRACEPTION VS DISTRICT BAR PLOT
2 create_bar_plot(Contraception, "district", "District")
```



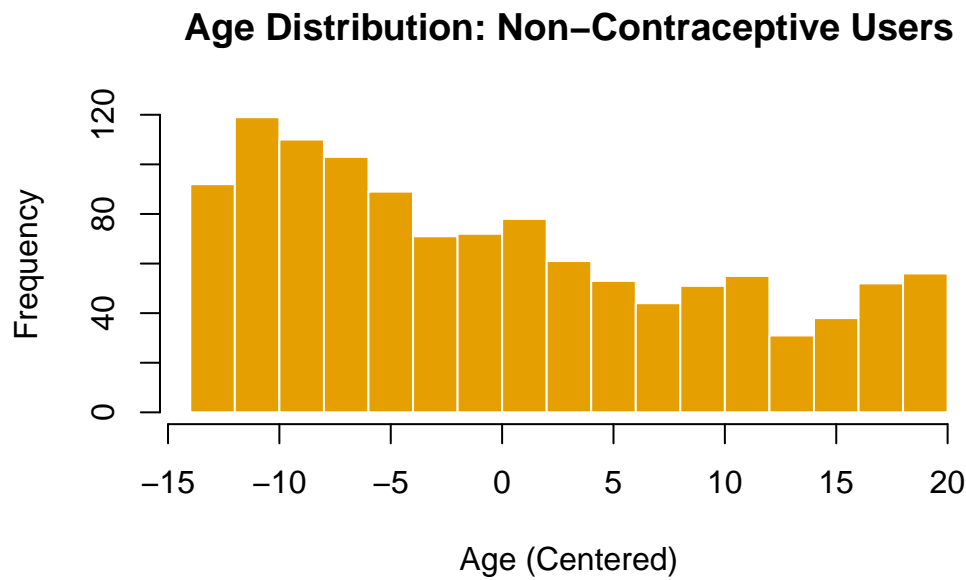
iii) Proportion of Contraceptive Use by District

The bar plot by district illustrates the variations in contraceptive use across different geographical regions. Each district exhibits unique patterns in contraceptive use, indicating that local policies, health services, and cultural factors may significantly influence these behaviors.

```

1 # Function to create histograms for age distribution
2 create_histogram <- function(data, use_num, color, title) {
3   hist(data$age[data$use_num == use_num],
4         xlab = "Age (Centered)",
5         ylab = "Frequency",
6         main = title,
7         col = color,
8         border = "white")
9 }
10
11 # Create histograms for age distribution and Non-Contraceptive Users
12 create_histogram(Contraception, 0, "#E69F00", "Age Distribution: Non-Contraceptive Users")

```

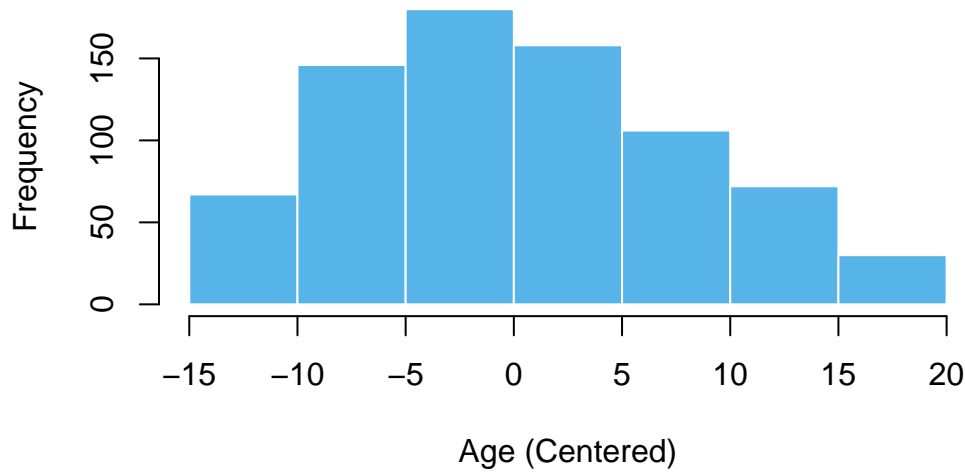


iv) Age Distribution of Non-Contraceptive Users

The histogram showing the age distribution of women who do not use contraception indicates a concentration of non-users in younger age groups. This suggests that younger women may either have limited knowledge about contraceptive options or may not yet feel the need for contraception. Addressing knowledge gaps.

```
1 # Create histograms for age distribution for Contraceptive Users
2 create_histogram(Contraception, 1, "#56B4E9", "Age Distribution: Contraceptive Users")
```


Age Distribution: Contraceptive Users

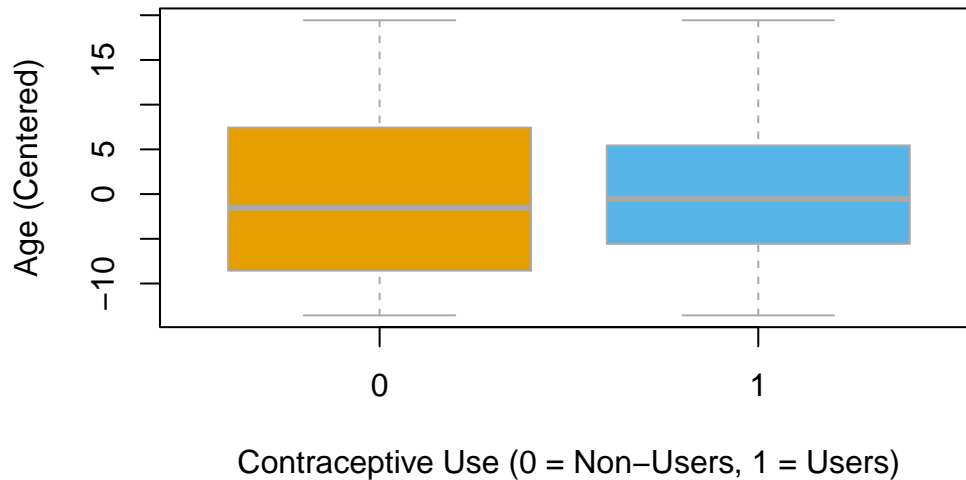


v) Age Distribution of Contraceptive Users

This histogram showcases the age distribution for women who do use contraception, similar to the previous plot but focused on users. As we had anticipated the distribution appears to be more evenly spread across age groups, with a notable presence of users in the middle and older age groups.

```
1 create_box_plot <- function(data) {  
2   boxplot(age ~ use_num,  
3           data = data,  
4           xlab = "Contraceptive Use (0 = Non-Users, 1 = Users)",  
5           ylab = "Age (Centered)",  
6           main = "Age Distribution by Contraceptive Use",  
7           col = c("#E69F00", "#56B4E9"),  
8           border = "darkgray")  
9 }  
10  
11 # Create the box plot for age distribution  
12 create_box_plot(Contraception)
```

Age Distribution by Contraceptive Use



c. Model Fit

```
1 # Fit the logistic regression model
2 model <- glm(use_num ~ age + livch + urban,
3               data = Contraception,
4               family = binomial(link = "logit"))
5
6 summary(model)
```

Call:

```
glm(formula = use_num ~ age + livch + urban, family = binomial(link = "logit"),
    data = Contraception)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-1.568044	0.126229	-12.422	< 2e-16	***
age	-0.023995	0.007536	-3.184	0.00145	**
livch1	1.059186	0.151954	6.970	3.16e-12	***
livch2	1.287805	0.167241	7.700	1.36e-14	***
livch3+	1.216385	0.170593	7.130	1.00e-12	***

```
urbanY      0.797181    0.105186    7.579 3.49e-14 ***
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 2590.9  on 1933  degrees of freedom
Residual deviance: 2456.7  on 1928  degrees of freedom
AIC: 2468.7
```

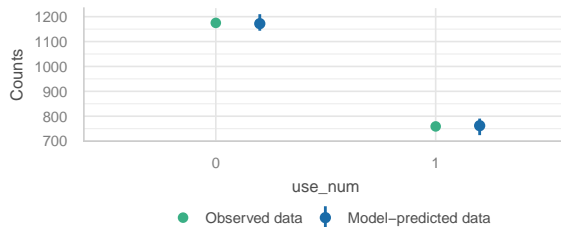
Number of Fisher Scoring iterations: 4

d. Comparison of the Diagnostic Plots

```
1 performance::check_model(model, panel = TRUE)
```

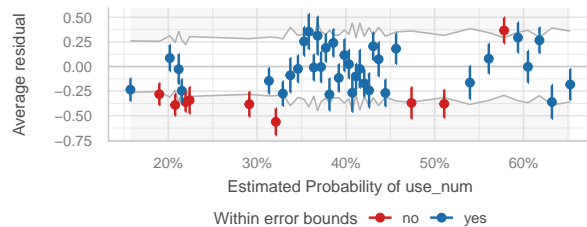
Posterior Predictive Check

Model-predicted intervals should include observed data points



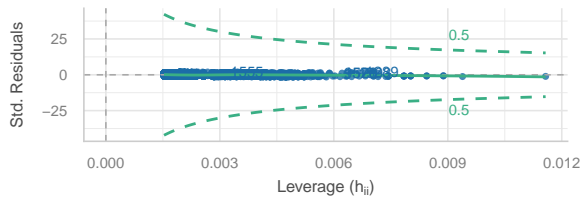
Binned Residuals

Points should be within error bounds



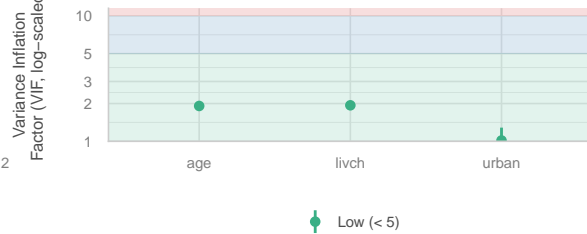
Influential Observations

Points should be inside the contour lines



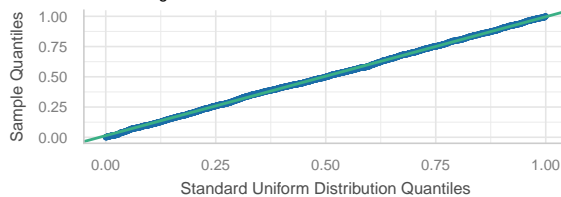
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



Distribution of Quantile Residuals

Dots should fall along the line



i) Posterior Predictive Check:

The observed and model-predicted intervals seem close, suggesting a reasonable fit.

ii) Binned Residuals:

The plot shows the model's errors across the probability range, and most residuals fall within the bounds, meaning no strong deviations, but a few points (in red) indicate areas with potential under- or over-prediction. Looking at the graph, there is possibility for overfitting but not something terrible. A good practice to detect data overfitting is by applying Cross-Validation, Bootstrap Resampling etc.

Below I am going test if there is an overfitting problem to my model by using a Bootstrap Resampling algorithm. This will give us a distribution of model coefficients across different resampled datasets, showing how much they vary.

```
1 set.seed(123)
2 boot_fit <- boot(data=Contraception, statistic=function(data, indices) {
3   d <- data[indices, ]
4   fit <- glm(use_num ~ age + livch + urban, data=d, family=binomial(link="logit"))
5   return(coef(fit))
6 }, R=1000)
7 boot_fit
```

ORDINARY NONPARAMETRIC BOOTSTRAP

Call:

```
boot(data = Contraception, statistic = function(data, indices) {
  d <- data[indices, ]
  fit <- glm(use_num ~ age + livch + urban, data = d, family = binomial(link = "logit"))
  return(coef(fit))
}, R = 1000)
```

Bootstrap Statistics :

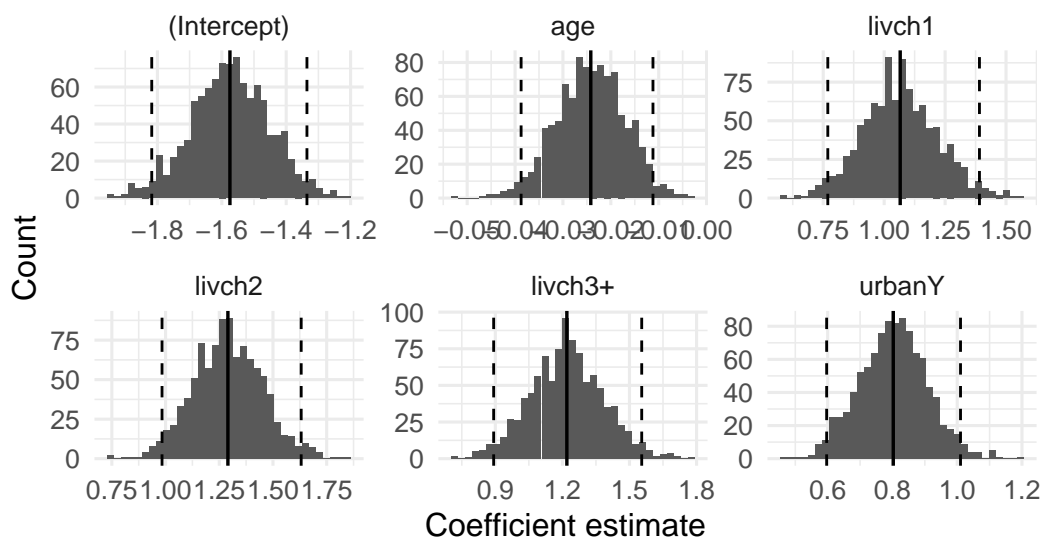
	original	bias	std. error
t1*	-1.56804374	-0.0067118991	0.123053057
t2*	-0.02399512	-0.0001941084	0.007193948
t3*	1.05918582	0.0065718308	0.155691426
t4*	1.28780501	0.0024604551	0.162848757

```
t5* 1.21638466 0.0035732271 0.165559373
t6* 0.79718138 0.0052819863 0.105728152
```

```
1 boot_df <- as.data.frame(boot_fit$t)
2 names(boot_df) <- names(boot_fit$t0)
3
4 boot_long <- boot_df %>%
5   pivot_longer(everything(), names_to = "term", values_to = "beta")
6
7 ci_df <- boot_long %>%
8   group_by(term) %>%
9   summarise(
10     mean = mean(beta),
11     lo = quantile(beta, 0.025),
12     hi = quantile(beta, 0.975),
13     .groups = "drop"
14   )
15
16 ggplot(boot_long, aes(x = beta)) +
17   geom_histogram(bins = 35) +
18   facet_wrap(~ term, scales = "free", ncol = 3) +
19   geom_vline(data = ci_df, aes(xintercept = mean), linewidth = 0.6) +
20   geom_vline(data = ci_df, aes(xintercept = lo), linetype = "dashed", linewidth = 0.5) +
21   geom_vline(data = ci_df, aes(xintercept = hi), linetype = "dashed", linewidth = 0.5) +
22   labs(
23     title = "Bootstrap distributions of coefficient estimates",
24     subtitle = "Solid = mean; dashed = 95% percentile interval (R = 1000)",
25     x = "Coefficient estimate",
26     y = "Count"
27   ) +
28   theme_minimal(base_size = 12) +
29   theme(
30     plot.title = element_text(face = "bold", hjust = 0.5),
31     plot.subtitle = element_text(hjust = 0.5)
32   )
```

Bootstrap distributions of coefficient estimates

Solid = mean; dashed = 95% percentile interval (R = 1000)



- The **bias** for all coefficients is relatively small, which is a good sign that the bootstrap estimates closely match the original estimates.
- The **standard errors** are also within reasonable ranges, indicating that the coefficients are relatively stable across the bootstrapped samples. However, **livch** and **urban** coefficients have somewhat higher variability compared to **age**.

This result suggests that the model is **not overfitting**, as the coefficients appear stable with small bias and reasonable variability. I run that bootstrap algorithm in order to support the robustness of my model.

iii) Influential Observations:

This plot identifies points with high leverage (potentially influential points) based on the distance of their leverage (horizontal axis) and standardized residuals (vertical axis).

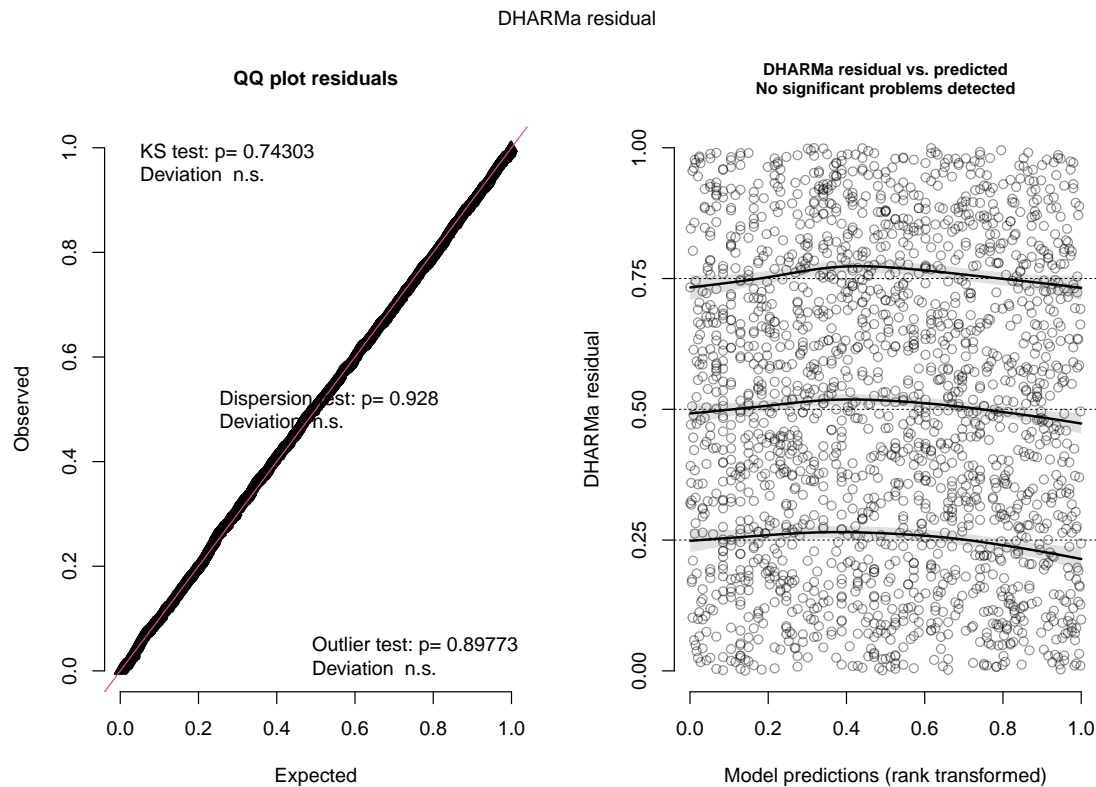
iv) Collinearity:

All predictors have a VIF below 5, which suggests no problematic collinearity that might affect model stability.

```

1 simulated_residuals <- simulateResiduals(
2   fittedModel = model
3 )
4
5 plot(simulated_residuals)

```



i) QQ Plot of Residuals:

Since the residuals fall almost perfectly along the line, this indicates that they are well-behaved and likely normally distributed. The Kolmogorov-Smirnov (KS) test shows no significant deviation from expectations ($p\text{-values} > 0.05$).

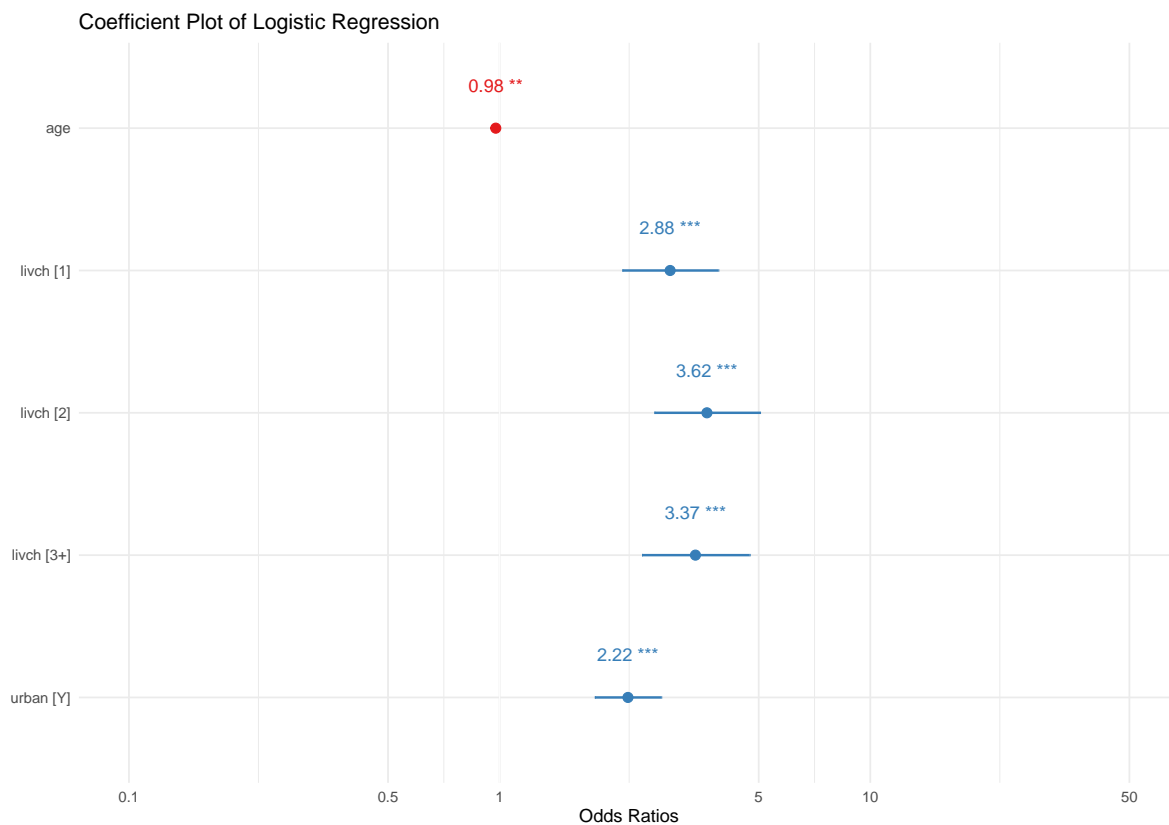
ii) Residual vs. Predicted (Rank Transformed):

The random scatter of residuals and lack of any clear pattern indicate that the model fits well, with no significant problems detected.

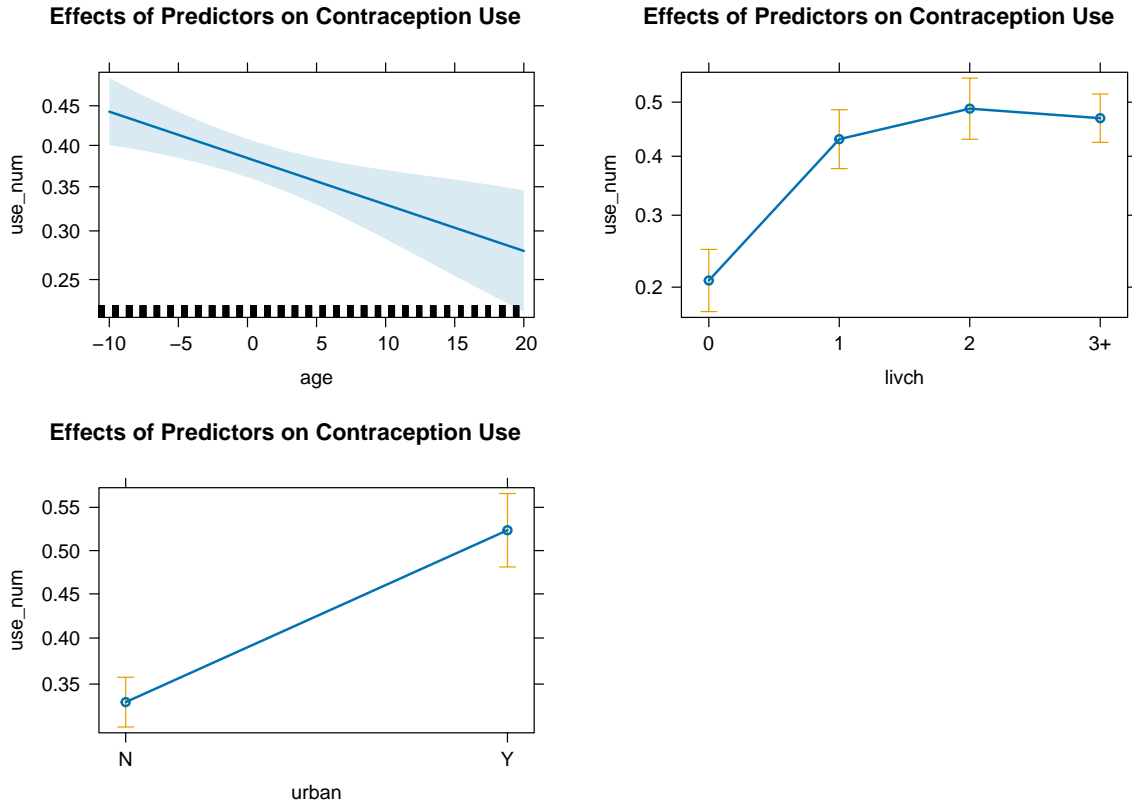
Eventually, I am not going to use the second model or any adjustment to the model as the first one seems to have a reasonable good fit without violating the assumptions.

e. Results Interpretation and Coefficient/Effect Plots

```
1 # Coefficient plot with `theme_minimal()`  
2 plot_model(model,  
3     show.values = TRUE,  
4     value.offset = 0.3,  
5     title = "Coefficient Plot of Logistic Regression") +  
6     theme_minimal()
```



```
1 # Plot the effects of the model  
2 plot(allEffects(model), main = "Effects of Predictors on Contraception Use")
```

The **log-odds coefficients** can be converted into **odds ratios (OR)** by exponentiating the coefficients. This helps in understanding the percentage change in the odds of the response variable. The odds ratio tells us the multiplicative change in the odds of the outcome for a one-unit change in the predictor. If the odds ratio is above 1, the odds of the event increase; if below 1, the odds decrease.

- **age**: The odds ratio is $\exp(-0.023995) = 0.976$, meaning that for each additional year of age, the odds of using contraception decrease by about 2.4%. This is less than the 5% threshold, so while it's statistically significant, it did not meet our criteria for a practically significant effect.
- **livch1**: The odds ratio for having one child is $\exp(1.059) = 2.884$, meaning the odds of using contraception are 188.4% higher compared to women with no children and much higher from 10% (our threshold).
- **livch2**: The odds ratio for having two children is $\exp(1.288) = 3.626$, meaning the odds of using contraception are 262.6% higher compared to women with no children and much higher from 10% (our threshold).

- **livch3+**: The odds ratio for having three or more children is $\exp(1.216) = 3.375$, meaning the odds of using contraception are 237.5% higher compared to women with no children and much higher from 10% (our threshold).
- **urbanY**: The odds ratio is $\exp(0.797) = 2.219$, meaning living in an urban area increases the odds of using contraception by 121.9% compared to rural areas and much higher from 10% (our threshold).

The predictors `livch` and `urban` have strong and significant effects on the odds of using contraception, with odds ratios well above 1, meaning their effects are both statistically and practically significant based on our 10% threshold.

In the logistic regression model examining the use of contraception (`use_num`) based on `age`, `livch` (number of living children), and `urban` (urban vs. non-urban), categorical predictors were automatically encoded by R into dummy variables. Specifically, `livch` and `urban` are categorical variables, and R created separate coefficients for each level of `livch` (e.g., `livch1`, `livch2`, `livch3+`), comparing each to a reference category (`livch = 0`). Similarly, for `urban`, the coefficient `urbanY` compares living in an urban area (Y) to the reference group living in a non-urban area (N). These coefficients reflect the change in the log-odds of using contraception compared to the reference categories. This encoding allows for a detailed understanding of how each level of the categorical variables affects the likelihood of using contraception.

Question 2: Analysis of Gopher Tortoise Data

```

1  ## LOAD DATA
2  g_url <- "https://raw.githubusercontent.com/bbolker/mm_workshops/master/data/gopherdat2.csv"
3  g_data <- read.csv(g_url)
4
5  ## Centering of the variable year
6  g_data$year_c <- g_data$year - mean(g_data$year)
7
8  head(g_data,10)

```

	Site	year	shells	type	Area	density	prev	year_c
1	BS	2004	0	Fresh	15.2	4.8	1.0	-1
2	BS	2005	0	Fresh	15.2	4.8	1.0	0
3	BS	2006	0	Fresh	15.2	4.8	1.0	1
4	CB	2004	1	Fresh	16.0	2.8	4.3	-1
5	CB	2005	0	Fresh	16.0	2.8	8.0	0
6	CB	2006	1	Fresh	16.0	2.8	17.6	1
7	Cent	2004	0	Fresh	6.9	29.1	28.6	-1

8	Cent 2005	1 Fresh	6.9	29.1	51.9	0
9	Cent 2006	1 Fresh	6.9	29.1	10.7	1
10	CF 2004	9 Fresh	43.2	4.2	80.7	-1

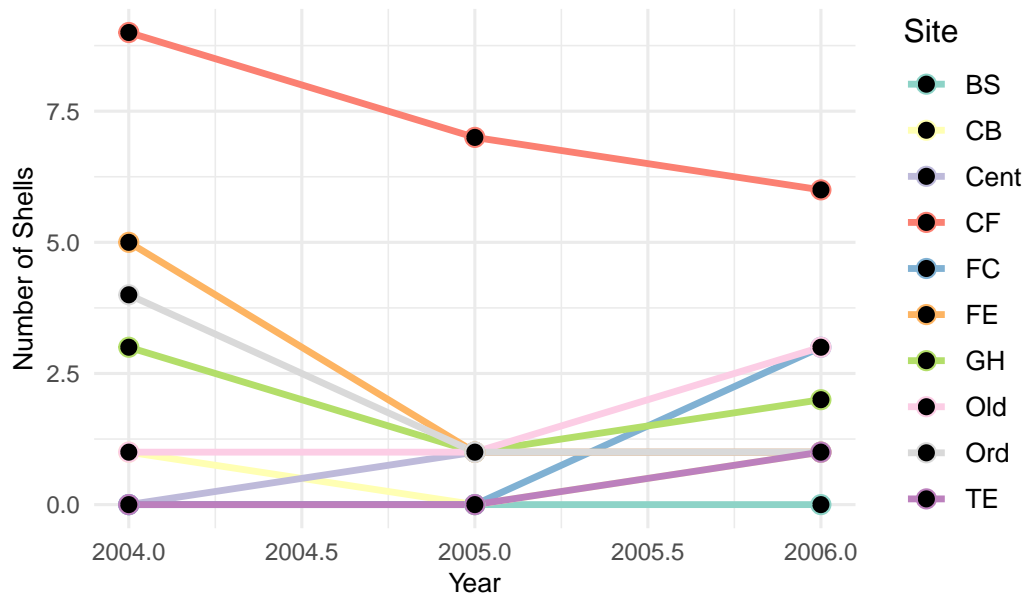
a. Data Visualization

```

1 # Line plot
2 ggplot(g_data, aes(x = year, y = shells, color = Site, group = Site)) +
3   geom_line(size = 1.2) + # Line size for visibility
4   geom_point(size = 3, shape = 21, fill = "black") + # Points with white fill for better con
5   labs(
6     title = "Trends in Gopher Shell Counts Over Time by Site",
7     x = "Year",
8     y = "Number of Shells",
9     color = "Site" # Legend title
10  ) +
11  theme_minimal(base_size = 12) + # Clean theme
12  theme(
13    legend.position = "right", # Legend positioning
14    plot.title = element_text(hjust = 0.5, size = 14, face = "bold"), # Smaller centered ti
15    axis.title = element_text(size = 10), # Axis title size
16    axis.text = element_text(size = 9) # Axis text size
17  ) +
18  scale_color_brewer(palette = "Set3") # Color palette

```

Trends in Gopher Shell Counts Over Time by Site



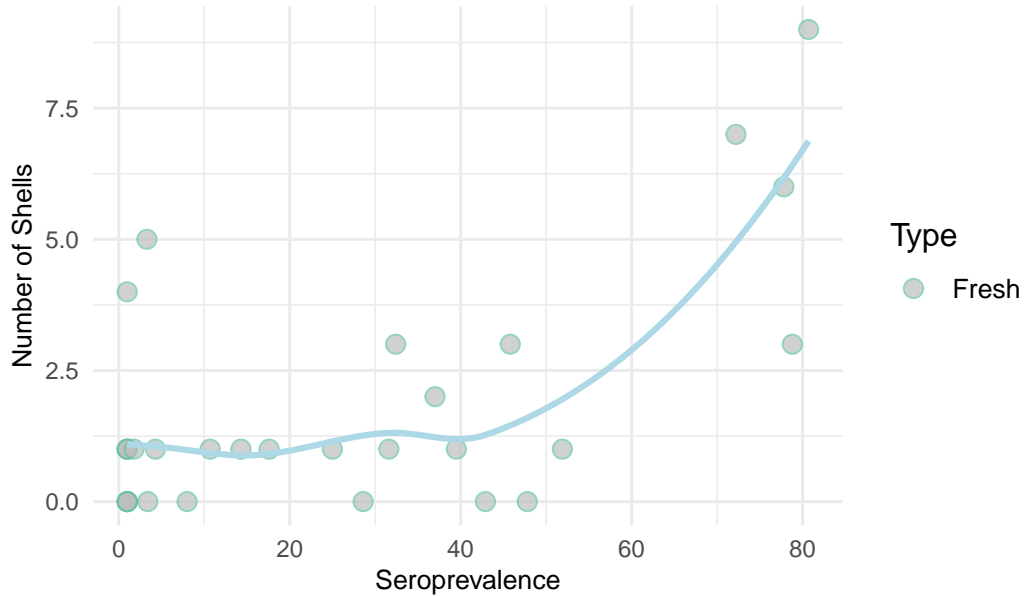
- The **first plot** shows the variability in shell numbers across different sites and years, with some showing increasing or decreasing trends.

```

1 # Scatterplot
2 ggplot(g_data, aes(x = prev, y = shells, color = type)) +
3   geom_point(size = 3, alpha = 0.7, shape = 21, fill = "grey") + # Points with transparency
4   labs(
5     title = "Relationship Between Shell Counts and Seroprevalence",
6     x = "Seroprevalence",
7     y = "Number of Shells",
8     color = "Type" # Legend title
9   ) +
10  geom_smooth(se = FALSE, method = "loess", color = "lightblue", formula = y ~ x) + # Smoother
11  theme_minimal(base_size = 12) + # Clean theme
12  theme(
13    legend.position = "right", # Legend positioning
14    plot.title = element_text(hjust = 0.5, size = 14, face = "bold"), # Smaller centered title
15    axis.title = element_text(size = 10), # Axis title size
16    axis.text = element_text(size = 9) # Axis text size
17  ) +
18  scale_color_brewer(palette = "Set2") # Color palette

```

Relationship Between Shell Counts and Seroprevalence



- The **second plot** suggests a positive correlation between seroprevalence and the number of shells, particularly when seroprevalence is high.

b. Model Fit

In this analysis, the response variable is the count of shells, making a Poisson Regression Model an appropriate choice given the nature of the data. To ensure robust estimation, we will adhere to the rule of requiring at least 10-20 observations per predictor. Therefore, the number of predictors will be minimized to meet this criterion, balancing model complexity and data sufficiency for accurate inference.

```
1 ## Model Fit
2 poisson_model <- glm(shells ~ year_c + prev + offset(log(Area)), data = g_data, family = poi
3 summary(poisson_model)
```

Call:

```
glm(formula = shells ~ year_c + prev + offset(log(Area)), family = poisson(link = "log"),
    data = g_data)
```

Coefficients:

Estimate	Std. Error	z value	Pr(> z)
----------	------------	---------	----------

```
(Intercept) -3.557101    0.241276 -14.743 < 2e-16 ***
year_c      -0.229100    0.164966  -1.389    0.165
prev         0.021828    0.004326   5.045 4.52e-07 ***
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

```
Null deviance: 49.800  on 29  degrees of freedom
Residual deviance: 24.317  on 27  degrees of freedom
AIC: 84.172
```

Number of Fisher Scoring iterations: 5

```
1 ## Over-dispersion Check
2 dispersion <- summary(poisson_model)$deviance / summary(poisson_model)$df.residual
3 print(c("Dispersion =", dispersion))
```

```
[1] "Dispersion ="      "0.900646372066475"
```

```
1 dispersiontest(poisson_model)
```

Overdispersion test

```
data: poisson_model
z = -1.0315, p-value = 0.8488
alternative hypothesis: true dispersion is greater than 1
sample estimates:
dispersion
0.7688125
```

The dispersion statistic is calculated as **0.901**, which is less than 1, indicating that the model does not exhibit overdispersion (The results of the dispersion test further confirm this, with a test statistic of **-1.0315** and a p-value of **0.8488**), so Poisson-Regression is an appropriate model for the problem.

c. Model Fit Using bbmle

```

1  ## Transforming year as a factor
2  g_data <- transform(
3    g_data,
4    year = as.factor(year)
5  )
6
7  # Fit the Poisson model using bbmle formula interface
8  poisson_model_bbmle <- mle2(shells ~ dpois(lambda = exp(b0 + b1 * year_c
9                                start = list(b0 = 0, b1 = 0, b2 = 0),
10                                data = g_data)
11
12  summary(poisson_model_bbmle)

```

Maximum likelihood estimation

Call:

```
mle2(minuslogl = shells ~ dpois(lambda = exp(b0 + b1 * year_c +
      b2 * prev + log(Area))), start = list(b0 = 0, b1 = 0, b2 = 0),
      data = g_data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(z)
b0	-3.5563450	0.2412167	-14.7434	< 2.2e-16 ***
b1	-0.2283314	0.1649610	-1.3842	0.1663
b2	0.0218136	0.0043262	5.0422	4.601e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

-2 log L: 78.17166

The results obtained from the Poisson regression models fitted using the `glm()` function and the `bbmle::mle2()` function are notably similar, indicating consistency across both methodologies. Furthermore, if the original factor variable for `year` is employed in the `glm()` model, the estimates would closely align with those derived from the `bbmle` approach.

d. Creation of a Negative Log-likelihood Function

```

1  # the Negative Log-Likelihood
2  NGLL <- function(b0, b1, b2) {

```

```

3   lamda <- exp(b0 + b1 * g_data$year_c + b2 * g_data$prev + log(g_data$Area))
4   negative_log_likelihood <- -sum(dpois(g_data$shells, lambda = lamda, log = TRUE))
5
6   return(negative_log_likelihood)
7 }
8
9 ## NGLL(0,0,0)      ## Test
10
11 # Using optim to Minimize the Negative Log-Likelihood
12 my_optim <- optim(par = c(b0 = 0, b1 = 0, b2 = 0),
13                  fn = function(params)
14                      NGLL(params[1], params[2], params[3]))

```

e. Comparison of Parameters for Different Approaches

```

1  ## Estimates from poisson_model
2  poisson_model_params <- coef(poisson_model)
3
4  ## Estimates from poisson_model_bbmle
5  poisson_model_bbmle_params <- coef(poisson_model_bbmle)
6
7  ## Estimates from my_optim
8  my_optim_params <- my_optim$par
9
10 # Creation of a data frame
11 comparisons <- data.frame(
12     poisson_model = poisson_model_params,
13     poisson_model_bbmle = poisson_model_bbmle_params,
14     my_optim = my_optim_params
15 )
16 print(comparisons)

```

	poisson_model	poisson_model_bbmle	my_optim
(Intercept)	-3.55710147	-3.55634500	-3.55661473
year_c	-0.22909974	-0.22833145	-0.22926177
prev	0.02182806	0.02181357	0.02182335

As we expected, the coefficients of all methods are nearly identical.

f. Wald and profile CIs

```
1  ## WALD CIs for Poisson GLM
2  # Extract the standard errors and compute the Wald CI
3  poisson_model_se <- summary(poisson_model)$coefficients[, "Std. Error"]
4  wald_ci_glm <- confint.default(poisson_model, level = 0.95) # Wald CI from GLM
5
6  ## WALD CIs for bbmle
7  # Get standard errors from bbmle fit
8  poisson_model_bbmle_se <- sqrt(diag(vcov(poisson_model_bbmle)))
9  wald_ci_bbmle <- cbind(
10     poisson_model_bbmle_params - 1.96 * poisson_model_bbmle_se,
11     poisson_model_bbmle_params + 1.96 * poisson_model_bbmle_se
12 )
13
14  ## WALD CIs for custom optim fit
15  # Assume that the Hessian matrix (returned by optim) is an approximation of the covariance matrix
16  hessian <- optimHess(par = my_optim$par, fn = function(params) NGLL(params[1], params[2], params[3]))
17  cov_matrix <- solve(hessian)
18  optim_se <- sqrt(diag(cov_matrix))
19
20  # Compute the Wald CIs for optim estimates
21  wald_ci_optim <- cbind(
22     my_optim_params - 1.96 * optim_se,
23     my_optim_params + 1.96 * optim_se
24 )
25
26  ## PROFILE CIs for bbmle
27  profile_ci_bbmle <- confint(poisson_model_bbmle)
28
29  ## Print Wald CIs and compare
30  wald_comparison <- data.frame(
31     Parameter = names(poisson_model_params),
32     Wald_CI_GLM = paste0(round(wald_ci_glm[, 1], 4), " to ", round(wald_ci_glm[, 2], 4)),
33     Wald_CI_bbmle = paste0(round(wald_ci_bbmle[, 1], 4), " to ", round(wald_ci_bbmle[, 2], 4)),
34     Wald_CI_optim = paste0(round(wald_ci_optim[, 1], 4), " to ", round(wald_ci_optim[, 2], 4))
35 )
36
37  print(wald_comparison)
```

Parameter	Wald_CI_GLM	Wald_CI_bbmle	Wald_CI_optim
-----------	-------------	---------------	---------------

1	(Intercept)	-4.03 to -3.0842	-4.0291 to -3.0836	-4.0293 to -3.0839
2	year_c	-0.5524 to 0.0942	-0.5517 to 0.095	-0.5526 to 0.094
3	prev	0.0133 to 0.0303	0.0133 to 0.0303	0.0134 to 0.0303

```

1 ## Compare Profile CIs for bbmle
2 profile_ci_comparison <- data.frame(
3   Parameter = names(poisson_model_bbmle_params),
4   Profile_CI_bbmle = paste0(round(profile_ci_bbmle[, 1], 4), " to ", round(profile_ci_bbmle[,
5 ]
6
7 print(profile_ci_comparison)

```

	Parameter	Profile_CI_bbmle
1	b0	-4.0618 to -3.1126
2	b1	-0.5554 to 0.0943
3	b2	0.0134 to 0.0304

Wald Confidence Intervals Comparison:

- **Wald CI for GLM:** These were calculated based on the standard errors from the GLM output. For example, for the intercept (b0), the Wald CI ranges from -4.03 to -3.08.
- **Wald CI for bbmle:** Similarly calculated using the standard errors from the `bbmle` model fit, yielding a very similar CI for b0 (-4.0291 to -3.0836), showing that both methods are almost identical in their results.
- **Wald CI for optim:** Using the Hessian matrix from `optim` as an estimate for the covariance matrix, the Wald CI for the intercept (b0) was again very close to the previous estimates, ranging from -4.0293 to -3.0839.

Conclusion: The Wald CIs are very consistent across all three approaches, indicating that the parameter estimates are robust regardless of the method used to fit the model.

Profile Confidence Intervals (for bbmle):

- These CIs were calculated using profile likelihood, which often provides more accurate confidence intervals, particularly for non-linear models or when the parameters are near the boundary of their possible range.
- For the intercept (b0), the profile CI ranges from -4.0618 to -3.1126, which is slightly wider than the Wald CIs. Similarly, the CIs for the other parameters (b1 and b2) are also slightly broader compared to the Wald CIs.

Comparison and Interpretation:

- **Wald vs Profile CIs:** Wald CIs assume normality of the estimates and may be narrower, especially when the model is highly non-linear. Profile CIs are generally considered more accurate as they account for the curvature of the likelihood surface. In our case, the profile CIs are slightly wider, suggesting a more conservative estimate of uncertainty around the parameters.
- **Consistency across methods:** The similarity in Wald CIs from GLM, bbmle, and optim suggests that all methods are implemented correctly and are producing nearly identical parameter estimates.

This shows that both Wald and profile CIs are in good agreement, though the profile CIs provide a slightly more conservative interval, as expected. These comparisons also confirm that your implementations across different methods are consistent.

Question 3: Endometrial Data

```
1 ## LOAD DATA
2 data("endometrial", package = "brglm2")
3 head(endometrial,10)
```

	NV	PI	EH	HG
1	0	13	1.64	0
2	0	16	2.26	0
3	0	8	3.14	0
4	0	34	2.68	0
5	0	20	1.28	0
6	0	5	2.31	0
7	0	17	1.80	0
8	0	10	1.68	0
9	0	26	1.56	0
10	0	17	2.31	0

```
1 summary(endometrial)
```

	NV	PI	EH	HG
Min.	:0.0000	Min. : 0.00	Min. :0.270	Min. :0.0000
1st Qu.:	:0.0000	1st Qu.:11.00	1st Qu.:1.180	1st Qu.:0.0000
Median	:0.0000	Median :16.00	Median :1.640	Median :0.0000

Mean	:0.1646	Mean	:17.38	Mean	:1.662	Mean	:0.3797
3rd Qu.	:0.0000	3rd Qu.	:21.00	3rd Qu.	:2.015	3rd Qu.	:1.0000
Max.	:1.0000	Max.	:49.00	Max.	:3.610	Max.	:1.0000

In this analysis, the response variable is the Hyperplasia Grade (NG), which is modeled as a binary outcome. The predictors used in the model are the number of vessels (NV), the Progesterone Index, and the Endometrial Index (EH). Based on Harrell's guidelines for binary logistic regression models [Harrell], the number of observations in the dataset is sufficient to include all selected predictors, ensuring that the model avoids overfitting while maintaining adequate statistical power.

To evaluate the relationship between NG and the predictors, three different modeling approaches will be employed:

1. **Standard Generalized Linear Model (GLM):** A logistic regression model will be fitted using the canonical logit link function to estimate the probability of a high hyperplasia grade given the predictor variables.
2. **Bayesian Logistic Regression:** A Bayesian approach will be applied to incorporate prior distributions for the model parameters, allowing for the integration of prior knowledge and uncertainty in the parameter estimates.
3. **Bias-Reduced Logistic Regression:** This approach will use Firth's correction or another bias-reduction method to mitigate the small-sample bias often encountered in maximum likelihood estimates in logistic regression, particularly when rare events are present in the binary response.

By comparing these methods, the aim is to assess their performance and suitability for modeling hyperplasia grade under different statistical frameworks, while ensuring robust inference.

```

1 ##HG vs Number of Vessels (NV)
2 ggplot(endometrial, aes(x = NV, y = HG)) +
3   geom_jitter(height = 0.05, width = 0) + # Add some jitter to separate the binary points
4   geom_smooth(method = "glm", method.args = list(family = "binomial"), se = FALSE, color = "red")
5   labs(title = "HG vs Number of Vessels",
6         x = "Number of Vessels (NV)",
7         y = "Hyperplasia Grade (HG)") +
8   theme_minimal() +
9   theme(text = element_text(size = 14)) # Adjust text size for clarity

```

```

1 ##HG vs Progesterone Index (PI)
2 ggplot(endometrial, aes(x = PI, y = HG)) +
3   geom_jitter(height = 0.05, width = 0) +
4   geom_smooth(method = "glm", method.args = list(family = "binomial"), se = FALSE, color = "red")

```

```

5 labs(title = "HG vs Progesterone Index",
6       x = "Progesterone Index (PI)",
7       y = "Hyperplasia Grade (HG)") +
8 theme_minimal() +
9 theme(text = element_text(size = 14))

```

```

1 ##HG vs Endometrial Height (EH)
2 ggplot(endometrial, aes(x = EH, y = HG)) +
3   geom_jitter(height = 0.05, width = 0) +
4   geom_smooth(method = "glm", method.args = list(family = "binomial"), se = FALSE, color = "red") +
5   labs(title = "HG vs Endometrial Height",
6         x = "Endometrial Height (EH)",
7         y = "Hyperplasia Grade (HG)") +
8   theme_minimal() +
9   theme(text = element_text(size = 14))

```

Number of Vessels (NV) and **Endometrial Height (EH)** have strong, nonlinear relationships with hyperplasia grade (HG). On the other hand, **Progesterone Index (PI)** shows a much weaker and more linear relationship with HG, suggesting that it may be less influential in predicting hyperplasia compared to NV and EH.

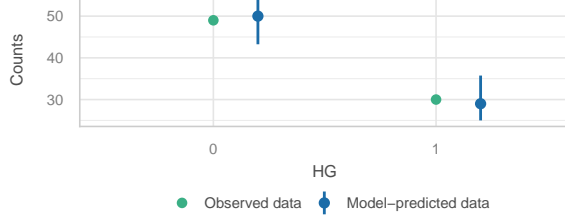
```

1 ## Regular GLM Fit
2 model_glm <- glm(HG ~ NV + PI + EH, data = endometrial, family = binomial(link = "logit"))
3 performance::check_model(model_glm)

```

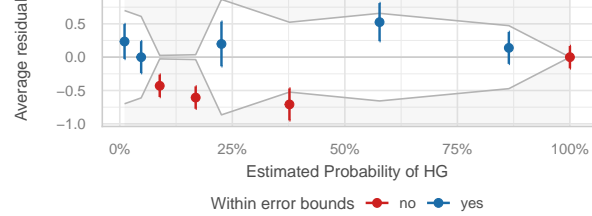
Posterior Predictive Check

Model-predicted intervals should include observed data points



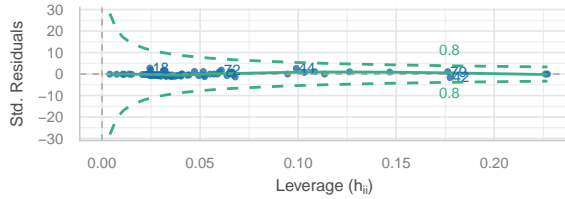
Binned Residuals

Points should be within error bounds



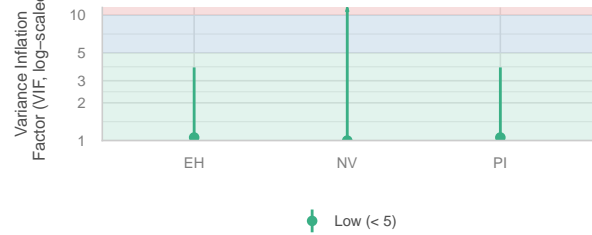
Influential Observations

Points should be inside the contour lines



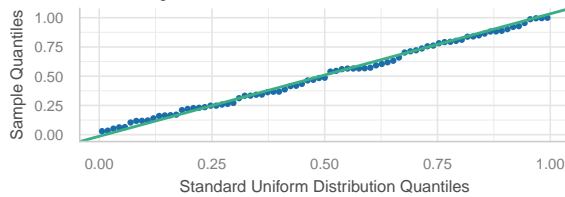
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



Distribution of Quantile Residuals

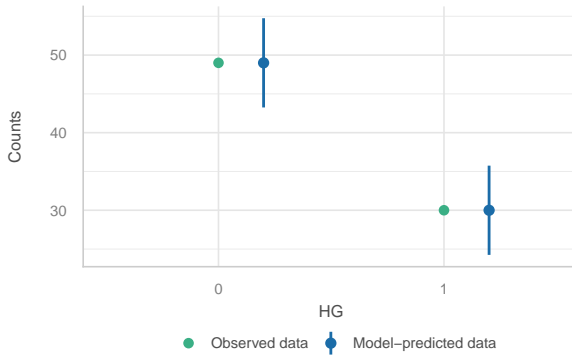
Dots should fall along the line



```
1 ## Bayesian Logistic Regression Fit
2 model_bayesglm <- bayesglm(HG ~ NV + PI + EH, data = endometrial, family = binomial(link = "logit"))
3 performance::check_model(model_bayesglm)
```

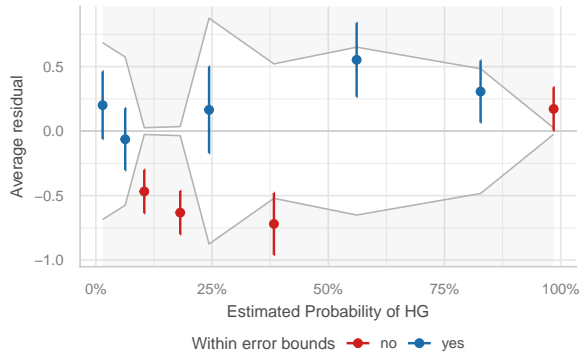
Posterior Predictive Check

Model-predicted intervals should include observed data points



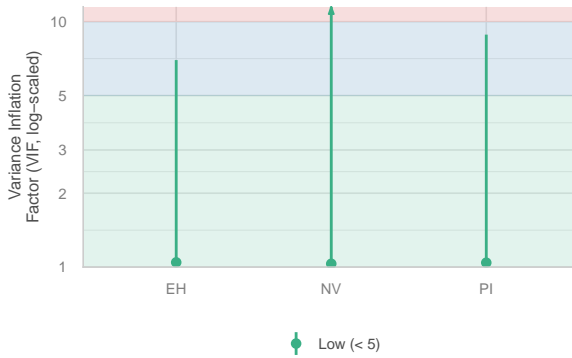
Binned Residuals

Points should be within error bounds



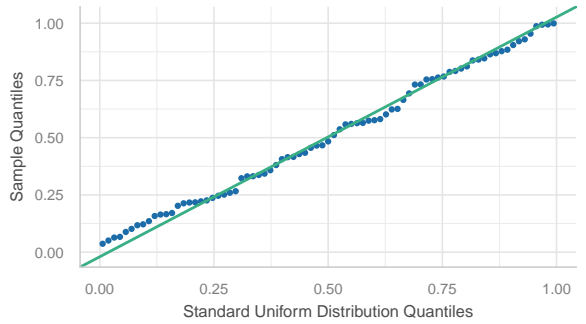
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



Distribution of Quantile Residuals

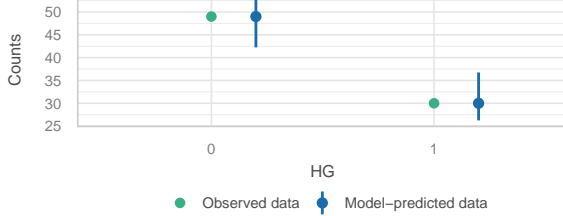
Dots should fall along the line



```
1 ## Bias-Reduced Logistic Regression Fit
2 model_brglmFit <- glm(HG ~ NV + PI + EH, data = endometrial, family = binomial(link = "logit")
3 performance::check_model(model_brglmFit)
```

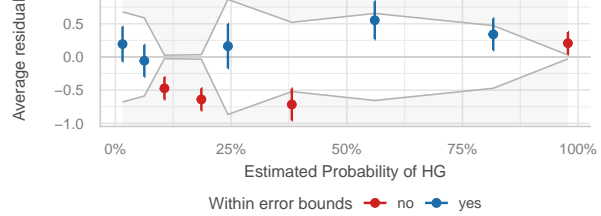
Posterior Predictive Check

Model-predicted intervals should include observed data points



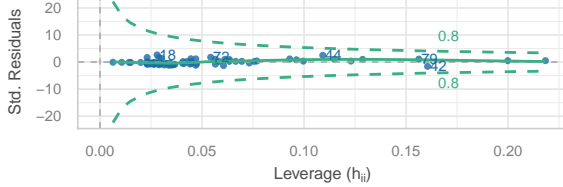
Binned Residuals

Points should be within error bounds



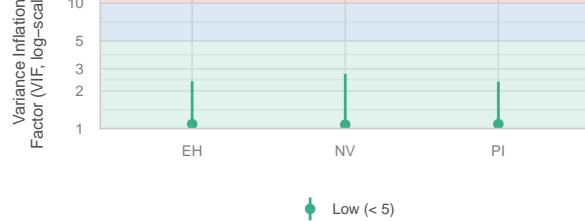
Influential Observations

Points should be inside the contour lines



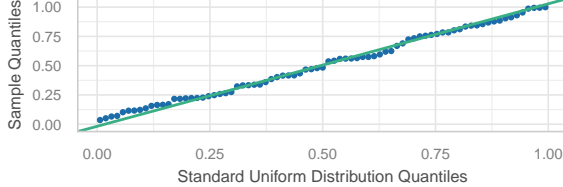
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



Distribution of Quantile Residuals

Dots should fall along the line



```
1 summary(model_glm)
```

Call:

```
glm(formula = HG ~ NV + PI + EH, family = binomial(link = "logit"),
     data = endometrial)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	4.30452	1.63730	2.629	0.008563 **
NV	18.18556	1715.75089	0.011	0.991543
PI	-0.04218	0.04433	-0.952	0.341333
EH	-2.90261	0.84555	-3.433	0.000597 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)


```
Null deviance: 104.903 on 78 degrees of freedom
Residual deviance: 55.393 on 75 degrees of freedom
AIC: 63.393
```

```
Number of Fisher Scoring iterations: 17
```

```
1 summary(model_bayesglm)
```

```
Call:
```

```
bayesglm(formula = HG ~ NV + PI + EH, family = binomial(link = "logit"),
  data = endometrial)
```

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.71159	1.38954	2.671	0.007560 **
NV	3.29816	1.58068	2.087	0.036929 *
PI	-0.02904	0.03657	-0.794	0.427261
EH	-2.62865	0.73865	-3.559	0.000373 ***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for binomial family taken to be 1)
```

```
Null deviance: 104.903 on 78 degrees of freedom
Residual deviance: 56.254 on 75 degrees of freedom
AIC: 64.254
```

```
Number of Fisher Scoring iterations: 20
```

```
1 summary(model_brglmFit)
```

```
Call:
```

```
glm(formula = HG ~ NV + PI + EH, family = binomial(link = "logit"),
  data = endometrial, method = "brglmFit")
```

```
Deviance Residuals:
```

Min	1Q	Median	3Q	Max
-1.4740	-0.6706	-0.3411	0.3252	2.6123

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.77456	1.48869	2.535	0.011229 *
NV	2.92927	1.55076	1.889	0.058902 .
PI	-0.03475	0.03958	-0.878	0.379915
EH	-2.60416	0.77602	-3.356	0.000791 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 104.903 on 78 degrees of freedom
Residual deviance: 56.575 on 75 degrees of freedom
AIC: 64.575

Type of estimator: AS_mixed (mixed bias-reducing adjusted score equations)
Number of Fisher Scoring iterations: 6

1. Comparison of Estimates:

```
1 glm_coefs <- coef(model_glm)
2 bayesglm_coefs <- coef(model_bayesglm)
3 brglmFit_coefs <- coef(model_brglmFit)
4
5 # Create a comparison data frame
6 comparison_df <- data.frame(
7   Coefficient = names(glm_coefs),
8   GLM = round(glm_coefs, 4),
9   BayesGLM = round(bayesglm_coefs, 4),
10  BRGLM = round(brglmFit_coefs, 4)
11 )
12
13 # Print the comparison
14 print(comparison_df)
```

	Coefficient	GLM	BayesGLM	BRGLM
(Intercept)	(Intercept)	4.3045	3.7116	3.7746
NV	NV	18.1856	3.2982	2.9293
PI	PI	-0.0422	-0.0290	-0.0348
EH	EH	-2.9026	-2.6286	-2.6042

```

1 # Long format
2 plot_df <- comparison_df %>%
3   pivot_longer(cols = c(GLM, BayesGLM, BRGLM),
4                 names_to = "Method",
5                 values_to = "Estimate") %>%
6   mutate(
7     Method = factor(Method, levels = c("GLM", "BayesGLM", "BRGLM")),
8     Coefficient = factor(Coefficient, levels = unique(Coefficient))
9   )
10
11 # Portfolio theme (centered titles)
12 theme_portfolio <- theme_minimal(base_size = 12) +
13   theme(
14     plot.title.position = "plot",
15     plot.title = element_text(face = "bold", size = 15, hjust = 0.5),
16     plot.subtitle = element_text(hjust = 0.5, margin = margin(b = 8)),
17     axis.title = element_text(face = "bold"),
18     panel.grid.minor = element_blank(),
19     panel.grid.major.y = element_blank(),
20     strip.text = element_text(face = "bold")
21   )
22
23 # Plot 1: Faceted coefficient comparison (one panel per coefficient)
24 p1 <- ggplot(plot_df, aes(x = Estimate, y = Method)) +
25   geom_vline(xintercept = 0, linetype = "dashed", linewidth = 0.6, alpha = 0.8) +
26   geom_point(size = 2.6) +
27   geom_text(
28     aes(label = sprintf("%.3f", Estimate)),
29     vjust = -0.8,
30     size = 3
31   ) +
32   facet_wrap(~ Coefficient, scales = "free_x", nrow = 1) +
33   labs(
34     title = "Coefficient estimates across methods",
35     subtitle = "GLM vs BayesGLM vs BRGLM",
36     x = "Estimate",
37     y = NULL
38   ) +
39   theme_portfolio
40
41
42 # Plot 2: Slope chart per coefficient (separate facets, not mixed)

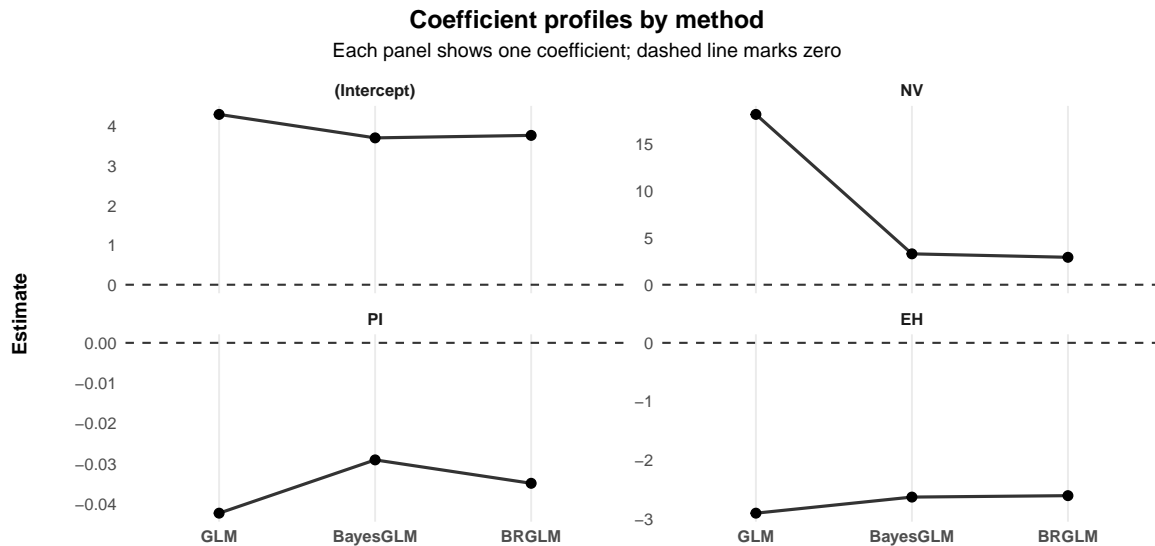
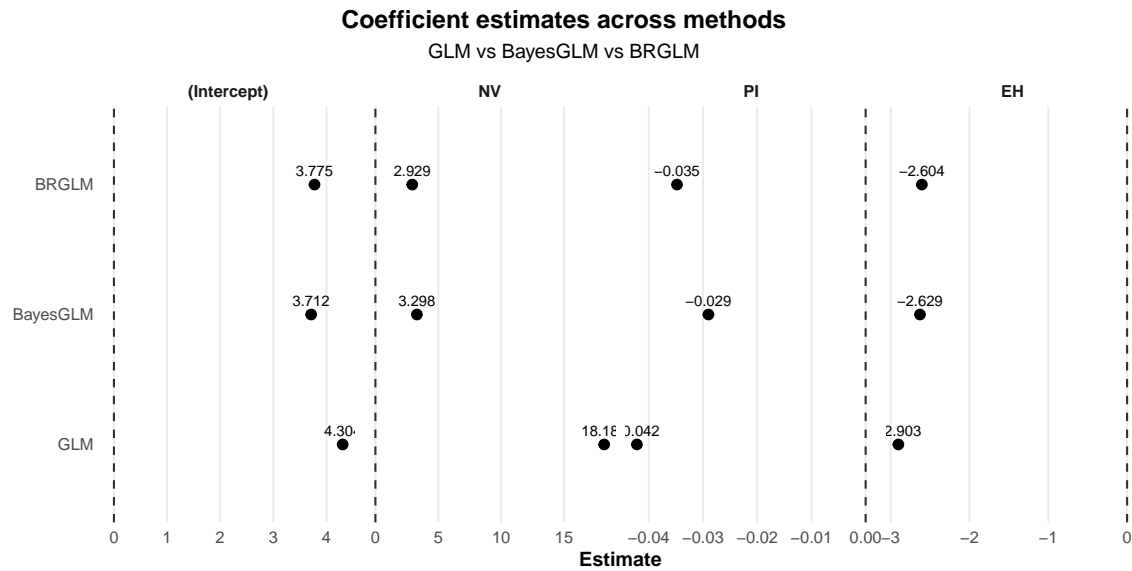
```

```

43 p2 <- ggplot(plot_df, aes(x = Method, y = Estimate, group = 1)) +
44   geom_hline(yintercept = 0, linetype = "dashed", linewidth = 0.6, alpha = 0.8) +
45   geom_line(linewidth = 0.9, alpha = 0.8) +
46   geom_point(size = 2.4) +
47   facet_wrap(~ Coefficient, scales = "free_y", ncol = 2) +
48   labs(
49     title = "Coefficient profiles by method",
50     subtitle = "Each panel shows one coefficient; dashed line marks zero",
51     x = NULL,
52     y = "Estimate"
53   ) +
54   theme_portfolio +
55   theme(axis.text.x = element_text(face = "bold"))
56
57 # Combine into ONE figure (two rows) without mixing plots
58 (p1 / p2) +
59   plot_annotation(
60     title = "Comparison of coefficient estimates across estimation methods",
61     theme = theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 16))
62   )

```

Comparison of coefficient estimates across estimation methods



The comparison of coefficient estimates from the GLM, BayesGLM, and BRGLM models shows notable differences, particularly for the **Intercept** and the predictor **NV**. The GLM model produced a very high estimate for NV (18.1856), suggesting a strong positive effect, while both the BayesGLM (3.2982) and BRGLM (2.9293) models showed much lower estimates, indicating they may mitigate the extreme influence of this predictor. For PI, all models yielded negative estimates, with GLM at -0.0422 and the Bayesian methods being slightly more consistent around -0.0290 and -0.0348. The EH variable also had negative estimates across all models, with GLM showing the most negative effect at -2.9026. Overall, the Bayesian and bias-reduced methods provide more stable and less extreme estimates compared to the traditional GLM, which may be

prone to overfitting.

2. Wald and likelihood profile confidence intervals

```
1 # Calculate Wald Confidence Intervals for GLM
2 wald_ci_glm <- confint.default(model_glm, level = 0.95)
3 wald_ci_glm <- as.data.frame(wald_ci_glm)
4 colnames(wald_ci_glm) <- c("lower", "upper")
5
6 # Calculate Profile Likelihood Confidence Intervals for GLM
7 profile_ci_glm <- confint(model_glm)
8 profile_ci_glm <- as.data.frame(profile_ci_glm)
9 colnames(profile_ci_glm) <- c("lower", "upper")
10
11 # Calculate Wald Confidence Intervals for bayesglm
12 wald_ci_bayesglm <- confint.default(model_bayesglm, level = 0.95)
13 wald_ci_bayesglm <- as.data.frame(wald_ci_bayesglm)
14 colnames(wald_ci_bayesglm) <- c("lower", "upper")
15
16 # Profile CI for bayesglm may not be straightforward, use the posterior predictive intervals
17 # Instead, we will stick to the Wald for bayesglm as it is commonly used
18
19 # Calculate Wald Confidence Intervals for brglmFit
20 wald_ci_brglmFit <- confint.default(model_brglmFit, level = 0.95)
21 wald_ci_brglmFit <- as.data.frame(wald_ci_brglmFit)
22 colnames(wald_ci_brglmFit) <- c("lower", "upper")
23
24 # Calculate Profile Likelihood Confidence Intervals for brglmFit
25 profile_ci_brglmFit <- confint(model_brglmFit)
26 profile_ci_brglmFit <- as.data.frame(profile_ci_brglmFit)
27 colnames(profile_ci_brglmFit) <- c("lower", "upper")
28
29 # Create a summary comparison data frame
30 comparison <- data.frame(
31   Parameter = rownames(wald_ci_glm),
32   Wald_CI_GLM = paste0(round(wald_ci_glm$lower, 4), " to ", round(wald_ci_glm$upper, 4)),
33   Profile_CI_GLM = paste0(round(profile_ci_glm$lower, 4), " to ", round(profile_ci_glm$upper, 4)),
34   Wald_CI_BayesGLM = paste0(round(wald_ci_bayesglm$lower, 4), " to ", round(wald_ci_bayesglm$upper, 4)),
35   Wald_CI_brglmFit = paste0(round(wald_ci_brglmFit$lower, 4), " to ", round(wald_ci_brglmFit$upper, 4)),
36   Profile_CI_brglmFit = paste0(round(profile_ci_brglmFit$lower, 4), " to ", round(profile_ci_brglmFit$upper, 4)),
37 )
```

```

38
39 # Print the comparison table
40 print(comparison)

```

	Parameter	Wald_CI_GLM	Profile_CI_GLM	Wald_CI_BayesGLM
1	(Intercept)	1.0955 to 7.5136	1.4332 to 7.955	0.9881 to 6.435
2	NV	-3344.6244 to 3380.9955	-69.2281 to 506.1938	0.2001 to 6.3962
3	PI	-0.1291 to 0.0447	-0.1371 to 0.0382	-0.1007 to 0.0426
4	EH	-4.5599 to -1.2454	-4.786 to -1.4366	-4.0764 to -1.1809
	Wald_CI_brglmFit	Profile_CI_brglmFit		
1	0.8568 to 6.6923	0.8568 to 6.6923		
2	-0.1102 to 5.9687	-0.1102 to 5.9687		
3	-0.1123 to 0.0428	-0.1123 to 0.0428		
4	-4.1251 to -1.0832	-4.1251 to -1.0832		

```

1 ci_df <- bind_rows(
2   # GLM
3   data.frame(
4     Parameter = rownames(wald_ci_glm),
5     lower = wald_ci_glm$lower,
6     upper = wald_ci_glm$upper,
7     Method = "GLM",
8     CI_Type = "Wald"
9   ),
10  data.frame(
11    Parameter = rownames(profile_ci_glm),
12    lower = profile_ci_glm$lower,
13    upper = profile_ci_glm$upper,
14    Method = "GLM",
15    CI_Type = "Profile"
16  ),
17  # BayesGLM (Wald only)
18  data.frame(
19    Parameter = rownames(wald_ci_bayesglm),
20    lower = wald_ci_bayesglm$lower,
21    upper = wald_ci_bayesglm$upper,
22    Method = "BayesGLM",
23    CI_Type = "Wald"
24  ),
25  # brglmFit
26  data.frame(
27    Parameter = rownames(wald_ci_brglmFit),

```

```

28   lower = wald_ci_brglmFit$lower,
29   upper = wald_ci_brglmFit$upper,
30   Method = "BRGLM",
31   CI_Type = "Wald"
32 ),
33 data.frame(
34   Parameter = rownames(profile_ci_brglmFit),
35   lower = profile_ci_brglmFit$lower,
36   upper = profile_ci_brglmFit$upper,
37   Method = "BRGLM",
38   CI_Type = "Profile"
39 )
40 ) %>%
41 filter(Parameter != "(Intercept)") %>%
42 mutate(
43   Parameter = factor(Parameter, levels = rev(unique(Parameter))),
44   CI_Type = factor(CI_Type, levels = c("Wald", "Profile"))
45 )
46
47
48
49 ggplot(ci_df, aes(x = (lower + upper) / 2, y = Parameter)) +
50   geom_vline(xintercept = 0, linetype = "dashed", linewidth = 0.6, alpha = 0.7) +
51   geom_errorbarh(
52     aes(xmin = lower, xmax = upper, color = CI_Type),
53     height = 0.25,
54     position = position_dodge(width = 0.6)
55   ) +
56   geom_point(
57     aes(color = CI_Type),
58     position = position_dodge(width = 0.6),
59     size = 2
60   ) +
61   facet_wrap(~ Method, nrow = 1) +
62   labs(
63     title = "Comparison of confidence intervals across estimation methods",
64     subtitle = "Wald vs profile likelihood intervals for logistic regression coefficients",
65     x = "Coefficient estimate",
66     y = NULL,
67     color = "CI type"
68   ) +
69   theme_minimal(base_size = 12) +

```



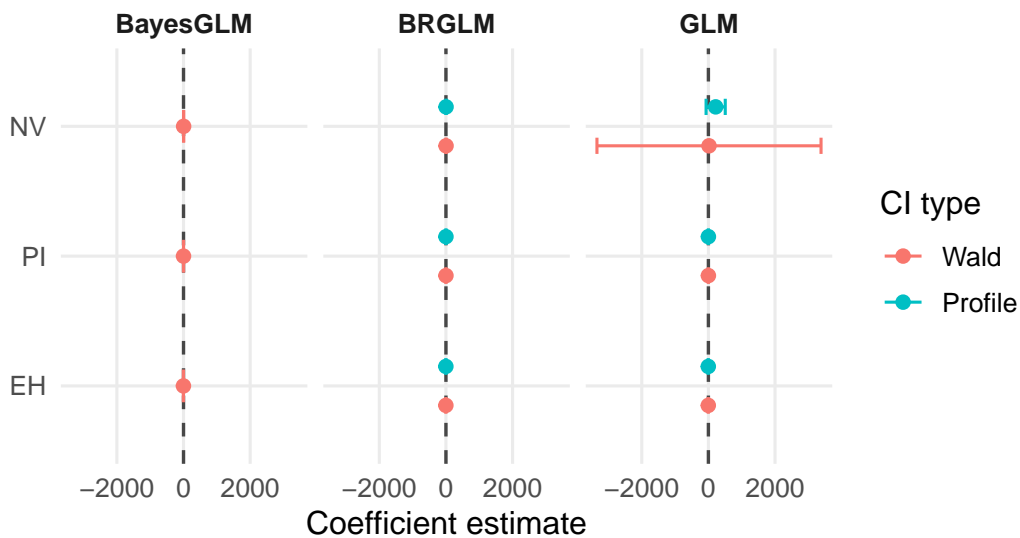
```

70 theme(
71   plot.title = element_text(face = "bold", hjust = 0.5),
72   plot.subtitle = element_text(hjust = 0.5),
73   strip.text = element_text(face = "bold"),
74   panel.grid.minor = element_blank()
75 )

```

Comparison of confidence intervals across estimation methods

Wald vs profile likelihood intervals for logistic regression coefficients



The comparison of the Wald and profile likelihood confidence intervals (CIs) across the three logistic regression models reveals important insights into the parameter estimates' uncertainty. For the **GLM model**, the Wald CIs are notably wider for the NV parameter, suggesting significant uncertainty, while the profile CIs are narrower, indicating a more concentrated estimate around the true parameter value. The profile CIs for both models show that the lower bound for NV is negative, raising concerns about potential non-identifiability in this parameter. In contrast, the **bayesglm model** presents relatively consistent Wald CIs, indicating robustness, though it lacks a profile CI due to complexities in Bayesian frameworks. For the **brglmFit model**, both the Wald and profile CIs provide nearly identical ranges, reflecting the model's stability in estimating the parameters. Overall, the profile likelihood CIs generally offer a more refined estimate compared to the Wald CIs, particularly for the NV parameter, emphasizing the value of profiling in models with potential non-linearity or parameter constraints.

3. Wald and likelihood ratio-test p-values for all three (non-intercept) coefficients

```
1 # Function to extract Wald p-values
2 wald_p_values <- function(model) {
3   coefs <- summary(model)$coefficients
4   p_values <- 2 * (1 - pnorm(abs(coefs[, "Estimate"] / coefs[, "Std. Error"])))
5   return(p_values[-1]) # Exclude the intercept
6 }
7
8 # Extract Wald p-values
9 wald_p_glm <- wald_p_values(model_glm)
10 wald_p_bayesglm <- wald_p_values(model_bayesglm)
11 wald_p_brglmFit <- wald_p_values(model_brglmFit)
12
13 # Likelihood Ratio Tests
14 lrt_glm <- anova(model_glm, test = "LRT")
15 lrt_bayesglm <- anova(model_bayesglm, test = "LRT")
16 lrt_brglmFit <- anova(model_brglmFit, test = "LRT")
17
18 # Extract LRT p-values
19 lrt_p_glm <- lrt_glm$`Pr(>Chi)`[-1] # Exclude the intercept
20 lrt_p_bayesglm <- lrt_bayesglm$`Pr(>Chi)`[-1] # Exclude the intercept
21 lrt_p_brglmFit <- lrt_brglmFit$`Pr(>Chi)`[-1] # Exclude the intercept
22
23 # Combine Wald and LRT p-values
24 comparison <- data.frame(
25   Coefficient = names(wald_p_glm),
26   Wald_p_GLM = wald_p_glm,
27   Wald_p_BayesGLM = wald_p_bayesglm,
28   Wald_p_BrglmFit = wald_p_brglmFit,
29   LRT_p_GLM = lrt_p_glm,
30   LRT_p_BayesGLM = lrt_p_bayesglm,
31   LRT_p_BrglmFit = lrt_p_brglmFit
32 )
33
34 # Print the comparison table
35 print(comparison)
```

	Coefficient	Wald_p_GLM	Wald_p_BayesGLM	Wald_p_BrglmFit	LRT_p_GLM
NV	NV	0.9915432347	0.0369292945	0.0589021443	5.322163e-08
PI	PI	0.3413329906	0.4272605796	0.3799145349	6.957899e-01

EH	EH	0.0005973924	0.0003726778	0.0007913435	8.777197e-06
	LRT_p_BayesGLM	LRT_p_BrglmFit			
NV	5.322163e-08	8.687300e-08			
PI	6.957899e-01	8.219755e-01			
EH	1.377741e-05	9.394201e-06			

```

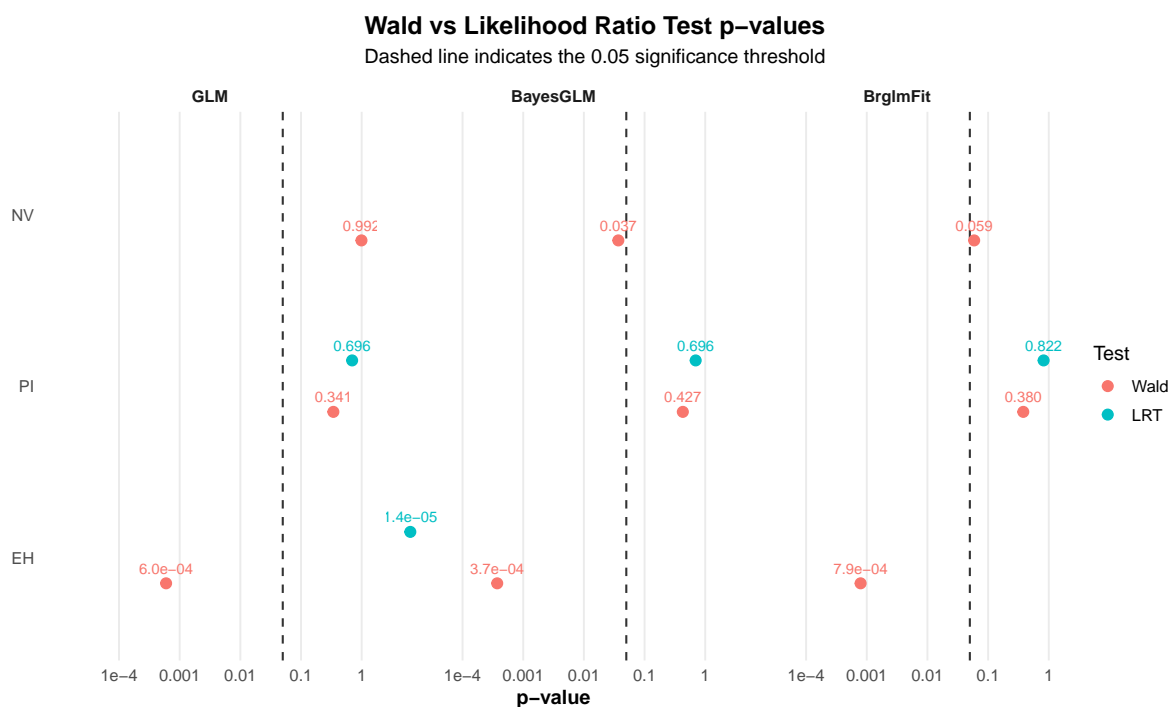
1 # Tidy p-values
2 pval_df <- comparison %>%
3   pivot_longer(
4     cols = -Coefficient,
5     names_to = "Test",
6     values_to = "p_value"
7   ) %>%
8   separate(Test, into = c("Type", "Method"), sep = "_p_") %>%
9   mutate(
10     Method = factor(Method, levels = c("GLM", "BayesGLM", "BrglmFit")),
11     Type = factor(Type, levels = c("Wald", "LRT")),
12     Coefficient = factor(Coefficient, levels = rev(unique(Coefficient))),
13     # Label formatting: scientific for very small p-values
14     p_label = ifelse(p_value < 0.001, format(p_value, scientific = TRUE, digits = 2),
15                     sprintf("%.3f", p_value))
16   )
17
18 # Portfolio theme (centered title)
19 theme_portfolio <- theme_minimal(base_size = 12) +
20   theme(
21     plot.title.position = "plot",
22     plot.title = element_text(face = "bold", size = 15, hjust = 0.5),
23     plot.subtitle = element_text(hjust = 0.5, margin = margin(b = 8)),
24     axis.title = element_text(face = "bold"),
25     strip.text = element_text(face = "bold"),
26     panel.grid.minor = element_blank(),
27     panel.grid.major.y = element_blank()
28   )
29
30 ggplot(pval_df, aes(x = p_value, y = Coefficient, color = Type)) +
31   geom_vline(xintercept = 0.05, linetype = "dashed", linewidth = 0.6, alpha = 0.8) +
32   geom_point(size = 2.7, position = position_dodge(width = 0.6)) +
33   geom_text(
34     aes(label = p_label),
35     position = position_dodge(width = 0.6),
36     vjust = -0.9,

```

```

37     size = 3,
38     show.legend = FALSE
39   ) +
40   facet_wrap(~ Method, nrow = 1) +
41   scale_x_log10(
42     breaks = c(1, 0.1, 0.01, 0.001, 1e-4),
43     labels = c("1", "0.1", "0.01", "0.001", "1e-4"),
44     limits = c(1e-5, 1)
45   ) +
46   labs(
47     title = "Wald vs Likelihood Ratio Test p-values",
48     subtitle = "Dashed line indicates the 0.05 significance threshold",
49     x = "p-value",
50     y = NULL,
51     color = "Test"
52   ) +
53   theme_portfolio

```



The comparison of Wald and likelihood ratio test (LRT) p-values for the coefficients of the models reveals some significant insights. For the variable **NV**, the Wald p-values across the three models (GLM: 0.992, BayesGLM: 0.037, BrglmFit: 0.059) indicate that NV is not statistically significant in the GLM, while it shows significance in the other two models, particularly in

BayesGLM. However, the LRT p-values confirm NV's strong significance across all models, with values close to zero (e.g., GLM: $5.32 \times 10^{-85.32}$, BayesGLM: $5.32 \times 10^{-85.32}$, BrglmFit: $8.69 \times 10^{-88.69}$). For the **PI** variable, all models yield high Wald p-values (ranging from 0.341 to 0.427), indicating non-significance, which is corroborated by the LRT p-values (GLM: 0.696, BayesGLM: 0.696, BrglmFit: 0.822). In contrast, **EH** shows a notable discrepancy, with Wald p-values suggesting significance (ranging from 0.0006 to 0.0008), while LRT p-values reinforce this finding with values below 0.0001, affirming EH as a significant predictor in all three models. Overall, the LRT p-values provide a more consistent measure of significance across the models, particularly for NV and EH, while the Wald p-values indicate variability in significance for NV depending on the modeling approach used.

Differences in results arise from the estimation techniques used, how each method handles sample size and data characteristics, the incorporation of prior information in Bayesian approaches, and the robustness of the confidence intervals and p-values generated by each method.

Question 4: Zero-inflation by simulation

```

1  ## LOAD DATA
2  data("bioChemists", package="pscl")
3
4  # Fit a negative binomial model
5  nb_model <- glm.nb(art ~ fem + mar + kid5 + phd + ment, data = bioChemists)
6
7  # Display summary of the model
8  summary(nb_model)

```

Call:

```
glm.nb(formula = art ~ fem + mar + kid5 + phd + ment, data = bioChemists,
       init.theta = 2.264387695, link = log)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	0.256144	0.137348	1.865	0.062191	.
femWomen	-0.216418	0.072636	-2.979	0.002887	**
marMarried	0.150489	0.082097	1.833	0.066791	.
kid5	-0.176415	0.052813	-3.340	0.000837	***
phd	0.015271	0.035873	0.426	0.670326	
ment	0.029082	0.003214	9.048	< 2e-16	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(2.2644) family taken to be 1)

Null deviance: 1109.0 on 914 degrees of freedom
Residual deviance: 1004.3 on 909 degrees of freedom
AIC: 3135.9

Number of Fisher Scoring iterations: 1

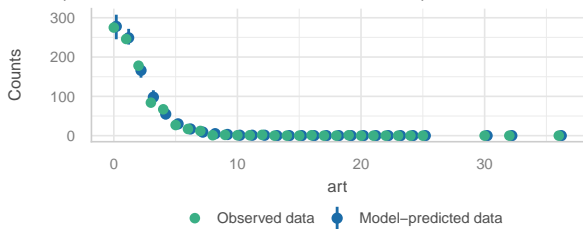
Theta: 2.264
Std. Err.: 0.271

2 x log-likelihood: -3121.917

```
1 # Check model performance
2 performance::check_model(nb_model)
```

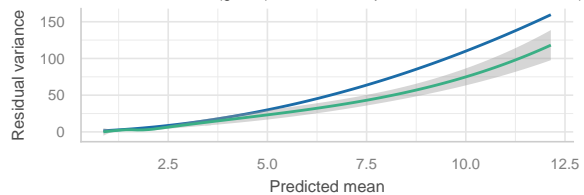
Posterior Predictive Check

Model-predicted intervals should include observed data points



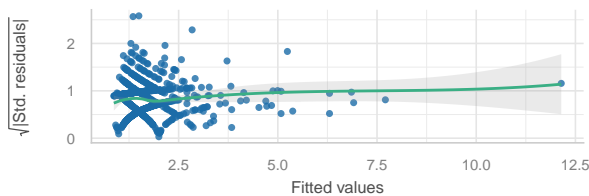
Misspecified dispersion and zero-inflation

Observed residual variance (green) should follow predicted residual variance (blue)



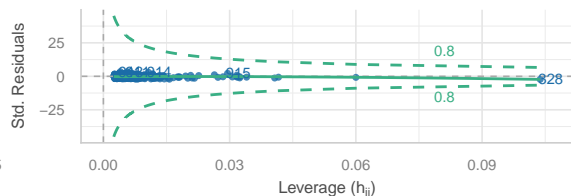
Homogeneity of Variance

Reference line should be flat and horizontal



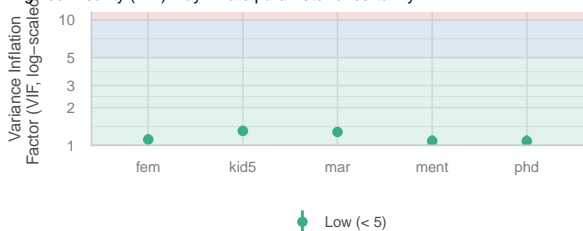
Influential Observations

Points should be inside the contour lines



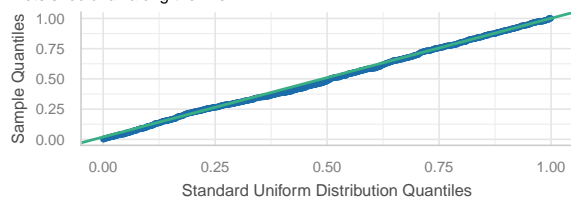
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



Distribution of Quantile Residuals

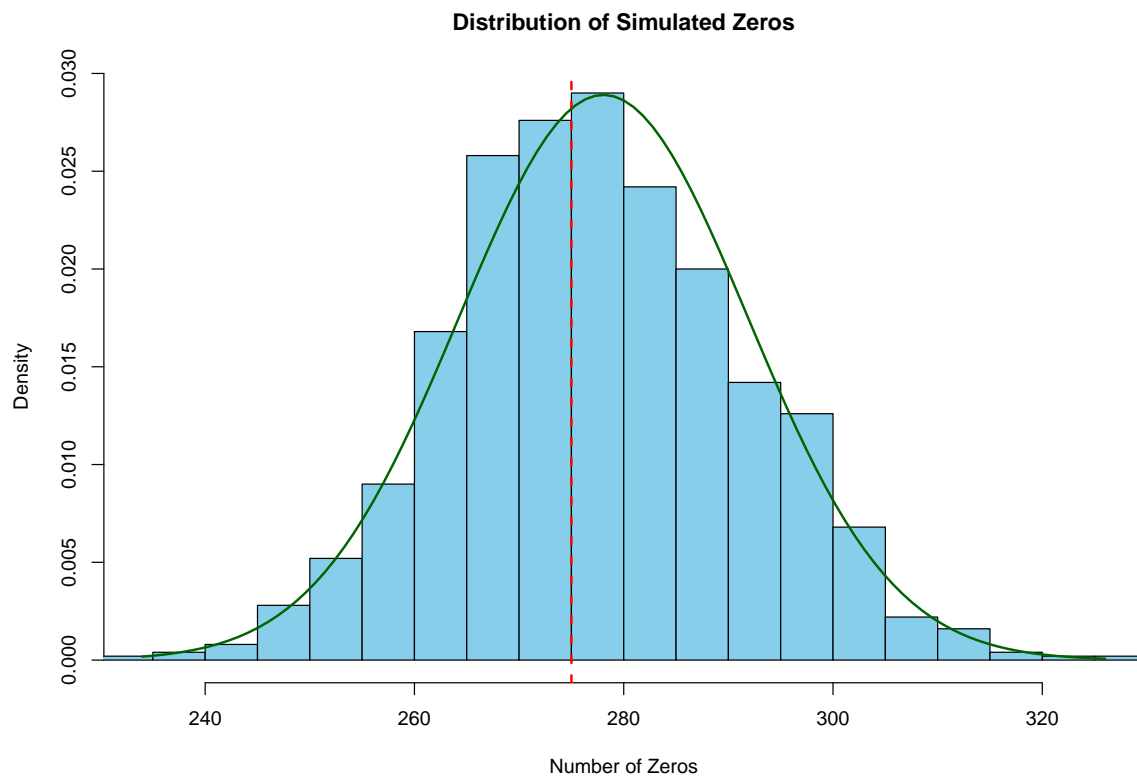
Dots should fall along the line



```

1 # Set seed for reproducibility
2 set.seed(123)
3
4 # Simulate new responses from the negative binomial model
5 sim_vals <- simulate(nb_model, nsim = 1000)
6
7 # Calculate the number of zeros in each simulation and in the observed data
8 zeros_sim <- colSums(sim_vals == 0)
9 zeros_obs <- sum(bioChemists$art == 0)
10
11 # Create a histogram of the number of zeros in the simulated data
12 hist(zeros_sim, breaks = 30, main = "Distribution of Simulated Zeros",
13      xlab = "Number of Zeros", col = "skyblue", border = "black",
14      xlim = range(c(zeros_sim, zeros_obs), na.rm = TRUE),
15      freq = FALSE)
16
17 # Add a vertical line representing the observed number of zeros
18 abline(v = zeros_obs, col = "red", lwd = 2, lty = 2)
19
20 # Overlay the normal distribution curve for reference
21 curve(dnorm(x, mean = mean(zeros_sim), sd = sd(zeros_sim)),
22      add = TRUE, col = "darkgreen", lwd = 2)

```

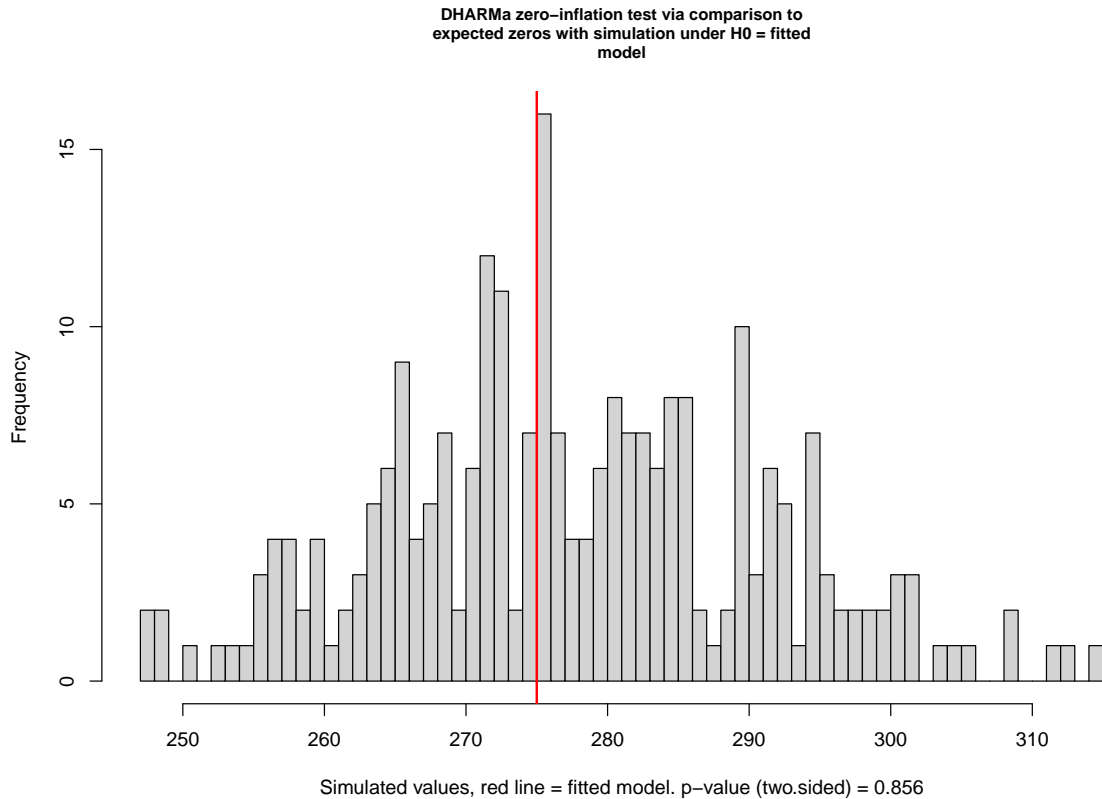


After simulating 1000 new responses from your fitted model, the distribution of zeros in the simulated datasets closely follows a normal curve. The vertical red line shows the actual number of zeros in the observed data. The fact that the observed zeros align well with the center of the distribution suggests that the model captures the number of zeros in the data quite well.

```
1 # Calculate p-value based on simulation results
2 p_value <- mean(zeros_sim >= zeros_obs)
3 cat("P-value from simulation: ", p_value, "\n")
```

P-value from simulation: 0.6

```
1 # Perform DHARMA test for zero-inflation
2 simulation_output <- simulateResiduals(fittedModel = nb_model)
3 dh_test <- testZeroInflation(simulation_output)
```

```
1 cat("P-value from DHARMa test: ", dh_test$p.value, "\n")
```

P-value from DHARMa test: 0.856

The calculated p-value based on the simulated zeros is 0.6. This indicates that the observed number of zeros is not unusually high or low compared to the simulated datasets, further confirming that the model appropriately accounts for the zeros in the data.

The calculated p-value based on the simulated zeros is 0.6. This indicates that the observed number of zeros is not unusually high or low compared to the simulated datasets, further confirming that the model appropriately accounts for the zeros in the data. The test returns a **p-value of 0.856**, which is well above the typical 0.05 threshold. This high p-value strongly suggests that there is no evidence of zero-inflation in the data. In other words, the number of zeros predicted by the model is consistent with what was observed, and there is no need for a more complex model (like a zero-inflated model).

Therefore, our model appropriately explains the factors influencing article production among biochemistry students, with **gender**, **number of kids under 5**, and **mentorship** being the key drivers.