

Report

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2/21/2020

Introduction

Our client, Reshma Satish, a Ph.D. student at Boston University's Department of Forensic Anthropology, administered a project involves fracturing 135 long deer bones using a standardized fracturing apparatus over 540 days. The bones are broken into 9 groups with 15 bones in each group and each group is fractured at different times (0 days, 30 days, 60 days, 90 days, 180 days, 270 days, etc.) Her goal was to investigate how the time of exposure of long bones affects variables such as the type of fracture angle, the type of fracture surface morphology, etc. which are created on the bones. Currently, our client only has data until day 360 since this experiment still keeps going so that we only have 7 groups bones right now.

This report will start with a description of the EDA, as well as Data cleaning/Data analysis/Data structure. Then we will describe the methods we will use on the modeling part, followed by our analysis.

Data Cleaning and EDA

Data structure

We are provided the data in an excel document with 7 groups of drying days and a total of 105 bones. There are 10 variables in the dataset, but we will only focus on 8 of them, with Bisect Fracture and Fracture-like as binary responses, Number of fragments as a numerical response, and Fracture Angle, Fracture Type, Fracture Surface, and Fracture Outline as unordered categorical responses. We will create dummy variables for Fractographic Features, considering there can be multiple features at the same time.

Data Cleaning

At first glance of the raw dataset, there are many NA inputs. After discussed with our client, we decide to change NA in Fracture Angle, Fracture Type, Fracture Surface, and Fracture Outline to non-applicable and change NA in Fractographic Features to No Feature. Moreover, we create numerical variable drying days from variable Bone Specimen for future analysis.

Create Dummy Variable

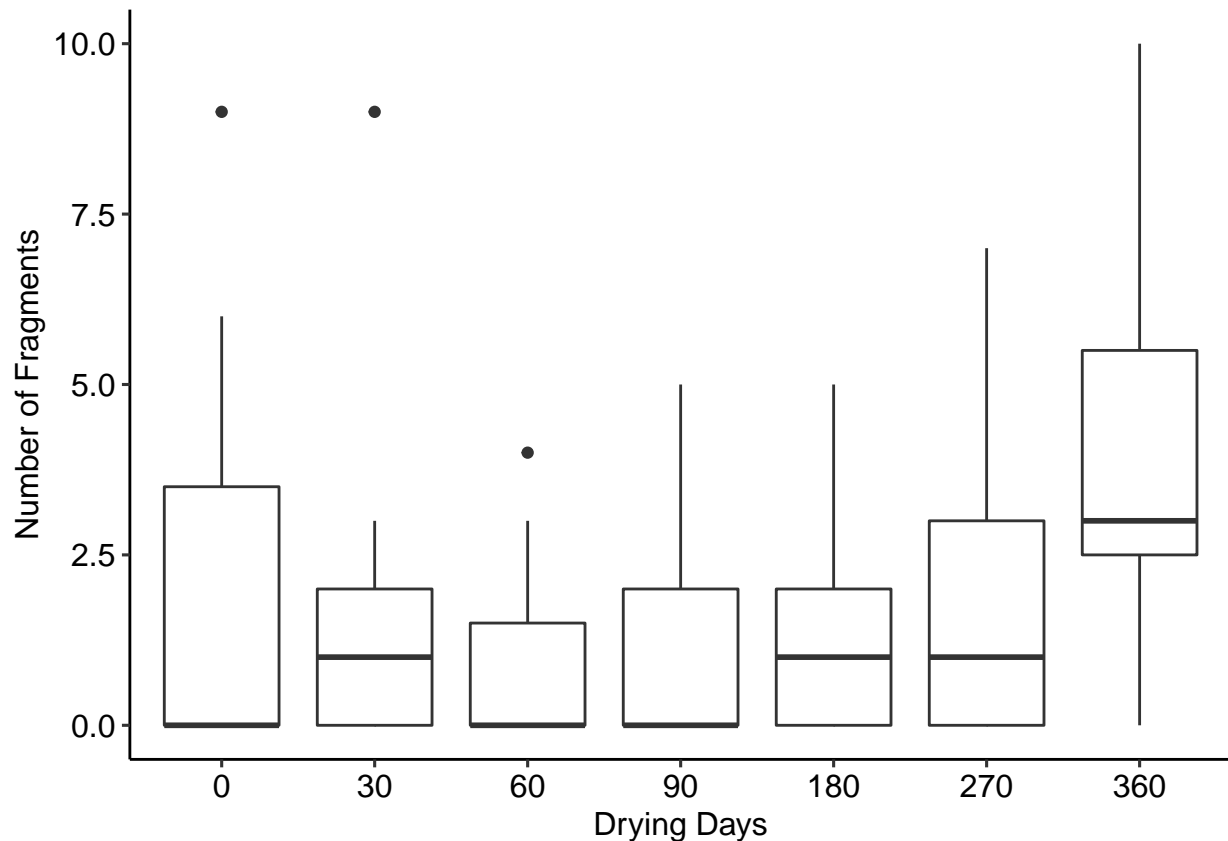
There are some observations have multiple features in the Fractographic Features variable. Thus, we create 6 dummy variables to indicate which feature appears for a given observation.

EDA

We conduct a basic exploratory data analysis (EDA) to visualize the data and find some patterns between variables. We focus on the two binary responses and the number of fragments.

Table 1: Bisecting Fracture and Fracture-like percentage for different drying-day groups

	0	30	60	90	180	270	360
Bisecting percentage	0.47	0.6	0.67	0.47	0.67	0.60	0.87
Fracture-like percentage	0.47	0.8	0.73	0.53	0.73	0.93	0.93



In the table, we give a bisecting percentage and fracture-like percentage for each group of bones in different drying days. We can see a pattern that with the drying days increasing, it's more likely to have a bisecting or fracture-like happened during the standardized fracturing apparatus.

In the boxplot, we can see several outliers in the first three groups and a large amount of zero value. It's hard to figure a clear pattern in the first four groups, but later on, the number of fragments is increased as the drying days increased.

Modeling & Interpretation

We used logistic regression, Poisson regression, negative binomial, and multinomial logit models based on different types of response variables in our dataset.

Fracture Type

According to the Fracture Type variable has 6 discrete outcomes and those outcomes aren't ordinal, which are non applicable, COMMINUTED SEGMENTAL, BUTTERFLY, OBLIQUE and TRANSVERSE. Then we used a normal multinomial logistic model.

```
## Call:
## multinom(formula = bone$`Fracture Type` ~ bone$days, trace = FALSE)
##
## Coefficients:
##              (Intercept) bone$days
## COMMINUTED           0.83   0.00217
## non applicable        1.52  -0.00245
## OBLIQUE              -0.19  -0.00278
## SEGMENTAL            -0.60  -0.00067
```

```
## TRANSVERSE          -1.98  -0.00437
##
## Std. Errors:
##              (Intercept) bone$days
## COMMUNITED          0.52    0.0026
## non applicable      0.50    0.0027
## OBLIQUE             0.69    0.0042
## SEGMENTAL           0.76    0.0041
## TRANSVERSE         1.43    0.0104
##
## Residual Deviance: 281
## AIC: 301
```

COMMUNITED relative to BUTTERFLY:

Intercept: This is the multinomial logit estimate for COMMUNITED relative to BUTTERFLY when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring COMMUNITED relative to BUTTERFLY is 0.83. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for COMMUNITED relative to BUTTERFLY. If a subject were to increase Days by one point, the multinomial log-odds of preferring COMMUNITED relative to BUTTERFLY would be expected to increase by 0.00217.

non applicable relative to BUTTERFLY

Intercept: This is the multinomial logit estimate for non-applicable relative to BUTTERFLY when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring non-applicable relative to BUTTERFLY is 1.52. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for non-applicable relative to BUTTERFLY. If a subject were to increase Days by one point, the multinomial log-odds of preferring non-applicable relative to BUTTERFLY would be expected to decrease by 0.00245.

OBLIQUE relative to BUTTERFLY:

Intercept: This is the multinomial logit estimate for OBLIQUE relative to BUTTERFLY when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring OBLIQUE relative to BUTTERFLY is -0.1913727. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for OBLIQUE relative to BUTTERFLY. If a subject were to increase Days by one point, the multinomial log-odds of preferring OBLIQUE relative to BUTTERFLY would be expected to decrease by 0.0027752170.

SEGMENTAL relative to BUTTERFLY:

Intercept: This is the multinomial logit estimate for SEGMENTAL relative to BUTTERFLY when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring SEGMENTAL relative to BUTTERFLY is -0.5994698. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for SEGMENTAL relative to BUTTERFLY. If a subject were to increase Days by one point, the multinomial log-odds of preferring SEGMENTAL relative to BUTTERFLY would be expected to decrease by 0.0006693986.

TRANSVERSE relative to BUTTERFLY:

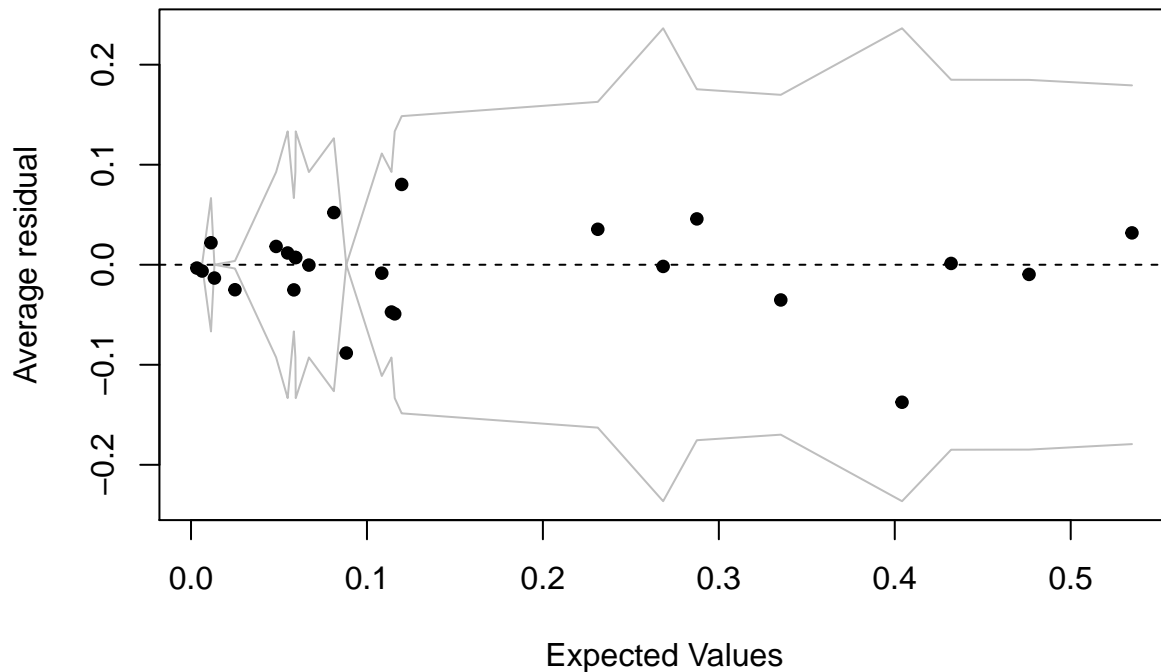
Intercept: This is the multinomial logit estimate for TRANSVERSE relative to BUTTERFLY when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring

TRANSVERSE relative to BUTTERFLY is -1.9804151. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for TRANSVERSE relative to BUTTERFLY. If a subject were to increase Days by one point, the multinomial log-odds of preferring TRANSVERSE relative to BUTTERFLY would be expected to decrease by 0.004371236.

Checking Residual

According to the Binned residual plot, there is not a clear pattern.

Binned residual plot



Checking P-values for each corresponding outcomes relative to baseline/BUTTERFLY

P-values of non-applicable is smaller than 0.05, so days makes a statistical significance for log-odds of preferring non-applicable relative to baseline/BUTTERFLY. P-values of COMMINUTED, OBLIQUE, SEGMENTAL and TRANSVERSE are larger than 0.05, so days make a statistically significant difference for log-odds of preferring COMMINUTED, OBLIQUE, SEGMENTAL and TRANSVERSE relative to baseline/BUTTERFLY.

	COMMUNUTED	non applicable	OBLIQUE	SEGMENTAL	TRANSVERSE
##	0.1141	0.0024	0.7824	0.4285	0.1652

Fracture Surface

```
## Call:
## multinom(formula = bone$`Fracture Surface` ~ bone$days, trace = FALSE)
##
## Coefficients:
##              (Intercept) bone$days
## non applicable          2.2  -0.0087
## ROUGH                 -23.6   0.0602
## SMOOTH                 2.3  -0.0075
##
```

```
## Std. Errors:
##              (Intercept) bone$days
## non applicable    5.7e-01    0.0025
## ROUGH            3.6e-05    0.0029
## SMOOTH           5.6e-01    0.0024
##
## Residual Deviance: 208
## AIC: 220
```

non applicable relative to INTERMEDIATE:

$\text{Log}(\text{Prob}(\text{non applicable})/\text{Prob}(\text{INTERMEDIATE})) = 2.185304 - 0.008706689 \cdot \text{Days}$

Intercept: This is the multinomial logit estimate for non-applicable relative to INTERMEDIATE when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring non-applicable relative to INTERMEDIATE is 2.185304. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for non-applicable relative to INTERMEDIATE. If a subject were to increase Days by one point, the multinomial log-odds of preferring non-applicable relative to INTERMEDIATE would be expected to decrease by 0.008706689.

ROUGH relative to INTERMEDIATE:

$\text{Log}(\text{Prob}(\text{ROUGH})/\text{Prob}(\text{INTERMEDIATE})) = -23.616556 + 0.060230466 \cdot \text{Days}$

Intercept: This is the multinomial logit estimate for ROUGH relative to INTERMEDIATE when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring ROUGH relative to INTERMEDIATE is -23.616556. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for ROUGH relative to INTERMEDIATE. If a subject were to increase Days by one point, the multinomial log-odds of preferring ROUGH relative to INTERMEDIATE would be expected to increase by 0.060230466.

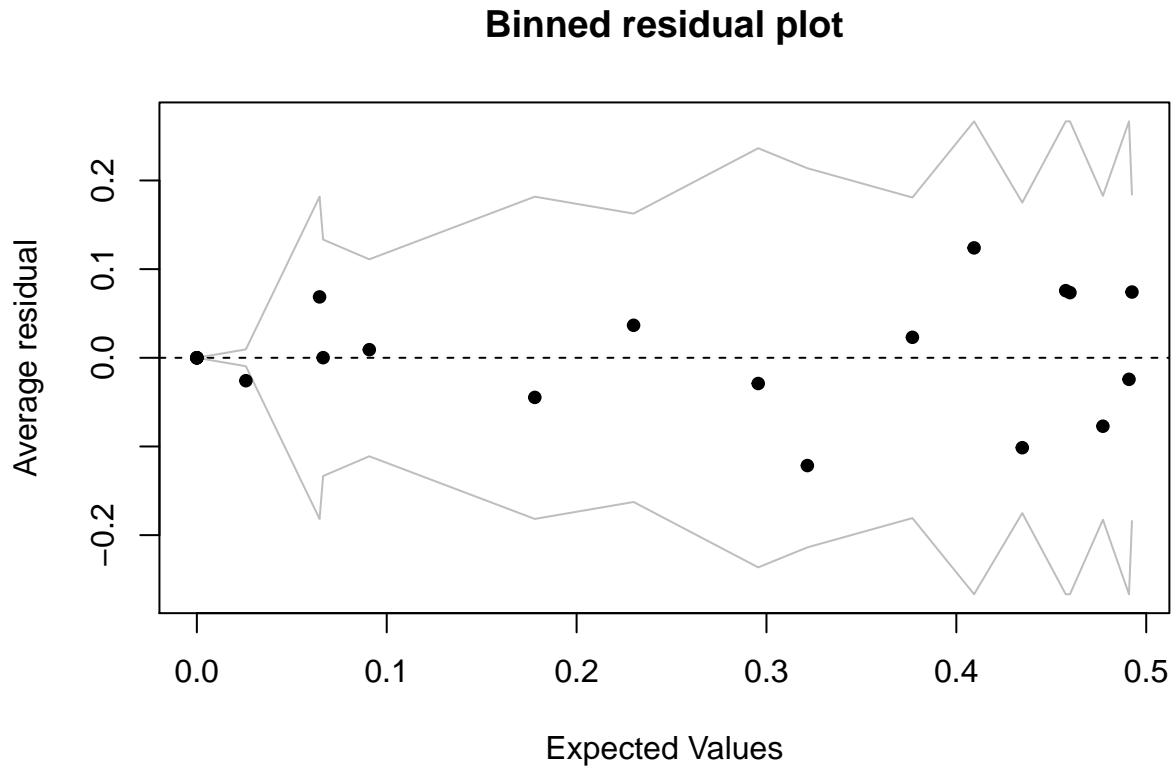
SMOOTH relative to INTERMEDIATE:

$\text{Log}(\text{Prob}(\text{SMOOTH})/\text{Prob}(\text{INTERMEDIATE})) = 2.255591 - 0.007492372 \cdot \text{Days}$

Intercept: This is the multinomial logit estimate for SMOOTH relative to INTERMEDIATE when the predictor variables in the model are evaluated at zero. For day equals to zero, the logit for preferring SMOOTH relative to INTERMEDIATE is 2.255591. Note that evaluating days equals to zero indicated that the day of starting the experiment Days: This is the multinomial logit estimate for a one-unit increase in Days for SMOOTH relative to INTERMEDIATE. If a subject were to increase Days by one point, the multinomial log-odds of preferring SMOOTH relative to INTERMEDIATE would be expected to decrease by 0.007492372.

Checking residual

According to the Binned residual plot, there is not a clear pattern.



Checking P-values for each corresponding outcomes relative to Baseline/INTERMEDIATE

P-values of ROUGH is smaller than 0.05, so days makes a statistical significance for log-odds of preferring ROUGH relatives to baseline/INTERMEDIATE.

P-values of non-applicable and SMOOTH are larger than 0.05, so days make a statistically significant difference for log-odds of preferring non-applicable and SMOOTH relative to baseline/INTERMEDIATE.

## non applicable	ROUGH	SMOOTH
## 0.1141	0.0024	0.7824

Bisect Fracture

Since the response variable “bisect fracture” is a binary outcome (0 or 1), we are using logistic regression to figure out the relationship between the probability of “bisect fracture” and the value of “days”.

In addition, when “bisect fracture” is 0, it means the bone did not break by the standard fracturing machine, otherwise, it means the bone broke by the machine.

```
##
## Call:
## glm(formula = bone$`Bisecting Fracture` ~ bone$days, family = binomial())
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
##    -1.73    -1.23     0.71     1.04     1.16
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.02996    0.30127   0.10   0.921
## bone$days    0.00339    0.00174   1.94   0.052 .
## ---
```

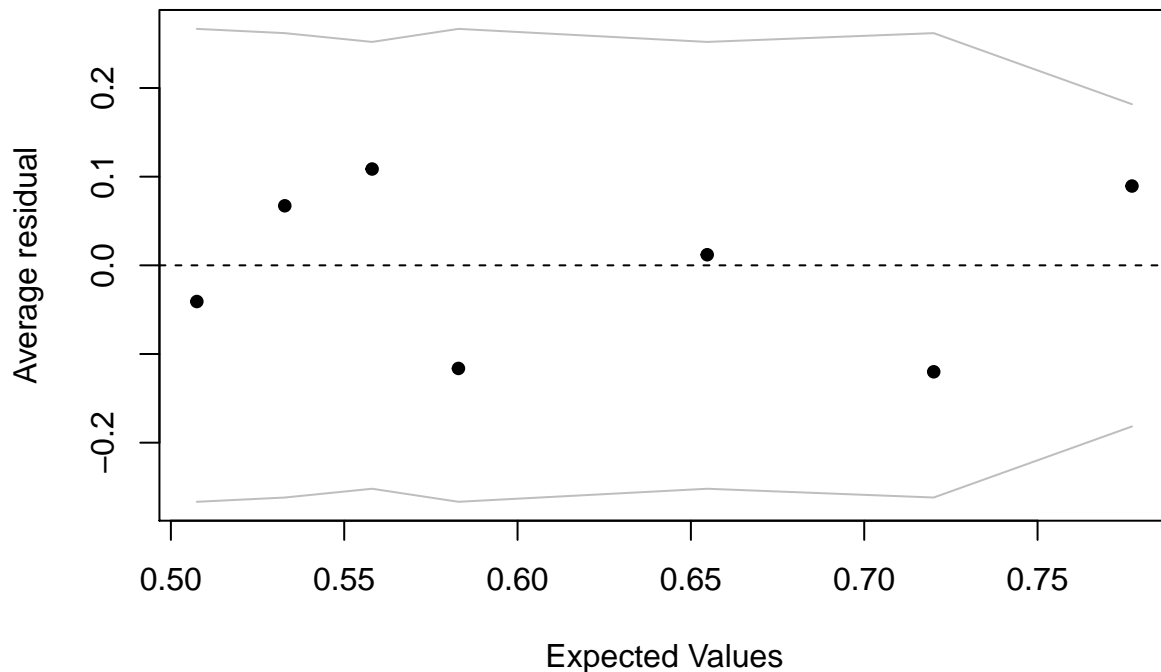
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 139.55  on 104  degrees of freedom
## Residual deviance: 135.53  on 103  degrees of freedom
## AIC: 139.5
##
## Number of Fisher Scoring iterations: 4
```

From the output, the estimated intercept coefficient 0.029 corresponds to the log odds of breaking the bone with average days, in other words, on average days, the expected probability of broke the bone is $\text{expit}(0.029)=0.4927=49\%$.

And a one-unit increase in the predictor “days” increases the log odds of breaking the bone (versus not broke the bone) by 0.0034.

Further, the p-value of days is 0.052 indicates that there is no strong evident but moderate evidence in support of the differences of the bone broke by the machine or not affected by drying time.

Binned residual plot



Since the discrete residual plot does not tell us much about the model fit, we are using Binned residual plot for this model. Due to every point fall within the bounds, our model fits well in this case.

Fracture like

Since “Fracture-like” is a binary outcome(0 or 1) as well, therefore, as an idea with the above part, we used logistic regression to figure out their relationship.

Besides, when “Fracture-like” is 0, it means the bone has no surface feature after cut by the standard fracturing machine, otherwise, it means fracturing machine made a mark on the bone.

```
##
## Call:
## glm(formula = bone$`Fracture-like` ~ bone$days, family = binomial())
```

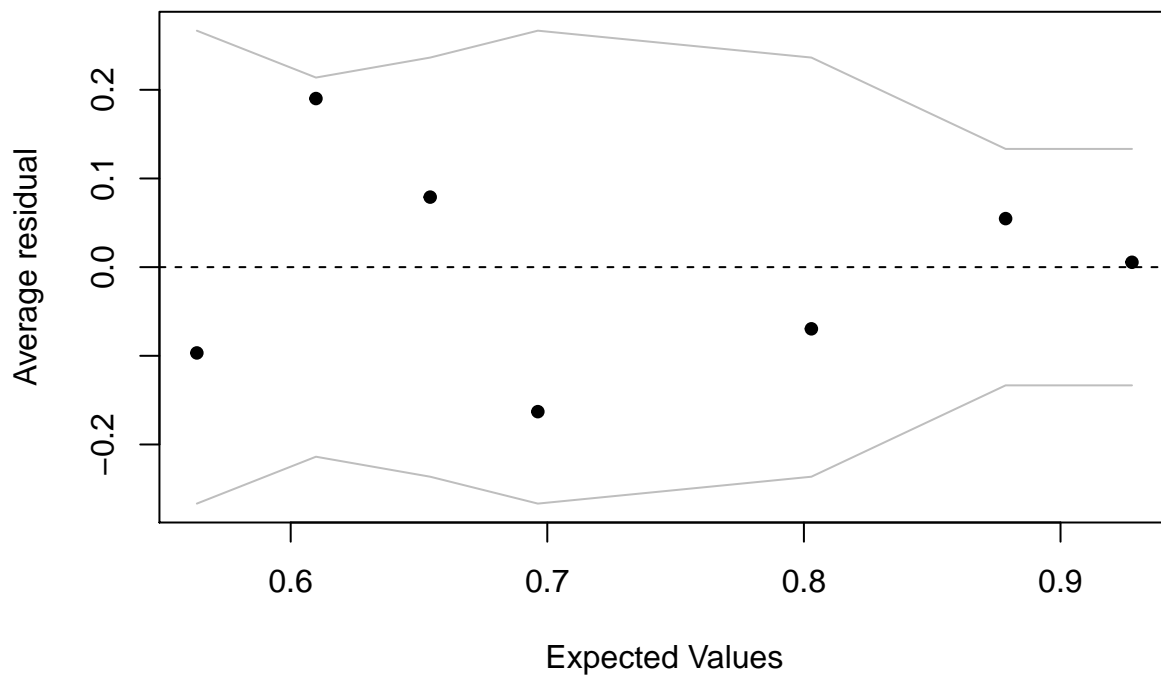
```
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.293  -1.288   0.509   0.921   1.071
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.25510    0.32022   0.80  0.4257
## bone$days    0.00639    0.00230   2.78  0.0055 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 121.78  on 104  degrees of freedom
## Residual deviance: 112.13  on 103  degrees of freedom
## AIC: 116.1
##
## Number of Fisher Scoring iterations: 4
```

From the output, the estimated intercept coefficient 0.2551 corresponds to the log odds of making a mark on the bone with average days, in other words, on average days, the expected probability of making a mark on bone is $\text{expit}(0.2551) = 0.436 = 43.6\%$.

And a one-unit increase in the predictor “days” increases the log odds of making a mark on the bone (versus no surface feature on the bone) by 0.0064.

Also, the p-value of days is 0.0055 indicates that there is strong evidence in determining whether the bone has any surface feature after cut by the machine affected by drying time.

Binned residual plot



Same logic with the above part, our model fits well in this case.

Fracture Angle

As “Fracture Angle” as no natural-order variable(nominal), since we cannot compare the order of angle of fresh bone and dry bone, and also N/A(non-applicable) in this variable, so we used a multinomial logit model in this case, that the outcome variable in this model has more than 2 levels.

```
## Call:
## multinom(formula = bone$`Fracture Angle` ~ bone$days, trace = FALSE)
##
## Coefficients:
##              (Intercept) bone$days
## non applicable          2.2   -0.0057
## OBLIQUE                 2.2   -0.0030
## RIGHT ANGLES           -1.2   -0.0077
##
## Std. Errors:
##              (Intercept) bone$days
## non applicable          0.63    0.0029
## OBLIQUE                 0.62    0.0027
## RIGHT ANGLES           1.48    0.0104
##
## Residual Deviance: 200
## AIC: 212
```

From the output, the baseline is Fracture Angle = Intermediate.

A one-unit increase in the variable “days” is associated with the decrease in the log odds of being in an Intermediate fracture angle vs. non-applicable fracture angle in the amount of 0.0057.

A one-unit increase in the variable “days” is associated with the decrease in the log odds of being in an Intermediate fracture angle vs. oblique fracture angle in the amount of 0.003.

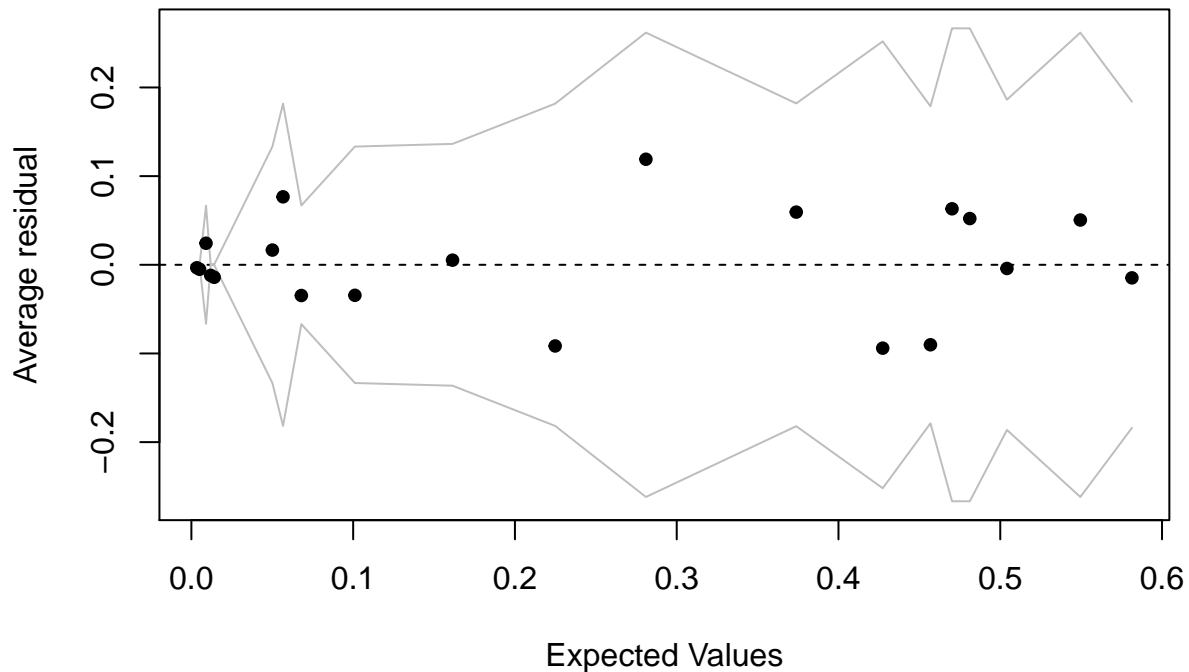
In other words, if the one-unit increase in “days”, your chances of staying in the intermediate fracture angle category are higher compared to staying in non-applicable and oblique.

Since summary of multinomial logit model does not provide p-values, we can get significance of the coefficients by calculating z score and input it into the formula: $z = (x_i - \bar{x})/s$ where coefficients of summary represents $x_i - \bar{x}$, and Std.Errors of summary represents s .

```
##              (Intercept) bone$days
## non applicable          0.00037    0.047
## OBLIQUE                 0.00034    0.266
## RIGHT ANGLES           0.41049    0.458
```

From the output, it represents the p-value of coefficients. Only non-applicable has strong evidence in determining whether affected by drying time because its p-value is $0.047 < 5\%$.

Binned residual plot



It looks like our model fit kind of well in this case, but there might not good enough when expected values small.

Number of Fragments

Considering “Number of Fragments” as a numerical variable, we use the Poisson regression at first.

```
fit.Number_of_Fragments1 <- glm(bone$`Number of Fragments` ~ bone$days, family="poisson")
summary(fit.Number_of_Fragments1) #estimated coefficients
```

```
##
## Call:
## glm(formula = bone$`Number of Fragments` ~ bone$days, family = "poisson")
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.480  -1.685  -0.741   0.649   4.522
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.196437   0.123824   1.59    0.11
## bone$days    0.002574   0.000549   4.69 2.8e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 296.20  on 104  degrees of freedom
## Residual deviance: 274.71  on 103  degrees of freedom
## AIC: 452
##
## Number of Fisher Scoring iterations: 6
```

```
pchisq(fit.Number_of_Fragments1$deviance,df=fit.Number_of_Fragments1$df.residual, lower.tail=FALSE)
```

```
## [1] 1.5e-17
```

```
regout <- glm(bone$`Number of Fragments`~bone$days, family=quasipoisson)
summary(glm(regout)$dispersion
```

```
## [1] 2.9
```

Here our null hypothesis is that our model is correctly specified. The low p-value shows that we can reject this hypothesis, thus the Poisson regression model fits poorly. Next, we check the dispersion of the data. We can see the variance of random component is roughly 3 times the size of the mean. There may be an over-dispersion problem. So we consider using a negative binomial model.

```
fit.Number_of_Fragments2 <- glm.nb(bone$`Number of Fragments` ~ bone$days)
summary(fit.Number_of_Fragments2)
```

```
##
```

```
## Call:
```

```
## glm.nb(formula = bone$`Number of Fragments` ~ bone$days, init.theta = 0.833740805,
##       link = log)
```

```
##
```

```
## Deviance Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -1.579  -1.301  -0.433   0.350   2.204
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.24931    0.20348   1.23    0.220
## bone$days    0.00225    0.00103   2.18    0.029 *
```

```
## ---
```

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

```
##
```

```
## (Dispersion parameter for Negative Binomial(0.83) family taken to be 1)
```

```
##
```

```
##      Null deviance: 117.06  on 104  degrees of freedom
```

```
## Residual deviance: 111.39  on 103  degrees of freedom
```

```
## AIC: 386.7
```

```
##
```

```
## Number of Fisher Scoring iterations: 1
```

```
##
```

```
##
```

```
##              Theta:  0.834
```

```
##            Std. Err.:  0.212
```

```
##
```

```
## 2 x log-likelihood:  -380.656
```

```
pchisq(fit.Number_of_Fragments2$deviance,df=fit.Number_of_Fragments2$df.residual, lower.tail=FALSE)
```

```
## [1] 0.27
```

Using the negative binomial model, we have a better fit. The only variable “days” has a coefficient of 0.002247, which is statistically significant. This means that for each one-unit increase in “days”, the expected log count of the number of fragments increases by 0.002247. It can be also interpreted as for each 100 unit increase in “days”, the expected count of the number of fragments will be increased by 1.25 times.

Fracture Outline

We assume “Fracture Outline” as no natural-order(nominal) variable, same reason as the “Fracture Angle” part, thus we used a multinomial logit model.

```
##                (Intercept) bone$days
## INTERMEDIATE      -1.71    -0.0155
## non applicable      0.13    -0.0043
## TRANSVERSE       -3.38    -0.0059
```

From the output, the baseline is Fracture Angle = Curved/Jagged.

A one-unit increase in the variable “days” is associated with the decrease in the log odds of being in curved fracture outline vs. intermediate fracture outline in the amount of 0.0155.

A one-unit increase in the variable “days” is associated with the decrease in the log odds of being in curved fracture outline vs. non-applicable fracture outline in the amount of 0.0043.

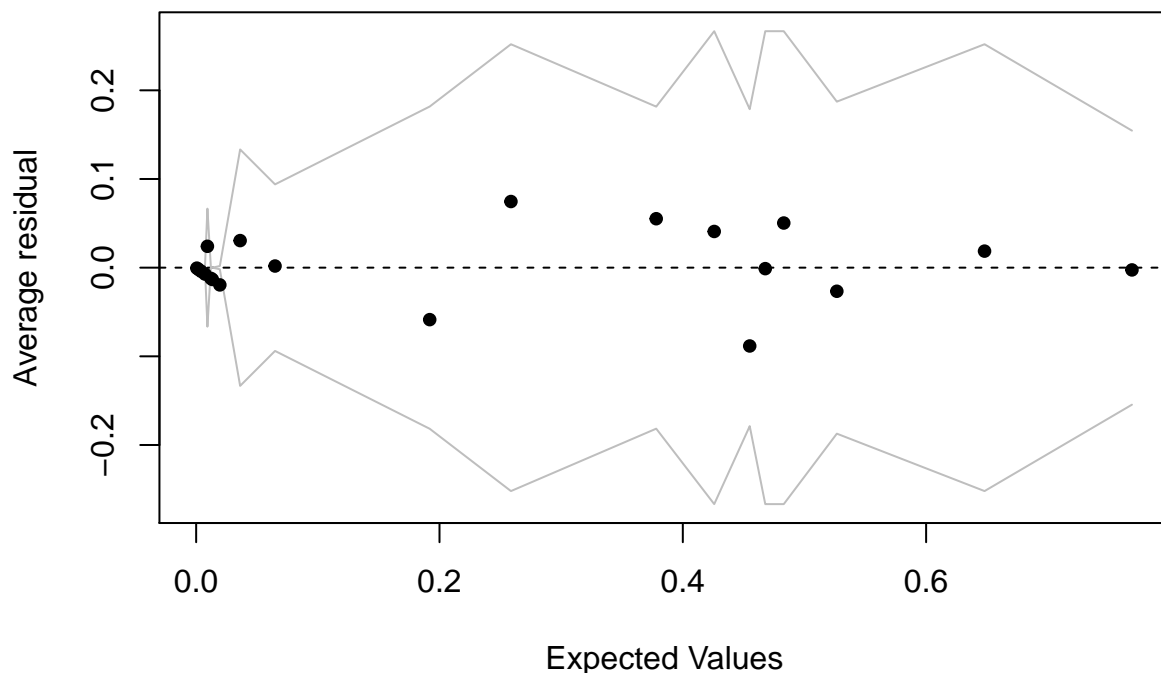
In other words, if a one-unit increase in “days”, your chances of staying in the curved/jagged fracture outline category are higher compared to staying in non-applicable, intermediate and transverse.

Get significance of the coefficients by calculating z score and input it into the formula:

```
##                (Intercept) bone$days
## INTERMEDIATE      0.027     0.184
## non applicable     0.686     0.017
## TRANSVERSE       0.014     0.565
```

From the output, it represents the p-value of coefficients. Only the non-applicable has strong evidence for determining whether it affected by drying time because its p-value is $0.017 < 5\%$.

Binned residual plot



It looks like our model fit kind of well in this case, except there might not good enough when expected values small.

Fractographic Features

We have 6 different features since some of the features appear at the same time, therefore we create 6 dummy variables for different features, and build a logistic regression model for each feature to figuring out their relationship. Then, we will use the chi-square test to evaluate whether 2 features are correlated.

Chi-square test for Independence

The null hypothesis of chi-square: 2 variables/features are independent with each other.

```
tb.1 = table(bone$`WAKE HACKLE`, bone$`BONE HACKLE`)
chisq.test(tb.1)
```

```
## Warning in chisq.test(tb.1): Chi-squared approximation may be incorrect
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.1
## X-squared = 12, df = 1, p-value = 5e-04
```

Since $p\text{-value } 0.0005 < 0.01$ significant level, therefore, we have strong evidence to reject the null hypothesis. Thus, “WAKE HACKLE” related to “BONE HACKLE”.

```
tb.2 = table(bone$`WAKE HACKLE`, bone$`BONE MIRROR`)
chisq.test(tb.2)
```

```
## Warning in chisq.test(tb.2): Chi-squared approximation may be incorrect
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.2
## X-squared = 5e-30, df = 1, p-value = 1
```

Since $p\text{-value } 1 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “WAKE HACKLE” is independent of “BONE MIRROR”.

```
tb.3 = table(bone$`WAKE HACKLE`, bone$`CANTILEVER CURL`)
chisq.test(tb.3)
```

```
## Warning in chisq.test(tb.3): Chi-squared approximation may be incorrect
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.3
## X-squared = 0.1, df = 1, p-value = 0.7
```

Since $p\text{-value } 0.7 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “WAKE HACKLE” is independent of “CANTILEVER CURL”.

```
tb.4 = table(bone$`WAKE HACKLE`, bone$`ARREST RIDGE`)
chisq.test(tb.4)
```

```
## Warning in chisq.test(tb.4): Chi-squared approximation may be incorrect
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.4
```

```
## X-squared = 5, df = 1, p-value = 0.03
```

Since $p\text{-value } 0.03 < 0.05$ significant level, therefore, we have somewhat strong evidence to reject the null hypothesis. Thus, “WAKE HACKLE” is related to “ARREST RIDGE”.

```
tb.5 = table(bone$`WAKE HACKLE`, bone$`WALLNER LINES`)
chisq.test(tb.5)
```

```
## Warning in chisq.test(tb.5): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: tb.5
```

```
## X-squared = 4, df = 1, p-value = 0.05
```

Since $p\text{-value } 0.05 = 0.05$ significant level, therefore, we have somewhat strong evidence to retain the null hypothesis. Thus, “WAKE HACKLE” is independent of “WALLNER LINES”.

```
tb.6 = table(bone$`BONE HACKLE`, bone$`BONE MIRROR`)
chisq.test(tb.6)
```

```
## Warning in chisq.test(tb.6): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: tb.6
```

```
## X-squared = 7e-31, df = 1, p-value = 1
```

Since $p\text{-value } 1 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “BONE HACKLE” is independent of “BONE MIRROR”.

```
tb.7 = table(bone$`BONE HACKLE`, bone$`CANTILEVER CURL`)
chisq.test(tb.7)
```

```
## Warning in chisq.test(tb.7): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: tb.7
```

```
## X-squared = 3e-30, df = 1, p-value = 1
```

Since $p\text{-value } 1 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “BONE HACKLE” is independent of “CANTILEVER CURL”.

```
tb.8 = table(bone$`BONE HACKLE`, bone$`ARREST RIDGE`)
chisq.test(tb.8)
```

```
## Warning in chisq.test(tb.8): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: tb.8
```

```
## X-squared = 8, df = 1, p-value = 0.005
```

Since $p\text{-value } 0.005 < 0.01$ significant level, therefore, we have strong evidence to reject the null hypothesis. Thus, “BONE HACKLE” is related to “ARREST RIDGE”.

```
tb.9 = table(bone$`BONE HACKLE`, bone$`WALLNER LINES`)
chisq.test(tb.9)
```

```
## Warning in chisq.test(tb.9): Chi-squared approximation may be incorrect
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.9
## X-squared = 2e-30, df = 1, p-value = 1
```

Since p-value $1 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “BONE HACKLE” is independent of “WALLER LINES”.

```
tb.10 = table(bone$`BONE MIRROR`, bone$`CANTILEVER CURL`)
chisq.test(tb.10)
```

```
## Warning in chisq.test(tb.10): Chi-squared approximation may be incorrect
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.10
## X-squared = 2e-30, df = 1, p-value = 1
```

```
tb.11 = table(bone$`BONE MIRROR`, bone$`ARREST RIDGE`)
chisq.test(tb.11)
```

```
## Warning in chisq.test(tb.11): Chi-squared approximation may be incorrect
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.11
## X-squared = 2e-30, df = 1, p-value = 1
```

```
tb.12 = table(bone$`BONE MIRROR`, bone$`WALLNER LINES`)
chisq.test(tb.12)
```

```
## Warning in chisq.test(tb.12): Chi-squared approximation may be incorrect
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.12
## X-squared = 1e-30, df = 1, p-value = 1
```

Since triple p-value $1 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “BONE MIRROR” is independent of “CANTILEVER CURL”, “ARREST RIDGE” and “WALLNER LINES”.

```
tb.13 = table(bone$`CANTILEVER CURL`, bone$`ARREST RIDGE`)
chisq.test(tb.13)
```

```
## Warning in chisq.test(tb.13): Chi-squared approximation may be incorrect
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tb.13
```

```
## X-squared = 2e-30, df = 1, p-value = 1
```

```
tb.14 = table(bone$`CANTILEVER CURL`, bone$`WALLNER LINES`)  
chisq.test(tb.14)
```

```
## Warning in chisq.test(tb.14): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: tb.14
```

```
## X-squared = 1e-30, df = 1, p-value = 1
```

Since both p-value $1 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “CANTILEVER CURL” is independent of “ARREST RIDGE” and “WALLNER LINES”.

```
tb.15 = table(bone$`ARREST RIDGE`, bone$`WALLNER LINES`)  
chisq.test(tb.15)
```

```
## Warning in chisq.test(tb.15): Chi-squared approximation may be incorrect
```

```
##
```

```
## Pearson's Chi-squared test with Yates' continuity correction
```

```
##
```

```
## data: tb.15
```

```
## X-squared = 1e-30, df = 1, p-value = 1
```

Since p-value $1 > 0.05$ significant level, therefore, we have strong evidence to retain the null hypothesis. Thus, “ARREST RIDGE” is independent of “WALLNER LINES”.

Logistic Regression for six feature v.s. days

```
##
```

```
## Call:
```

```
## glm(formula = bone$`WAKE HACKLE` ~ bone$days, family = binomial())
```

```
##
```

```
## Deviance Residuals:
```

```
##      Min       1Q   Median       3Q      Max
```

```
## -0.683  -0.676  -0.664  -0.645   1.829
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept) -1.337128   0.367130  -3.64  0.00027 ***
```

```
## bone$days   -0.000352   0.001985  -0.18  0.85938
```

```
## ---
```

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

```
##
```

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

```
##
```

```
##      Null deviance: 105.08  on 104  degrees of freedom
```

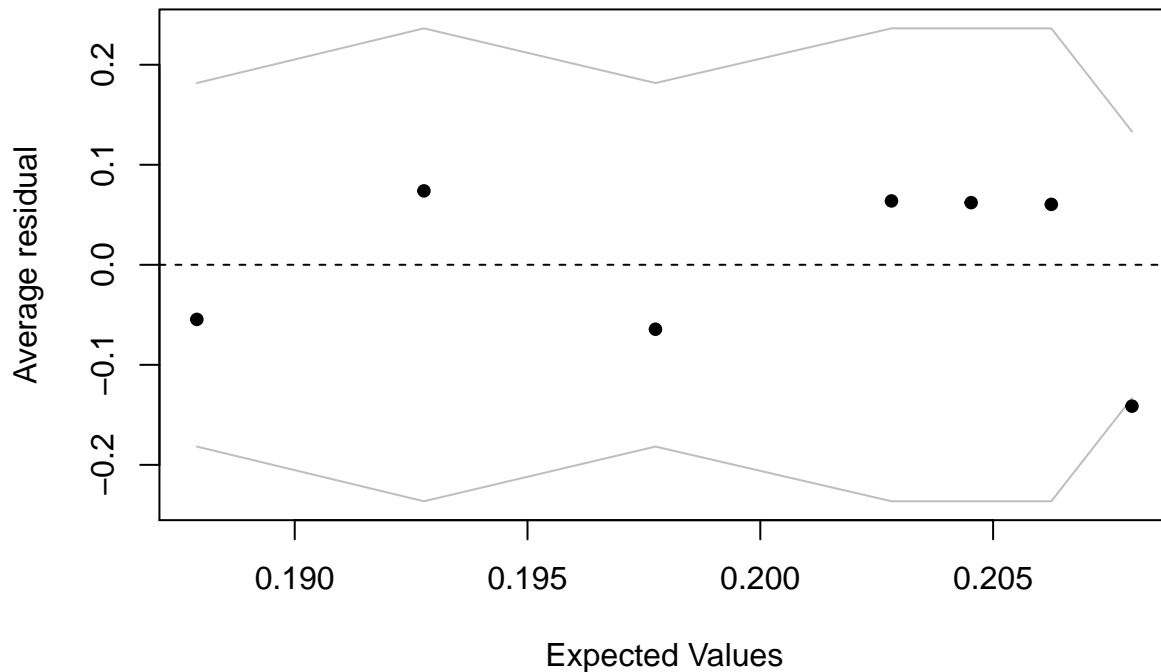
```
## Residual deviance: 105.05  on 103  degrees of freedom
```

```
## AIC: 109.1
```

```
##
```

```
## Number of Fisher Scoring iterations: 4
```


Binned residual plot



From the output, the estimated intercept coefficient -1.337 corresponds to the log odds of having a wake hackle feature on the bone with average days, in other words, on average days, expected probability of having a wake hackle feature on bone is $\text{expit}(-1.337)=0.208=20.8\%$.

And the one-unit increase in the predictor “days” increases the log odds of having a wake hackle feature on the bone (versus no-wake hackle feature on the bone) by -0.00035.

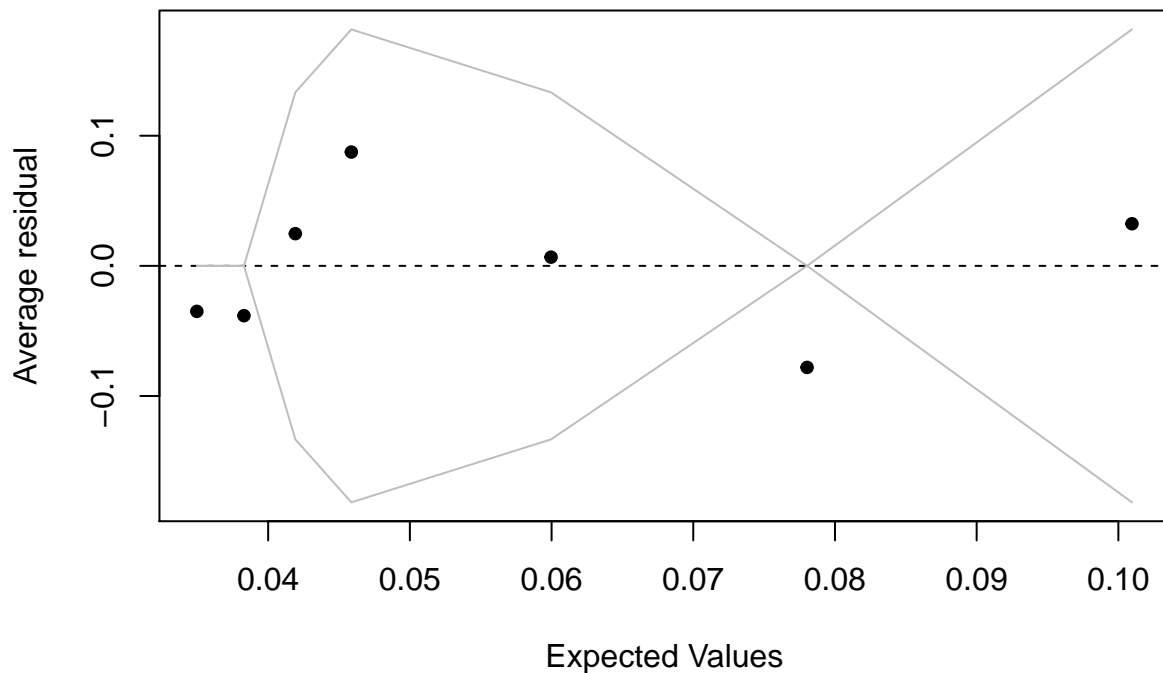
We can see the influence of drying days is relatively small and the 0.86 p-value shows no evidence in support of the differences of the wake hackle feature when drying time changes.

Binned residual plot shows our model fits well in this case.

```
##
## Call:
## glm(formula = bone$`BONE HACKLE` ~ bone$days, family = binomial())
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.461  -0.403  -0.306  -0.279   2.519
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.31778    0.73705  -4.50  6.7e-06 ***
## bone$days    0.00314    0.00324   0.97    0.33
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 45.997  on 104  degrees of freedom
## Residual deviance: 45.067  on 103  degrees of freedom
## AIC: 49.07
##
```

```
## Number of Fisher Scoring iterations: 6
```

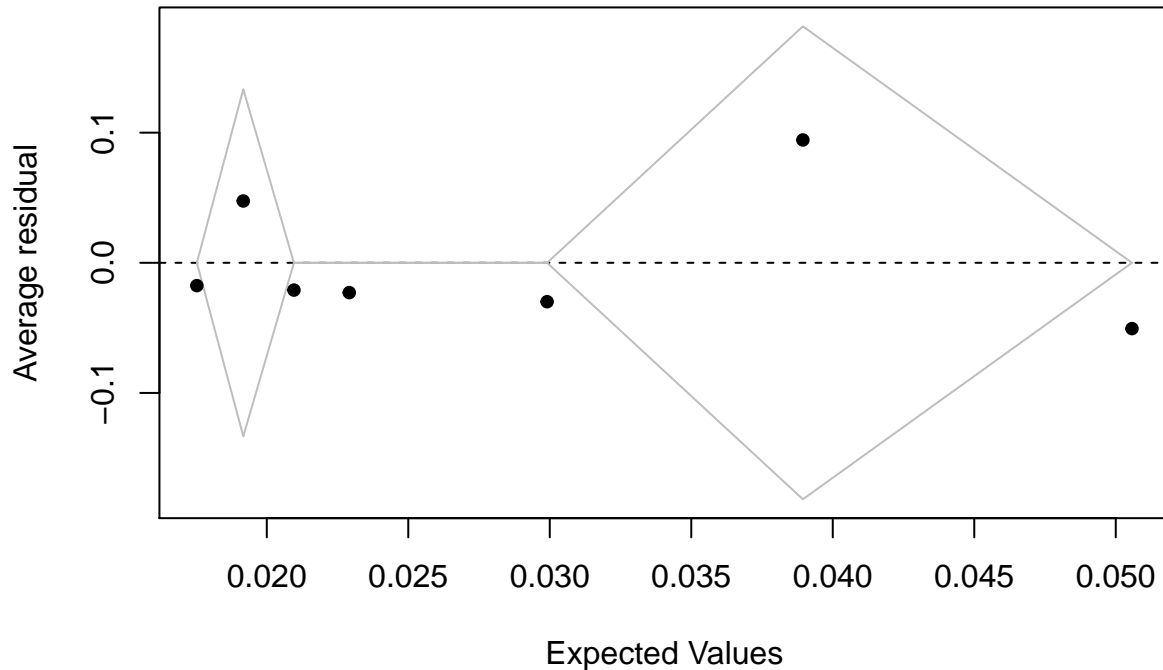
Binned residual plot



Again,
the low coefficient and p-value of the variable days show no evidence in support of the differences in the bone
hackle feature when drying time changes.
Binned residual plot with only a few points outside the bound shows our model fits quite well in this case.

```
##
## Call:
## glm(formula = bone$`BONE MIRROR` ~ bone$days, family = binomial())
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.322  -0.282  -0.215  -0.197   2.812
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -4.02622    1.02982  -3.91 9.2e-05 ***
## bone$days    0.00304    0.00449   0.68    0.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 27.246  on 104  degrees of freedom
## Residual deviance: 26.795  on 103  degrees of freedom
## AIC: 30.8
##
## Number of Fisher Scoring iterations: 6
```

Binned residual plot



Again, the low coefficient and p-value of the variable days show no evidence in support of the differences in the bone mirror feature when drying time changes.

Binned residual plot with most points outside the bound shows our model fits bad in this case.

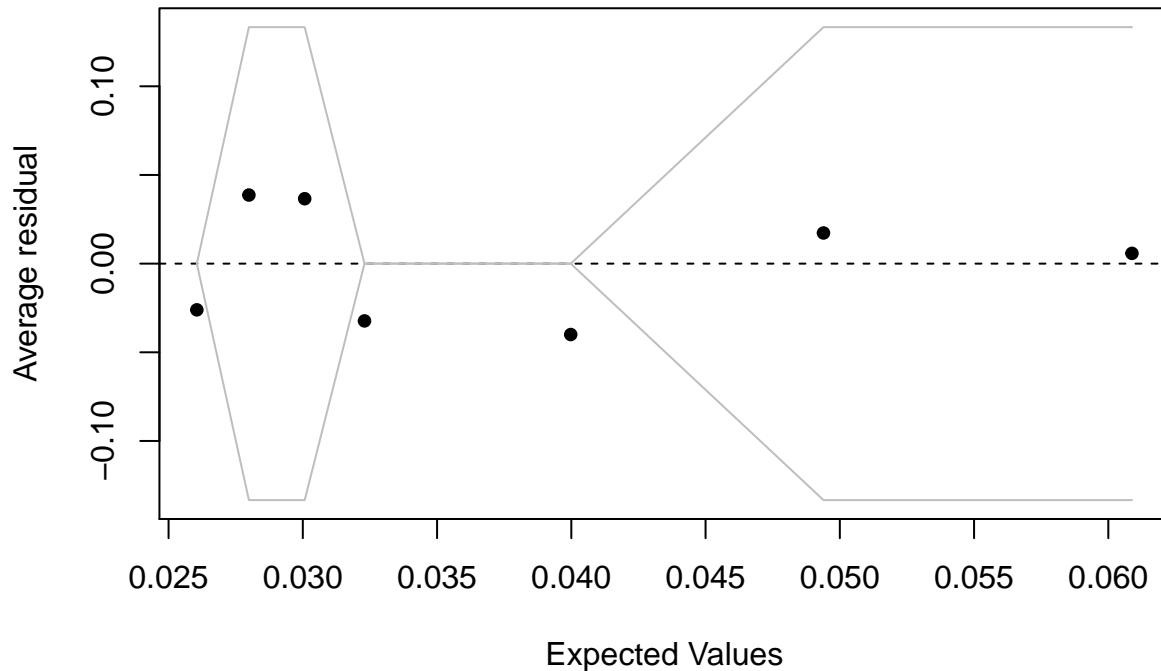
```
## # A tibble: 2 x 2
##   `BONE MIRROR`    n
##   <fct>          <int>
## 1 0             102
## 2 1              3
```

We only have 3 bones have the bone mirror feature, that may be the reason for the poor fitting.

```
##
## Call:
## glm(formula = bone$`CANTILEVER CURL` ~ bone$days, family = binomial())
##
## Deviance Residuals:
##   Min       1Q   Median       3Q      Max
## -0.354  -0.318  -0.256  -0.238   2.674
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.62120    0.86550  -4.18  2.9e-05 ***
## bone$days    0.00246    0.00392   0.63    0.53
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##   Null deviance: 33.987  on 104  degrees of freedom
## Residual deviance: 33.601  on 103  degrees of freedom
```

```
## AIC: 37.6
##
## Number of Fisher Scoring iterations: 6
```

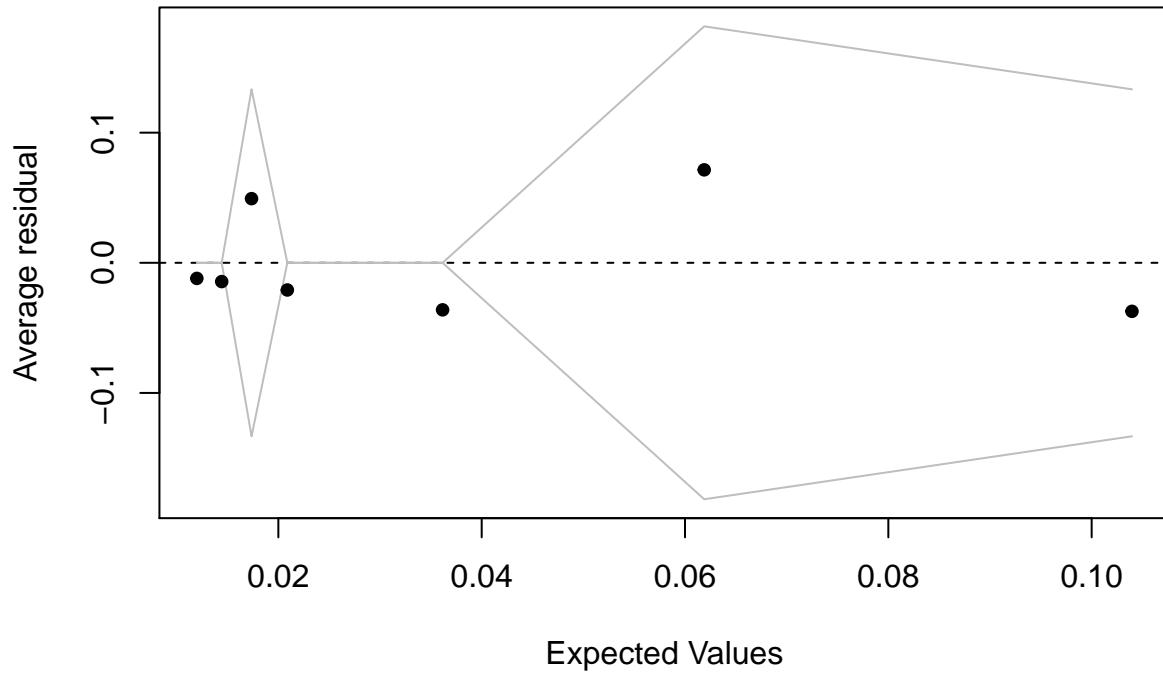
Binned residual plot



Again, the low coefficient and p-value of the variable days show no evidence in support of the differences in the cantilever curl feature when drying time changes. Binned residual plot with most points inside the bound shows our model fits quite good in this case.

```
##
## Call:
## glm(formula = bone$`ARREST RIDGE` ~ bone$days, family = binomial())
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.469  -0.357  -0.205  -0.171   2.847
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -4.41229    1.10916  -3.98  6.9e-05 ***
## bone$days    0.00627    0.00417   1.50    0.13
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 33.987  on 104  degrees of freedom
## Residual deviance: 31.525  on 103  degrees of freedom
## AIC: 35.52
##
## Number of Fisher Scoring iterations: 6
```

Binned residual plot



```
## # A tibble: 2 x 2
##   `ARREST RIDGE`      n
##   <fct>          <int>
## 1 0             101
## 2 1              4
```

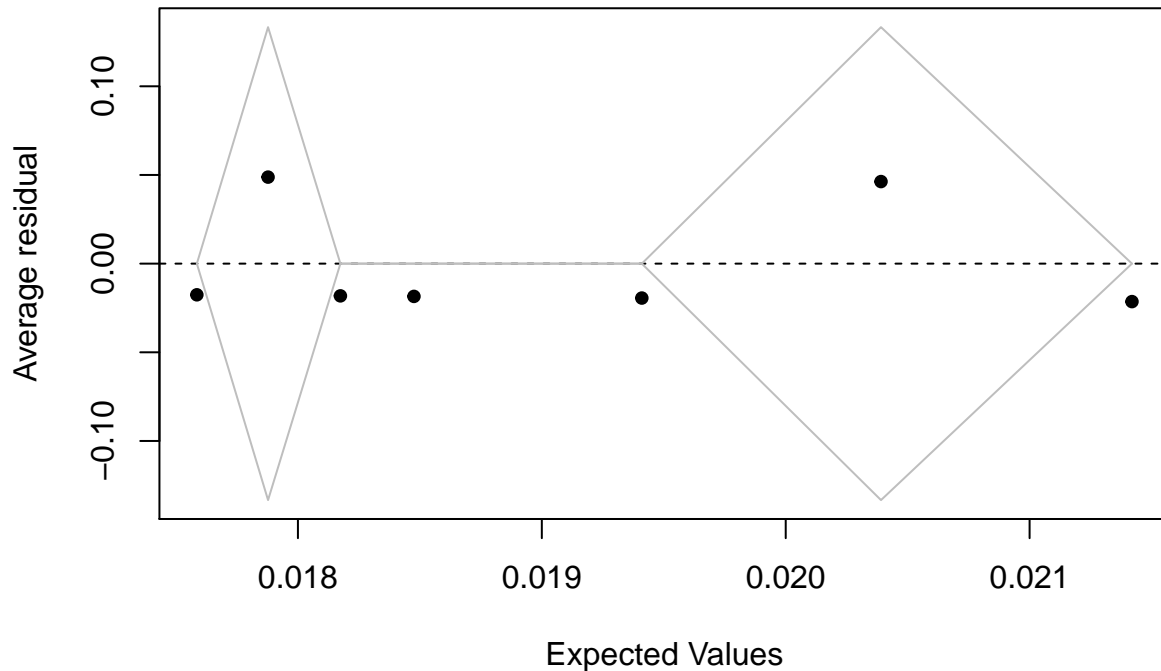
Again, the low coefficient and p-value of the variable days show no evidence in support of the differences in the arrest ridge feature when drying time changes.

Binned residual plot with most points outside the bound shows our model fits poor in this case. The possible reason is that we only have 4 bones have the arrest ridge feature

```
##
## Call:
## glm(formula = bone$`WALLNER LINES` ~ bone$days, family = binomial())
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.208  -0.203  -0.193  -0.190   2.837
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -4.022938   1.108503  -3.63  0.00028 ***
## bone$days    0.000559   0.005660   0.10  0.92136
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 19.805  on 104  degrees of freedom
## Residual deviance: 19.795  on 103  degrees of freedom
```

```
## AIC: 23.8
##
## Number of Fisher Scoring iterations: 6
```

Binned residual plot



```
## # A tibble: 2 x 2
##   `WALLNER LINES`      n
##   <fct>           <int>
## 1 0             103
## 2 1              2
```

Again, the low coefficient and p-value of the variable days show no evidence in support of the differences in the wallner lines feature when drying time changes.

Binned residual plot with most points outside the bound shows our model fits poor in this case. The possible reason is that we only have 2 bones have the wallner lines feature

Conclusion

According to the previous models, we have some confusion about how does the days' variable impacts 7 response variables and 6 dummy variables.

In the model (fit.Fracture_Type), days make a statistically significant difference for log-odds of preferring COMMUNUTED, OBLIQUE, SEGMENTAL and TRANSVERSE relative to baseline/BUTTERFLY.

In the model (fit.Fracture_Surface), days make a statistically significant difference for log-odds of preferring non-applicable and SMOOTH relative to baseline/INTERMEDIATE.

In the model (fit.Bisect_Fracture), days make moderate evidence that it makes the difference of the bone break.

In the model (fit.Fracture_like), days are a statistically significant predictor in predicting the probability of Fracture_like.

In the model (fit.Fracture_Angle), days make a statistically significant difference for log-odds of preferring non-applicable and OBLIQUE relative to baseline/INTERMEDIATE.

In the model (fit.Number_of_Fragments2), days are statistically significant in predicting the number of fragments.

In the model (fit.Fracture_Outline), days make a statistically significant difference for log-odds of preferring INTERMEDIATE and TRANSVERSE relative to baseline/CURVED/JAGGED.

Based on the chi-square test, there are some feature is correlated to other dummy variables. Another sign to indicated correlated variables is there are too much zero in those dummy variable. In the model (fit.Feature.1), there is no evidence in support of the differences of the wake hackle feature when drying time changes.

In the model (fit.Feature.2), there is no evidence in support of the differences in the bone hackle feature when drying time changes.

In the model (fit.Feature.3), there is no evidence in support of the differences in the bone mirror feature when drying time changes.

In the model (fit.Feature.4), there is no evidence in support of the differences of the cantilever curl feature when drying time changes.

In the model (fit.Feature.5), there is no evidence in support of the differences of the arrest ridge feature when drying time changes.

In the model (fit.Feature.6), there is no evidence in support of the differences of the Wallner lines feature when drying time changes.