

inital EDA

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2/7/2020

Data Cleaning

```
## [1] "integer"
```

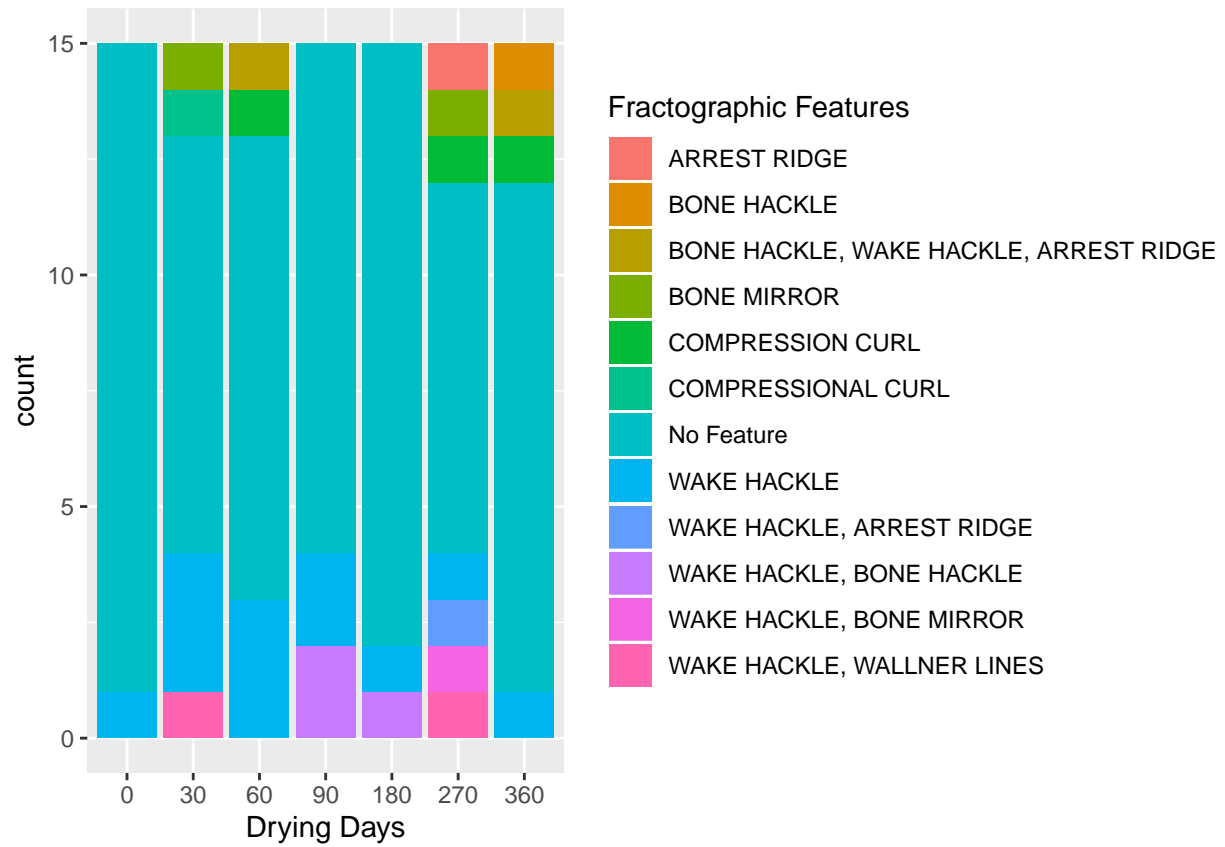
EDA

```
options(digits = 2)
table1<-rbind(table(bone$`Bisecting Fracture`,bone$`Bone Specimen`)[2,]/15,table(bone$`Fracture-like`,bone$`Bone Specimen`)[2,]/15)
row.names(table1)<-c('Bisecting percentage','Fracture-like percentage')
kable(table1,caption = 'Bisecting Fracture and Fracture-like percentage for different drying-day groups')
```

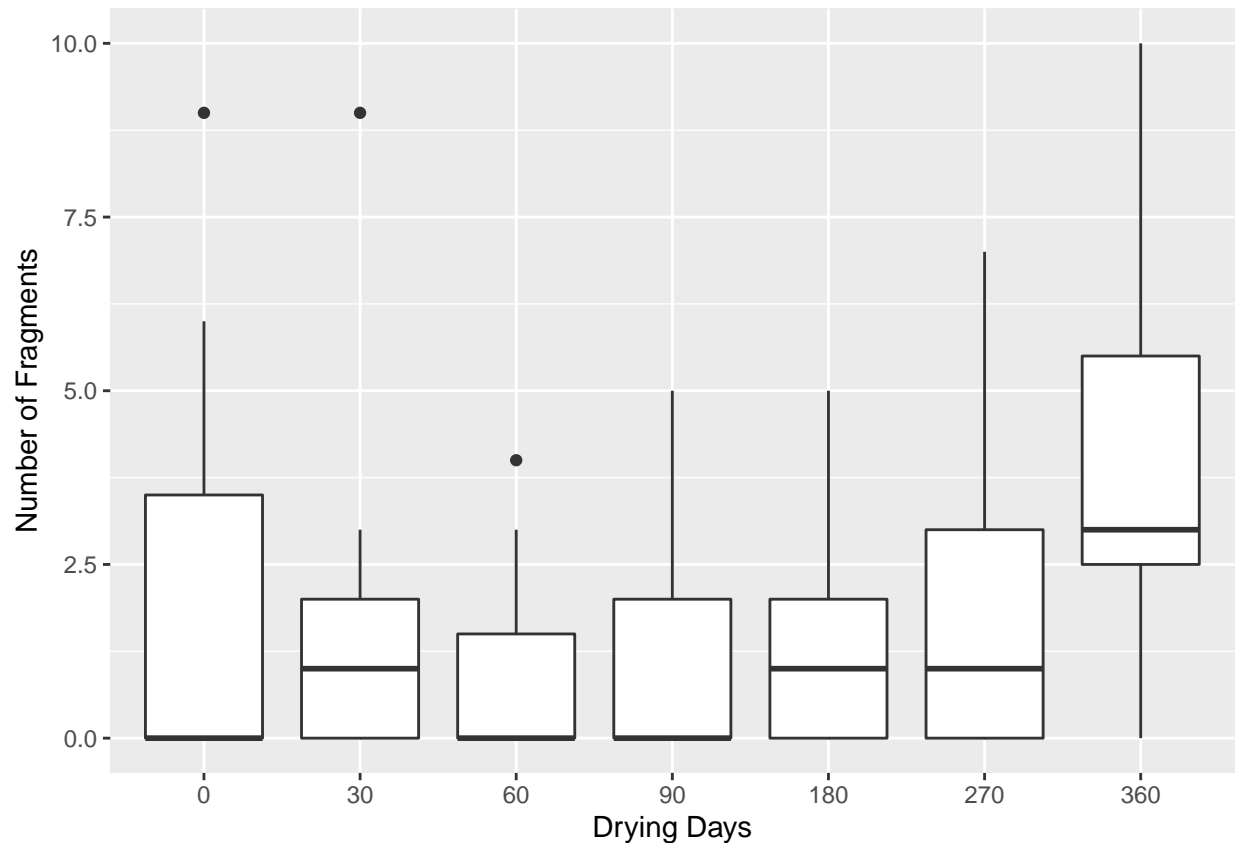
Table 1: Bisecting Fracture and Fracture-like percentage for different drying-day groups

	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

```
ggplot(data = bone) + geom_bar(mapping = aes(x = `Bone Specimen`, fill = `Fractographic Features`))+labs(x = 'Bone Specimen', fill = 'Fractographic Features')
```



```
ggplot(data = bone, mapping = aes(x = `Bone Specimen`, y = `Number of Fragments`)) + geom_boxplot()+lab
```



Models

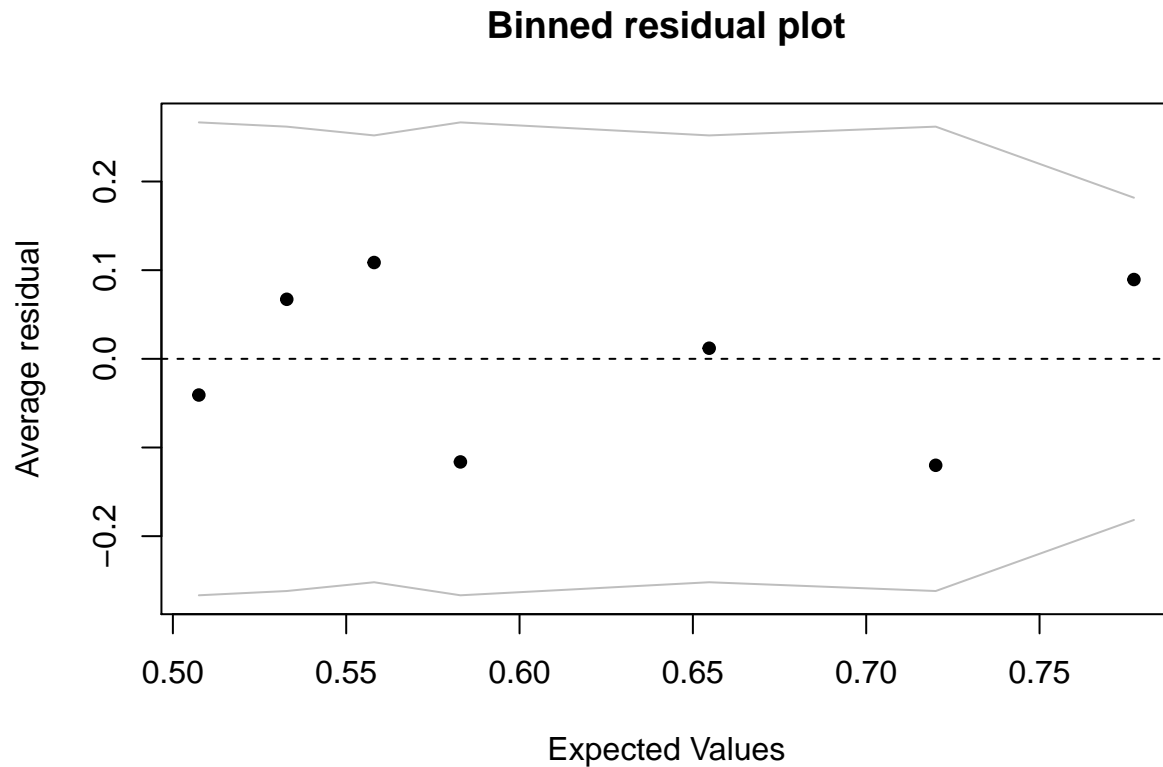
Bisect Fracture

```
fit.Bisect_Fracture<-glm(bone$`Bisecting Fracture`~bone$days,family = binomial())
summary(fit.Bisect_Fracture)
```

```
##
## 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
```

```
binnedplot(fitted(fit.Bisect_Fracture),resid(fit.Bisect_Fracture,type="response"))
```

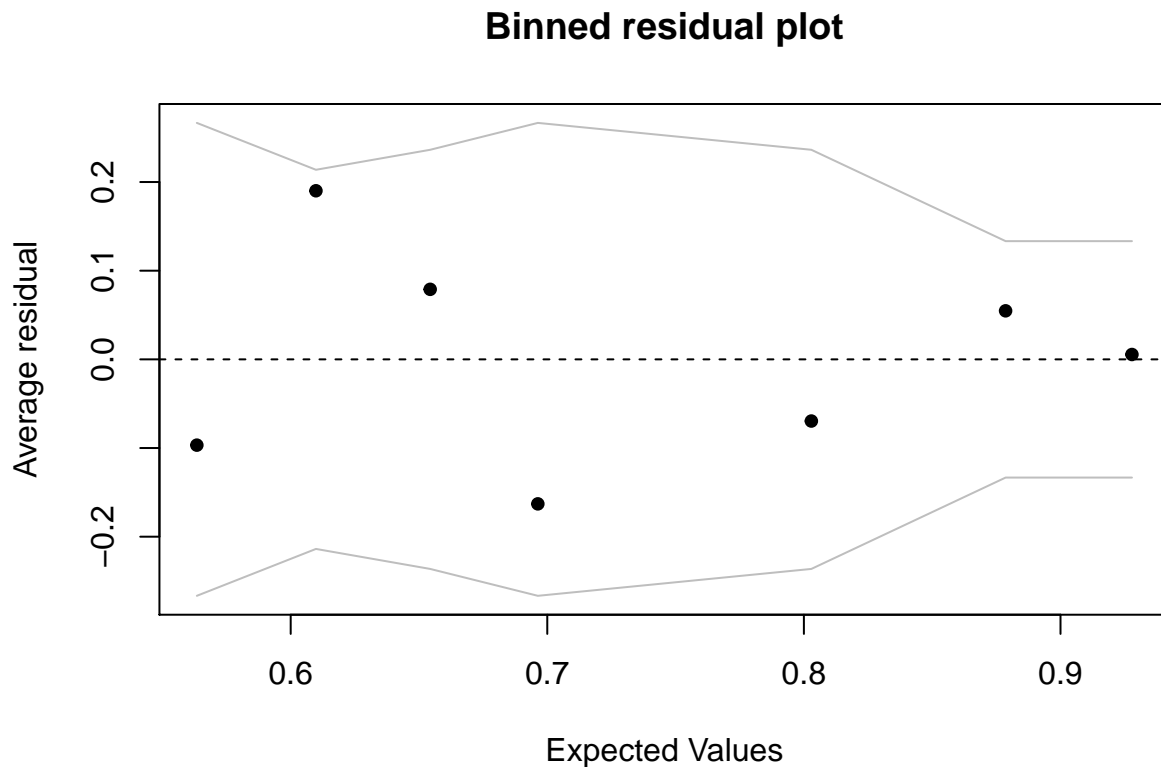


Fracture like

```
fit.Fracture_like<-glm(bone$`Fracture-like`~bone$days,family = binomial())
summary(fit.Fracture_like)
```

```
##
## 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
binnedplot(fitted(fit.Fracture_like), resid(fit.Fracture_like, type="response"))
```

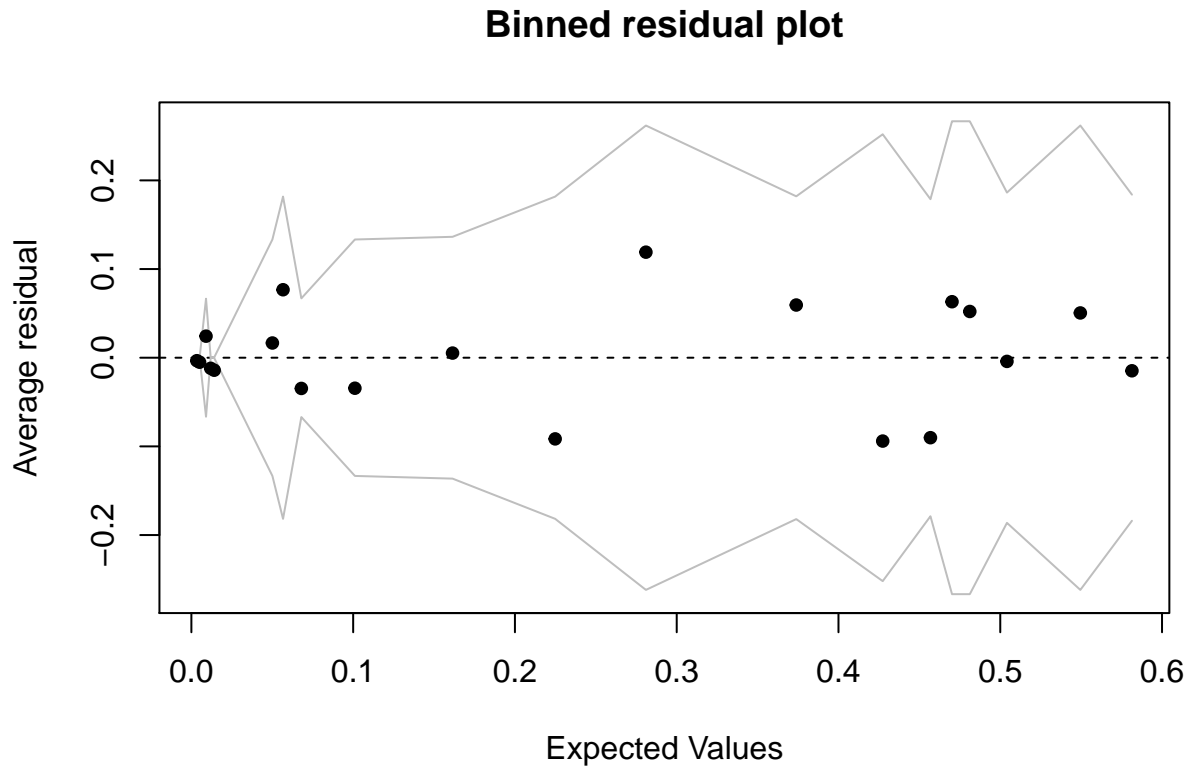


```
## Fracture Angle
fit.Fracture_Angle<-multinom(bone$`Fracture Angle`~bone$days,trace = FALSE)
summary(fit.Fracture_Angle)
```

```
## 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
```

```
binnedplot(fitted(fit.Fracture_Angle),resid(fit.Fracture_Angle,type="response"))
```



Number of Fragments

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

```
##
## 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
deviance(fit.Number_of_Fragments)/fit.Number_of_Fragments$df.residual

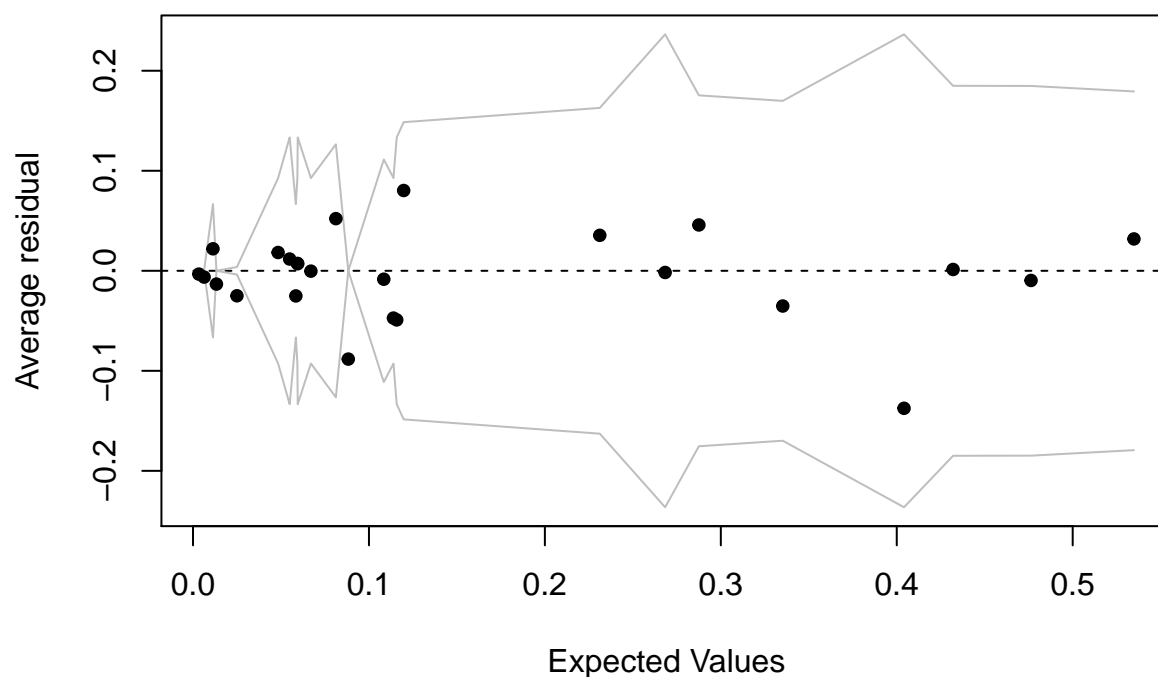
## [1] 2.7
```

Fracture Type

```
fit.Fracture_Type<-multinom(bone$`Fracture Type`~bone$days,trace = FALSE)
summary(fit.Fracture_Type)

## 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
## COMMINUTED           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
binnedplot(fitted(fit.Fracture_Type),resid(fit.Fracture_Type,type="response"))
```

Binned residual plot



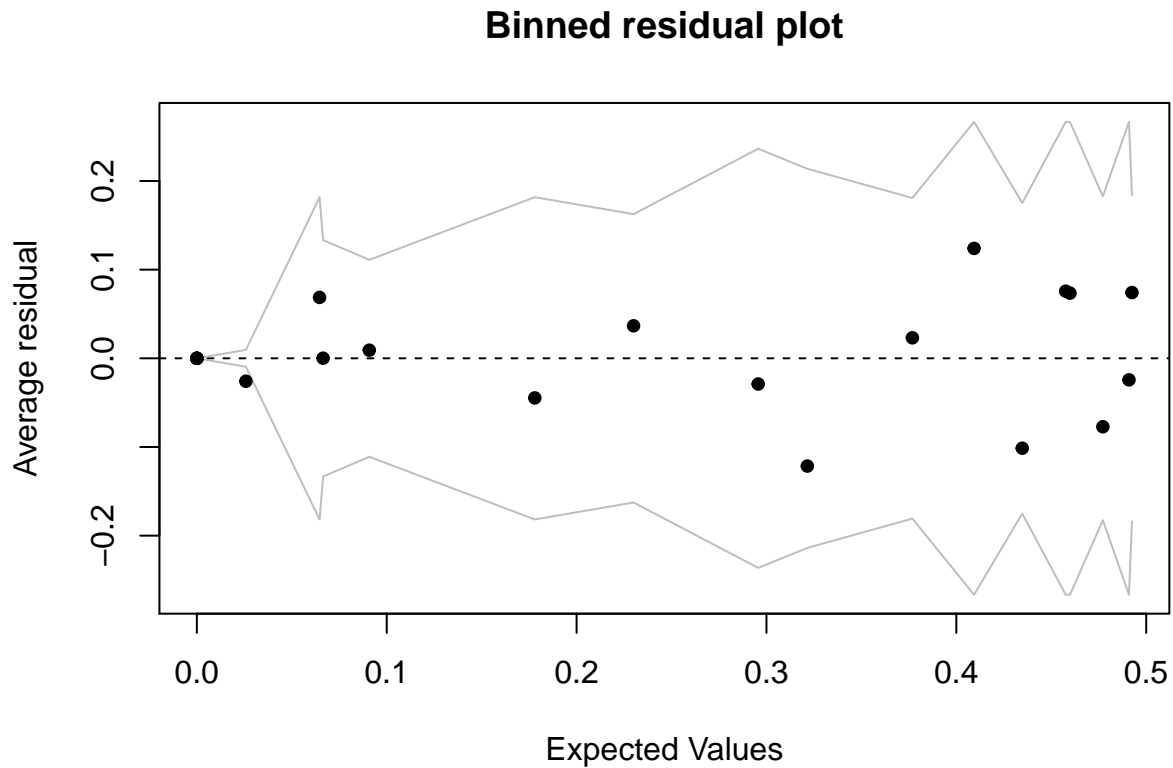
Fracture Surface

```
fit.Fracture_Surface<-multinom(bone$`Fracture Surface`~bone$days,trace = FALSE)
summary(fit.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
```



```
binnedplot(fitted(fit.Fracture_Surface),resid(fit.Fracture_Surface,type="response"))
```



Fracture Outline

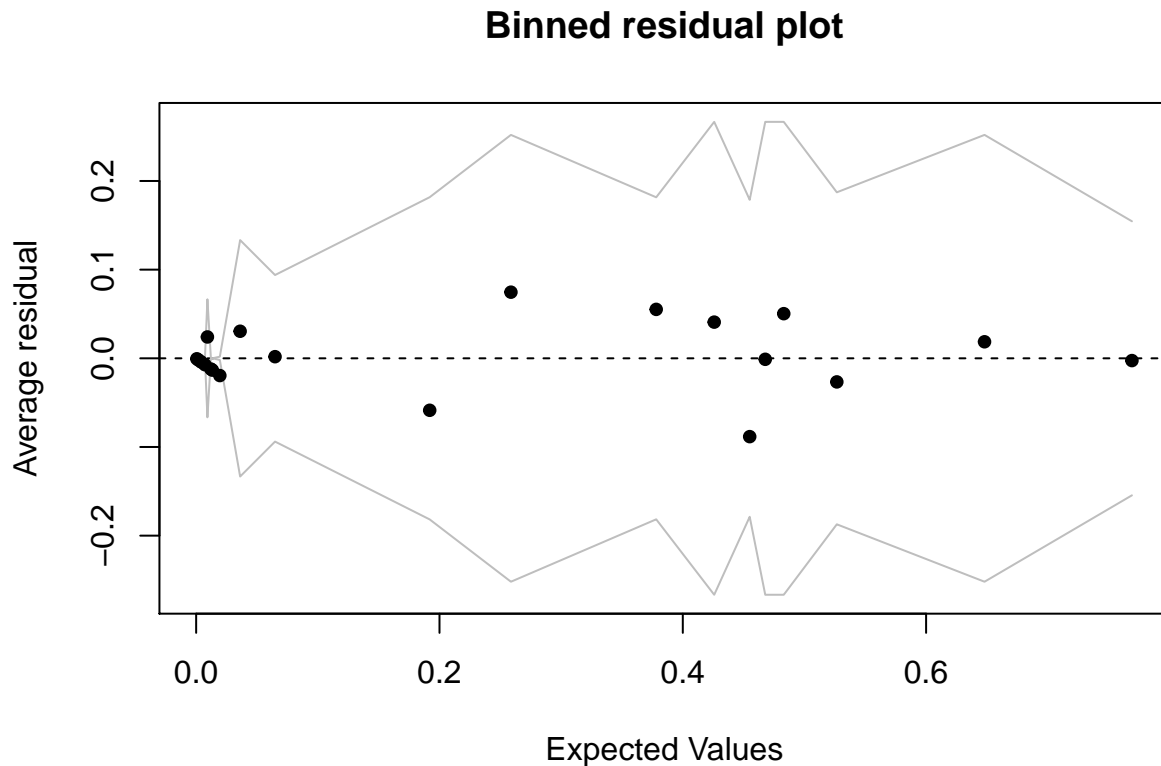
```
fit.Fracture_Outline<-multinom(bone$`Fracture Outline`~bone$days,trace = FALSE)
summary(fit.Fracture_Outline)
```

```
## Call:
## multinom(formula = bone$`Fracture Outline` ~ bone$days, trace = FALSE)
##
## Coefficients:
##              (Intercept) bone$days
## INTERMEDIATE      -1.71   -0.0155
## non applicable       0.13   -0.0043
## TRANSVERSE       -3.38   -0.0059
##
## Std. Errors:
##              (Intercept) bone$days
## INTERMEDIATE       0.78    0.0116
## non applicable      0.31    0.0018
## TRANSVERSE        1.38    0.0103
##
## Residual Deviance: 164
## AIC: 176
```

```

binnedplot(fitted(fit.Fracture_Outline),resid(fit.Fracture_Outline,type="response"))

```



Fractographic Features

```

fit.Fractographic_Features<-multinom(bone$`Fractographic Features`~bone$days,trace = FALSE)
summary(fit.Fractographic_Features)

```

```

## Call:
## multinom(formula = bone$`Fractographic Features` ~ bone$days,
##   trace = FALSE)
##
## Coefficients:
##
## (Intercept) bone$days
## BONE HACKLE -4.5e+01 1.3e-01
## BONE HACKLE, WAKE HACKLE, ARREST RIDGE 1.7e+00 -4.2e-03
## BONE MIRROR 2.4e+00 -7.9e-03
## COMPRESSION CURL 1.8e+00 -2.9e-03
## COMPRESSIONAL CURL 3.0e+00 -2.7e-02
## No Feature 6.1e+00 -8.8e-03
## WAKE HACKLE 4.6e+00 -1.1e-02
## WAKE HACKLE, ARREST RIDGE -1.3e-04 4.5e-07
## WAKE HACKLE, BONE HACKLE 3.1e+00 -1.0e-02
## WAKE HACKLE, BONE MIRROR 1.9e-04 -8.1e-07
## WAKE HACKLE, WALLNER LINES 2.4e+00 -7.9e-03
##

```

```
## Std. Errors:
##
## (Intercept) bone$days
## BONE HACKLE 0.00007 0.0046
## BONE HACKLE, WAKE HACKLE, ARREST RIDGE 2.99833 0.0107
## BONE MIRROR 2.89390 0.0108
## COMPRESSION CURL 2.93423 0.0103
## COMPRESSIONAL CURL 2.96299 0.0274
## No Feature 2.67886 0.0092
## WAKE HACKLE 2.70497 0.0096
## WAKE HACKLE, ARREST RIDGE 3.77439 0.0130
## WAKE HACKLE, BONE HACKLE 2.80202 0.0105
## WAKE HACKLE, BONE MIRROR 3.77421 0.0130
## WAKE HACKLE, WALLNER LINES 2.89390 0.0108
##
## Residual Deviance: 226
## AIC: 270
```

```
binnedplot(fitted(fit.Fractographic_Features), resid(fit.Fractographic_Features, type="response"))
```

