

STAT6420
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Pledge:

I have neither given nor received any unauthorized aid for this project. I abide by the academic honor code of UGA.

Contents

1	Introduction	4
2	Exploratory Data Analyses	4
2.1	First research question	4
2.2	Second research question	6
2.3	Third research question	8
2.4	Fifth research question	10
3	Statistical Analyses	11
3.1	First research question	11
3.2	Second research question	11
3.3	Fourth research question	12
3.4	Fifth research question	12
4	Conclusions	13
5	Appendix: R code	14

List of Figures

1	Residual vs fitted plot of regular linear regression	7
2	Deviance plot of logistic regression	8
3	Residual vs Fitted Plot and Boxcox Plot of Linear regression	9
4	Fitted response vs original response for both linear regression fit and gamma regression fit	9
5	Leverage Plot and Cooks Distance Plot. The red dots are the entries 137, 385 and 1541.	10
6	Cooks distances when the exceptional entries are removed	10

List of Tables

1	Confusion matrix for logistic regression	13
2	Confusion matrix for logistic regression with cross-validation	13

Summary

In this report, we will do some analysis on the dataset comprising of samples taken in different farms from different animal sources. We would like to answer these five questions using generalized linear regression analysis:

1. Are `Camplyobacter`, `Salmonella`, and `Listeria` predictive of each other.
2. Model the probability of `Camplyobacter` in terms of the `Type` and `Month` variable
3. Model the variable `EcoliLog10` in terms of the `Type` and `Month` variable
4. Are `Farm` and `Flock` needed to be controlled to answer the previous two research questions.
5. Can both the `SampleType` and `PastureTime` be predicted using the proportion of bacteria found? If not, can the `SampleType` alone be predicted using the proportion of bacteria found?

After analyzing the data, setting up some models and perform some specific test, we arrived at these conclusions for our questions: With our results, we can finally answer our questions presented in the Introduction.

1. We do not have enough information to show that `Camplyobacter`, `Salmonella`, and `Listeria` are predictive of each other.
2. A model was fitted and we get a dispersion effect of approximately 0.89. So there is lack of overdispersion but there is sign of underdispersion.
3. A model was fitted and it was shown that there are no influential points in our dataset. So those problematic points found can be considered to be outliers.
4. The `Farm` and `Flock` should not be controlled to answer the previous questions because the predictors used in the previous questions are not consistent in every `Farm` and every `Flock`.
5. We could not predict both the `SampleType` and `PastureTime` variables in unison. Rather, we predicted only the `SampleType` using the proportion of the bacteria samples found. Using the entire dataset, we have a small classification error rate of 6.45%. Using cross-validation, we get an average classification error rate of 7%.

1 Introduction

In this project, we will study the dataset that contains information on the. The goal of these report is to answer these five questions

1. Are Camplyobacter, Salmonella, and Listeria predictive of each other.
2. Model the probability of Camplyobacter in terms of the Type and Month variable
3. Model the variable EcoliLog10 in terms of the Type and Month variable
4. Are Farm and Flock needed to be controlled to answer the previous two research questions.
5. Can both the SampleType and PastureTime be predicted using the proportion of bacteria found?
If not, can the SampleType alone be predicted using using the proportion of bacteria found?

2 Exploratory Data Analyses

2.1 First research question

We want to see the predictive power of Camplyobacter, Salmonella, and Listeria with each other. Hence, we will make three models as follows

$$\text{Camplyobacter} = \beta_0 + \beta_1 \cdot \text{Salmonella} + \beta_2 \cdot \text{Listeria}$$

$$\text{Salmonella} = \beta_0 + \beta_1 \cdot \text{Camplyobacter} + \beta_2 \cdot \text{Listeria}$$

$$\text{Listeria} = \beta_0 + \beta_1 \cdot \text{Salmonella} + \beta_2 \cdot \text{Camplyobacter}$$

The summary of these models are shown below:

```
> summary(model_Camplyobact)

Call:
lm(formula = "Camplyobact~Listeria+Salmonella", data = broilers)

Residuals:
    Min       1Q   Median       3Q      Max
-0.4676 -0.4405 -0.4395  0.5595  0.5605

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.4404735   0.0134922  32.647  <2e-16 ***
Listeria     -0.0009209   0.0320169  -0.029   0.977
Salmonella    0.0271414   0.0303931   0.893   0.372
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4973 on 1887 degrees of freedom
(2 observations deleted due to missingness)
Multiple R-squared:  0.0004237, Adjusted R-squared:  -0.0006358
```

F-statistic: 0.3999 on 2 and 1887 DF, p-value: 0.6704

```
> summary(model_Salmonella)
```

Call:

```
lm(formula = "Salmonella~Campylobact+Listeria", data = broilers)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.1830	-0.1830	-0.1674	-0.1601	0.8555

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.16742	0.01219	13.739	<2e-16 ***
Campylobact	0.01556	0.01743	0.893	0.372
Listeria	-0.02291	0.02424	-0.945	0.345

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

Residual standard error: 0.3766 on 1887 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.0008964, Adjusted R-squared: -0.0001626

F-statistic: 0.8465 on 2 and 1887 DF, p-value: 0.4291

```
> summary(model_Listeria)
```

Call:

```
lm(formula = "Listeria~Salmonella+Campylobact", data = broilers)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.1540	-0.1540	-0.1535	-0.1333	0.8671

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.1540067	0.0116058	13.270	<2e-16 ***
Salmonella	-0.0206572	0.0218524	-0.945	0.345
Campylobact	-0.0004761	0.0165519	-0.029	0.977

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

Residual standard error: 0.3575 on 1887 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.0004746, Adjusted R-squared: -0.0005848

F-statistic: 0.448 on 2 and 1887 DF, p-value: 0.639

We see that the predictors in all the models are not significant which shows signs of colinearity so we will check the correlation matrix.

```
> cor(broilers[,c("Campylobact", "Listeria", "Salmonella")],  
+      use = "complete.obs")  
          Campylobact    Listeria    Salmonella
```

```

Campylobact  1.0000000000 -0.001109826  0.02057247
Listeria     -0.001109826  1.0000000000 -0.02177444
Salmonella   0.020572470 -0.021774441  1.000000000

```

We see that the correlations between different bacteria samples are very low so signs are slim.

To also consider all possible cases, we will consider a logistic model for each of the

2.2 Second research question

We will study the effect on the sample type and the months on the presence/absence of *Campylobacter*. We first fit a linear model without interaction terms because there will be too many characters ($4 \times 7 = 28$). The summary of the model is shown below:

```

Call:
lm(formula = "Campylobact~factor(SampleType)+factor(Month) ",
    data = broilers)

Residuals:
    Min       1Q   Median       3Q      Max
-1.01568 -0.21013 -0.01568  0.26482  0.99110

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.13945    0.04212  27.052 < 2e-16 ***
factor(SampleType)Feces -0.23628    0.03053  -7.738 1.64e-14 ***
factor(SampleType)Soil  -0.70929    0.03053 -23.229 < 2e-16 ***
factor(SampleType)WCR-F -0.91052    0.03704 -24.582 < 2e-16 ***
factor(SampleType)WCR-P -0.85714    0.03695 -23.199 < 2e-16 ***
factor(Month)5        -0.12377    0.03950  -3.133  0.00176 **
factor(Month)6        -0.19727    0.03705  -5.324 1.13e-07 ***
factor(Month)7        -0.22003    0.03754  -5.862 5.40e-09 ***
factor(Month)8        -0.23105    0.03917  -5.898 4.34e-09 ***
factor(Month)9        -0.24527    0.04029  -6.088 1.38e-09 ***
factor(Month)10       -0.16800    0.04007  -4.193 2.88e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3786 on 1879 degrees of freedom
(2 observations deleted due to missingness)
Multiple R-squared:  0.423, Adjusted R-squared:  0.4199
F-statistic: 137.8 on 10 and 1879 DF, p-value: < 2.2e-16

```

We see that all of the predictors are significant but the R^2 is moderately low. We check the residual vs fitted plot in Figure 1.

We see in Figure 1 that there is a lack of a horizontal band but rather a downward pattern shown. So we will also consider logistic regression (not probit because we are considering odds). The summary is shown below:

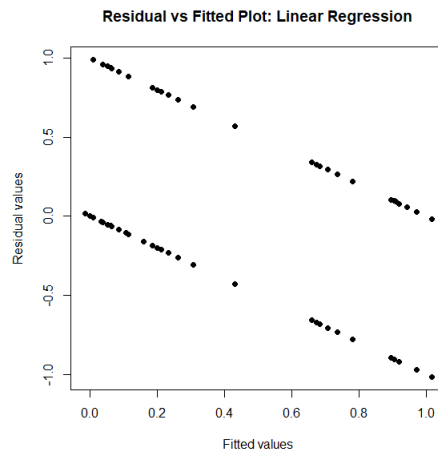


Figure 1: Residual vs fitted plot of regular linear regression

```
Call:
glm(formula = "Campylobact~factor(SampleType)+factor(Month)",
     family = binomial(link = "logit"), data = broilers)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)      3.8825     0.3640  10.667 < 2e-16 ***
factor(SampleType)Feces -1.9172     0.3123  -6.140 8.27e-10 ***
factor(SampleType)Soil -4.0581     0.3151 -12.881 < 2e-16 ***
factor(SampleType)WCR-F -6.5206     0.5428 -12.012 < 2e-16 ***
factor(SampleType)WCR-P -5.2329     0.3883 -13.477 < 2e-16 ***
factor(Month)5      -0.5767     0.2534  -2.276 0.02287 *
factor(Month)6      -1.0494     0.2396  -4.380 1.19e-05 ***
factor(Month)7      -1.2041     0.2430  -4.954 7.26e-07 ***
factor(Month)8      -1.3088     0.2603  -5.027 4.97e-07 ***
factor(Month)9      -1.3930     0.2668  -5.221 1.78e-07 ***
factor(Month)10     -0.8052     0.2676  -3.009 0.00262 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2597.2  on 1889  degrees of freedom
Residual deviance: 1670.0  on 1879  degrees of freedom
(2 observations deleted due to missingness)
AIC: 1692

Number of Fisher Scoring iterations: 6

We will check the deviance plot to see if a transformation is required.
```

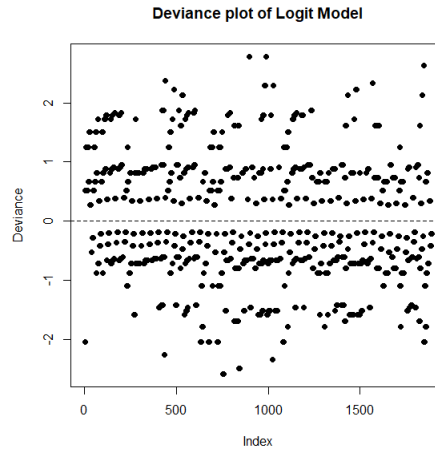


Figure 2: Deviance plot of logistic regression

We see in Figure 2 that the points are distributed evenly so there is no need for a transformation.

2.3 Third research question

We will study the effect on the sample type and the animal source on the logarithmic scale of the *E. coli* concentration in the sample. We first fit a linear model with interaction terms and the `EcoliLog10` is shifted by 0.1 so the boxcox plot can be shown. The summary is shown below:

Call:

```
lm(formula = "I(EcoliLog10 + 0.1) ~ factor(SampleType)+ factor(AnimalSource)
+ factor(SampleType)*factor(AnimalSource)", data = fecalsoil)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-5.7246	-0.8384	0.0370	0.9811	4.3188

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.63741	0.05691	116.629	< 2e-16 ***
factor(SampleType) Soil	-2.11200	0.08061	-26.200	< 2e-16 ***
factor(AnimalSource) Cattle	-1.68056	0.22025	-7.630	3.98e-14 ***
factor(AnimalSource) Layer	0.59819	0.16086	3.719	0.000207 ***
factor(AnimalSource) Swine	-0.81281	0.20972	-3.876	0.000111 ***
factor(SampleType) Soil:factor(AnimalSource) Cattle	-0.90452	0.31151	-2.904	0.003739 **
factor(SampleType) Soil:factor(AnimalSource) Layer	-1.26201	0.22753		
factor(SampleType) Soil:factor(AnimalSource) Swine	-2.41290	0.29662		


```

factor(SampleType) Soil:factor(AnimalSource) Layer    -5.547  3.40e-08 ***
factor(SampleType) Soil:factor(AnimalSource) Swine   -8.135  8.16e-16 ***
---

```

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

Residual standard error: 1.427 on 1616 degrees of freedom

(8 observations deleted due to missingness)

Multiple R-squared: 0.5042, Adjusted R-squared: 0.5021

F-statistic: 234.8 on 7 and 1616 DF, p-value: < 2.2e-16

We see that the interaction terms are very significant. We see that there is not much fanning in or out in the residual plot and the boxcox plot shows that there is no need for a transformation in Figure 3.

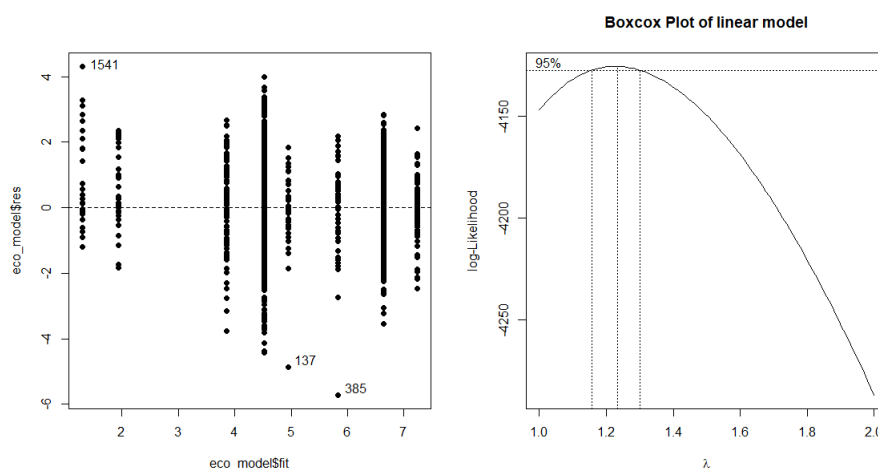


Figure 3: Residual vs Fitted Plot and Boxcox Plot of Linear regression

A Gamma model can be considered but we see from Figure 4, a fitted Gamma model and the linear model have the same fit.

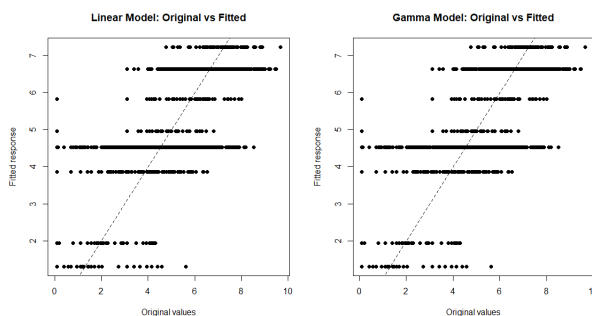


Figure 4: Fitted response vs original response for both linear regression fit and gamma regression fit

So we will stick with the linear model we fitted. Hence, we will check the leverage plot and the cooks distance plot: We see in Figures 3 and 5 that entry 385, 137 and 1541 have high residuals, high leverages

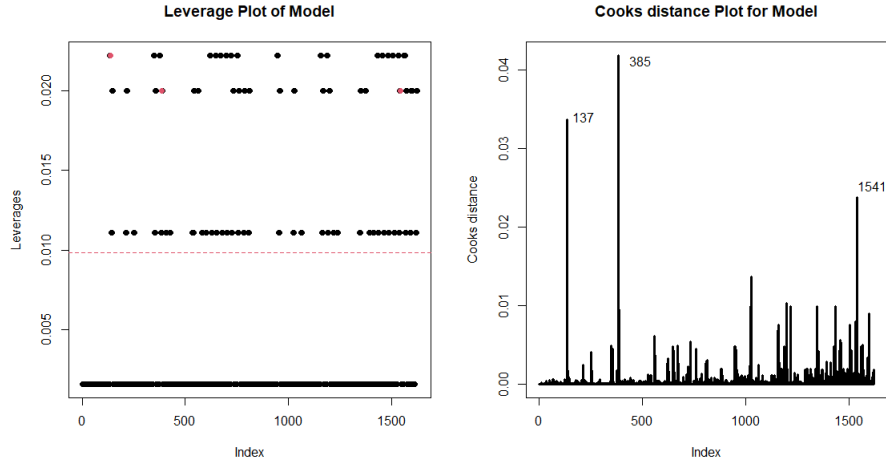


Figure 5: Leverage Plot and Cooks Distance Plot. The red dots are the entries 137, 385 and 1541.

and high cooks distances relative to the other entries. So they are considered to be either outliers or influential points. For more information, we will check the cooks distance if we remove each entry from the model.

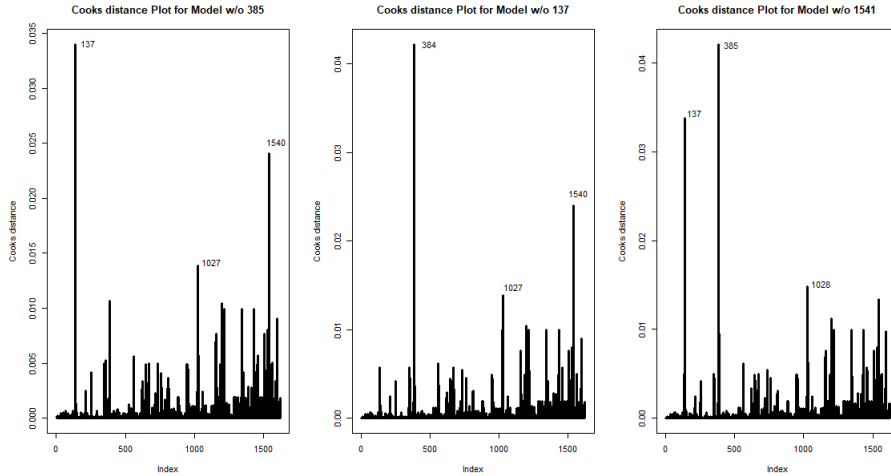


Figure 6: Cooks distances when the exceptional entries are removed

We see that not much changes in the cooks distance, so those entries are not considered to be influential points. So there are no strong influential points in this dataset.

2.4 Fifth research question

The question is if we can predict both the Sample Type and Pasture time by using the proportions of bacteria found (A, B, C, D, E). We cannot predict both the Sample Type and the Pasture time because they are two different groups which could be independent. However, we can predict the Sample Type because there are only two variable in the Sample Type so we can use logistic regression. We only need four predictors

because $A + B + C + D + E = 1$. If we run all four possible combinations of the four parameters, we see that the deviance for all of them are significant so we will choose the model that has the most significant predictors. The summary of our chosen model is shown below:

```
Call:
glm(formula = Sample_dummy ~ A + B + C + D, family = binomial)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    50.70      12.00   4.225 2.39e-05 ***
A             -55.60      12.20  -4.557 5.19e-06 ***
B             -50.93      12.28  -4.149 3.34e-05 ***
C             -43.03      12.64  -3.404 0.000665 ***
D             -53.97      19.27  -2.801 0.005098 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 300.711  on 216  degrees of freedom
Residual deviance:  69.343  on 212  degrees of freedom
AIC: 79.343

Number of Fisher Scoring iterations: 8
```

3 Statistical Analyses

3.1 First research question

Let $\beta_{Campylobacter}$, $\beta_{Salmonella}$ and $\beta_{Listeria}$ be the coefficients of the respective predictors. Our hypotheses are as follow:

$$H_0 : \beta_{Campylobacter} = \beta_{Salmonella} = \beta_{Listeria} = 0$$

$$H_A : \text{at least one of these parameters is } 0$$

We will use is a t -test in our process using the models we prepared. As we see in both the linear and logistic models, none of the predictors are significant so we fail to reject the null hypothesis. Hence, we do not have enough to show that *Campylobacter*, *Salmonella*, and *Listeria* are predictive of each other.

3.2 Second research question

We will check for overdispersion in the binomial model fitted. The calculation of the dispersion factor is as follows:

$$\frac{\text{Deviance}}{\text{Error degree of freedom}}$$

Since this is a binomial model, the dispersion factor is expected to be very close to 1. Hence, the dispersion factor of our model is shown below:

```
> campyl_model_binom_logit$deviance/campyl_model_binom_logit$df.residual
[1] 0.8887724
```

The dispersion factor is smaller than 1 so there is no sign of overdispersion but a small sign of underdispersion.

3.3 Fourth research question

The models used in the second and third response should not be controlled for the `Farm` and `Flock` variables because it is possible that the predictors used in the previous research questions might not be in each `Farm` or `Flock`. For instance, we will predict the presence of `Campylobacter` using the `Type` and `Month` but only for the `Farm` labeled as `A`.

```
Call:
glm(formula = "Campylobact~factor(SampleType)+factor(Month)",
     family = binomial(link = "logit"), data = broilers[broilers$Farm ==
"A", ])

```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	6.5748	1.1852	5.547	2.90e-08	***
factor(SampleType)Feces	-1.6478	1.0649	-1.547	0.121765	
factor(SampleType)Soil	-5.1429	1.0502	-4.897	9.73e-07	***
factor(SampleType)WCR-F	-22.9223	883.4291	-0.026	0.979300	
factor(SampleType)WCR-P	-8.2900	1.4567	-5.691	1.26e-08	***
factor(Month)5	-0.8190	0.7092	-1.155	0.248167	
factor(Month)6	-2.3167	0.6347	-3.650	0.000262	***
factor(Month)7	-2.0530	0.6532	-3.143	0.001672	**
factor(Month)8	-3.2910	0.7047	-4.670	3.01e-06	***
factor(Month)9	-3.1195	0.7630	-4.088	4.34e-05	***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 619.91 on 449 degrees of freedom
Residual deviance: 256.00 on 440 degrees of freedom
(2 observations deleted due to missingness)
AIC: 276

Number of Fisher Scoring iterations: 17

We see `Farm A` lacks the 10 `Month` data so there will be a vast difference in the estimate of the other parameters.

3.4 Fifth research question

We will check the confusion matrix of our results. The matrix is shown in table 1:

Hence, the error rate can be evaluated as $\frac{10+4}{107+10+4+96} = \frac{14}{217} = 6.45\%$.

Now we will perform cross-validation on our dataset: breaking our training set and test set by 70 to 30. The confusion matrix for our cross-validation is shown in Table 2

We see that our error rate is $\frac{1+1}{40+1+1+30} = \frac{2}{72} \approx 2.78\%$.

		Actual values	
		Fecal	Soil
Predicted values	Fecal	107	10
	Soil	4	96

Table 1: Confusion matrix for logistic regression

		Actual values	
		Fecal	Soil
Predicted values	Fecal	40	1
	Soil	1	30

Table 2: Confusion matrix for logistic regression with cross-validation

If we repeat the cross-validation 10 times, we get this list of error rates, the summary of our list is shown below:

```
> summary(1-accuracy_score_list)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.04167 0.05903 0.07639 0.07083 0.08333 0.09722
```

We see that the error rate average and median is around 7% and the error rate does not get larger than 10%.

4 Conclusions

With our results, we can finally answer our questions presented in the Introduction.

1. We do not have enough information to show that `Campylobacter`, `Salmonella`, and `Listeria` are predictive of each other.
2. A model was fitted and we get a dispersion effect of approximately 0.89. So there is lack of overdispersion but there is sign of underdispersion.
3. A model was fitted and it was shown that there are no influential points in our dataset. So those problematic points found can be considered to be outliers.
4. The Farm and Flock should not be controlled to answer the previous questions because the predictors used in the previous questions are not consistent in every Farm and every Flock.
5. We could not predict both the `SampleType` and `PastureTime` variables in unison. Rather, we predicted only the `SampleType` using the proportion of the bacteria samples found. Using the entire dataset, we have a small classification error rate of 6.45%. Using cross-validation, we get an average classification error rate of 7%.

5 Appendix: R code

```
1 library(readxl)
2 library(faraway)
3 library(MASS)
4 library(leaps)
5
6 dev.new()
7
8 broilers <- read_excel("PasturedPoultryFarms.xlsx", sheet = "Broilers")
9
10 fecalsoil <- read_excel("PasturedPoultryFarms.xlsx", sheet =
11   ↪ "FecalSoil")
12
13 Compositional <- read_excel("PasturedPoultryFarms.xlsx", sheet =
14   ↪ "Compositional")
15 #####
16 #
17   ↪ #
18 #                               First Ques
19   ↪ #
20 #
21   ↪ #
22 #####
23 model_Campylobact <- lm("Campylobact~Listeria+Salmonella", data =
24   ↪ broilers)
25 model_Salmonella <- lm("Salmonella~Campylobact+Listeria", data =
26   ↪ broilers)
27 model_Listeria <- lm("Listeria~Salmonella+Campylobact", data = broilers)
28
29 summary(model_Campylobact)
30 summary(model_Salmonella)
31 summary(model_Listeria)
32
33 model_Campylobact_binom <- glm("Campylobact~Listeria+Salmonella", data =
34   ↪ broilers,
35                                   family = binomial)
36 model_Salmonella_binom <- glm("Salmonella~Campylobact+Listeria", data =
37   ↪ broilers,
```

```

34         family = binomial)
35 model_Listeria_binom <- glm("Listeria~Salmonella+Campylobact",data =
  ↳ broilers,
36         family = binomial)
37
38 cor(broilers[,c("Campylobact", "Listeria", "Salmonella")],
39     use = "complete.obs")
40
41
42 summary(model_Campylobact_binom)
43 summary(model_Salmonella_binom)
44 summary(model_Listeria_binom)
45
46
47
48
49 #####
50 #
  ↳ #
51 #
  ↳ #
52 #                               Second Ques
  ↳ #
53 #
  ↳ #
54 #
  ↳ #
55 #####
56
57
58 campyl_model <- lm("Campylobact~factor(SampleType)+factor(Month)",
59                   data = broilers)
60 summary(campyl_model)
61 plot(campyl_model$fit, campyl_model$res,pch = 19,xlab = "Fitted
  ↳ values",
62      ylab = "Residual values",main = "Residual vs Fitted Plot: Linear
  ↳ Regression")
63
64 boxcox(lm("I (Campylobact+0.1)~factor(SampleType)+factor(Month)",
65          data = broilers))
66
67 campyl_model_1 <-
  ↳ lm("log (Campylobact+0.1)~factor(SampleType)+factor(Month)",
68      data = broilers)
69 summary(campyl_model_1)

```

```

70
71 plot(campyl_model_1$fit, campyl_model_1$res, pch = 19)
72
73
74 campyl_model_binom_logit <-
  ↪ glm("Campylobact~factor(SampleType)+factor(Month)",
75       data = broilers, family = binomial(link =
  ↪ "logit"))
76 summary(campyl_model_binom_logit)
77
78
79 plot(residuals(campyl_model_binom_logit, type = "deviance"), pch = 19,
80       ylab="Deviance", main = "Deviance plot of Logit Model")
81 abline(h = 0, lty = 2)
82
83 #Dispersion factor
84 campyl_model_binom_logit$deviance/campyl_model_binom_logit$df.residual
85
86 #####
87 #
88 ↪ #
89 #
90 ↪ #
91 #
92 ↪ #
93 #####
94
95
96 fecalsoil$EcoliLog10 <- as.numeric(fecalsoil$EcoliLog10)
97
98 eco_model <- lm("I(EcoliLog10 + 0.1) ~ factor(SampleType)+
  ↪ factor(AnimalSource) + factor(SampleType)*factor(AnimalSource)",
99       data = fecalsoil)
100 summary(eco_model)
101
102
103 par(mfrow = c(1,2))
104 plot(eco_model$fit, eco_model$res, pch = 19)
105 abline(h=0, lty = 2)
106 identify(eco_model$fit, eco_model$res, atpen = T, tolerance = 0.5)

```



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107
108 boxcox(eco_model, lambda = seq(1,2,by = 0.05))
109 title("Boxcox Plot of linear model")
110 par(mfrow = c(1,1))
111
112 step(eco_model)
113
114 Cpplot(leaps(model.matrix(eco_model)[,-1],na.omit(fecalsoil$EcoliLog10)+0.1))
115
116 maxadjr(leaps(model.matrix(eco_model)[,-1],na.omit(fecalsoil$EcoliLog10)+0.1,
117             method="adjr2"), best = 8)
118
119 eco_model_gamma <- glm("I(EcoliLog10+0.1) ~ factor(SampleType)+
120   ↪ factor(AnimalSource) + factor(SampleType)*factor(AnimalSource)",
121   data = fecalsoil, family = Gamma(link = "inverse"))
122
123 summary(eco_model_gamma)
124
125 par(mfrow = c(1,2))
126 plot(na.omit(fecalsoil$EcoliLog10)+0.1,eco_model$fit,pch = 19,
127       xlab = "Original values",ylab="Fitted response",main = "Linear
128   ↪ Model: Original vs Fitted")
129
130 abline(a=0,b=1,lty = 2)
131
132 plot(na.omit(fecalsoil$EcoliLog10)+0.1,eco_model_gamma$fit,pch = 19,
133       xlab = "Original values",ylab="Fitted response",main = "Gamma
134   ↪ Model: Original vs Fitted")
135
136 abline(a=0,b=1,lty = 2)
137 par(mfrow = c(1,1))
138
139 par(mfrow = c(1,2))
140 plot(hat(model.matrix(eco_model)),pch = 19,ylab = 'Leverages',
141       main = 'Leverage Plot of Model')
142
143 abline(h =
144   ↪ 2*ncol(model.matrix(eco_model))/nrow(model.matrix(eco_model)),lty =
145   ↪ 2, col = 2)
146
147 points(137,hat(model.matrix(eco_model))[137], col = 2,pch = 19)
148 points(385,hat(model.matrix(eco_model))[385], col = 2,pch = 19)
149 points(1541,hat(model.matrix(eco_model))[1541], col = 2,pch = 19)
150
151
152 plot(cooks.distance(eco_model),type = 'h',lwd = 3,ylab = 'Cooks
153   ↪ distance',
154       main = 'Cooks distance Plot for Model')

```

```

146 identify(1:nrow(model.matrix(eco_model)), cooks.distance(eco_model),
147           tolerance = 0.5, atpen = TRUE)
148 par(mfrow = c(1,1))
149
150 eco_model_385 <- lm("I(EcoliLog10 + 0.1) ~ factor(SampleType)+
151   ↪ factor(AnimalSource) + factor(SampleType)*factor(AnimalSource)",
152   data = na.omit(fecalsoil)[-385,])
153
154 eco_model_137 <- lm("I(EcoliLog10 + 0.1) ~ factor(SampleType)+
155   ↪ factor(AnimalSource) + factor(SampleType)*factor(AnimalSource)",
156   data = na.omit(fecalsoil)[-137,])
157
158 eco_model_1541 <- lm("I(EcoliLog10 + 0.1) ~ factor(SampleType)+
159   ↪ factor(AnimalSource) + factor(SampleType)*factor(AnimalSource)",
160   data = na.omit(fecalsoil)[-1541,])
161
162 par(mfrow = c(1,3))
163 plot(cooks.distance(eco_model_385), type = 'h', lwd = 3, ylab = 'Cooks
164   ↪ distance',
165   main = 'Cooks distance Plot for Model w/o 385')
166 identify(1:nrow(model.matrix(eco_model_385)), cooks.distance(eco_model_385),
167   tolerance = 0.5, atpen = TRUE)
168
169 plot(cooks.distance(eco_model_137), type = 'h', lwd = 3, ylab = 'Cooks
170   ↪ distance',
171   main = 'Cooks distance Plot for Model w/o 137')
172 identify(1:nrow(model.matrix(eco_model_137)), cooks.distance(eco_model_137),
173   tolerance = 0.5, atpen = TRUE)
174
175 plot(cooks.distance(eco_model_1541), type = 'h', lwd = 3, ylab = 'Cooks
176   ↪ distance',
177   main = 'Cooks distance Plot for Model w/o 1541')
178 identify(1:nrow(model.matrix(eco_model_1541)), cooks.distance(eco_model_1541),
179   tolerance = 0.5, atpen = TRUE)
180
181 par(mfrow = c(1,1))
182 #####
183 #
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182  #
183  ↪ #
184  #####
185
186
187  summary(glm("Campylobact~factor(SampleType)+factor(Month)",
188             data = broilers[broilers$Farm == "A",], family =
189             ↪ binomial(link = "logit")))
190
191
192  #####
193  #
194  ↪ #
195  #
196  ↪ #
197  #
198  ↪ #
199  #####
200
201  attach(Compositional)
202  Sample_dummy <- factor(Compositional$Sampletype, labels = c(0,1))
203
204  summary(glm(Sample_dummy~A + B + C + D, family = binomial))
205  summary(glm(Sample_dummy~A + C + D + E, family = binomial))
206  summary(glm(Sample_dummy~A + B + D + E, family = binomial))
207  summary(glm(Sample_dummy~A + B + C + E, family = binomial))
208
209  compositional_model <- glm(Sample_dummy~A+ B + C + D, family =
210  ↪ binomial)
211  summary(compositional_model_A)
212  compositional_model_E <- glm(Sample_dummy~ B+ C+D+E, family = binomial)
213  summary(compositional_model_E)
214
215  #Predicted values
216  Pred_sample <- compositional_model_A$fit > 0.5
217

```

```

218 #Confusion matrix
219 table(Pred_sample, Samplettype)
220
221 ##Cross-Validation
222 test_num <- as.integer(nrow(Compositional)/3)
223 index <- sample(nrow(Compositional), test_num)
224 Sample_dummy_cross_val <- factor(Samplettype[-index], labels = c(0,1))
225 compos_cross_val_model <- glm("factor(Samplettype, labels = c(0,1)) ~
  ↪ A+B+C+D",
226                               data = Compositional[-index,], family =
  ↪ binomial)
227 Pred_sample_cross_val <- predict(compos_cross_val_model,
  ↪ Compositional[index, c("A", "B", "C", "D", "E")],
228                               type = "response") > 0.5
229 table(Pred_sample_cross_val, Samplettype[index])
230
231
232 ##Cross-Validation multiple loops
233 accuracy_score_list <- c()
234
235 for (i in seq(1,10)){
236   test_num <- as.integer(nrow(Compositional)/3)
237   index <- sample(nrow(Compositional), test_num)
238   Sample_dummy_cross_val <- factor(Samplettype[-index], labels = c(0,1))
239   compos_cross_val_model <- glm("factor(Samplettype, labels = c(0,1)) ~
  ↪ A+B+C+D",
240                               data = Compositional[-index,], family =
  ↪ binomial)
241   Pred_sample_cross_val <- predict(compos_cross_val_model,
  ↪ Compositional[index, c("A", "B", "C", "D", "E")],
242                               type = "response") > 0.5
243   correct_obs <-
  ↪ sum(diag(table(Pred_sample_cross_val, Samplettype[index])))
244   accuracy_score_list <-
  ↪ append(accuracy_score_list, (correct_obs/test_num))
245
246
247 }
248
249 summary(1-accuracy_score_list)
250
251 1-c(1,2,3)
252 predict(compos_cross_val_model,
  ↪ Compositional[index, c("A", "B", "C", "D", "E")],
253         type = "response")

```

```
254 detach(Compositional)
255
```