Stage 2: Exploratory Data Analysis

Isaac Slagel and Jack Welsh

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Main Report

Pitbulls in Dallas Shelters

In our EDA we found a distinct difference between outcomes for pitbulls compared to other breeds of dogs. What we saw was that pitbulls tend to be killed at a higher rate than other dogs. However we also found there were other variables that influence the outcome of dogs like chip status, outcome month, and intake condition. Inorder to quantify the difference in treatment between dog breeds, we condensed our large dataset into a smaller form and conducted a series of binomial regressions described in Table 1.

Table 1: Modeling Dog Outcomes in Dallas Animal Shelters

	Dependent variable:		
	Proportion of dogs who died		
	(1)	(2)	(3)
Intercept	0.116***	0.111***	0.552***
	(0.069,0.186)	(0.069,0.170)	(0.454,0.669)
Pitbull	3.440***	3.424***	3.489***
	(1.795,6.557)	(1.905,6.130)	(3.022,4.027)
Scannable Chip	0.789	0.799	0.781***
	(0.377,1.566)	(0.412,1.483)	(0.667,0.911)
Summer Outcome	1.461	1.447	1.478***
	(0.725,2.852)	(0.771,2.649)	(1.271,1.718)
Contagious		7.286**	3.975***
		(1.324,44.137)	(2.568,6.168)
Treatable At Intake			0.161***
			(0.133,0.196)
Overdisperson Parameter	139.72	111.46	6.27
Nested F Test		$F : 5.1142^{*}$	$F : 313.62^{***}$
Note:			*p<0.1; **p<0.05; ***p<0.01

See from the above table that all of our models has variable estimates that are significant including Model 3 which accounted for whether or not an animal was deemed "treatable" at the time of intake. For some reason our table does not indicate the significance of the treatable intake variable in model 3, it is indeed significant. Further, by two F tests we see each of our models is an improvement on the one before it (Model 1 → Model 2: F = 5.1141, p-value = 0.031) (Model 2 → Model 3: F = 313.62, p-value <<< .05).

Using model 3 as our best model of dog outcomes from the animal shelter, we glean several insights about how certain characteristics of dogs have relationships with those animal's outcome from the animal shelter.

For instance, if a dog is a pitbull, we expect it's odds of leaving the animal shelter dead increase by 348%, after controlling for chip status, season, and intake condition. Yikes! On the other hand, if a dog comes into the shelter with a scannable chip, we expect the animals odds of dying within the shelter system to drop by about 22%, after controlling for pitbull, season, and intake condition. Interestingly enough, if a dog has its outcome in the summer, the odds of that outcome being death are about 47% higher, controlling for breed, chip status, and intake condition.

Dogs and Cats

Interestingly enough, we were not able to find any significant relationships between dog and cat outcomes. We tried multiple binomial models accounting for stray, summer, and chip status. None of these models showed any significance. This suprised us a lot, as we saw a few trends in our EDA and have heard stories about poorer outcomes for cats in animal shelters. We may consider looking into a few other outcomes for our final report (we only considered death at outcome).

Annotated Appendix

Pitbulls

One of our research interests was to look into how different species of dogs fare in the animal shelter system. Specifically, we were interested in why pitbulls are more likely to be dead at the outcome of their time in the shelter. Does this trend continue after controlling for other variables in our dataset?

Initially we fit a model which factors in the chip status, whether or not the outcome was in the summer, and whether the dog was a pitbull or not.

```r
pitbull_binom <- adoptions %>%
  filter(!str_detect(intake_subtype, "(DEAD)|(DIED)")) %>%
  filter(dog == 1) %>%
  mutate(out_dead = outcome_type %in% c("DEAD ON ARRIVAL", "EUTHANIZED", "DIED"),
         summer = ifelse(month %in% c(5, 6, 7, 8, 9), 1, 0)) %>%
  mutate(chip_status = ifelse(chip_status=="SCAN CHIP", 1, 0)) %>%
  group_by(pitbull, chip_status, summer, month) %>%
  summarize(prop_dead = sum(out_dead)/n(), count = n())


pitbull_model1_binom <- glm(prop_dead ~ pitbull + chip_status + summer , weights = count, family = binom

pitbull_model1_quasi <- glm(prop_dead ~ pitbull + chip_status + summer , weights = count, family = quasi

summary(pitbull_model1_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ pitbull + chip_status + summer, family = binomial,
##     data = pitbull_binom, weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -7.4184  -1.8174  -0.4575   1.5859   9.4807
##
## Coefficients:
##              Estimate Std. Error  z value Pr(>|z|)
## (Intercept) -2.15259    0.02131 -100.994  < 2e-16 ***
## pitbull      1.23537    0.02783   44.387  < 2e-16 ***
```

```
## chip_status -0.23649    0.03050   -7.753 8.97e-15 ***
## summer       0.37879    0.02938   12.891  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2641.29  on 51  degrees of freedom
## Residual deviance:  544.19  on 48  degrees of freedom
##    (2 observations deleted due to missingness)
## AIC: 867.48
##
## Number of Fisher Scoring iterations: 4
```

```r
exp(confint(pitbull_model1_binom))
```

```
## Waiting for profiling to be done...

##                   2.5 %     97.5 %
## (Intercept) 0.1114096 0.1211179
## pitbull     3.2569778 3.6324244
## chip_status 0.7434426 0.8378715
## summer      1.3786281 1.5469365
```

```r
summary(pitbull_model1_quasi)
```

```
##
## Call:
## glm(formula = prop_dead ~ pitbull + chip_status + summer, family = quasibinomial,
##     data = pitbull_binom, weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -7.4184  -1.8174  -0.4575   1.5859   9.4807
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.15259    0.06971 -30.880  < 2e-16 ***
## pitbull      1.23537    0.09103  13.572  < 2e-16 ***
## chip_status -0.23649    0.09976  -2.371 0.021826 *
## summer       0.37879    0.09610   3.942 0.000262 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 10.69677)
##
##     Null deviance: 2641.29  on 51  degrees of freedom
## Residual deviance:  544.19  on 48  degrees of freedom
##    (2 observations deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```r
exp(confint(pitbull_model1_quasi))
```

```
## Waiting for profiling to be done...
```

```
##                   2.5 %     97.5 %
## (Intercept) 0.1011467 0.1329404
## pitbull     2.8769183 4.1109439
## chip_status 0.6478111 0.9580232
## summer      1.2082342 1.7612914
```

Initially we see that all variables included have a significant relationship to the proportion of dogs who are dead at the end of their time in the shelter, even after inflating our standard errors to account for the variance structure of our data.

Next lets try to control for whether or not a animal was contagious when it was brought into the shelter.

```r
pitbull_binom <- adoptions %>%
  filter(!str_detect(intake_subtype, "(DEAD)|(DIED)")) %>%
  filter(dog == 1) %>%
  mutate(out_dead = outcome_type %in% c("DEAD ON ARRIVAL", "EUTHANIZED", "DIED"),
         summer = ifelse(month %in% c(5, 6, 7, 8, 9), 1, 0),
         chip_status = ifelse(chip_status=="SCAN CHIP", 1, 0),
         contagious=ifelse(grepl(".*[^NON-]CONTAGIOUS", intake_condition),1,0)) %>%
  group_by(pitbull, chip_status, summer, contagious) %>%
  summarize(prop_dead = sum(out_dead)/n(), count = n())

pitbull_model2_binom <- glm(prop_dead ~ pitbull + chip_status +
                     summer + contagious, weights = count,
                 family = binomial, data = pitbull_binom)

pitbull_model2_quasi <- glm(prop_dead ~ pitbull + chip_status +
                     summer + contagious , weights = count,
                 family = quasibinomial, data = pitbull_binom)

summary(pitbull_model2_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ pitbull + chip_status + summer + contagious,
##     family = binomial, data = pitbull_binom, weights = count)
##
## Deviance Residuals:
##      Min       1Q    Median       3Q      Max
## -2.89655  -1.32251  -0.08517   1.08867   2.12765
##
## Coefficients:
##             Estimate Std. Error  z value Pr(>|z|)
## (Intercept) -2.20165    0.02169 -101.518  < 2e-16 ***
## pitbull      1.23078    0.02814   43.742  < 2e-16 ***
## chip_status -0.22483    0.03077   -7.306 2.74e-13 ***
## summer       0.36978    0.02969   12.456  < 2e-16 ***
## contagious   1.98593    0.08113   24.477  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2699.882  on 15  degrees of freedom
## Residual deviance:   32.758  on 11  degrees of freedom
##   (2 observations deleted due to missingness)
```

```
## AIC: 143.79
##
## Number of Fisher Scoring iterations: 3
```

```r
exp(confint(pitbull_model2_binom))
```

```
## Waiting for profiling to be done...
```

```
##                   2.5 %     97.5 %
## (Intercept) 0.1059964 0.1154017
## pitbull     3.2401347 3.6179798
## chip_status 0.7517627 0.8481433
## summer      1.3654369 1.5339545
## contagious  6.2166833 8.5454709
```

```r
summary(pitbull_model2_quasi)
```

```
##
## Call:
## glm(formula = prop_dead ~ pitbull + chip_status + summer + contagious,
##     family = quasibinomial, data = pitbull_binom, weights = count)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.89655  -1.32251  -0.08517   1.08867   2.12765
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.20165    0.03766 -58.455 4.54e-15 ***
## pitbull      1.23078    0.04887  25.187 4.45e-11 ***
## chip_status -0.22483    0.05344  -4.207  0.00147 **
## summer       0.36978    0.05156   7.172 1.82e-05 ***
## contagious   1.98593    0.14091  14.094 2.19e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 3.01608)
##
##     Null deviance: 2699.882  on 15  degrees of freedom
## Residual deviance:   32.758  on 11  degrees of freedom
##   (2 observations deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 3
```

```r
exp(confint(pitbull_model2_quasi))
```

```
## Waiting for profiling to be done...
```

```
##                   2.5 %     97.5 %
## (Intercept) 0.1026891 0.1190278
## pitbull     3.1110085 3.7678996
## chip_status 0.7188083 0.8863497
## summer      1.3078316 1.6007855
## contagious  5.5323688 9.6176550
```

Next lets try to control for whether or not a animal was treatable when it was brought into the shelter.

```
pitbull_binom <- adoptions %>%
  filter(!str_detect(intake_subtype, "(DEAD)|(DIED)")) %>%
  filter(dog == 1) %>%
  mutate(out_dead = outcome_type %in% c("DEAD ON ARRIVAL", "EUTHANIZED", "DIED"),
         summer = ifelse(month %in% c(5, 6, 7, 8, 9), 1, 0),
         chip_status = ifelse(chip_status=="SCAN CHIP", 1, 0),
         contagious=ifelse(grepl(".*[^NON-]CONTAGIOUS", intake_condition),1,0),
         treatable=ifelse(grepl("^TREATABLE.*", intake_condition),1,0)) %>%
  group_by(pitbull, chip_status, summer, month, contagious, treatable) %>%
  summarize(prop_dead = sum(out_dead)/n(), count = n())

pitbull_model3_binom <- glm(prop_dead ~ pitbull + chip_status +
                     summer + contagious + treatable, weights = count,
                  family = binomial, data = pitbull_binom)

pitbull_model3_quasi <- glm(prop_dead ~ pitbull + chip_status +
                     summer + contagious + treatable,
                     weights = count,
                     family = quasibinomial, data = pitbull_binom)

summary(pitbull_model3_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ pitbull + chip_status + summer + contagious +
##     treatable, family = binomial, data = pitbull_binom, weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -6.0491  -1.4236  -0.1897   0.9336   9.5936
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.59457    0.03949  -15.06  < 2e-16 ***
## pitbull      1.24955    0.02925   42.72  < 2e-16 ***
## chip_status -0.24774    0.03176   -7.80 6.21e-15 ***
## summer       0.39095    0.03070   12.73  < 2e-16 ***
## contagious   1.38010    0.08913   15.48  < 2e-16 ***
## treatable   -1.82378    0.03953  -46.14  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 5475.42  on 194  degrees of freedom
## Residual deviance:  842.76  on 189  degrees of freedom
##   (2 observations deleted due to missingness)
## AIC: 1514.1
##
## Number of Fisher Scoring iterations: 4
```

```
exp(confint(pitbull_model3_binom))
```

```
## Waiting for profiling to be done...
```

6

```
##                2.5 %     97.5 %
## (Intercept) 0.5106406 0.5961339
## pitbull     3.2943807 3.6946299
## chip_status 0.7333041 0.8305406
## summer      1.3918868 1.5699049
## contagious  3.3384762 4.7351594
## treatable   0.1493824 0.1744212
```

```
summary(pitbull_model3_quasi)
```

```
##
## Call:
## glm(formula = prop_dead ~ pitbull + chip_status + summer + contagious +
##     treatable, family = quasibinomial, data = pitbull_binom,
##     weights = count)
##
## Deviance Residuals:
##     Min      1Q   Median      3Q      Max
## -6.0491  -1.4236  -0.1897   0.9336   9.5936
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.59457    0.08240  -7.216 1.26e-11 ***
## pitbull      1.24955    0.06104  20.472  < 2e-16 ***
## chip_status -0.24774    0.06628  -3.738 0.000246 ***
## summer       0.39095    0.06407   6.102 5.80e-09 ***
## contagious   1.38010    0.18600   7.420 3.86e-12 ***
## treatable   -1.82378    0.08249 -22.110  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 4.354402)
##
##     Null deviance: 5475.42  on 194  degrees of freedom
## Residual deviance:  842.76  on 189  degrees of freedom
##    (2 observations deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
exp(confint(pitbull_model3_quasi))
```

```
## Waiting for profiling to be done...
```

```
##                2.5 %     97.5 %
## (Intercept) 0.4692407 0.6482124
## pitbull     3.0952904 3.9321196
## chip_status 0.6848701 0.8881191
## summer      1.3032732 1.6754195
## contagious  2.7616713 5.7307395
## treatable   0.1373228 0.1897619
```

Note that these models have different confidence intervals than the ones mentioned in the main report of our paper. While each of the three models in the appendix was fit on a dataset summarised specifically for each model, the models in the main report were all fit using the same dataset. By using the same dataset we can compare models using nested F tests, but SEs may be artificially small.

Dogs vs Cats

```
cat_dog_binom <- adoptions %>%
  filter(!str_detect(intake_subtype, "(DEAD)|(DIED)")) %>%
  filter(dog == 1 | cat == 1) %>%
  mutate(out_dead = outcome_type %in% c("DEAD ON ARRIVAL", "EUTHANIZED", "DIED"),
         summer = ifelse(month %in% c(5, 6, 7, 8, 9), 1, 0))%>%
  mutate(chip_status = ifelse(chip_status=="SCAN CHIP", 1, 0)) %>%
  group_by(dog, chip_status, summer, stray) %>%
  summarize(prop_dead = sum(out_dead)/n(), count = n())


####### MODEL 1: dog #########

dogcat_model1_binom <- glm(prop_dead ~ dog, weights = count, family = binomial, data = cat_dog_binom)

dogcat_model1_quasi <- glm(prop_dead ~ dog, weights = count, family = quasibinomial, data = cat_dog_bino

summary(dogcat_model1_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ dog, family = binomial, data = cat_dog_binom,
##     weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -19.837   -7.385   -2.250    4.985   15.639
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.43741    0.02199  -65.38   <2e-16 ***
## dog         -0.30509    0.02563  -11.90   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
## Residual deviance: 1745.6  on 16  degrees of freedom
## AIC: 1866
##
## Number of Fisher Scoring iterations: 4
```
```
exp(confint(dogcat_model1_binom))
```

```
## Waiting for profiling to be done...

##                  2.5 %     97.5 %
## (Intercept) 0.2274800 0.2479563
## dog         0.7010303 0.7751213
```
```
summary(dogcat_model1_quasi)
```

```
##
## Call:
## glm(formula = prop_dead ~ dog, family = quasibinomial, data = cat_dog_binom,
```

```
##       weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -19.837   -7.385   -2.250    4.985   15.639
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.4374     0.2249  -6.393 8.91e-06 ***
## dog          -0.3051     0.2621  -1.164    0.261
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 104.5899)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
## Residual deviance: 1745.6  on 16  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```r
exp(confint(dogcat_model1_quasi))
```

```
## Waiting for profiling to be done...

##                  2.5 %    97.5 %
## (Intercept) 0.1495373 0.3624932
## dog         0.4457027 1.2501118
```

```
####### MODEL 2: summer #########
```

```r
dogcat_model2_binom <- glm(prop_dead ~ summer, weights = count, family = binomial, data = cat_dog_binom

dogcat_model2_quasi <- glm(prop_dead ~ summer, weights = count, family = quasibinomial, data = cat_dog_

summary(dogcat_model2_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ summer, family = binomial, data = cat_dog_binom,
##     weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -18.202   -7.386   -4.440    5.671   17.663
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.81259    0.01405  -129.0   <2e-16 ***
## summer       0.45539    0.02372    19.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
```

```
## Residual deviance: 1524.9  on 16  degrees of freedom
## AIC: 1645.3
##
## Number of Fisher Scoring iterations: 4
```

```
exp(confint(dogcat_model2_binom))
```

```
## Waiting for profiling to be done...
```

```
##                 2.5 %     97.5 %
## (Intercept) 0.1587829 0.1677739
## summer      1.5050770 1.6517349
```

```
summary(dogcat_model2_quasi)
```

```
##
## Call:
## glm(formula = prop_dead ~ summer, family = quasibinomial, data = cat_dog_binom,
##     weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -18.202   -7.386   -4.440    5.671   17.663
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.8126     0.1344 -13.490 3.71e-10 ***
## summer        0.4554     0.2268   2.008   0.0619 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 91.44736)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
## Residual deviance: 1524.9  on 16  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
exp(confint(dogcat_model2_quasi))
```

```
## Waiting for profiling to be done...
```

```
##                 2.5 %     97.5 %
## (Intercept) 0.1243408 0.2107409
## summer      1.0043970 2.4491693
```

```
####### MODEL 3: chip ######
```

```
dogcat_model3_binom <- glm(prop_dead ~ dog + chip_status, weights = count, family = binomial, data = ca
```

```
dogcat_model3_quasi <- glm(prop_dead ~ dog + chip_status, weights = count, family = quasibinomial, data
```

```
summary(dogcat_model3_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ dog + chip_status, family = binomial,
```

```
##     data = cat_dog_binom, weights = count)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -15.6677   -4.1391   0.1846   10.8318   14.4792
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.40636    0.02211 -63.599   <2e-16 ***
## dog         -0.24565    0.02620  -9.377   <2e-16 ***
## chip_status -0.29305    0.02828 -10.363   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1750.8  on 15  degrees of freedom
## Residual deviance: 1503.0  on 13  degrees of freedom
##   (2 observations deleted due to missingness)
## AIC: 1625.4
##
## Number of Fisher Scoring iterations: 4
```

`exp(confint(dogcat_model3_binom))`

```
## Waiting for profiling to be done...
```

```
##                   2.5 %     97.5 %
## (Intercept) 0.2345951 0.2558385
## dog         0.7431337 0.8235017
## chip_status 0.7056151 0.7883420
```

`summary(dogcat_model3_quasi)`

```
##
## Call:
## glm(formula = prop_dead ~ dog + chip_status, family = quasibinomial,
##     data = cat_dog_binom, weights = count)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -15.6677   -4.1391   0.1846   10.8318   14.4792
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.4064     0.2391  -5.883 5.38e-05 ***
## dog          -0.2456     0.2832  -0.867    0.401
## chip_status  -0.2931     0.3057  -0.959    0.355
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 116.867)
##
##     Null deviance: 1750.8  on 15  degrees of freedom
## Residual deviance: 1503.0  on 13  degrees of freedom
##   (2 observations deleted due to missingness)
```

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

```r
exp(confint(dogcat_model3_quasi))
```

```
## Waiting for profiling to be done...
```

```
##                 2.5 %    97.5 %
## (Intercept) 0.1496550 0.3838132
## dog         0.4540004 1.3839138
## chip_status 0.3987708 1.3312323
```

```
####### MODEL 4: summer + dog + summer:dog ######
```

```r
dogcat_model4_binom <- glm(prop_dead ~ summer+dog+ summer:dog, weights = count, family = binomial, data

dogcat_model4_quasi <- glm(prop_dead ~ summer+dog+ summer:dog, weights = count, family = quasibinomial,

summary(dogcat_model4_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ summer + dog + summer:dog, family = binomial,
##     data = cat_dog_binom, weights = count)
##
## Deviance Residuals:
##     Min       1Q    Median       3Q      Max
## -17.392   -7.749    -4.789    6.527   18.670
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.67600    0.03030 -55.313  < 2e-16 ***
## summer       0.56018    0.04434  12.634  < 2e-16 ***
## dog         -0.17185    0.03420  -5.024 5.05e-07 ***
## summer:dog  -0.18718    0.05275  -3.549 0.000387 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
## Residual deviance: 1421.8  on 14  degrees of freedom
## AIC: 1546.2
##
## Number of Fisher Scoring iterations: 4
```

```r
exp(confint(dogcat_model4_binom))
```

```
## Waiting for profiling to be done...
```

```
##                 2.5 %    97.5 %
## (Intercept) 0.1762591 0.1984903
## summer      1.6052408 1.9099840
## dog         0.7877336 0.9007624
## summer:dog  0.7478053 0.9195843
```

```
summary(dogcat_model4_quasi)
```

```
##
## Call:
## glm(formula = prop_dead ~ summer + dog + summer:dog, family = quasibinomial,
##     data = cat_dog_binom, weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -17.392   -7.749   -4.789    6.527   18.670
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.6760     0.2978  -5.628 6.23e-05 ***
## summer        0.5602     0.4358   1.285    0.220
## dog          -0.1718     0.3362  -0.511    0.617
## summer:dog   -0.1872     0.5185  -0.361    0.723
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 96.60753)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
## Residual deviance: 1421.8  on 14  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
exp(confint(dogcat_model4_quasi))
```

```
## Waiting for profiling to be done...
```

```
##                   2.5 %    97.5 %
## (Intercept) 0.09987833 0.324086
## summer      0.74071253 4.144038
## dog         0.44621757 1.682512
## summer:dog  0.29772816 2.292399
```

```
####### MODEL 5: stray ######
```

```
dogcat_model5_binom <- glm(prop_dead ~ stray, weights = count, family = binomial, data = cat_dog_binom)
```

```
dogcat_model5_quasi <- glm(prop_dead ~ stray, weights = count, family = quasibinomial, data = cat_dog_bi
```

```
summary(dogcat_model5_binom)
```

```
##
## Call:
## glm(formula = prop_dead ~ stray, family = binomial, data = cat_dog_binom,
##     weights = count)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -18.398   -7.178   -2.626    4.353   23.455
##
## Coefficients:
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.44258    0.01775  -81.28   <2e-16 ***
## stray       -0.36155    0.02303  -15.70   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
## Residual deviance: 1640.2  on 16  degrees of freedom
## AIC: 1760.6
##
## Number of Fisher Scoring iterations: 4
```

```
exp(confint(dogcat_model5_binom))
```

```
## Waiting for profiling to be done...
```

```
##                2.5 %     97.5 %
## (Intercept) 0.228210 0.2446524
## stray       0.665877 0.7287805
```

```
summary(dogcat_model5_quasi)
```

```
##
## Call:
## glm(formula = prop_dead ~ stray, family = quasibinomial, data = cat_dog_binom,
##     weights = count)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -18.398  -7.178  -2.626   4.353  23.455
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.4426     0.1803  -8.002 5.53e-07 ***
## stray         -0.3616     0.2339  -1.546    0.142
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 103.1719)
##
##     Null deviance: 1883.0  on 17  degrees of freedom
## Residual deviance: 1640.2  on 16  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
exp(confint(dogcat_model5_quasi))
```

```
## Waiting for profiling to be done...
```

```
##                2.5 %     97.5 %
## (Intercept) 0.1636774 0.3324977
## stray       0.4414678 1.1069417
```

Multilevel on Council District