

# Running Models

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## Model One: Poisson Regression (Comparing Across (g) = Zipcodes)

$$s_g = \text{Poisson}(p_g * e^{\mu + \alpha c_g + \beta r_g})$$

- $g$  is zipcode
- $s_{\{g\}}$  is the number of ‘drug arrests’ in zipcode ( $g$ )
- $p_{\{g\}}$  is the total population in zipcode ( $g$ )
- $c_{\{g\}}$  is # of EMS Dispatches concerning drugs made in zipcode ( $g$ ) - this is our measure of ‘drug activity’ for this model
- $r_{\{g\}}$  is the racial composition of zipcode ( $g$ ) in this case it would be (proportion non-white)
- Some notes about this model is that we must be less granular and use zip if our measure of drug activity is ems calls bc that is the only measure that EMS data goes down too (it is pretty deidentified).

### Load Data

```
mod1dat <- read.csv("data/ModelDatasets/zipcodeModel1.csv")
```

### Fit Poisson Model

```
mod1dat$zip <- factor(mod1dat$zip)
names(mod1dat)[4] <- "Total.Pop"
```

```
mod1 <- glm(formula = no.drug.arrests.13.18 ~ no.ems.calls.13.18 + proportionNonWhite,
  , offset = log(Total.Pop), family = poisson, data = mod1dat)
```

```
arm::display(mod1)
```

```
## glm(formula = no.drug.arrests.13.18 ~ no.ems.calls.13.18 + proportionNonWhite,
##      family = poisson, data = mod1dat, offset = log(Total.Pop))
##               coef.est coef.se
## (Intercept)      -4.39    0.02
## no.ems.calls.13.18  0.00    0.00
## proportionNonWhite  2.40    0.06
## ---
##      n = 12, k = 3
##      residual deviance = 1308.1, null deviance = 4439.9 (difference = 3131.9)
```

```
summary(mod1)
```

```
##
## Call:
## glm(formula = no.drug.arrests.13.18 ~ no.ems.calls.13.18 + proportionNonWhite,
##      family = poisson, data = mod1dat, offset = log(Total.Pop))
```

```
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -18.0348   -4.2371   -0.5872    4.1594   25.3984
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -4.386e+00  2.015e-02 -217.60  <2e-16 ***
## no.ems.calls.13.18  1.118e-04  7.488e-06   14.94  <2e-16 ***
## proportionNonWhite  2.405e+00  5.737e-02   41.92  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 4439.9  on 11  degrees of freedom
## Residual deviance: 1308.1  on  9  degrees of freedom
## AIC: 1419.5
##
## Number of Fisher Scoring iterations: 4
```

- *Intercept* - no interpretation
- *Measure of drug activity* - coefficient is practically 0
- *Proportion non white* - The greater the proportion of nonwhite people, the greater the number of drug arrests. A one unit increase in the proportion of nonwhite people, the number of drug arrests will increase with a multiplicative effect of 11.02.

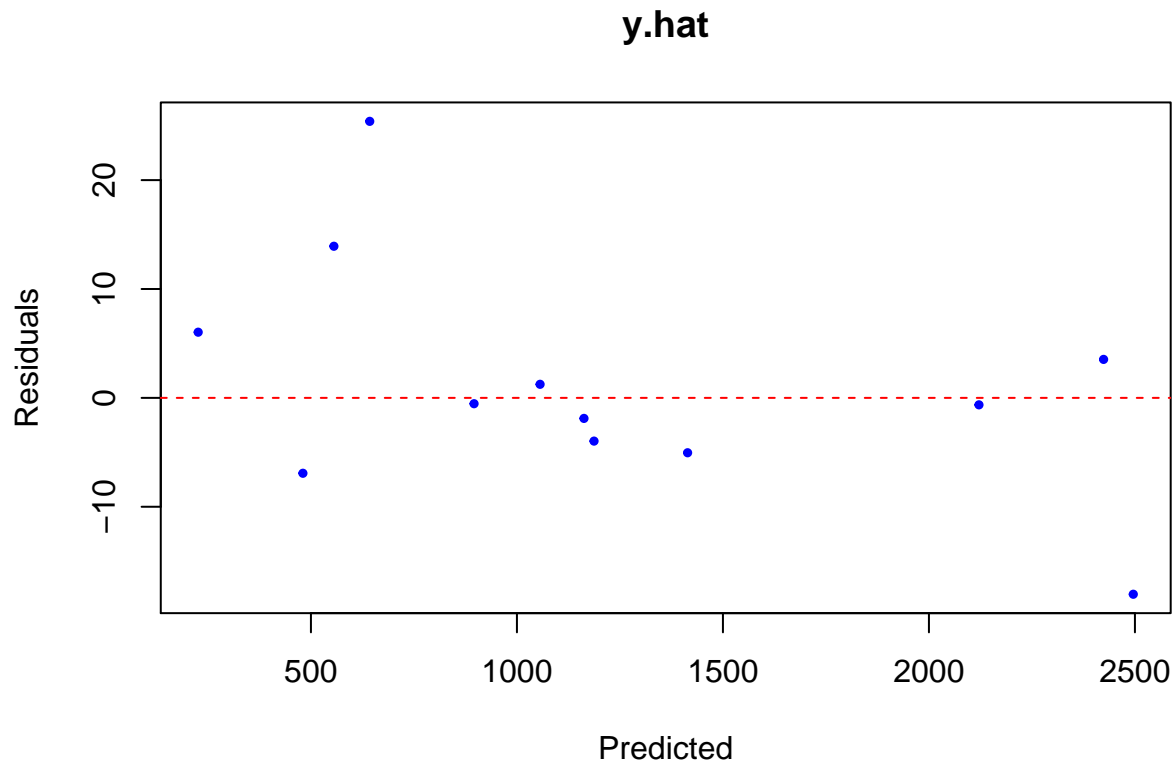
## Test for overdispersion

```
yhat <- predict(mod1, type = 'response')
z <- (mod1dat$no.drug.arrests.13.18 - yhat) / sqrt(yhat)
cat('overdispersion ratio is', sum(z^2)/(12-3), "\n")

## overdispersion ratio is 169.1272
cat('p-value of overdispersion test is', pchisq(sum(z^2), 12-3), "\n")

## p-value of overdispersion test is 1
y.hat <- predict(mod1, type = 'response')
u <- resid(mod1)
sigma <- arm::sigma.hat(mod1)

arm::residual.plot(y.hat,u, sigma)
```



- ALOT of overdispersion (169) and it is significant.

#### Attempt to Fix Overdispersion with Quasipoisson

```
mod1quasi <- glm(formula = no.drug.arrests.13.18 ~ no.ems.calls.13.18 + proportionNonWhite, offset = log(Total.Pop))
summary(mod1quasi)
```

```
##
## Call:
## glm(formula = no.drug.arrests.13.18 ~ no.ems.calls.13.18 + proportionNonWhite,
##      family = quasipoisson, data = mod1dat, offset = log(Total.Pop))
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -18.0348  -4.2371  -0.5872   4.1594  25.3984
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -4.386e+00  2.621e-01 -16.732 4.35e-08 ***
## no.ems.calls.13.18  1.118e-04  9.738e-05   1.149  0.2803
## proportionNonWhite  2.405e+00  7.461e-01   3.223  0.0104 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 169.1274)
##
##      Null deviance: 4439.9  on 11  degrees of freedom
## Residual deviance: 1308.1  on  9  degrees of freedom
```

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

## Model Two: Poisson Regression (Comparing Across Zipcodes (g) + Time (t))

$$s_{g,t} = \text{Poisson}(p_{g,t} * e^{\mu + \alpha c_{g,t} + \beta r_{g,t}})$$

```
mod2dat <- read.csv("data/ModelDatasets/zipcodeModel12.csv")
```

- g is zipcode
- s\_{g} is the number of 'drug arrests' in zipcode (g)
- p\_{g,t} is the total population in zipcode (g) at time (t)
- c\_{g,t} is # of EMS Dispatches concerning drugs made in zipcode (g) at time (t)- this is our measure of 'drug activity' for this model
- r\_{g,t} is the racial composition of zipcode (g) at time (t) in this case it would be (proportion non-white)

```
mod2dat$zip <- factor(mod2dat$zip)
```

### Fit Poisson Model

```
mod2 <- glm(formula = no.drug.arrests.14.17 ~ no.ems.calls.14.17 + proportionNonWhite, offset = log(Total.Population),
            family = poisson, data = mod2dat)
```

```
arm::display(mod2)
```

```
## glm(formula = no.drug.arrests.14.17 ~ no.ems.calls.14.17 + proportionNonWhite,
##      family = poisson, data = mod2dat, offset = log(Total.Population))
##               coef.est coef.se
## (Intercept)      -6.11    0.02
## no.ems.calls.14.17  0.00    0.00
## proportionNonWhite  2.45    0.07
## ---
##      n = 48, k = 3
##      residual deviance = 1829.1, null deviance = 3902.8 (difference = 2073.6)
```

```
summary(mod2)
```

```
##
## Call:
## glm(formula = no.drug.arrests.14.17 ~ no.ems.calls.14.17 + proportionNonWhite,
##      family = poisson, data = mod2dat, offset = log(Total.Population))
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -15.4887  -3.8196   0.4086   3.0315  21.5564
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -6.113e+00  2.373e-02 -257.63  <2e-16 ***
## no.ems.calls.14.17  4.872e-04  4.517e-05   10.79  <2e-16 ***
```

```
## proportionNonWhite 2.452e+00 6.809e-02 36.00 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 3902.8 on 47 degrees of freedom
## Residual deviance: 1829.1 on 45 degrees of freedom
## AIC: 2170.1
##
## Number of Fisher Scoring iterations: 4
```

- *Intercept* - not interpretable
- *no.ems.calls.14.17* - again basically 0
- *proportionNonWhite* - so this is similar to the coefficient estimate from before, the greater the proportion of nonwhite people, the greater the number of drug arrests. A one unit increase in the proportion of nonwhite people, the number of drug arrests will increase with a multiplicative effect of 11.58.

### Test for overdispersion

```
yhat <- predict(mod2, type = 'response')
z <- (mod2dat$no.drug.arrests.14.17 - yhat) / sqrt(yhat)
cat('overdispersion ratio is', sum(z^2)/(48-3), "\n") #n -k
```

```
## overdispersion ratio is 48.12283
```

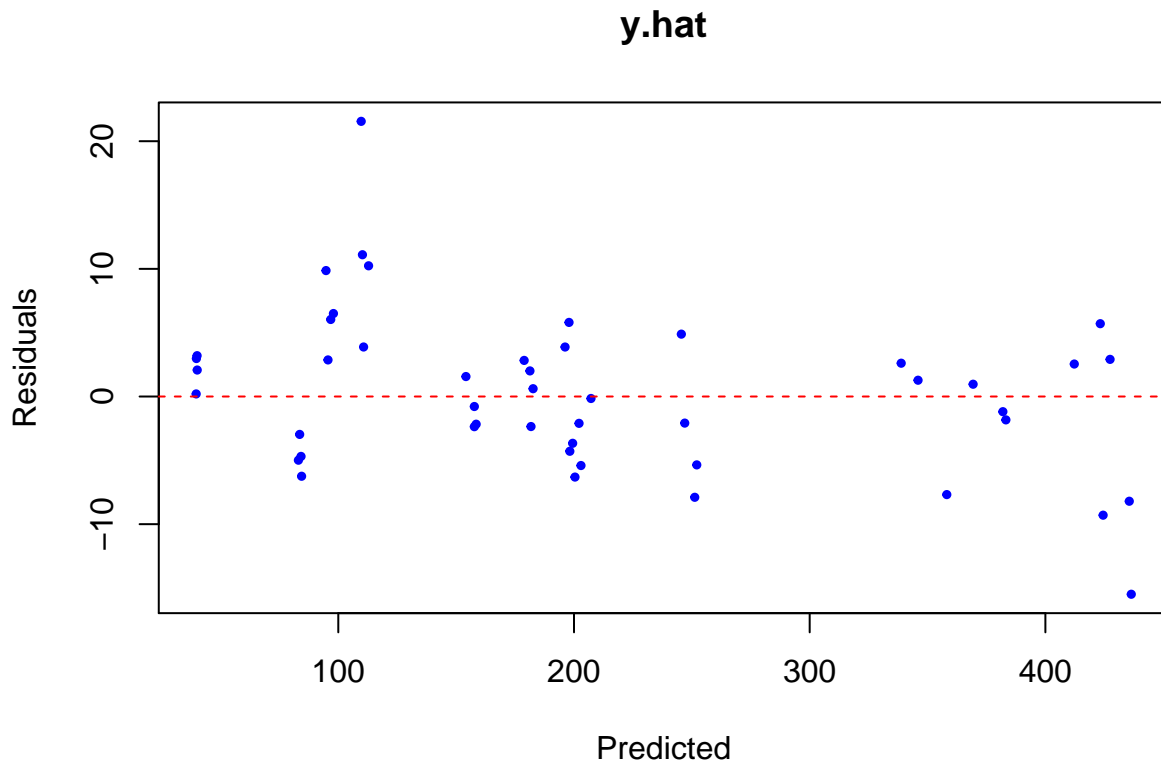
```
cat('p-value of overdispersion test is', pchisq(sum(z^2), 48-3), "\n")
```

```
## p-value of overdispersion test is 1
```

- Again overdispersion is a problem it is 48.12, and the p-value attached is 1, but adding the extra observations did seem to decrease it, which is a good thing I guess.

```
y.hat <- predict(mod2, type = 'response')
u <- resid(mod2)
sigma <- arm::sigma.hat(mod2)
```

```
arm::residual.plot(y.hat,u, sigma)
```



### Quasipoisson

```
mod2quasi <- glm(formula = no.drug.arrests.14.17 ~ no.ems.calls.14.17 + proportionNonWhite, offset = log(Total.Population))
arm::display(mod2quasi)
```

```
## glm(formula = no.drug.arrests.14.17 ~ no.ems.calls.14.17 + proportionNonWhite,
##      family = quasipoisson, data = mod2dat, offset = log(Total.Population))
##               coef.est coef.se
## (Intercept)    -6.11    0.16
## no.ems.calls.14.17  0.00    0.00
## proportionNonWhite  2.45    0.47
## ---
##  n = 48, k = 3
##  residual deviance = 1829.1, null deviance = 3902.8 (difference = 2073.6)
##  overdispersion parameter = 48.1
```

- The coefficient standard errors are definitely bigger than the model fit w. the poisson link, but they are not 'very big' in that I am definitely not worried about them.
- With this model, the proportionNonWhite parameter stays significant, but the no.ems.calls variable does not

### Model Three: Same as Model One with Extra Drug Activity Measures

$$s_g = \text{Poisson}(p_g * e^{\mu + \alpha c_g + \beta r_g + \beta d_g + \beta z_g})$$

- $g$  is zipcode
- $s_{\{g\}}$  is the number of 'drug arrests' in zipcode ( $g$ )

- $p_{\{g\}}$  is the total population in zipcode (g) - population over age 18
- $c_{\{g\}}$  is # of EMS Dispatches concerning drugs made in zipcode (g) - this is our measure of ‘drug activity’ for this model
- $r_{\{g\}}$  is the racial composition of zipcode (g) in this case it would be (proportion non-white)