

# Crab Poisson GLM

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## Poisson vs Quasi-Poisson GLM

```
count <- c(0, 0, 22, 3, 17, 0, 0,
7, 11, 11, 73, 33, 0, 65,
13, 44, 20, 27, 48, 104,
233, 81, 22, 9, 2, 0,
0, 56, 0, 8, 0, 3, 1,
16, 55, 142, 10, 2, 145,
6, 4, 5, 124, 24, 204,
415, 466, 6, 14, 12, 0,
0, 4, 13, 5, 1, 1, 4,
4, 36, 407, 0, 0, 18,
4, 14, 0, 24, 52, 314,
245, 107, 5, 6, 2, 0,
0, 0, 4, 2, 2, 5, 4,
2, 1, 0, 12, 1, 30, 0,
3, 28, 2, 21, 8, 82, 12,
10, 2, 0, 0, 1, 1, 2,
2, 1, 2, 29, 2, 2, 0,
13, 0, 19, 1, 3, 26, 30,
5, 4, 94, 1, 9, 3, 0,
0, 0, 0, 2, 3, 0, 0,
4, 0, 5, 4, 22, 0, 64,
4, 4, 43, 3, 16, 19, 95,
6, 22, 0, 0)

site <- as.factor(c(1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1,
2, 2, 2, 2, 2, 2, 2, 2,
2, 2, 2, 2, 2, 2, 2, 2,
2, 2, 2, 2, 2, 2, 2, 2,
2, 3, 3, 3, 3, 3, 3, 3,
3, 3, 3, 3, 3, 3, 3, 3,
3, 3, 3, 3, 3, 3, 3, 3,
3, 3, 4, 4, 4, 4, 4, 4,
4, 4, 4, 4, 4, 4, 4, 4,
4, 4, 4, 4, 4, 4, 4, 4,
4, 4, 4, 5, 5, 5, 5, 5,
5, 5, 5, 5, 5, 5, 5, 5,
5, 5, 5, 5, 5, 5, 5, 5,
```

```

5, 5, 5, 5, 6, 6, 6, 6,
6, 6, 6, 6, 6, 6, 6, 6,
6, 6, 6, 6, 6, 6, 6, 6,
6, 6, 6, 6, 6))

# Create a generalized linear model with a Poisson family on count vs site.
pois_glm <- glm(count ~ site,
               family = poisson)

# Summarize the model.
summary(pois_glm)

##
## Call:
## glm(formula = count ~ site, family = poisson)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -11.7235  -6.7252  -3.3662   0.1082  31.4551
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   3.52046    0.03440 102.336 <2e-16 ***
## site2         0.70958    0.04202  16.888 <2e-16 ***
## site3         0.40428    0.04442   9.101 <2e-16 ***
## site4        -1.29692    0.07425 -17.468 <2e-16 ***
## site5        -1.21788    0.07200 -16.916 <2e-16 ***
## site6        -0.98359    0.06594 -14.917 <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: 12735  on 149  degrees of freedom
## Residual deviance: 10255  on 144  degrees of freedom
## AIC: 10765
##
## Number of Fisher Scoring iterations: 6

# Create a generalized linear model with a Quasi-Poisson family on count vs site.
# This will give us an overdispersion factor to work with.
quasi_pois_glm <- glm(count ~ site,
                    family = quasipoisson)

# Summarize the model.
summary(quasi_pois_glm)

##
## Call:
## glm(formula = count ~ site, family = quasipoisson)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -11.7235  -6.7252  -3.3662   0.1082  31.4551
##

```

```
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.5205     0.3569   9.865 <2e-16 ***
## site2        0.7096     0.4359   1.628  0.1057
## site3        0.4043     0.4608   0.877  0.3818
## site4       -1.2969     0.7702  -1.684  0.0944 .
## site5       -1.2179     0.7469  -1.631  0.1052
## site6       -0.9836     0.6840  -1.438  0.1526
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 107.6158)
##
##      Null deviance: 12735  on 149  degrees of freedom
## Residual deviance: 10255  on 144  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 6
# Divide our deviance by our overdispersion factor to get the scaled deviance.
10255/107.6158

## [1] 95.2927
```