MATH 523: EXAMPLE - POISSON DATA CODE & RESULTS

```
site<-gl(3,1,12)
tumor<-gl(4,3)
Y<-c(22,2,10,16,54,115,19,33,73,11,17,28)
cancer<-data.frame(tumor,site,Y)
cancer.m0 <- glm(Y ~ 1, family=poisson,data=cancer)
cancer.m1 <- glm(Y ~ tumor, family=poisson,data=cancer)
cancer.m2 <- glm(Y ~ site, family=poisson,data=cancer)
cancer.m3 <- glm(Y ~ tumor + site, family=poisson,data=cancer)

summary(cancer.m0)
summary(cancer.m1)
summary(cancer.m2)
summary(cancer.m3)
```

Note: The `gl` function generates levels of a factor.

```
> summary(cancer.m0)
Call: glm(formula = Y ~ 1, family = poisson, data = cancer)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-7.170  -3.633  -2.398   0.777  11.022

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)    3.507      0.050   70.13   <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: 295.20  on 11  degrees of freedom
Residual deviance: 295.20  on 11  degrees of freedom
AIC: 356.31

> summary(cancer.m1)
Call: glm(formula = Y ~ tumor, family = poisson, data = cancer)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-6.940  -2.299  -0.701   2.208   6.055

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.4277     0.1715  14.156  < 2e-16 ***
tumor2        1.6940     0.1866   9.079  < 2e-16 ***
tumor3        1.3020     0.1934   6.731 1.68e-11 ***
tumor4        0.4990     0.2174   2.295   0.0217 *
---
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1     1
(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 295.20  on 11  degrees of freedom
Residual deviance: 150.10  on  8  degrees of freedom
AIC: 217.21
```

```
> summary(cancer.m2)
Call:
glm(formula = Y ~ site, family = poisson, data = cancer)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-7.6398  -2.5337   0.1155   1.4367   6.8161

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.8332     0.1213  23.363  < 2e-16 ***
site2         0.4439     0.1554   2.857  0.00427 **
site3         1.2010     0.1383   8.683  < 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: 295.20  on 11  degrees of freedom
Residual deviance: 196.90  on  9  degrees of freedom
AIC: 262.01

> summary(cancer.m3)
Call:glm(formula = Y ~ tumor + site, family = poisson, data = cancer)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.0453  -1.0741   0.1297   0.5857   5.1354

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.7544     0.2040   8.600  < 2e-16 ***
tumor2        1.6940     0.1866   9.079  < 2e-16 ***
tumor3        1.3020     0.1934   6.731 1.68e-11 ***
tumor4        0.4990     0.2174   2.295  0.02173 *
site2         0.4439     0.1554   2.857  0.00427 **
site3         1.2010     0.1383   8.683  < 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: 295.203  on 11  degrees of freedom
Residual deviance:  51.795  on  6  degrees of freedom
AIC: 122.91
```