- ➤ To fit the zero-truncated Poisson model, we use the vglm function in the VGAM package.
- This function fits a very flexible class of models called vector generalized linear models to a wide range of assumed distributions.
- ▶ In our case, we believe the data are Poisson, but without zeros.
- Thus the values are strictly positive Poisson, for which we use the positive Poisson family via the pospoisson function passed to vglm.

Fitting the Model with R

We will use the *hospitalstay* data.

```
m1 <- vglm(stay ~ age + hmo + died,
    family = pospoisson(),
    data = hospitalstay)
summary(m1)</pre>
```

Fitting the Model with R

Model Summary

```
## Coefficients:
```

```
## Estimate Std. Error z value

## (Intercept) 2.436 0.027 89.1

## age -0.014 0.005 -2.9

## hmo1 -0.136 0.024 -5.7

## died1 -0.204 0.018 -11.1
```

- ▶ The value of the coefficient for age, -0.0144 suggests that the log count of stay decreases by 0.0144 for each year increase in age.
- The coefficient for hmo, -0.1359 indicates that the log count of stay for HMO patient is 0.1359 less than for non-HMO patients.
- ► The log count of stay for patients who died while in the hospital was 0.2038 less than those patients who did not die.
- ► Finally, the value of the constant 2.4358 is the log count of the stay when all of the predictors equal zero.

- Can compute Cls using boot package
- Age does not have a significant effect, but hmo and died both do.

