BST210 Project Check-in 2: Appendix

Linear Regression

All of our potential dependent variables are in the form of counts, rates and percentages, however for the purposes of this assignment, we treated the emergency department visits per 1,000 beneficiaries as a linear variable and fit a multiple linear regression to determine the effects of Medicaid expansion on this rate. For our analysis, we plan to run this model as a Poisson model.

To evaluate the effects of Medicaid Expansion on health outcomes among the Medicare population in 2018, we fit a multiple linear regression model:

$$E(\text{Number of ED visits}/1{,}000 \text{ beneficiaries}) = \beta_0 + \beta_1 * \text{Average Age} +$$
$$\beta_2 * I(\text{State Expanded in 2014}) +$$
$$\beta_3 * I(\text{State Expanded after 2014}) +$$
$$\beta_4 * I(\text{State has not Expanded}) +$$
$$\beta_5 * \text{Percent Eligible for Medicaid} +$$
$$\beta_6 * \text{Percent Eligible for Medicaid}^2$$

```r
mod.lm <- lm(emergency_department_visits_per_1000_beneficiaries ~ average_age +
             expansion_status + percent_eligible_for_medicaid +
             percent_eligible_for_medicaid_2, data = medicare %>% mutate(percent_eligible_for_medicaid

# Model interpretation
summary(mod.lm)
```

```
##
## Call:
## lm(formula = emergency_department_visits_per_1000_beneficiaries ~
##     average_age + expansion_status + percent_eligible_for_medicaid +
##         percent_eligible_for_medicaid_2, data = medicare %>%
##     mutate(percent_eligible_for_medicaid_2 = percent_eligible_for_medicaid^2))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -655.61  -66.17    3.30   69.00 1056.20
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      1479.308    128.124  11.546  < 2e-16 ***
## average_age                       -15.953      1.688  -9.451  < 2e-16 ***
## expansion_status2                  36.771      8.627   4.262 2.08e-05 ***
## expansion_status3                  16.459      9.581   1.718   0.0859 .
## expansion_status4                  55.867      8.260   6.763 1.60e-11 ***
## percent_eligible_for_medicaid    2139.196     94.964  22.526  < 2e-16 ***
## percent_eligible_for_medicaid_2 -2710.022    165.888 -16.336  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## 
## Residual standard error: 112.9 on 3122 degrees of freedom
##   (15 observations deleted due to missingness)
## Multiple R-squared:  0.4149, Adjusted R-squared:  0.4138
## F-statistic:    369 on 6 and 3122 DF,  p-value: < 2.2e-16
```

```
confint(mod.lm)
```

```
##                                    2.5 %      97.5 %
## (Intercept)                   1228.09271  1730.52411
## average_age                    -19.26243   -12.64340
## expansion_status2               19.85531    53.68695
## expansion_status3               -2.32591    35.24445
## expansion_status4               39.67072    72.06293
## percent_eligible_for_medicaid 1952.99814  2325.39465
## percent_eligible_for_medicaid_2 -3035.28232 -2384.76099
```

According to this model, for counties with the same expansion status level and percent eligible for Medicaid, a one year increase in the average age of Medicare beneficiaries results in about 16 less emergency department visits per 1,000 beneficiaries. For counties with the same average age of Medicare beneficiaries and percent eligible for Medicaid, being in a state that expanded Medicaid in 2014 results in about 37 (95% CI: (19.86, 53.69)) more emergency department visits per 1,000 beneficiaries than counties that are in states that expanded Medicaid before 2014. For counties with the same average age of Medicare beneficiaries and percent eligible for Medicaid, being in a state that expanded Medicaid in years after 2014 results in about 16 (95% CI: (-2.326, 35.24)) more emergency department visits per 1,000 beneficiaries than counties that are in states that expanded Medicaid before 2014. For counties with the same average age of Medicare beneficiaries and percent eligible for Medicaid, being in a state that has not expanded Medicaid results in about 56 (95% CI: (39.67, 72.06)) more emergency department visits per 1,000 beneficiaries than counties that are in states that expanded Medicaid before 2014. For counties in states with the same expansion category and average age of Medicare beneficiaries, a one percent increase in the percent eligible for Medicaid results in about 571 less emergency department visits per 1,000 beneficiaries. All p-values, with the exception of that for the expansion category 3 (state expanded Medicaid after 2014), is < 0.001.

```
# Model evaluation
par(mfrow = c(2, 2))
hist(mod.lm$residuals, main = "Histogram of Residuals", xlab = "Residuals")
qqnorm(residuals(mod.lm), pch = 20, col = "tomato", main = "Unstandardized Residuals")
qqline(residuals(mod.lm)) #NJP Added line
plot(fitted(mod.lm), residuals(mod.lm), main = "Plot of Residuals against Fitted Values", xlab = "Fitte
abline(h = 0, col = "cornflowerblue", lwd = 2)
```
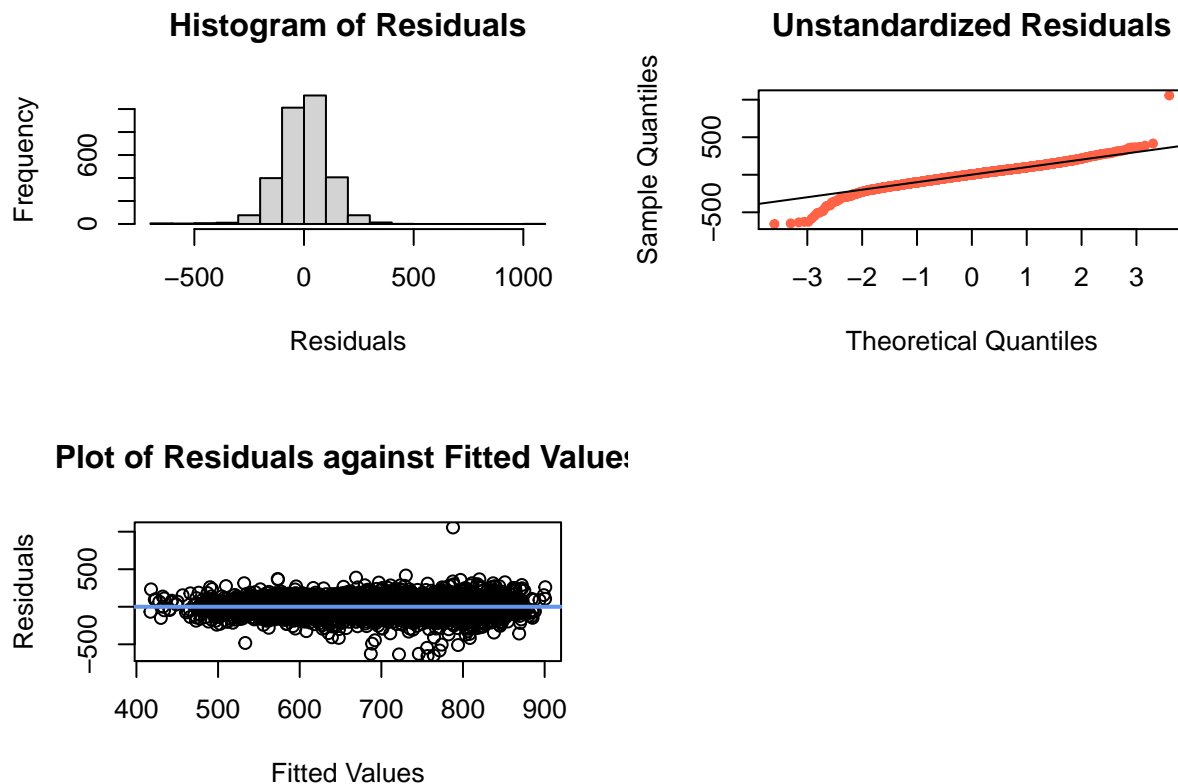
Histogram of Residuals

Unstandardized Residuals

Plot of Residuals against Fitted Values

In evaluating this linear model, we have determined that the linearity assumption holds, as there is no pattern in the residuals. The residuals are pretty normally distributed, although there is some evidence of left skew in the qqplot.

Poisson Regression

FQHC/RHC centers are centers that provide services to Medicare beneficiaries in geographic areas that have a shortage of health services. To determine the effect of Medicaid expansion on the rate of FQHC/RHC visits per 1,000 beneficiaries, we fit a Poisson model. The form of the model is:

$$
\begin{aligned}
log(\lambda) = \beta_0 &+ \beta_1 * AverageAge+ \\
\beta_2 &* I(\text{State Expanded Medicaid in 2014})+ \\
\beta_3 &* I(\text{State Expanded Medicaid after 2014})+ \\
\beta_4 &* I(\text{State has not expanded Medicaid})+ \\
\beta_5 &* I(\text{Percent Eligible for Medicaid})+ \\
\beta_6 &* I(\text{Percent Eligible for Medicaid}^2)
\end{aligned}
$$

where λ is the incidence rate or FQHRC/RHC visits per 1,000 beneficiaries.

```
mod.pois <-  glm(`fqhc/rhc_visits_per_1000_beneficiaries` ~ average_age + expansion_status + percent_el
summary(mod.pois)
```

```
##
## Call:
## glm(formula = `fqhc/rhc_visits_per_1000_beneficiaries` ~ average_age +
##     expansion_status + percent_eligible_for_medicaid + percent_eligible_for_medicaid_2,
##     family = poisson(), data = na.omit(medicare[, c("county",
```

```
##          "percent_eligible_for_medicaid", "average_age", "expansion_status",
##          "fqhc/rhc_visits_per_1000_beneficiaries")]) %>% mutate(percent_eligible_for_medicaid_2 = per
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -94.57  -32.26  -14.06   17.87  110.44
##
## Coefficients:
##                                  Estimate Std. Error  z value Pr(>|z|)
## (Intercept)                    -1.143e+01  3.186e-02 -358.690  < 2e-16 ***
## average_age                     2.405e-01  4.147e-04  579.943  < 2e-16 ***
## expansion_status2               2.031e-01  2.260e-03   89.835  < 2e-16 ***
## expansion_status3              -1.871e-02  2.620e-03   -7.141 9.29e-13 ***
## expansion_status4               1.689e-01  2.178e-03   77.545  < 2e-16 ***
## percent_eligible_for_medicaid   6.664e+00  2.298e-02  290.015  < 2e-16 ***
## percent_eligible_for_medicaid_2 -4.219e+00  3.683e-02 -114.544  < 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: 3866643  on 3108  degrees of freedom
## Residual deviance: 3429374  on 3102  degrees of freedom
## AIC: 3454731
##
## Number of Fisher Scoring iterations: 5
```

```
exp(confint(mod.pois))
```

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

```
##                                      2.5 %        97.5 %
## (Intercept)                   1.023444e-05 1.159580e-05
## average_age                   1.270841e+00 1.272908e+00
## expansion_status2             1.219736e+00 1.230592e+00
## expansion_status3             9.764351e-01 9.865171e-01
## expansion_status4             1.178939e+00 1.189047e+00
## percent_eligible_for_medicaid 7.492959e+02 8.199245e+02
## percent_eligible_for_medicaid_2 1.368768e-02 1.581387e-02
```

By our model, for counties that have the same average age of Medicare beneficiaries and same percentage of beneficiaries who are eligible for Medicaid, counties in states that expanded in 2014 have an incidence rate of FQHC/RHC visits that is 1.225 (95% CI: (1.219, 1.231)) times the incidence rate of FQHC/RHC visits in counties whose state expanded before 2014. For counties that have the same average age of Medicare beneficiaries and same percentage of beneficiaries who are eligible for Medicaid, counties in states that expanded after 2014 have an incidence rate of FQHC/RHC visits that is 0.981 (95% CI: (.976, .987)) times the incidence rate of FQHC/RHC visits in counties whose state expanded before 2014. For counties that have the same average age of Medicare beneficiaries and same percentage of beneficiaries who are eligible for Medicaid, counties in states that have not expanded have an incidence rate of FQHC/RHC visits that is 1.184 (95% CI: (1.179, 1.189)) times the incidence rate of FQHC/RHC visits in counties whose state expanded before 2014.

Overdispersion

```
# Checking for Overdispersion (Latitude-only model)
deviance(mod.pois)/mod.pois$df.residual
```

```
## [1] 1105.537
```

```
pearson.stat1 <- sum((na.omit(medicare[, c("county", "percent_eligible_for_medicaid", "average_age", "e
pearson.stat1/mod.pois$df.residual
```

```
## [1] 1173.745
```

The deviance/degrees of freedom is about 1105, and the Pearson χ^2 statistic divided by degrees of freedom is around 1174. This indicates that there is overdisperson in the model. To account for this, we will need to try fitting a negative binomial model.

Data Prep

```
state_demo %>%
  filter(!county %in% c("NATIONAL TOTAL", "STATE TOTAL") & !is.na(expansion_status)) %>%
  group_by(expansion_status) %>%
  summarize(avg_mcd_elig = mean(percent_eligible_for_medicaid, na.rm = T),
            cnt_counties = n())
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 4 x 3
##   expansion_status avg_mcd_elig cnt_counties
##   <chr>                  <dbl>        <int>
## 1 1                      0.220          218
## 2 2                      0.213          902
## 3 3                      0.215          408
## 4 4                      0.196         1662
```

```
state_demo$exp <- ifelse(state_demo$expansion_status == "4", 0, 1)
state_demo$exp <- as.factor(state_demo$exp)
state_demo$not_exp <- ifelse(state_demo$expansion_status == "4", 1, 0)
state_demo$not_exp <- as.factor(state_demo$not_exp)

county_dat <- state_demo %>% filter(!county %in% c("NATIONAL TOTAL", "STATE TOTAL"))


county_dat <- county_dat %>% filter(!is.na(percent_eligible_for_medicaid) &
                                    !is.na(emergency_department_visits_per_1000_beneficiaries) &
                                    !is.na(average_age) &
                                    !is.na(hospital_readmission_rate))
```

Data Analysis

Binomial Logistic Regression Initially we planned to examine Preventive Quality Indicators as a measure of health quality in a population, but these data points are only publically available at the state level, which would limit our analysis to only 50 observations. Thus, we have modified our analysis approach to consider data at the county level and use alternative measures for quality of health.

```
pqi3 <- state_demo %>% filter(county == 'STATE TOTAL') %>% rename(pqi_03_less_65 = 'pqi03_diabetes_lt_c

summary(glm(not_exp ~ pqi_03_less_65, family = binomial(), data=pqi3))
```

```
##
## Call:
## glm(formula = not_exp ~ pqi_03_less_65, family = binomial(),
##     data = pqi3)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.0362  -0.9883  -0.9397   1.3702   1.4831
```

1

```
## 
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -0.8320144  1.0832267  -0.768    0.442
## pqi_03_less_65  0.0005229  0.0015878   0.329    0.742
## 
## (Dispersion parameter for binomial family taken to be 1)
## 
##     Null deviance: 66.406  on 49  degrees of freedom
## Residual deviance: 66.298  on 48  degrees of freedom
##   (3 observations deleted due to missingness)
## AIC: 70.298
## 
## Number of Fisher Scoring iterations: 4
```

This reduced model confirms that the precentage of people eligible for medicaid in the Medicare population (i.e. dual eligible) is associated with whether the state has expanded Medicaid access as part of the Affordable Care Act.

```
mod.1 <- glm(not_exp ~ percent_eligible_for_medicaid, family = binomial(),
         data= county_dat)
summary(mod.1)
```

```
## 
## Call:
## glm(formula = not_exp ~ percent_eligible_for_medicaid, family = binomial(),
##     data = county_dat)
## 
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.396  -1.215   1.018   1.119   1.722
## 
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                    0.60237    0.09589   6.282 3.35e-10 ***
## percent_eligible_for_medicaid -2.48259    0.43084  -5.762 8.30e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for binomial family taken to be 1)
## 
##     Null deviance: 4216.4  on 3045  degrees of freedom
## Residual deviance: 4182.4  on 3044  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 4186.4
## 
## Number of Fisher Scoring iterations: 4
```

This extended model considers the additional covariates of health quality measures (hospital readmission rate & number of emergency department visits) and also controls for average age in the county population when predicting the county's Medicaid expansion status.

```r
mod.binary = glm(not_exp ~
                 emergency_department_visits_per_1000_beneficiaries +
                 hospital_readmission_rate +
                 average_age +
                 percent_eligible_for_medicaid,
                 family = binomial(), data = county_dat)
summary(mod.binary)
```

```
##
## Call:
## glm(formula = not_exp ~ emergency_department_visits_per_1000_beneficiaries +
##     hospital_readmission_rate + average_age + percent_eligible_for_medicaid,
##     family = binomial(), data = county_dat)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5556  -1.2048   0.9571   1.1102   1.8422
##
## Coefficients:
##                                                     Estimate Std. Error
## (Intercept)                                       -6.1305202  2.4005702
## emergency_department_visits_per_1000_beneficiaries  0.0015904  0.0003563
## hospital_readmission_rate                           2.6013322  1.4463722
## average_age                                         0.0754098  0.0315594
## percent_eligible_for_medicaid                      -3.3928890  0.6566558
##                                                    z value Pr(>|z|)
## (Intercept)                                         -2.554   0.0107 *
## emergency_department_visits_per_1000_beneficiaries   4.463 8.06e-06 ***
## hospital_readmission_rate                            1.799   0.0721 .
## average_age                                          2.389   0.0169 *
## percent_eligible_for_medicaid                       -5.167 2.38e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 4216.4  on 3045  degrees of freedom
## Residual deviance: 4149.5  on 3041  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 4159.5
##
## Number of Fisher Scoring iterations: 4
```

```r
exp(100*0.0015904)
```

```
## [1] 1.172385
```

```r
CI=c(exp(100*(0.0015904-1.96*0.0003563)),exp(100*(0.0015904+1.96*0.0003563)))
CI
```

```
## [1] 1.093305 1.257185
```

```
exp(2.6013322)
```

```
## [1] 13.48169
```

```
CI=c(exp((2.6013322-1.64*1.4463722)),exp((2.6013322+1.64*1.4463722)))
CI
```

```
## [1]   1.257696 144.514899
```

```
anova(mod.1, mod.binary, test="Chisq" )
```

```
## Analysis of Deviance Table
##
## Model 1: not_exp ~ percent_eligible_for_medicaid
## Model 2: not_exp ~ emergency_department_visits_per_1000_beneficiaries +
##     hospital_readmission_rate + average_age + percent_eligible_for_medicaid
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      3044     4182.4
## 2      3041     4149.5  3   32.851 3.463e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
library(nnet)
mod.all_multi <- multinom(expansion_status ~ hospital_readmission_rate +
                          average_age  +
                          emergency_department_visits_per_1000_beneficiaries +
                          percent_eligible_for_medicaid,
                          data = county_dat)
```

Multinomial Logistic Regression (y - expansion status category of 1, 2, 3, or 4)

```
## # weights:  24 (15 variable)
## initial  value 4222.652624
## iter  10 value 3447.502738
## iter  20 value 3430.078544
## iter  30 value 3430.047519
## final  value 3430.047329
## converged
```

```
summary(mod.all_multi)
```

```
## Call:
## multinom(formula = expansion_status ~ hospital_readmission_rate +
##     average_age + emergency_department_visits_per_1000_beneficiaries +
##     percent_eligible_for_medicaid, data = county_dat)
##
## Coefficients:
##   (Intercept) hospital_readmission_rate average_age
```

```
## 2   -1.800253                      2.4989419  0.02842874
## 3    6.088403                     -0.5764894 -0.08309832
## 4   -4.747857                      3.9555005  0.07170940
##    emergency_department_visits_per_1000_beneficiaries
## 2                                         0.001833953
## 3                                         0.001588072
## 4                                         0.003080513
##    percent_eligible_for_medicaid
## 2                     -2.183894
## 3                     -2.584953
## 4                     -5.317456
##
## Std. Errors:
##    (Intercept) hospital_readmission_rate average_age
## 2 6.372788e-05              6.501529e-06 0.004814838
## 3 7.153420e-05              6.783909e-06 0.005421215
## 4 6.103099e-05              5.847374e-06 0.004650734
##    emergency_department_visits_per_1000_beneficiaries
## 2                                          0.0004967208
## 3                                          0.0005558584
## 4                                          0.0004809703
##    percent_eligible_for_medicaid
## 2                  2.989936e-06
## 3                  1.931632e-06
## 4                  2.651484e-06
##
## Residual Deviance: 6860.095
## AIC: 6890.095
```

```r
exp(2.49)
```

```
## [1] 12.06128
```

```r
CI=c(exp((2.49-1.96*6.501529e-06)),exp((2.49+1.96*6.501529e-06)))
CI
```

```
## [1] 12.06112 12.06143
```

```r
exp(-0.57)
```

```
## [1] 0.5655254
```

```r
CI=c(exp((-0.57-1.96* 6.783909e-06)),exp((-0.57+1.96* 6.783909e-06)))
CI
```

```
## [1] 0.5655179 0.5655330
```

```r
exp(3.95)
```

```
## [1] 51.93537
```

```
CI=c(exp((3.95-1.96*5.847374e-06)),exp((3.95+1.96*5.847374e-06)))
CI
```

```
## [1] 51.93477 51.93596
```

```
library(VGAM)
```

Ordinal Logistic Regression

```
## Loading required package: stats4
```

```
## Loading required package: splines
```

```
##
## Attaching package: 'VGAM'
```

```
## The following object is masked from 'package:tidyr':
##
##     fill
```

```
mod.no.po <- vglm(as.numeric(expansion_status) ~ emergency_department_visits_per_1000_beneficiaries +
                  average_age ,
                  cumulative(parallel=FALSE, reverse=T), data=county_dat)
```

```
## Warning in Deviance.categorical.data.vgam(mu = mu, y = y, w = w, residuals =
## residuals, : fitted values close to 0 or 1
```

```
## Warning in slot(family, "validparams")(eta, y = y, extra = extra): It seems
## that the nonparallelism assumption has resulted in intersecting linear/additive
## predictors. Try propodds() or fitting a partial nonproportional odds model or
## choosing some other link function, etc.
```

```
## Warning in Deviance.categorical.data.vgam(mu = mu, y = y, w = w, residuals =
## residuals, : fitted values close to 0 or 1
```

```
## Warning in slot(family, "validparams")(eta, y = y, extra = extra): It seems
## that the nonparallelism assumption has resulted in intersecting linear/additive
## predictors. Try propodds() or fitting a partial nonproportional odds model or
## choosing some other link function, etc.
```

```
## Warning in Deviance.categorical.data.vgam(mu = mu, y = y, w = w, residuals =
## residuals, : fitted values close to 0 or 1
```

```
## Warning in slot(family, "validparams")(eta, y, extra = extra): It seems that
## the nonparallelism assumption has resulted in intersecting linear/additive
## predictors. Try propodds() or fitting a partial nonproportional odds model or
## choosing some other link function, etc.
```

```
## Warning in slot(family, "validparams")(eta, y, extra = extra): It seems that
## the nonparallelism assumption has resulted in intersecting linear/additive
## predictors. Try propodds() or fitting a partial nonproportional odds model or
## choosing some other link function, etc.
```

```
## Warning in vglm.fitter(x = x, y = y, w = w, offset = offset, Xm2 = Xm2, : some
## quantities such as z, residuals, SEs may be inaccurate due to convergence at a
## half-step
```

```
summary(mod.no.po)
```

```
##
## Call:
## vglm(formula = as.numeric(expansion_status) ~ emergency_department_visits_per_1000_beneficiaries +
##     average_age, family = cumulative(parallel = FALSE, reverse = T),
##     data = county_dat)
##
## Pearson residuals:
##                             Min     1Q Median     3Q    Max
## logitlink(P[Y>=2]) -5.498  0.1467 0.1645 0.4207 0.7922
## logitlink(P[Y>=3]) -1.510 -1.3180 0.3945 0.4129 3.3851
## logitlink(P[Y>=4]) -4.091 -0.6207 0.6581 0.8443 1.3592
##
## Coefficients:
##                                                     Estimate Std. Error
## (Intercept):1                                      -8.652e+00  3.654e+00
## (Intercept):2                                      -6.179e+00  1.910e+00
## (Intercept):3                                      -1.352e+01  1.913e+00
## emergency_department_visits_per_1000_beneficiaries:1  2.259e-03  5.661e-04
## emergency_department_visits_per_1000_beneficiaries:2  7.979e-04  3.010e-04
## emergency_department_visits_per_1000_beneficiaries:3  1.152e-03  2.970e-04
## average_age:1                                       1.364e-01  4.852e-02
## average_age:2                                       8.739e-02  2.528e-02
## average_age:3                                       1.796e-01  2.525e-02
##                                                     z value Pr(>|z|)
## (Intercept):1                                        -2.368 0.017893 *
## (Intercept):2                                        -3.235 0.001218 **
## (Intercept):3                                        -7.068 1.57e-12 ***
## emergency_department_visits_per_1000_beneficiaries:1  3.990 6.61e-05 ***
## emergency_department_visits_per_1000_beneficiaries:2    NA       NA
## emergency_department_visits_per_1000_beneficiaries:3  3.879 0.000105 ***
## average_age:1                                          NA       NA
## average_age:2                                         3.458 0.000545 ***
## average_age:3                                         7.112 1.14e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Names of linear predictors: logitlink(P[Y>=2]), logitlink(P[Y>=3]),
## logitlink(P[Y>=4])
##
## Residual deviance: 6886.45 on 9129 degrees of freedom
##
## Log-likelihood: -3443.225 on 9129 degrees of freedom
```

```
##
## Number of Fisher scoring iterations: 15
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):3', 'emergency_department_visits_per_1000_beneficiaries:2', 'average_age:1', 'average_a
##
##
## Exponentiated coefficients:
## emergency_department_visits_per_1000_beneficiaries:1
##                                             1.002261
## emergency_department_visits_per_1000_beneficiaries:2
##                                             1.000798
## emergency_department_visits_per_1000_beneficiaries:3
##                                             1.001152
##                                           average_age:1
##                                             1.146087
##                                           average_age:2
##                                             1.091326
##                                           average_age:3
##                                             1.196728
```