# Friday, Mar 4

#### Poisson Regression for Rates

The *i*-th observed  $rate R_i$  can be written as

$$R_i = C_i/S_i$$

where  $C_i$  is a *count* and  $S_i$  is the "size" of the interval in which the counts are observed. Examples include fish per minute, epileptic episodes per day, or defects per (square) meter. In some cases  $S_i$  is referred to as the "exposure" of the *i*-th observation.

Assume that the count  $C_i$  has a Poisson distribution and that

$$E(C_i) = S_i \underbrace{\exp(\beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik})}_{\lambda_i},$$

where  $\lambda_i$  is the expected count per unit (e.g., per minute) so that  $S_i\lambda_i$  is then the expected count per  $S_i$  (e.g., per hour if  $S_i = 60$ , per day if  $S_i = 1440$ , or per second if  $S_i = 1/60$ ). The expected rate is then

$$E(R_i) = E(C_i/S_i) = E(C_i)/S_i = \exp(\beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik}),$$

if we treat exposure as fixed (like we do  $x_{i1}, x_{i2}, \ldots, x_{ik}$ ). But rather than using  $R_i$  as the response variable we can use  $C_i$  as the response variable in a Poisson regression model where

$$E(C_i) = S_i \exp(\beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik}) = \exp(\beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik} + \log S_i),$$

and where  $\log S_i$  is an "offset" variable (i.e., basically an explanatory variable where it's  $\beta_j$  is "fixed" at one).

Note: If  $S_i$  is a constant for all observations so that  $S_i = S$  then we can write the model as

$$E(C_i) = \exp(\beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik} + \log S_i) = \exp(\beta_0^* + \beta_1 x_{i1} + \beta_2 x_{i2} + \dots + \beta_k x_{ik}),$$

where  $\beta_0^* = \log(S) + \beta_0$  so that the offset is "absorbed" into  $\beta_0$ , and we do not need to be concerned about it. Including an offset is only necessary if  $S_i$  is not the same for all observations.

#### Variance of Rates

Using rates as response variables in a linear or nonlinear model without accounting for  $S_i$  is not advisable because of heteroscedasticity due to unequal  $S_i$ .

Note that  $E(C_i) = S_i E(R_i)$  and that  $Var(C_i) = S_i E(R_i)$  if  $C_i$  has a Poisson distribution. The variance of  $R_i$  is then

$$Var(R_i) = Var(C_i/S_i) = Var(C_i)/S_i^2 = E(S_iR_i)/S_i^2 = S_iE(R_i)/S_i^2 = E(R_i)/S_i$$

if we treat  $S_i$  as fixed. So the variance of a rate is inversely proportional to  $S_i$ . For example, suppose  $E(R_i) = E(R_{i'}) = 0.5$ , but  $S_i = 2$  and  $S_{i'} = 100$  so that  $R_i = C_i/2$  and  $R_{i'} = C_{i'}/100$ . Then

$$Var(R_i) = 0.5/2 = 0.25 > Var(R_{i'}) = 0.5/100 = 0.005.$$

For this reason it is usually not advised to use rates as response variables without either (a) using an appropriate offset variable in Poisson regression or a related model or (b) using weights of  $w_i = S_i/E(R_i)$  (via iteratively weighted least squares with weights of  $w_i = S_i/\hat{y}_i$ ).

### Modeling Rates with Poisson Regression

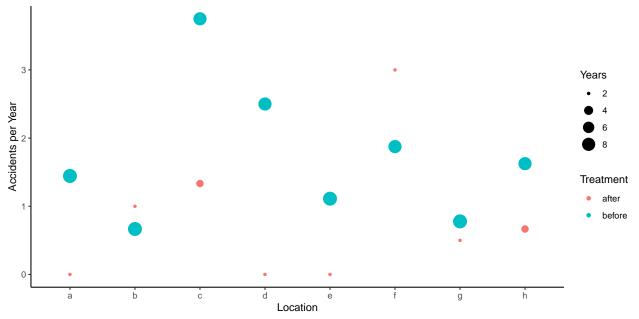
Software for GLMs (and sometimes linear models) will often permit specification of an offset variable. In R this is done using offset in the model formula.

**Example:** Consider the following data from an observational study of auto accidents.

```
library(trtools)
head(accidents)
```

```
accidents years location treatment
1
         13
                 9
                                 before
                           a
2
          6
                 9
                           b
                                 before
3
         30
                 8
                           С
                                 before
4
         20
                 8
                           d
                                 before
5
                 9
         10
                                 before
                           е
         15
                           f
                                 before
  geom_point(aes(size = years, color = treatment)) +
```

```
p <- ggplot(accidents, aes(x = location, y = accidents/years)) +
  geom_point(aes(size = years, color = treatment)) +
  labs(x = "Location", y = "Accidents per Year",
      size = "Years", color = "Treatment") + theme_classic()
plot(p)</pre>
```

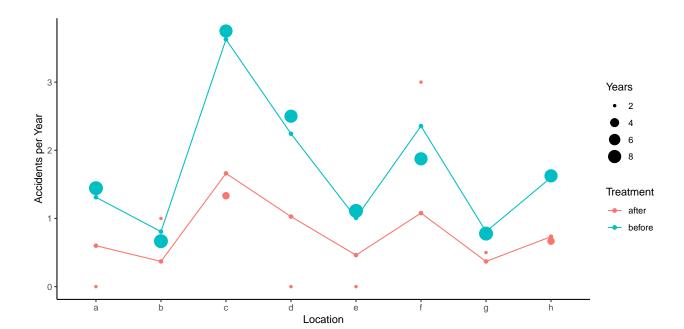


```
m <- glm(accidents ~ location + treatment + offset(log(years)),
    data = accidents, family = poisson)
cbind(summary(m)$coefficients, confint(m))</pre>
```

```
Estimate Std. Error z value Pr(>|z|)
                                                         2.5 % 97.5 %
(Intercept)
                 -0.5099
                             0.3734 -1.3656 0.172075 -1.29243 0.1770
locationb
                 -0.4855
                             0.4494 -1.0804 0.279943 -1.41219 0.3784
locationc
                  1.0176
                             0.3264 3.1174 0.001825 0.40267 1.6939
locationd
                  0.5371
                             0.3563 1.5075 0.131683 -0.15098 1.2601
locatione
                 -0.2624
                             0.4206 -0.6238 0.532790 -1.11363 0.5588
locationf
                  0.5859
                             0.3529 1.6601 0.096897 -0.09389 1.3036
                             0.4494 -1.0804 0.279943 -1.41219 0.3784
locationg
                 -0.4855
```

```
locationh
                  0.1993
                             0.3792 0.5255 0.599208 -0.54592 0.9578
treatmentbefore
                  0.7807
                             0.2754 2.8343 0.004593 0.27407 1.3616
exp(cbind(coef(m), confint(m)))
                        2.5 % 97.5 %
(Intercept)
                0.6006 0.2746 1.194
locationb
                0.6154 0.2436 1.460
locationc
               2.7666 1.4958 5.441
locationd
               1.7110 0.8599 3.526
               0.7692 0.3284 1.749
locatione
               1.7966 0.9104 3.683
locationf
locationg
               0.6154 0.2436 1.460
                1.2205 0.5793 2.606
locationh
treatmentbefore 2.1829 1.3153 3.902
When using contrast we do need to specify the offset. Think of it as another explanatory variable.
  a = list(treatment = "before", location = letters[1:8], years = 1),
  b = list(treatment = "after", location = letters[1:8], years = 1),
 cnames = letters[1:8], tf = exp)
  estimate lower upper
     2.183 1.272 3.745
b
     2.183 1.272 3.745
    2.183 1.272 3.745
d
    2.183 1.272 3.745
    2.183 1.272 3.745
е
f
    2.183 1.272 3.745
    2.183 1.272 3.745
g
    2.183 1.272 3.745
h
contrast(m,
  a = list(treatment = "after", location = letters[1:8], years = 1),
  b = list(treatment = "before", location = letters[1:8], years = 1),
  cnames = letters[1:8], tf = exp)
  estimate lower upper
a 0.4581 0.267 0.786
b
  0.4581 0.267 0.786
  0.4581 0.267 0.786
C
   0.4581 0.267 0.786
  0.4581 0.267 0.786
е
f 0.4581 0.267 0.786
  0.4581 0.267 0.786
   0.4581 0.267 0.786
We also need to specify the offset when computing estimated expected rates.
d <- expand.grid(treatment = c("before", "after"),</pre>
  location = letters[1:8], years = 1)
d$yhat <- predict(m, newdata = d, type = "response")</pre>
   treatment location years
                              yhat
1
     before a 1 1.3110
2
                         1 0.6006
      after
                  a
```

```
3
      before
                            1 0.8068
4
       after
                            1 0.3696
                     b
5
      before
                     С
                            1 3.6269
6
                            1 1.6615
       after
                     С
7
      before
                     d
                            1 2.2431
8
       after
                     d
                            1 1.0276
9
      before
                            1 1.0085
                     е
                            1 0.4620
10
       after
                     е
11
      before
                     f
                            1 2.3553
12
                     f
       after
                            1 1.0789
13
      before
                            1 0.8068
                     g
14
       after
                            1 0.3696
                     g
                            1 1.6001
15
      before
                     h
                     h
                            1 0.7330
16
       after
p <- p + geom_point(aes(y = yhat, color = treatment), data = d)</pre>
p <- p + geom_line(aes(y = yhat, group = treatment, color = treatment), data = d)
plot(p)
```



#### Computing Estimated Expected Rates

Using predict will produce estimated expected rates. Confidence intervals for estimating expected counts can be obtained using either contrast or glmint. We can estimate the expected number of accidents per year at each location before treatment.

```
contrast(m, a = list(treatment = "before", location = letters[1:8], years = 1),
    cnames = paste("before at", letters[1:8]), tf = exp)
```

```
estimate lower upper before at a 1.3110 0.7595 2.263 before at b 0.8068 0.4027 1.616 before at c 3.6269 2.5678 5.123 before at d 2.2431 1.4421 3.489 before at e 1.0085 0.5415 1.878
```

```
before at f
              2.3553 1.5302 3.625
before at g
              0.8068 0.4027 1.616
before at h
              1.6001 0.9587 2.671
We can also estimate the expected number of accidents per decade.
contrast(m, a = list(treatment = "before", location = letters[1:8], years = 10),
 cnames = paste("before at", letters[1:8]), tf = exp)
            estimate lower upper
              13.110 7.595 22.63
before at a
               8.068 4.027 16.16
before at b
before at c
              36.269 25.678 51.23
before at d 22.431 14.421 34.89
before at e
              10.085 5.415 18.78
before at f
              23.553 15.302 36.25
before at g
               8.068 4.027 16.16
before at h
            16.001 9.587 26.71
Alternatively the glmint function can be used, which is more convenient for producing plots.
d <- expand.grid(treatment = c("before", "after"),</pre>
 location = letters[1:8], years = 1)
glmint(m, newdata = d)
      fit
             low
                    upp
1 1.3110 0.7595 2.2629
2 0.6006 0.2889 1.2485
3 0.8068 0.4027 1.6161
  0.3696 0.1582 0.8635
5 3.6269 2.5678 5.1228
6 1.6615 0.9393 2.9388
7 2.2431 1.4421 3.4890
8 1.0276 0.5347 1.9747
9 1.0085 0.5415 1.8780
10 0.4620 0.2096 1.0180
11 2.3553 1.5302 3.6253
12 1.0789 0.5654 2.0589
13 0.8068 0.4027 1.6161
14 0.3696 0.1582 0.8635
15 1.6001 0.9587 2.6706
16 0.7330 0.3697 1.4532
cbind(d, glmint(m, newdata = d))
   treatment location years
                               fit
                                      low
                                              upp
                          1 1.3110 0.7595 2.2629
1
      before
                    a
2
       after
                    a
                          1 0.6006 0.2889 1.2485
3
      before
                    b
                          1 0.8068 0.4027 1.6161
4
       after
                    b
                          1 0.3696 0.1582 0.8635
5
                          1 3.6269 2.5678 5.1228
      before
                    С
6
                          1 1.6615 0.9393 2.9388
       after
                    С
7
      before
                    d
                          1 2.2431 1.4421 3.4890
```

1 1.0276 0.5347 1.9747

1 1.0085 0.5415 1.8780

1 0.4620 0.2096 1.0180

1 2.3553 1.5302 3.6253

8

9

10

11

after

before

before

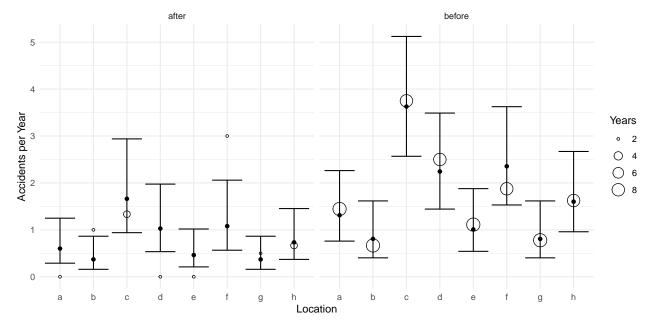
after

d

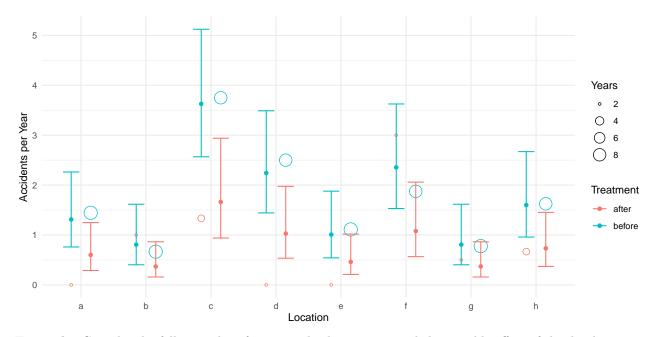
е

е

```
12
                           1 1.0789 0.5654 2.0589
       after
13
      before
                           1 0.8068 0.4027 1.6161
                    g
       after
                           1 0.3696 0.1582 0.8635
14
                    g
15
      before
                           1 1.6001 0.9587 2.6706
                    h
                           1 0.7330 0.3697 1.4532
16
       after
                    h
d <- cbind(d, glmint(m, newdata = d))</pre>
p \leftarrow ggplot(accidents, aes(x = location)) +
  geom_point(aes(y = accidents/years, size = years), shape = 21, fill = "white") +
  facet_wrap(~ treatment) + theme_minimal() +
  labs(x = "Location", y = "Accidents per Year", size = "Years") +
  geom_errorbar(aes(ymin = low, ymax = upp), data = d) +
 geom_point(aes(y = fit), data = d)
plot(p)
```



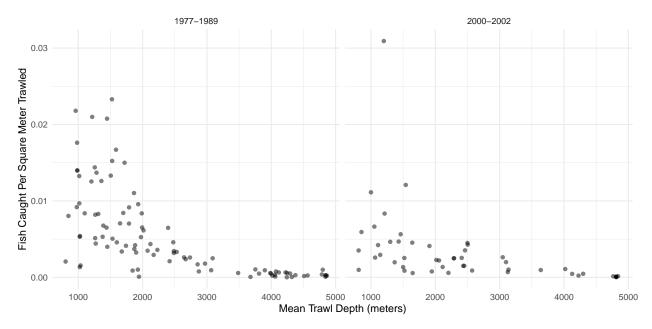
```
p <- ggplot(accidents, aes(x = location, color = treatment)) +
  geom_point(aes(y = accidents/years, size = years),
    position = position_dodge(width = 0.6), shape = 21, fill = "white") +
  labs(x = "Location", y = "Accidents per Year",
    size = "Years", color = "Treatment") + theme_minimal() +
  geom_errorbar(aes(ymin = low, ymax = upp), data = d,
    position = position_dodge(width = 0.6), width = 0.5) +
  geom_point(aes(y = fit), data = d, position = position_dodge(width = 0.6))
  plot(p)</pre>
```



**Example**: Consider the following data from a study that investigated the possible effect of the development of a commercial fishery on deep sea fish abundance. The figure below shows the number of fish per square meter of swept area from 147 trawls by mean depth in meters, and by whether the trawl was during one of two periods. The 1977-1989 period was from before the development of a commercial fishery, and the period 2000-2002 was when the fishery was active.

```
library(COUNT)
data(fishing)
head(fishing)
```

```
site totabund
                   density meandepth year
                                              period sweptarea
     1
             76 0.0020703
                                 804 1978 1977-1989
                                                          36710
1
2
     2
            161 0.0035198
                                 808 2001 2000-2002
                                                          45741
3
     3
             39 0.0009805
                                 809 2001 2000-2002
                                                          39775
4
     4
            410 0.0080392
                                 848 1979 1977-1989
                                                          51000
5
     5
            177 0.0059334
                                 853 2002 2000-2002
                                                          29831
            695 0.0218005
                                 960 1980 1977-1989
                                                          31880
p \leftarrow ggplot(fishing, aes(x = meandepth, y = totabund/sweptarea)) +
  geom_point(alpha = 0.5) + facet_wrap(~ period) + theme_minimal() +
  labs(x = "Mean Trawl Depth (meters)",
    y = "Fish Caught Per Square Meter Trawled")
plot(p)
```



An appropriate model for these data might be as follows.

```
m <- glm(totabund ~ period * meandepth + offset(log(sweptarea)),
    family = poisson, data = fishing)
summary(m)$coefficients</pre>
```

```
Estimate Std. Error z value Pr(>|z|)

(Intercept) -3.4228194 1.490e-02 -229.672 0.000e+00

period2000-2002 -0.7711169 2.973e-02 -25.937 2.547e-148

meandepth -0.0009713 7.965e-06 -121.945 0.000e+00

period2000-2002:meandepth 0.0001318 1.524e-05 8.651 5.090e-18

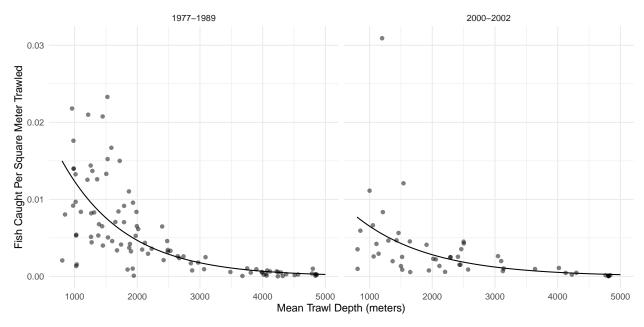
d <- expand.grid(sweptarea = 1, period = c("1977-1989","2000-2002"),

meandepth = seq(800, 5000, length = 100))

d$yhat <- predict(m, newdata = d, type = "response")

p <- p + geom_line(aes(y = yhat), data = d)

plot(p)
```



What is the expected number of fish per square meter in 1977-1989 at depths of 1000, 2000, 3000, 4000, and 5000 meters? What is it in 2000-2002?

```
contrast(m,
  a = list(sweptarea = 1,
    meandepth = c(1000, 2000, 3000, 4000, 5000), period = "1977-1989"),
 cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
       estimate
                    lower
                               upper
1000m 0.0123500 0.0121470 0.0125564
2000m 0.0046757 0.0046128 0.0047395
3000m 0.0017702 0.0017281 0.0018134
4000m 0.0006702 0.0006450 0.0006963
5000m 0.0002537 0.0002406 0.0002676
contrast(m.
  a = list(sweptarea = 1,
    meandepth = c(1000, 2000, 3000, 4000, 5000), period = "2000-2002"),
  cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
       estimate
                    lower
                               upper
1000m 0.0065168 0.0063254 0.0067139
2000m 0.0028149 0.0027508 0.0028806
3000m 0.0012159 0.0011702 0.0012635
4000m 0.0005252 0.0004942 0.0005582
```

Note that we can change the units of swept area very easily here. There are 10,000 square meters in a hectare. Here are the expected number of fish per hectare.

```
contrast(m,
    a = list(sweptarea = 10000,
    meandepth = c(1000,2000,3000,4000,5000), period = "1977-1989"),
    cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
```

```
estimate lower upper 1000m 123.500 121.470 125.564
```

5000m 0.0002269 0.0002084 0.0002470

```
46.757 46.128 47.395
2000m
3000m
       17.702 17.281 18.134
4000m
        6.702 6.450 6.963
5000m
         2.537
                 2.406
                         2.676
contrast(m,
 a = list(sweptarea = 10000,
   meandepth = c(1000, 2000, 3000, 4000, 5000), period = "2000-2002"),
 cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
      estimate lower upper
1000m
       65.168 63.254 67.139
2000m
       28.149 27.508 28.806
      12.159 11.702 12.635
3000m
4000m
        5.252 4.942 5.582
        2.269 2.084 2.470
5000m
What is the rate ratio of fish per square meter in 2000-2002 versus 1977-1989 at 1000, 2000, 3000, 4000, and
5000 meters?
contrast(m,
 a = list(sweptarea = 1,
   meandepth = c(1000, 2000, 3000, 4000, 5000), period = "2000-2002"),
  b = list(sweptarea = 1,
   meandepth = c(1000, 2000, 3000, 4000, 5000), period = "1977-1989"),
 cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
      estimate lower upper
1000m 0.5277 0.5100 0.5460
2000m
      0.6020 0.5861 0.6183
3000m 0.6869 0.6565 0.7187
4000m 0.7837 0.7293 0.8421
5000m 0.8941 0.8087 0.9885
Here it is for 1977-1989 versus 2000-2002.
contrast(m,
 a = list(sweptarea = 1,
   meandepth = c(1000, 2000, 3000, 4000, 5000), period = "1977-1989"),
 b = list(sweptarea = 1,
   meandepth = c(1000, 2000, 3000, 4000, 5000), period = "2000-2002"),
 cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
      estimate lower upper
1000m
         1.895 1.832 1.961
2000m
         1.661 1.617 1.706
      1.456 1.391 1.523
3000m
4000m
      1.276 1.188 1.371
5000m
      1.118 1.012 1.237
How does the expected number of fish per square meter change per 1000m of depth?
# increasing depth by 1000m
contrast(m,
 a = list(sweptarea = 1, meandepth = 2000, period = c("1977-1989","2000-2002")),
 b = list(sweptarea = 1, meandepth = 1000, period = c("1977-1989", "2000-2002")),
```

cnames = c("1977-1989","2000-2002"), tf = exp)

```
estimate lower upper
1977-1989
          0.3786 0.3727 0.3846
2000-2002 0.4320 0.4211 0.4431
# decreasing depth by 1000m
contrast(m.
  a = list(sweptarea = 1, meandepth = 1000, period = c("1977-1989", "2000-2002")),
 b = list(sweptarea = 1, meandepth = 2000, period = c("1977-1989","2000-2002")),
 cnames = c("1977-1989", "2000-2002"), tf = exp)
          estimate lower upper
1977-1989
             2.641 2.600 2.683
2000-2002
             2.315 2.257 2.375
Ratios are unit-less, so we get the same rate ratios when considering fish per hectare (i.e., per 10000 square
# increasing depth by 1000m
contrast(m,
  a = list(sweptarea = 10000,
   meandepth = 2000, period = c("1977-1989","2000-2002")),
  b = list(sweptarea = 10000,
   meandepth = 1000, period = c("1977-1989", "2000-2002")),
  cnames = c("1977-1989", "2000-2002"), tf = exp)
          estimate lower upper
1977-1989 0.3786 0.3727 0.3846
2000-2002 0.4320 0.4211 0.4431
# decreasing depth by 1000m
contrast(m,
  a = list(sweptarea = 10000,
    meandepth = 1000, period = c("1977-1989","2000-2002")),
  b = list(sweptarea = 10000,
```

```
estimate lower upper
1977-1989 2.641 2.600 2.683
2000-2002 2.315 2.257 2.375
```

#### Standardized Mortality Ratios

meandepth = 2000, period = c("1977-1989","2000-2002")),

cnames = c("1977-1989","2000-2002"), tf = exp)

In epidemiology, the *standardized mortality ratio* (SMR) is the ratio of the *observed* number of deaths and the (estimated) *expected* number of deaths. Poisson regression with an offset can be used to model the SMR to determine if the number of deaths tends to be higher or lower than we would expect.

**Example**: Here is an example of an observational study using a Poisson regression model to investigate the relationship between lung cancer and radon exposure in counties in Minnesota.

Note: The data manipulation and plotting is quite a bit more complicated than what you will normally see in this class, but I have included it in case you might be interested to see the code.

First we will process the data containing the observed and expected number of deaths due to lung cancer, where the latter are based on the known distribution of age and gender in the county.

```
lung <- read.table("http://faculty.washington.edu/jonno/book/MNlung.txt",
header = TRUE, sep = "\t") %>%
mutate(obs = obs.M + obs.F, exp = exp.M + exp.F) %>%
```

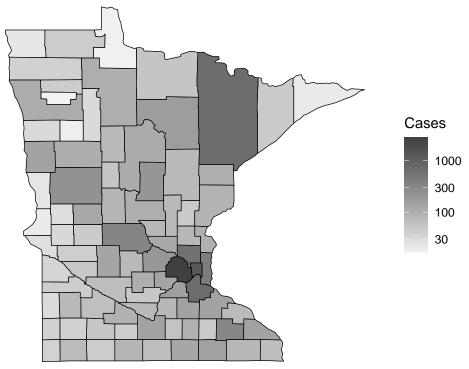
```
dplyr::select(X, County, obs, exp) %>%
  rename(county = County) %>%
  mutate(county = tolower(county)) %>%
  mutate(county = ifelse(county == "red", "red lake", county))
head(lung)
  Х
       county obs
                    exp
1 1
       aitkin 92 76.9
2 2
       anoka 677 600.5
       becker 105 107.9
3 3
4 4 beltrami 101 105.7
5 5
       benton 61 81.4
6 6 big stone 32 27.4
Now we will read in data to estimate the average radon exposure of residents of each county.
radon <- read.table("http://faculty.washington.edu/jonno/book/MNradon.txt",</pre>
  header = TRUE) %>% group_by(county) %>%
  summarize(radon = mean(radon)) %>% rename(X = county)
head(radon)
# A tibble: 6 x 2
      X radon
  <int> <dbl>
      1 2.08
1
      2 3.21
2
3
      3 3.18
4
      4 3.66
5
      5 3.78
      6 4.93
Next we merge the two data frames.
radon <- left_join(lung, radon) %>% dplyr::select(-X)
head(radon)
     county obs
                  exp radon
     aitkin 92 76.9 2.075
1
     anoka 677 600.5 3.212
3
     becker 105 107.9 3.175
4 beltrami 101 105.7 3.657
     benton 61 81.4 3.775
6 big stone 32 27.4 4.933
For fun we can make some plots of the data by county.
library(maps)
dstate <- map_data("state") %>%
  filter(region == "minnesota")
dcounty <- map_data("county") %>%
  filter(region == "minnesota") %>%
  rename(county = subregion)
dcounty <- left_join(dcounty, radon) %>%
  mutate(smr = obs/exp)
no_axes <- theme_minimal() + theme(</pre>
axis.text = element_blank(),
```

```
axis.line = element_blank(),
axis.ticks = element_blank(),
panel.border = element_blank(),
panel.grid = element_blank(),
axis.title = element_blank()
)

p <- ggplot(dcounty, aes(x = long, y = lat, group = group)) + coord_fixed(1.3) +
geom_polygon(aes(fill = exp), color = "black", size = 0.25) +
scale_fill_gradient(low = grey(0.95), high = grey(0.25),
    trans = "log10", na.value = "pink") +
theme(legend.position = c(0.8,0.4)) + no_axes +
ggtitle("Expected Number of Cases") + labs(fill = "Cases")

plot(p)</pre>
```

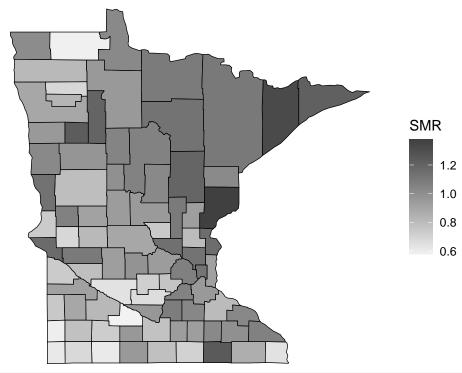
## **Expected Number of Cases**



```
p <- ggplot(dcounty, aes(x = long, y = lat, group = group)) + coord_fixed(1.3) +
    geom_polygon(aes(fill = smr), color = "black", size = 0.25) +
    scale_fill_gradient(low = grey(0.95), high = grey(0.25), na.value = "pink") +
    theme(legend.position = c(0.8,0.4)) + no_axes +
    ggtitle("Standardized Mortality Ratio") + labs(fill = "SMR")

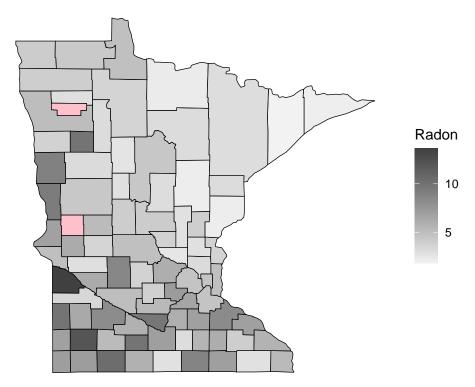
plot(p)</pre>
```

## Standardized Mortality Ratio



```
p <- ggplot(dcounty, aes(x = long, y = lat, group = group)) + coord_fixed(1.3) +
    geom_polygon(aes(fill = radon), color = "black", size = 0.25) +
    scale_fill_gradient(low = grey(0.95), high = grey(0.25), na.value = "pink") +
    theme(legend.position = c(0.8,0.4)) + no_axes +
    ggtitle("Average Radon (pCi/liter)") + labs(fill = "Radon")</pre>
plot(p)
```

### Average Radon (pCi/liter)



How does the expected SMR relate to radon? Consider the Poisson regression model

$$\log E(Y_i/E_i) = \beta_0 + \beta_1 r_i,$$

where  $Y_i$  and  $E_i$  are the observed and expected number of lung cancer deaths (or cases), respectively, in the *i*-th county, and  $r_i$  is the average radon exposure in the *i*-th county. Here  $Y_i/E_i$  is the SMR for the *i*-th county. We can also write this model as

$$\log E(Y_i) = \log E_i + \beta_0 + \beta_1 r_i,$$

so  $\log E_i$  is an offset.

```
m <- glm(obs ~ offset(log(exp)) + radon,
  family = poisson, data = dcounty)
summary(m)$coefficients</pre>
```

```
Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.2107 0.005619 37.51 6.954e-308
radon -0.0421 0.001195 -35.24 4.366e-272
exp(cbind(coef(m), confint(m)))
```

2.5 % 97.5 % (Intercept) 1.2346 1.2211 1.248 radon 0.9588 0.9565 0.961

We should be careful and remember the ecological fallacy which states that relationships at the group level (e.g., county) do not necessarily hold at the individual level. Radon may be related to other variables (e.g., smoking) that affect the risk of lung cancer.