Friday, Mar 1

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

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

where λ_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

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

if we treat exposure as *fixed* (like we do $x_{i1}, x_{i2}, \dots, x_{ik}$). 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

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

and where $\log S_i$ is an "offset" variable (i.e., basically an explanatory variable where it's β_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

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

where $\beta_0^* = \log(S) + \beta_0$ so that the offset is "absorbed" into β_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 $\text{Var}(C_i) = S_i E(R_i)$ if C_i has a Poisson distribution. The variance of R_i is then

$$\text{Var}(R_i) = \text{Var}(C_i/S_i) = \text{Var}(C_i)/S_i^2 = E(S_i R_i)/S_i^2 = S_i E(R_i)/S_i^2 = E(R_i)/S_i,$$

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

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

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

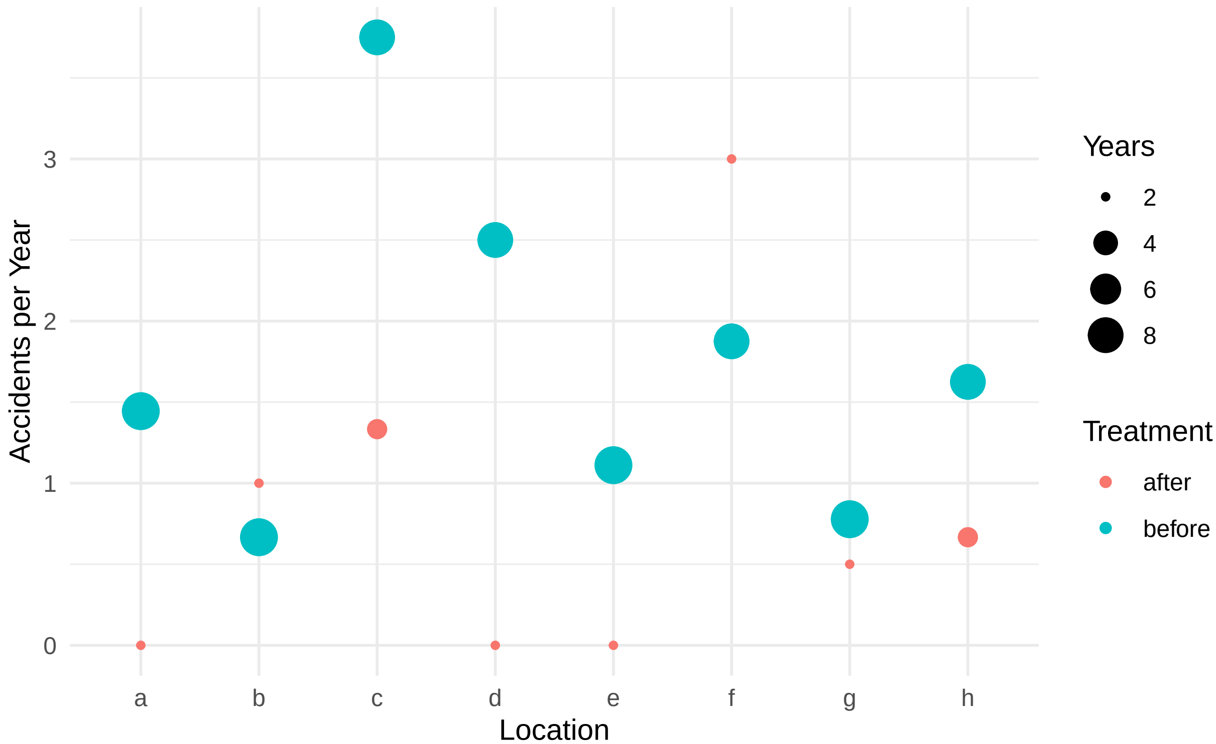
Software for GLMs (and sometimes linear models) will often permit specification of an offset variable. In R this is done using `offset` in the model formula.

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

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

```
  accidents years location treatment
1        13     9        a    before
2         6     9        b    before
3        30     8        c    before
4        20     8        d    before
5        10     9        e    before
6        15     8        f    before
```

```r
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_minimal()
plot(p)
```




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

```
            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
locationg        -0.4855     0.4494 -1.0804 0.279943 -1.41219 0.3784
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
```

```r
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
locatione       0.7692 0.3284  1.749
locationf       1.7966 0.9104  3.683
locationg       0.6154 0.2436  1.460
locationh       1.2205 0.5793  2.606
treatmentbefore 2.1829 1.3153  3.902
```

When using other tools like `contrast` or functions from the **emmeans** package, be sure to specify the offset (if necessary). Here are the rate ratios for the treatment.

```r
trtools::contrast(m,
  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
a    2.183 1.272 3.745
b    2.183 1.272 3.745
c    2.183 1.272 3.745
d    2.183 1.272 3.745
e    2.183 1.272 3.745
f    2.183 1.272 3.745
g    2.183 1.272 3.745
h    2.183 1.272 3.745
```

```r
trtools::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
c   0.4581 0.267 0.786
d   0.4581 0.267 0.786
e   0.4581 0.267 0.786
f   0.4581 0.267 0.786
g   0.4581 0.267 0.786
h   0.4581 0.267 0.786
```

Here are the estimated expected number of accidents per year at location `a`.

```r
trtools::contrast(m, a = list(treatment = c("before","after"), location = "a", years = 1),
  cnames = c("before","after"), tf = exp)
```

```
       estimate  lower upper
```

```
before   1.3110 0.7595 2.263
after    0.6006 0.2889 1.248
```

Here are the estimated expected number of accidents *per decade* at location `a`.

```r
trtools::contrast(m, a = list(treatment = c("before","after"), location = "a", years = 10),
  cnames = c("before","after"), tf = exp)
```

```
       estimate lower upper
before   13.110 7.595 22.63
after     6.006 2.889 12.48
```

When using functions from the **emmeans** package we use the `offset` argument with the value specified on the log scale. Here are the estimated number of accidents per decade.

```r
library(emmeans)
emmeans(m, ~treatment|location, type = "response", offset = log(10))
```

```
location = a:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after      6.01 2.24 Inf      2.89     12.48
 before    13.11 3.65 Inf      7.59     22.63

location = b:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after      3.70 1.60 Inf      1.58      8.64
 before     8.07 2.86 Inf      4.03     16.16

location = c:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after     16.62 4.83 Inf      9.39     29.39
 before    36.27 6.39 Inf     25.68     51.23

location = d:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after     10.28 3.42 Inf      5.35     19.75
 before    22.43 5.06 Inf     14.42     34.89

location = e:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after      4.62 1.86 Inf      2.10     10.18
 before    10.08 3.20 Inf      5.42     18.78

location = f:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after     10.79 3.56 Inf      5.65     20.59
 before    23.55 5.18 Inf     15.30     36.25

location = g:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after      3.70 1.60 Inf      1.58      8.64
 before     8.07 2.86 Inf      4.03     16.16

location = h:
 treatment  rate   SE  df asymp.LCL asymp.UCL
 after      7.33 2.56 Inf      3.70     14.53
```

```
 before    16.00 4.18 Inf      9.59     26.71

Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

Here is the rate ratio for the effect of treatment.

```r
pairs(emmeans(m, ~treatment|location, type = "response", offset = log(10)), infer = TRUE)
```

```
location = a:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

location = b:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

location = c:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

location = d:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

location = e:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

location = f:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

location = g:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

location = h:
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

Use `reverse = TRUE` to “flip” the rate ratio. Also for rate ratios the size of the offset does not matter since it “cancels-out” in the ratio. Also since there is no interaction in this model which means the rate ratio does not depend on location, we can omit it when using `emmeans` (but not `contrast`).

```r
pairs(emmeans(m, ~treatment, type = "response"), infer = TRUE)
```

```
 contrast       ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 after / before 0.458 0.126 Inf     0.267     0.786    1  -2.834  0.0046

Results are averaged over the levels of: location
Confidence level used: 0.95
```

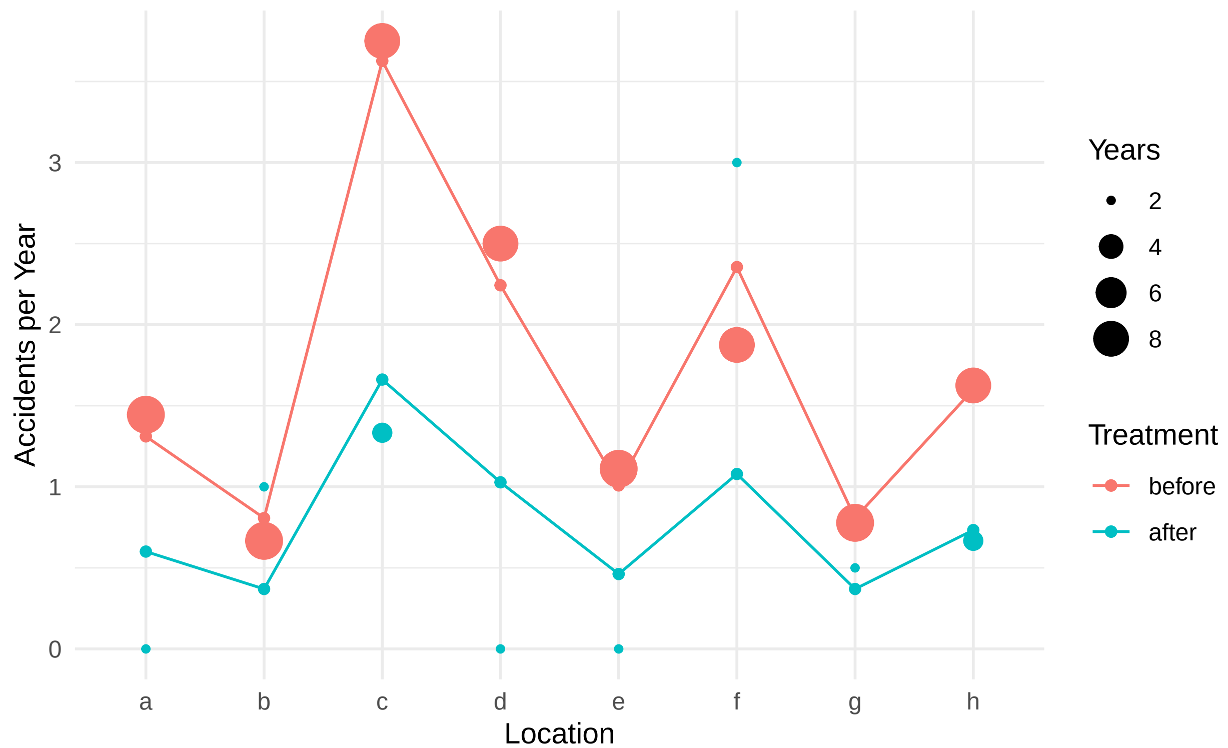
```
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

When using `predict` we need to be sure to also include the offset amount.

```
d <- expand.grid(treatment = c("before","after"), location = letters[1:8], years = 1)
d$yhat <- predict(m, newdata = d, type = "response")
head(d)
```

```
  treatment location years   yhat
1    before        a     1 1.3110
2     after        a     1 0.6006
3    before        b     1 0.8068
4     after        b     1 0.3696
5    before        c     1 3.6269
6     after        c     1 1.6615
```

```
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_minimal() +
  geom_point(aes(y = yhat, color = treatment), data = d) +
  geom_line(aes(y = yhat, group = treatment, color = treatment), data = d)
plot(p)
```



We can use the `glmint` function from the **trtools** package if we want to produce confidence intervals for plots.

```
d <- expand.grid(treatment = c("before","after"), location = letters[1:8], years = 1)
d$yhat <- predict(m, newdata = d, type = "response")
glmint(m, newdata = d)
```

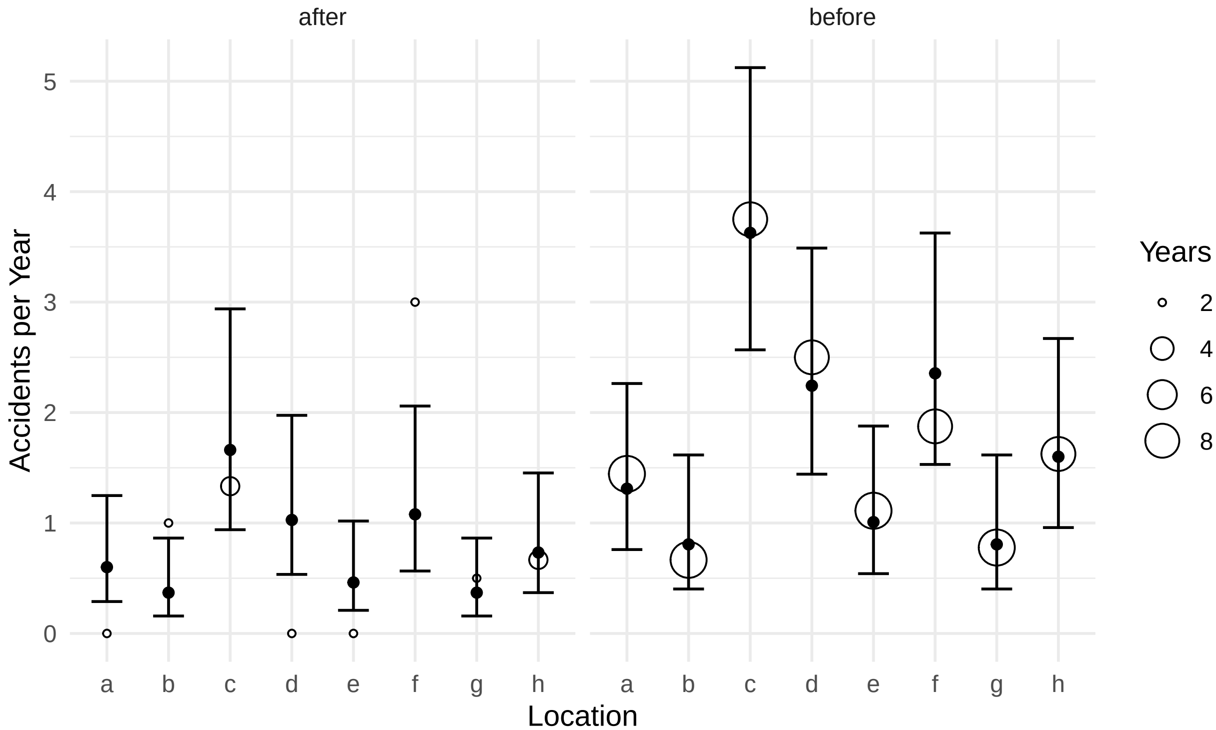
```
     fit    low    upp
```

```
1  1.3110 0.7595 2.2629
2  0.6006 0.2889 1.2485
3  0.8068 0.4027 1.6161
4  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
```

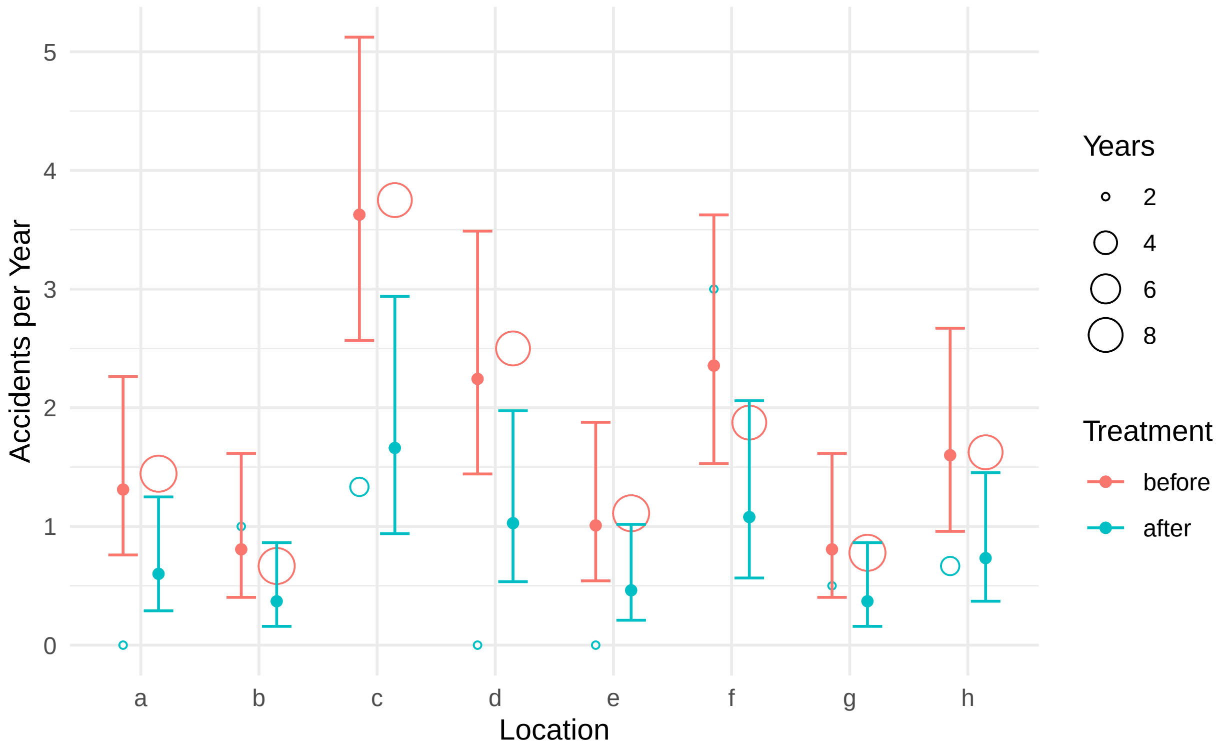
```
cbind(d, glmint(m, newdata = d))
```

```
   treatment location years   yhat    fit    low    upp
1     before        a     1 1.3110 1.3110 0.7595 2.2629
2      after        a     1 0.6006 0.6006 0.2889 1.2485
3     before        b     1 0.8068 0.8068 0.4027 1.6161
4      after        b     1 0.3696 0.3696 0.1582 0.8635
5     before        c     1 3.6269 3.6269 2.5678 5.1228
6      after        c     1 1.6615 1.6615 0.9393 2.9388
7     before        d     1 2.2431 2.2431 1.4421 3.4890
8      after        d     1 1.0276 1.0276 0.5347 1.9747
9     before        e     1 1.0085 1.0085 0.5415 1.8780
10     after        e     1 0.4620 0.4620 0.2096 1.0180
11    before        f     1 2.3553 2.3553 1.5302 3.6253
12     after        f     1 1.0789 1.0789 0.5654 2.0589
13    before        g     1 0.8068 0.8068 0.4027 1.6161
14     after        g     1 0.3696 0.3696 0.1582 0.8635
15    before        h     1 1.6001 1.6001 0.9587 2.6706
16     after        h     1 0.7330 0.7330 0.3697 1.4532
```

```
d <- cbind(d, glmint(m, newdata = d))
p <- 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, width = 0.5) +
  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)
```

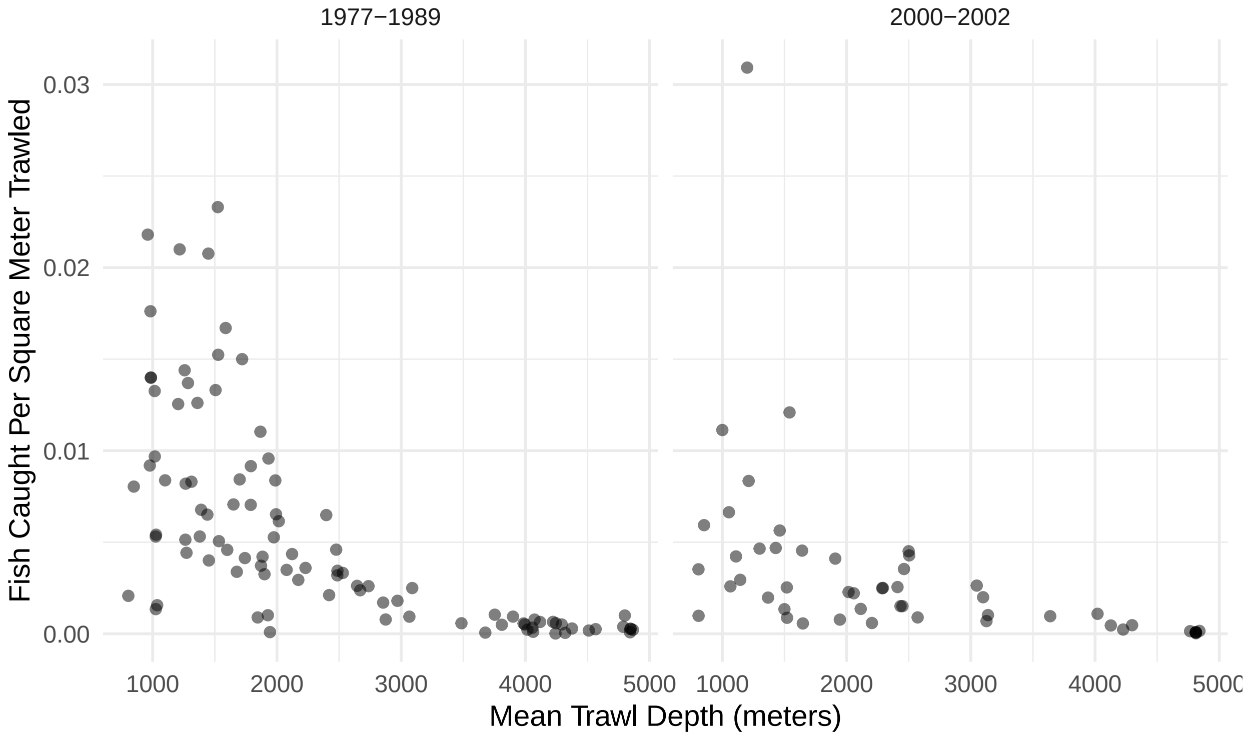


Example: Consider the following data from an observational study that investigated the possible effect of the development of a commercial fishery on deep sea fish abundance. The figure below shows the number of fish per square meter of swept area from 147 trawls by mean depth in meters, and by whether 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.

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

```
  site totabund   density meandepth year    period sweptarea
1    1       76 0.0020703       804 1978 1977-1989     36710
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
6    6      695 0.0218005       960 1980 1977-1989     31880
```

```r
p <- 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)
```

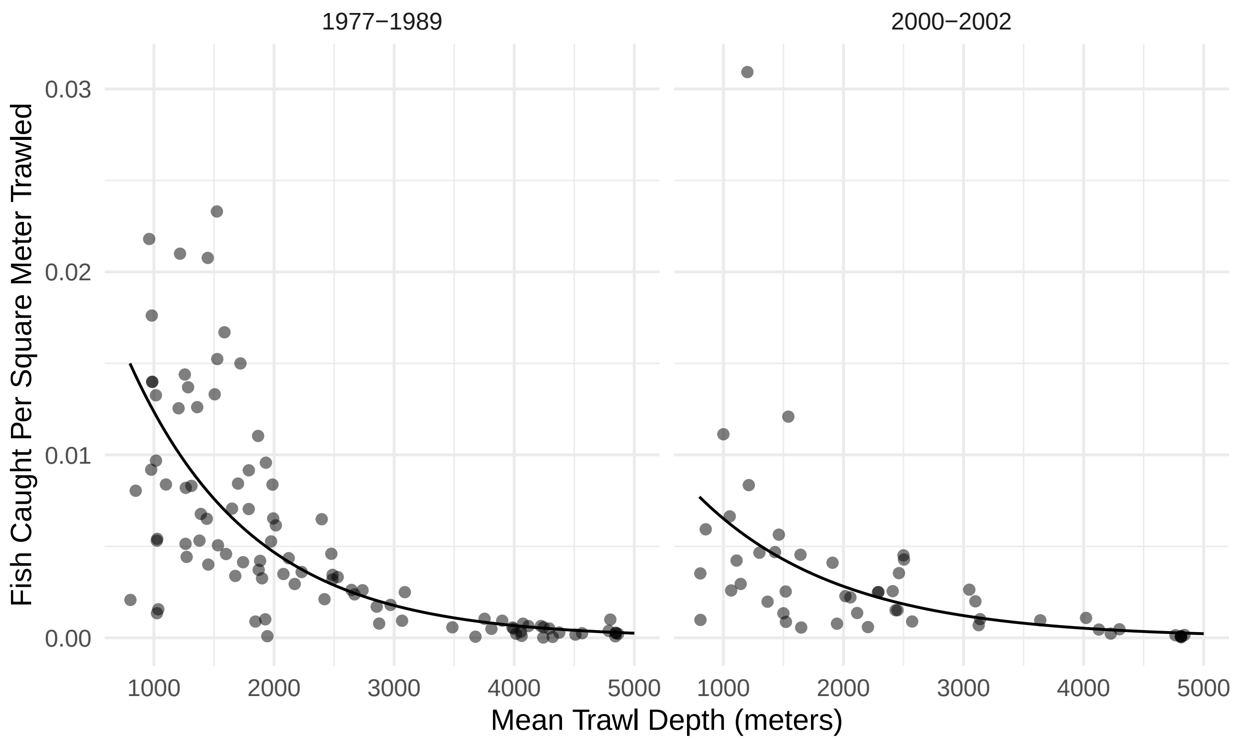


An appropriate model for these data might be as follows.

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

```
                            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?

```
trtools::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
```

```
trtools::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
5000m 0.0002269 0.0002084 0.0002470
```

Here is how we can do that with **emmeans**.

```
library(emmeans)
emmeans(m, ~meandepth|period, at = list(meandepth = seq(1000, 5000, by = 1000)),
  type = "response", offset = log(1))
```

```
period = 1977-1989:
 meandepth     rate       SE  df asymp.LCL asymp.UCL
      1000 0.012350 1.04e-04 Inf  0.012147  0.012556
      2000 0.004676 3.23e-05 Inf  0.004613  0.004739
      3000 0.001770 2.18e-05 Inf  0.001728  0.001813
      4000 0.000670 1.31e-05 Inf  0.000645  0.000696
      5000 0.000254 6.89e-06 Inf  0.000241  0.000268

period = 2000-2002:
 meandepth     rate       SE  df asymp.LCL asymp.UCL
      1000 0.006517 9.91e-05 Inf  0.006325  0.006714
      2000 0.002815 3.31e-05 Inf  0.002751  0.002881
      3000 0.001216 2.38e-05 Inf  0.001170  0.001263
      4000 0.000525 1.63e-05 Inf  0.000494  0.000558
      5000 0.000227 9.85e-06 Inf  0.000208  0.000247

Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

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.

```
trtools::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
2000m   46.757  46.128  47.395
3000m   17.702  17.281  18.134
4000m    6.702   6.450   6.963
5000m    2.537   2.406   2.676
```

```
trtools::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
3000m   12.159 11.702 12.635
4000m    5.252  4.942  5.582
5000m    2.269  2.084  2.470
```

```
emmeans(m, ~meandepth|period, at = list(meandepth = seq(1000, 5000, by = 1000)),
  type = "response", offset = log(10000))
```

```
period = 1977-1989:
 meandepth   rate     SE  df asymp.LCL asymp.UCL
      1000 123.50 1.0443 Inf    121.47    125.56
      2000  46.76 0.3232 Inf     46.13     47.39
      3000  17.70 0.2175 Inf     17.28     18.13
      4000   6.70 0.1308 Inf      6.45      6.96
      5000   2.54 0.0689 Inf      2.41      2.68
```

```
period = 2000-2002:
 meandepth   rate     SE  df asymp.LCL asymp.UCL
      1000  65.17 0.9910 Inf     63.25     67.14
      2000  28.15 0.3310 Inf     27.51     28.81
      3000  12.16 0.2379 Inf     11.70     12.63
      4000   5.25 0.1632 Inf      4.94      5.58
      5000   2.27 0.0985 Inf      2.08      2.47

Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

What is the rate ratio of fish per square meter in 2000-2002 versus 1977-1989 at 1000, 2000, 3000, 4000, and 5000 meters?

```r
trtools::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.

```r
trtools::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
3000m    1.456 1.391 1.523
4000m    1.276 1.188 1.371
5000m    1.118 1.012 1.237
```

Now using **emmeans**.

```r
pairs(emmeans(m, ~meandepth*period, at = list(meandepth = seq(1000, 5000, by = 1000)),
  type = "response", offset = log(1)), by = "meandepth", infer = TRUE)
```

```
meandepth = 1000:
 contrast                  ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 (1977-1989) / (2000-2002)  1.90 0.0330 Inf      1.83      1.96    1  36.740  <.0001

meandepth = 2000:
 contrast                  ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 (1977-1989) / (2000-2002)  1.66 0.0227 Inf      1.62      1.71    1  37.200  <.0001

meandepth = 3000:
 contrast                  ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 (1977-1989) / (2000-2002)  1.46 0.0336 Inf      1.39      1.52    1  16.260  <.0001

meandepth = 4000:
```

```
 contrast                  ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 (1977-1989) / (2000-2002)  1.28 0.0468 Inf      1.19      1.37    1   6.640  <.0001

meandepth = 5000:
 contrast                  ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 (1977-1989) / (2000-2002)  1.12 0.0573 Inf      1.01      1.24    1   2.190  0.0288

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

How does the expected number of fish per square meter change per 1000m of depth?

```r
# increasing depth by 1000m
trtools::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
```

```r
# decreasing depth by 1000m
trtools::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
```

Here is how to do the latter with **emmeans**.

```r
pairs(emmeans(m, ~meandepth*period, at = list(meandepth = c(1000,2000)),
  offset = log(1), type = "response"), by = "period", infer = TRUE)
```

```
period = 1977-1989:
 contrast                      ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 meandepth1000 / meandepth2000  2.64 0.0210 Inf      2.60      2.68    1 121.940  <.0001

period = 2000-2002:
 contrast                      ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 meandepth1000 / meandepth2000  2.32 0.0301 Inf      2.26      2.37    1  64.610  <.0001

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

Standardized Mortality Ratios

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)
```

```
  X    county obs   exp
1 1    aitkin  92  76.9
2 2     anoka 677 600.5
3 3    becker 105 107.9
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",
  header = TRUE) %>% group_by(county) %>%
  summarize(radon = mean(radon)) %>% rename(X = county)
head(radon)
```

```
# A tibble: 6 x 2
      X radon
  <int> <dbl>
1     1  2.08
2     2  3.21
3     3  3.18
4     4  3.66
5     5  3.78
6     6  4.93
```

Next we merge the two data frames.

```
radon <- left_join(lung, radon) %>% dplyr::select(-X)
head(radon)
```

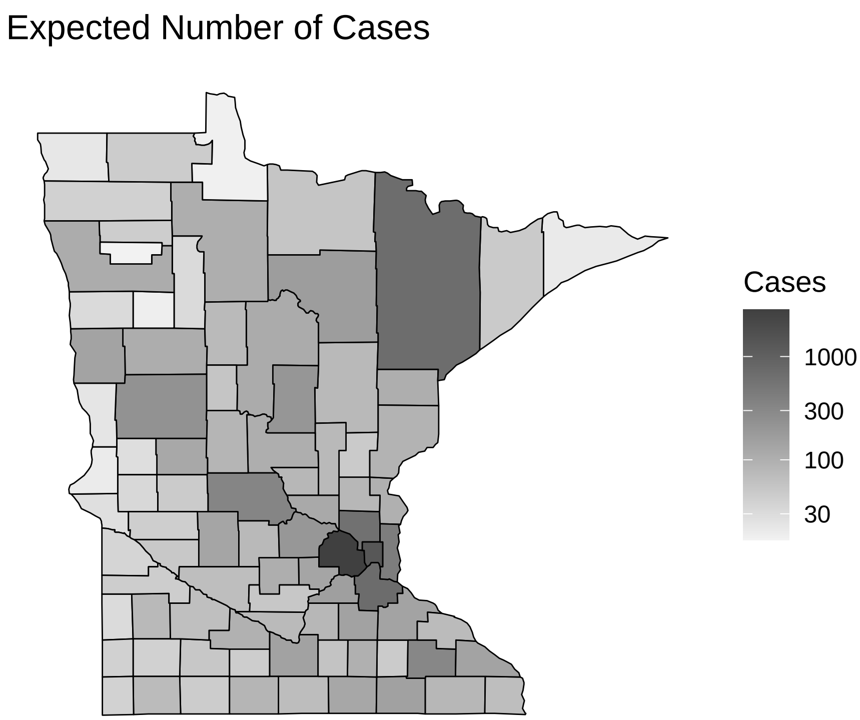
```
     county obs   exp radon
1    aitkin  92  76.9 2.075
2     anoka 677 600.5 3.212
3    becker 105 107.9 3.175
4  beltrami 101 105.7 3.657
5    benton  61  81.4 3.775
6 big stone  32  27.4 4.933
```

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") %>%
```

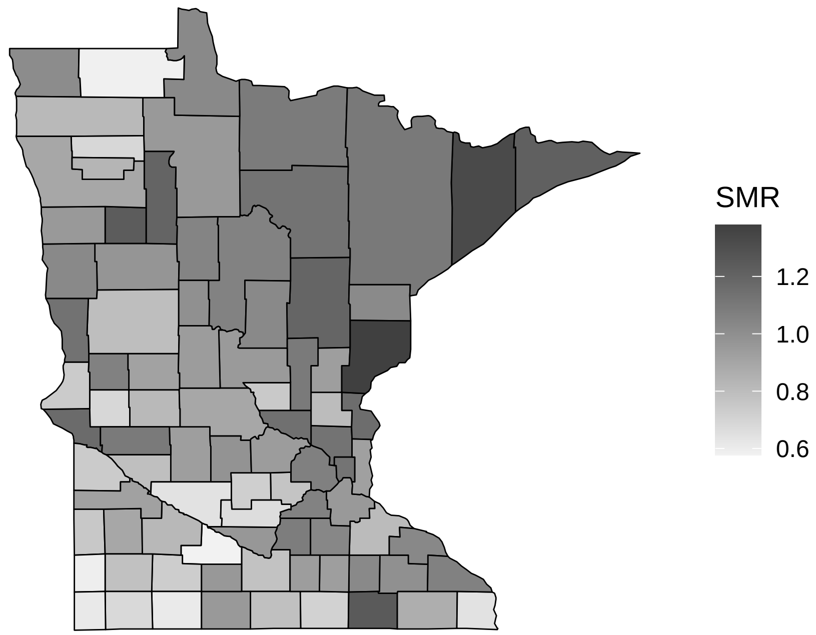
```
  filter(region == "minnesota") %>%
  rename(county = subregion)
dcounty <- left_join(dcounty, radon) %>%
  mutate(smr = obs/exp)
```

```
no_axes <- theme_minimal() + theme(
  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", linewidth = 0.25) +
  scale_fill_gradient(low = grey(0.95), high = grey(0.25),
    trans = "log10", na.value = "pink") +
  theme(legend.position = "inside", legend.position.inside = c(0.8,0.4)) +
  no_axes + ggtitle("Expected Number of Cases") + labs(fill = "Cases")

plot(p)
```



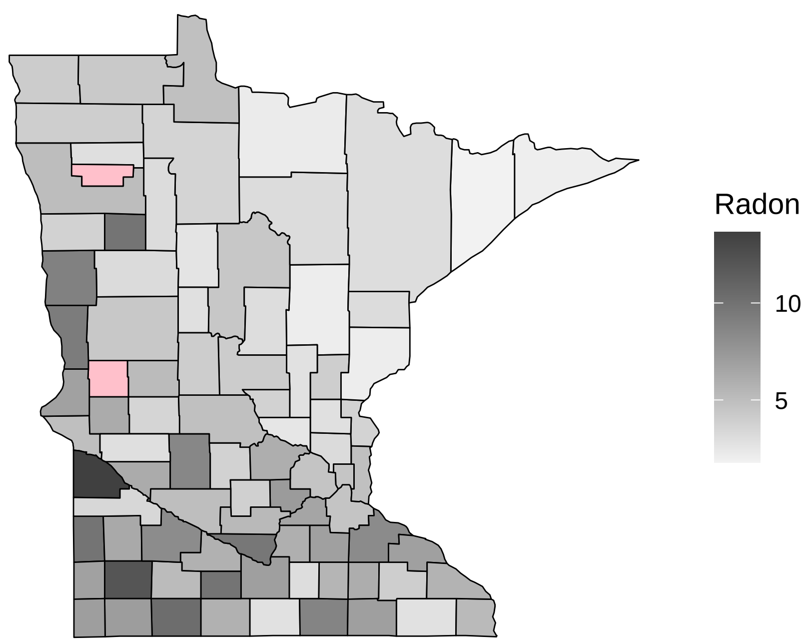

```
p <- ggplot(dcounty, aes(x = long, y = lat, group = group)) + coord_fixed(1.3) +
  geom_polygon(aes(fill = smr), color = "black", linewidth = 0.25) +
  scale_fill_gradient(low = grey(0.95), high = grey(0.25), na.value = "pink") +
  theme(legend.position = "inside", legend.position.inside = c(0.8,0.4))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

plot(p)
```

Standardized Mortality Ratio




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

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
```

```
            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.