Wednesday, Mar 9

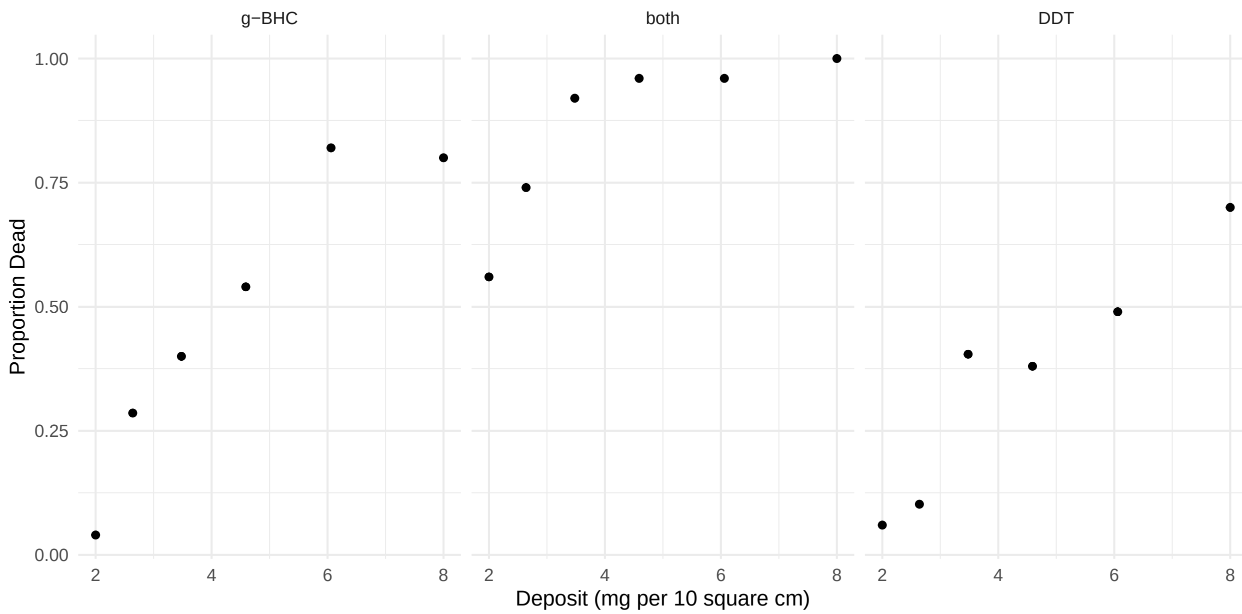
Odds Ratios Examples

Consider the following data from an experiment that investigated the effects of three insecticides on four beetles.

```
library(trtools) # contains the insecticide data frame
insecticide
```

```
   insecticide deposit deaths total
1          DDT    2.00      3    50
2          DDT    2.64      5    49
3          DDT    3.48     19    47
4          DDT    4.59     19    50
5          DDT    6.06     24    49
6          DDT    8.00     35    50
7        g-BHC    2.00      2    50
8        g-BHC    2.64     14    49
9        g-BHC    3.48     20    50
10       g-BHC    4.59     27    50
11       g-BHC    6.06     41    50
12       g-BHC    8.00     40    50
13        both    2.00     28    50
14        both    2.64     37    50
15        both    3.48     46    50
16        both    4.59     48    50
17        both    6.06     48    50
18        both    8.00     50    50
```

```
p <- ggplot(insecticide, aes(x = deposit, y = deaths/total)) +
  geom_point() + facet_wrap(~ insecticide) + theme_minimal() +
  labs(x = "Deposit (mg per 10 square cm)", y = "Proportion Dead")
plot(p)
```

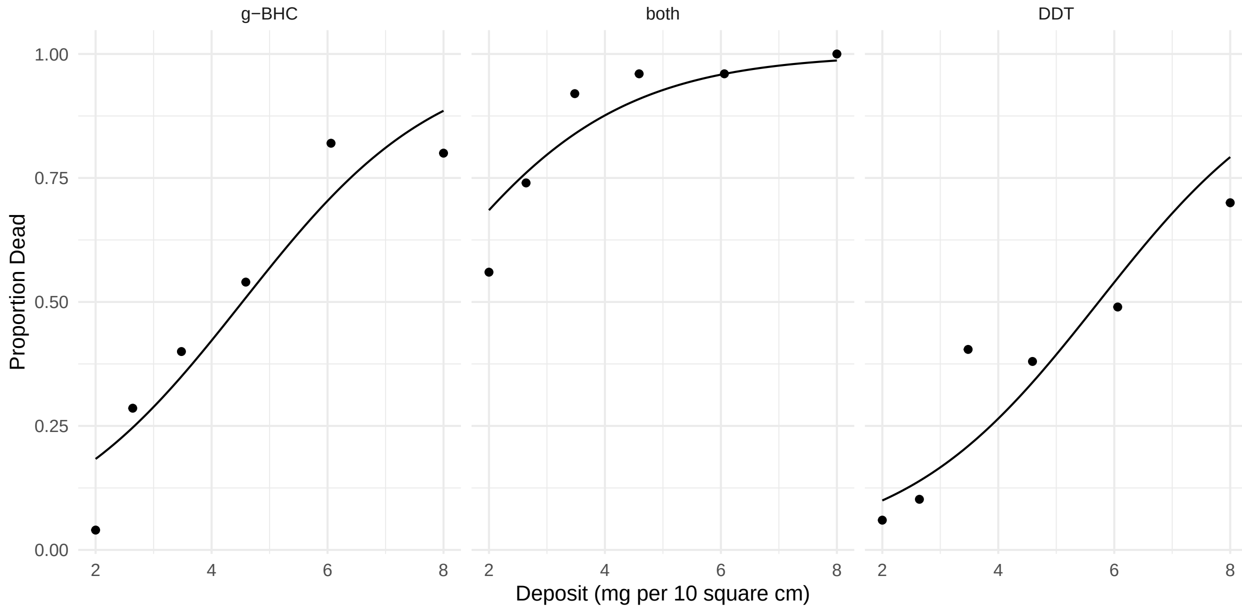


First consider an "additive" logistic regression model (i.e., a model with no interaction).

```
m <- glm(cbind(deaths, total-deaths) ~ insecticide + deposit,
  family = binomial, data = insecticide)
summary(m)$coefficients
```

```
                 Estimate Std. Error z value  Pr(>|z|)
(Intercept)       -2.6731    0.24968 -10.706 9.548e-27
insecticideboth    2.2704    0.22583  10.054 8.839e-24
insecticideDDT    -0.7074    0.19726  -3.586 3.356e-04
deposit            0.5898    0.04926  11.973 4.943e-33
```

```
d <- expand.grid(deposit = seq(2, 8, length = 100),
  insecticide = c("DDT","g-BHC","both"))
d$yhat <- predict(m, newdata = d, type = "response")
p <- p + geom_line(aes(y = yhat), data = d)
plot(p)
```



A model for the *odds* of death can be written as

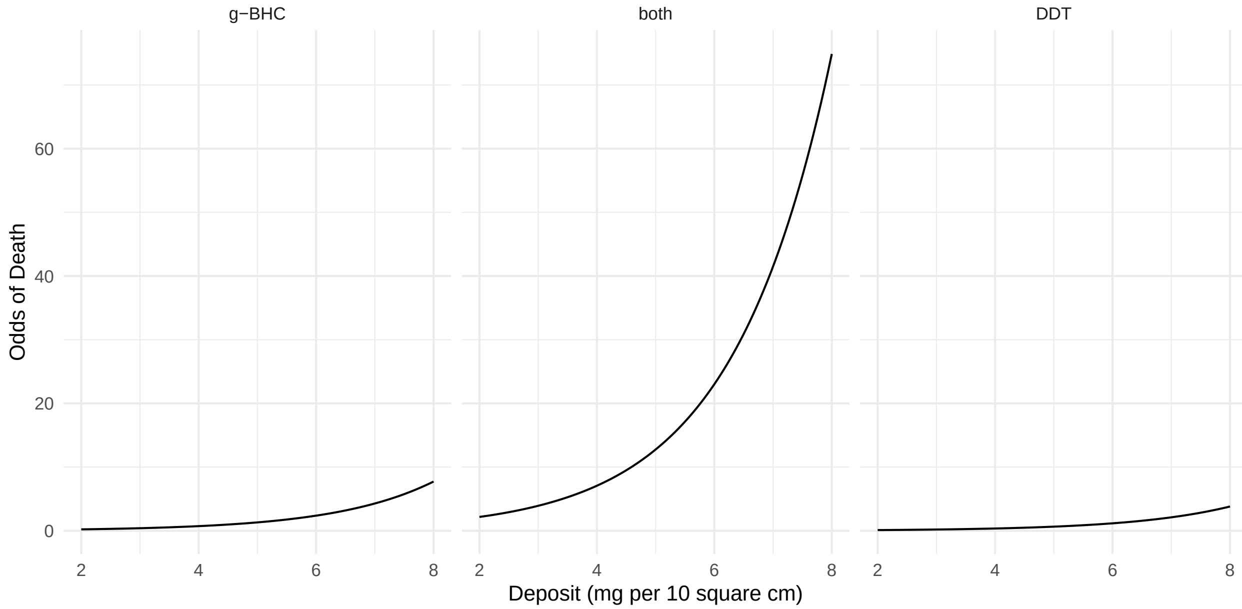
$$O_i = e^{\beta_0} e^{\beta_1 x_{i1}} e^{\beta_2 x_{i2}} e^{\beta_3 x_{i3}}$$

where x_{i1} and x_{i2} are indicator variables for the insecticides `both` and `DDT`, respectively, and x_{i3} is deposit. This can be written case-wise as

$$O_i = \begin{cases} e^{\beta_0} e^{\beta_3 d_i}, & \text{if the } i\text{-th observation of insecticide is g-BHC,} \\ e^{\beta_0} e^{\beta_1} e^{\beta_3 d_i}, & \text{if the } i\text{-th observation of insecticide is both,} \\ e^{\beta_0} e^{\beta_2} e^{\beta_3 d_i}, & \text{if the } i\text{-th observation of insecticide is DDT,} \end{cases}$$

and where $d_i = x_{i3}$ is the deposit. We could plot the estimated *odds* of death as a function of deposit and insecticide type.

```
d <- expand.grid(deposit = seq(2, 8, length = 100),
  insecticide = c("g-BHC","both","DDT"))
d$yhat <- predict(m, newdata = d, type = "response")
d$odds <- d$yhat / (1 - d$yhat)

p <- ggplot(d, aes(x = deposit, y = odds)) +
  geom_line() + facet_wrap(~ insecticide) + theme_minimal() +
  labs(x = "Deposit (mg per 10 square cm)", y = "Odds of Death")
plot(p)
```



It can be shown that the odds ratio for a one unit increase in deposit is e^{β_3} (regardless of insecticide used), and the odds ratio for comparing `both` with `g-BHC` is e^{β_1} (regardless of deposit amount). We can get these odds ratios as follows.

```
exp(cbind(coef(m), confint(m)))
```

```
                              2.5 %  97.5 %
(Intercept)     0.06904 0.04182  0.1114
insecticideboth 9.68342 6.27529 15.2250
insecticideDDT  0.49292 0.33359  0.7235
deposit         1.80362 1.64187  1.9921
```

But using `contrast` allows us to do this without having to figure out the parameterization.

```
# estimate the odds ratio for dose (one unit increase)
contrast(m,
  a = list(deposit = 3, insecticide = c("DDT","g-BHC","both")),
  b = list(deposit = 2, insecticide = c("DDT","g-BHC","both")),
  cnames = c("DDT","g-BHC","both"), tf = exp)
```

```
      estimate lower upper
DDT      1.804 1.638 1.986
g-BHC    1.804 1.638 1.986
both     1.804 1.638 1.986
```

```
# estimate the odds ratio for type of insecticide (both versus DDT)
contrast(m,
  a = list(deposit = c(2,5,8), insecticide = "both"),
  b = list(deposit = c(2,5,8), insecticide = "g-BHC"),
  cnames = c("2mg","5mg","8mg"), tf = exp)
```

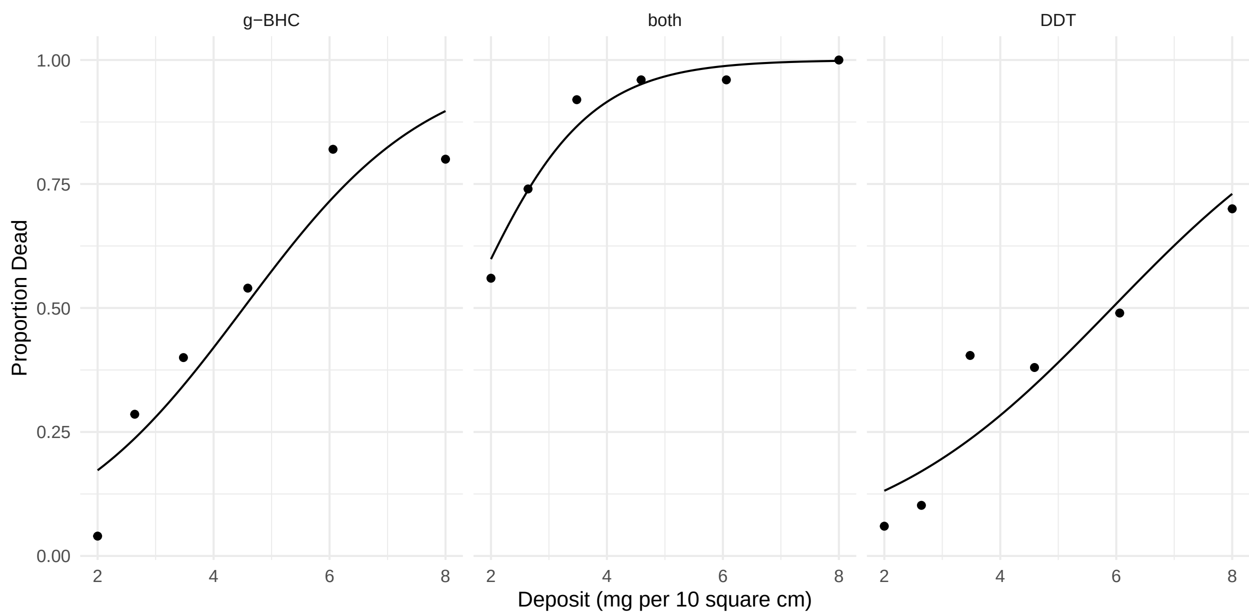
```
    estimate lower upper
2mg    9.683  6.22 15.07
5mg    9.683  6.22 15.07
8mg    9.683  6.22 15.07
```

Now suppose we include an interaction between dose and type of insecticide.

```r
m.int <- glm(cbind(deaths, total-deaths) ~ insecticide * deposit,
  family = binomial, data = insecticide)
summary(m.int)$coefficients
```

```
                        Estimate Std. Error  z value  Pr(>|z|)
(Intercept)             -2.81091    0.35845 -7.84177 4.442e-15
insecticideboth          1.22575    0.67176  1.82468 6.805e-02
insecticideDDT          -0.03893    0.50722 -0.07676 9.388e-01
deposit                  0.62207    0.07786  7.98986 1.351e-15
insecticideboth:deposit  0.37010    0.20897  1.77109 7.655e-02
insecticideDDT:deposit  -0.14143    0.10376 -1.36301 1.729e-01
```

```r
d <- expand.grid(deposit = seq(2, 8, length = 100),
  insecticide = c("DDT","g-BHC","both"))
d$yhat <- predict(m.int, newdata = d, type = "response")

p <- ggplot(insecticide, aes(x = deposit, y = deaths/total)) +
  geom_point() + facet_wrap(~ insecticide) + theme_minimal() +
  labs(x = "Deposit (mg per 10 square cm)", y = "Proportion Dead") +
  geom_line(aes(y = yhat), data = d)
plot(p)
```




```r
# estimate the odds ratio for the effect of dose
contrast(m.int,
  a = list(deposit = 3, insecticide = c("DDT","g-BHC","both")),
  b = list(deposit = 2, insecticide = c("DDT","g-BHC","both")),
  cnames = c("DDT","g-BHC","both"), tf = exp)
```

```
      estimate lower upper
DDT      1.617 1.414 1.850
g-BHC    1.863 1.599 2.170
both     2.697 1.844 3.944
```

```r
# estimate the odds ratio for the effect of type of insecticide (both versus g-BHC)
contrast(m.int,
```

```
  a = list(deposit = c(2,5,8), insecticide = "both"),
  b = list(deposit = c(2,5,8), insecticide = "g-BHC"),
  cnames = c("2mg","5mg","8mg"), tf = exp)
```

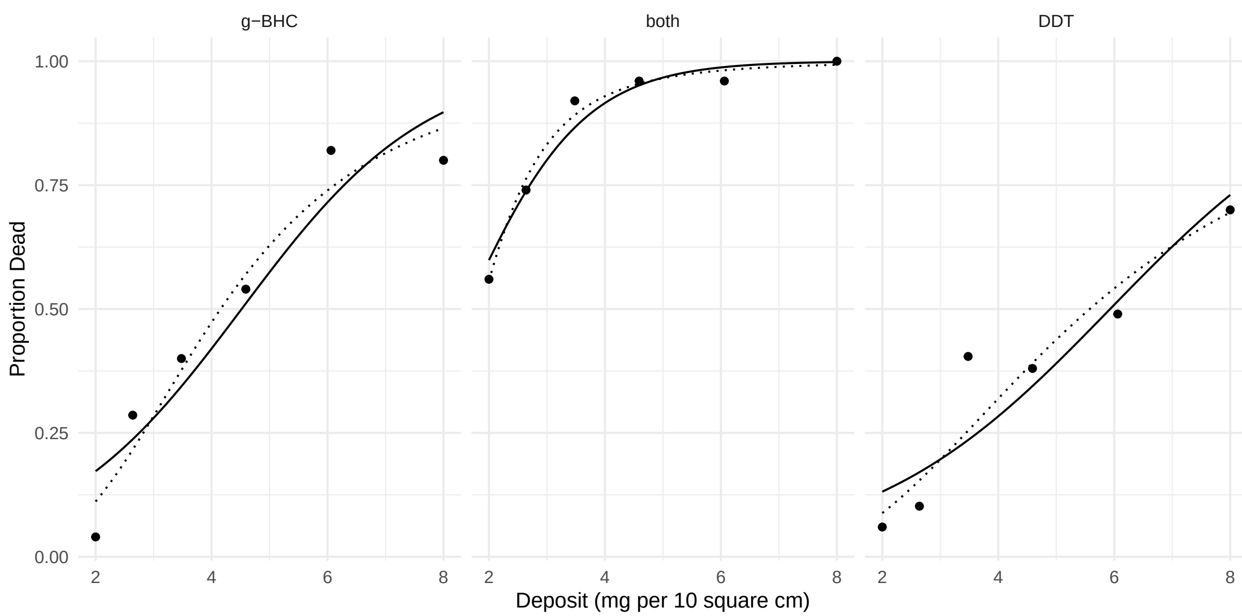
```
    estimate lower  upper
2mg    7.142 3.785  13.47
5mg   21.677 8.293  56.67
8mg   65.797 7.956 544.14
```

Now consider a model where we use log transformation of dose.

```
m <- glm(cbind(deaths, total-deaths) ~ insecticide * log(deposit),
  family = binomial, data = insecticide)
summary(m)$coefficients
```

```
                             Estimate Std. Error z value  Pr(>|z|)
(Intercept)                   -4.0428     0.4972 -8.1306 4.271e-16
insecticideboth                1.9221     0.7722  2.4892 1.280e-02
insecticideDDT                 0.1278     0.7118  0.1796 8.575e-01
log(deposit)                   2.8381     0.3392  8.3666 5.931e-17
insecticideboth:log(deposit)   0.5503     0.6662  0.8261 4.088e-01
insecticideDDT:log(deposit)   -0.5602     0.4680 -1.1971 2.313e-01
```

```
d <- expand.grid(deposit = seq(2, 8, length = 100),
  insecticide = c("DDT","g-BHC","both"))
d$yhat <- predict(m, newdata = d, type = "response")
p <- p + geom_line(aes(y = yhat), data = d, linetype = 3)
plot(p)
```



Now the odds ratio shows the effect of *doubling* the dose.

```
# odds ratio for the effect of increasing dose from 1 to 2 (doubling)
contrast(m,
  a = list(deposit = 2, insecticide = c("DDT","g-BHC","both")),
  b = list(deposit = 1, insecticide = c("DDT","g-BHC","both")),
  cnames = c("DDT","g-BHC","both"), tf = exp)
```

```
      estimate lower  upper
DDT      4.850 3.130  7.515
g-BHC    7.151 4.510 11.337
both    10.471 4.805 22.818
```

```
# odds ratio for the effect of increasing dose from 2 to 4 (doubling)
contrast(m,
  a = list(deposit = 4, insecticide = c("DDT","g-BHC","both")),
  b = list(deposit = 2, insecticide = c("DDT","g-BHC","both")),
  cnames = c("DDT","g-BHC","both"), tf = exp)
```

```
      estimate lower  upper
DDT      4.850 3.130  7.515
g-BHC    7.151 4.510 11.337
both    10.471 4.805 22.818
```

```
# odds ratio for the effect of increasing dose from 2 to 3 (not doubling)
contrast(m,
  a = list(deposit = 3, insecticide = c("DDT","g-BHC","both")),
  b = list(deposit = 2, insecticide = c("DDT","g-BHC","both")),
  cnames = c("DDT","g-BHC","both"), tf = exp)
```

```
      estimate lower upper
DDT      2.518 1.949 3.254
g-BHC    3.161 2.414 4.138
both     3.951 2.505 6.231
```

Contrasts between insecticides can proceed in the usual way although the results are not quite the same as when we did not transform dose.

```
# odds ratio to compare two insecticides at three doses
contrast(m,
  a = list(deposit = c(2,5,8), insecticide = "both"),
  b = list(deposit = c(2,5,8), insecticide = "g-BHC"),
  cnames = c("2mg","5mg","8mg"), tf = exp)
```

```
    estimate lower upper
2mg    10.01 4.826 20.76
5mg    16.57 7.087 38.76
8mg    21.47 5.351 86.11
```

At some point we will want to visit the issue of how to evaluate/select models.

Binary/Bernoulli Logistic Regression Example

Consider the following data from a study that investigated the relationship between vasoconstriction and the rate and volume of air breathed by human subjects. Here the response variable is *binary* and thus has a *Bernoulli* distribution (a special case of the binomial distribution).

```
library(catdata)
data(vaso)
head(vaso)
```

```
      vol     rate vaso
1  1.3083 -0.19237    1
2  1.2528  0.08618    1
3  0.2231  0.91629    1
```

```
4 -0.2877  0.40547    1
5 -0.2231  1.16315    1
6 -0.3567  1.25276    1
```

Volume (`vol`) is the logarithm of volume in liters, and rate (`rate`) is the logarithm of liters per second. For this example I am going to transform these variables to the volume and rate in deciliters.

```
vaso$dvolume <- exp(vaso$vol)*10        # transform to deciliters
vaso$drate <- exp(vaso$rate)*10         # transform to deciliters per sec
```

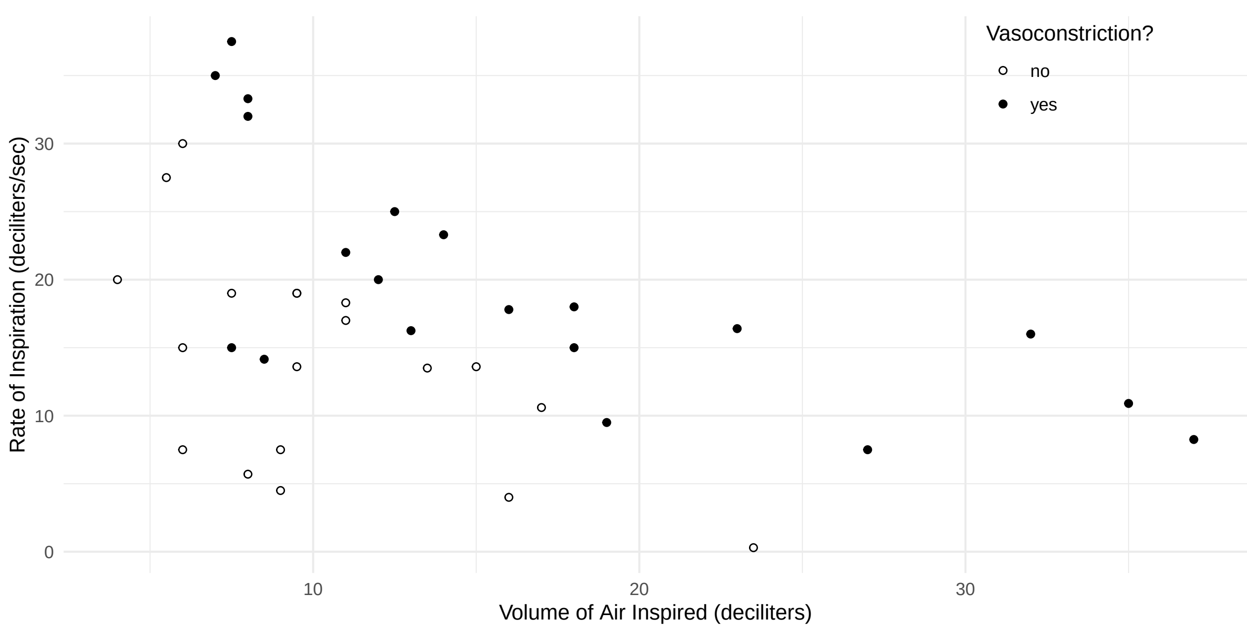
I am also going to create a couple different versions of the response variable: one that is a character for plotting and one that is binary for modeling (note that the help file for `vaso` has coding on the `vaso` variable backwards).

```
vaso$vasoconstriction <- ifelse(vaso$vaso == 1, "yes", "no")
vaso$y <- ifelse(vaso$vaso == 1, 1, 0) # create binary response
head(vaso)
```

```
      vol     rate vaso dvolume drate vasoconstriction y
1  1.3083 -0.19237    1    37.0  8.25              yes 1
2  1.2528  0.08618    1    35.0 10.90              yes 1
3  0.2231  0.91629    1    12.5 25.00              yes 1
4 -0.2877  0.40547    1     7.5 15.00              yes 1
5 -0.2231  1.16315    1     8.0 32.00              yes 1
6 -0.3567  1.25276    1     7.0 35.00              yes 1
```

Here is a scatterplot of volume and rate, with point color indicating vasoconstriction.

```
p <- ggplot(vaso, aes(x = dvolume, y = drate)) +
  geom_point(aes(fill = vasoconstriction), shape = 21) +
  scale_fill_manual(values = c("white","black")) +
  labs(x = "Volume of Air Inspired (deciliters)",
    y = "Rate of Inspiration (deciliters/sec)",
    fill = "Vasoconstriction?") +
  theme_minimal() + theme(legend.position = c(0.85, 0.9))
plot(p)
```



If the response variable is *binary* (i.e., 0 or 1) then we can use `glm(y ~ ...)` rather than `glm(cbind(y, 1-y) ~ ...)`.

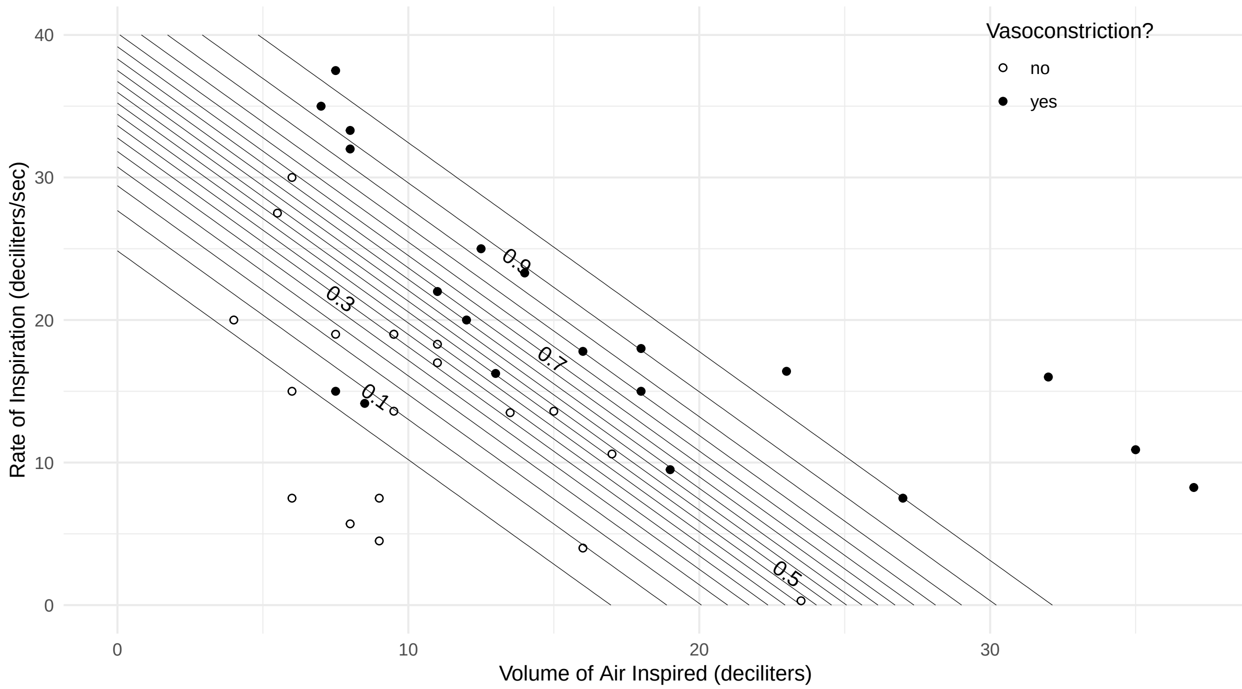
```
m <- glm(y ~ dvolume + drate, family = binomial, data = vaso)
cbind(summary(m)$coefficients, confint(m))
```

```
            Estimate Std. Error z value Pr(>|z|)    2.5 %  97.5 %
(Intercept)  -9.5296    3.23319  -2.947 0.003204 -17.5593 -4.4560
dvolume       0.3882    0.14286   2.717 0.006579   0.1654  0.7385
drate         0.2649    0.09142   2.898 0.003759   0.1177  0.4895
```

```
exp(cbind(coef(m), confint(m)))
```

```
                          2.5 %  97.5 %
(Intercept) 7.267e-05 2.366e-08 0.01161
dvolume     1.474e+00 1.180e+00 2.09281
drate       1.303e+00 1.125e+00 1.63151
```

```
d <- expand.grid(dvolume = seq(0, 40, length = 100),
  drate = seq(0, 40, length = 100))
d$yhat <- predict(m, newdata = d, type = "response")

library(metR) # for geom_text_contour

p <- ggplot(vaso, aes(x = dvolume, y = drate)) +
  geom_point(aes(fill = vasoconstriction), shape = 21) +
  scale_fill_manual(values = c("white","black")) +
  geom_contour(aes(z = yhat), data = d, color = "black",
    size = 0.15, breaks = seq(0.05, 0.95, by = 0.05)) +
  geom_text_contour(aes(z = yhat), data = d) +
  labs(x = "Volume of Air Inspired (deciliters)",
    y = "Rate of Inspiration (deciliters/sec)",
    fill = "Vasoconstriction?") +
  theme_minimal() + theme(legend.position = c(0.85, 0.9))
plot(p)
```




```
# odds ratio for the effect of volume
contrast(m, tf = exp,
  a = list(dvolume = 2, drate = c(10,20,30)),
  b = list(dvolume = 1, drate = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl/sec")))
```

```
             estimate lower upper
at 10 dl/sec    1.474 1.114 1.951
at 20 dl/sec    1.474 1.114 1.951
at 30 dl/sec    1.474 1.114 1.951
```

```
# odds ratios for rate
contrast(m, tf = exp,
  a = list(drate = 2, dvolume = c(10,20,30)),
  b = list(drate = 1, dvolume = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl")))
```

```
         estimate lower upper
at 10 dl    1.303  1.09 1.559
at 20 dl    1.303  1.09 1.559
at 30 dl    1.303  1.09 1.559
```

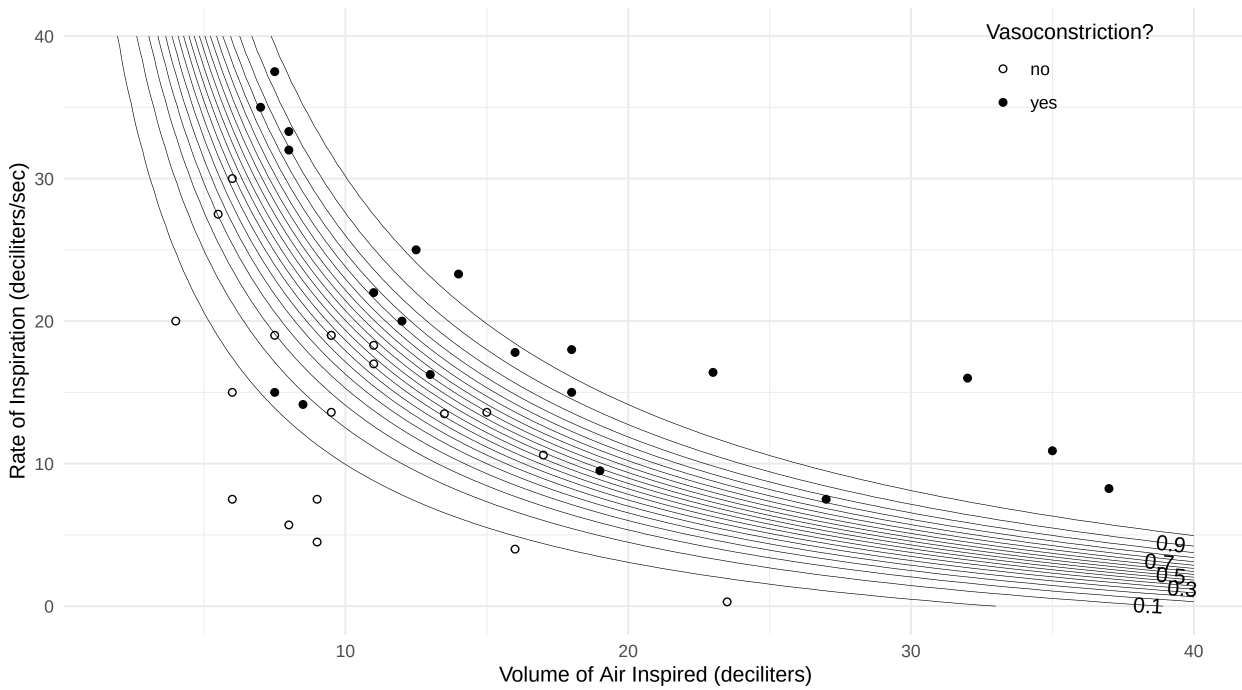
Now consider a model with a product term (i.e., "interaction") for volume and rate.

```
m <- glm(y ~ dvolume + drate + dvolume*drate, family = binomial, data = vaso)
summary(m)$coefficients
```

```
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -7.11496    3.34853 -2.1248   0.0336
dvolume        0.12637    0.21471  0.5886   0.5561
drate          0.05112    0.15082  0.3390   0.7346
dvolume:drate  0.02408    0.01662  1.4490   0.1473
```

```
d <- expand.grid(dvolume = seq(0, 40, length = 100), drate = seq(0, 40, length = 100))
```

```r
d$yhat <- predict(m, newdata = d, type = "response")
p <- ggplot(vaso, aes(x = dvolume, y = drate)) +
  geom_point(aes(fill = vasoconstriction), shape = 21) +
  scale_fill_manual(values = c("white","black")) +
  geom_contour(aes(z = yhat), data = d, color = "black",
    size = 0.15, breaks = seq(0.05, 0.95, by = 0.05)) +
  geom_text_contour(aes(z = yhat), data = d) +
  labs(x = "Volume of Air Inspired (deciliters)",
    y = "Rate of Inspiration (deciliters/sec)",
    fill = "Vasoconstriction?") +
  theme_minimal() + theme(legend.position = c(0.85, 0.9))
plot(p)
```




```r
# odds ratios for the effect of volume
contrast(m, tf = exp,
  a = list(dvolume = 2, drate = c(10,20,30)),
  b = list(dvolume = 1, drate = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl/sec")))
```

```
              estimate lower upper
at 10 dl/sec     1.444 1.087 1.918
at 20 dl/sec     1.837 1.179 2.861
at 30 dl/sec     2.337 1.133 4.820
```

```r
# odds ratios for the effect of rate
contrast(m, tf = exp,
  a = list(drate = 2, dvolume = c(10,20,30)),
  b = list(drate = 1, dvolume = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl")))
```

```
          estimate lower upper
at 10 dl     1.339 1.096 1.636
```

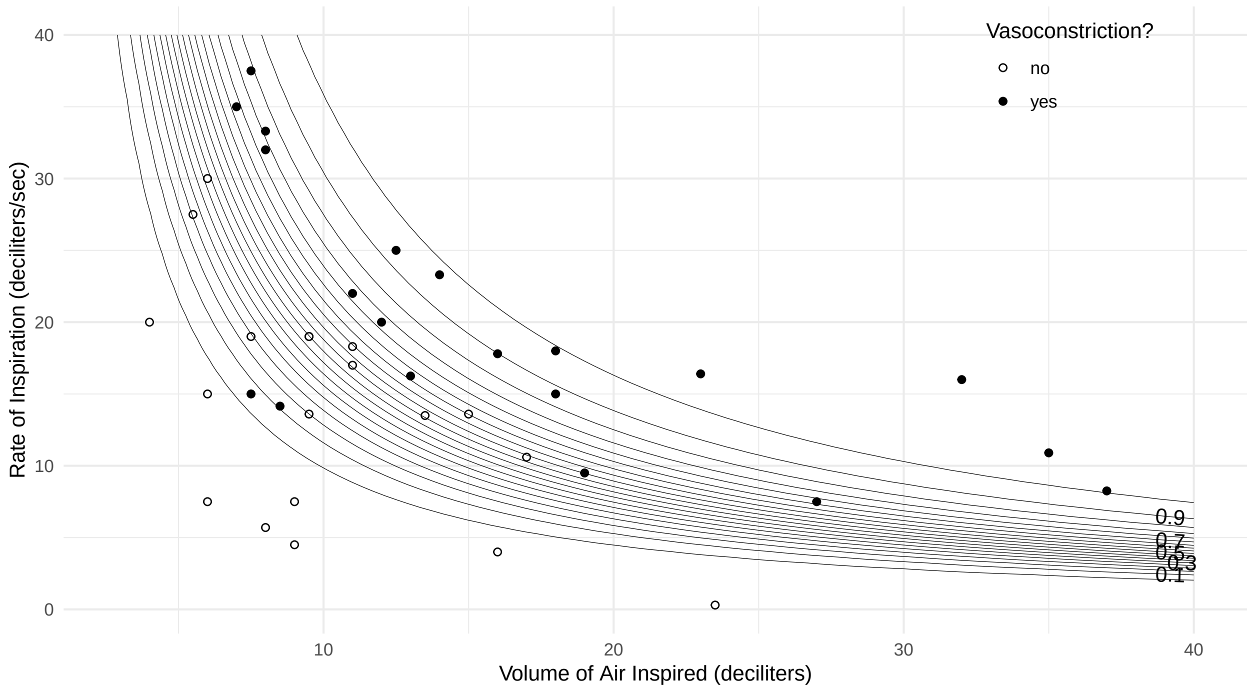
```
at 20 dl    1.704 1.083 2.680
at 30 dl    2.167 1.010 4.649
```

Now about a model where we transform volume and rate to make it additive on the log scale?

```r
m <- glm(y ~ log(dvolume) + log(drate), family = binomial, data = vaso)
exp(cbind(coef(m), confint(m)))
```

```
Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

                           2.5 %    97.5 %
(Intercept)  1.024e-11 8.144e-22 1.435e-05
log(dvolume) 1.776e+02 9.911e+00 1.902e+04
log(drate)   9.574e+01 5.540e+00 8.398e+03
```

```r
d <- expand.grid(dvolume = seq(0, 40, length = 100),
  drate = seq(0, 40, length = 100))
d$yhat <- predict(m, newdata = d, type = "response")

p <- ggplot(vaso, aes(x = dvolume, y = drate)) +
  geom_point(aes(fill = vasoconstriction), shape = 21) +
  scale_fill_manual(values = c("white","black")) +
  geom_contour(aes(z = yhat), data = d, color = "black",
    size = 0.15, breaks = seq(0.05, 0.95, by = 0.05)) +
  geom_text_contour(aes(z = yhat), data = d) +
  labs(x = "Volume of Air Inspired (deciliters)",
    y = "Rate of Inspiration (deciliters/sec)",
    fill = "Vasoconstriction?") +
  theme_minimal() + theme(legend.position = c(0.85, 0.9))
plot(p)
```




```
# odds ratios for the effect of volume
contrast(m, tf = exp,
  a = list(dvolume = 2, drate = c(10,20,30)),
  b = list(dvolume = 1, drate = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl/sec")))
```

```
             estimate lower upper
at 10 dl/sec    36.24 2.877 456.3
at 20 dl/sec    36.24 2.877 456.3
at 30 dl/sec    36.24 2.877 456.3
```

```
# odds ratios for the effect of rate
contrast(m, tf = exp,
  a = list(drate = 2, dvolume = c(10,20,30)),
  b = list(drate = 1, dvolume = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl")))
```

```
         estimate lower upper
at 10 dl    23.62 1.945 286.7
at 20 dl    23.62 1.945 286.7
at 30 dl    23.62 1.945 286.7
```

Doubling the volume or rate is a relatively large change. How about increasing it by only, say, 10% rather than 100%?

```
# odds ratios for the effect of volume
contrast(m, tf = exp,
  a = list(dvolume = 1.1, drate = c(10,20,30)),
  b = list(dvolume = 1.0, drate = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl/sec")))
```

```
             estimate lower upper
at 10 dl/sec    1.638 1.156 2.321
at 20 dl/sec    1.638 1.156 2.321
```

```
at 30 dl/sec    1.638 1.156 2.321
```

```
# odds ratios for the effect of rate
contrast(m, tf = exp,
  a = list(drate = 1.1, dvolume = c(10,20,30)),
  b = list(drate = 1.0, dvolume = c(10,20,30)),
  cnames = c(paste("at", c(10,20,30), "dl")))
```

```
         estimate lower upper
at 10 dl    1.545 1.096 2.177
at 20 dl    1.545 1.096 2.177
at 30 dl    1.545 1.096 2.177
```

Note that we'd get the same results for *any* 10% increase in volume or rate (e.g., from 2.0 to 2.2) because both are on the log scale.