Monday, Feb 5

Modeling Nonlinearity

Four approaches to modeling a nonlinear relationship between the expected response and a quantitative explanatory variable.

1. polynomials
2. transformations
3. splines
4. nonlinear regression

The first three can be done with *linear models*.

Polynomial Regression

If we have a single explanatory variable x_i, then a *polynomial regression model* of degree k is

$$E(Y_i) = \beta_0 + \beta_1 x_i + \beta_2 x_i^2 + \cdots + \beta_k x_i^k.$$

Note that this *is* a linear *model* since we can write it as

$$E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik},$$

where $x_{i1} = x_i, x_{i2} = x_i^2, \dots, x_{ik} = x_i^k$.

Example: Consider again the `ToothGrowth` data but with dose treated as a quantitative explanatory variable, and ignoring supplement type for now. Note the use of the "inhibit" function `I` here.

```
m <- lm(len ~ dose + I(dose^2), data = ToothGrowth)
summary(m)$coefficients
```

```
            Estimate Std. Error t value  Pr(>|t|)
(Intercept)    -2.49      3.178 -0.7836 4.365e-01
dose           30.15      6.147  4.9052 8.148e-06
I(dose^2)      -7.93      2.366 -3.3514 1.432e-03
```

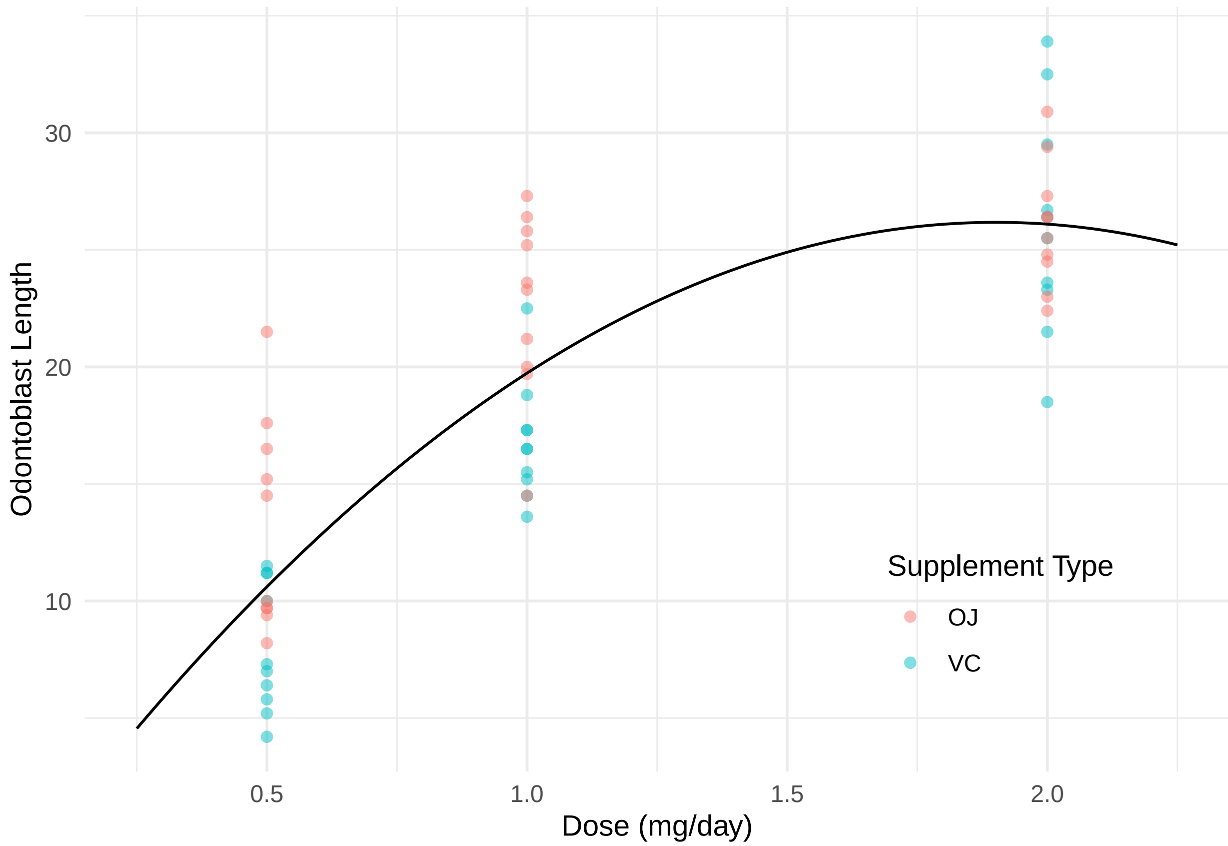
This model is

$$E(L_i) = \beta_0 + \beta_1 d_i + \beta_2 d_i^2,$$

where d_i is dose.

```
d <- expand.grid(dose = seq(0.25, 2.25, length = 100))
d$yhat <- predict(m, newdata = d)

p <- ggplot(ToothGrowth, aes(x = dose, y = len)) +
  geom_point(aes(color = supp), alpha = 0.5) +
  geom_line(aes(y = yhat), data = d) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length",
    color = "Supplement Type") +
  theme_minimal() + theme(legend.position = c(0.8,0.2))
plot(p)
```



Note that the following are equivalent ways to specify this model.

```
# create a new variable for squared dose
ToothGrowth$dose2 <- ToothGrowth$dose^2
m <- lm(len ~ dose + dose2, data = ToothGrowth)

# specify squared dose in the model formula using the "inhibit" function
m <- lm(len ~ dose + I(dose^2), data = ToothGrowth)

# use the poly function to create the extra term
m <- lm(len ~ poly(dose, degree = 2), data = ToothGrowth)
```

I recommend not using the first approach of creating a new variable only because it is easier to have the transformation "built in" to the model when applying other functions to the model object like `predict` or `contrast`.

Note: Using `poly` without the option `raw = TRUE` will produce "orthogonal polynomials" which is a reparameterization of the model. This approach is sometimes recommended due to numerical instability of "raw" polynomials, but in many cases this is not an issue. But the `poly` function is sometimes convenient, especially for polynomials of higher degree.

Clearly in such a model the rate of change in expected length is *not* necessarily constant.

```
library(trtools)
contrast(m, a = list(dose = 1), b = list(dose = 0.5)) # 0.5 to 1
```

```
 estimate    se lower upper tvalue df    pvalue
     9.13 1.341 6.444 11.82  6.806 57 6.697e-09
```

```r
contrast(m, a = list(dose = 1.5), b = list(dose = 1)) # 1 to 1.5
```

```
 estimate     se lower upper tvalue df   pvalue
    5.165 0.4472  4.27  6.06  11.55 57 1.47e-16
```

This can also be seen mathematically by writing the model as

$$E(L_i) = \beta_0 + \beta_1 x_i + \beta_2 x_i^2 = \beta_0 + \underbrace{(\beta_1 + \beta_2 x_i)}_{\delta_i} x_i = \beta_0 + \delta_i x_i,$$

so that the rate of change in length per unit increase in dose *depends on dose* (if $\beta_2 \neq 0$). In a sense, dose is "interacting with itself" — i.e., the "effect" of a one unit increase in dose depends on the dose.

We can have the polynomial depend on (i.e, interact with) supplement type.

```r
m <- lm(len ~ dose + I(dose^2) + supp + dose:supp + I(dose^2):supp, data = ToothGrowth)
summary(m)$coefficients
```

```
                  Estimate Std. Error t value  Pr(>|t|)
(Intercept)         -1.433      3.847 -0.3726 7.109e-01
dose                34.520      7.442  4.6384 2.272e-05
I(dose^2)          -10.387      2.864 -3.6260 6.383e-04
suppVC              -2.113      5.440 -0.3885 6.992e-01
dose:suppVC         -8.730     10.525 -0.8295 4.105e-01
I(dose^2):suppVC     4.913      4.051  1.2129 2.305e-01
```

Note that we could also have written

```r
m <- lm(len ~ poly(dose, 2)*supp, data = ToothGrowth)
```

In a model formula argument, `a*b` expands to `a + b + a:b`.

This model can be written as

$$E(L_i) = \begin{cases} \beta_0 + \beta_1 d_i + \beta_2 d_i^2, & \text{if supplement type is OJ,} \\ \beta_0 + \beta_3 + (\beta_1 + \beta_4) d_i + (\beta_2 + \beta_5) d_i^2, & \text{if supplement type is VC,} \end{cases}$$

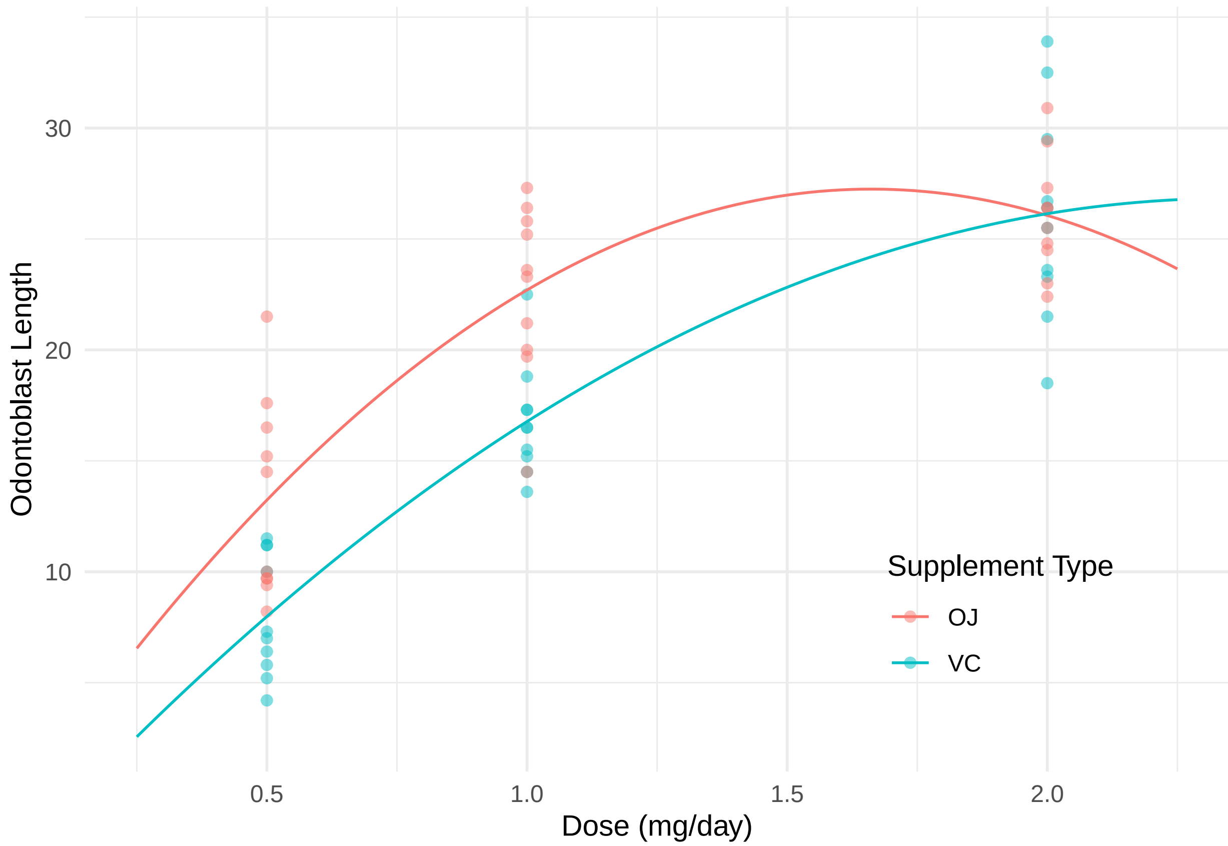
where d_i is dose, or alternatively as

$$E(L_i) = \begin{cases} \beta_0 + \beta_1 d_i + \beta_2 d_i^2, & \text{if supplement type is OJ,} \\ \gamma_0 + \gamma_1 d_i + \gamma_2 d_i^2, & \text{if supplement type is VC,} \end{cases}$$

where $\gamma_0 = \beta_0 + \beta_3$, $\gamma_1 = \beta_1 + \beta_4$, and $\gamma_2 = \beta_2 + \beta_5$. There is a distinct polynomial of degree two for each supplement type.

```r
d <- expand.grid(supp = c("OJ", "VC"), dose = seq(0.25, 2.25, length = 100))
d$yhat <- predict(m, newdata = d)

p <- ggplot(ToothGrowth, aes(x = dose, y = len, color = supp)) +
  geom_point(alpha = 0.5) + geom_line(aes(y = yhat), data = d) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length",
    color = "Supplement Type") + theme_minimal() +
  theme(legend.position = c(0.8,0.2))
plot(p)
```



Polynomials are, in principle, quite general. But in many cases we would like to have a monotonic relationship, and/or have a model exhibit an asymptote. Finally, the parameters of a polynomial model are not easily to interpret.

Logarithmic Transformations

Applying a *logarithmic transformation* to an explanatory variable may be useful for explanatory variables that tend to have "diminishing returns" with respect to the expected response.

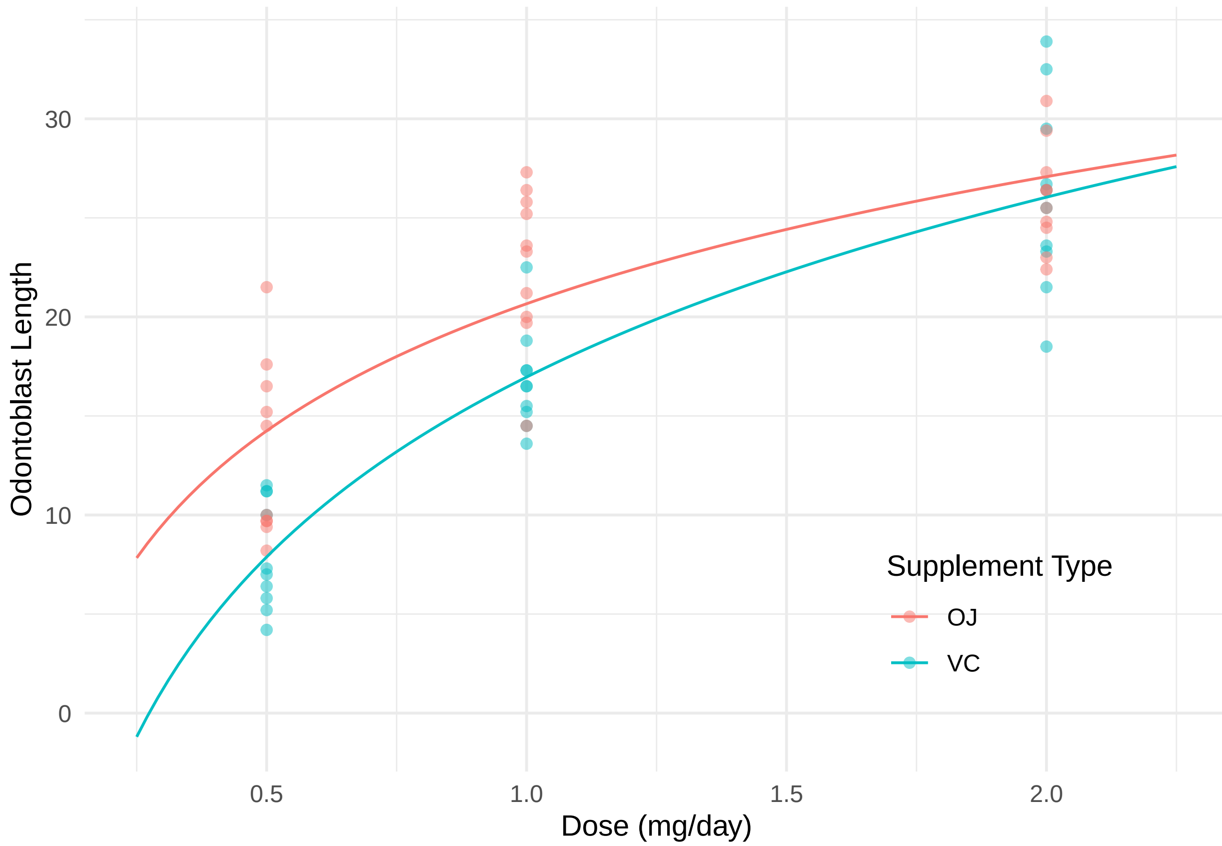
Example: Consider a linear model for expected length but now with log(dose) as the explanatory variable.

```
m <- lm(len ~ log(dose) + supp + log(dose):supp, data = ToothGrowth)
summary(m)$coefficients
```

```
                 Estimate Std. Error t value  Pr(>|t|)
(Intercept)        20.663     0.6791  30.425 1.629e-36
log(dose)           9.255     1.2000   7.712 2.303e-10
suppVC             -3.700     0.9605  -3.852 3.033e-04
log(dose):suppVC    3.845     1.6971   2.266 2.737e-02
```

```
d <- expand.grid(supp = c("OJ", "VC"), dose = seq(0.25, 2.25, length = 100))
d$yhat <- predict(m, newdata = d)

p <- ggplot(ToothGrowth, aes(x = dose, y = len, color = supp)) +
  geom_point(alpha = 0.5) + geom_line(aes(y = yhat), data = d) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length",
    color = "Supplement Type") + theme_minimal() +
  theme(legend.position = c(0.8,0.2))
plot(p)
```



Note that `log` is the "natural" logarithm or base-e logarithm sometimes written as $\ln(x)$ or $\log_e(x)$. Here are few things to remember about logarithms when using them for transformations of explanatory variables.

1. Logarithms of different bases are *proportional*. In general

$$\log_b(x) = c \log_a(x),$$

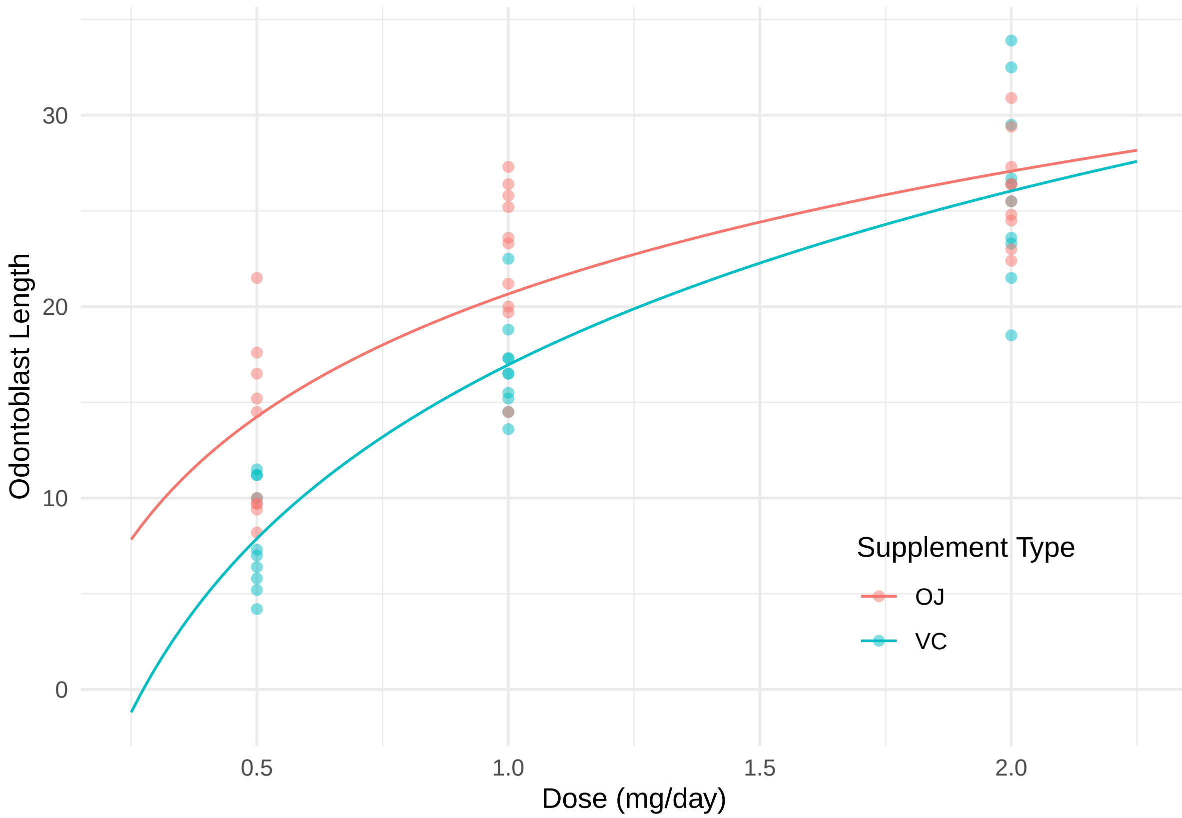
where $c = 1/\log_a(b)$. So usually when we are using things like `contrast` or the **emmeans** package to facilitate our inferences the base does not matter. You can use `log2` for $\log_2(x)$ and `log10` for $\log_{10}(x)$, and for an arbitrary base b you can use `log(x,b)` for $\log_b(x)$.

```
m <- lm(len ~ log2(dose) + supp + log2(dose):supp, data = ToothGrowth)
summary(m)$coefficients
```

```
                   Estimate Std. Error t value  Pr(>|t|)
(Intercept)          20.663     0.6791  30.425 1.629e-36
log2(dose)            6.415     0.8318   7.712 2.303e-10
suppVC               -3.700     0.9605  -3.852 3.033e-04
log2(dose):suppVC     2.665     1.1763   2.266 2.737e-02
```

```
d <- expand.grid(supp = c("OJ", "VC"), dose = seq(0.25, 2.25, length = 100))
d$yhat <- predict(m, newdata = d)

p <- ggplot(ToothGrowth, aes(x = dose, y = len, color = supp)) +
  geom_point(alpha = 0.5) + geom_line(aes(y = yhat), data = d) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length",
    color = "Supplement Type") + theme_minimal() +
  theme(legend.position = c(0.8,0.2))
plot(p)
```



2. If we apply a log transformation to x, then the effect of increasing/decreasing x by some amount is not constant, but the effect of increasing/decreasing x by a *factor* is constant. For example, suppose we have the model
$$E(Y) = \beta_0 + \beta_1 \log(x).$$

   Then for any $c > 0$ then
$$\beta_0 + \beta_1 \log(cx) = \beta_0 + \beta_1 \log(c) + \beta_1 \log(x) = E(Y) + \beta_1 \log(c)$$

   so then $E(Y)$ increases/decreases by $\beta_1 \log(c)$. For example, the effect of *doubling* of *halving* dose is constant in this model.

```
contrast(m,
  a = list(dose = 1, supp = c("OJ","VC")),
  b = list(dose = 0.5, supp = c("OJ","VC")),
  cnames = c("OJ", "VC"))
```

```
   estimate     se lower  upper tvalue df    pvalue
OJ    6.415 0.8318 4.749  8.081  7.712 56 2.303e-10
VC    9.080 0.8318 7.414 10.746 10.916 56 1.733e-15
```

```
contrast(m,
  a = list(dose = 2, supp = c("OJ","VC")),
  b = list(dose = 1, supp = c("OJ","VC")),
  cnames = c("OJ", "VC"))
```

```
   estimate     se lower  upper tvalue df    pvalue
OJ    6.415 0.8318 4.749  8.081  7.712 56 2.303e-10
VC    9.080 0.8318 7.414 10.746 10.916 56 1.733e-15
```

3. Recall that $\log(x)$ is only defined for $x > 0$.

Exponential Transformations

Consider the linear model

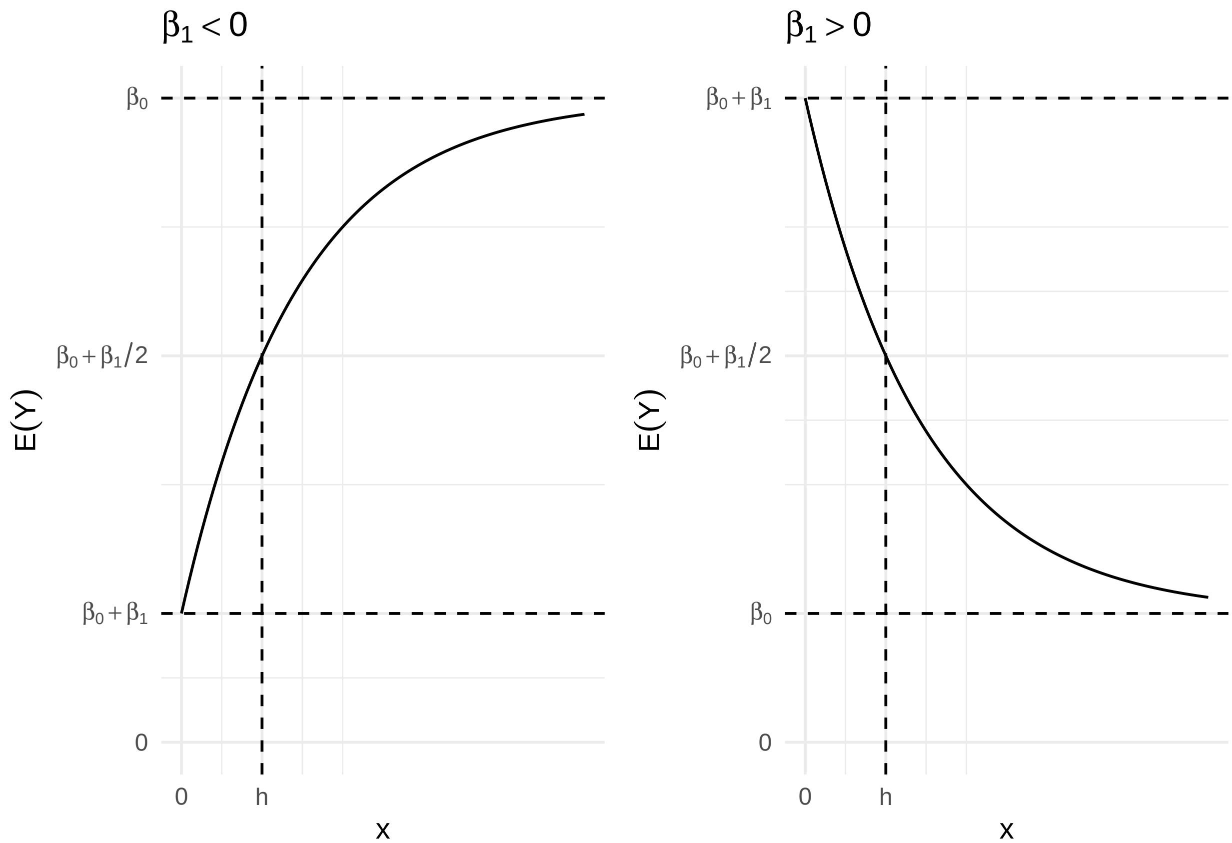
$$E(Y) = \beta_0 + \beta_1 2^{-x/h}$$

where $h > 0$ is some specified value. This applies an *exponential* transformation to x with the following properties.

1. If $x = 0$ then $E(Y) = \beta_0 + \beta_1$, so the "y-intercept" is $\beta_0 + \beta_1$.
2. As x increases then $E(Y)$ approaches an asymptote of β_0. This is an *upper* (if $\beta_1 < 0$) or *lower* (if $\beta_1 > 0$) asymptote.[1]
3. The quantity h can be interpreted as the "half-life" of the curve in the sense that it is the value of x at which the expected responses is half way between the intercept at $\beta_0 + \beta_1$ and its upper/lower asymptote at β_0 because if $x = h$ then

$$E(Y) = \beta_0 + \beta_1 2^{-x/h} = \beta_0 + \beta_1/2,$$

   and $\beta_0 + \beta_1/2$ is the midpoint between the "intercept" of $E(Y) = \beta_0 + \beta_1$ and the asymptote of β_0.
4. If $\beta_1 < 0$ then $-\beta_1$ is how much $E(Y)$ *increases* from $x = 0$ as it approaches the asymptote, while if $\beta_1 > 0$ then β_1 is how much $E(Y)$ *decreases* from when $x = 0$ as it approaches the asymptote.



Consider again a linear model for the `ToothGrowth` data with an exponential transformation of dose with h = 1.

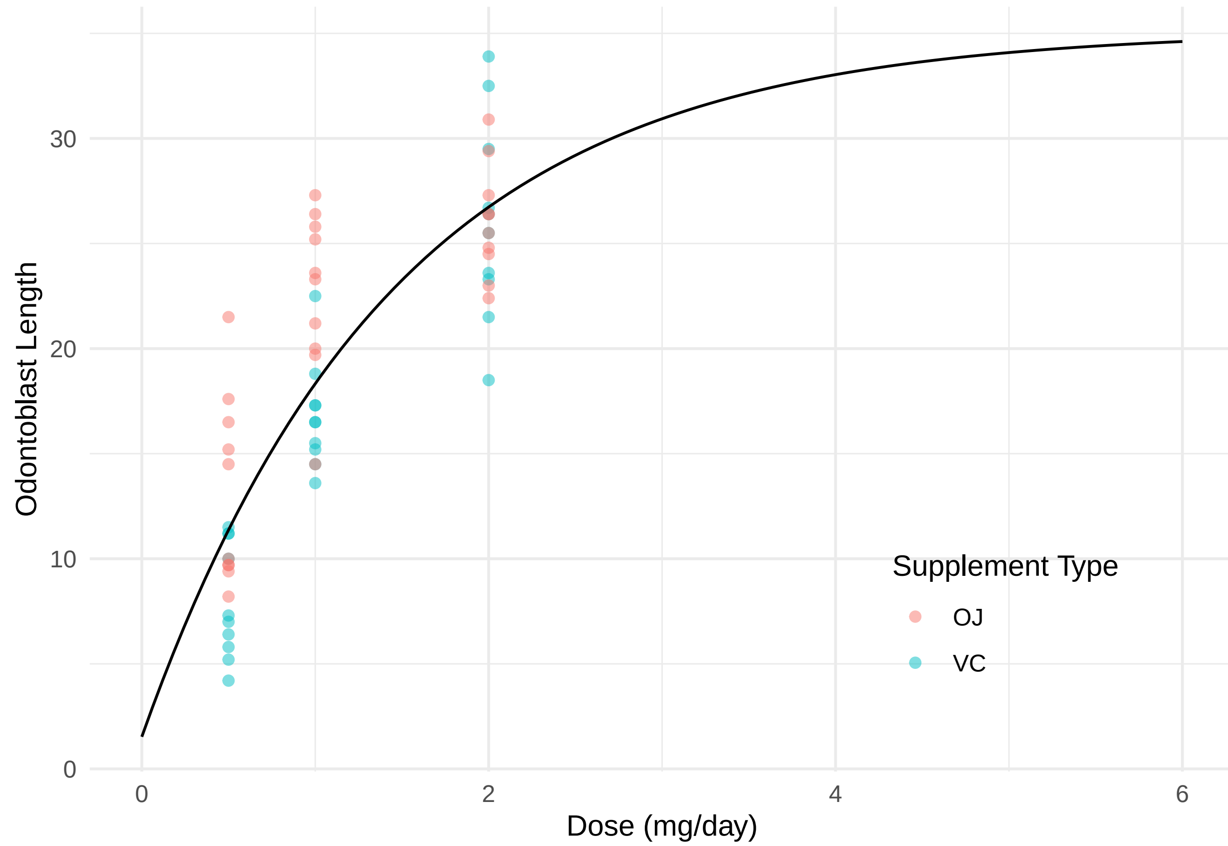
[1]This can be seen by showing that $\lim_{x\to\infty} \beta_0 + \beta_1 2^{-x/h} = \beta_0$ if $h > 0$, and by showing that the first derivative of $\beta_0 + \beta_1 2^{-x/h}$ with respect to x is positive if $\beta_1 < 0$ and negative if $\beta_1 > 0$ if $h > 0$.

```r
m <- lm(len ~ I(2^(-dose/1)), data = ToothGrowth)
summary(m)$coefficients
```

```
               Estimate Std. Error t value  Pr(>|t|)
(Intercept)       35.14      1.555   22.60 1.942e-30
I(2^(-dose/1))   -33.61      2.988  -11.25 3.303e-16
```

```r
d <- expand.grid(supp = c("OJ", "VC"), dose = seq(0, 6, length = 100))
d$yhat <- predict(m, newdata = d)

p <- ggplot(ToothGrowth, aes(x = dose, y = len, color = supp)) +
  geom_point(alpha = 0.5) + xlim(0,6) +
  geom_line(aes(y = yhat), color = "black", data = d) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length",
    color = "Supplement Type") + theme_minimal() +
  theme(legend.position = c(0.8,0.2))
plot(p)
```




```r
lincon(m, a = c(1,1)) # intercept
```

```
        estimate    se  lower upper tvalue df pvalue
(1,1),0    1.528 1.635 -1.745   4.8 0.9345 58 0.3539
```

Now suppose that we let the effect of dose "interact" with supplement type.

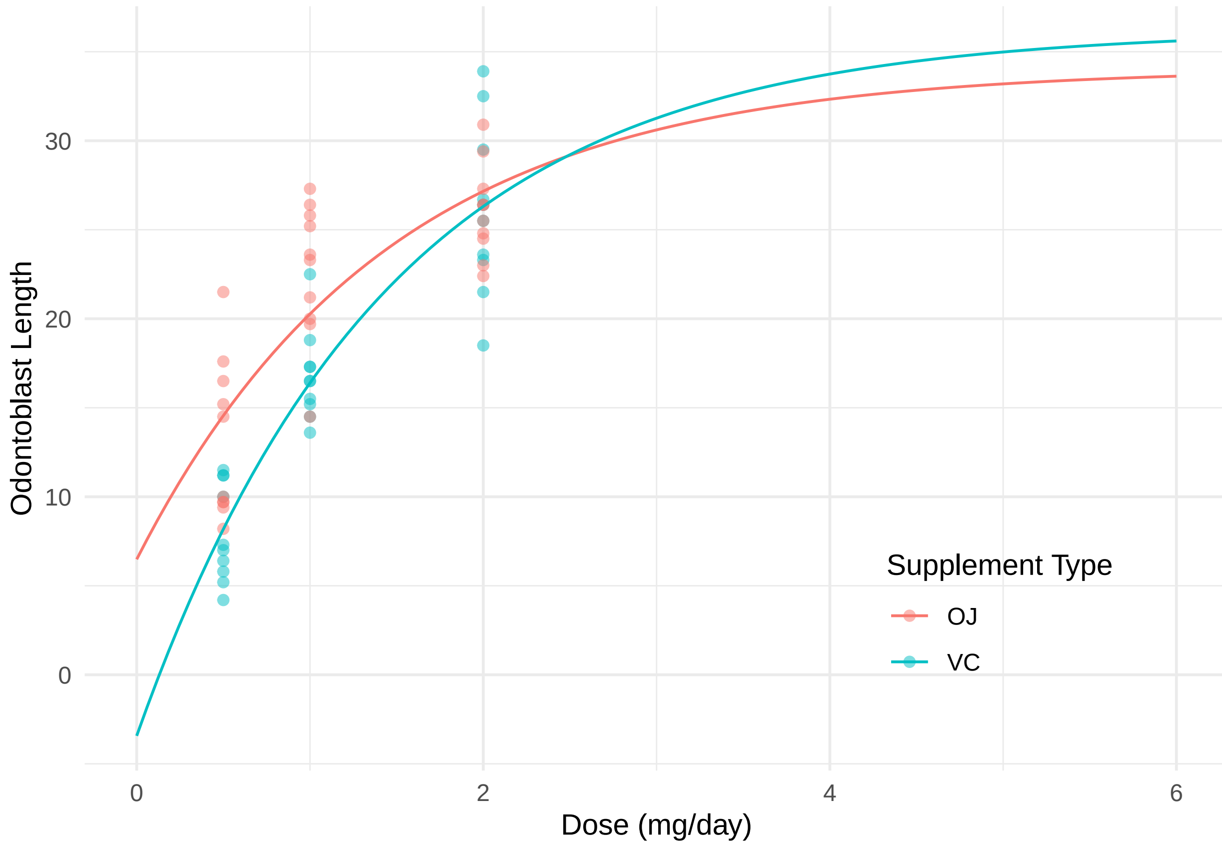
```r
m <- lm(len ~ I(2^(-dose/1)) + supp + supp:I(2^(-dose/1)), data = ToothGrowth)
summary(m)$coefficients
```

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

```
(Intercept)             34.054      1.925 17.6872 1.375e-24
I(2^(-dose/1))         -27.569      3.700 -7.4519 6.199e-10
suppVC                   2.169      2.723  0.7964 4.291e-01
I(2^(-dose/1)):suppVC  -12.083      5.232 -2.3094 2.463e-02
```

```r
d <- expand.grid(supp = c("OJ", "VC"), dose = seq(0, 6, length = 100))
d$yhat <- predict(m, newdata = d)

p <- ggplot(ToothGrowth, aes(x = dose, y = len, color = supp)) +
  geom_point(alpha = 0.5) + xlim(0,6) +
  geom_line(aes(y = yhat), data = d) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length",
    color = "Supplement Type") + theme_minimal() +
  theme(legend.position = c(0.8,0.2))
plot(p)
```



This model can be written as

$$E(Y_i) = \beta_0 + \beta_1 2^{-x_i/h} + \beta_2 d_i + \beta_3 d_i 2^{-x_i/h},$$

where $d_i = 1$ if the supplement type is VC, and $d_i = 0$ otherwise, and $h = 1$. We can also write this model case-wise as

$$E(Y_i) = \begin{cases} \beta_0 + \beta_1 2^{-x_i/h}, & \text{if the supplement type of the } i\text{-th observation is OJ,} \\ \beta_0 + \beta_2 + (\beta_1 + \beta_3) 2^{-x_i/h}, & \text{if the supplement type of the } i\text{-th observation is VC,} \end{cases}$$

or

$$E(Y_i) = \begin{cases} \beta_0 + \beta_1 2^{-x_i/h}, & \text{if the supplement type of the } i\text{-th observation is OJ,} \\ \gamma_0 + \gamma_1 2^{-x_i/h}, & \text{if the supplement type of the } i\text{-th observation is VC,} \end{cases}$$

where $\gamma_0 = \beta_0 + \beta_2$ and $\gamma_1 = \beta_1 + \beta_3$. We can make inferences for the intercepts and asymptotes for *each* supplement type using `lincon`.

```
lincon(m, a = c(1,1,0,0)) # b0 + b1 = intercept for OJ
```

```
             estimate    se lower upper tvalue df    pvalue
(1,1,0,0),0     6.485 2.024 2.429 10.54  3.203 56 0.002243
```

```
lincon(m, a = c(1,1,1,1)) # g0 + g1 = b0 + b2 + b1 + b3 = intercept for VC
```

```
             estimate    se  lower  upper tvalue df   pvalue
(1,1,1,1),0    -3.429 2.024 -7.485 0.6261 -1.694 56 0.09582
```

```
lincon(m, a = c(1,0,1,0)) # g0 = b0 + b2 = asymptote for VC
```

```
             estimate    se lower upper tvalue df    pvalue
(1,0,1,0),0     36.22 1.925 32.37 40.08  18.81 56 7.07e-26
```

We can also obtain (approximate) inferences using `contrast`.

```
contrast(m, a = list(dose = 0, supp = c("OJ","VC")),
    cname = c("OJ intercept","VC intercept"))
```

```
             estimate    se  lower   upper tvalue df   pvalue
OJ intercept    6.485 2.024  2.429 10.5401  3.203 56 0.002243
VC intercept   -3.429 2.024 -7.485  0.6261 -1.694 56 0.095824
```

```
contrast(m, a = list(dose = 100, supp = c("OJ","VC")),
    cname = c("OJ asymptote","VC asymptote"))
```

```
             estimate    se lower upper tvalue df    pvalue
OJ asymptote    34.05 1.925 30.20 37.91  17.69 56 1.375e-24
VC asymptote    36.22 1.925 32.37 40.08  18.81 56 7.070e-26
```

But wouldn't it make sense to have something like the following?

$$E(Y_i) = \begin{cases} \beta_0 + \beta_1 2^{-x_i/h_{\text{OJ}}}, & \text{if the supplement type of the } i\text{-th observation is OJ}, \\ \beta_0 + \beta_1 2^{-x_i/h_{\text{VC}}}, & \text{if the supplement type of the } i\text{-th observation is VC}, \end{cases}$$

because at $x = 0$ and as $x \to \infty$ there should be no difference in the supplement type, but there might be a difference in how "fast" the expected response increases with dose. But unless we *know* h_{OJ} and h_{VC}, this model would be *nonlinear* (i.e., the model is not linear if h_{OJ} and h_{VC} are *unknown parameters* as opposed to known values).