Friday, Feb 10

The Von Bertalanffy Growth Model

Consider the data frame `walleye` from the package **alr4**.

```
library(alr4)
head(walleye)
```

```
  age length period
1   1  215.3      1
2   1  193.3      1
3   1  202.6      1
4   1  201.5      1
5   1  232.0      1
6   1  191.0      1
```

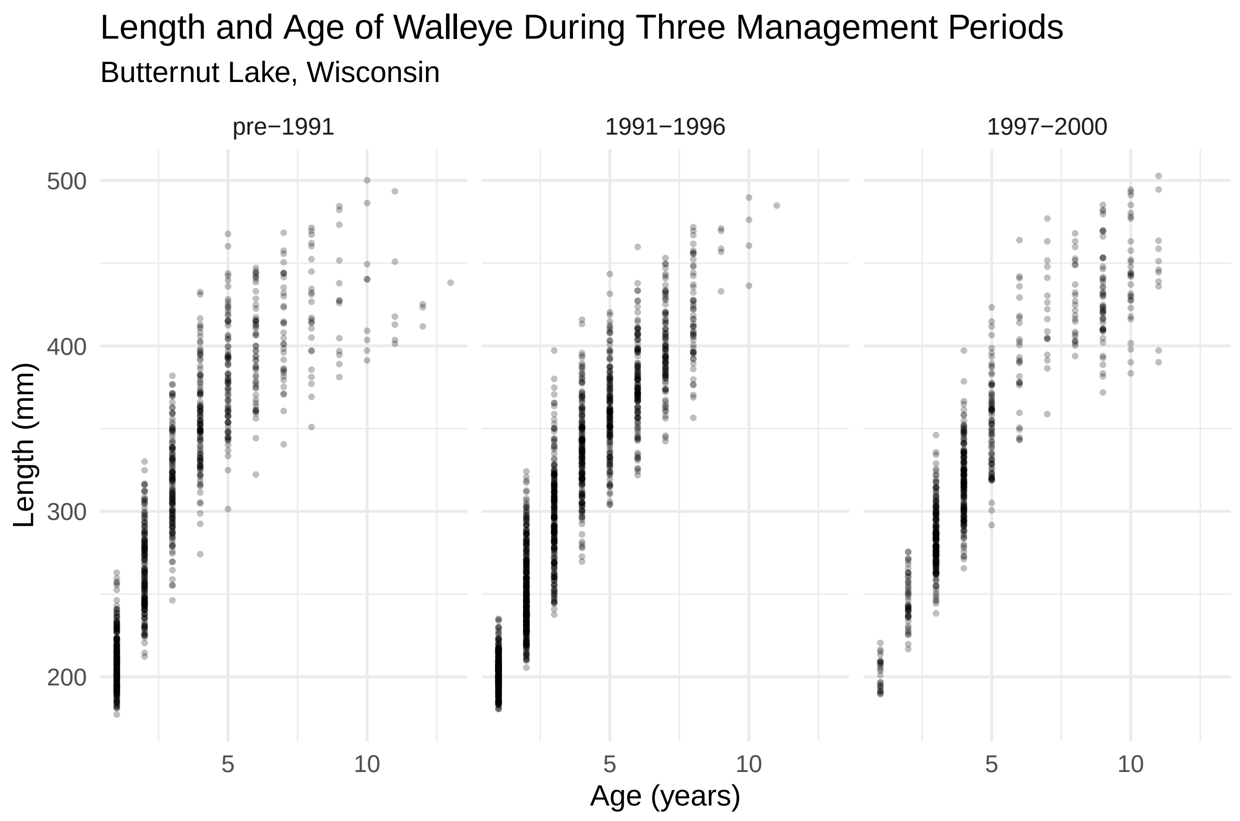
The `period` variable refers to three distinct management periods: pre 1990, 1991-1996, and 1997-2000. It will be useful to explicitly define that as a categorical variable (i.e., a `factor` in R) with descriptive category labels.

```
walleye$periodf <- factor(walleye$period, levels = c(1,2,3),
  labels = c("pre-1991","1991-1996","1997-2000"))
head(walleye)
```

```
  age length period  periodf
1   1  215.3      1 pre-1991
2   1  193.3      1 pre-1991
3   1  202.6      1 pre-1991
4   1  201.5      1 pre-1991
5   1  232.0      1 pre-1991
6   1  191.0      1 pre-1991
```

Let's visualize the data.

```
p <- ggplot(walleye, aes(y = length, x = age)) + facet_wrap(~ periodf) +
  theme_minimal() + geom_point(alpha = 0.25, size = 0.5) +
  labs(x = "Age (years)", y = "Length (mm)",
   title = "Length and Age of Walleye During Three Management Periods",
   subtitle = "Butternut Lake, Wisconsin",
   caption = "Source: Weisberg, S. (2014). Applied Linear Regression, 4th edition. Hoboken, NJ: Wiley.")
plot(p)
```



Source: Weisberg, S. (2014). Applied Linear Regression, 4th edition. Hoboken, NJ: Wiley.

A common nonlinear regression model for these kind of data is the Von Bertalanffy growth model. This model can be written many different ways. One that is similar to the exponential model we used earlier is

$$E(L) = \alpha + (\delta - \alpha)2^{-a/\gamma},$$

where L and a are length and age, respectively. The parameters can be interpreted as follows.

1. α is the asymptote of $E(L)$ as a increases.
2. δ is the value of $E(L)$ when $a = 0$.
3. γ is the value of a at which $E(L)$ is half way between δ and α.

Consider first a model in which there are no differences in the function between management periods. The starting values were obtained by "eyeballing" the plot.

```
m <- nls(length ~ alpha + (delta - alpha) * 2^(-age / gamma),
   data = walleye, start = list(alpha = 500, delta = 200, gamma = 5))
cbind(summary(m)$coefficients, confint(m))
```

```
      Estimate Std. Error t value  Pr(>|t|)    2.5%   97.5%
alpha  487.724     4.7688  102.27  0.00e+00 478.878 497.394
delta  140.729     2.0780   67.72  0.00e+00 136.654 144.732
gamma    3.424     0.1021   33.54 1.46e-211   3.236   3.632
```

Now suppose we want to allow the α and γ parameters to vary over management periods, but not δ. The model we want could be written case-wise as

$$E(L_i) = \begin{cases} \alpha_1 + (\delta - \alpha_1)2^{-a_i/\gamma_1}, & \text{if the } i\text{-th observation is from the first period,} \\ \alpha_2 + (\delta - \alpha_2)2^{-a_i/\gamma_2}, & \text{if the } i\text{-th observation is from the second period,} \\ \alpha_3 + (\delta - \alpha_3)2^{-a_i/\gamma_3}, & \text{if the } i\text{-th observation is from the third period.} \end{cases}$$

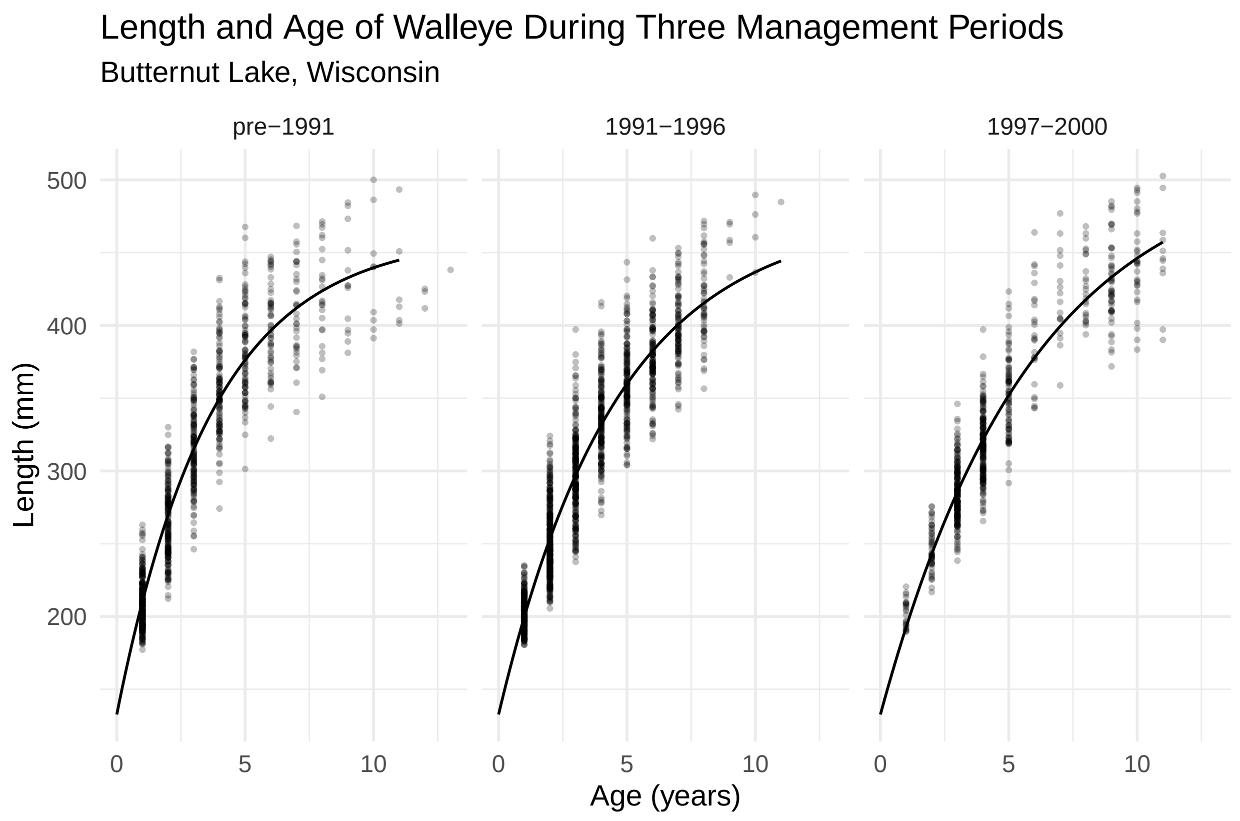
Perhaps the easiest way to specify this model is to use the `case_when` function from the **dplyr** package.

```
library(dplyr)
m <- nls(length ~ case_when(
  periodf == "pre-1991"  ~ alpha1 + (delta - alpha1) * 2^(-age / gamma1),
  periodf == "1991-1996" ~ alpha2 + (delta - alpha2) * 2^(-age / gamma2),
  periodf == "1997-2000" ~ alpha3 + (delta - alpha3) * 2^(-age / gamma3)
  ), start = list(alpha1 = 500, alpha2 = 500, alpha3 = 500,
    delta = 200, gamma1 = 5, gamma2 = 5, gamma3 = 5), data = walleye)
cbind(summary(m)$coefficients, confint(m))
```

```
       Estimate Std. Error t value   Pr(>|t|)    2.5%   97.5%
alpha1  461.912    4.82053   95.82  0.000e+00 453.119 471.429
alpha2  475.839    6.30129   75.51  0.000e+00 464.110 489.135
alpha3  516.907    7.76416   66.58  0.000e+00 502.581 532.897
delta   132.667    2.22347   59.67  0.000e+00 128.307 136.939
gamma1    2.574    0.08383   30.70 1.299e-181   2.423   2.740
gamma2    3.194    0.12046   26.51 3.746e-140   2.971   3.448
gamma3    4.095    0.15206   26.93 4.080e-144   3.817   4.410
```

```
d <- expand.grid(age = seq(0, 11, length = 100),
   periodf = levels(walleye$periodf))
d$yhat <- predict(m, newdata = d)

p <- ggplot(walleye, aes(y = length, x = age)) + facet_wrap(~ periodf) +
  theme_minimal() + geom_point(alpha = 0.25, size = 0.5) +
  geom_line(aes(y = yhat), data = d) +
  labs(x = "Age (years)", y = "Length (mm)",
   title = "Length and Age of Walleye During Three Management Periods",
   subtitle = "Butternut Lake, Wisconsin",
   caption = "Source: Weisberg, S. (2014). Applied Linear Regression, 4th edition. Hoboken, NJ: Wiley.")
plot(p)
```



Source: Weisberg, S. (2014). Applied Linear Regression, 4th edition. Hoboken, NJ: Wiley.

Here `summary` and `confint` provide inferences for each parameter in each period, but do not provide inferences about the *differences* in the parameters *between* periods. But we can use `lincon` to do this. Suppose we wanted to compare the second and third periods with the first.

```
library(trtools) # for lincon
lincon(m, a = c(-1,1,0,0,0,0,0)) # alpha2 - alpha1
```

```
                   estimate    se lower upper tvalue   df  pvalue
(-1,1,0,0,0,0,0),0    13.93 6.758 0.675 27.18  2.061 3191 0.03942
```

```
lincon(m, a = c(-1,0,1,0,0,0,0)) # alpha3 - alpha1
```

```
                   estimate    se lower upper tvalue   df   pvalue
(-1,0,1,0,0,0,0),0    54.99 8.449 38.43 71.56  6.509 3191 8.75e-11
```

```
lincon(m, a = c(0,0,0,0,-1,1,0)) # gamma2 - gamma1
```

```
                   estimate     se  lower  upper tvalue   df    pvalue
(0,0,0,0,-1,1,0),0   0.6199 0.1061 0.4118 0.8281   5.84 3191 5.736e-09
```

```
lincon(m, a = c(0,0,0,0,-1,0,1)) # gamma3 - gamma1
```

```
                   estimate    se lower upper tvalue   df    pvalue
(0,0,0,0,-1,0,1),0    1.521 0.145 1.237 1.805  10.49 3191 2.372e-25
```

Sometimes it is helpful to write the model as a *function* to keep the code tidy. We can program the function

$$E(L) = \alpha + (\delta - \alpha)2^{-a/\gamma}$$

as follows.

```r
vbf <- function(age, alpha, delta, gamma) {
  alpha + (delta - alpha) * 2^(-age / gamma)
}
```

Now we can use `vbf` in `nls`.

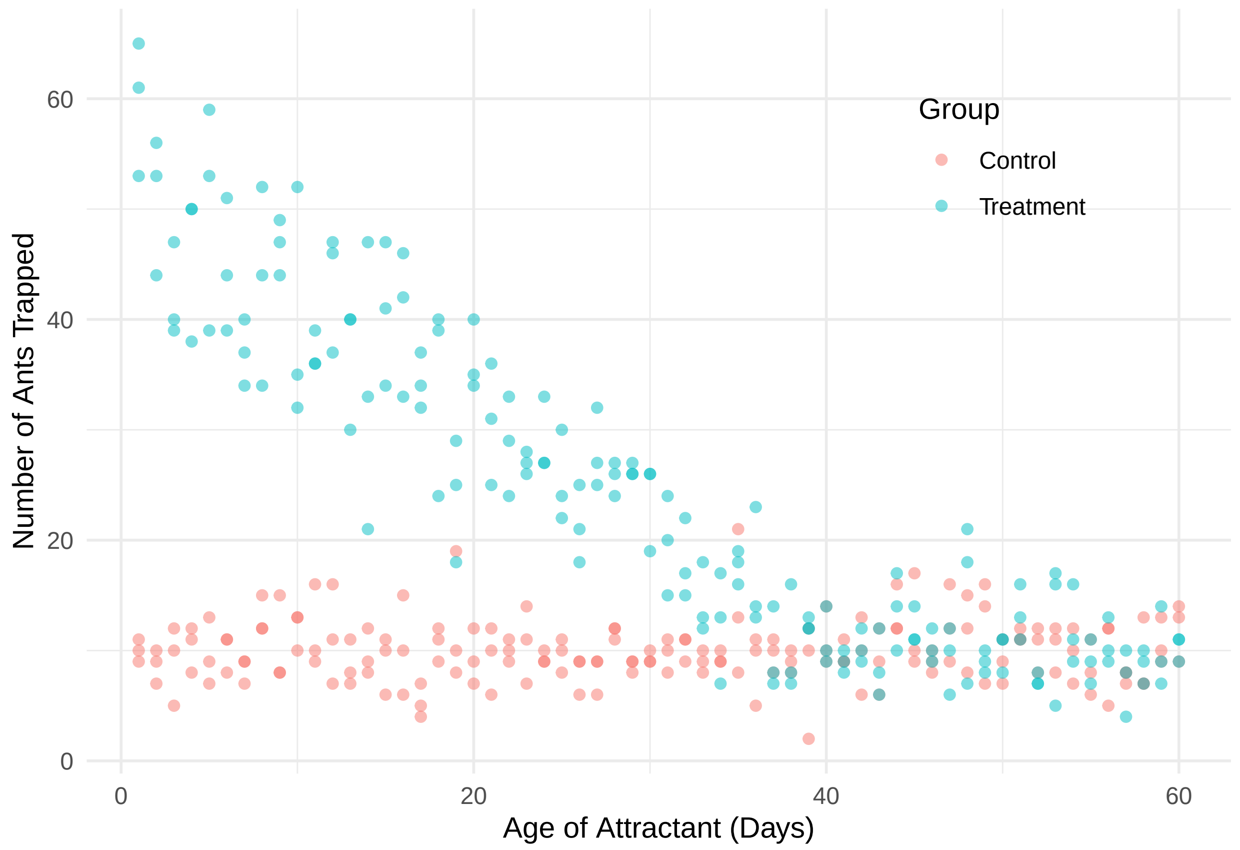
```r
m <- nls(length ~ case_when(
  periodf == "pre-1991"  ~ vbf(age, alpha1, delta, gamma1),
  periodf == "1991-1996" ~ vbf(age, alpha2, delta, gamma2),
  periodf == "1997-2000" ~ vbf(age, alpha3, delta, gamma3)
  ), start = list(alpha1 = 500, alpha2 = 500, alpha3 = 500,
    delta = 200, gamma1 = 5, gamma2 = 5, gamma3 = 5), data = walleye)
cbind(summary(m)$coefficients, confint(m))
```

```
       Estimate Std. Error t value   Pr(>|t|)    2.5%   97.5%
alpha1  461.912    4.82053   95.82  0.000e+00 453.119 471.429
alpha2  475.839    6.30129   75.51  0.000e+00 464.110 489.135
alpha3  516.907    7.76416   66.58  0.000e+00 502.581 532.897
delta   132.667    2.22347   59.67  0.000e+00 128.307 136.939
gamma1    2.574    0.08383   30.70 1.299e-181   2.423   2.740
gamma2    3.194    0.12046   26.51 3.746e-140   2.971   3.448
gamma3    4.095    0.15206   26.93 4.080e-144   3.817   4.410
```

Segmented Regression as a Linear Model

Consider data from a study of the effect of attractant age on attracting fire ants.

```r
library(trtools) # for fireants data
p <- ggplot(fireants, aes(x = day, y = count, color = group)) +
  geom_point(alpha = 0.5) + theme_minimal() +
  theme(legend.position = c(0.8,0.8)) +
  labs(x = "Age of Attractant (Days)", y = "Number of Ants Trapped",
   color = "Group")
plot(p)
```



Consider first this model for only the treatment group:

$$E(Y_i) = \beta_0 + \beta_1 x_i + \beta_2 I(x_i < \delta)(x_i - \delta),$$

where Y_i and x_i are the fire ant count and age of attractant, respectively, and I is an *indicator function* defined as

$$I(x_i < \delta) = \begin{cases} 1, & \text{if } x_i < \delta, \\ 0, & \text{if } x_i \geq \delta. \end{cases}$$

In general, an indicator function is a function such that

$$I(\text{statement}) = \begin{cases} 1, & \text{if the statement is true,} \\ 0, & \text{if the statement is false.} \end{cases}$$

Note: Don't confuse the *indicator function* I with the "inhibit" function `I` in R. An *indicator function* is a *mathematical function* that returns a 1 or 0 depending on if its argument is true or false, respectively. The inhibit function is a R function that is used to force R to treat something "as is" — usually in a model formula argument.

Writing the model case-wise for $x_i < \delta$ versus $x_i \geq \delta$ we have

$$E(Y_i) = \begin{cases} \beta_0 - \beta_2\delta + (\beta_1 + \beta_2)x_i, & \text{if } x_i < \delta, \\ \beta_0 + \beta_1 x_i, & \text{if } x_i \geq \delta. \end{cases}$$

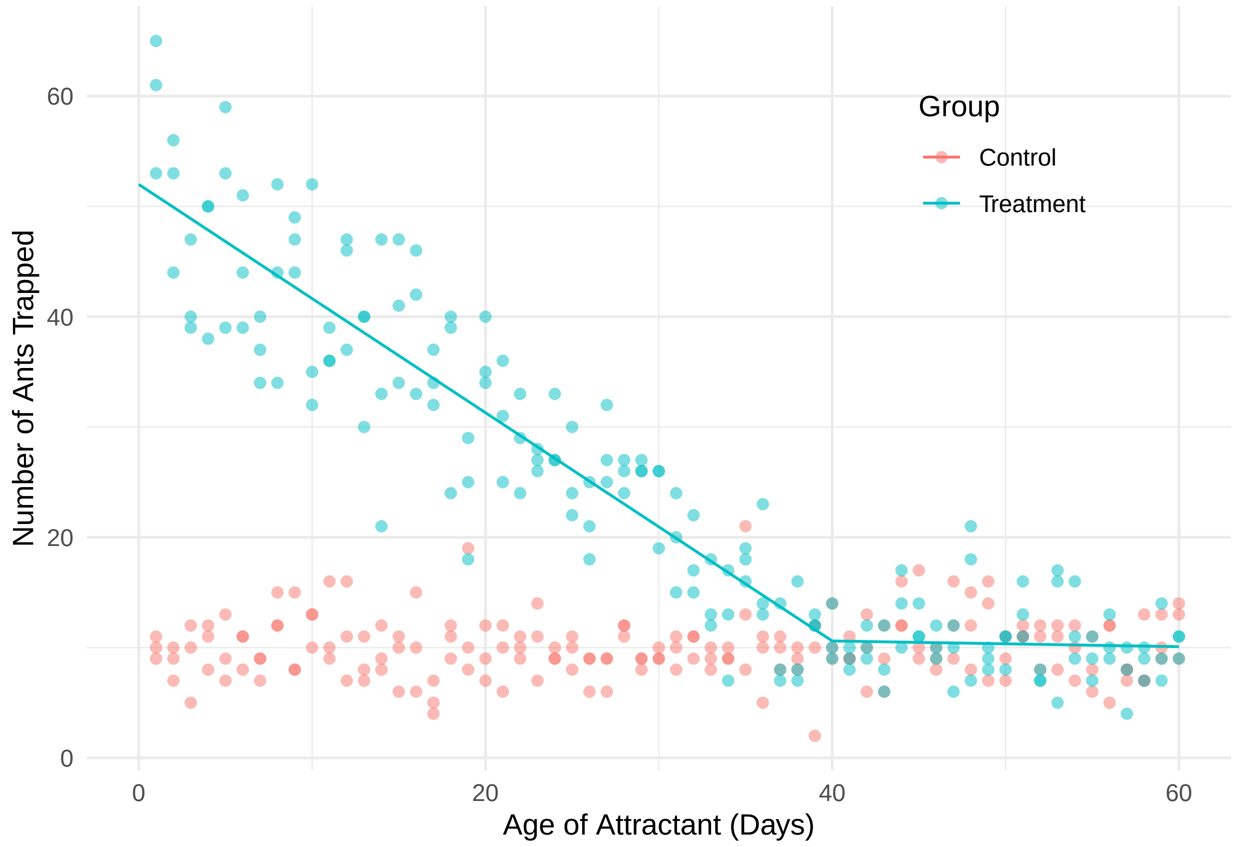
This is sometimes called *segmented*, *piece-wise*, or *broken-stick* regression. It is also a special case of a *spline*. The δ is called a "knot" of the spline. If the knot is known then this is a *linear* model.

```r
treated <- subset(fireants, group == "Treatment")
m <- lm(count ~ day + I((day < 40)*(day - 40)), data = treated)
summary(m)$coefficients
```

```
                           Estimate Std. Error t value  Pr(>|t|)
(Intercept)                11.62723    3.74415  3.1054 2.213e-03
day                        -0.02574    0.07898 -0.3259 7.449e-01
I((day < 40) * (day - 40)) -1.00914    0.10389 -9.7138 3.798e-18
```

Note that we can write the indicator function $I(x_i < 40)$ as `(day < 40)` in R.

```r
d <- expand.grid(day = seq(0, 60, length = 100), group = "Treatment")
d$yhat <- predict(m, newdata = d)
p <- p + geom_line(aes(y = yhat), data = d)
plot(p)
```



Now it would be useful to extend the model to include the control group, but subject to a couple of constraints:

1. The relationship between expected count and age for the *control* group should not have a break (because there is no attractant to wear off).
2. After 40 days the relationship between expected count and age should be *identical* for the control and treatment groups (because the attractant has worn off).

Here's a model that will accomplish that:

$$E(Y_i) = \beta_0 + \beta_1 x_i + \beta_2 I(x_i < \delta)(x_i - \delta)g_i,$$

where

$$g_i = \begin{cases} 1, & \text{if the } i\text{-th observation is from the treatment group,} \\ 0, & \text{otherwise,} \end{cases}$$

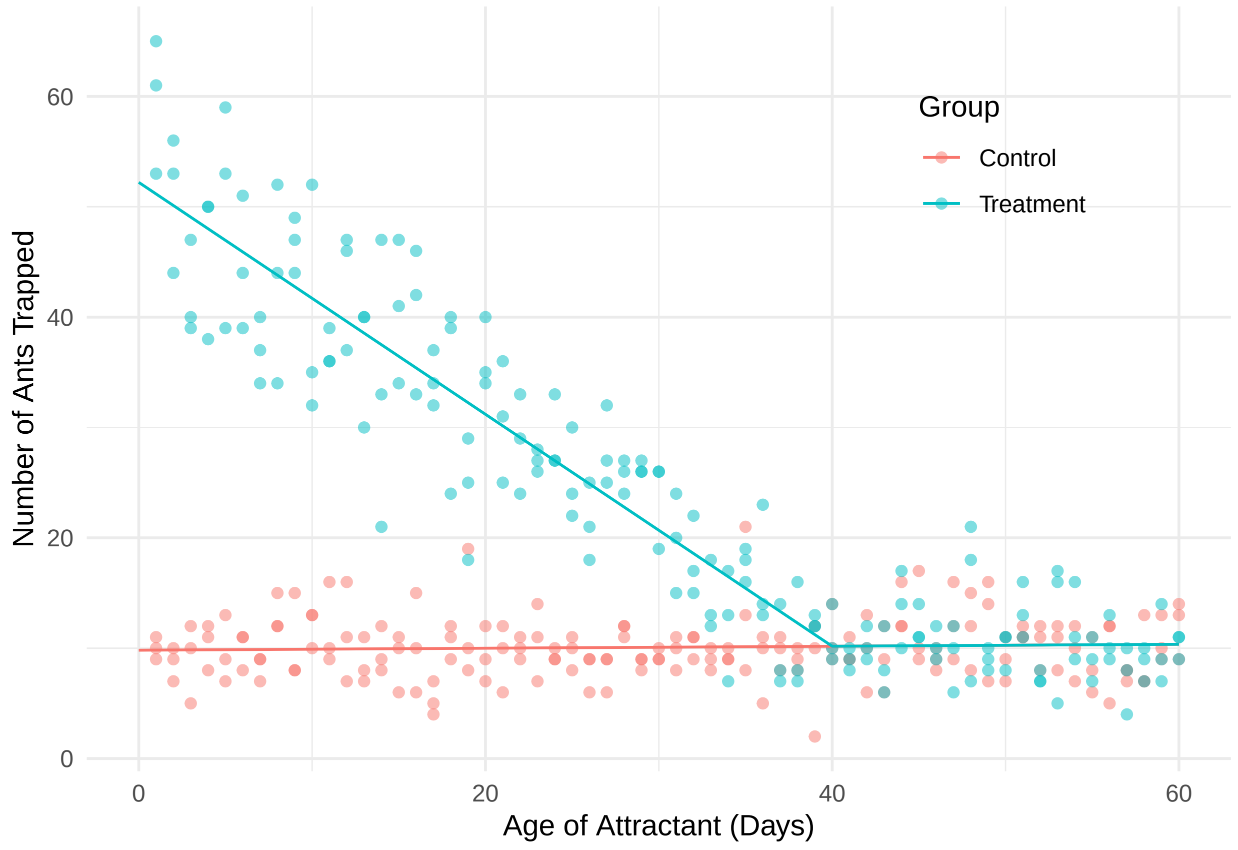
so that the model can be written as

$$E(Y_i) = \begin{cases} \beta_0 - \beta_2\delta + (\beta_1 + \beta_2)x_i, & \text{if the } i\text{-th observation is from the treatmnt group and } x_i < \delta, \\ \beta_0 + \beta_1 x_i, & \text{otherwise.} \end{cases}$$

```r
m <- lm(count ~ day + I((day < 40)*(day - 40)*(group == "Treatment")),
   data = fireants)

d <- expand.grid(day = seq(0, 60, length = 100),
   group = c("Control","Treatment"))
d$yhat <- predict(m, newdata = d)

p <- ggplot(fireants, aes(x = day, y = count, color = group)) +
  geom_point(alpha = 0.5) + theme_minimal() +
  theme(legend.position = c(0.8,0.8)) +
  labs(x = "Age of Attractant (Days)",
   y = "Number of Ants Trapped", color = "Group") +
  geom_line(aes(y = yhat), data = d)
plot(p)
```



Now we can make some inferences.

```r
# expected counts at day 0
contrast(m, a = list(group = c("Control","Treatment"), day = 0),
  cnames = c("Control","Treatment"))
```

```
          estimate     se  lower upper tvalue  df     pvalue
Control      9.819 0.5982  8.642 11.00  16.41 357  1.665e-45
Treatment   52.211 0.6770 50.880 53.54  77.12 357 1.145e-224
```

```
# expected counts at day 40
contrast(m, a = list(group = c("Control","Treatment"), day = 40),
  cnames = c("Control","Treatment"))
```

```
          estimate     se lower upper tvalue  df     pvalue
Control      10.18 0.2573 9.671 10.68  39.56 357 1.523e-132
Treatment    10.18 0.2573 9.671 10.68  39.56 357 1.523e-132
```

```
# slopes before day 40
contrast(m,
  a = list(group = c("Control","Treatment"), day = 1),
  b = list(group = c("Control","Treatment"), day = 0),
  cnames = c("Control","Treatment"))
```

```
           estimate      se    lower    upper   tvalue  df     pvalue
Control    0.008954 0.01509 -0.02072  0.03863   0.5935 357  5.532e-01
Treatment -1.050865 0.01926 -1.08873 -1.01299 -54.5726 357 2.658e-175
```

```
# slopes after day 40
contrast(m,
  a = list(group = c("Control","Treatment"), day = 41),
  b = list(group = c("Control","Treatment"), day = 40),
  cnames = c("Control","Treatment"))
```

```
          estimate      se    lower   upper tvalue  df pvalue
Control   0.008954 0.01509 -0.02072 0.03863 0.5935 357 0.5532
Treatment 0.008954 0.01509 -0.02072 0.03863 0.5935 357 0.5532
```

```
# difference in expected counts at day 20
contrast(m,
  a = list(group = "Treatment", day = 20),
  b = list(group = "Control", day = 20))
```

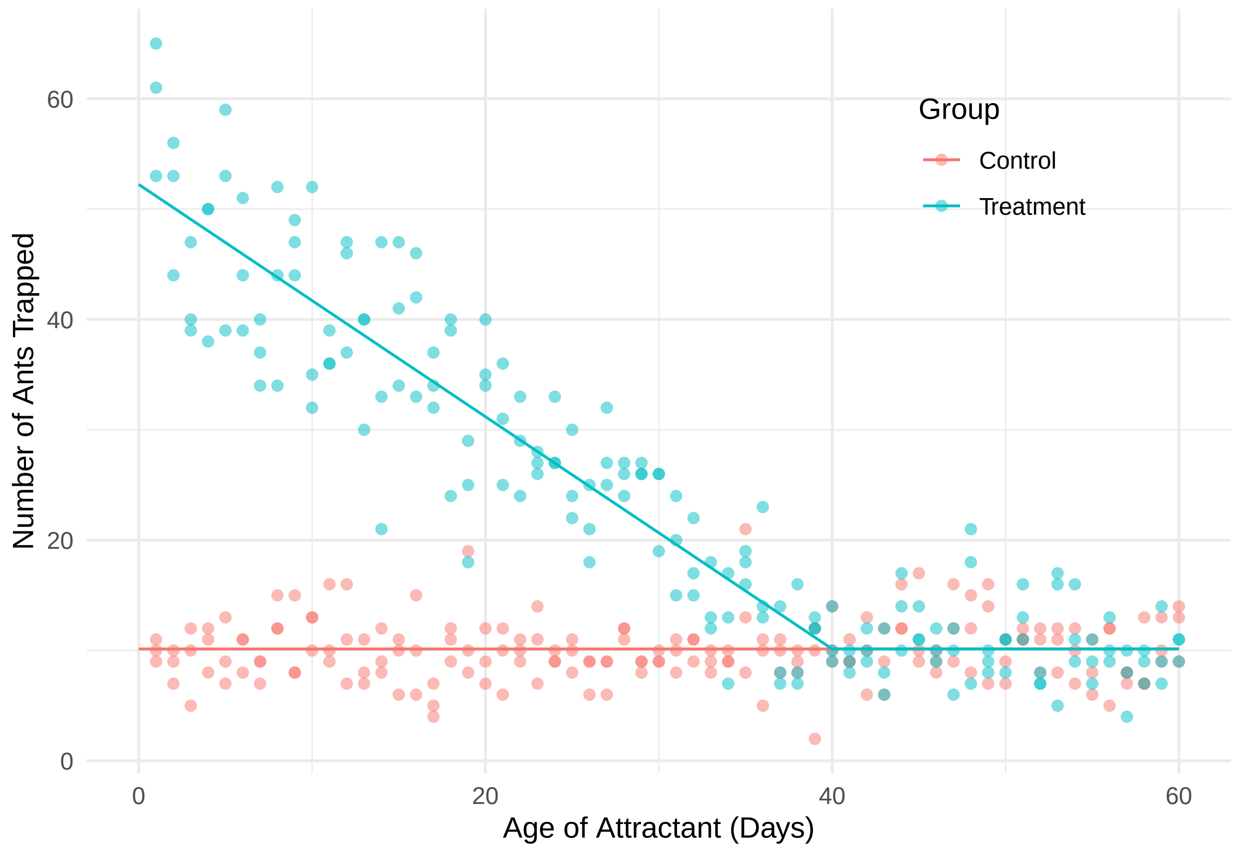
```
 estimate     se lower upper tvalue  df     pvalue
     21.2 0.4602 20.29  22.1  46.05 357 2.908e-152
```

We could go one step further by assuming that for the control group and after the knot the expected count is constant. This would require us to drop the term $\beta_1 x_i$.

```
m <- lm(count ~ I((day < 40) * (day - 40) *
   (group == "Treatment")), data = fireants)

d <- expand.grid(day = seq(0, 60, length = 100),
   group = c("Control","Treatment"))
d$yhat <- predict(m, newdata = d)

p <- ggplot(fireants, aes(x = day, y = count, color = group)) +
  geom_point(alpha = 0.5) + theme_minimal() +
  theme(legend.position = c(0.8,0.8)) +
  labs(x = "Age of Attractant (Days)",
    y = "Number of Ants Trapped", color = "Group") +
  geom_line(aes(y = yhat), data = d)
plot(p)
```



Now consider the following inferences.

```
# slopes before day 40
contrast(m,
  a = list(group = c("Control","Treatment"), day = 1),
  b = list(group = c("Control","Treatment"), day = 0),
  cnames = c("Control","Treatment"))
```

```
          estimate     se lower  upper tvalue  df     pvalue
Control      0.000 0.0000  0.00  0.000    NaN 358        NaN
Treatment   -1.052 0.0191 -1.09 -1.015 -55.08 358 7.001e-177
```

```
# slopes after day 40
contrast(m,
  a = list(group = c("Control","Treatment"), day = 41),
  b = list(group = c("Control","Treatment"), day = 40),
  cnames = c("Control","Treatment")) # slopes after day 40
```

```
          estimate se lower upper tvalue  df pvalue
Control          0  0     0     0    NaN 358    NaN
Treatment        0  0     0     0    NaN 358    NaN
```

Segmented Regression as a Nonlinear Model

If the knot δ is *known* then the model is *linear*. We can write

$$E(Y_i) = \beta_0 + \beta_1 x_i + \beta_2 I(x_i < \delta)(x_i - \delta)g_i$$

as

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

where $x_{i1} = x_i$ (day) and $x_{i2} = I(x_i < \delta)(x_i - \delta)g_i$, provided we *know* δ. But what if δ is unknown and is to be estimated? Then we have a *nonlinear* model.

Let's start estimating a *linear* model with `nls` by guessing the value of δ. This will give us some good starting values.

```r
m <- nls(count ~ b0 + b1 * day + b2 * (day < 40) * (day - 40) *
   (group == "Treatment"), data = fireants,
   start = list(b0 = 0, b1 = 1, b2 = 1))
cbind(summary(m)$coefficients, confint(m))
```

```
    Estimate Std. Error  t value   Pr(>|t|)     2.5%    97.5%
b0  9.818633    0.59822  16.4131  1.665e-45  8.64216 10.99511
b1  0.008954    0.01509   0.5935  5.532e-01 -0.02072  0.03863
b2 -1.059819    0.02301 -46.0541 2.908e-152 -1.10508 -1.01456
```

Now consider a model where the knot (δ) is a *parameter*, using the estimate from the linear model as starting values.

```r
m <- nls(count ~ b0 + b1 * day + b2 * (day < delta) * (day - delta) *
   (group == "Treatment"), data = fireants,
   start = list(b0 = 10, b1 = 0, b2 = -1, delta = 40))
cbind(summary(m)$coefficients, confint(m))
```

```
       Estimate Std. Error  t value   Pr(>|t|)     2.5%    97.5%
b0     9.807069    0.60056  16.3298  3.885e-45  8.62598 10.98816
b1     0.008604    0.01516   0.5674  5.708e-01 -0.02122  0.03843
b2    -1.052444    0.03597 -29.2590  9.772e-97 -1.12822 -0.98318
delta 40.200079    0.75454  53.2776 1.061e-171 38.60885 41.69578
```

The `contrast` function does not work with a `nls` object, but we can use `lincon` provided that the quantity of interest is a linear combination of parameters. For example, recall that the model can be written as

$$E(Y_i) = \begin{cases} \beta_0 - \beta_2\delta + (\beta_1 + \beta_2)x_i, & \text{if } x_i < \delta \text{ and treatment,} \\ \beta_0 + \beta_1 x_i, & \text{otherwise,} \end{cases}$$

so the slope before the knot for the treatment group is $\beta_1 + \beta_2$. This can be written as

$$\ell = a_0\beta_0 + a_1\beta_1 + a_2\beta_2 + a_3\delta + b$$

where $a_0 = 0$, $a_1 = 1$, $a_2 = 1$, $a_3 = 0$, and $b = 0$.

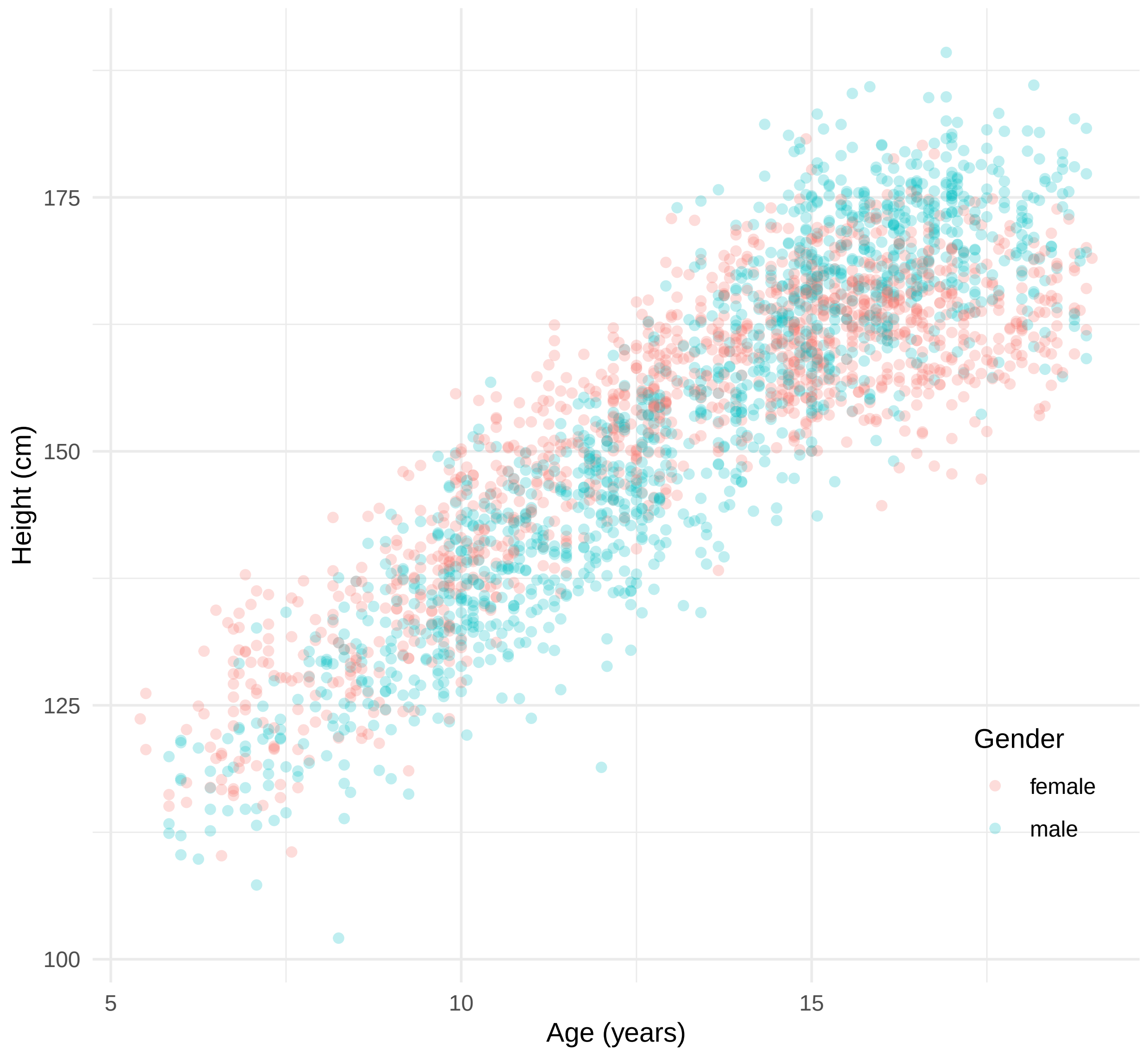
```r
# slope before knot for treatment group
lincon(m, a = c(0, 1, 1, 0))
```

```
             estimate      se  lower   upper tvalue  df     pvalue
(0,1,1,0),0    -1.044 0.03262 -1.108 -0.9797    -32 356 8.718e-107
```

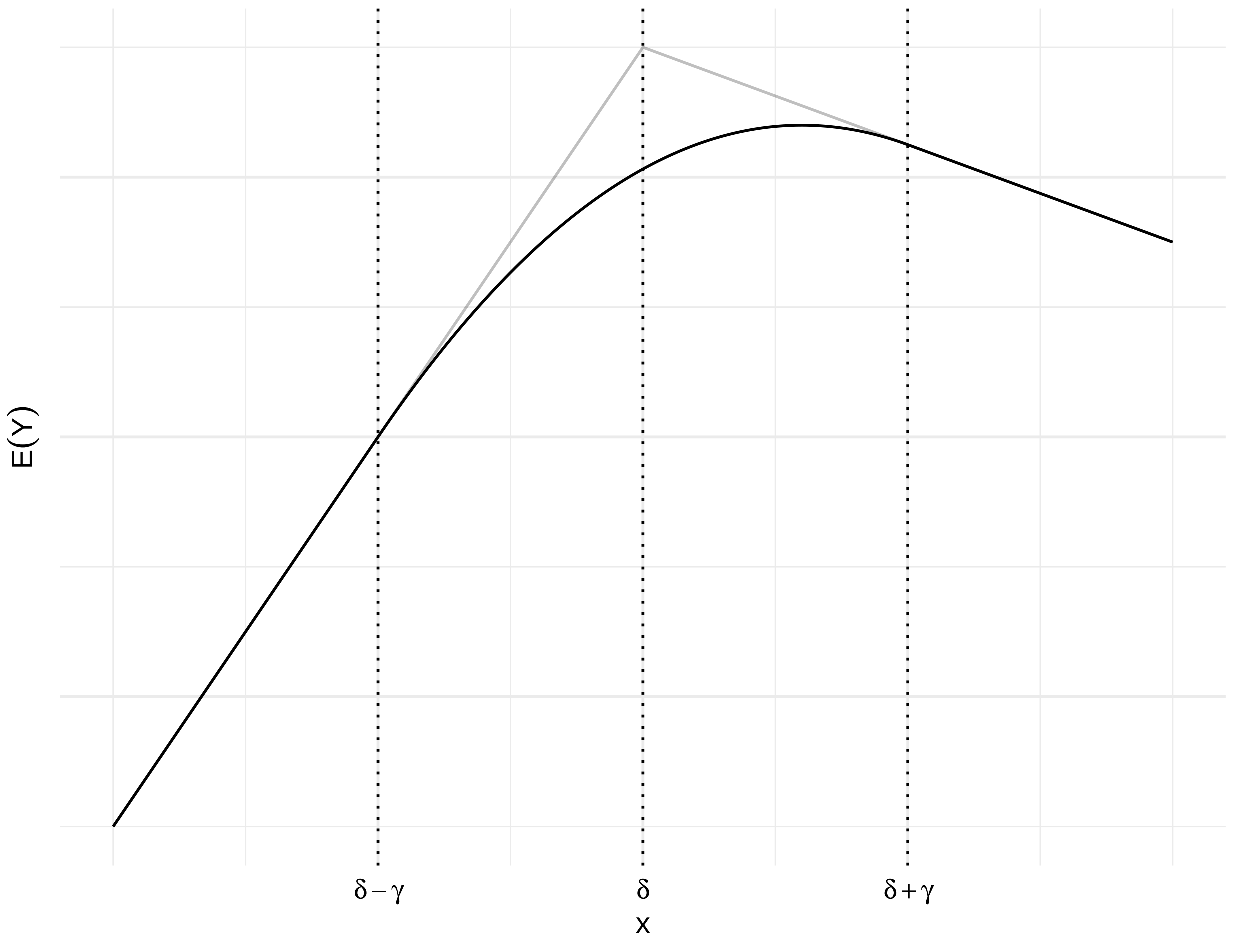
Bent Cable Regression

The data frame `children` in the package **npregfast** contains 2500 observations of the age and height of children.

```r
library(ggplot2)
library(npregfast)
p <- ggplot(children, aes(x = age, y = height, color = sex)) +
  geom_point(alpha = 0.25) + theme_minimal() +
  labs(x = "Age (years)", y = "Height (cm)", color = "Gender") +
  theme(legend.position = c(0.9,0.2))
plot(p)
```



The “bent cable” regression model can be used as kind of crude growth model for these data. It can be viewed as a generalization of the segmented regression model where rather than having two lines meet at a sharp angle, one line gradually transitions into the other by attaching them by what looks like a bent cable. The figure below shows a bent cable model.



The grey lines show a segmented regression model while the solid curve shows a bent cable model. Essentially there are two lines: one line to the left of $\delta - \gamma$ and one line to the right of $\delta + \gamma$. And between the two lines (i.e., between $\delta - \gamma$ and $\delta + \gamma$) is a quadratic polynomial that joins the two lines in such a way that the whole piece-wise function is smooth. The parameter δ represents the point at which the two lines would meet if there was no bend, and γ is the half of the distance between the points $\delta - \gamma$ and $\delta + \gamma$. As γ gets closer to zero this function approaches a segmented regression model (as shown by the grey lines).

The bent cable regression model can be written as

$$E(Y) = \beta_0 + \beta_1 x + \beta_2 q(x, \delta, \gamma),$$

where $q(x, \delta, \gamma)$ is a function defined as

$$q(x, \delta, \gamma) = \frac{(x - \delta + \gamma)^2}{4\gamma} I(\delta - \gamma \le x \le \delta + \gamma) + I(x > \delta + \gamma)(x - \delta).$$

This can be written case-wise as

$$E(Y) = \begin{cases} \beta_0 + \beta_1 x, & \text{if } x < \delta - \gamma, \\ \beta_0 + \beta_1 x + \beta_2 \frac{(x_i - \delta + \gamma)^2}{4\gamma}, & \text{if } \delta - \gamma \le x \le \delta + \gamma, \\ \beta_0 - \delta\beta_2 + (\beta_1 + \beta_2)x, & \text{if } x > \delta + \gamma. \end{cases}$$

So when $x < \delta - \gamma$ we have a line with intercept β_0 and slope β_1, and after $x > \delta + \gamma$ we have another line with intercept $\beta_0 - \delta\beta_2$ and slope $\beta_1 + \beta_2$. Between $\delta - \gamma$ and $\delta + \gamma$ is what is basically a quadratic regression model. And all three functions are constrained so that they form one smooth and continuous function.

Given the complexity of the function $q(x, \delta, \gamma)$, it is useful to program it.

```
q <- function(x, delta, gamma) {
  (x - delta + gamma)^2 / (4 * gamma) *
    (delta - gamma <= x & x <= delta + gamma) +
    (x > (delta + gamma)) * (x - delta)
}
```

First I will estimate a *linear* model with crude guesses of δ and γ.

```
m <- nls(height ~ b0 + b1 * age + b2 * q(age, 15, 1), data = children,
   start = list(b0 = 0, b1 = 0, b2 = 0))
   summary(m)$coefficients
```

```
   Estimate Std. Error t value Pr(>|t|)
b0   84.886    0.80646  105.26 0.00e+00
b1    5.320    0.06612   80.46 0.00e+00
b2   -4.172    0.21769  -19.16 1.78e-76
```

Next we can use the estimates of β_0, β_1, and β_2 as starting values in a nonlinear model.

```
m <- nls(height ~ b0 + b1 * age + b2 * q(age, delta, gamma), data = children,
   start = list(b0 = 85, b1 = 5.3, b2 = -5, delta = 15, gamma = 1))
summary(m)$coefficients
```

```
      Estimate Std. Error t value  Pr(>|t|)
b0      85.898    0.95916  89.555 0.000e+00
b1       5.217    0.08468  61.613 0.000e+00
b2      -5.239    0.68653  -7.631 3.297e-14
delta   15.662    0.27560  56.828 0.000e+00
gamma    1.483    0.51344   2.889 3.897e-03
```

The slope after the bend is $\beta_1 + \beta_2$, but if $\beta_2 = -\beta_1$ then the slope after the bend would be zero. This model would then be

$$E(Y) = \beta_0 + \beta_1 x - \beta_1 q(x, \delta, \gamma).$$

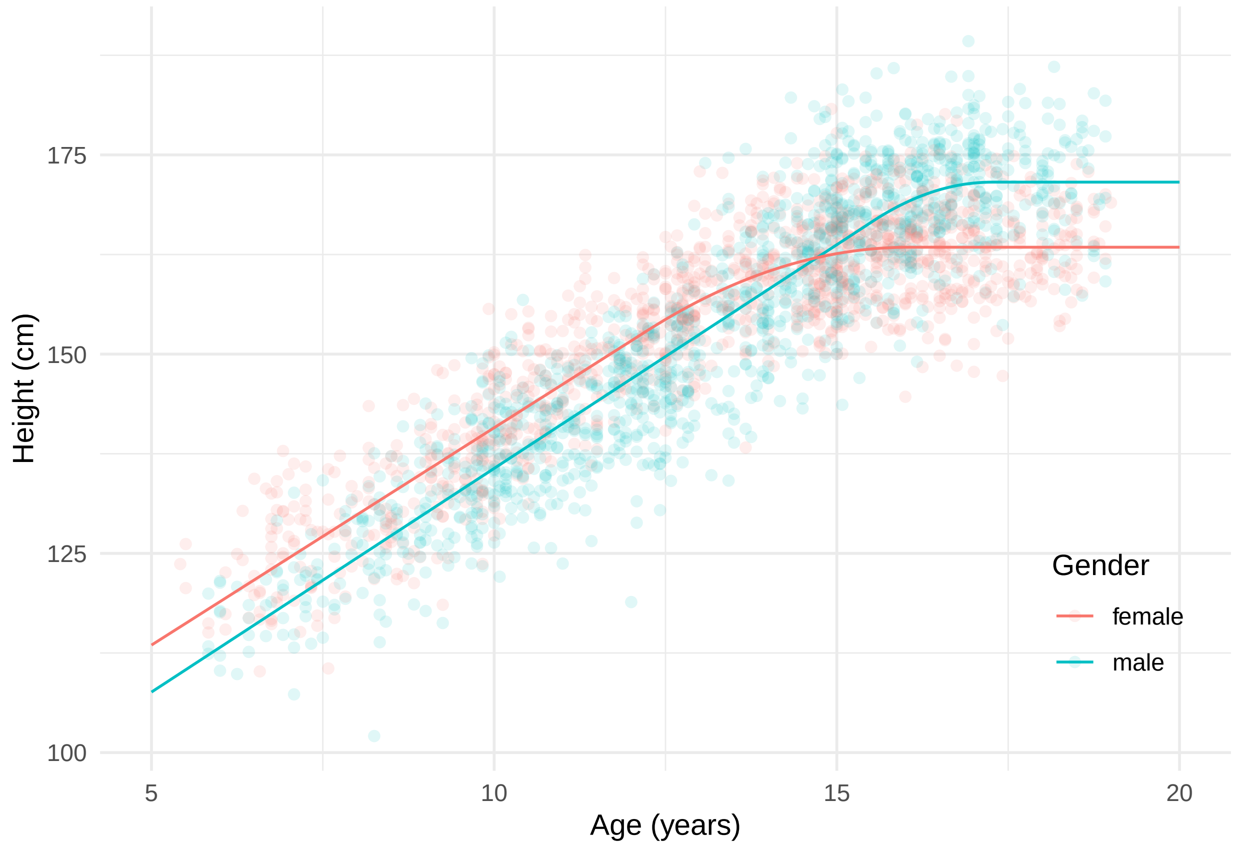
Let's consider using this model but now with a separate growth curve for males and females.

```
m <- nls(height ~ case_when(
   sex == "male"   ~ b0m + b1m*age - b1m*q(age, deltam, gammam),
   sex == "female" ~ b0f + b1f*age - b1f*q(age, deltaf, gammaf)),
   data = children, start = list(b0m = 86, b0f = 86, b1m = 5, b1f = 5,
   deltam = 15, deltaf = 15, gammam = 1.5, gammaf = 1.5))
summary(m)$coefficients
```

```
       Estimate Std. Error t value   Pr(>|t|)
b0m     79.5271    1.04815  75.874  0.000e+00
b0f     86.2213    1.65345  52.146  0.000e+00
b1m      5.6137    0.08511  65.959  0.000e+00
b1f      5.4542    0.16443  33.171 3.665e-200
deltam  16.3983    0.12218 134.209  0.000e+00
deltaf  14.1533    0.14833  95.416  0.000e+00
gammam   0.8673    0.49692   1.745  8.105e-02
gammaf   1.9069    0.43727   4.361  1.348e-05
```

```
d <- expand.grid(sex = c("male","female"), age = seq(5, 20, length = 200))
d$yhat <- predict(m, newdata = d)

p <- ggplot(children, aes(x = age, y = height, color = sex)) +
  geom_point(alpha = 0.125) + theme_minimal() +
  geom_line(aes(y = yhat), data = d) +
  labs(x = "Age (years)", y = "Height (cm)", color = "Gender") +
  theme(legend.position = c(0.9,0.2))
plot(p)
```


Height (cm)
Age (years)
Gender
female
male