Wednesday, Feb 22

Iteratively Weighted Least Squares

Iteratively weighted least squares can be used when we assume that the variance is proportional to a function of the mean so that

$$\mathrm{Var}(Y_i) \propto h[E(Y_i)],$$

where h is some specified function, implying that our weights should be

$$w_i = \frac{1}{h[E(Y_i)]}.$$

Because $E(Y_i)$ is unknown we can use the estimate $\hat{y}_i$ to obtain weights

$$w_i = \frac{1}{h(\hat{y}_i)}.$$

Because $\hat{y}_i$ depends on the weights used in the weighted least squares algorithm, and w_i depends on $\hat{y}_i$, we can use the following algorithm known as *iteratively weighted least squares*.

1. Estimate the model using *ordinary least squares* where all $w_i = 1$.
2. Compute weights as $w_i = 1/h(\hat{y}_i)$.
3. Estimate the model using *weighted least squares* with the weights $w_i = 1/h(\hat{y}_i)$.

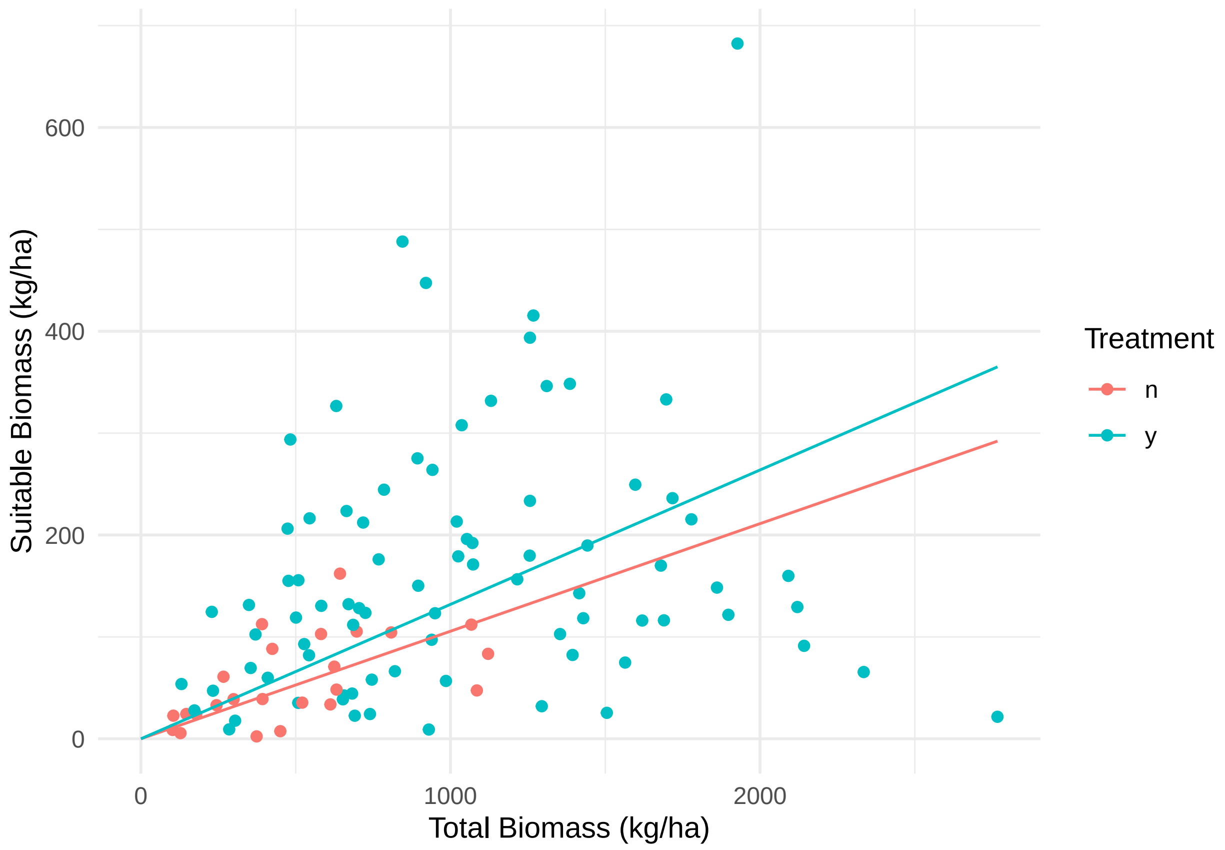
The second and third steps can be repeated until the estimates and thus the weights stop changing. Typically only a few iterations are necessary.

Example: Consider again following data from a study on the effects of fuel reduction on biomass.

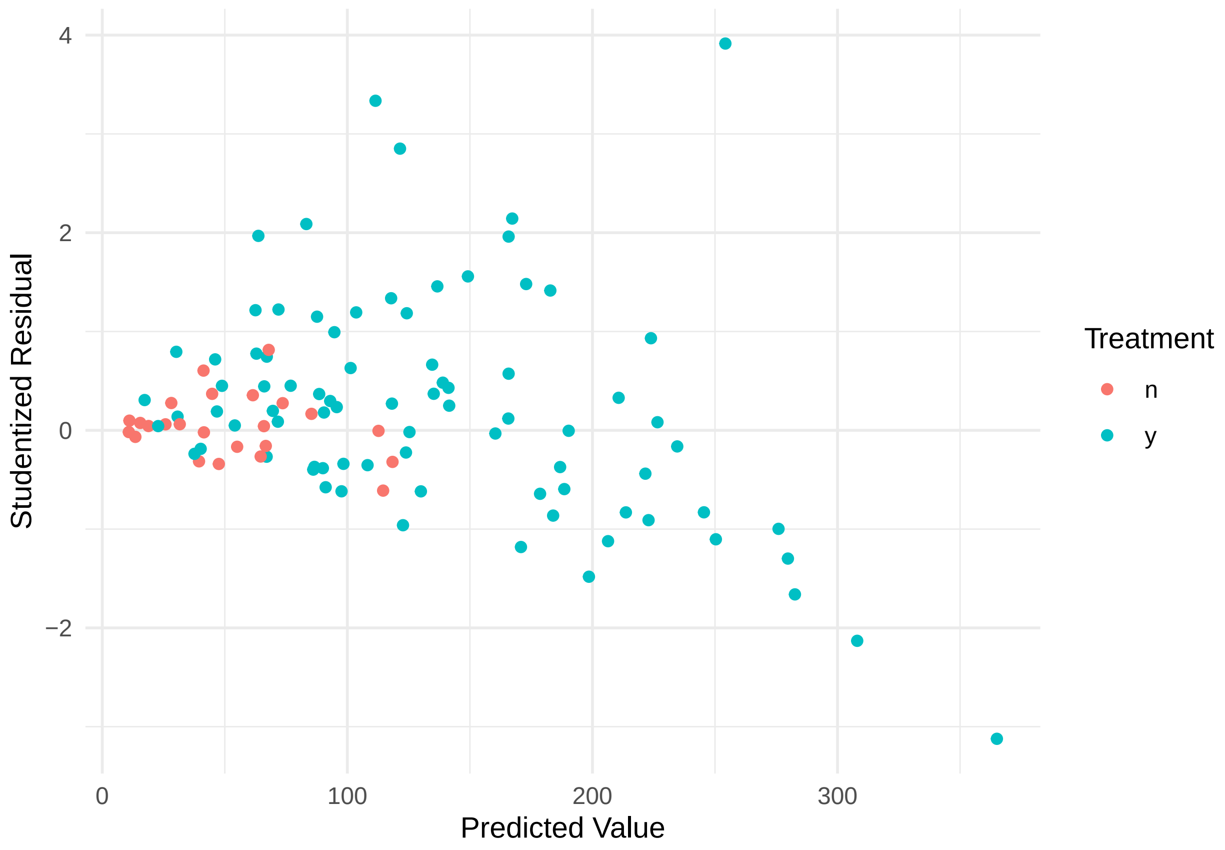
```r
library(trtools) # for biomass data

m.ols <- lm(suitable ~ -1 + treatment:total, data = biomass)
summary(m.ols)$coefficients
```

```
                  Estimate Std. Error t value Pr(>|t|)
treatmentn:total   0.1056    0.04183   2.524 1.31e-02
treatmenty:total   0.1319    0.01121  11.773 7.61e-21
```

```r
d <- expand.grid(treatment = c("n","y"), total = seq(0, 2767, length = 10))
d$yhat <- predict(m.ols, newdata = d)

p <- ggplot(biomass, aes(x = total, y = suitable, color = treatment)) +
  geom_point() + geom_line(aes(y = yhat), data = d) + theme_minimal() +
  labs(x = "Total Biomass (kg/ha)", y = "Suitable Biomass (kg/ha)",
    color = "Treatment")
plot(p)
```



```r
biomass$yhat <- predict(m.ols)
biomass$rest <- rstudent(m.ols)

p <- ggplot(biomass, aes(x = yhat, y = rest, color = treatment)) +
  geom_point() + theme_minimal() +
  labs(x = "Predicted Value", y = "Studentized Residual",
    color = "Treatment")
plot(p)
```



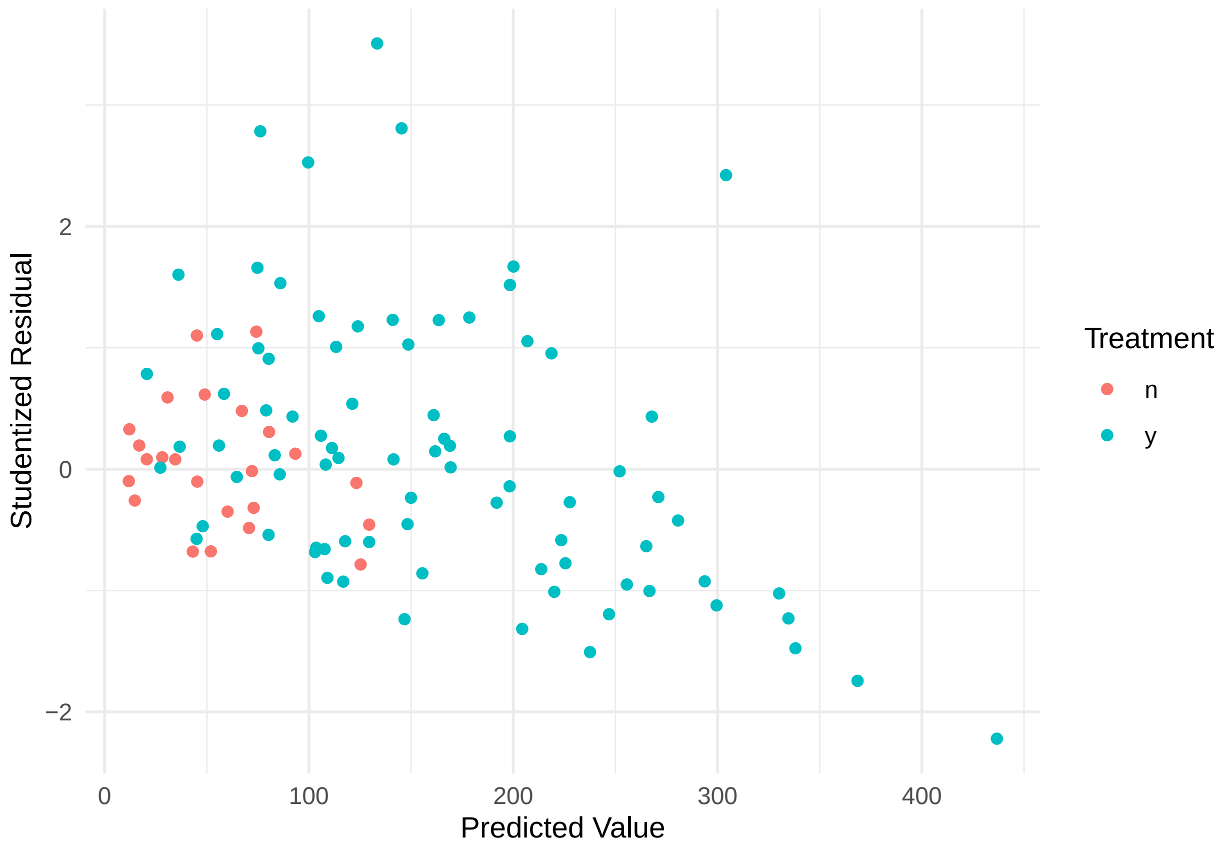
Assume that $\text{Var}(Y_i) \propto E(Y_i)$, which means the weights should be $w_i = 1/E(Y_i)$. We can program the iteratively weighted least squares algorithm as follows.

```
biomass$w <- 1 # initial weights are all equal to one
for (i in 1:5) {
  m.wls <- lm(suitable ~ -1 + treatment:total, weights = w, data = biomass)
  print(coef(m.wls)) # optional
  biomass$w <- 1 / predict(m.wls)
}
```

```
treatmentn:total treatmenty:total
          0.1056           0.1319
treatmentn:total treatmenty:total
          0.1155           0.1578
treatmentn:total treatmenty:total
          0.1155           0.1578
treatmentn:total treatmenty:total
          0.1155           0.1578
treatmentn:total treatmenty:total
          0.1155           0.1578
```

Now let's take a look at the residuals.

```
biomass$yhat <- predict(m.wls)
biomass$rest <- rstudent(m.wls)

p <- ggplot(biomass, aes(x = yhat, y = rest, color = treatment)) +
  geom_point() + theme_minimal() +
  labs(x = "Predicted Value", y = "Studentized Residual",
    color = "Treatment")
plot(p)
```

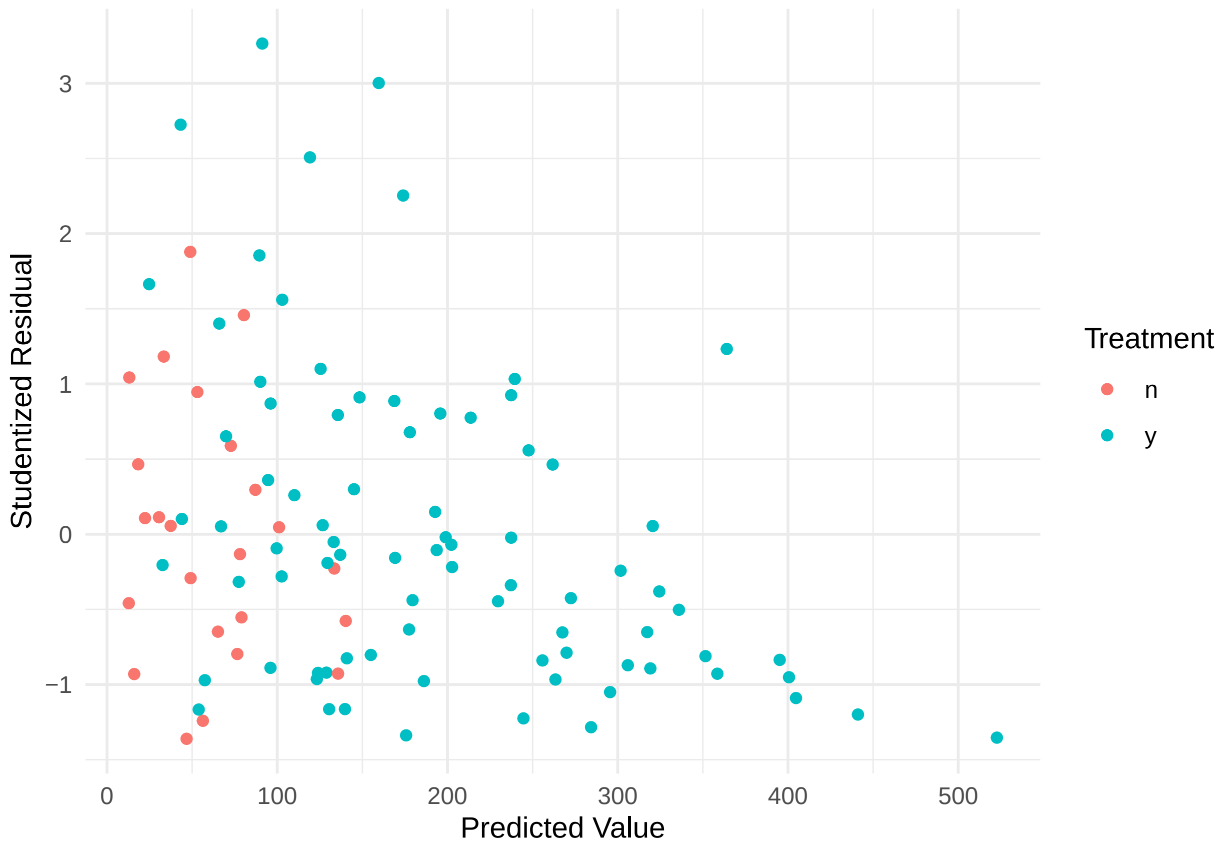


That may not be quite enough. Suppose we assume that $\text{Var}(Y_i) \propto E(Y_i)^p$ where $p = 2$.

```
biomass$w <- 1 # initial weights are all equal to one
for (i in 1:5) {
  m.wls <- lm(suitable ~ -1 + treatment:total, weights = w, data = biomass)
  biomass$w <- 1 / predict(m.wls)^2
}
```

Now let's take a look at the residuals.

```
biomass$yhat <- predict(m.wls)
biomass$rest <- rstudent(m.wls)

p <- ggplot(biomass, aes(x = yhat, y = rest, color = treatment)) +
  geom_point() + theme_minimal() +
  labs(x = "Predicted Value", y = "Studentized Residual",
    color = "Treatment")
plot(p)
```



Better. Maybe too much? We could try $p = 1.5$ or something like that. The residuals do get a little strange for higher predicted values, but we'll leave it here.

The model is $E(S_i) = \beta_1 n_i t_i + \beta_2 y_i t_i$, where n_i and y_i are indicator variables for if the i-th plot was treated or not by fuel reduction. We can also write the model as

$$E(S_i) = \begin{cases} \beta_1 t_i, & \text{if the } i\text{-th plot was not treated by fuel reduction,} \\ \beta_2 t_i, & \text{if the } i\text{-th plot was treated by fuel reduction.} \end{cases}$$

We can use $\beta_2 - \beta_1$ for inferences about the treatment effect.

```
lincon(m.ols, a = c(-1,1))
```

```
          estimate      se    lower  upper tvalue  df pvalue
(-1,1),0   0.02634 0.0433 -0.05953 0.1122 0.6082 104 0.5444
```

```
lincon(m.wls, a = c(-1,1))
```

```
          estimate      se    lower  upper tvalue  df   pvalue
(-1,1),0   0.06386 0.02359 0.01708 0.1106  2.707 104 0.007937
```

The `contrast` function from the **trtools** package can also do this. It can make inferences for a *difference of differences*.

```
contrast(m.wls,
  a = list(treatment = "y", total = 1),
  b = list(treatment = "y", total = 0),
  u = list(treatment = "n", total = 1),
  v = list(treatment = "n", total = 0))
```

```
 estimate      se   lower  upper tvalue  df   pvalue
```

```
  0.06386 0.02359 0.01708 0.1106  2.707 104 0.007937
```

This estimates $E(Y_a) - E(Y_b) - [E(Y_u) - E(Y_v)]$. This can also be done using the `emtrends` function from the **emmeans** package.

```
library(emmeans)
emtrends(m.wls, ~treatment, var = "total") # estimate slopes
```

```
 treatment total.trend     SE  df lower.CL upper.CL
 n               0.125 0.0183 104   0.0888    0.161
 y               0.189 0.0149 104   0.1593    0.219

Confidence level used: 0.95
```

```
pairs(emtrends(m.wls, ~ treatment, var = "total")) # estimate difference between slopes
```

```
 contrast estimate     SE  df t.ratio p.value
 n - y     -0.0639 0.0236 104  -2.707  0.0079
```

Recall that both the **emmeans** and **trtools** packages have a `contrast` function. To avoid conflicts or having to use `trtools::contrast` to call te `contrast` function from the **trtools** package later, we can unload the **emmeans** package usin `detach`.

```
detach(package:emmeans)
```

Yet another approach to compare the slopes is to change the parameterization. Consider the following model.

```
m.wls <- lm(suitable ~ -1 + total + total:treatment, weights = w, data = biomass)
summary(m.wls)$coefficients
```

```
                  Estimate Std. Error t value  Pr(>|t|)
total              0.18892    0.01493  12.656 8.836e-23
total:treatmentn -0.06386    0.02359  -2.707 7.937e-03
```

From `summary` we can see that this model can be written as

$$E(S_i) = \beta_1 t_i + \beta_2 t_i n_i,$$

where n_i is an indicator variable where $n_i = 1$ if the treatment was not appiled to the i-th plot, add $n_i = 0$ otherwise, so we can also write the model as

$$E(S_i) = \begin{cases} (\beta_1 + \beta_2)t_i, & \text{if the } i\text{-th plot was not treated by fuel reduction,} \\ \beta_1 t_i, & \text{if the } i\text{-th plot was treated by fuel reduction.} \end{cases}$$

Note that the meaning of β_1 and β_2 have changed here. The slopes of the lines with and without treatment are β_1 and $\beta_1 + \beta_2$, respectively, and the difference between the slopes is $\beta_1 - (\beta_1 + \beta_2) = -\beta_2$. So inferences for β_2 are for the difference in the slopes (after we reverse the sign). Although not necessary, we can change the reference category to avoid having to reverse the sign.

```
biomass$treatment <- relevel(biomass$treatment, ref = "y")
m.wls <- lm(suitable ~ -1 + total + total:treatment, weights = w, data = biomass)
summary(m.wls)$coefficients
```

```
                  Estimate Std. Error t value  Pr(>|t|)
total              0.12506    0.01827   6.847 5.428e-10
total:treatmenty  0.06386    0.02359   2.707 7.937e-03
```

Now the model can be written as

$$E(S_i) = \beta_1 t_i + \beta_2 t_i n_i,$$

or

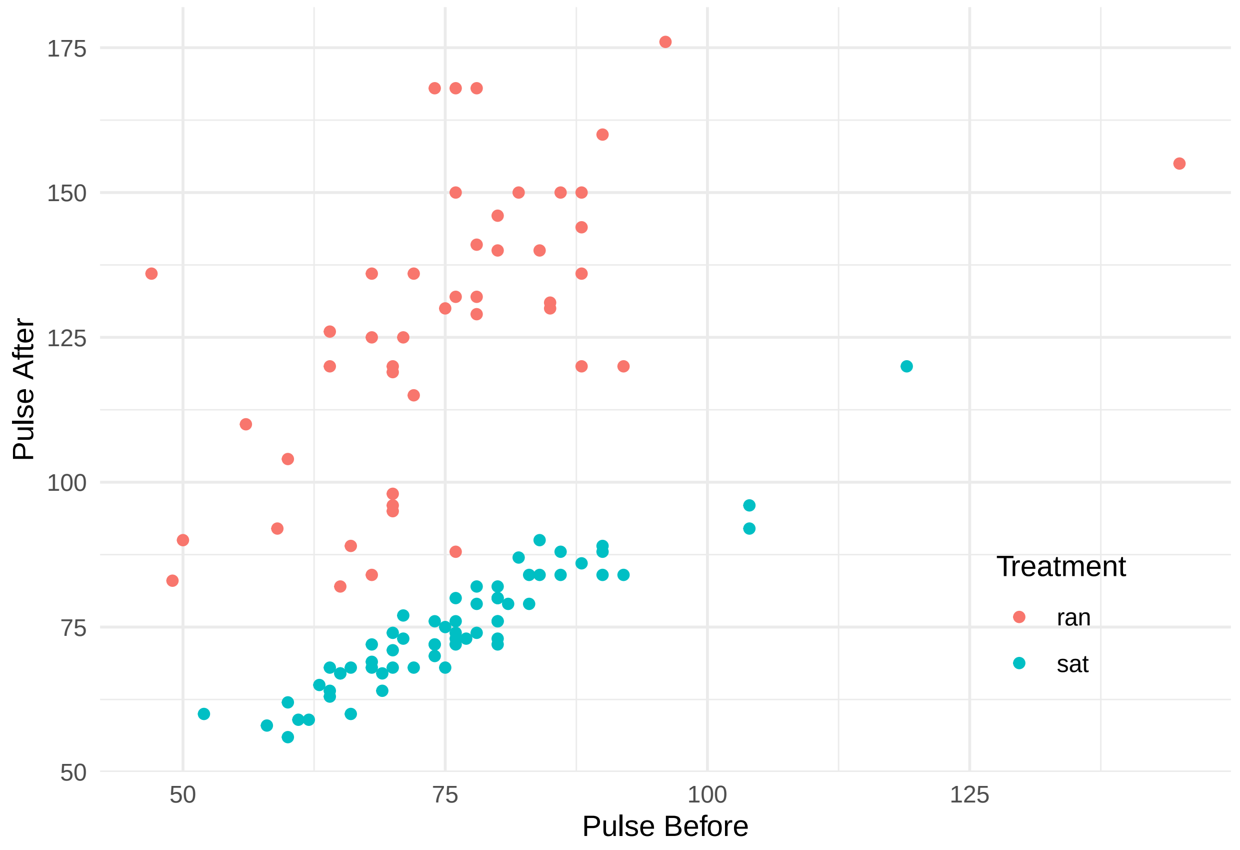
$$E(S_i) = \begin{cases} \beta_1 t_i, & \text{if the } i\text{-th plot was not treated by fuel reduction,} \\ (\beta_1 + \beta_2) t_i, & \text{if the } i\text{-th plot was treated by fuel reduction.} \end{cases}$$

Note: For some reason the reference category (y) is getting an indicator variable here, where normally it does not. I am not sure if this is a bug or intentional, but it appears to be due to the somewhat unusual parameterization I am using.

Parametric Models for Heteroscedasticity

Example: Consider the following data where variability appears to vary by treatment.

```
library(trtools) # for pulse data
p <- ggplot(pulse, aes(x = pulse1, y = pulse2, color = treatment)) +
  geom_point() + theme_minimal() +
  labs(x = "Pulse Before", y = "Pulse After", color = "Treatment") +
  theme(legend.position = c(0.85,0.2))
plot(p)
```



There is one case with missing values on `pulse1` and `pulse2`.

```
subset(pulse, !complete.cases(pulse)) # show observations with missing data
```

```
   height weight age gender smokes alcohol exercise treatment pulse1 pulse2 year
76    173     64  20 female     no     yes moderate       sat     NA     NA   97
```

This will cause problems so we are going to remove it.

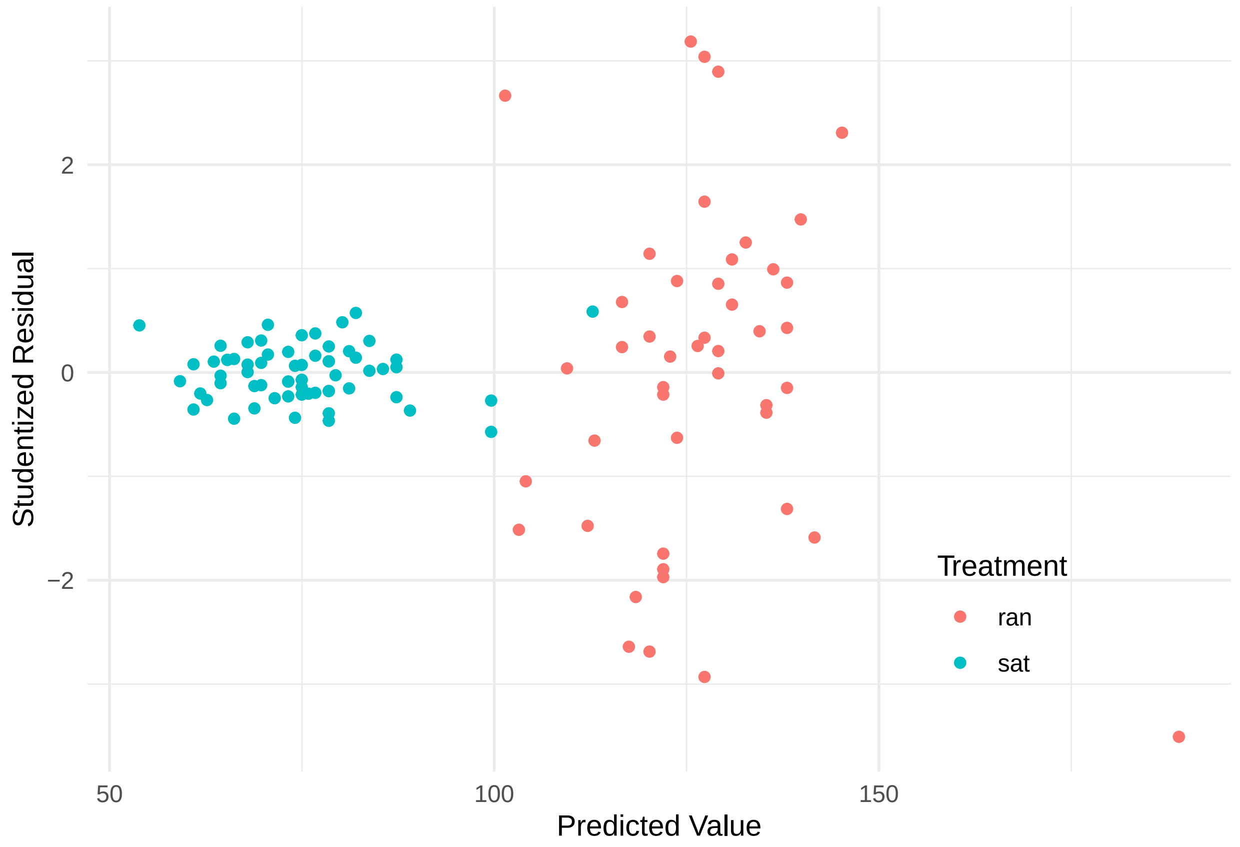
```
pulse <- subset(pulse, complete.cases(pulse)) # overwrite pulse with only complete cases
```

Let's consider a simple linear model.

```r
m <- lm(pulse2 ~ treatment + pulse1 + treatment:pulse1, data = pulse)
summary(m)$coefficients
```

```
                     Estimate Std. Error  t value  Pr(>|t|)
(Intercept)          59.41757    10.4467  5.68767 1.171e-07
treatmentsat        -51.25896    15.7451 -3.25554 1.524e-03
pulse1                0.89363     0.1357  6.58544 1.841e-09
treatmentsat:pulse1  -0.01437     0.2049 -0.07011 9.442e-01
```

```r
pulse$yhat <- predict(m)
pulse$rest <- rstudent(m)
p <- ggplot(pulse, aes(x = yhat, y = rest, color = treatment)) +
  geom_point() + theme_minimal() +
  labs(x = "Predicted Value", y = "Studentized Residual",
    color = "Treatment") +
  theme(legend.position = c(0.8,0.2))
plot(p)
```



Consider that the model assumed by `lm` is

$$E(Y_i) = \beta_0 + \beta_1 t_i + \beta_2 x_i + \beta_3 t_i x_i, \quad (1)$$

$$\text{Var}(Y_i) = \sigma^2, \quad (2)$$

where Y_i is the second pulse measurement, t_i is an indicator variable for the treatment (i.e., $t_i = 1$ if the i-th observation was from the sitting treatment condition, and $t_i = 0$ otherwise), and x_i is the first pulse measurement. Maybe it would make sense to have something like

$$\mathrm{Var}(Y_i) = \begin{cases} \sigma_s^2, & \text{if the } i\text{-th observation is from the sitting treatment,} \\ \sigma_r^2, & \text{if the } i\text{-th observation is from the running treatment.} \end{cases}$$

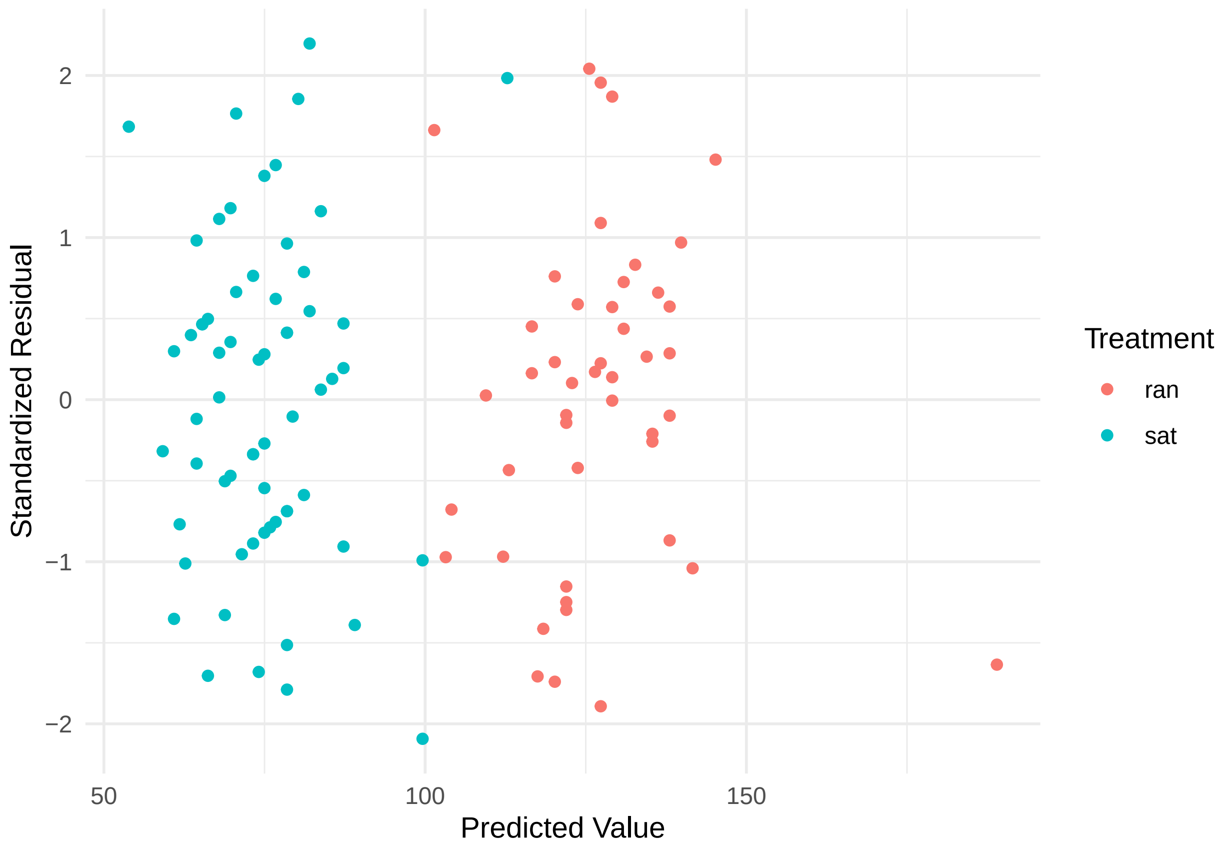
We can estimate such a model using the `gls` function from the **nlme** package.

```
library(nlme) # should come with R
m <- gls(pulse2 ~ treatment + pulse1 + treatment:pulse1, data = pulse,
  method = "ML", weights = varIdent(form = ~ 1|treatment))
summary(m)
```

```
Generalized least squares fit by maximum likelihood
  Model: pulse2 ~ treatment + pulse1 + treatment:pulse1
  Data: pulse
    AIC   BIC logLik
  763.1 779.3 -375.6

Variance function:
 Structure: Different standard deviations per stratum
 Formula: ~1 | treatment
 Parameter estimates:
  sat   ran
1.000 5.723

Coefficients:
                     Value Std.Error t-value p-value
(Intercept)          59.42    15.755   3.771  0.0003
treatmentsat        -51.26    16.058  -3.192  0.0019
pulse1                0.89     0.205   4.367  0.0000
treatmentsat:pulse1  -0.01     0.209  -0.069  0.9452

 Correlation:
                    (Intr) trtmnt pulse1
treatmentsat        -0.981
pulse1              -0.980  0.962
treatmentsat:pulse1  0.962 -0.980 -0.981

Standardized residuals:
    Min      Q1     Med      Q3     Max
-2.0920 -0.7688  0.1026  0.5886  2.1968

Residual standard error: 3.634
Degrees of freedom: 109 total; 105 residual
```

Note the different syntax for extracting standardized residuals.

```
pulse$yhat <- predict(m)
pulse$resz <- residuals(m, type = "p") # note different syntax
p <- ggplot(pulse, aes(x = yhat, y = resz, color = treatment)) +
  geom_point() + theme_minimal() +
  labs(x = "Predicted Value", y = "Standardized Residual",
    color = "Treatment")
plot(p)
```



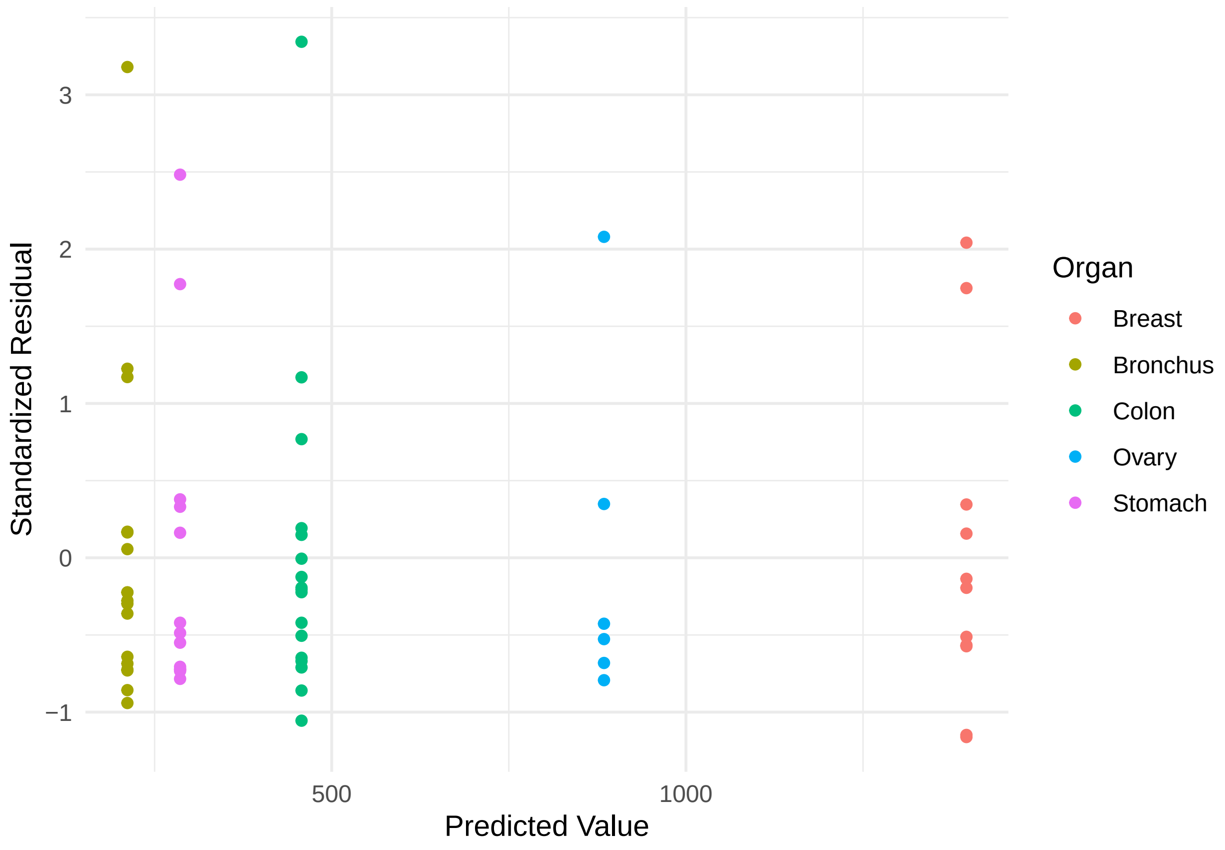
Here is an example with the `CancerSurvival` data.

```
library(Stat2Data)
data(CancerSurvival)
m <- gls(Survival ~ Organ, data = CancerSurvival,
  method = "ML", weights = varIdent(form = ~ 1|Organ))
summary(m)
```

```
Generalized least squares fit by maximum likelihood
  Model: Survival ~ Organ
  Data: CancerSurvival
    AIC   BIC logLik
  976.8 998.4 -478.4

Variance function:
 Structure: Different standard deviations per stratum
 Formula: ~1 | Organ
 Parameter estimates:
 Stomach Bronchus    Colon    Ovary   Breast
  1.0000   0.6119   1.2455   3.0141   3.5504

Coefficients:
                Value Std.Error t-value p-value
(Intercept)    1395.9     371.0   3.763  0.0004
OrganBronchus -1184.3     374.5  -3.162  0.0025
OrganColon     -938.5     385.5  -2.435  0.0179
OrganOvary     -511.6     565.2  -0.905  0.3691
OrganStomach  -1109.9     383.2  -2.896  0.0053
```

```
 Correlation:
              (Intr) OrgnBr OrgnCl OrgnOv
OrganBronchus -0.991
OrganColon    -0.962  0.953
OrganOvary    -0.656  0.650  0.632
OrganStomach  -0.968  0.959  0.932  0.635

Standardized residuals:
    Min      Q1     Med      Q3     Max
-1.1613 -0.6824 -0.2878  0.1748  3.3435

Residual standard error: 332.7
Degrees of freedom: 64 total; 59 residual
```

```r
CancerSurvival$yhat <- predict(m)
CancerSurvival$resz <- residuals(m, type = "p")
p <- ggplot(CancerSurvival, aes(x = yhat, y = resz, color = Organ)) +
  geom_point() + theme_minimal() +
  labs(x = "Predicted Value", y = "Standardized Residual", color = "Organ")
plot(p)
```



Comments about parametric models for heteroscedasticity.

Advantages: Potentially very effective *if* we can specify an accurate model for the variance.

Disadvantages: If we do not specify an accurate model for the variance, it may bias estimation of parameters concerning the expected response.

Heteroscedastic Consistent Standard Errors

The idea is to estimate the model parameters using ordinary least squares, but estimate the standard errors in such a way that we do not assume homoscedasticity This is sometimes called *heteroscedastic consistent standard errors*, *robust standard errors*, or *sandwich estimators*.

Example: Consider again the cancer survival data.

```
m <- lm(Survival ~ Organ, data = CancerSurvival)
```

The **sandwich** package provides resources for using heteroscedastic-consistent standard errors. Technically, what is being estimated is the *covariance matrix* of the parameter estimators.

```
library(sandwich) # for vcovHC used below
vcov(m)    # bad estimate if there is heteroscedasticity
```

```
               (Intercept) OrganBronchus OrganColon OrganOvary OrganStomach
(Intercept)          40752        -40752     -40752     -40752       -40752
OrganBronchus       -40752         67121      40752      40752        40752
OrganColon          -40752         40752      67121      40752        40752
OrganOvary          -40752         40752      40752     115464        40752
OrganStomach        -40752         40752      40752      40752        75235
```

```
vcovHC(m) # better estimate if there is heteroscedasticity
```

```
               (Intercept) OrganBronchus OrganColon OrganOvary OrganStomach
(Intercept)         153504       -153504    -153504    -153504      -153504
OrganBronchus      -153504        156256     153504     153504       153504
OrganColon         -153504        153504     164908     153504       153504
OrganOvary         -153504        153504     153504     394879       153504
OrganStomach       -153504        153504     153504     153504       163498
```

The square root of the diagonal elements are the standard errors.

```
sqrt(diag(vcov(m)))    # bad estimates of the standard errors
```

```
  (Intercept) OrganBronchus    OrganColon    OrganOvary  OrganStomach 
        201.9         259.1         259.1         339.8         274.3 
```

```
sqrt(diag(vcovHC(m))) # better estimates of the standard errors
```

```
  (Intercept) OrganBronchus    OrganColon    OrganOvary  OrganStomach 
        391.8         395.3         406.1         628.4         404.3 
```

But the usual way to interface with the functions in the **sandwich** package is through other functions.

```
               Estimate Std. Error t value  Pr(>|t|) 2.5 % 97.5 %
(Intercept)      1395.9      201.9   6.915 3.770e-09   992 1799.9
OrganBronchus   -1184.3      259.1  -4.571 2.530e-05 -1703 -665.9
OrganColon       -938.5      259.1  -3.622 6.083e-04 -1457 -420.1
OrganOvary       -511.6      339.8  -1.506 1.375e-01 -1192  168.4
OrganStomach    -1109.9      274.3  -4.046 1.533e-04 -1659 -561.1
```

```
confint(m) # bad confidence intervals due to bad standard error estimates
```

```
               2.5 % 97.5 %
(Intercept)      992 1799.9
OrganBronchus  -1703 -665.9
OrganColon     -1457 -420.1
OrganOvary     -1192  168.4
OrganStomach   -1659 -561.1
```

```
library(lmtest) # for coeftest and coefci used below
coeftest(m, vcov = vcovHC) # better standard error estimates
```

```

t test of coefficients:

              Estimate Std. Error t value Pr(>|t|)    
(Intercept)       1396        392    3.56  0.00073 ***
OrganBronchus    -1184        395   -3.00  0.00400 ** 
OrganColon        -938        406   -2.31  0.02434 *  
OrganOvary        -512        628   -0.81  0.41886    
OrganStomach     -1110        404   -2.74  0.00801 ** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
coefci(m, vcov = vcovHC)   # better confidence intervals
```

```
                2.5 % 97.5 %
(Intercept)     611.9 2179.9
OrganBronchus -1975.3 -393.3
OrganColon    -1751.1 -125.9
OrganOvary    -1769.0  745.8
OrganStomach  -1919.0 -300.8
```

Both `lincon` and `contrast` will accept a `fcov` argument to provide a function to estimate standard errors.

```
lincon(m, fcov = vcovHC)
```

```
              estimate    se   lower  upper  tvalue df    pvalue
(Intercept)     1395.9 391.8   611.9 2179.9  3.5628 59 0.0007337
OrganBronchus  -1184.3 395.3 -1975.3 -393.3 -2.9961 59 0.0039950
OrganColon      -938.5 406.1 -1751.1 -125.9 -2.3111 59 0.0243421
OrganOvary      -511.6 628.4 -1769.0  745.8 -0.8141 59 0.4188611
OrganStomach   -1109.9 404.3 -1919.0 -300.8 -2.7449 59 0.0080080
```

```
organs <- sort(unique(CancerSurvival$Organ)) # sorted organ names
contrast(m, a = list(Organ = organs),
  cnames = organs, fcov = vcovHC)
```

```
         estimate     se  lower  upper tvalue df    pvalue
Breast     1395.9 391.80 611.93 2179.9  3.563 59 7.337e-04
Bronchus    211.6  52.46 106.61  316.6  4.033 59 1.604e-04
Colon       457.4 106.79 243.72  671.1  4.283 59 6.884e-05
Ovary       884.3 491.30 -98.75 1867.4  1.800 59 7.698e-02
Stomach     286.0  99.97  85.96  486.0  2.861 59 5.836e-03
```

```
lincon(m, a = c(1,0,0,0,1), fcov = vcovHC)
```

```
              estimate    se lower upper tvalue df   pvalue
(1,0,0,0,1),0      286 99.97 85.96   486  2.861 59 0.005836
```

You can use a similar approach with the `emmeans` function from the **emmeans** package, but there the argument is `vcov`.

```
library(emmeans)
emmeans(m, ~Organ, vcov = vcovHC)
```

```
 Organ    emmean    SE df lower.CL upper.CL
 Breast     1396 391.8 59    611.9     2180
 Bronchus    212  52.5 59    106.6      317
 Colon       457 106.8 59    243.7      671
 Ovary       884 491.3 59    -98.8     1867
 Stomach     286 100.0 59     86.0      486

Confidence level used: 0.95
```

```
pairs(emmeans(m, ~Organ, vcov = vcovHC), adjust = "none", infer = TRUE)
```

```
 contrast           estimate  SE df lower.CL upper.CL t.ratio p.value
 Breast - Bronchus    1184.3 395 59      393   1975.3   2.996  0.0040
 Breast - Colon        938.5 406 59      126   1751.1   2.311  0.0243
 Breast - Ovary        511.6 628 59     -746   1769.0   0.814  0.4189
 Breast - Stomach     1109.9 404 59      301   1919.0   2.745  0.0080
 Bronchus - Colon     -245.8 119 59     -484     -7.7  -2.066  0.0432
 Bronchus - Ovary     -672.7 494 59    -1661    315.9  -1.362  0.1785
 Bronchus - Stomach    -74.4 113 59     -300    151.5  -0.659  0.5124
 Colon - Ovary        -426.9 503 59    -1433    579.1  -0.849  0.3992
 Colon - Stomach       171.4 146 59     -121    464.1   1.172  0.2460
 Ovary - Stomach       598.3 501 59     -405   1601.6   1.193  0.2375

Confidence level used: 0.95
```

Use the function `waldtest` in place of `anova` when using heteroscedastic-consistent standard errors.

```
m.full <- lm(Survival ~ Organ, data = CancerSurvival)
m.null <- lm(Survival ~ 1, data = CancerSurvival)
waldtest(m.null, m.full, vcov = vcovHC)
```

```
Wald test

Model 1: Survival ~ 1
Model 2: Survival ~ Organ
  Res.Df Df    F Pr(>F)
1     63
2     59  4 3.52  0.012 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Comments about heteroscedastic-consistent standard errors:

Advantages: Does not require us to specify a variance structure/function. We let the data inform the estimator.

Disadvantages: Highly dependent on the data to help produce better estimates of the standard errors, and tends to work well only if n is relatively large.

Note: There are a variety of variations of the "sandwich" estimator. Different estimators can be specified through the `type` argument to `vcovHC` so instead of writing `vcov = vcovHC` or `fcov = vcovHC` we write `vcov = function(m) vcovHC(m, type = "HC0")` or `vcov = function(m) vcovHC(m, type = "HC0")` if we wanted to use that particular type of estimator (sometimes called "White's estimator").