Case Study 9.3: Water Hardness and Mortality

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The data in this case study were collected in an investigation of environmental causes of disease. They show the annual mortality rate per 100,000 for males, averaged over the years 1958–1964, and the calcium concentration (in parts per million) in the drinking water supply for 61 large towns in England and Wales. (The higher the calcium concentration, the harder the water.) Towns at least as far north as Derby are identified in the data set with the code `N`. In this study we will use R to investigate how are mortality and water hardness related, and if there a geographical factor in the relationship. The data is in the file `water.csv` on Canvas

```
water.df = read.csv("WATER.csv")
head(water.df)
```

```
##   Mortality  Ca Location
## 1      1247 105
## 2      1668  17        N
## 3      1466   5
## 4      1800  14        N
## 5      1609  18        N
## 6      1558  10        N
```

It's always useful to check for missing values.

```
sum(is.na(water.df))
```

```
## [1] 0
```

No missing values. All good. How about a plot? The ideal plot would use `Location` as a plotting symbol, however we can see that the towns to the South are coded as blanks. We should change that. How? How about making all the values that are not `N` be `S`?

```
water.df$Location[water.df$Location != 'N'] = 'S'
```

```
## Warning in `[<-.factor`(`*tmp*`, water.df$Location != "N", value =
## structure(c(NA, : invalid factor level, NA generated
```

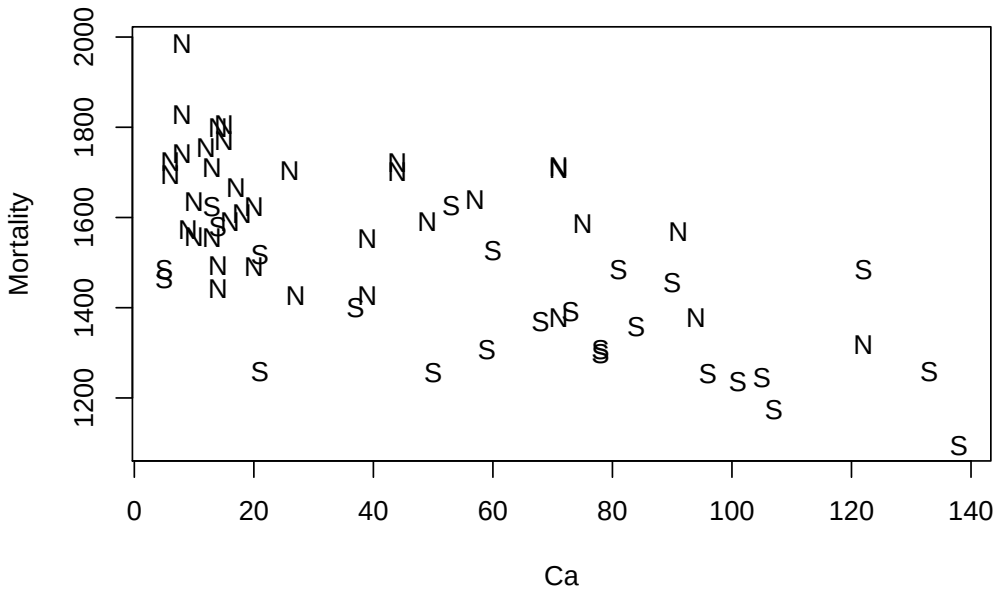
Hmm. That did not work, as planned. That is because `Location` is a factor. We have a number of choices. One is to make a new variable. The other is to make `Location` a character vector, make the change and, then make it a factor again. Although this second option sounds like a lot of work it is really only one line of code. It is preferable because we will not clutter our workspace with redundant information.

```
water.df$Location = with(water.df, {
  Location = as.character(Location);
  Location[is.na(Location)] = 'S';
  Location = factor(Location)
})
water.df$Location
```

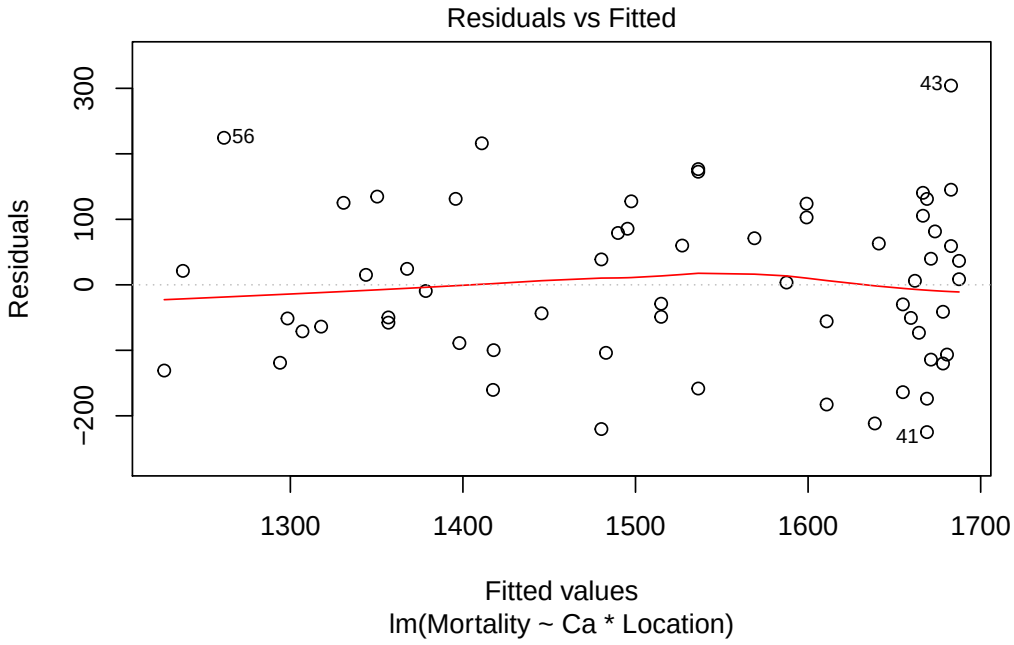
```
##  [1] S N S N N N N S N S S S N S S N N N N S N N N N N S N S N S S S N N S
## [36] S S N S N N N N N S S N N N N N S N S S S N N N S N
## Levels: N S
```

Much better. Now how about that plot?

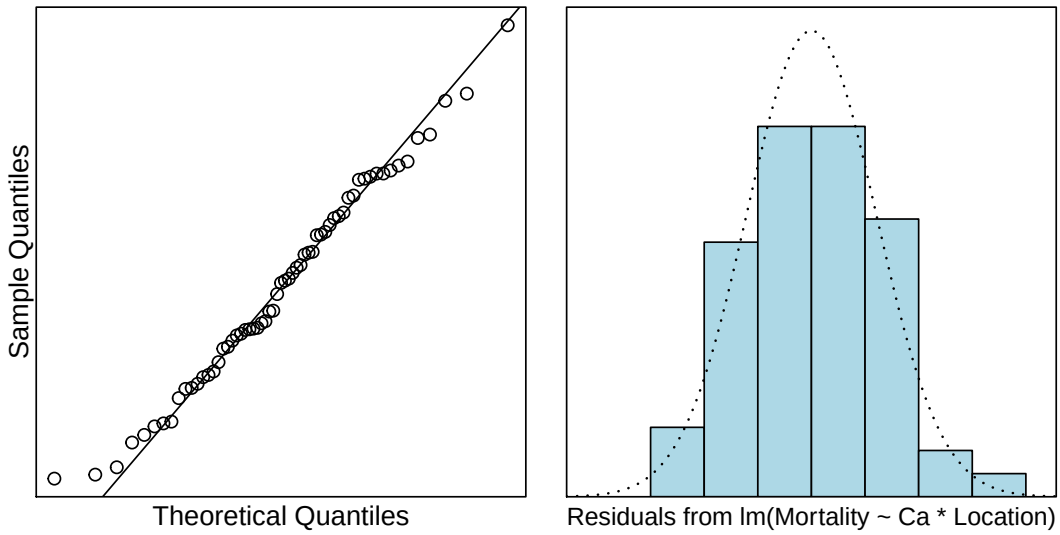
```
plot(Mortality~Ca, pch = as.character(water.df$Location), data = water.df)
```



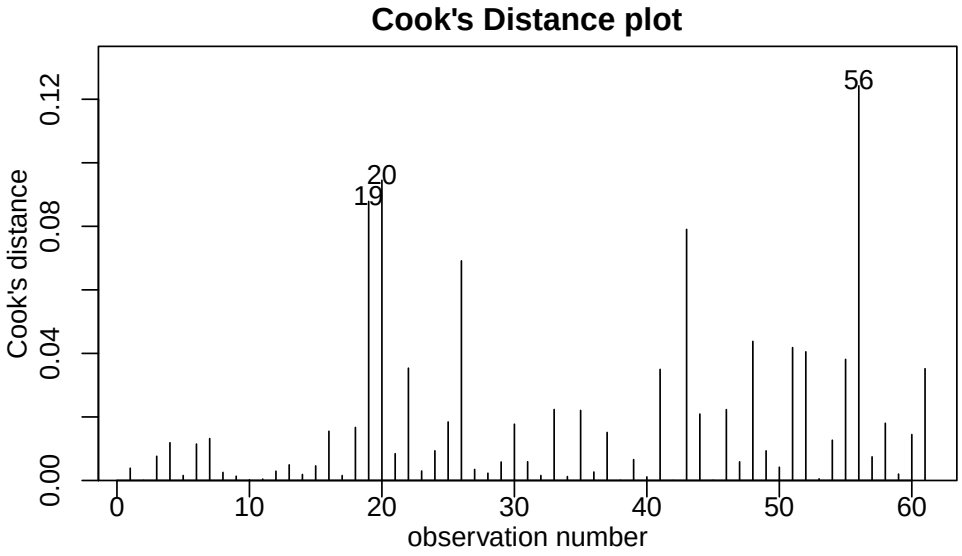

```
water.fit = lm(Mortality ~ Ca * Location, data = water.df)
plot(water.fit, which = 1)
```




```
normcheck(water.fit)
```




```
cooks20x(water.fit)
```



All looks pretty good.

```
summary(water.fit)
```

```
##
## Call:
```

```
## lm(formula = Mortality ~ Ca * Location, data = water.df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -224.878  -88.953    3.495   85.617  304.172
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1701.4272    30.9493  54.975  < 2e-16 ***
## Ca             -2.3249     0.6996  -3.323  0.00156 **
## LocationS    -175.7321    58.5586  -3.001  0.00399 **
## Ca:LocationS    0.1598     0.9460   0.169  0.86643
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 123.9 on 57 degrees of freedom
## Multiple R-squared:  0.5857, Adjusted R-squared:  0.5639
## F-statistic: 26.86 on 3 and 57 DF,  p-value: 5.855e-11
```

It does not look like there is any evidence of different slopes. Do we get any additional info from the ANOVA table?

```
anova(water.fit)
```

```
## Analysis of Variance Table
##
## Response: Mortality
##             Df Sum Sq Mean Sq F value    Pr(>F)
## Ca           1 906185  906185 59.0005 2.330e-10 ***
## Location     1 331091  331091 21.5569 2.065e-05 ***
## Ca:Location  1    438     438  0.0285    0.8664
## Residuals   57 875459   15359
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Nope. We only have two levels so we do not need the ANOVA table for this analysis.

So we do not have interaction, but it looks like there is a relationship with hardness and it looks like there is a North/South effect (`Location`). We should refit the model.

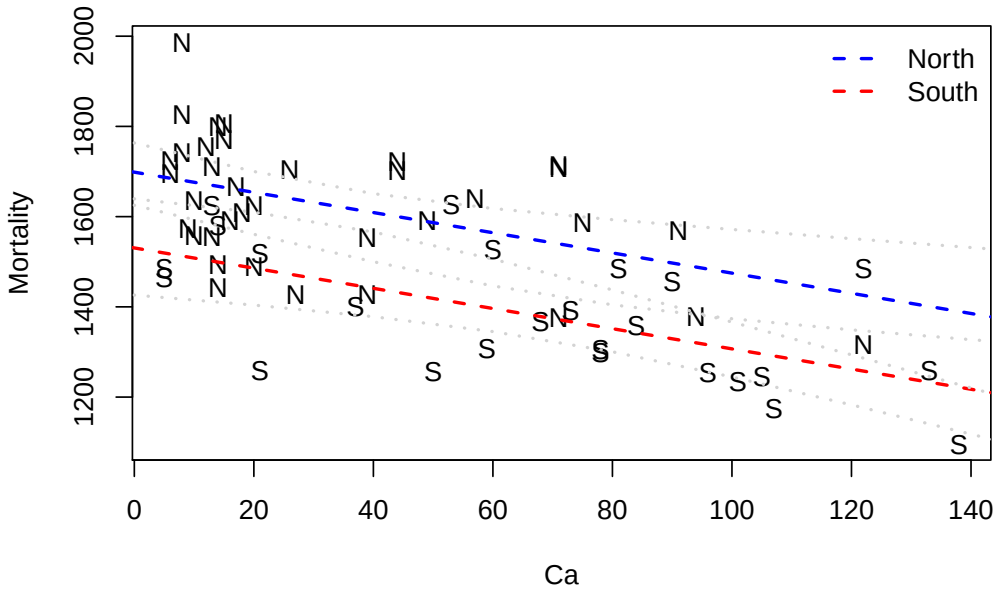
```
water.fit2 = lm(Mortality ~ Ca + Location, data = water.df)
summary(water.fit2)
```

```
##
## Call:
## lm(formula = Mortality ~ Ca + Location, data = water.df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -223.607  -89.582    2.091   83.303  306.353
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1698.5472    25.6148  66.311  < 2e-16 ***
## Ca            -2.2375     0.4669  -4.792 1.19e-05 ***
## LocationS   -167.9518    35.8694  -4.682 1.75e-05 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 122.9 on 58 degrees of freedom
## Multiple R-squared:  0.5855, Adjusted R-squared:  0.5712
## F-statistic: 40.96 on 2 and 58 DF,  p-value: 8.091e-12
```

Minimal change in R^2. How do the fitted lines look on the plot?

```
b = coef(water.fit2)
plot(Mortality~Ca, pch = as.character(water.df$Location), data = water.df)
abline(b[1:2], col = "blue", lty = 2, lwd = 2)
abline(b[1] + b[3], b[2], col = "red", lty = 2, lwd = 2)
legend("topright", lty = 2, lwd = 2, col = c("blue", "red"),
    legend = c("North", "South"), bty = "n")
# This code puts some confidence bounds around the lines.
# It's pretty complicated if you don't know R and it isn't examinable
pred.df = data.frame(Ca = rep(seq(0, 160, by = 20), 2),
    Location = rep(c('N', 'S'), c(9, 9)))
water.pred = predict(water.fit, newdata = pred.df, interval = "confidence")
for(i in 1:2){
  idx = 1:9 + (i - 1) * 9
  for(j in c("lwr", "upr")){
      lines(pred.df$Ca[idx], water.pred[idx, j], lty = 3, lwd = 2, col = "lightgrey");
  }
}
```



So it looks like mortality decreases as the calcium concentration in the water increases, and that mortality is lower in the South than the North.