Analysis of Covariance in Completely Randomized Design

Example:

Effect of Treatment on *Leprosy Bacilli*:

An experiment was conducted to examine the effects of use of certain drugs-treatments on leprosy at the Eversley Childs' Sanitarium in the Philippines (see Statistical Methods, 6th edition, by Snedecor and Cochran).

On each patient six sites on the body at which leprosy bacilli tend to congregate were selected. The variate **X**, based on laboratory tests, is a score representing the abundance of leprosy bacilli at these sites before the experiment began. The variate **Y** is a similar score after several months of treatment. Drugs **A** and **D** are antibiotics while drug **F** is an inert drug included as a control. Ten patients were selected for each treatment for this example. The data of leprosy bacilli score before and after treatment are given below in Table 1:

Scores.A.X	Scores.A.Y	Scores.D.X	Scores.D.Y	Scores.F.X	Scores.F.Y
11	6	6	0	16	13
8	0	6	2	13	10
5	2	7	3	11	18
14	8	8	1	9	5
19	11	18	18	21	23
6	4	8	4	16	12
10	13	19	14	12	5
6	1	8	9	12	16
11	8	5	1	7	1
3	0	15	9	12	20

Table 1: **Leprosy bacilli scores**

Solution:

Method of Analysis of variance (ANCOVA) in CRD using formula approach:

Although we have very simple way to analyze the analysis of covariance in CRD using `R` models, we must also know the manual way of analyzing to understand the underlying procedure.

1 **Total Sums of Squares:**

For this we must recall the following formulae of S_{YY}, S_{XX}, and S_{XY} from Equation 1 to Equation 3, which are used to compute **total sums of squares** of **X**, **Y** and their products respectively:

$$S_{\text{YY}} = \sum_{[i=1]}^{n} Y_i^2 - \frac{\left(\sum_{[i=1]}^{n} Y_i\right)^2}{n} \tag{1}$$

with df=(n-1).

$$S_{\mathrm{XX}} = \sum_{[i=1]}^{n} X_i^2 - \frac{\left(\sum_{[i=1]}^{n} X_i\right)^2}{n} \tag{2}$$

with df=(n-1)

$$S_{\mathrm{XY}} = \sum_{[i=1]}^{n} X_i Y_i - \frac{\left(\sum_{[i=1]}^{n} X_i\right)\left(\sum_{[i=1]}^{n} Y_i\right)}{n} \tag{3}$$

with df=(n-1).

```
data=read.csv("Leprosy.csv"); data; rowMeans(data);
```

```
##    Scores.A.X Scores.A.Y Scores.D.X Scores.D.Y Scores.F.X Scores.F.Y
## 1          11          6          6          0         16         13
## 2           8          0          6          2         13         10
## 3           5          2          7          3         11         18
## 4          14          8          8          1          9          5
## 5          19         11         18         18         21         23
## 6           6          4          8          4         16         12
## 7          10         13         19         14         12          5
## 8           6          1          8          9         12         16
## 9          11          8          5          1          7          1
## 10          3          0         15          9         12         20
```

```
##  [1]  8.666667  6.500000  7.666667  7.500000 18.333333  8.333333 12.166667
##  [8]  8.666667  5.500000  9.833333
```

```
plot(1:10,1:10,type="l",col="red");
```


![plot of chunk unnamed-chunk-1](figure/unnamed-chunk-1-1.png)