# Factors and Model Matrices

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## The Big Picture

- A *factor* is a categorical variable.
- The possible values are called *levels*.
- In a regression framework, a single factor with $k$ levels is represented by $k - 1$ columns in the design matrix (or model matrix).
- There are several ways to represent the same factor with columns.
- The most usual parameterization uses 0s and 1s with a column corresponding to each level but one.
- The fitted values are the same for each parameterization, but the parameter estimates differ.

# Sugar

- An experiment examines the sugar content in four plant lines including a control (wild type) and three treatments (genetically modified forms).
- Data are sugar weights in mg after breaking down cellulose.
- There are three individuals sampled in each group.

| Control | A | B | C |
|---|---|---|---|
| 82.0 | 58.3 | 68.1 | 50.7 |
| 97.8 | 67.9 | 70.8 | 47.1 |
| 69.9 | 59.3 | 63.6 | 48.9 |

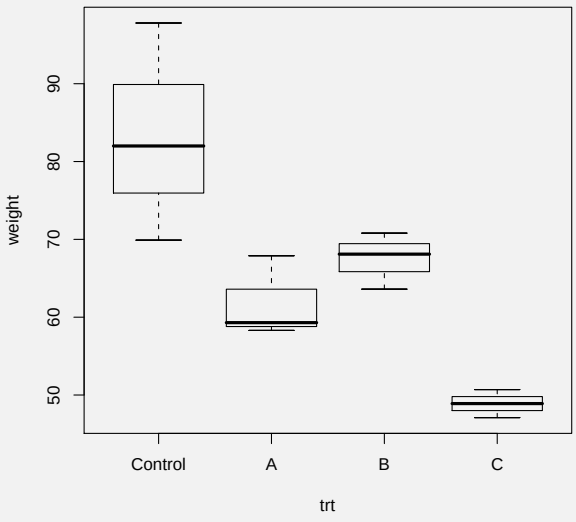




# Side-by-side Box Plots

- Side-by-side boxplots are good for examining differences in center and spread as well as skewness.

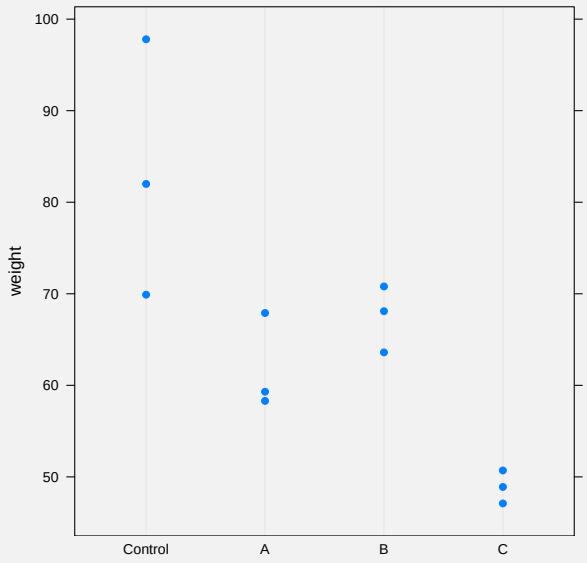
```
> library(DAAG)
> data(sugar)
> attach(sugar)
> plot(weight ~ trt)
```



# Dot Plots

- For very small data sets, dot plots show the exact locations of points.
- Lattice graphics in R are useful here.
- We note that the control group is much more spread out than the genetically modified groups.

```
> library(lattice)
> print(dotplot(weight ~ trt))
```



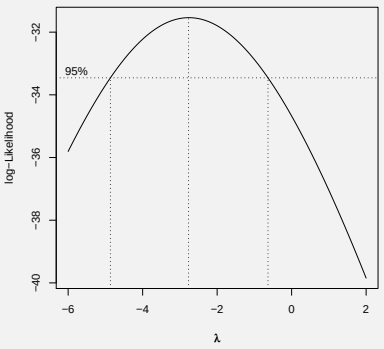


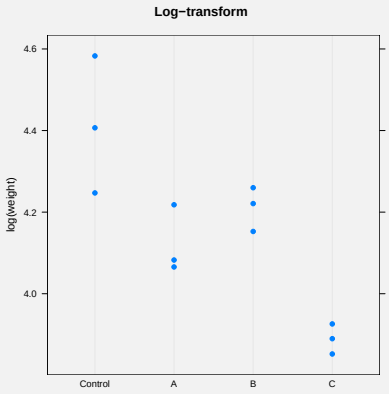


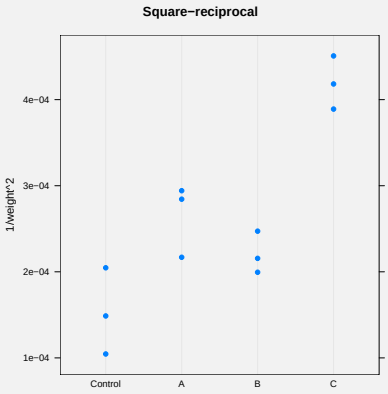

# Transformations

- A log transformation would lessen the spread.
- According to Box-Cox, a more extreme transformation (such as $1/y^2$) would do better.
- I will show both transformations and their effects on the dot plots, but will simply analyze the untransformed data for simplicity.

# Box-Cox Transformations








# Standard Parameterization

- For this example, the single factor `trt` is parameterized with three columns of 0s and 1s.
- The intercept corresponds to the control group.
- The other variables correspond to differences between each other level and the control group.
- R will use the first level name in alphabetical order as the reference.

```
> sugar1.lm = lm(weight ~ trt)
> model.matrix(sugar1.lm)

   (Intercept) trtA trtB trtC
1            1    0    0    0
2            1    0    0    0
3            1    0    0    0
4            1    1    0    0
5            1    1    0    0
6            1    1    0    0
7            1    0    1    0
8            1    0    1    0
9            1    0    1    0
10           1    0    0    1
11           1    0    0    1
12           1    0    0    1
attr(,"assign")
[1] 0 1 1 1
attr(,"contrasts")
attr(,"contrasts")$trt
[1] "contr.treatment"
```

# Alternative Parameterization

- An alternative parameterization has a mean effect of 0 for the four groups.
- The model matrix is more complicated for this parameterization.
- You change the `contrasts` option to achieve this in R.

```
> old = options(contrasts = c("contr.sum", "contr.poly"))
> sugar2.lm = lm(weight ~ trt)
> model.matrix(sugar2.lm)

   (Intercept) trt1 trt2 trt3
1            1    1    0    0
2            1    1    0    0
3            1    1    0    0
4            1    0    1    0
5            1    0    1    0
6            1    0    1    0
7            1    0    0    1
8            1    0    0    1
9            1    0    0    1
10           1   -1   -1   -1
11           1   -1   -1   -1
12           1   -1   -1   -1
attr(,"assign")
[1] 0 1 1 1
attr(,"contrasts")
attr(,"contrasts")$trt
[1] "contr.sum"

> options(old)
```





# Coefficients

- Different parameterizations lead to different estimates.
- The p-values correspond to different hypothesis tests.

```
> summary(sugar1.lm)$coefficients

             Estimate Std. Error   t value     Pr(>|t|)
(Intercept)  83.23333   4.472757 18.608955 7.173441e-08
trtA        -21.40000   6.325434 -3.383167 9.596536e-03
trtB        -15.73333   6.325434 -2.487313 3.767970e-02
trtC        -34.33333   6.325434 -5.427823 6.249550e-04

> summary(sugar2.lm)$coefficients

             Estimate Std. Error    t value     Pr(>|t|)
(Intercept) 65.366667   2.236379 29.2288028 2.033089e-09
trt1        17.866667   3.873521  4.6125129 1.726990e-03
trt2        -3.533333   3.873521 -0.9121761 3.883370e-01
trt3         2.133333   3.873521  0.5507478 5.968464e-01
```

# ANOVA

- However, the ANOVA tables are identical.

```
> anova(sugar1.lm)

Analysis of Variance Table

Response: weight
          Df  Sum Sq Mean Sq F value   Pr(>F)
trt        3 1822.21  607.40  10.121 0.004248 **
Residuals  8  480.13   60.02
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(sugar2.lm)

Analysis of Variance Table

Response: weight
          Df  Sum Sq Mean Sq F value   Pr(>F)
trt        3 1822.21  607.40  10.121 0.004248 **
Residuals  8  480.13   60.02
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```





# ANOVA

- The fitted values are also identical.

```
> cbind(sugar, fitted(sugar1.lm), fitted(sugar2.lm))

   weight     trt fitted(sugar1.lm) fitted(sugar2.lm)
1    82.0 Control          83.23333          83.23333
2    97.8 Control          83.23333          83.23333
3    69.9 Control          83.23333          83.23333
4    58.3       A          61.83333          61.83333
5    67.9       A          61.83333          61.83333
6    59.3       A          61.83333          61.83333
7    68.1       B          67.50000          67.50000
8    70.8       B          67.50000          67.50000
9    63.6       B          67.50000          67.50000
10   50.7       C          48.90000          48.90000
11   47.1       C          48.90000          48.90000
12   48.9       C          48.90000          48.90000
```