

## Balanced

```
## comparison of summary t-tests and F-tests from anova,
## with a balanced design
> reg <- lm(time ~ treatment + poison, boxcox.f)
> reg2 <- lm(time ~ poison + treatment, boxcox.f)

#####
> summary(reg) # output edited
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.31417    0.04366   6.880 2.16e-08 ***
treatmentB   0.36250    0.06458   5.614 1.43e-06 ***
treatmentC   0.07833    0.06458   1.213 0.231894
treatmentD   0.22000    0.06458   3.407 0.001459 **
poison1      0.13813    0.03229   4.278 0.000107 ***
poison2      0.06500    0.03229   2.013 0.050540 .

Residual standard error: 0.1582 on 42 degrees of freedom
Multiple R-Squared:  0.6503, Adjusted R-squared:  0.6087
F-statistic: 15.62 on 5 and 42 DF,  p-value: 1.123e-08

> summary(reg2) # output edited
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.31417    0.04366   6.880 2.16e-08 ***
poison1      0.13813    0.03229   4.278 0.000107 ***
poison2      0.06500    0.03229   2.013 0.050540 .
treatmentB   0.36250    0.06458   5.614 1.43e-06 ***
treatmentC   0.07833    0.06458   1.213 0.231894
treatmentD   0.22000    0.06458   3.407 0.001459 **

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#####
# Notice that the summary output is essentially the same,
# except for the order in which the coefficients appear in the table. Why?
#####

> anova(reg) # output edited
Analysis of Variance Table

Response: time
          Df Sum Sq Mean Sq F value    Pr(>F)
treatment  3  0.92121  0.30707   12.273 6.697e-06 ***
poison     2  1.03301  0.51651   20.643 5.704e-07 ***
Residuals 42  1.05086  0.02502

> anova(reg2)
Analysis of Variance Table

Response: time
          Df Sum Sq Mean Sq F value    Pr(>F)
poison     2  1.03301  0.51651   20.643 5.704e-07 ***
treatment  3  0.92121  0.30707   12.273 6.697e-06 ***
Residuals 42  1.05086  0.02502

#####
# Notice that the anova tables are essentially the same. Why?
#####
```

## Unbalanced

```
## comparison of summary t-tests and F-tests from anova,
## with an unbalanced design

> bc48 <- boxcox.fl[48,] # destroy the balance by discarding last case
> reg <- lm(time ~ treatment + poison, bc48)
> reg2 <- lm(time ~ poison + treatment, bc48)

#####
> summary(reg) # output edited
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.31417    0.04622   6.798 3.18e-08 ***
treatmentB   0.36230    0.06536   5.546 1.91e-06 ***
treatmentC   0.07833    0.06536   1.199 0.237601
treatmentD   0.22010    0.06690   3.290 0.002064 **
poison1      0.13810    0.03287   4.201 0.000140 ***
poison2      0.06498    0.03287   1.977 0.034848 .

Residual standard error: 0.1601 on 41 degrees of freedom
Multiple R-Squared:  0.6476, Adjusted R-squared:  0.6047
F-statistic: 13.07 on 5 and 41 DF,  p-value: 2.134e-08

> summary(reg2) # output edited
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.31417    0.04622   6.798 3.18e-08 ***
poison1      0.13810    0.03287   4.201 0.000140 ***
poison2      0.06498    0.03287   1.977 0.034848 .
treatmentB   0.36230    0.06536   5.546 1.91e-06 ***
treatmentC   0.07833    0.06536   1.199 0.237601
treatmentD   0.22010    0.06690   3.290 0.002064 **

Residual standard error: 0.1601 on 41 degrees of freedom
Multiple R-Squared:  0.6476, Adjusted R-squared:  0.6047
F-statistic: 13.07 on 5 and 41 DF,  p-value: 2.134e-08

#####
# Notice that the summary output is again essentially the same,
# except for the order in which the coefficients appear in the table. Why?
#####

> anova(reg) # output edited
      Analysis of Variance Table

      Response: time
            Df Sum Sq Mean Sq  F value    Pr(>F)
treatment   3  0.94389  0.31463   12.275 7.219e-06 ***
poison      2  0.98734  0.49377   19.265 1.263e-06 ***
Residuals  41  1.05086  0.02563

> anova(reg2)
      Analysis of Variance Table

      Response: time
            Df Sum Sq Mean Sq  F value    Pr(>F)
poison      2  1.01331  0.50665   19.767 9.739e-07 ***
treatment   3  0.91813  0.30604   11.940 9.361e-06 ***
Residuals  41  1.05086  0.02563

#####
# Notice that the anova tables are different. Why?
#####
```