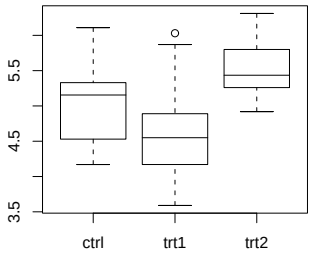
Plant Growth

```
> PlantGrowth
   weight group
1    4.17  ctrl
2    5.58  ctrl
[ . . . ]
29   5.80  trt2
30   5.26  trt2
> summary(PlantGrowth)
     weight       group
 Min.   :3.590   ctrl:10
 1st Qu.:4.550   trt1:10
 Median :5.155   trt2:10
 Mean   :5.073
 3rd Qu.:5.530
 Max.   :6.310
> attach(PlantGrowth)
> tapply(weight,group,mean)
 ctrl  trt1  trt2
5.032 4.661 5.526
> tapply(weight,group,sd)
     ctrl      trt1      trt2
0.5830914 0.7936757 0.4425733
> plot(group,weight)
>
```



One-Factor ANOVA

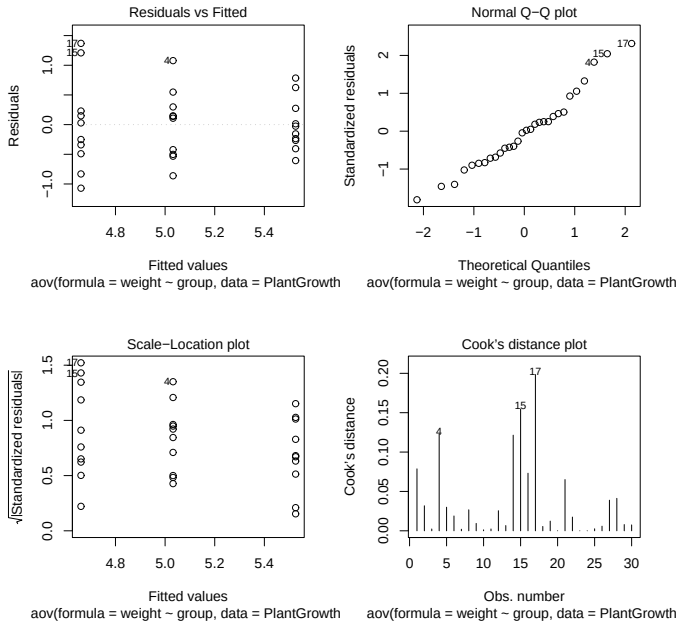
```
> pg.aov <- aov(weight ~ group, data=PlantGrowth)
> pg.aov
Call:
   aov(formula = weight ~ group, data = PlantGrowth)

Terms:
                    group Residuals
Sum of Squares   3.76634  10.49209
Deg. of Freedom        2        27

Residual standard error: 0.6233746
Estimated effects may be unbalanced
> summary(pg.aov)
            Df  Sum Sq Mean Sq F value  Pr(>F)
group        2  3.7663  1.8832  4.8461 0.01591 *
Residuals   27 10.4921  0.3886
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> coef(pg.aov)
(Intercept)   grouptrt1   grouptrt2
      5.032      -0.371       0.494
> resid(pg.aov)
     1      2      3      4      5      6      7
-0.862  0.548  0.148  1.078 -0.532 -0.422  0.138  [ . . . ]
>
```


ANOVA Model Matrix

```
> model.matrix(pg.aov)
   (Intercept) grouptrt1 grouptrt2
1            1         0         0
2            1         0         0
3            1         0         0
4            1         0         0
5            1         0         0
6            1         0         0
7            1         0         0
8            1         0         0
9            1         0         0
10           1         0         0
11           1         1         0
12           1         1         0
13           1         1         0
14           1         1         0
15           1         1         0
16           1         1         0
17           1         1         0
18           1         1         0
19           1         1         0
20           1         1         0
21           1         0         1
22           1         0         1
23           1         0         1
24           1         0         1
25           1         0         1
26           1         0         1
27           1         0         1
28           1         0         1
29           1         0         1
30           1         0         1
[ . . . ]
>
```


Regression Diagnostics

```
> plot(pg.aov)
```



Compare aov and lm

```
> pg.aov <- aov(weight ~ group, data=PlantGrowth)
> pg.lm <- lm(weight ~ group, data=PlantGrowth)
> pg.aov
Call:
   aov(formula = weight ~ group, data = PlantGrowth)

Terms:
                    group Residuals
Sum of Squares   3.76634  10.49209
Deg. of Freedom        2        27

Residual standard error: 0.6233746
Estimated effects may be unbalanced
> pg.lm

Call:
lm(formula = weight ~ group, data = PlantGrowth)

Coefficients:
(Intercept)    grouptrt1    grouptrt2
      5.032       -0.371        0.494
>
```


Compare aov and lm

```
> summary(pg.aov)
            Df  Sum Sq Mean Sq F value  Pr(>F)
group        2  3.7663  1.8832  4.8461 0.01591 *
Residuals   27 10.4921  0.3886
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> summary(pg.lm)

Call:
lm(formula = weight ~ group, data = PlantGrowth)

Residuals:
    Min      1Q  Median      3Q     Max
-1.0710 -0.4180 -0.0060  0.2627  1.3690

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.0320     0.1971  25.527   <2e-16 ***
grouptrt1    -0.3710     0.2788  -1.331   0.1944
grouptrt2     0.4940     0.2788   1.772   0.0877 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.6234 on 27 degrees of freedom
Multiple R-Squared: 0.2641,Adjusted R-squared: 0.2096
F-statistic: 4.846 on 2 and 27 DF,  p-value: 0.01591


>
```


Compare aov and lm

```
> coef(pg.aov)
(Intercept)   grouptrt1   grouptrt2
      5.032      -0.371       0.494
> coef(pg.lm)
(Intercept)   grouptrt1   grouptrt2
      5.032      -0.371       0.494
> resid(pg.aov)
     1      2      3      4      5      6      7
-0.862  0.548  0.148  1.078 -0.532 -0.422  0.138 [ . . . ]
> resid(pg.lm)
     1      2      3      4      5      6      7
-0.862  0.548  0.148  1.078 -0.532 -0.422  0.138 [ . . . ]
>
```