STAT 425

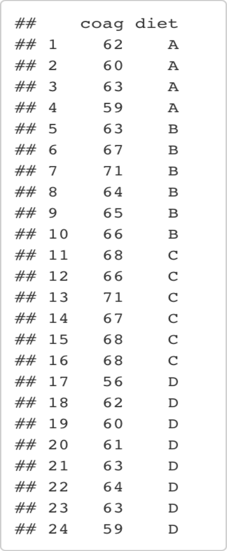
One Way ANOVA

Comparative Experiments

- A comparative experiment is intended to answer research questions regarding the differences between the effects of imposing two or more different conditions.
- The imposed conditions are the treatments, and they are imposed on the experimental units. The effects are measured using the responses (usually values of a single response variable).
- The way treatments are assigned to experimental units is called the design of the experiment. Some form of randomization is usually used. In that case, it is a randomized experiment (or sometimes randomized study).

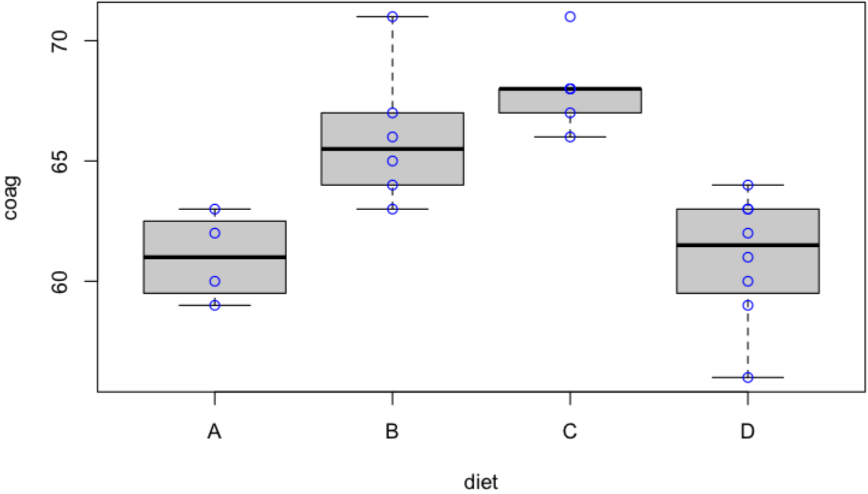
Blood Coagulation Example

- 24 animals were randomly assigned to 4 different diets with goal to study blood coagulation times.
- The samples were taken in a random order.
- This data set can be found in the *faraway* library.



```
##    coag diet
## 1    62    A
## 2    60    A
## 3    63    A
## 4    59    A
## 5    63    B
## 6    67    B
## 7    71    B
## 8    64    B
## 9    65    B
## 10   66    B
## 11   68    C
## 12   66    C
## 13   71    C
## 14   67    C
## 15   68    C
## 16   68    C
## 17   56    D
## 18   62    D
## 19   60    D
## 20   61    D
## 21   63    D
## 22   64    D
## 23   63    D
## 24   59    D
```

Blood Coagulation Example



Terminology

- Factor: an Independent variable. They can be experimental or observational. In our example: *Diet*

- Level: A particular form of the factor. In our example: *Levels of the Diet: A, B, C, D*

- Treatments: Factor levels or factor level combinations (if the study contains more than one factors). They provide insights into mechanisms causing the variation being studied.
Control treatments?

- Complete Randomized Design: Experimental units are randomly split into r groups, and r treatments are assigned, one per group.

One-Way ANOVA Model

- Data:

$$\begin{array}{ccccc} \text{group } 1 & y_{11}, & y_{12} & \ldots & y_{1n_1} \\ \text{group } 2 & y_{21}, & y_{22} & \ldots & y_{2n_2} \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ \text{group } r & y_{r1}, & y_{r2} & \ldots & y_{rn_r} \end{array}$$

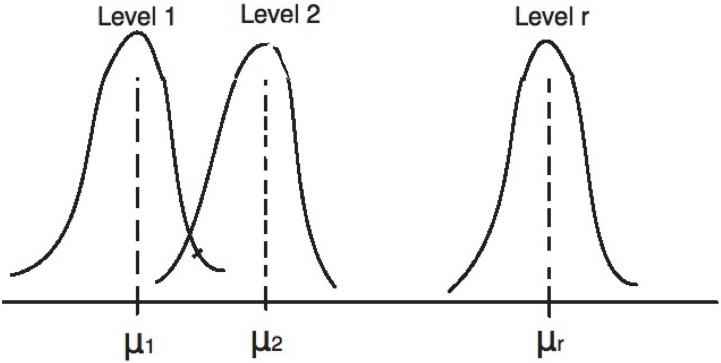
- r is the number of groups
- n_i denotes the number of obs in the ith group
- $n = \sum_{i=1}^{r} n_i$ is the total sample size
- y_{ij} = observation j for the ith factor.

ANOVA Means Model

$$y_{ij} = \mu_i + e_{ij},\ i = 1, \ldots, r; \quad j = 1, \ldots, n_i$$

- y_{ij}: the value of the response in the jth trial for the ith factor.
- μ_i: the population mean for the ith factor level (treatment).
- $e_{ij} \sim^{iid} N(0, \sigma^2)$

ANOVA Model Representation



ANOVA Factor Effects Model

Define the effect of factor level i on the response, i.e. the treatment effect as

$$\alpha_i = \mu_i - \mu$$

where μ is the overall mean.

Factor Effects Model

$$y_{ij} = \mu + \alpha_i + e_{ij},\ i = 1, \ldots, r;\ j = 1, \ldots, n_i$$

$$e_{ij} \sim^{iid} N(0, \sigma^2)$$

Model Parametrization

$$y_{ij} = \mu + \alpha_i + e_{ij}$$

- The factor effects model has $r + 1$ model parameters, i.e.

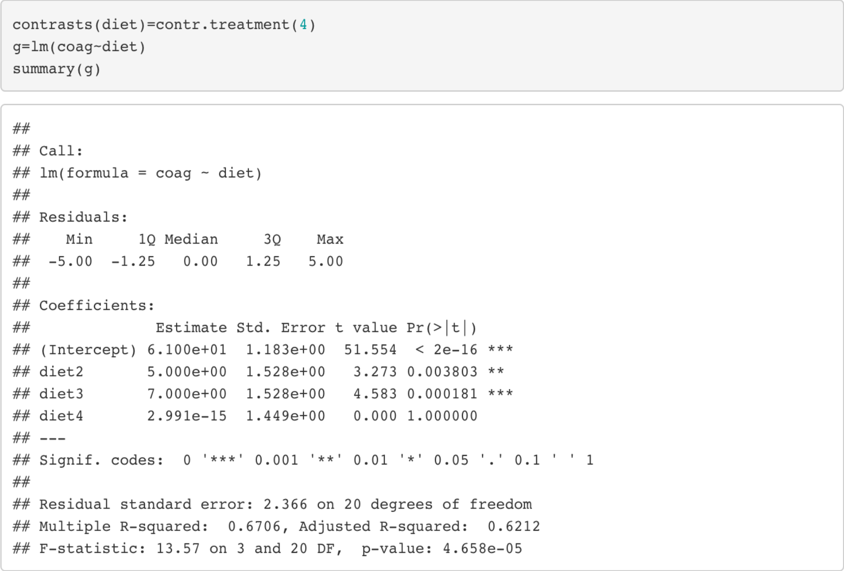
$$(\mu, \alpha_1, \ldots, \alpha_r)$$

- In order for the α's to be (uniquely) estimated, we need to impose restrictions.
- The restrictions on the α's depend on how μ is defined.

Model	μ Definition	α's Restriction
Reference Cell	$\mu = \mu_1$	$\alpha_1 = 0$
Sum-to-Zero	$\mu = \frac{1}{r}\sum_i \mu_i$	$\sum_i \alpha_i = 0$
Weighted Sum-to-Zero	$\mu = \frac{1}{n}\sum_i n_i\mu_i$	$\sum_i n_i\alpha_i = 0$

- The default in R is the Reference Cell model.

Coagulation Example: Reference Cell (default)



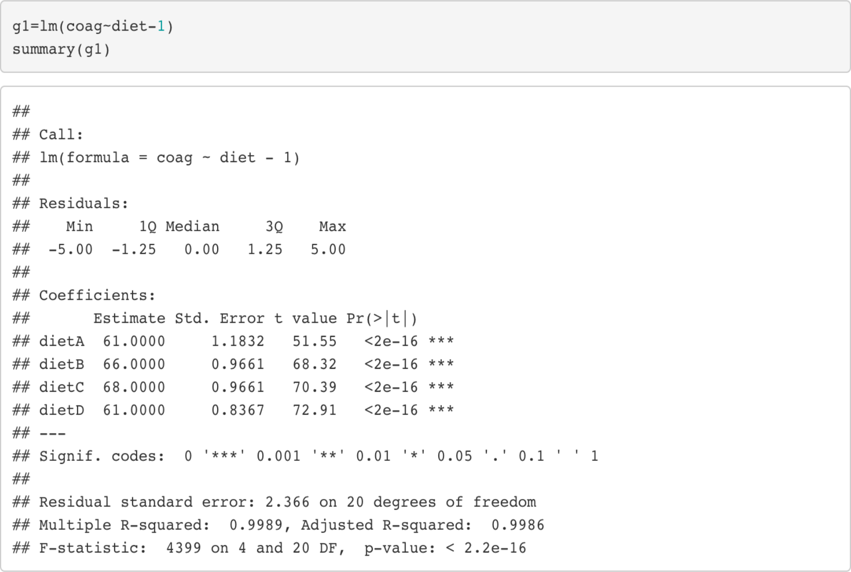
```
contrasts(diet)=contr.treatment(4)
g=lm(coag~diet)
summary(g)
```

```
##
## Call:
## lm(formula = coag ~ diet)
##
## Residuals:
##    Min     1Q Median     3Q    Max
##  -5.00  -1.25   0.00   1.25   5.00
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 6.100e+01  1.183e+00  51.554  < 2e-16 ***
## diet2       5.000e+00  1.528e+00   3.273 0.003803 **
## diet3       7.000e+00  1.528e+00   4.583 0.000181 ***
## diet4       2.991e-15  1.449e+00   0.000 1.000000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.366 on 20 degrees of freedom
## Multiple R-squared:  0.6706, Adjusted R-squared:  0.6212
## F-statistic: 13.57 on 3 and 20 DF,  p-value: 4.658e-05
```

```
model.matrix(g)
```

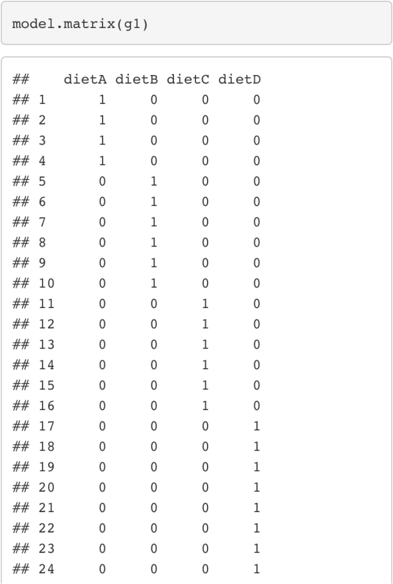
```
##    (Intercept) dietB dietC dietD
## 1            1     0     0     0
## 2            1     0     0     0
## 3            1     0     0     0
## 4            1     0     0     0
## 5            1     1     0     0
## 6            1     1     0     0
## 7            1     1     0     0
## 8            1     1     0     0
## 9            1     1     0     0
## 10           1     1     0     0
## 11           1     0     1     0
## 12           1     0     1     0
## 13           1     0     1     0
## 14           1     0     1     0
## 15           1     0     1     0
## 16           1     0     1     0
## 17           1     0     0     1
## 18           1     0     0     1
## 19           1     0     0     1
## 20           1     0     0     1
## 21           1     0     0     1
## 22           1     0     0     1
## 23           1     0     0     1
## 24           1     0     0     1
```

Coagulation Example: A coding that fits the Mean Model



```
g1=lm(coag~diet-1)
summary(g1)
```

```
##
## Call:
## lm(formula = coag ~ diet - 1)
##
## Residuals:
##    Min     1Q Median     3Q    Max
##  -5.00  -1.25   0.00   1.25   5.00
##
## Coefficients:
##       Estimate Std. Error t value Pr(>|t|)
## dietA  61.0000     1.1832   51.55   <2e-16 ***
## dietB  66.0000     0.9661   68.32   <2e-16 ***
## dietC  68.0000     0.9661   70.39   <2e-16 ***
## dietD  61.0000     0.8367   72.91   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.366 on 20 degrees of freedom
## Multiple R-squared:  0.9989, Adjusted R-squared:  0.9986
## F-statistic:  4399 on 4 and 20 DF,  p-value: < 2.2e-16
```



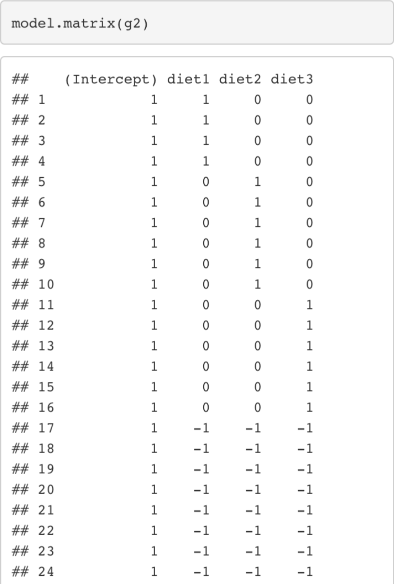
```
model.matrix(g1)
```

```
##    dietA dietB dietC dietD
## 1      1     0     0     0
## 2      1     0     0     0
## 3      1     0     0     0
## 4      1     0     0     0
## 5      0     1     0     0
## 6      0     1     0     0
## 7      0     1     0     0
## 8      0     1     0     0
## 9      0     1     0     0
## 10     0     1     0     0
## 11     0     0     1     0
## 12     0     0     1     0
## 13     0     0     1     0
## 14     0     0     1     0
## 15     0     0     1     0
## 16     0     0     1     0
## 17     0     0     0     1
## 18     0     0     0     1
## 19     0     0     0     1
## 20     0     0     0     1
## 21     0     0     0     1
## 22     0     0     0     1
## 23     0     0     0     1
## 24     0     0     0     1
```

Coagulation Example: $\sum_i \alpha_i = 0$

```
contrasts(diet) = contr.sum(4)
g2 = lm(coag~diet)
summary(g2)
```

```
##
## Call:
## lm(formula = coag ~ diet)
##
## Residuals:
##    Min     1Q Median     3Q    Max
##  -5.00  -1.25   0.00   1.25   5.00
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  64.0000     0.4979 128.537  < 2e-16 ***
## diet1        -3.0000     0.9736  -3.081 0.005889 **
## diet2         2.0000     0.8453   2.366 0.028195 *
## diet3         4.0000     0.8453   4.732 0.000128 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.366 on 20 degrees of freedom
## Multiple R-squared:  0.6706, Adjusted R-squared:  0.6212
## F-statistic: 13.57 on 3 and 20 DF,  p-value: 4.658e-05
```



```
model.matrix(g2)
```

```
##    (Intercept) diet1 diet2 diet3
## 1            1     1     0     0
## 2            1     1     0     0
## 3            1     1     0     0
## 4            1     1     0     0
## 5            1     0     1     0
## 6            1     0     1     0
## 7            1     0     1     0
## 8            1     0     1     0
## 9            1     0     1     0
## 10           1     0     1     0
## 11           1     0     0     1
## 12           1     0     0     1
## 13           1     0     0     1
## 14           1     0     0     1
## 15           1     0     0     1
## 16           1     0     0     1
## 17           1    -1    -1    -1
## 18           1    -1    -1    -1
## 19           1    -1    -1    -1
## 20           1    -1    -1    -1
## 21           1    -1    -1    -1
## 22           1    -1    -1    -1
## 23           1    -1    -1    -1
## 24           1    -1    -1    -1
```

Model Properties

1. $E(y_{ij}) = \mu_i$
2. $Var(y_{ij}) = Var(e_{ij}) = \sigma^2$
   Thus, all observations have the same variance, regardless of factor level.
3. $e_{ij} \sim N(0, \sigma^2)$ and independent.
4. $y_{ij} \sim \mathcal{N}(\mu_i, \sigma^2)$ and independent.

We can re-state the model as

$$y_{ij} \text{ are independent } \mathcal{N}(\mu_i, \sigma^2)$$

Fitting of ANOVA Model

Minimize the sum of squared deviations of the observations around their expected values with respect to the parameters:

$$Q = \sum_{i=1}^{r} \sum_{j=1}^{n_i} (y_{ij} - \mathbb{E}(y_{ij}))^2$$

If we re-write Q we have

$$Q = \sum_{j} (y_{1j} - \mu_1)^2 + \sum_{j} (y_{2j} - \mu_2)^2 + \ldots + \sum_{j} (y_{rj} - \mu_r)^2$$

So the least squares estimator of μ_i, denoted by $\hat{\mu}_i$ is

$$\hat{\mu}_i = \bar{y}_{i\cdot} = \frac{1}{n_i} \sum_{j=1}^{n_i} y_{ij}$$

Using the appropriate constraints, we can easily extract the estimators for μ and α_i.

Using the model ‘g2‘ with constraint $\sum_{i=1}^{4} \alpha_i = 0$ we have:

```
g2$coef
```

```
## (Intercept)       diet1       diet2       diet3
##          64          -3           2           4
```

This implies that $\hat{\mu} = 64$ and

$$\begin{array}{ll} \hat{\alpha}_1 = -3 & \hat{\mu}_1 = 64 - 3 = 61 \\ \hat{\alpha}_2 = 2 & \hat{\mu}_2 = 64 + 2 = 66 \\ \hat{\alpha}_3 = 4 & \hat{\mu}_3 = 64 + 4 = 68 \end{array}$$

The estimators for α_4 and the corresponding mean μ_4, are obtained them using the constraints:

$$\hat{\alpha}_4 = -\hat{\alpha}_1 - \hat{\alpha}_2 - \hat{\alpha}_3 = 3 - 2 - 4 = -3 \text{ and } \hat{\mu}_4 = 64 - 3 = 61$$

Fitted Values & Residuals

- The LS fit for y_{ij} is the corresponding group mean

$$\hat{y}_{ij} = \bar{y}_{i\cdot}$$

- Residuals

$$r_{ij} = y_{ij} - \hat{y}_{ij} = y_{ij} - \bar{y}_{i\cdot}$$

- RSS

$$\sum_{i=1}^{r} \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_{i\cdot})^2,$$

i.e. the within-group variation.

ANOVA Table

Source of Variation	SS	df	MS
Between Groups	$FSS = \sum n_i(\bar{y}_{i\cdot} - \bar{y}_{\cdot\cdot})^2$	$r - 1$	$\frac{FSS}{r-1}$
Error (within groups)	$RSS = \sum\sum(y_{ij} - \bar{y}_{i\cdot})^2$	$n - r$	$\frac{RSS}{n-r}$
Total	$TSS = \sum\sum(y_{ij} - \bar{y}_{\cdot\cdot})^2$	$n - 1$	

F-test

- We want to test whether the means of the groups are really different. We can express this as

$$\begin{cases} H_0 : \mu_1 = \mu_2 = \ldots = \mu_r \\ H_\alpha : \text{ not all } \mu_i,\; i = 1, \ldots, r \text{ are equal} \end{cases}$$

- or in terms of models

$$\begin{cases} H_0 : y_{ij} = \mu + e_{ij} \\ H_a : y_{ij} = \mu + \alpha_i + e_{ij} \end{cases}$$

F-test

- They are two nested models, so we can use the F-test

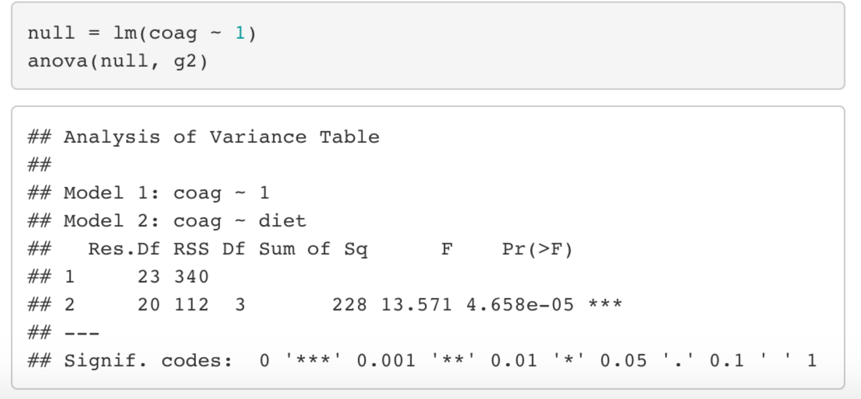
$$\frac{(RSS_0 - RSS_a)/(r-1)}{RSS_a/(n-r)} \sim F_{r-1,n-r},$$

under H_0.

- The test statistic can also be written as

$$\frac{FSS/(r-1)}{RSS/(n-r)} = \frac{\text{Between-group Variation}/(r-1)}{\text{Within-group Variation}/(n-r)},$$

where FSS, RSS are defined in the ANOVA table.

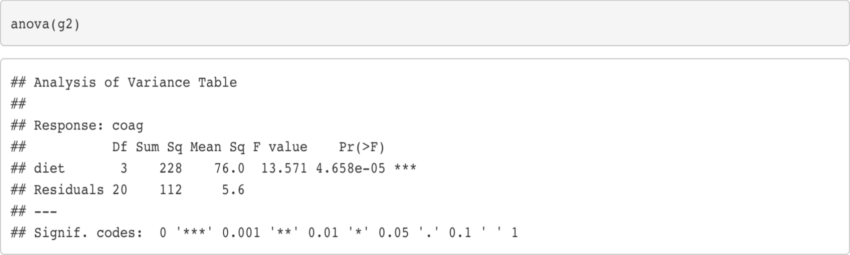


```
null = lm(coag ~ 1)
anova(null, g2)
```

```
## Analysis of Variance Table
##
## Model 1: coag ~ 1
## Model 2: coag ~ diet
##   Res.Df RSS Df Sum of Sq      F    Pr(>F)
## 1     23 340
## 2     20 112  3       228 13.571 4.658e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- It does not matter which coding is used for the mean/effects. The results would be the same.

Equivalently, we can get the ANOVA table that contains the same F test and p-value:



```
anova(g2)
```

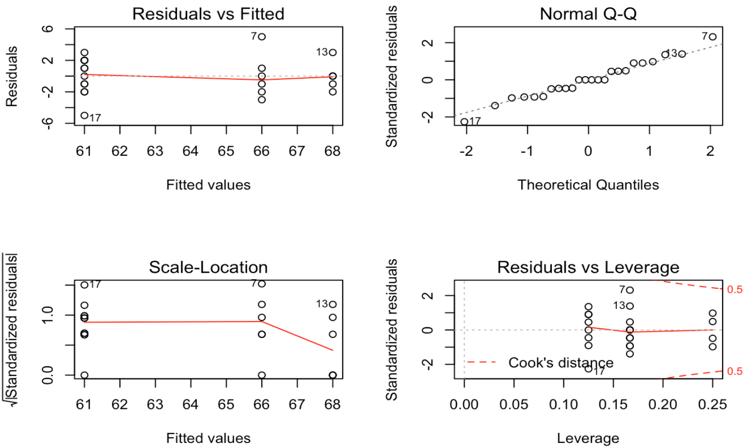
```
## Analysis of Variance Table
##
## Response: coag
##           Df Sum Sq Mean Sq F value    Pr(>F)
## diet       3    228    76.0  13.571 4.658e-05 ***
## Residuals 20    112     5.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The p-value is much less than $\alpha = 5\%$, so we reject the null and conclude that there are differences among the different types of diet.

Diagnostics for ANOVA Models

- Check for outliers/ unusual observations.
- Check the residuals vs. fitted values plot for departures from the constant variance assumption.
- Check the Q-Q plot for departures from the normality assumption.

```r
par(mfrow=c(2,2))
plot(g2)
```

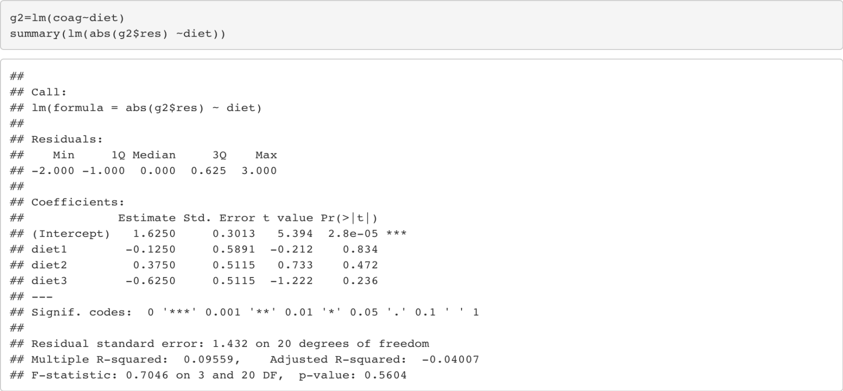


Levene's Test for Equality of Variances:

- Run Regression abs(residuals)$\sim$ X, i.e. use abs(residuals) as the response in a new one-way ANOVA.

- If the p-value for the F-test is greater than 1% level, then we conclude that there is no evidence of a non-constant variance.

H_0 : All group variances are equal.



```
g2=lm(coag~diet)
summary(lm(abs(g2$res) ~diet))
```

```
##
## Call:
## lm(formula = abs(g2$res) ~ diet)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -2.000 -1.000  0.000  0.625  3.000
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.6250     0.3013   5.394  2.8e-05 ***
## diet1        -0.1250     0.5891  -0.212    0.834
## diet2         0.3750     0.5115   0.733    0.472
## diet3        -0.6250     0.5115  -1.222    0.236
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.432 on 20 degrees of freedom
## Multiple R-squared:  0.09559,    Adjusted R-squared:  -0.04007
## F-statistic: 0.7046 on 3 and 20 DF,  p-value: 0.5604
```

- Since the p-value is greater than 0.01, there is no evidence of unequal variances.