4.1a.   The completed table is as follows:

Source	DF	SS	MS	F	P
Treatment	4	1010.56	**252.640**	29.84	**< 0.00001**
Block	**5**	**323.82**	64.765	**7.649**	**< 0.00001**
Error	20	169.33	**8.467**		
Total	29	1503.71			

DF: **5** $= 20/4$
SS: **323.82** $= 1503.71 - 169.33 - 1010.56$
MS: **252.640** $= 1010.56/4$
       8.467 $= 169.33/20$
F: **7.649** $= 64.765/8.467$
P: **< 0.00001** $=$ using online calculator

4.1b. $df = b - 1 = 5$, so $b = 6$, so 6 blocks were used.

4.1c.   Because the p-value is much smaller than 0.05, at the significance level of 0.05, we will reject
        the null hypothesis to conclude that the means of the five treatments as well as the means of
        the six blocks are significantly different from each other and thus not equal. Basically,
        different types of treatments and different types of blocks do have an effect on the response
   variable.

4.3

```
> fit4 <- aov(Strength~factor(Chemical) + factor(Bolt), data = chem)
> summary(fit4)
                 Df Sum Sq Mean Sq F value   Pr(>F)
factor(Chemical)  3  12.95    4.32   2.376    0.121
factor(Bolt)      4 157.00   39.25  21.606 2.06e-05 ***
Residuals        12  21.80    1.82
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
~
```

For Chemical, since the p-value is greater than 0.05, at the significance level of 0.05, the null
hypothesis is failed to be rejected. Thus, we conclude that different chemical types have no
effect on strength. However, the p-value of Bolt is significant at the 0.05 level since it's
smaller than that. Hence, we conclude that different types of bolts have an effect on
strength.

Residuals vs Fitted

aov(Strength ~ factor(Chemical) + factor(Bolt))
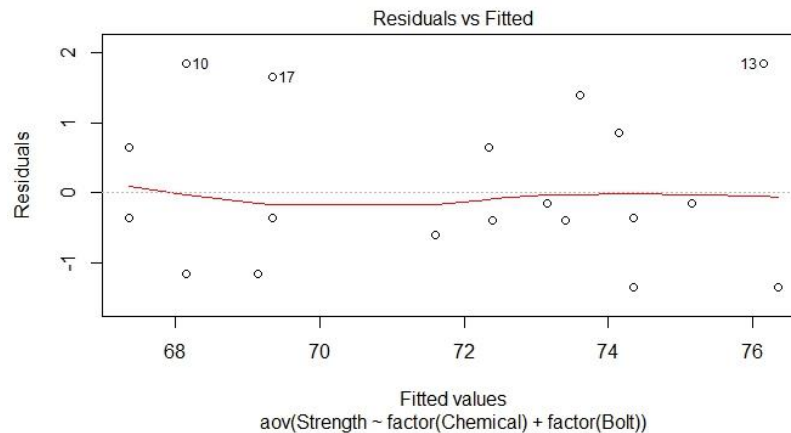
Moreover, the residual plot is for the most part randomly scattered and show no significant pattern. However, using a test of normality can help us to determine whether our model is valid. Regardless, there is no strong violation of the constant variance assumption as well as the linearity one.

4.8a.
```
> fit <- aov(Responses~factor(Region)+factor(Design), data = sales)
> summary(fit)
                Df Sum Sq Mean Sq F value  Pr(>F)
factor(Region)   3  49036   16345   18.07 0.00208 **
factor(Design)   2  90755   45378   50.15 0.00018 ***
Residuals        6   5429     905
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
13 observations deleted due to missingness
```

From the ANOVA table, we see that the p-value for both Region and Design is significant at a significance level of 0.05 since it is smaller than that. Thus, we can reject the null hypothesis and conclude that design type and region type do have an effect on responses.

4.8b. Using R code, I have used the Tukey method:

```
> sales$Region <- as.factor(sales$Region)
>
> tukey <- TukeyHSD(fit)
> tukey
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = Responses ~ factor(Region) + factor(Design), data = sales)

$`factor(Region)`
            diff        lwr        upr      p adj
NW-NE    96.66667   11.64632 181.68701 0.0292948
SE-NE   -38.66667 -123.68701  46.35368 0.4560435
SW-NE   113.33333   28.31299 198.35368 0.0142872
SE-NW  -135.33333 -220.35368 -50.31299 0.0060311
SW-NW    16.66667  -68.35368 101.68701 0.9015669
SW-SE   152.00000   66.97966 237.02034 0.0033310

$`factor(Design)`
        diff        lwr        upr      p adj
2-1   175.25  109.98853  240.51147 0.0004236
3-1   -17.25  -82.51147   48.01147 0.7104869
3-2  -192.50 -257.76147 -127.23853 0.0002508
```

Because the p-value is smaller than 0.05 between designs 2 and 1 as well as 3 and 2, we can reject the null hypothesis and say that their mean responses are significantly different from each other. The mean responses garnered from designs 3 and 1 are not significantly different from each other, so we fail to reject the null hypothesis. Basically, the mean responses garnered from design 2 is different from the mean responses garnered from designs 1 and 3, while the mean responses garnered between designs 1 and 3 do not differ.

4.8c.
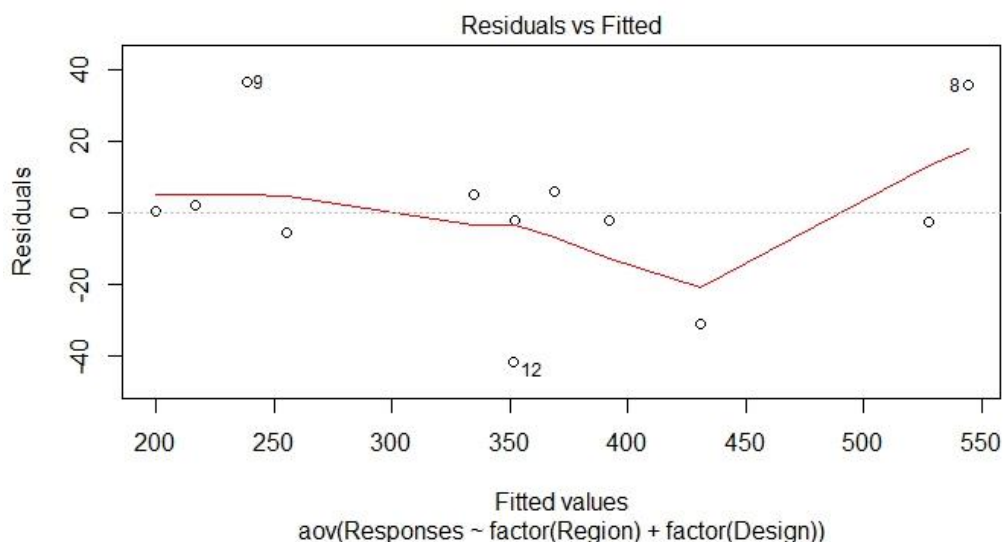
Residuals vs Fitted

Fitted values
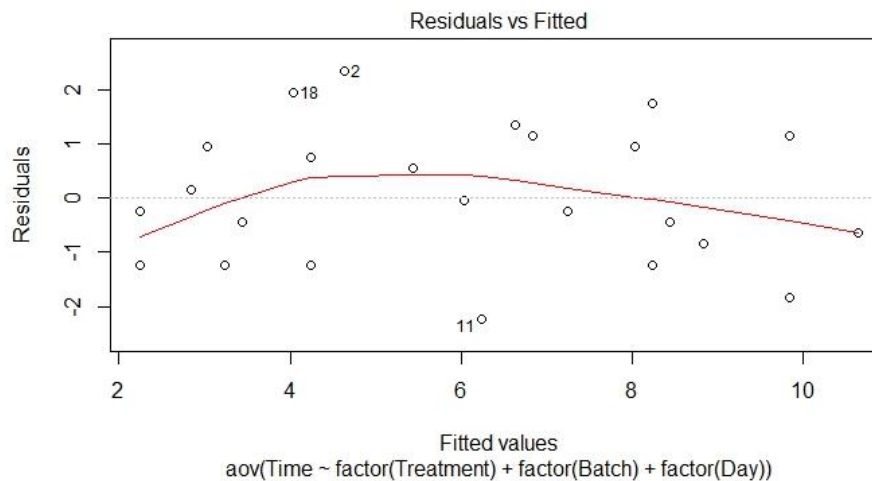aov(Responses ~ factor(Region) + factor(Design))

The residual plot is for the most part randomly scattered and show no significant pattern. However, using a test of normality can help us to determine whether our model is valid. Regardless, there is no strong violation of the constant variance assumption as well as the linearity one.

4.22

```
> fit2 <- aov(Time~factor(Treatment)+factor(Batch)+factor(Day), data = batch)
> summary(fit2)
                 Df Sum Sq Mean Sq F value   Pr(>F)
factor(Treatment)  4 141.44   35.36  11.309 0.000488 ***
factor(Batch)      4  15.44    3.86   1.235 0.347618
factor(Day)        4  12.24    3.06   0.979 0.455014
Residuals         12  37.52    3.13
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> |
```

The following is the ANOVA output from R. As we can see, the p-value for Treatment is significant at the 0.05 significance level since it is smaller than 0.05, while Batch and Day are not significant. The treatment refers to the ingredients, so we conclude that the chemical ingredients have a significant effect on the mean reaction time (we reject the null hypothesis), while the effects of Batch and Day do not have any effect on the mean reaction time (we fail to reject the null hypothesis). Basically, only ingredients have an effect on the mean reaction time, while Batch and Days do not.

Residuals vs Fitted

Fitted values
aov(Time ~ factor(Treatment) + factor(Batch) + factor(Day))

We can also confirm that the residual plot is for the most part randomly scattered and show no significant pattern. Although it seems like a quadratic trend may be seen, the trend is negligible. However, using a test of normality can help us to determine whether our model is valid. Regardless, there is no strong violation of the constant variance assumption as well as the linearity one.

4.35 Using R code, I have outputted the following ANOVA table:
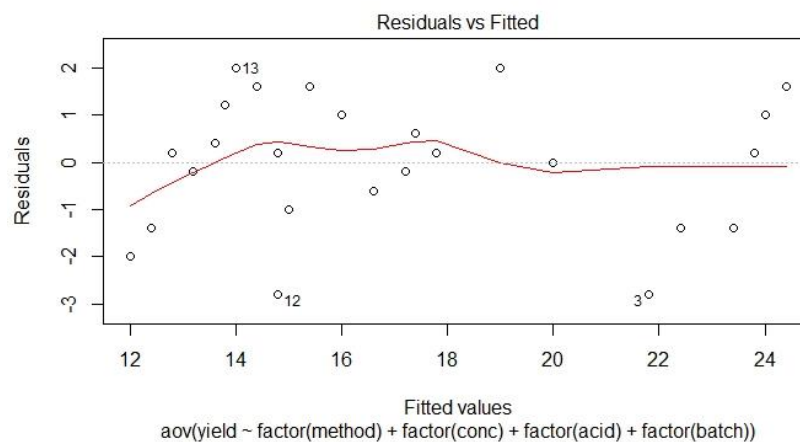
```
> assemblyDF = data.frame(acid, batch, method,
+                         conc, yield)
>
> a2.aov = aov(yield ~ factor(method) + factor(conc) +  factor(acid) + factor(batch),
+             data = assemblyDF)
> summary(a2.aov)
               Df Sum Sq Mean Sq F value   Pr(>F)
factor(method)  4  342.8   85.70  14.650 0.000941 ***
factor(conc)    4   12.0    3.00   0.513 0.728900
factor(acid)    4   24.4    6.10   1.043 0.442543
factor(batch)   4   10.0    2.50   0.427 0.785447
Residuals       8   46.8    5.85
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> qf(0.95, df1 = 4-1, df2 = (4-2)*(4-1))
[1] 4.757063
```

We see from the output that at a significance level of 0.05, the p-value is only significant for method, which is the standing time (thus we reject the null hypothesis). For concentration, acid, and batch, we must fail to reject the null hypothesis.

Thus, we conclude that the five standing times are significantly different from each other as their means do not match and thus the standing time has a significant effect on yield. We also conclude that the five catalyst concentrations, the five acid concentrations, and the five batches of raw materials have no significant effect on the yields since their p-values are too large.

The residual plot is for the most part randomly scattered and show no significant pattern. However, using a test of normality can help us to determine whether our model is valid. Regardless, there is no strong violation of the constant variance assumption as well as the linearity one.