1. **Two-factor factorial** - R code is provided below. This code shows how to do side-by-side box plots for the different treatment groups, how to compute a table of means, and how to (crudely) plot the treatment group means. Following that it computes the ANOVA table, plots the residuals and tests the contrasts.

(a) Examining the table of means (especially looking at averages for each factor individually) suggests that reinforcement improves memory on average (though not for each level of isolation time) and that there are differences across the isolation times (memory scores are higher after 40 minutes of isolation than they are after 20 or 60 minutes). The table of means and the graphs shows that there appears to be an interaction because verbal reinforcement appears to have a big effect for longer (60 minute) isolation times but little (or even a negative) effect for shorter times.

(b) ANOVA table shows reinforcement, isolation, and their interaction are each significant at the .05 level.

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>reinforce</td>
<td>1</td>
<td>196.000000</td>
<td>196.000000</td>
<td>12.42</td>
<td>0.0014</td>
</tr>
<tr>
<td>isolation</td>
<td>2</td>
<td>156.222222</td>
<td>78.111111</td>
<td>4.95</td>
<td>0.0139</td>
</tr>
<tr>
<td>reinforce*isolation</td>
<td>2</td>
<td>1058.666667</td>
<td>529.333333</td>
<td>33.55</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>30</td>
<td>473.333333</td>
<td>15.777778</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(c) The residual plots appear to be consistent with constant variance. The normal probability plot exhibits a fairly straight line indicating the normal error assumption is met.

(d) Note that I used a contrast function from the package "lsmeans" to carry out the contrast tests. You can see in the code below how that package works. Contrast results:

<table>
<thead>
<tr>
<th>contrast</th>
<th>estimate</th>
<th>SE</th>
<th>df</th>
<th>t.ratio</th>
<th>p.value</th>
</tr>
</thead>
<tbody>
<tr>
<td>lin</td>
<td>1.000000</td>
<td>1.621613</td>
<td>30</td>
<td>0.617</td>
<td>0.5421</td>
</tr>
<tr>
<td>quad</td>
<td>8.666667</td>
<td>2.808717</td>
<td>30</td>
<td>3.086</td>
<td>0.0043</td>
</tr>
</tbody>
</table>

i. The quadratic contrast for isolation time is significant but the linear contrast is not.
ii. There is no contrast required for reinforcement since this factor has only two levels and thus 1 d.f. In other words there is only one contrast (weights (-1,1)) and this is the contrast reported in the usual ANOVA output.
iii. The main effect shows that reinforcement does work to increase memory retention. The interaction suggests that verbal reinforcement does not work equally well for all isolation times. The interaction is the difference in the reinforcement effect over different isolation times (the effect of verbal reinforcement is small (even negative) at 20 and 40 minutes and big at 60 minutes).

(e) Summary: Positive verbal reinforcement does tend to enhance children’s memory. The effect is especially noticeable when there is a long time before the recall event. In fact there is no difference between the reinforcement and non-reinforcement groups at lower isolation times. The results are relevant for 4th graders in the city. It is not clear that we can generalize the results to include other cities or even other grades in this city.

```r
library(tidyverse)
library(lsmeans)
library(car)
# read in data and identify variables as categorical factors
datainput <- read_csv("H://HAL/Courses/Stat210//paragraphdata.csv")
paragraph <- data.frame(datainput)
paragraph$reinforce <- as.factor(paragraph$reinforce)
paragraph$isolation <- as.factor(paragraph$isolation)
# plot side-by-side box plots of the data from each group
boxplot(score ~ reinforce*isolation,data=paragraph)
# carry out two-way ANOVA
paragraph_anova <- aov(score ~ reinforce + isolation + reinforce*isolation, data=paragraph)
anova(paragraph_anova)
# plot residuals
plot(paragraph_anova$fitted.values,paragraph_anova$residuals,pch="x")
qqnorm(paragraph_anova$residuals)
# use the lsmeans package to test the contrasts
leastsquare = lsmeans(paragraph_anova, "isolation")

contrasts = list(lin = c(-1, 0, 1),
                quad = c(-1, 2, -1))
contrast(leastsquare, contrasts)
```
2. Three-factor factorial

(a) | d.f. | SS   | MS   | F    | pvalue |
---|------|------|------|------|--------|
*species* | 2    | 9900.0 | 4950.0 | 50.11 | 0.0000 |
*soil* | 2    | 16436.1 | 8218.0 | 83.19 | 0.0000 |
*fungicide* | 1    | 1932.0 | 1932.0 | 19.56 | 0.0001 |
spec*soil | 4    | 658.4 | 164.6 | 1.67  | 0.1792 |
spec*fung | 2    | 194.0 | 97.0 | 0.98  | 0.3844 |
*soil*fung | 2    | 1851.1 | 925.6 | 9.37  | 0.0005 |
*threeway* | 4    | 1069.7 | 267.4 | 2.71  | 0.0454 |
error | 36    | 3556.2 | 98.8 | ---- | significant at the .05 level |

(b) 

i. Means for the levels of each main factor are given below. From the means, we see that sweet clover emerges slowly, clay is problematic, and fungicide works.

<table>
<thead>
<tr>
<th>Species</th>
<th>Alfalfa</th>
<th>Red clover</th>
<th>Sweet clover</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>76.7</td>
<td>82.2</td>
<td>51.0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Soil Type</th>
<th>Silt loam</th>
<th>Sand</th>
<th>Clay</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>77.8</td>
<td>86.2</td>
<td>45.8</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fungicide</th>
<th>No</th>
<th>Yes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>64.0</td>
<td>75.9</td>
</tr>
</tbody>
</table>

ii. The ANOVA table tells us that the Soil*Fungicide interaction is most significant. For interpretation, we should look at the table of means for this interaction (and perhaps make a plot of the means in the table).

<table>
<thead>
<tr>
<th>Soil Type</th>
<th>Fungicide</th>
<th>No</th>
<th>Yes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Silt loam</td>
<td>74.7</td>
<td>81.0</td>
<td></td>
</tr>
<tr>
<td>Sand</td>
<td>85.7</td>
<td>86.7</td>
<td></td>
</tr>
<tr>
<td>Clay</td>
<td>31.7</td>
<td>60.0</td>
<td></td>
</tr>
</tbody>
</table>

Interpretation: Main effects indicate that fungicide is effective. The interaction shows that the fungicide is very effective in clay, less so in the other soils. The fungicide effect is not the same for all soils.

3. Randomized block ANOVA

(a) There are 6 treatments so 5 d.f. for treatment. There are 6*8=48 total measurements (6 treatments at each of 8 locations). Thus the d.f. for within group is 42 = (8-1)*6. The completed ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>Sum Squares</th>
<th>d.f.</th>
<th>MS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>96.99</td>
<td>5</td>
<td>19.40</td>
</tr>
<tr>
<td>WithinGroup</td>
<td>91.47</td>
<td>42</td>
<td>2.18</td>
</tr>
<tr>
<td>Total</td>
<td>188.46</td>
<td>47</td>
<td></td>
</tr>
</tbody>
</table>

We can test the hypothesis of equal treatment means using the usual ANOVA F-test. F=19.40/2.18 = 8.9 which yields p < .0001 when compared to the $F_{5,42}$ distribution. We can reject the hypothesis of equal treatment means.

(b) We should look at the residuals $e_{ij} = Y_{ij} - \bar{Y}_j$ (where $i$ indexes blocks and $j$ indexes treatments) and plot them vs location (i.e., block). If there is a location effect then we might expect to see the residuals cluster in such a plot (i.e., tend to be high for some locations and low for others) instead of being evenly spread out around zero in each location.

(c) The revised ANOVA table is as follows:

<table>
<thead>
<tr>
<th>Source</th>
<th>Sum Squares</th>
<th>d.f.</th>
<th>MS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blocks</td>
<td>76.24</td>
<td>7</td>
<td>10.89</td>
</tr>
<tr>
<td>Treatments</td>
<td>96.99</td>
<td>5</td>
<td>19.40</td>
</tr>
<tr>
<td>WithinGroup</td>
<td>15.23</td>
<td>35</td>
<td>0.44</td>
</tr>
<tr>
<td>Total</td>
<td>188.46</td>
<td>47</td>
<td></td>
</tr>
</tbody>
</table>

Here too we can clearly reject the hypotheses of equal treatment means (now comparing $F=19.40/0.44 = 44.58$ to a $F_{5,35}$ distribution. Notice that the MS(WithinGroup) is much smaller now. Once we remove the location effect the precision with which we can compare treatments has improved considerably.

(d) The MS(WithinGroup) in part (c) is 0.44. This is an estimate of the variance due to individual variation (sometimes called the error variance) but it also includes any interactions between treatment and block. The additional information provided suggests that the true variance due to individual variation is 0.30. This allows us to potentially judge the magnitude of the interaction by comparing those two estimates. The ratio (about 1.47) is an F-statistic – this would be compared to the F-distribution with 35 and 48 degrees of freedom (the 48 is because we have two observations of every treatment/block combination). The p-value is about .12. This suggests there might be some interaction of treatment and block but the interaction effect would not typically be judged significant enough that we would reject the randomized block analysis.
4. Randomized block ANOVA in R

(a) There seem to be several places where the curves cross suggesting a possible interaction between treatment and block. In particular there are a couple of varieties where the measurement for the treatment 4 is much higher than the measurement for treatment 2 while most varieties don’t have much difference. As usual it is hard to really judge though because the square root of the MSE is 977 when we do the ANOVA (in a subsequent part of the problem). This value of the square root of the MSE means that points can be up to 1900 away from their “true” value just due to random variation found among individual observations.

(b) The normal probability plot shows that the residuals look roughly normal. The plot shows fairly constant variance across treatments. There is some evidence of non-constant variance across varieties but this is hard (impossible) to judge with only 3 observations per block.

(c) The F-test statistic for the treatment effect is 38.52 with \( p < .0001 \). There is strong evidence of treatment differences.

(d) We can use the Bonferroni procedure (or the Tukey procedure as they agree in this case) and detect that the control (mean = 4557.5) is worse than the two treatments (mean = 2150 for 4 weeks and mean = 1758 for 2 weeks). The difference between the two treatments (2 weeks or 4 weeks) does not appear to be significant. The first result is what we would expect - some herbicide application is better than none. Early application is a bit better than late application but the difference is not significant.

(e) Blocks are not significantly different at the .05 level or even at the .10 level. This DOES NOT however mean that blocking was ineffective. This is an important point. Blocking is mildly effective in this study. The MSE would be higher had we not blocked. The quantity I mentioned in class estimates MSE for an unblocked study is 18\% higher than the MSE in the blocked study. This means we’d need 18\% more data (perhaps 19 measurements per treatment instead of the 16 blocks) in a completely randomized experiment to attain the same level of significance as we found in the blocked study.

R code:

```r
library(tidyverse)
datainput <- read_csv("H://HAL/Courses/Stat210//weedctrl2.csv")
weedsall <- data.frame(datainput)
weedsall$treat <- as.factor(weedsall$treat)
weeds <- weedsall[weedsall$loc==1,]

# plot data with each block in a different color; connect points with lines
ggplot() +
  geom_point(data=weeds, mapping=aes(x=treat, y=biomass, color=variety)) +
  geom_line(data=weeds, mapping=aes(x=treat, y=biomass, color=variety, group=variety)) +
  scale_x_discrete(name="Treatment", labels=c("ctl","2 weeks","4 weeks")) +
  ylab("Biomass")

# fit randomized block analysis of variance and obtain summary table
weeds_rb <- aov(weeds$biomass ~ weeds$variety + weeds$treat)
summary(weeds_rb)

# check assumptions - residuals vs treatment
ggplot() +
  geom_point(data=weeds, mapping=aes(x=treat, y=weeds_rb$residuals), position = position_jitter(width = 0.1, height = 0.0))

# check assumptions - residuals vs block
ggplot() +
  geom_point(data=weeds, mapping=aes(x=variety, y=weeds_rb$residuals), position = position_jitter(width=0.1))

# check assumptions - normality
qqnorm(weeds_rb$residuals)

# obtain treatment means for subsequent analysis
tapply(weeds$biomass, weeds$treat, describe)
TukeyHSD(weeds_rb, "weeds$treat")
```
5. Random/fixed effects

(a) The key point in the factor effects model is that the overall mean and the $J$ treatment effects are too many parameters. All of these parameters can’t be estimated without a constraint of some kind because the data (really the likelihood) can’t distinguish between parameter values $\mu, \tau_1, \tau_2$ and $\mu + c, \tau_1 - c, \tau_2 - c$ (for any $c$ we want). Both sets of parameters yield identical means for all observations under the model. Note that it is not possible to prove that we must have $\sum_j \tau_j = 0$; we must have a restriction but it need not be that one. We like to choose that restriction because it gives the parameters a natural interpretation ($\mu$ is the grand mean and $\tau_j$ is the treatment $j$ effect) but we don’t have to choose that one.

(b) Inference for treatment mean

i. Fixed effects ($\sum_i \beta_i = 0$): Start by noting that $\bar{Y}_j$ is a linear combination of normal random variables and hence will be normal. Then, $E(\bar{Y}_j) = \frac{1}{I} E(\sum_i (\mu + \beta_i + \tau_j + \epsilon_{ij})) = \frac{1}{I} E(\mu + 0 + \sum_i \epsilon_{ij}) = \mu + \tau_j$ and $Var(\bar{Y}_j) = \frac{1}{I^2} \sum_i Var(\mu + \beta_i + \tau_j + \epsilon_{ij}) = \sigma^2/I$. The problem asked how you’d use these results ... you can form a $t$ confidence interval for $\mu + \tau_j$ from this mean and variance (after plugging in the MSE for $\sigma^2$).

ii. Random effects ($\beta_i \sim N(0, \sigma^2_b)$): The initial part of the argument proceeds as above to find that $\bar{Y}_j$ is normal. The mean calculation is similar to the one given above. In the variance calculation $\beta_i$ and $\epsilon_{ij}$ are random and both contribute variance terms so that we end up with a mean of $\mu + \tau_j$ and a variance of $(\sigma^2_b + \sigma^2)/I$. The interpretation is that if we hope to draw inferences about treatment $j$ that generalizes to a population of blocks (i.e., the population of blocks from which our random blocks were sampled), then the variance associated with our estimated treatment effect should be larger to account for differences among blocks. If we only want to draw inferences about the blocks in the study (the fixed effects case) then we will have more precise inferences.

(c) Here notice that $\bar{Y}_j - \bar{Y}_{j'}$ is $\frac{1}{I} (\sum_i Y_{ij} - Y_{ij'}) = \frac{1}{I} (\sum_i \tau_j - \tau_{j'} + \epsilon_{ij} - \epsilon_{ij'})$. Note that this difference in means doesn’t depend on the block effects since they cancel out of the sum. The mean is $\tau_j - \tau_{j'}$ and the variance is $2\sigma^2/I$ (same as in the usual completely randomized ANOVA!). Here too the explanation should provide the intuition (about the block effects cancelling) rather than merely report that the calculations result in the same mean and variance.

(d) The natural quantity to examine in this case is the sample contrast $\sum_j c_j \bar{Y}_j$. As in the previous part it helps to first simplify this sum as $\sum_j c_j (\mu + \beta_i + \tau_j + \epsilon_j) = \sum_j c_j \tau_j + \sum_j c_j \epsilon_j$ where we use the fact that the sum of contrast weights is zero and the first two terms do not depend on $j$. From this last expression we can easily see that the mean is $\sum_j c_j \tau_j$ and the variance is $\sum_j c^2_j \sigma^2/I$. Here too the block effects cancel out in computing the contrast so it doesn’t matter whether we think of them as fixed or random. (Another plus of contrasts!)