1. For example, if t=3,

1	2	3	1
1	1	2	3
3	1	1	2
2	3	1	$\overline{1}$

(a)
$$\mathcal{I}_{2|1} = \mathbf{X}_2' \mathbf{X}_2 - \mathbf{X}_2' \mathbf{H}_1 \mathbf{X}_2$$

$$\mathbf{X}_{2}'\mathbf{X}_{2} = diag(2(t+1), (t+1), (t+1), ..., (t+1))$$

$$\mathbf{H}_1'\mathbf{X}_2 = [\mathbf{X}_1(\mathbf{X}_1'\mathbf{X}_1)^-]\mathbf{X}_1'\mathbf{X}_2$$

 $\{\mathbf{X}_1'\mathbf{X}_2\}_{ij}$ is the number of times treatment j appears in block i, so

 $\mathbf{X}_1'\mathbf{X}_2 = (2 \times \mathbf{1}, \mathbf{1}, \mathbf{1}, ... \mathbf{1})$, and is of dimension 2(t+1)-by-t if the α column is left out of \mathbf{X}_1 .

But we can also write $X'_{1\frac{1}{t+1}}(2 \times 1, 1, 1, ... 1)_{(t+1)^2 \times t} = (2 \times 1, 1, 1, ... 1)_{2(t+1) \times t}$ because each column of X_1 contains t+1 ones.

So $\mathbf{H}_1\mathbf{X}_2 = \mathbf{H}_1(\frac{1}{t+1}(2\times 1,1,1,...1)) = \frac{1}{t+1}(2\times 1,1,1,...1)$ since the columns of the second

matrix factor are all in the vector space spanned by the columns of
$$\mathbf{X}_1$$
.
From here, it follows that $\mathbf{X}_2'\mathbf{H}_1\mathbf{X}_2 = \frac{1}{t+1}\begin{pmatrix} 4(t+1) & -2(t+1) \times \mathbf{1}' \\ -2(t+1) \times \mathbf{1} & (t+1)\mathbf{I} - \mathbf{J} \end{pmatrix} = \begin{pmatrix} 4 & 2 \times \mathbf{1}' \\ 2 \times \mathbf{1} & \mathbf{J} \end{pmatrix}$

So,
$$\mathcal{I}_{2|1} = \begin{pmatrix} 2(t+1) - 4 & -2 \times \mathbf{1}' \\ -2 \times \mathbf{1} & (t+1)\mathbf{I} - \mathbf{J} \end{pmatrix}_{t \times t}$$

(b) The X_2 matrices for the two designs do have the same rows (in kind, and number of each kind). Further, $\mathbf{H}_1 = \frac{1}{N}\mathbf{J}$, so $\mathbf{H}_1\mathbf{X}_2 = \frac{1}{N}(2(t+1)\times\mathbf{1},(t+1)\times\mathbf{1},(t+1)\times\mathbf{1},...(t+1)\times\mathbf{1}) =$ $\frac{1}{t+1}(2\times 1,1,1,...1)$. So the design we're analyzing is Condition E-equivalent to this CRD.

8.

(a)

source	d.f.	sum of squares
blocks	6	0.0459375
treatments	3	0.1281875
residual	6	0.0018375
corrected total	15	0.0605938

F = [0.01281875/3]/[0.0018375/6] = 13.9524. If testing at level 0.05, this is compared to $F_{0.95}(3,6) = 4.75706$; the hypothesis of equal treatments is rejected.

(b) $\bar{p} = 0.495625$, $\hat{\sigma}^2 = \bar{p}(1-\bar{p})/100 = 0.002499809$, $\chi^2 = 0.0018375/0.002499809 = 0.7350562$. If testing at level 0.05, this is compared to $\chi^2_{0.95}(6) = 12.59159$; the assumed model is not rejected.

(a) The problem with this data set, relative to the model we would like to use, is that the value is row 2 and column 3, with treatment 4, is far out-of-line with all the other data values. Consider only the data in cells (2,1), (2,3), (4,1), and (4,3). According to the model, the expected value for the contrast:

$$(2,1)$$
 - $(2,3)$ - $(4,1)$ + $(4,3)$

should be

$$(\beta_2 + \gamma_1 + \tau_2) - (\beta_2 + \gamma_3 + \tau_4) - (\beta_4 + \gamma_1 + \tau_4) + (\beta_4 + \gamma_3 + \tau_2) = 2(\tau_2 - \tau_4)$$

and the observed value is -5.23. But a similar calculation with cells:

$$(1,2)$$
 - $(1,4)$ - $(3,2)$ + $(3,4)$

has an observed value near zero, and the same expectation (under the model). Of course, in order to formally claim that these contrasts shouldn't have values this different, we would need to know something about σ^2 . No "pure error" sum of squares can be calculated from these data, so no model-free estimate of the variance is available. However, aside from the value in the (2,3) cell, all other values are very similar, suggesting that block and treatment effects, and σ^2 , are likely relatively small.

(b) Two possible model failures that could lead to this are the presence of row-block-by-column-block interaction, and a much larger variance for the (2,3) cell than for the rest of the experiment (i.e. an outlier).