HW #5

5.4, 5.10, 5.16, 5.17, 5.18, 5.23

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5.4

A treatment usually is associated with a change in the mean but not the variance, so the best estimate of σ is s_p from all the groups.

5.10

Fewer degrees of freedom, especially in the denominator, result in distributions where larger F-statistics are more likely.

5.16

term	df	sumsq	meansq	statistic	p.value
Judge	6	1927.1	321.18	6.718	6.096e-05
Residuals	39	1864.4	47.81		

5.17

Source	DF	SumSq	MeanSq	Fstat	Pval
Between Groups	7	35819	5117	3.5	0.0099
Within Groups	24	35088	1462		

There were 8 groups, and there is evidence at the $\alpha = 0.01$ level that the group means are *not* identical.

5.18

a

Treatment	mean.treat
CPFA150	171.7
CPFA300	146.7
CPFA450	151.0
CPFA50	168.3
CPFA600	152.3
Control	185.6
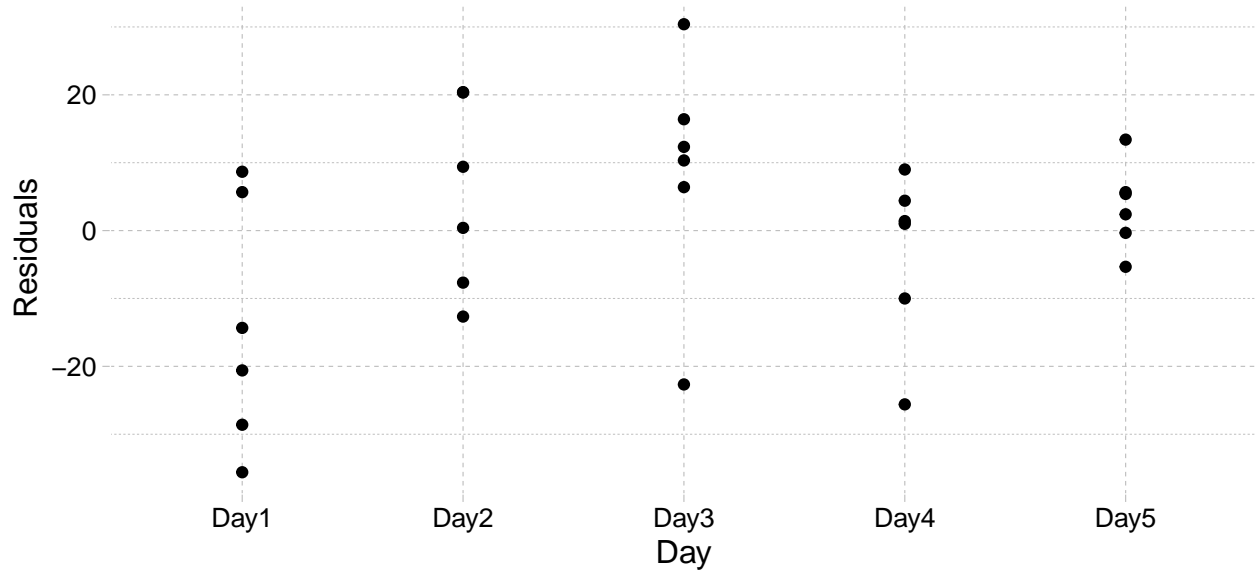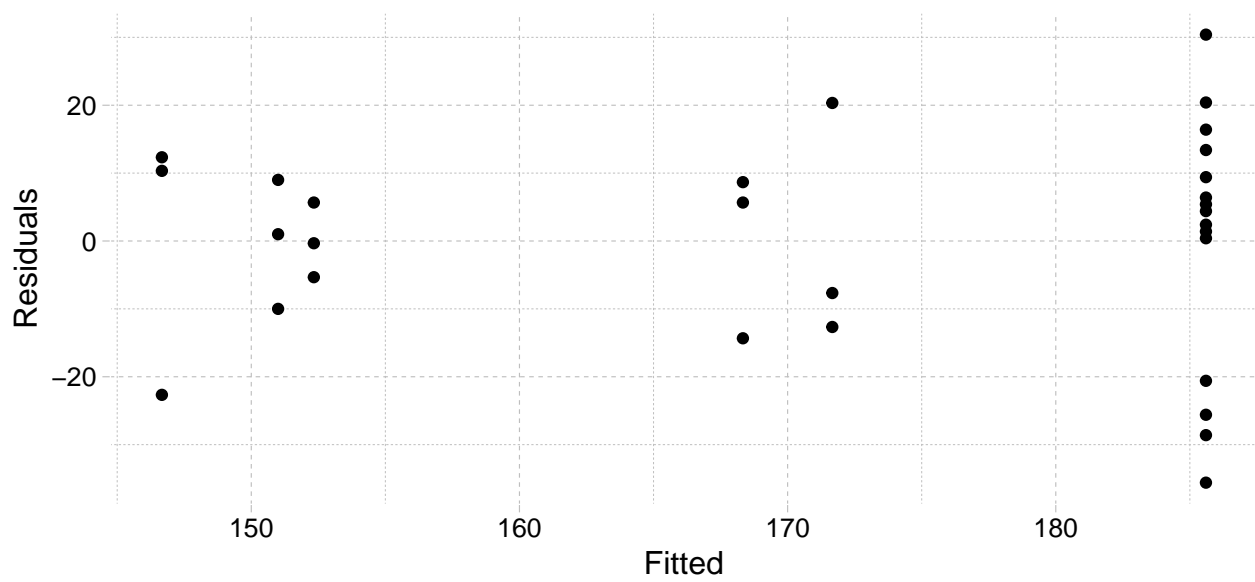
b

Treatment	Day1	Day2	Day3	Day4	Day5
CPFA50	168.3				
CPFA150		171.7			
CPFA300			146.7		
CPFA450				151	
CPFA600					152.3
Control	157.3	195.7	203.3	179	192.7

term	df	sumsq	meansq	statistic	p.value
TrtDayGroup	9	11147.5	1238.61	7.801	7e-05
Residuals	20	3175.3	158.77		

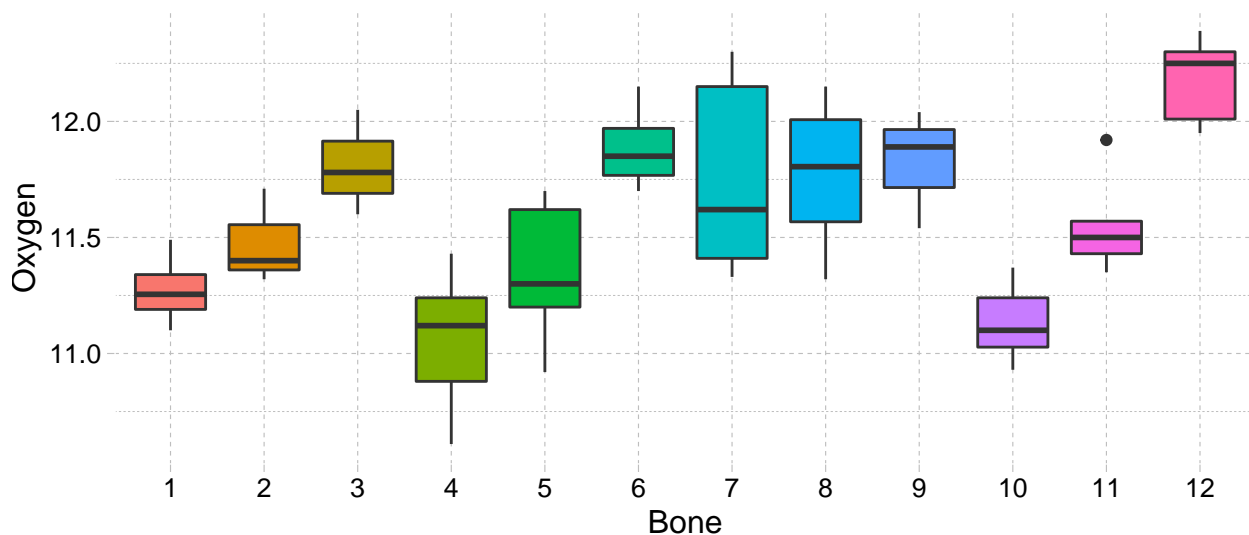From this we can conclude that the means of all 10 groups are *not* equal.

c

We compare the two models as follows:

term	df.residual	rss	df	sumsq	statistic	p.value
Protein ~ Treatment	24	7100.3				
Protein ~ Treatment + Day	20	3175.3	4	3924.9	6.18	0.002

This gives strong evidence that the means between days are different.

5.23

A boxplot of the data is given below:

The results of an ANOVA test are given below:

term	df	sumsq	meansq	statistic	p.value
Bone	11	6.07	0.552	7.43	1e-06
Residuals	40	2.97	0.074		

Based on these results, there is strong evidence against the means being equal.