group report

March 12, 2019

```
In [35]: data <- read.table("apple.txt",
                            sep="",
                            col.names=c("Variety", "FusariumStrain", "Days", "AppleWeight",
                                        "Radius", "FungalRadialAdvance", "RateOfAdvance"))
```

```
In [36]: data
```

Variety	FusariumStrain	Days	AppleWeight	Radius	FungalRadialAdvance	RateOfAdvance
1	1	70	156.2	3.66	2.04	0.0291
1	2	70	153.9	3.65	1.23	0.0176
1	3	70	137.8	3.51	1.25	0.0179
1	4	70	141.0	3.53	1.66	0.0237
1	5	70	145.8	3.58	1.74	0.0249
1	6	70	147.8	3.60	1.88	0.0269
1	7	70	174.9	3.81	2.26	0.0323
2	1	103	91.3	3.07	1.16	0.0113
2	2	103	115.5	3.05	1.26	0.0122
2	3	103	99.5	3.15	0.41	0.0040
2	4	103	101.2	3.17	2.39	0.0232
2	5	103	106.8	3.23	2.01	0.0195
2	6	103	88.1	3.03	1.98	0.0192
2	7	103	100.2	3.16	2.26	0.0219
3	1	54	66.5	2.66	2.29	0.0424
3	2	54	67.6	2.68	1.02	0.0189
3	3	54	64.8	2.64	0.27	0.0050
3	4	54	59.3	2.57	2.63	0.0487
3	5	54	70.1	2.71	2.58	0.0478
3	6	54	68.1	2.69	2.11	0.0391
3	7	54	64.0	2.63	2.73	0.0506
4	1	138	68.7	2.74	1.46	0.0106
4	2	138	66.7	2.71	0.53	0.0038
4	3	138	72.4	2.78	0.05	0.0004
4	4	138	68.6	2.74	1.69	0.0122
4	5	138	68.0	2.73	1.60	0.0116
4	6	138	62.2	2.65	2.15	0.0156
4	7	138	73.1	2.79	1.67	0.0121
5	1	89	62.7	2.46	1.33	0.0149
5	2	89	60.6	2.44	0.59	0.0066
5	3	89	67.8	2.53	0.60	0.0067
5	4	89	64.4	2.44	1.95	0.0219
5	5	89	54.5	2.35	1.76	0.0198
5	6	89	57.4	2.40	1.25	0.0140
5	7	89	60.9	2.44	2.05	0.0230

```
In [48]: data$RateOfAdvance
```

1. 0.0291 2. 0.0176 3. 0.0179 4. 0.0237 5. 0.0249 6. 0.0269 7. 0.0323 8. 0.0113 9. 0.0122 10. 0.004 11. 0.0232 12. 0.0195 13. 0.0192 14. 0.0219 15. 0.0424 16. 0.0189 17. 0.005 18. 0.0487 19. 0.0478 20. 0.0391 21. 0.0506 22. 0.0106 23. 0.0038 24. 4e-04 25. 0.0122 26. 0.0116 27. 0.0156 28. 0.0121 29. 0.0149 30. 0.0066 31. 0.0067 32. 0.0219 33. 0.0198 34. 0.014 35. 0.023

```
In [49]: round(data$FungalRadialAdvance / data$Days, 4) == data$RateOfAdvance
```

1. TRUE 2. TRUE 3. TRUE 4. TRUE 5. TRUE 6. TRUE 7. TRUE 8. TRUE 9. TRUE 10. TRUE 11. TRUE 12. TRUE 13. TRUE 14. TRUE 15. TRUE 16. TRUE 17. TRUE 18. TRUE 19. TRUE 20. TRUE

21. TRUE 22. TRUE 23. TRUE 24. TRUE 25. TRUE 26. TRUE 27. TRUE 28. TRUE 29. TRUE 30. TRUE 31. TRUE 32. TRUE 33. TRUE 34. TRUE 35. TRUE

We can see that RateOfAdvance is a function of the other two function, so it might not be very relevant to our analysis. So in our model, we might want to model the FungalRadialAdvace based on the variety, strain type and apple weight.

```
In [55]: model <- aov(FungalRadialAdvance ~ Variety * FusariumStrain * AppleWeight, data=data)
```

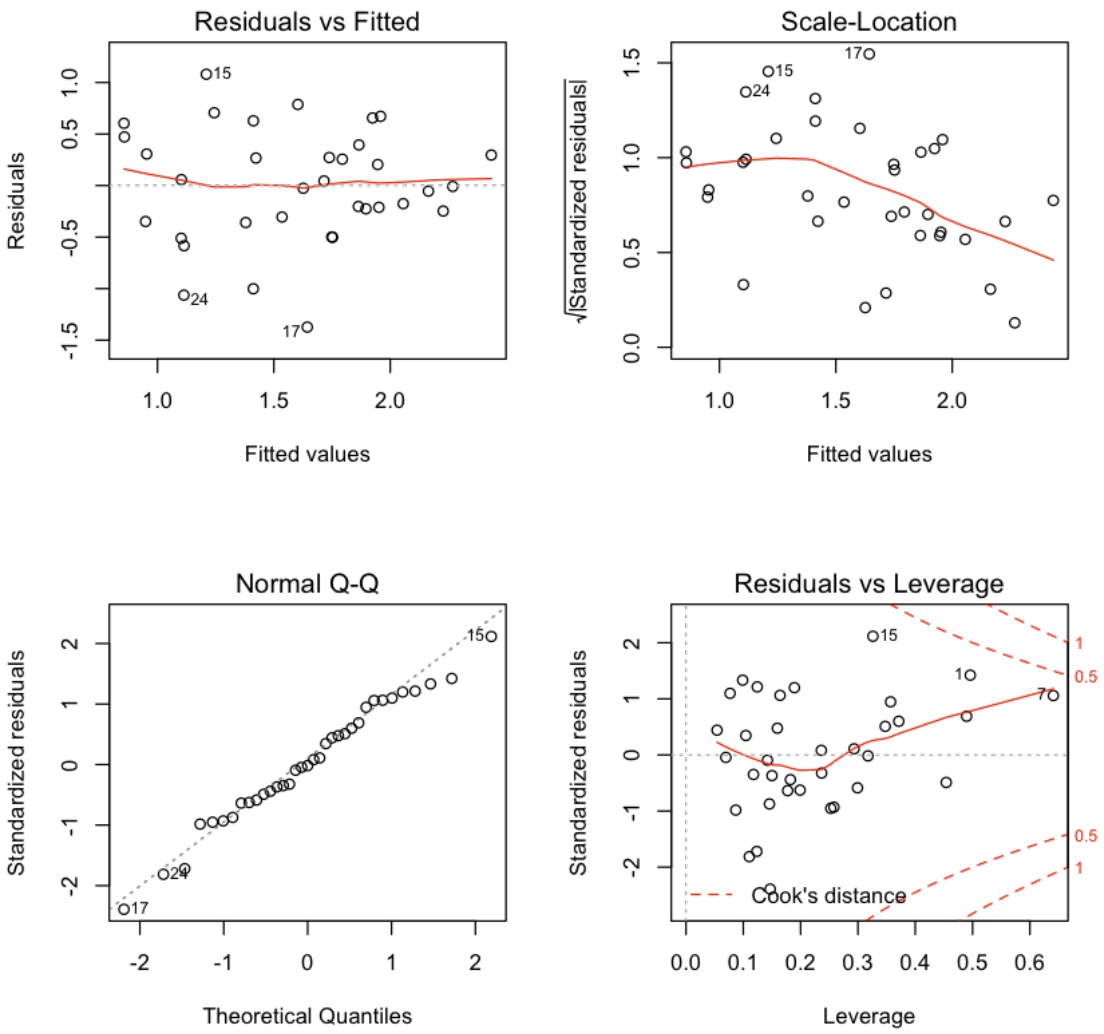
```
In [59]: summary(model)
```

```
                                  Df Sum Sq Mean Sq F value  Pr(>F)
Variety                            1  0.778   0.778   2.012 0.16754
FusariumStrain                     1  4.344   4.344  11.230 0.00239 **
AppleWeight                        1  0.417   0.417   1.078 0.30831
Variety:FusariumStrain             1  0.025   0.025   0.063 0.80308
Variety:AppleWeight                1  0.444   0.444   1.148 0.29348
FusariumStrain:AppleWeight         1  0.165   0.165   0.426 0.51931
Variety:FusariumStrain:AppleWeight 1  0.060   0.060   0.154 0.69768
Residuals                         27 10.443   0.387
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

```
In [60]: coef(model)
```

(Intercept) 1.08535318159217 **Variety** 0.601065359232265 **FusariumStrain** 0.424498234755231 **AppleWeight** 0.0103955792840682 **Variety:FusariumStrain** -0.110538582619801 **Variety:AppleWeight** -0.0128664269602559 **FusariumStrain:AppleWeight** -0.00272548227989302 **Variety:FusariumStrain:AppleWeight** 0.00142971207042958

```
In [61]: layout(matrix(1:4,ncol=2))
         plot(model)
```


Residuals vs Fitted
Residuals
Fitted values
15
24
17
Scale-Location
√|Standardized residuals|
Fitted values
17
15
24
Normal Q-Q
Standardized residuals
Theoretical Quantiles
15
24
17
Residuals vs Leverage
Standardized residuals
Leverage
Cook's distance
15
10
7
1
0.5
0.5
1