Thinning will increase the number of tree hollows across both treatments relative to the control

1. Construct a new variable, the difference between the tree hollows, that is diff =
2. Add a field to each tree to label which treatment the tree is applied
3. Use the glm() in r to run the regression: diff ~ treatment
4. Apply the different model family to see the diagnosis plot, choose the best performance model family, the supposed model family is
5. Binomial
6. Gamma
7. Poisson
8. Guassian

The poisson family will be applicable here, since tree hollows are supposed to be there and never disappear, so no negative value here.

1. And see the coefficient for each treatment is positive or not and the significance level for it

Note: the data might not be fitted the “best model” well, we will only choose the one with better performance than others

There will be a greater number of tree hollows develop in T2 as compared to T1

We could still use the model above, and check whether the coefficient for T2 is larger than T1, and we need to notice whether both coefficients are statistically significant

**CWD data**

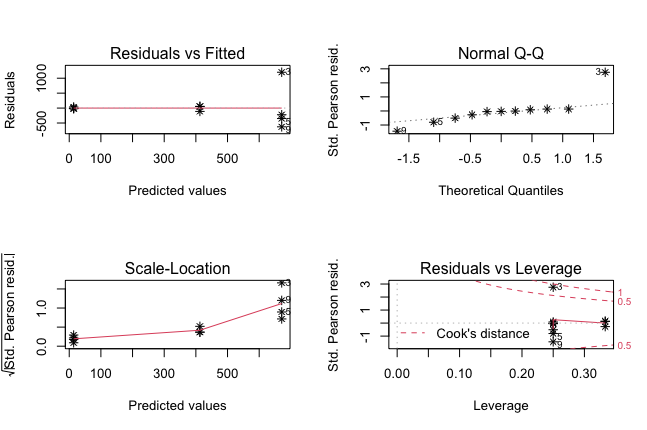
There will be a greater increase in coarse woody debris in years post thinning in T1 & T2 compared to the control

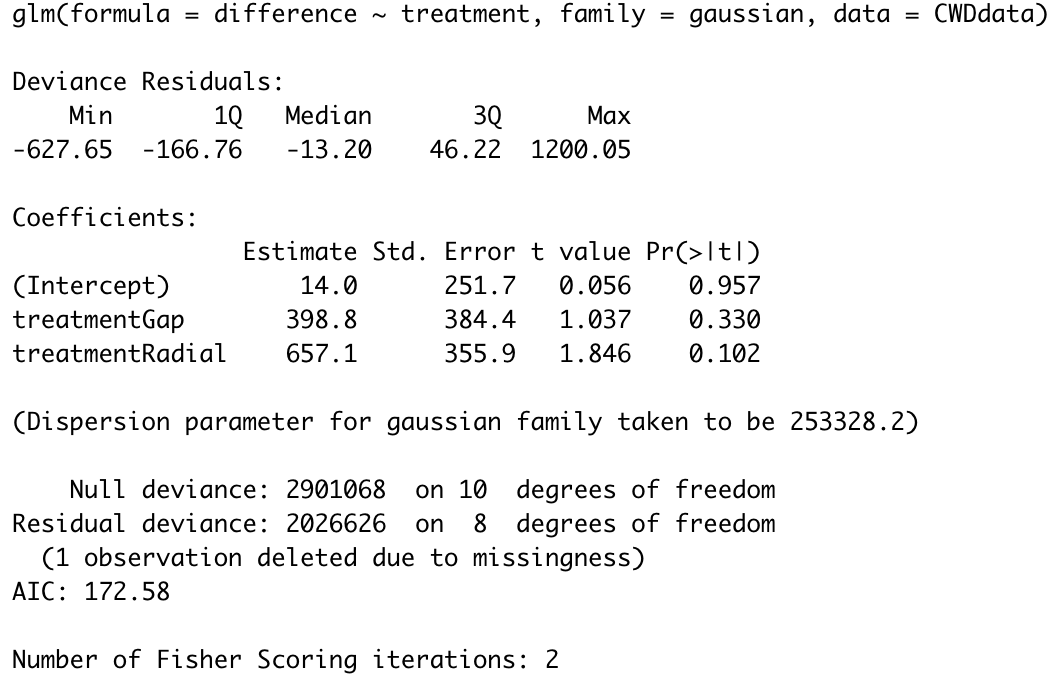
1. Construct a new variable, the difference between the CWD total, that is difference
2. Add a field to each plot to label which treatment the plot is applied
3. Use the glm() in r to run the regression: difference ~ treatment
4. Apply the different model family to see the diagnosis plot, choose the best performance model family, the supposed model family is
5. Guassian
6. ~~Binomial~~
7. Gamma
8. Poisson

Binomial is not applicable in this case, because the dependent variable is not in [0, 1], so the model is failed to fit.

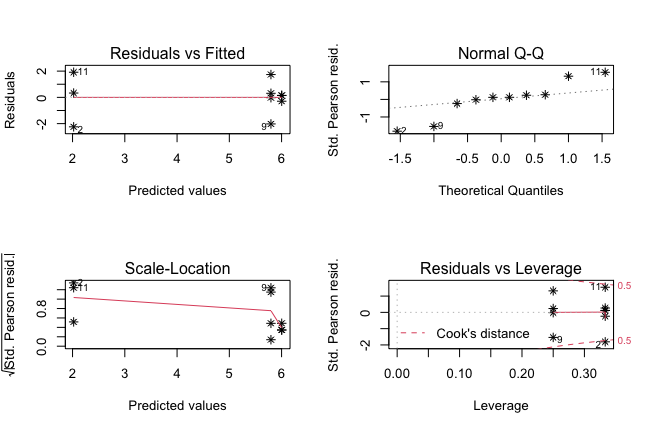
Played a trick in fitting the Gamma and Poisson model, convert the negative different to its absolute value, and then use this value to fit the model.

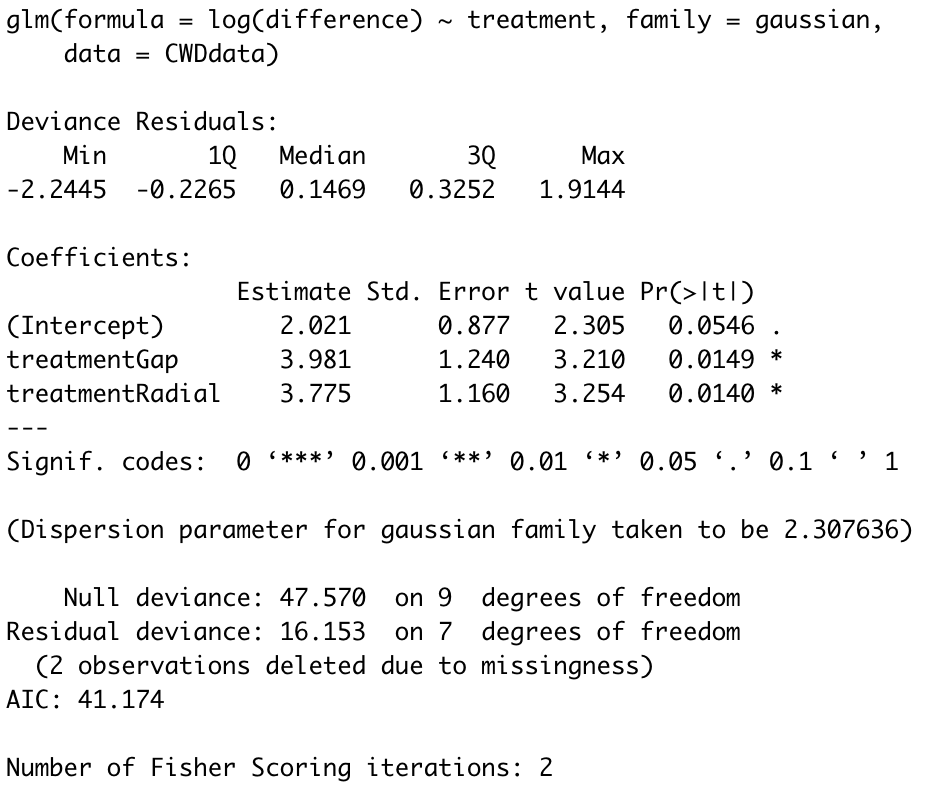
The guassian family might not fit the model well. The scale-location plot shows an increasing trend, it states the heteroskedasticity, that is the spread of the residuals is not equal, and the cook’s distance shows that the point 3 are a significant influential point. All 3, 5, 9 are outliers, and all of them are from treatment Radial. All the coefficient is not significant in this case, but all of them are positive.



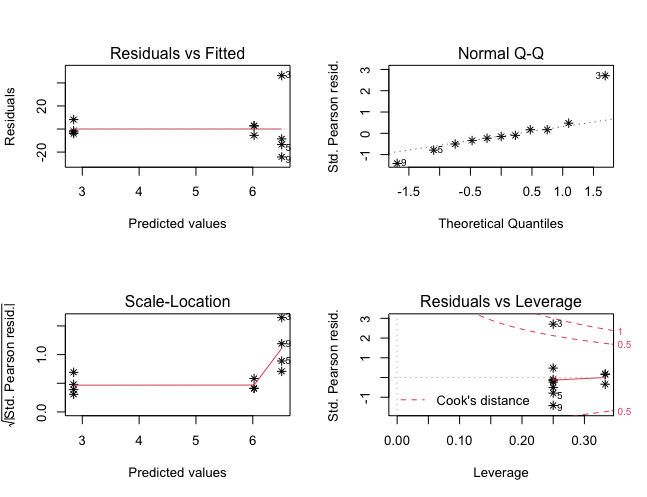


Since the increasing trend appears, so we fit the log\_guassian model, this time the scale-location shows a negative trend, and cook’s distance plot states that the point 2 & 11 are influential points, but its influence is less than point 3 in previous normal guassian model. And the QQ plots states the significant violation that the residual is normally distributed.





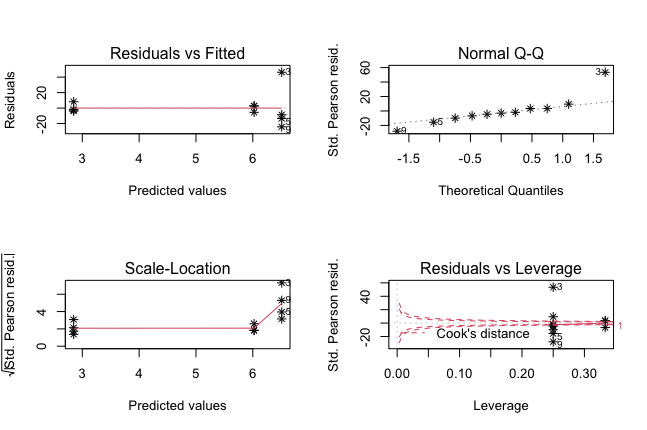
The quansi-poisson cannot be used directly, since the one of the difference in CWD is -6.5, so if we want to fit the quansi-poisson model, we have to convert all different to positive using the abs() in r, the scale-location still shows an increasing trend, the outlier this time is point 3,5,9, and all of them are from the treatment Radial. But all the coefficients are not significant but are positive.

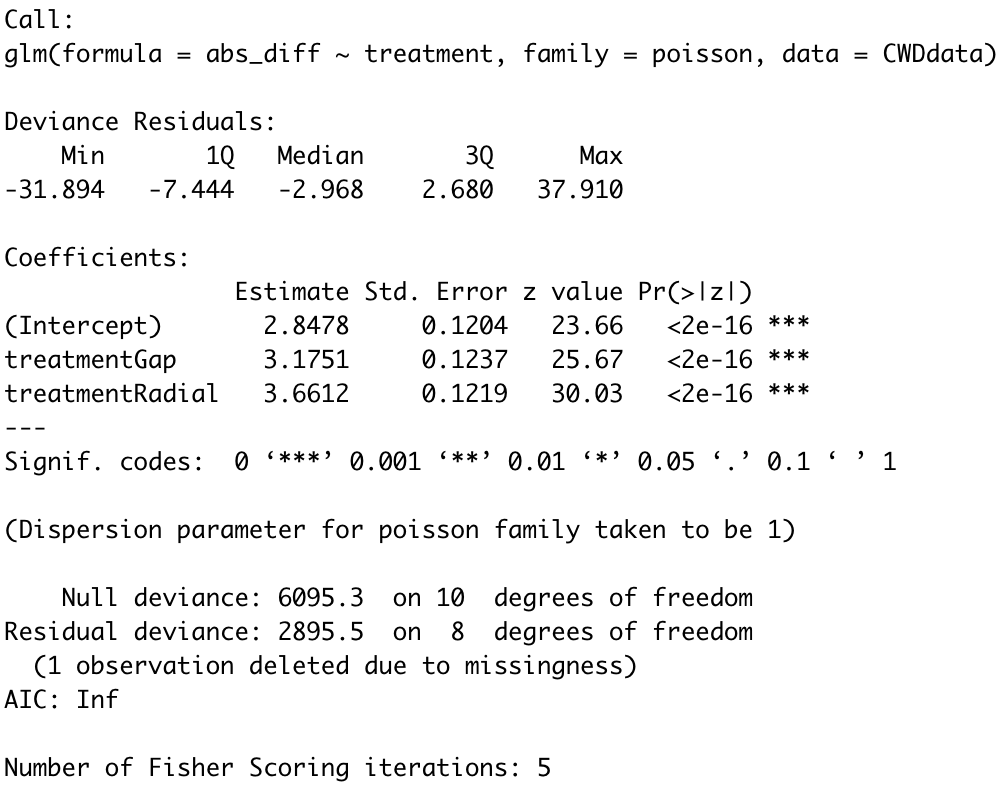


Table

Description automatically generated

The poisson model cannot be used directly, since the one of the difference in CWD is -6.5, so if we want to fit the poisson model, we have to convert all different to positive using the abs() in r. this time the scale-location model seems better, but it still shows an increasing trend, all 3,5, 9 becomes significant influential this time, almost all points become influential. So, this fitting is worse than the original guassian model fitting. All the coefficient is statistically significant and positive.





The Gamma also takes no negative values, so the outlier becomes 2,11(Control), 3(Radial), and no significant points are presented, but the normal QQ plot is left-skewed, and the scale-location is showed a decreasing trend first and then increasing trend. All the coefficients from the model are positive but not statistically significant.Diagram

Description automatically generated

