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Two-Way ANOVA

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Interpret the key results for Two-way ANOVA

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Complete the following steps to interpret a two-way ANOVA. Key output includes the group means, R^2 , and the residual plots.

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Step 1: Determine whether the main effects and interaction effect are statistically significant

To determine whether each main effect and the interaction effect is statistically significant, compare the p-value for each term to your significance level to assess the null hypothesis. A significance level (denoted as α or alpha) of 0.05 works well. A significance level of 0.05 indicates that an effect exists when there is no actual effect.

- The null hypothesis for a main effect is that the response mean for all factor levels is the same.
- The null hypothesis for an interaction effect is that the response mean for the combination of factor levels does not depend on the value of the other factor level.

The statistical significance of the effect depends on the p-value, as follows:

- If the p-value is greater than the significance level you selected, the effect is not statistically significant.
- If the p-value is less than or equal to the significance level you selected, then the effect is statistically significant.

The following shows how to interpret significant main effects and interaction effects:

- If the main effect of a factor is significant, the difference between some group means are statistically significant.
- If an interaction term is statistically significant, the relationship between the response and the factor differs by the level of the other factor. In this case, you should interpret the main effects without considering the interaction effect.

Source	DF	Adj SS	Adj MS	F-Value	P-Value
SinterTime	2	8.222	4.1111	1.71	0.2094
MetalType	2	20.222	10.1111	4.20	0.0318
SinterTime*MetalType	4	46.222	11.5556	4.80	0.0082
Error	18	43.333	2.4074		
Total	26	118.000			

Key Result: P-Value

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- In these results, you can conclude the following, based on the p-values and a significance level
- The p-value for MetalType is 0.0318, which indicates that the levels of MetalType are ass different strengths.
 - The p-value for SinterTime is 0.2094, which indicates that the levels of SinterTime are no different strengths.
 - The p-value for the interaction between MetalType*SinterTime is 0.0082, which indicate: relationship between MetalType and Strength depends on the value of SinterTime.
 - Because the interaction effect between MetalType and SinterTime is statistically significa interpret the main effects without considering the interaction effect.

Step 2: Assess the means

If the p-value in the ANOVA table indicates a statistically significant main effect or i the means table to understand the group differences.

For main effects, the table displays the groups within each factor and their fitted n interaction effects, the table displays all possible combinations of groups across b

Means

Term	Fitted Mean	SE Mean
SinterTime		
100	20.3333	0.5172
150	21.4444	0.5172
200	20.2222	0.5172
MetalType		
1	19.6667	0.5172
2	21.7778	0.5172
3	20.5556	0.5172
SinterTime*MetalType		
100 1	21.3333	0.8958
100 2	20.3333	0.8958
100 3	19.3333	0.8958
150 1	20.3333	0.8958
150 2	23.6667	0.8958
150 3	20.3333	0.8958
200 1	17.3333	0.8958
200 2	21.3333	0.8958
200 3	22.0000	0.8958

Key Result: Fitted Mean

Examine the means table to understand the differences between the groups in your data. Look in group means. If the interaction term is statistically significant, do not interpret the main effe considering the interaction effects.

In these results, the interaction effect is statistically significant. The interaction effect indicates relationship between MetalType and Strength depends on the value of SinterTime. For exampl MetalType 2, SinterTime150 is associated with the highest mean strength. However, if you use SinterTime 100 is associated with the highest mean strength.

Step 3: Determine how well the model fits your data

To determine how well the model fits your data, examine the goodness-of-fit statis summary table.

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However, a low S value by itself does not indicate that the model meets the model assumptions. You should check the residual plots to verify the assumptions.

R-sq

R² is the percentage of variation in the response that is explained by the model. The higher the R² value, the better the model fits your data. R² is always between 0% and 100%.

R² always increases when you add additional predictors to a model. For example, a full predictor model will always have an R² that is at least as high as the best four-predictor model. Therefore, R² is most useful when you compare models of the same size.

A high R² value does not indicate that the model meets the model assumptions. You should check the residual plots to verify the assumptions.

R-sq (adj)

Use adjusted R² when you want to compare models that have different numbers of predictors. Adjusted R² always increases when you add a predictor to the model, even when there is no improvement in the model. The adjusted R² value incorporates the number of predictors in the model. Choose the correct model.

R-sq (pred)

Use predicted R² to determine how well your model predicts the response for new observations. Models that have larger predicted R² values have better predictive ability.

A predicted R² that is substantially less than R² may indicate that the model is overfitted. Overfitting occurs when you add terms for effects that are not important in the population. They may appear important in the sample data. The model becomes tailored to the sample data and therefore, may not be useful for making predictions about the population.

Predicted R² can also be more useful than adjusted R² for comparing models based on new observations that are not included in the model calculation.

Model Summary

S	R-sq	R-sq(adj)	R-sq(pred)
1.55158	63.28%	46.96%	17.37%

Key Results: S, R-sq, R-sq (adj), R-sq (pred)

In these results, the predictors explain 63.28% of the variation in the response. The adjusted R² is a decrease of 17%. The low predicted R² value (17.37%) indicates that the model does not predict new observations as well as it fits the sample data. Thus, you should not use the model to make generalizations beyond the sample data.

Step 4: Determine whether your model meets the assumptions of the analysis

Use the residual plots to help you determine whether the model is adequate and meets the assumptions of the analysis. If the assumptions are not met, the model may not fit the data. You should use caution when you interpret the results.

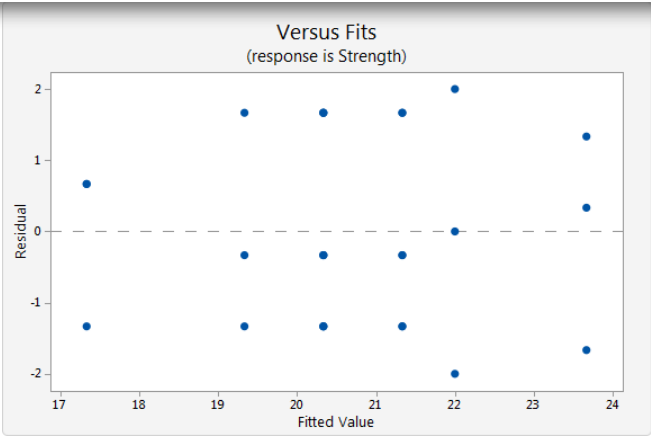
Residuals versus fits plot

Use the residuals versus fits plot to verify the assumption that the residuals are random and have constant variance. Ideally, the points should fall randomly on both sides of the center line with no recognizable patterns in the points.

The patterns in the following table may indicate that the model does not meet the assumptions of the analysis.

Pattern	What the pattern indicates
Fanning or uneven spreading of residuals across fitted values	Nonconstant variance

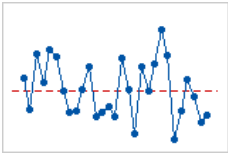
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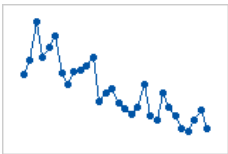
In this residual versus fits plot, the points appear randomly scattered on the plot. None of the residuals have substantially different variability.

Residuals versus order plot

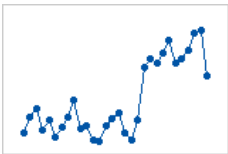
Use the residuals versus order plot to verify the assumption that the residuals are independent. Independent residuals show no trends or patterns when displayed in order. Patterns in the points may indicate that residuals near each other may be correlated. Ideally, the residuals on the plot should fall randomly around the center line.



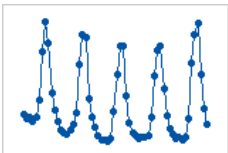
If you see a pattern, investigate the cause. The following types of patterns may indicate that residuals are dependent.



Trend

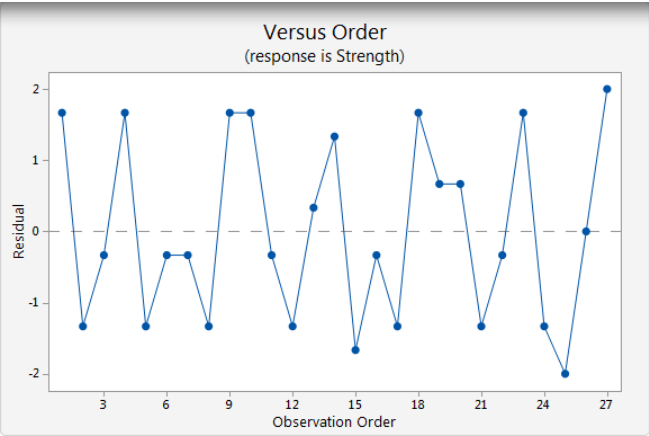


Shift



Cycle

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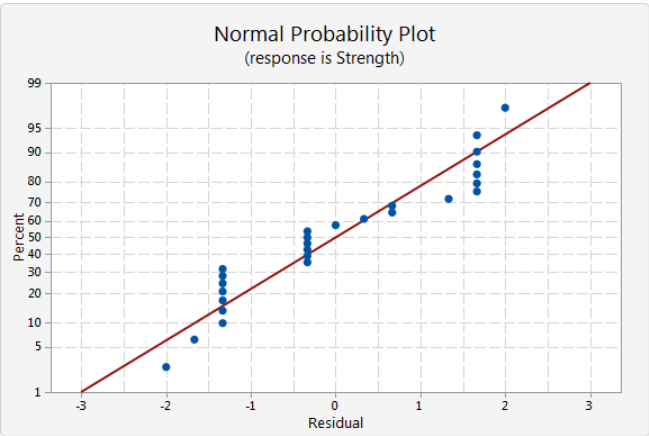
In this residual versus order plot, the residuals fall randomly around the centerline.

Normality plot of the residuals

Use the normal probability plot of residuals to verify the assumption that the residuals are normally distributed. The normal probability plot of the residuals should approximately follow a straight line.

The patterns in the following table may indicate that the model does not meet the assumptions of ANOVA.

Pattern	What the pattern may indicate
Not a straight line	Nonnormality
A point that is far away from the line	An outlier
Changing slope	An unidentified variable



In this normal probability plot, the residuals appear to deviate from the straight line. Even though the residuals are nonnormally distributed, ANOVA test results are often robust to violations of this assumption.