

DOE Fractional Factorial Analysis

This guide provides instructions on analyzing fractional factorial experiments (experiments where not every possible treatment combination in a full factorial design is run) using the Fit Model platform.

Specify the Model and Analyze

- Experiments designed in JMP® will have a **Model** script saved to the data table. The model specification window will be populated with this model. To generate the model manually:

From an open JMP table (for a completed fractional factorial experiment) select **Analyze > Fit Model**.

- Click on the response under **Select Columns**, and click **Y**.
- Select the factors of interest, and click **Add** (under **Construct Model Effects**).
- To add specific interaction terms, select the variables under **Select Columns** and click **Cross**. In this experiment, all but two of the 2-way interactions are confounded with main effects. These two 2-way interactions are confounded with other 2-way interactions:
 $\text{Feed Rate} * \text{Stir Rate} = \text{Catalyst} * \text{Temperature}$, and
 $\text{Feed Rate} * \text{Catalyst} = \text{Stir Rate} * \text{Concentration}$.

- Check the **Keep dialog open** box, and click **Run**.

Note: If aliased effects were entered into the model, JMP will display **Singularity Details** and will indicate that estimates are **zeroed** or **biased**.

Note: If your design is **saturated** (there are no error degrees of freedom) as the case here, select **Estimates > Sorted Estimates** from the top red triangle to see p-values based on **Lenth Pseudo Standard Error** (PSE, an estimate of residual standard error).

- Reduce the model** as desired, removing non-significant terms starting with 2-way interactions until a final model containing only significant terms (including all main effects that are involved in significant 2-way interactions).

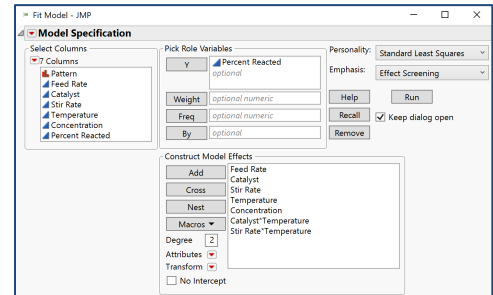
- Use the **Prediction**, **Surface**, and **Response Profiler**, and **Interaction Plots** to visualize the results.
- Model diagnostics** and **savings columns** to the data table are available under the **red triangle**.

Note: The **Easy DOE** platform (under DOE menu) provides a guided workflow to step through the process of creating and analyzing experiments and is an alternative to the steps above for analyzing the experimental data.

Visit **Design of Experiments Guide** in **JMP Help** to learn more.

Reactor 8 Runs.jmp (Help > Sample Data Folder > Design Experiment).

This is a unrepliated 8 run 2^{5-2} Resolution III



Term	Details
Concentration(3,6)	= Feed Rate*Temperature=Catalyst*Stir Rate
Temperature(140,180)	= Feed Rate*Concentration
Feed Rate*Stir Rate	= Catalyst*Temperature
Stir Rate(100,120)	= Catalyst*Concentration
Feed Rate*Catalyst	= Stir Rate*Temperature
Catalyst(1,2)	= Stir Rate*Concentration
Feed Rate(10,15)	= Temperature*Concentration

Term	Estimate	Relative Std Error	Pseudo t-Ratio	Pseudo p-Value
Catalyst(1,2)	10.125	0.353553	1.38	0.2837
Feed Rate*Stir Rate	6.125	0.353553	0.84	0.4793
Temperature(140,180)	5.875	0.353553	0.80	0.4954
Feed Rate(10,15)	-4.875	0.353553	-0.67	0.5649
Concentration(3,6)	-3.375	0.353553	-0.46	0.6839
Stir Rate(100,120)	1.875	0.353553	0.26	0.8185
Feed Rate*Catalyst	0.375	0.353553	0.05	0.9632

No error degrees of freedom, so ordinary tests uncomputable.
 Relative Std Error corresponds to residual standard error of 1.
 Pseudo t-Ratio and p-Value calculated using Lenth PSE = 7.3125 and DFE=2.3333

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Feed Rate(10,15)	1	1	190.12500	169.0000	0.0489*
Catalyst(1,2)	1	1	820.12500	729.0000	0.0236*
Stir Rate(100,120)	1	1	28.12500	25.0000	0.1257
Temperature(140,180)	1	1	276.12500	245.4444	0.0406*
Concentration(3,6)	1	1	91.12500	81.0000	0.0704
Feed Rate*Stir Rate	1	1	300.12500	266.7778	0.0389*