

DOE Screening Experiment Analysis

This guide provides instructions on analyzing screening experiments (e.g., fractional factorial) using the **Fit Two Level Screening** platform. Though the **Fit Model** platform can also be used, the **Fit Two Level Screening** platform produces graphs and analysis results designed for identifying the important effects in a fully saturated experiment. This example is a 20 run 2^5 screening experiment generated from the **Custom Design** platform. This design allows estimation of all main effects and two-factor interactions.

Specify the Model and Analyze

Reactor 20 Custom.jmp (Help > Sample Data Folder > Design Experiment)

Most experiments designed in JMP will have **Screening** and **Model** scripts saved to the data table. The **Screening** script launches the **Screening** analysis platform and automatically fits a saturated model.

- Launch the Fit Two Level Screening platform under DOE > Classical > Two Level Screening or Click on the green triangle next to Screening to run the script if saved to the data table.
- JMP fits a saturated model (here, 19 terms plus the intercept). The Contrasts table and Half Normal Plot identify active factors using Lenth Pseudo Standard Error (PSE).

Notes: In screening experiments, we assume that most effects are inactive and their estimates are essentially random noise.

The line in the **Half Normal Plot** is drawn with a slope equal to the **Lenth PSE** (an estimate of the residual standard error). Most effects are inactive and fall close to this line. Effects that deviate substantially from this line are labeled as active.

3. Select **Run Model** (at the bottom) to launch the **Fit Model** platform with only the active effects. Note: You need to include the main effects for any factors that are included in a significant interaction regardless of the p-value for that main effect. Add those terms by selecting them in the table while holding the command key.

Results include: Effect Summary, Lack of Fit (if replicated points), Summary of Fit, ANOVA table and more.

Other options – such as **residuals or normal plot, profiler** and **interaction plots** – are available under the **top red triangle**.

Tips:

- Individual and Simultaneous p-Values in the Fit Two Level Screening platform are based on Monte Carlo simulation (and will vary).
- An alternative approach to running the analysis is to use **Analyze** > **Fit Model** specifying the model or run the **Model** script. See the "DOE Fractional Factorial Analysis" guide.

Reactor 20 Custom - JMP Pro File Edit Tables Rows Cols DOE Reactor 20 Custom Cocked File C:\Program Files\SAS\JMP\16\ Design Custom Design Criterion D Optimal Source A subset of Reactor 32 Runs.jmp, Screening Model D OE Dialog Reduced Model

				Lenth	Individual	Simultaneou
Term	Contrast			t-Ratio	p-Value	p-Valu
Catalyst	9.48756			10.28	<.0001*	0.0004
Stir Rate	0.63302			0.69	0.4764	1.0000
Feed Rate	0.23699			0.26	0.8166	1.0000
Catalyst*Temperature						
Catalyst*Concentration	0.50061			0.54	0.6176	1.0000
Temperature*Concentration	-5.07962			-5.51	0.00111	0.0128
Catalyst"Stir Rate	0.68123			0.74	0.4405	1.0000
Temperature*Stir Rate	0.43577			0.47	0.6629	1.0000
Concentration*Stir Rate	0.69765			0.76	0.4303	1.0000
Catalyst*Feed Rate	0.04911			0.05	0.9618	1.0000
Temperature*Feed Rate	-0.61513			-0.67	0.5319	1.0000
Concentration*Feed Rate	0.82061	• • • • •		0.89	0.3533	1.0000
Stir Rate*Feed Rate	0.04482			0.05	0.9649	1.0000
Catalyst*Temperature*Concentration	0.51387			0.56	0.6084	1.0000
Catalyst*Temperature*Stir Rate	-0.38797	•		-0.42	0.7000	1.0000
Catalyst*Concentration*Stir Rate	1.29099			1.40	0.1584	0.9168
Temperature*Concentration*Stir Rate	1.22984		1011	1.33	0.1775	0.9426
Half Normal Plot						
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10 -	+Catalyst					
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