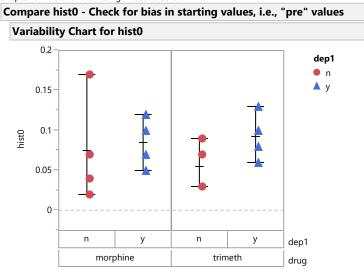
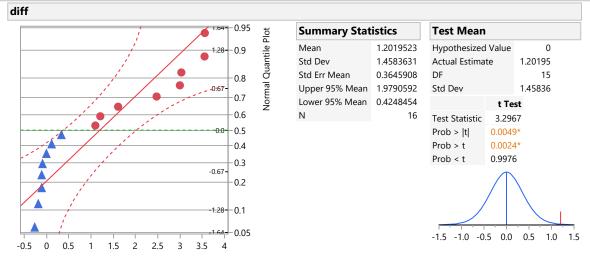
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- JMP Sample Data Dogs.jmp
- Cole and Grizzle (1966) Sixteen Dogs. Biometrics 22 810. A multivariate with repeated measures example. The 4 loghist columns are responses (Y), drug and depl are effects (Xs). See Chapter on Multivariate Fitting in User's Guide.



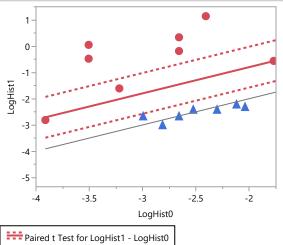
- diff = LogHist1 LogHist0, i.e., post pre
- A 1-factor paired test, typically, tests if the difference is zero. So find the difference and look at the distribution, test if is look like random variation about zero.
- Another is to graph post (LogHist1) pre (LogHist0), and determine
 if the points look like random variation about the line Y=X. This is
 one with Fit Y by X, and request a paired test.

Distributions Test if diff = LogHist1 - LogHist0 is a random normal distribuation about zero. Mean =1.202 and p-value 0.0049



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Bivariate Fit of LogHist1 By LogHist0 paired test



Paired t Test for LogHist1 - LogHist0

 LogHist1 - LogHist1

 Mean Difference
 1.201952
 Prob > |t| 0.0049*

 Std Error Dif
 0.364591
 Prob > t 0.0024*

 t Ratio
 3.296716
 Prob < t 0.9976</td>

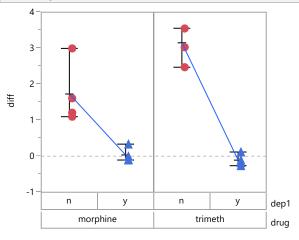
 DF
 15

- Note both methods return the same result.
- Of course, this data set has has other factors so the above analyses were shown as an example. Maybe your two experiments represent another factor.
- diff can be analyzed as Fit Model with drug and dep1 as factors, or as LogHist1 vs. drug and dep1 as factors and LogHist0 as a covariable.
- But first look at the data. Additional graphs and analyses are below.

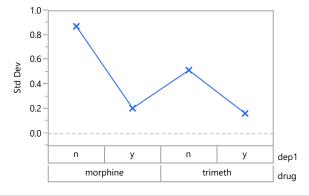
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Variability diff vs. drug and dep1 post-pre is near zero when dep1 = y

Variability Chart for diff

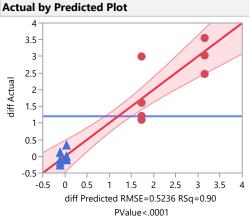


Variability Summary for diff Std Err Std Dev Mean Lower 95% Upper 95% Minimum Mean Range Median diff 1.201952 1.458363 0.364591 0.424845 1.979059 -0.26236 3.555348 3.817712 0.717542 16 drug[morphine] 0.882215 -0.10536 8 1.078413 0.381276 -0.01936 1.783791 2.995732 3.101093 0.717542 drug[trimeth] 1.521689 1.777873 0.628573 0.035351 3.008028 -0.26236 8 3.555348 3.817712 1.295357 drug[morphine] dep1[n] 1.728405 0.872892 0.436446 0.339439 3.117371 1.098612 2.995732 1.89712 1.409638 drug[morphine] dep1[y] 0.036025 0.205503 -0.29098 0.363026 -0.10536 0.336472 -0.04351 4 drug[trimeth] dep1[n] 3.151445 0.51532 0.25766 2.331456 3.971433 2.47293 3.555348 1.082418 3.28875 drug[trimeth] dep1[y] -0.10807 0.163643 0.081821 -0.36846 0.152326 -0.26236 0.117783 0.380147 -0.14384 4



Response diff vs. drug and dep1, maine effects and interaction

Whole Model

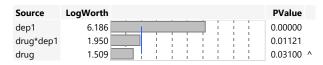


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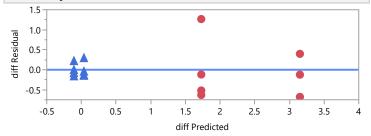
Response diff vs. drug and dep1, maine effects and interaction

Whole Model

Effect Summary



Residual by Predicted Plot



Summary of Fit

 RSquare
 0.896888

 RSquare Adj
 0.87111

 Root Mean Square Error
 0.523571

 Mean of Response
 1.201952

 Observations (or Sum Wgts)
 16

Analysis of Variance

		Sum of		
Source	DF	Squares	Mean Square	F Ratio
Model	3	28.612829	9.53761	34.7928
Error	12	3.289516	0.27413	Prob > F
C. Total	15	31.902345		<.0001*

Parameter Estimates

Term	Estimate	Std Error	t Ratio	Prob> t
Intercept	1.2019523	0.130893	9.18	<.0001*
drug[morphine]	-0.319737	0.130893	-2.44	0.0310*
dep1[n]	1.2379727	0.130893	9.46	<.0001*
drug[morphine]*dep1[n]	-0 391783	0.130893	-2 99	0.0112*