

Studies on Nonregular Fractional Factorial Designs

Dan Huang

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1 Introduction

Nonregular factorial designs are widely used in various experiments to identify effective factors in economic and flexible runs such as Plackett-Burman designs (Xu, Phoa, Wong, 2009). In this project, the primary purpose will focus on evaluating the results of experiments shown in the literature paper and investigate further on the research of nonregular fractional factorial design. Complex aliasing structure in nonregular fractional designs motivated the researchers to investigate some useful criteria for selection of significant effects in the assumed model such as generalized minimum aberration and generalized word length pattern. In following sections, it will include the analysis of some examples plus the simulation results.

Nonregular designs such as Plackett-Burman designs and supersaturated designs have partial aliased structure that is difficult to distinguish and analyze the effects of factors. However, this feature gives experimenters to identify potential interactions for improving the efficiency of designs (Wolters and Bingham, 2011). In nonregular fractional factorial designs, the partial aliasing structure can affect the effects negatively and positively. Partial fractions provide estimation for more models than fully confounded effects in regular fraction. However, the simplicity from results can be reduced due to the partial aliasing.

2 Literature Review

Commonly, we can classify orthogonal factorial designs into regular fractional factorials and nonregular fractional factorials. Any two factorial effects in regular fractional factorial design are either orthogonal or fully aliased. However, a nonregular fractional factorial design displays some complicated aliasing structure in which some effects are neither orthogonal nor fully confounded. This feature provides the possibility to detect interaction effects. Deng and Tang (1999) proposed generalized resolution and minimum aberration criteria for assessing, ranking and comparing

nonregular designs. Hamada and Wu (1992) introduced an analysis strategy that consists of three steps. The first step is to fit a model including all main effects and two-factor interactions that are orthogonal to the main effects by using standard analysis methods like normal plots. The second step is to entertain the model with significant main effects and two-factor interactions based on effect heredity and effect sparsity. Finally, significant terms identified in the previous steps and all main effects are included into the model by using forward selection regression procedure. Response surface methodology is the effective tool for evaluating the relationship in response variables and experimental factors and includes three stages: initial screening stage, sequential experimentation to find the optimal region and fitting a second-order model in this region. Cheng and Wu (2001) also introduced a two-stage analysis strategy that includes screening analysis and response surface exploration by fitting a second-order model. Other analysis strategies have been already developed such as a Bayesian method for screening experiments. For nonregular designs, Yuan, Joseph and Lin (2007) extended the general least angle regression (LARS).

3 Methods

(1) Lenth's method

Lenth (1989) propose a statistical method to test effects for unreplicated factorial designs by comparing to critical values. Using half-normal plot can also detect the active effects and diminish the subjectivity. The Lenth method can not only estimate factorial effects for 2^k full factorial and 2^{k-p} fractional factorial designs but also can be used to handle nonregular designs based on the orthogonal estimates. Under the assumption that there are only few active effects, Lenth (1989) introduced an estimator called pseudo standard error (PSE) based on the contrasts. Assume X_i as the estimates factorial effects, the $PSE = 1.5 \text{median}_{|X_i| < 2.5s_0} |X_i|$ where $s_0 = 1.5 \text{median}|x_i|$. The t-statistics is obtained by dividing the $|X_i|$ by the PSE, which is referred to $t_{(Lenth,i)} = \frac{X_i}{PSE}$. Individual error rate (IER) is the error rate of

individual effects after being tested active by using t-distribution. Experimentwise error rate (EER) is the error rate of at least one inactive effect that are tested as active. Compared to IER, EER could be used more often since it is obvious to see the critical values of EER should be larger than that of IER. We can also obtain confidence intervals for the estimated values easily by Lenth method.

(2)Forward selection

Traditional model selection methods such as forward selection, backward selection and stepwise selection are very common for experimenters to determine useful variables into models. Choosing valuable variables into models depends on the objective of models. Some models' primary purpose is for prediction while some models are built for parameters estimation, which causes the different selection criteria. Several of statistics can determine the model fit to select the best model such as coefficient of determination R^2 , adjusted R^2 and mean square error $\hat{\sigma}^2$. Clearly, we want a chosen model that maximizes R^2 and adjusted R^2 while minimizing mean square error $\hat{\sigma}^2$ at the same time. The advantage of all possible regression model selection methods allows us to compare the statistics for models mostly. However, those procedures can not make a direct comparison to determine the best model. Forward selection method begins with no variables in the model. Then we do k partial F-tests and add the variable that has the largest significant partial F. However, this procedure is not flexible since once a variable is added it cannot be eliminated. Therefore, the best model could never be considered and is particularly a problem if multicollinearity exists.

(3)Simulated Annealing Model Research

Model selection in some nonregular designs is difficult due to the large variables sets and small treatment runs in the designs. Wolters and Bingham (2011) proposed a nonconvergent stochastic search for fitting models with same number of variables and good interpretation as well that is called simulated annealing model search (SAMS) in which you could find larger models fitted nicely instead of a single best

model. Two general principles are assumed in SAMS that are effect sparsity and effect heredity. SAMS consists of model search algorithm and associated visualization methods to find larger good models but it is hard to identify single truly model. There are two major steps to complete model selection by handling SAMS. The first step is to determine the maximum plausible size of the true model considering the effect sparsity, denoted S_{max} . Then we need to find out a large set of promising oversized models such as $p=S_{max}+2$. We can say this model denoted M is a good model. The next step is to identify combination of S_{max} or few variables that can be best represented in M. Overall, simulating annealing is a search algorithm instead of an optimization algorithm. Also, this method is a heredity-respecting search without visiting nonheredity models.

4 Replication on strength-2 Screening Designs

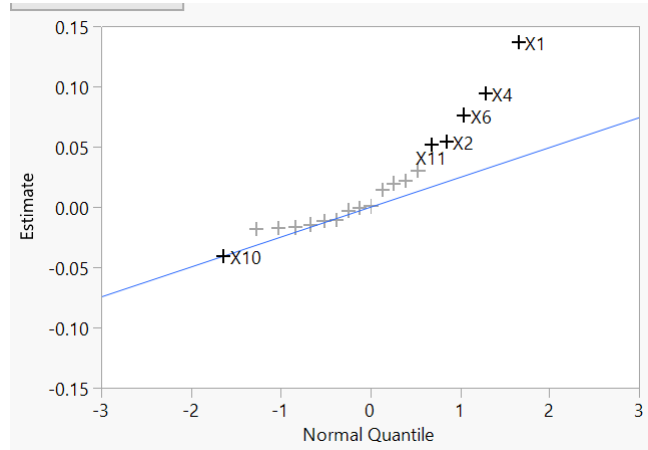
In the review paper, two 20-run Plackett-Burman designs with 19 factors were analyzed.

4.1 Wu et al.'s Image-Processing Experiment

Wu et al.'s image-processing experiment has nineteen 2-level factors and mean correlation as the response. Three methods such as Lenth's method, forward selection method and SAMS are replicated in this project for each experiments. In the first analysis, only main effects are considered in the model.

a) Lenth's method

From the normal plot below, it can tell us that 1, 2, 4, 6 and 11 five main factors are important in this main effect model. From the parameter estimate table, factors 1, 2, 4, 6 and 11 have t statistics exceeding 2.113. Factor 11, having $t=2.113$, is less than the individual error rate (IER) critical value of 2.121. The Lenth PSE=0.02478, which is the estimation for standard error. The result obtained is the same as the review paper.



Lenth PSE			
0.02478			
Parameter Estimate Population			
Term	Estimate	Pseudo t-Ratio	Pseudo p-Value
Intercept	0.764550	30.8535	<.0001*
X1	0.137700	5.5569	0.0012*
X2	0.054920	2.2163	0.0662
X3	-0.016180	-0.6529	0.5368
X4	0.095200	3.8418	0.0077*
X5	-0.002130	-0.0860	0.9342
X6	0.077010	3.1077	0.0395*
X7	-0.016860	-0.6804	0.5203
X8	0.022780	0.9193	0.3916
X9	0.020380	0.8224	0.4407
X10	-0.039800	-1.6061	0.1568
X11	0.052360	2.1130	0.0766
X12	0.001290	0.0521	0.9601
X13	0.000040	0.0016	0.9988
X14	-0.013820	-0.5577	0.5962
X15	0.015050	0.6073	0.5647
X16	-0.017460	-0.7046	0.5061
X17	0.031000	1.2510	0.2552
X18	-0.010560	-0.4262	0.6841
X19	-0.010070	-0.4064	0.6978

b) Forward selection

In the second analysis, the two-factor interaction model is considered, which contains all main effects and all two-factor interactions by using stepwise regression. I chose single step to add terms into the model until p-value first exceeds $\alpha = 0.01$ like the paper suggests. In step 11, the p-value of adding term 12*14 is 0.0205, larger than critical value which causes the forward selection terminated. The result obtained by this method is the same as the review paper looking at the **Table 1**. However, using weak heredity restricted forward selection identifies main effect x2 at the fourth step while in the review paper, two-factor interaction x4*x6 was detected.

Table 1. Unrestricted Forward Selection

Step	Term	p-value	R ²
1	X1	0.00186	0.4244
2	X15*X19	0.00213	0.6748
3	X18*X19	0.00548	0.8021
4	X4	0.00453	0.8863
5	X4*X8	0.00247	0.9422
6	X5*X15	0.00362	0.9706
7	X17*X18	0.00611	0.9847
8	X3*X7	0.00692	0.9923
9	X2*X5	0.00936	0.9962
10	X6*X16	0.004	0.9986

There is a disadvantage of forward selection that it overfits the model by includ-

Table 2. Weak heredity restricted forward selection

	Step	Term	p-value	R ²
	1	x1	0.0019	0.4244
	2	x4	0.0074	0.6272
	3	x1*x4	0.00159	0.8038
H	4	x2	0.1068	0.8359

ing inactive terms into the model (Westfall et al, 1998). Thus, forward selection with weak effect heredity was imposed. In the **Table 2**, it indicates that the restriction does not allow $x_{15} * x_{18}$ and $x_{18} * x_{19}$ to enter the model. When interaction $x_1 * x_4$ is added in step 3, the other 17 main effects has p-values that are larger than 0.1, which contradicts the terms included in table 1. Mee (2013) found out two two-factor interactions $x_1 * x_4$ and $x_4 * x_6$ are added in the model while in table 2, main effect x_2 is included by this restriction.

c) Simulated annealing model search

Here, the maximum reasonable size could be defined by $S_{max}=6$ for the true model. Specifying $p=S_{max}+2=8$ means over-specified model has eight terms. Implementing SAMS to fit 10000 individual models of size eight and the active terms with the smallest SSE will show up in the raster plot. (Plots produced by a matlab implementation of SAMS). The link plot is created for the complement to the raster plot, illustrating the relationship between variables and identifying the models. From the raster plot in the figure 1, seven frequent terms appear in the models: x_1 , x_4 , x_6 , $x_1 * x_4$, $x_1 * x_6$, $x_1 * x_{11}$, x_2 . In the link plot (figure 2), variables appearing frequently have a larger marker and greater spacing from their neighboring points, which indicates main effects x_1 , x_4 and $x_1 * x_4$ occur most frequently. In this PB 20-run design, the correlation between main effect contrasts and two-factor interaction contrasts is 0.2 or 0.6. SAMS suggests two-factor interaction $x_1 * x_4$ should be included in the model. The first two clusters have two models standing out that are (x_1, x_4, x_6)

and $(x_1, x_4, x_1 * x_4)$. Therefore, it is difficult to distinguish the main effect x_6 and interaction $x_1 * x_4$. SAMS indicates the influence of this partial aliasing. Compared with the result in the review paper, we don't include two interactions that are $x_4 * x_6$ and $x_4 * x_9$.

Figure 1. Raster Plot

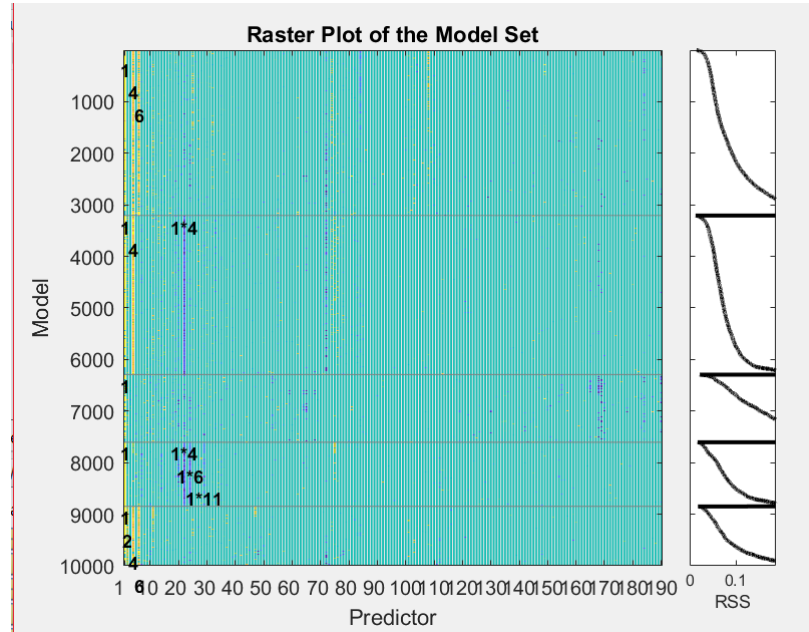


Figure 2. Link Plot

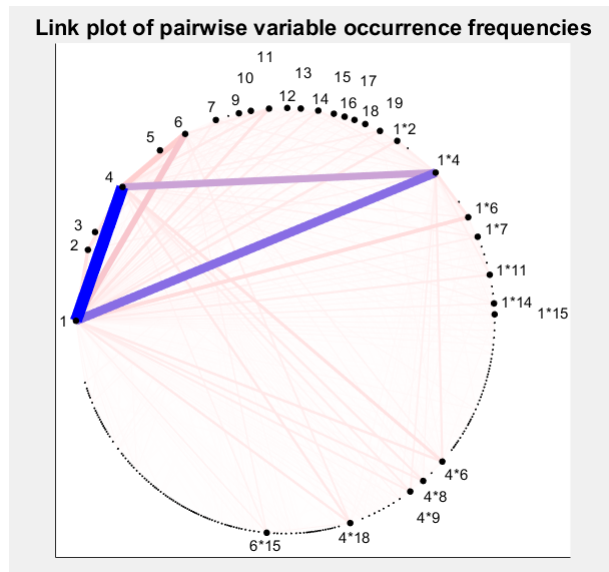
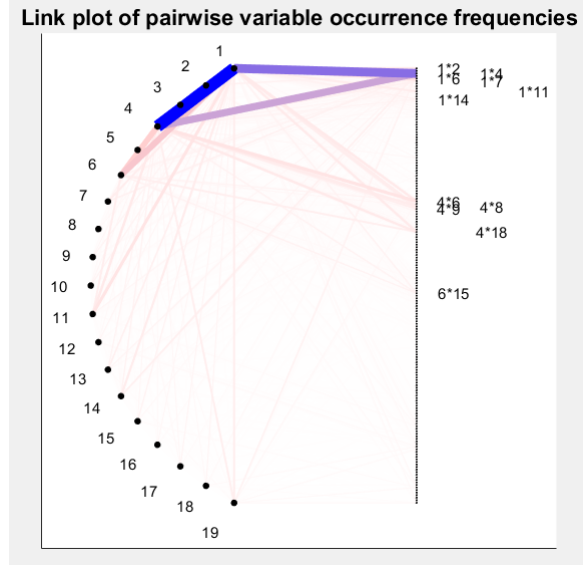


Figure 3. Link Plot



Overall, Lenth’s method for main effects only identifies four or five active factors. However, forward selection analysis suggests the $x_1 * x_4$ interaction as active. The model with x_1 , x_4 and $x_1 * x_4$ is also the second highest entropy model from SAMS. It is also possible that main effect x_6 could be significant.

4.2 Bell et al.’s Credit-Card-Offer Experiment

Bell et al.’s credit-card-offer experiment contains 19 factors and the number responding count as the response.

a) After transforming the response for $\arcsin[\sqrt{\text{Count}/5000}]$, using the Lenth’s method detects that there may be five important main effects that are x_2 , x_{14} , x_{12} , x_3 and x_{11} with $\text{PSE}=0.0026$. The parameter estimates table indicates main effects x_2 and x_{14} are significant.

Figure 4. Normal Plot

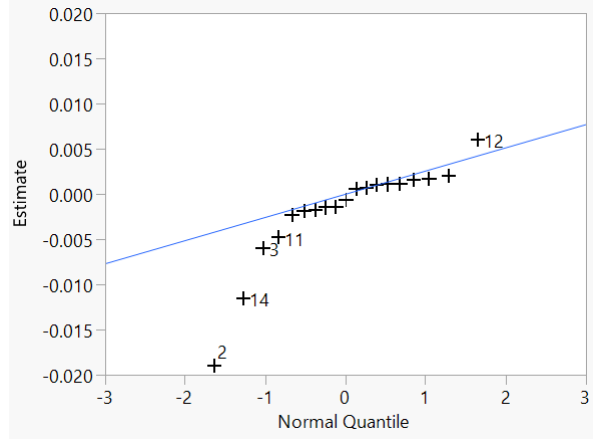


Figure 5. Parameter Estimates

Parameter Estimate Population			
Term	Estimate	Pseudo t-Ratio	Pseudo p-Value
Intercept	0.111522	43.4590	<.0001*
1	0.001078	0.4201	0.6883
2	-0.018847	-7.3445	0.0003*
3	-0.005907	-2.3017	0.0587
4	-0.001356	-0.5285	0.6152
5	-0.002208	-0.8604	0.4210
6	0.001758	0.6850	0.5176
7	-0.000521	-0.2029	0.8455
8	-0.001387	-0.5407	0.6072
9	-0.001800	-0.7015	0.5079
10	0.001255	0.4892	0.6412
11	-0.004697	-1.8302	0.1144
12	0.006145	2.3948	0.0515
13	0.001711	0.6668	0.5284
14	-0.011427	-4.4531	0.0038*
15	-0.001711	-0.6667	0.5285

b) Forward selection

Taking weak effect heredity into account, forward selection adds interaction $x_2 * x_{14}$ in step 3. After step 3, there are five main effects added in the next steps. The p-values of x_1 and x_5 are larger than 0.05. Compared to the results in the review paper, we include main effects x_{11} , x_5 and x_{16} instead of interactions $x_2 * x_{15}$, $x_{10} * x_{14}$, and $x_2 * x_{17}$.

Figure 6. Weak Heredity Forward Selection

Step	Term	p-value	R ²
1	X2	0.0001	0.5812
2	X14	0.0006	0.7949
3	X2*X14	0.00843	0.8688
4	X12	0.02296	0.9081
5	X11	0.057	0.9297
6	X3	0.0251	0.9529
7	X5	0.0709	0.9645
8	X16	0.0334	0.9769

c) SAMS method

From the raster plot, obviously there are five clusters shown in figure 7. The largest cluster displays main factors x_2 , x_{14} and two-factor interaction $x_2 * x_{14}$ with the smallest residual sum of squares (RSS). In the second cluster, it contains main effects x_2 , x_3 , x_{12} , x_{14} and interaction $x_2 * x_{15}$. When x_3 is absent, interaction $x_2 * x_{14}$ appears in the largest cluster. In the link plot, variables that occur most frequently are main effects x_2 and x_{14} . Compared to the results in the review paper, we have five clusters in the raster plot. The first cluster identifies three significant effects that are x_2 , x_{14} and $x_2 * x_{14}$, which is slightly different from results of the review paper.

Figure 7. Raster Plot

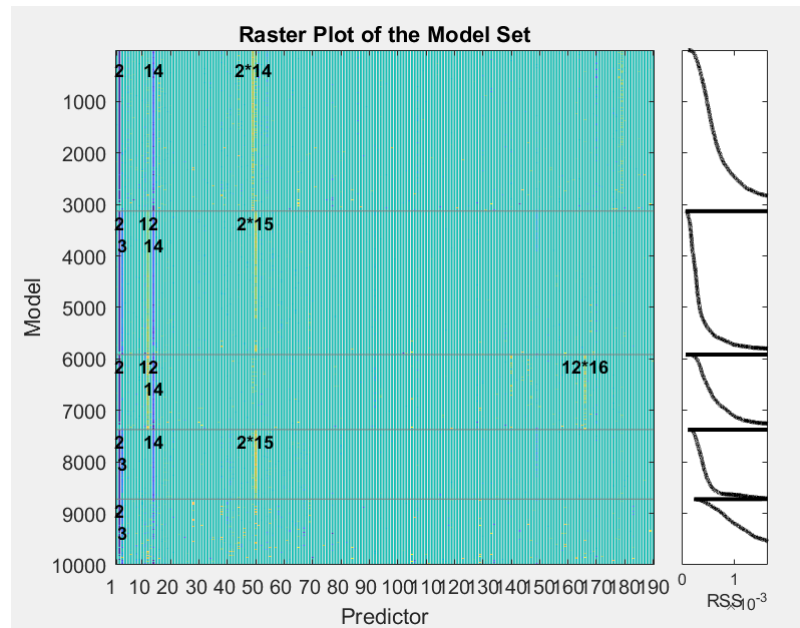


Figure 8. Link Plot

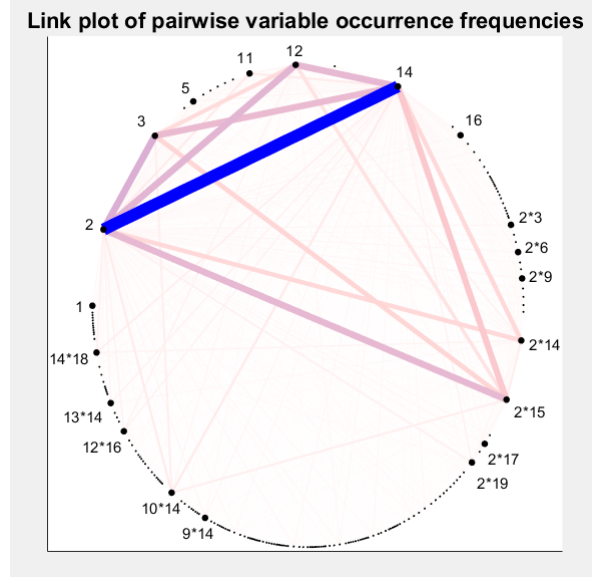
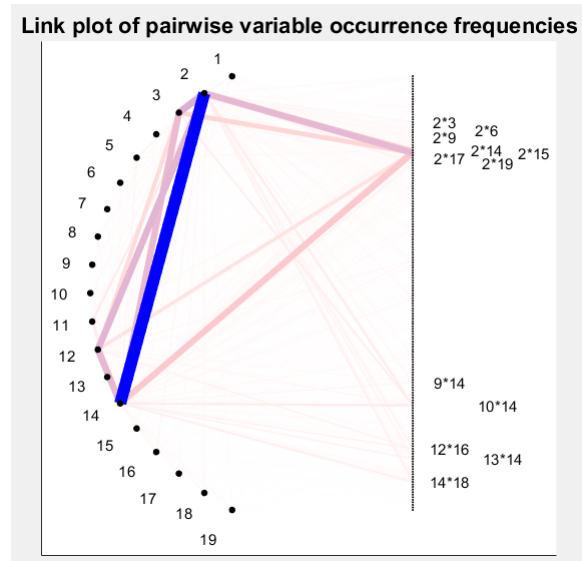


Figure 9. Link Plot



The three methods select different models. For main effect model, Lenth's method selects five significant effects that are x_2 , x_3 , x_{11} , x_{12} and x_{14} . Forward selection identifies interaction $x_2 * x_{14}$ except main effects. SAMS suggests a model containing effects x_2 , x_{14} and $x_2 * x_{14}$.

5 Analyzing Strength-3 Designs

5.1 Yi et al.' Computer-Architecture Experiment

Yi et al.'s computer-architecture experiment has 41 factors plus three additional orthogonal columns not being assigned factors and cycles per instruction (CPI) as the response.

a) Lenth's method

Using Lenth's method, we have main effects 4, 5, 10, 11, 12, 14, 15, 16, 17, 28, 31, 35, 38, 40, 41 selected having Lenth t statistics that exceed 2.0469 at Lenth PSE=0.04. JMP's Modeling Screening is the improvement compared to Lenth's method by adding terms until the model is saturated. Here, no two-factor interactions active are detected in JMP's Modeling Screening. Main effects 5, 11, 12, 31, 14, 41, 28, 15, 38 are active according to the individual p-values. Compared to results in the review paper, we have several different active effects being identified.

Figure 10. Parameter Estimates 1

Lenth PSE			
0.040892			
Parameter Estimate Population			
Term	Estimate	t Ratio	Prob> t
Intercept	1.28810	45.5564	<.0001*
X1	0.05342	1.8893	0.0654
X2	0.01974	0.6981	0.4888
X3	0.00551	0.1949	0.8464
X4	0.06308	2.2309	0.0308*
X5	-0.16213	-5.7339	<.0001*
X6	-0.00892	-0.3155	0.7539
X7	0.02431	0.8597	0.3946
X8	0.00542	0.1917	0.8489
X9	0.05178	1.8314	0.0738
X10	0.05788	2.0469	0.0467*
X11	-0.15372	-5.4365	<.0001*
X12	-0.14956	-5.2894	<.0001*
X13	0.01842	0.6515	0.5181
X14	0.08592	3.0388	0.0040*
X15	0.07524	2.6610	0.0108*
X16	0.06258	2.2133	0.0321*
X17	0.06540	2.3129	0.0255*
X18	0.00685	0.2423	0.8096
X19	0.02883	1.0196	0.3135
X20	-0.01756	-0.6209	0.5378
X21	0.03790	1.3403	0.1870

Figure 11. Parameter Estimates 2

X22	-0.02274	-0.8042	0.4256
X23	-0.00978	-0.3460	0.7310
X24	0.05490	1.9416	0.0586
X25	0.02569	0.9087	0.3685
X26	-0.05583	-1.9745	0.0546
X27	-0.02058	-0.7278	0.4706
X28	-0.08417	-2.9769	0.0047*
X29	-0.04149	-1.4673	0.1494
X30	0.00072	0.0253	0.9799
X31	0.10685	3.7790	0.0005*
X32	-0.04269	-1.5099	0.1382
X33	0.00024	0.0084	0.9933
X34	-0.00072	-0.0253	0.9799
X35	0.06683	2.3636	0.0226*
X36	0.00919	0.3251	0.7466
X37	0.00242	0.0856	0.9322
X38	0.07165	2.5340	0.0149*
X39	-0.01028	-0.3637	0.7178
X40	0.06885	2.4351	0.0190*
X41	0.08526	3.0154	0.0043*
X42	-0.00726	-0.2568	0.7985
X43	-0.02378	-0.8412	0.4048

Figure 12. JMP Modeling Screening

Term	Contrast		Lenth t-Ratio	Individual p-Value	Simultaneous p-Value
X5	-0.162125		-4.75	0.0001*	0.0049*
X11	-0.153716		-4.51	0.0002*	0.0089*
X12	-0.149557		-4.38	0.0002*	0.0129*
X31	0.106852		3.13	0.0050*	0.2246
X14	0.085920		2.52	0.0167*	0.6096
X41	0.085261		2.50	0.0170*	0.6130
X28	-0.084170		-2.47	0.0183*	0.6422
X15	0.075239		2.21	0.0333*	0.8420
X38	0.071648		2.10	0.0428*	0.9018
X40	0.068852		2.02	0.0500	0.9372
X35	0.066830		1.96	0.0558	0.9571
X17	0.065398		1.92	0.0604	0.9689
X4	0.063080		1.85	0.0680	0.9831
X16	0.062580		1.83	0.0705	0.9841
X10	0.057875		1.70	0.0930	0.9971
X26	-0.055830		-1.64	0.1047	0.9987
X24	0.054898		1.61	0.1101	0.9995
X1	0.053420		1.57	0.1201	0.9998
X9	0.051784		1.52	0.1329	1.0000

b) Forward selection method

Here, forward selection method with weak heredity and strong heredity are both undertaken to identify active main effects and two-factor interactions, assuming higher order interactions are negligible. Main effects 5, 11, 12, 31, 14, 41, 28 show significance under weak heredity. However, interactions 6*7 and 12*24 don't stand out compared to the result from the review paper.

Figure 13. Weak Heredity Restricted Forward Selection

Step	Parameter	Action	"Sig Prob"	Seq SS	RSquare	Cp	p	AICc	BIC
1	X5	Entered	0.0005	2.313037	0.1328	5.9e+6	2	100.938	108.084
2	X11	Entered	0.0004	2.079315	0.2522	5.1e+6	3	90.1018	99.5292
3	X12	Entered	0.0002	1.968317	0.3652	4.3e+6	4	77.9354	89.5904
4	X31	Entered	0.0051	1.004732	0.4228	3.9e+6	5	71.858	85.685
5	X14	Entered	0.0196	0.649645	0.4601	3.7e+6	6	68.3422	84.2836
6	X41	Entered	0.0172	0.639716	0.4969	3.4e+6	7	64.565	82.5609
7	X28	Entered	0.0154	0.623451	0.5327	3.2e+6	8	60.5558	80.5441

With strong heredity, there are same active main effects plus two two-factor interactions 5*6 and 11*23 while interaction 12*24 is determined in the review paper.

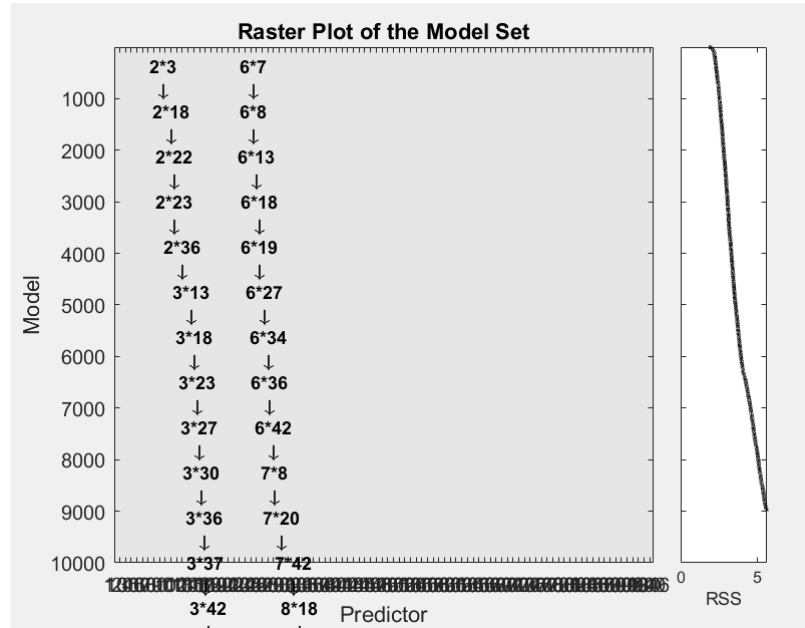
Figure 14. Strong Heredity Restricted Forward Selection

Step	Parameter	Action	"Sig Prob"	Seq SS	RSquare	Cp	p	AICc	BIC
1	X5	Entered	0.0005	2.313037	0.1328	5.9e+6	2	100.938	108.084
2	X11	Entered	0.0004	2.079315	0.2522	5.1e+6	3	90.1018	99.5292
3	X12	Entered	0.0002	1.968317	0.3652	4.3e+6	4	77.9354	89.5904
4	X5*X6	Entered	0.0049	1.009867	0.4231	3.9e+6	5	71.8131	85.64
5	X31	Entered	0.0034	1.004732	0.4808	3.5e+6	6	64.9049	80.8463
6	X14	Entered	0.0143	0.649645	0.5181	3.3e+6	7	60.7674	78.7633
7	X41	Entered	0.0121	0.639716	0.5548	3e+6	8	56.2761	76.2644
8	X28	Entered	0.0103	0.623451	0.5906	2.8e+6	9	51.4492	73.3654
9	X11*X23	Entered	0.0081	0.616316	0.6260	2.5e+6	10	46.1105	69.8875
10	X15	Entered	0.0136	0.498155	0.6546	2.4e+6	11	41.7959	67.3639

c)SAMS

Under weak effect heredity, the number of terms used in the model is $p=31$. However, the result displayed in the figure below indicates there is no main effects appearing. In review paper, Mee (2013) repeated SAMS with $p=20$ and found out only main effects are included in the highest entropy models.

Figure 15. Raster Plot



5.2 TNO's Mirror-Polishing Experiment

TNO's mirror-polishing experiment has been conducted to choose the best diamond-turning process for a mirror. Here, a 48-run experiment to detect the best diamond-turning process for a mirror was introduced with 13 factors that are sharpness (A), machine (B), operator (C), orientation (D), angle (E), radius (F), feed rate (G), depth (H), speed (I), material (J), lubrication amount (K), lubrication pressure (L) and shape (M). The mean surface roughness (Rq) is considered as the response.

a) Lenth's method

If we use Lenth's method only on 13 main effects, the potential interactions over some main effects could be ignored because we have 47 df in the experiment. Hence, JMP's Modeling Screening of Lenth's method is undertaken in two-factor interaction model. From the figures below, it is obvious that main effects B, G, I, A and two-factor interactions G*I, B*E and A*D are important in the assumed model. Lenth PSE=0.10176. If we want to make model hierarchical, adding D and E could be considered. Therefore, a model with six main effects and three two-factor interactions can be formulated. The result is the same as that in the review paper.

Figure 16. JMP's Modeling Screening Analysis for Rq

Term	Contrast		Lenth t-Ratio	Individual p-Value	Simultaneous p-Value
B	0.652938		6.42	<.0001*	0.0006*
G	0.498146		4.90	0.0001*	0.0077*
I	-0.410175		-4.03	0.0006*	0.0378*
A	-0.397912		-3.91	0.0007*	0.0469*
E	-0.244575		-2.40	0.0248*	0.5100
J	-0.151538		-1.49	0.1462	0.9922
L	-0.130883		-1.29	0.2078	0.9995
F	-0.106671		-1.05	0.2975	1.0000
C	0.077983		0.77	0.4417	1.0000
H	0.054713		0.54	0.6062	1.0000
D	0.045333		0.45	0.6675	1.0000
K	0.043287		0.43	0.6807	1.0000
M	-0.001125		-0.01	0.9922	1.0000
B*G	0.059463		0.58	0.5762	1.0000
B*I	-0.108125		-1.06	0.2911	1.0000
G*I	-0.428650		-4.21	0.0003*	0.0270*
B*A	-0.080871		-0.79	0.4251	1.0000
G*A	0.099271		0.98	0.3327	1.0000
I*A	-0.076225		-0.75	0.4510	1.0000
B*E	-0.264633		-2.60	0.0172*	0.4055
G*E	0.002117		0.02	0.9855	1.0000
I*E	0.005712		0.06	0.9561	1.0000
A*E	0.041167		0.40	0.6967	1.0000
B*J	0.142871 *		1.40	0.1693	0.9973
G*J	-0.039179		-0.39	0.7114	1.0000
I*J	-0.016399 *		-0.16	0.8765	1.0000
A*J	0.104896		1.03	0.3065	1.0000
E*J	-0.034940 *		-0.34	0.7427	1.0000
B*L	-0.143235 *		-1.41	0.1685	0.9972
G*L	-0.002210 *		-0.02	0.9846	1.0000

Figure 17. JMP's Modeling Screening Analysis for Rq

I*L	-0.048082 *		-0.47	0.6480	1.0000
A*L	0.002583		0.03	0.9806	1.0000
E*L	0.079032 *		0.78	0.4347	1.0000
J*L	-0.148302 *		-1.46	0.1541	0.9951
B*F	-0.006360 *		-0.06	0.9505	1.0000
G*F	0.039859 *		0.39	0.7068	1.0000
I*F	0.102549 *		1.01	0.3166	1.0000
A*F	0.114946		1.13	0.2631	1.0000
E*F	-0.099433 *		-0.98	0.3322	1.0000
J*F	-0.188482 *		-1.85	0.0757	0.8929
I*C	0.067841 *		0.67	0.5159	1.0000
A*C	0.042692		0.42	0.6847	1.0000
A*H	-0.019429		-0.19	0.8533	1.0000
F*H	0.037593 *		0.37	0.7210	1.0000
A*D	0.315767		3.10	0.0065*	0.1852
A*K	0.059737		0.59	0.5750	1.0000
A*M	-0.152567		-1.50	0.1437	0.9916

b) Forward selection method

There are six main effects and two interactions that are B, G, I, A, E, J, G*I, B*E identified by using forward selection. Adding interactions into model, we get $R^2=0.7825$. However, there are other more two interactions A*D and E*H displayed in the review paper.

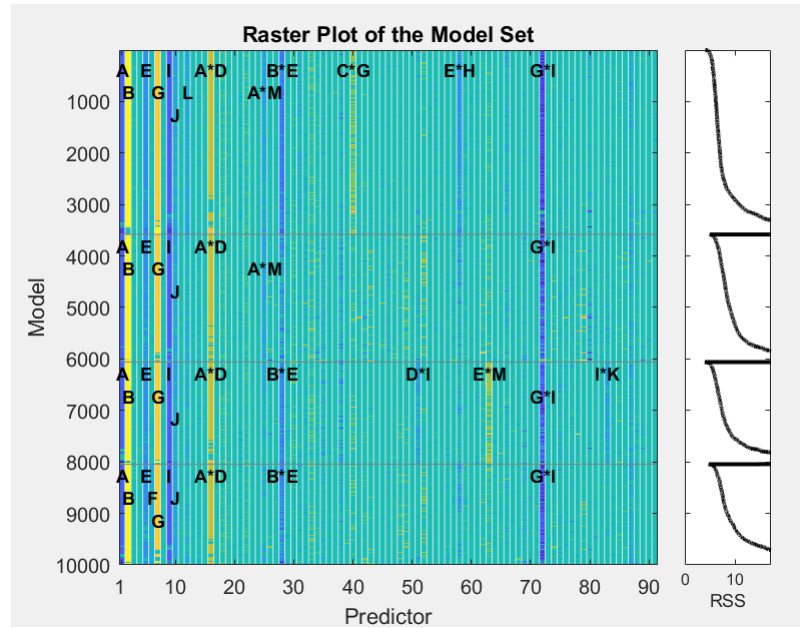
Figure 18. Weak Heredity Restricted Forward Selection for Rq

Step	Term	p-value	R ²
1	B	0.0003	0.2494
2	G	0.0012	0.3946
3	I	0.0055	0.493
4	G*I	0.0015	0.6005
5	A	0.0009	0.6931
6	E	0.0268	0.7281
7	B*E	0.0111	0.7281
8	J	0.1287	0.7825

c) SAMS

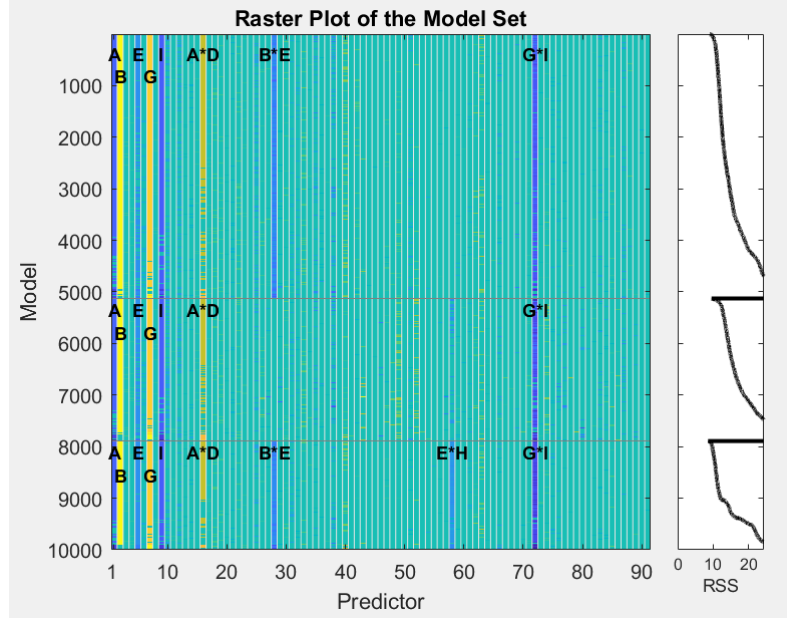
The raster plot was produced with four clusters by SAMS with $p=18$. There are six interactions presented in the first cluster. Only A*D and G*I are presented in every cluster. Each cluster identifies main effects A, B, E, G, I, J. SAMS obtains the same model as was chosen by forward selection.

Figure 19. Raster Plot



By classifying more clarity, SAMS produced a raster plot with three clusters with $p=12$. In each raster plot, main effects A, B, E, G, I and two interactions A*D, G*I are included.

Figure 20. Raster Plot



6 Analyzing Strength-2 Designs with $n \geq 2k$

In strength-3 designs, two-factor interactions are not biased with main effects. In addition, strength-3 design requires that n must be multiple of 8. However, $OA(24, 2^7, 2)$ allows to estimate 16 two-factor interactions even though there are small correlations between main effects and two-factor interactions. Here, we analyze a strength-2, 7-factor, 24-run design in two different known models.

6.1 Model $Y_1 = -A + A*B + z$

a) Lenth's method

Using Modeling Screening Lenth's method identifies the main effect A and interaction $A*B$ with Lenth $PSE=0.217$.

Figure 21. Parameter Estimates

Term	Contrast		Lenth t-Ratio	Individual p-Value	Simultaneous p-Value
A	-0.950869		-4.39	0.0021*	0.0314*
C	-0.415206		-1.92	0.0659	0.6621
D	-0.410243		-1.89	0.0689	0.6782
E	-0.144487		-0.67	0.5002	1.0000
B	0.089546		0.41	0.6916	1.0000
G	-0.020271		-0.09	0.9279	1.0000
F	-0.002298		-0.01	0.9924	1.0000
A*C	0.041501 *		0.19	0.8541	1.0000
A*D	0.139090 *		0.64	0.5458	1.0000
C*D	0.158622		0.73	0.4457	1.0000
A*E	-0.295930 *		-1.37	0.1748	0.9634
C*E	-0.183867 *		-0.85	0.3802	1.0000
D*E	0.102608 *		0.47	0.6524	1.0000
A*B	0.734969 *		3.39	0.0080*	0.1122
C*B	0.229971 *		1.06	0.2779	0.9992
D*B	0.291202 *		1.34	0.1811	0.9691
E*B	-0.130092 *		-0.60	0.5730	1.0000

b) Forward selection method

Using forward selection method with weak heredity also detects A and A*B both in the model at $R^2=0.8373$.

c) SAMS

Implementing SAMS with $p=10$ suggested by Wolters and Bingham (2011), we obtain A and A*B in each cluster. In the link plot, it indicates that effects A, D, A*B, A*E appear most frequently.

Figure 22. Raster Plot

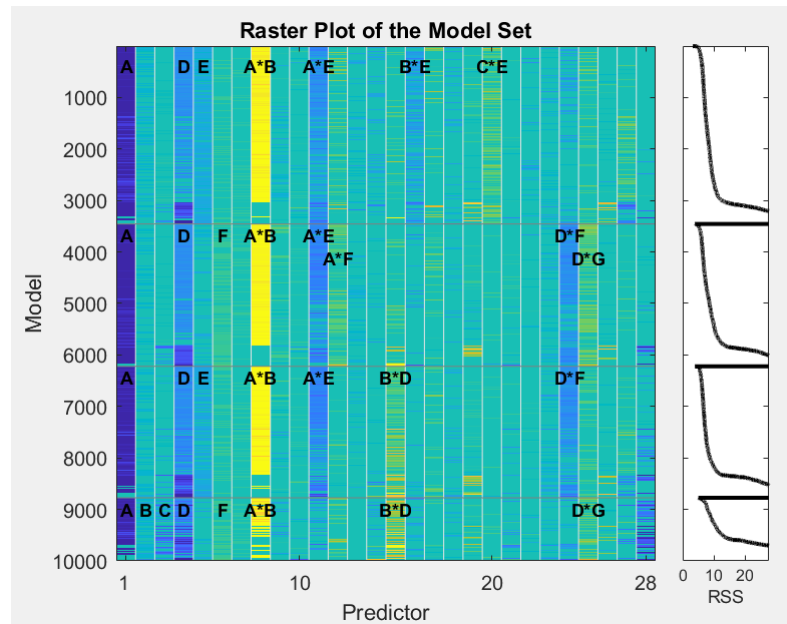
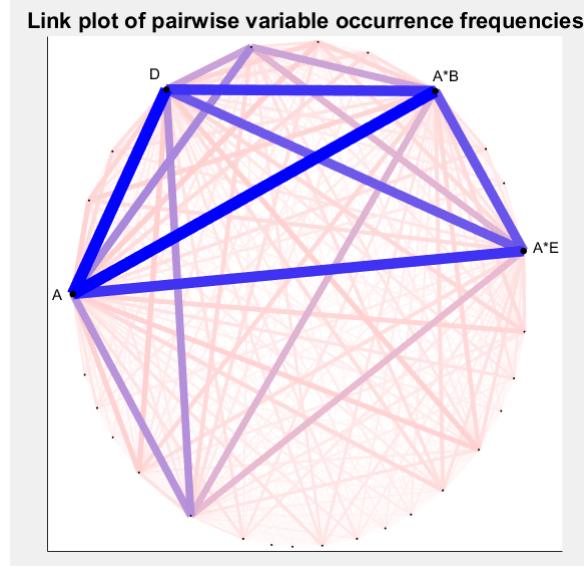


Figure 23. Link Plot



In summary, Lenth's method performs the best for this case, which identifies effects A and A*B based on the individual p-values. However, the best method used in the review paper for this case is stepwise regression.

6.2 Model $Y_2 = -A + 2B + 1.5C + D + E + A*B + 1.5B*C - A*D + D*E + z$

a) Lenth's method

Modeling Screening identifies main effects A, B, C, D, E, A*B. Interactions B*C and E*D could be significant too.

Figure 24. Parameter Estimates

Contrasts						
Term	Contrast			Lenth t-Ratio	Individual p-Value	Simultaneous p-Value
B	2.20329			8.80	0.0002*	0.0010*
A	-1.54227			-6.16	0.0005*	0.0055*
C	1.26411			5.05	0.0014*	0.0181*
E	0.79145			3.16	0.0127*	0.1544
D	0.66906			2.67	0.0225*	0.2761
G	0.08266			0.33	0.7549	1.0000
F	0.05149			0.21	0.8451	1.0000
B*A	1.12117 *			4.48	0.0026*	0.0319*
B*C	0.78460 *			3.13	0.0132*	0.1602
A*C	-0.16697 *			-0.67	0.5002	1.0000
B*E	0.12928			0.52	0.6218	1.0000
A*E	0.16427			0.66	0.5353	1.0000
C*E	0.02691			0.11	0.9160	1.0000
B*D	0.04880 *			0.19	0.8533	1.0000
A*D	-0.51825 *			-2.07	0.0550	0.5485
C*D	-0.29261 *			-1.17	0.2386	0.9942
E*D	-1.00084 *			-4.00	0.0038*	0.0557
B*G	-0.27581 *			-1.10	0.2646	0.9979
A*G	-0.30221 *			-1.21	0.2246	0.9896
C*G	-0.12328 *			-0.49	0.6392	1.0000
E*G	0.12297 *			0.49	0.6400	1.0000

b) Forward selection

Using forward selection method with weak heredity identifies same active terms as Lenth's method.

Figure 25. Weak Heredity Forward Selection

Step	Parameter	Action	"Sig Prob"	Seq SS	RSquare	Cp	p	AICc	BIC
1	B	Entered	0.0020	116.508	0.3586	.	2	127.178	129.513
2	A	Entered	0.0104	57.08634	0.5344	.	3	122.4	125.006
3	C	Entered	0.0169	38.35142	0.6524	.	4	118.61	121.167
4	A*B	Entered	0.0945	15.83247	0.7011	.	5	118.593	120.72
5	D	Entered	0.0221	25.07936	0.7783	.	6	115.48	116.726
6	E	Entered	0.0492	15.03352	0.8246	.	7	114.46	114.285
7	B*C	Entered	0.0309	14.77445	0.8701	.	8	112.514	110.259
8	D*E	Entered	0.0038	18.4816	0.9270	.	9	104.753	99.6109
9	A*D	Entered	0.0168	8.177026	0.9521	.	10	101.687	92.6454

c) SAMS

Implementing SAMS with $p=10$, we obtain main effects A, B, C in each cluster while A*B is not included in the highest entropy model.

Figure 26. Raster Plot

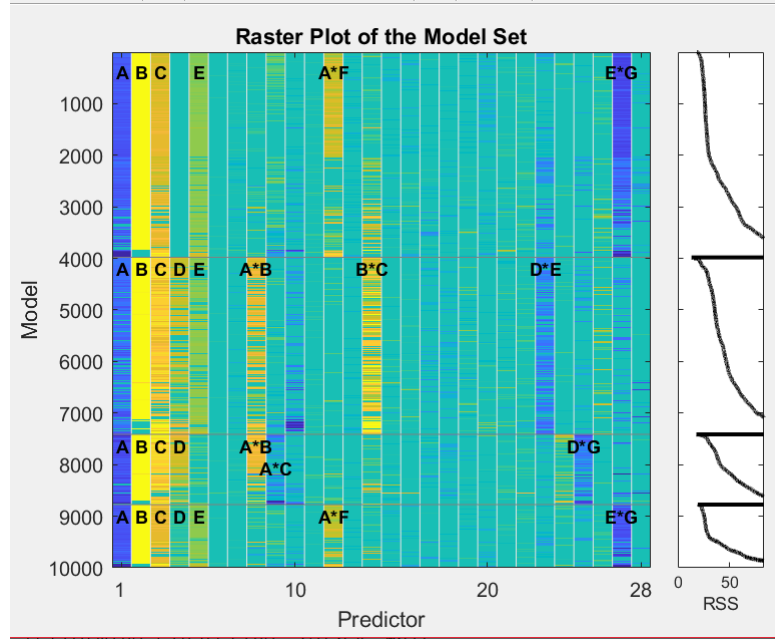
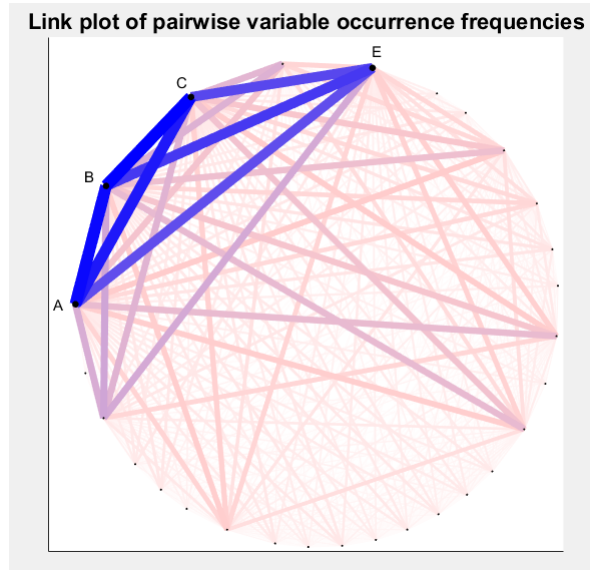


Figure 27. Link Plot



Overall, Lenth's method and forward selection method obtain same active effects.

7 Further Analysis on 3/4 Nonregular Designs

John (1962, 1969) proposed three quarter replicates of 2^n designs of 6, 12, 24, 48, \dots , runs to investigate the active terms in the assumed model. However, the aliasing

structure in nonregular designs is too complicated to analyze the effects since some two factorial effects are partially confounded. Typically, subsetting is a method to determine which runs to omit by using the columns of design matrix (Briggs, 2011). Here, Wu et al.'s image-processing experiment that is 20-run Plackett-Burman design is conducted for subsetting three quarter designs. There are two columns of PB design selected with a treatment combination of $(+,+)$, $(+,-)$, $(-,+)$, $(-,-)$. If columns 1 and 2 with $(+,+)$ are chosen, then each row with $(+,+)$ in columns 1 and 2 is deleted as below. After deleting five rows related to $(+,+)$ in columns 1 and 2, we obtain 15 rows left to analyze the new design. Operating the deletion of $1/4$ rows of the design, there are two approaches estimation efficiency and degree of freedom efficiency that can be implemented to test the efficiency of the new design. In this case, the new design is supersaturated design that the number of variables is greater than the number of runs. How we rank the new design or provide follow-up experimentation could be the further research.

Figure 28. $1/4$ fraction Deletion

	1	2
1	1	-1
2	1	1
3	-1	1
4	-1	-1
5	1	-1
6	1	1
7	1	1
8	1	1
9	-1	1
10	1	-1
11	-1	1
12	1	-1
13	-1	1
14	-1	-1
15	-1	-1
16	-1	-1
17	1	-1
18	1	1
19	-1	1
20	-1	-1

8 Reference

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