
Augmentation of definitive screening designs (DSD+)

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Abstract: Run efficient second order designs suitable for both factor screening and the fitting of a second-order response model are of interest in complex system characterisation efforts particularly when those efforts encounter budgetary constraints limiting their test programme. Leading designs are the smaller sized definitive screening design and the larger sized design, fractional Box-Behken design. When specific domain knowledge of system factor interactions is available, either *a priori* or *a posteriori*, that domain knowledge can be exploited to generate the definitive screening design plus. This paper describes how to generate the single DSD+, how to augment a DSD to arrive at the DSD+ and compares the performance of the two designs under a variety of effect sparsity, effect heredity and model noise conditions. The DSD+, with its extra $k - 1$ runs for k factors is shown to greatly improve the screen and model fitting capabilities of the DSD.

Keywords: empirical analysis; definitive screening; experimental design.

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1 Introduction

Response surface methodology (RSM) focuses on approximating a real world system response typically with either a first-order or second-order polynomial model. While the choice of experimental designs for first-order models is fairly straight forward depending upon the shape of the experimental design region and number of available experimental runs, choosing an experimental design to fit a second-order model,

$$\eta = \beta_0 + \sum_{i=1}^k \beta_i x_i + \sum_{i=1}^k \beta_{ii} x_i^2 + \sum_{i=1}^{k-1} \sum_{j=i+1}^k \beta_{ij} x_i x_j, \quad (1)$$

is more complex due to the variety of design criteria and characteristics to consider.

Usually, the experimenter does not have *a priori* knowledge regarding the appropriate polynomial model to use to approximate the system response. As such it is common practice in RSM to employ experiments sequentially. Box and Liu (1999) illustrated the RSM philosophy of sequential learning where first-order designs are typically used to perform factor screening and second-order designs are used to fit a response surface exhibiting some degree of curvature. Since the *a posteriori* knowledge about a system response possessing curvature comes from analysis of the first-order design, the typically sequential nature of RSM allows developing second-order designs by augmenting first-order designs with additional experimental runs.

Unfortunately, whether due to time, budget, or other constraints, there are times when conducting multiple experiments is unrealistic. For instance, Lawson (2003) points out fixed deadlines for scale up and production of prototype engineering designs may not allow the possibility of follow-up experimentation. Couple this with the fact that military systems, particularly aerodynamic systems, are complex and often exhibit nonlinear behaviour, there are times when a single experimental design capable of performing both factor screening and higher order response surface exploration may be required.

Recent literature has proposed second-order screening design methodologies, sometimes referred to as one-step RSM or definitive screening, employing a single experimental design capable of both factor screening and fitting a second-order polynomial model.

Edwards and Truong (2011) performed a simulation study examining several second-order screening designs focusing on the design's ability to correctly identify active factors under a variety of conditions. The truth models used assumed both factor sparsity and strong effect heredity.

Sparsity and heredity are two important principles considered during the development of successful screening designs. The sparsity principle stems from the Pareto principle which has led to an assumption in screening designs that only a small number of factors, *factor sparsity*, are significant in their contribution to an appropriate polynomial model approximation of a system response. However, the degree to which factor sparsity holds as the number of factors being investigated grows has been debated. The term *effect sparsity* has been used to identify with the assumption that instead of the number of active factors being relatively small in the polynomial model approximation, the number of active effects is relatively small. As a result, it is possible for the assumption of effect sparsity to hold while factor sparsity does not.

Heredity, either strong or weak, is the second screening principle considered during model selection. Strong heredity means that if a model includes a two-factor interaction, then its constituent main effects are included in the model. Conversely, weak heredity requires only one of the two constituent main effects be included in the model.

Dougherty et al. (2013) examined the robustness of definitive screening designs (DSDs) and fractional Box-Behken designs (FBBDD), two second order screening designs, with respect to the assumptions of sparsity (factor or effect) and heredity (strong or weak). Dougherty et al. (2013) showed that regardless of the heredity (weak or strong), sparsity (effect or factor), or noise level combination, the DSD is robust in its ability to correctly identify active main effects. At lower noise levels, the DSD performs favourably in identifying active two-factor interactions but as the noise level increases the DSD performance suffers. Additionally, the run-efficient DSD had trouble identifying active pure quadratic effects when two-factor interactions are present. However, if the experimenter has *a priori* knowledge regarding the importance of a particular factor, or that factor's second-order effects, augmentation of the DSD could reduce the correlation between a factors second-order effects without sacrificing too much in the way of design run efficiency while maintaining the requirement for a single design. Alternatively, if the experimenter has *a posteriori* knowledge about a particular factor to include any second-order effects, augmenting the DSD demonstrates the feasibility of follow-up design runs for DSD.

The remainder of this paper is organised as follows: Section 2 briefly discusses the literature relevant to second order screening designs while Section 3 focuses on the DSD generation and augmentation. In Section 4, we present a side-by-side comparison of the DSD examined in Dougherty et al. (2013) with an augmented design focusing on improved robustness to the assumptions of heredity and sparsity and significant second-order factor identification. Section 5 examines the effect of replicating the analysis on the designs ability to identify important factors of interest and Section 6 concludes the article.

2 Second order screening designs

Initial attempts at identifying second-order screening designs relied upon the design's projection capacity. When the *factor sparsity* principle holds any regular fractional factorial design of resolution R , projects onto any subset of $R - 1$ factors as a full factorial. For example, a 2_{III}^{3-1} design ($R = 3$) can project into a 2^2 design (Myers et al., 2009). This projection property extends to non-regular designs like the Plackett-Burman designs discussed in Lin and Draper (1992), and Wang and Wu (1995).

Cheng and Wu (2001), hereafter referred to as CW, studied three orthogonal array (OA) designs ($OA(18, 3^7)$, $OA(27, 3^8)$, and $OA(36, 3^{12})$). The $OA(N, 3^k)$ connotation shows the design's number of runs N and number of factors k . In contrast to 3^{n-k} designs which have defining contrast subgroups to describe the design structure, the $OA(N, 3^k)$ designs studied by CW required computer search to classify the possible projected designs.

Because a design can project onto many different combinations of factors, CW developed a projection-efficiency criterion to compare designs based upon:

- 1 the number of eligible projected designs
- 2 the estimation efficiency for eligible projected designs determined by the ratio of each design's D - and G -efficiencies (Cheng and Wu 2001).

Eligible designs are designs to fit a second-order model and the D - and G -efficiencies, denoted D_{eff} and G_{eff} , respectively, criteria compare the performance of a design against a corresponding optimal design (Myers et al., 2009).

Under the assumptions of factor sparsity and strong heredity, CW introduced a two-stage analysis method. The first stage consisted of performing a main effect factor screening analysis and the second stage involved fitting a second-order model with the identified main effects from the first stage. The key linkage between stage one and two was the ability to project the initial larger factor space onto a smaller factor space capable of fitting a second-order model. Unfortunately, the designs CW studied have no guarantee as to their ability to project down to a specific subset of the original factors and no flexibility in modifying the number of design runs.

Improving on the designs of CW, Xu et al. (2004), hereafter referred to by XCW, proposed a combinatorial method for constructing new and efficient OA designs and a design selection approach based upon a *projection aberration criterion* which combines the generalised word-length pattern of the generalised minimum aberration criterion (Xu and Wu, 2001) for factor screening and the projection-efficiency criteria (Cheng and Wu, 2001) for interaction detection. XCW assessed the projection performance of three combinatorially non-isomorphic $OA(18, 3^7)$ s and three combinatorially non-isomorphic $OA(27, 3^{13})$ s. Their three-step approach involves:

- 1 screening out poor orthogonal arrays for factor screening using the generalised word-length pattern
- 2 applying the projection aberration criterion to select a best design from step 1
- 3 determining the best level permutations of the design from step 2 to improve design projection eligibility and estimation efficiency under the second-order polynomial model.

Ye et al. (2007), hereafter referred to as YTL, also examined 3-level 18-run and 27-run orthogonal designs; however, in addition to considering the projection properties of designs, their design choices were based on both model estimation and model discrimination criteria. The two model estimation criteria employed examine the proportion of estimable models, *estimation capacity* (*EC*), and average *D*-efficiency of all models, *information capacity* (*IC*). YTL employed two of the six non-Bayesian criteria, *average expected prediction differences* (*AEPD*) and *minimum maximum prediction difference* (*MMPD*), proposed by Jones et al. (2007) for model discrimination.

While previous work focused primarily on the designs projection capacity, Edwards and Truong (2011) applied the method of Jones and Nachtsheim (2011b) for finding efficient designs with minimal aliasing between main effects and two-factor interactions. Deemed MA designs, Edwards and Truong (2011) constructed 18, 27, and 30-run designs for simultaneous screening and response surface optimisation for $k = 4 - 7$, $k = 4 - 13$, and $k = 6 - 14$ factors, respectively, by minimising the sum of squares of the elements of the alias matrix, \mathbf{A} , subject to a lower bound on the primary model *D*-efficiency. Edwards and Truong (2011) compared the 27-run OAs of XCW and YTL with MA designs in terms of *D*-efficiency of projection and, via a simulation study, the proportion of active factors declared significant (Power 1) as well as the proportion of simulations in which only the true active factors are declared significant (Power 2). Although ranked last in terms of *D*-efficiency, the MA designs showed superior performance in their ability to detect active factors (Edwards and Truong, 2011).

For simplicity, the CW, XCW, YTL, and MA designs use linear and quadratic main-effects only analysis for factor screening but the Bayesian approaches of Box and Meyer (1993) or Chipman et al. (1997) can also be used to screen for significant factors outside of main effects. However, these methods are not readily available in statistical software packages and are computationally intensive procedures, thus likely making their use impractical (Edwards and Truong, 2011). Unfortunately, as shown by Truong (2010), if the strong heredity principle fails to hold important effects can be missed leading to a mis-specified second-order polynomial model.

Edwards and Mee (2011) introduced the spherical FBBDD aimed at overcoming the projection deficiencies and main/quadratic effect only analysis issues found in the CW/XCW/YTL/MA designs. The FBBDD provide the ability to explore interactions during the screening stage and to fit second-order models via a backward elimination analysis strategy to each of the $(k - 1)$ -factor projections. In contrast to the CW/XCW/YTL/MA designs, Edwards and Mee (2011) assumed an effect sparsity vice factor sparsity model and searched for designs having eligible projections greater than the up to $p = 5$ factor projections provided by the CW/XCW/YTL/MA designs by taking subsets of the two-level fractional factorial designs which compose a BBD. While FBBDDs require more runs than CW/XCW/YTL/MA designs, their ease of construction and aliasing structure facilitate an analysis strategy which cannot be applied to the CW/XCW/YTL/MA designs.

Jones and Nachtsheim (2011a) introduced a class of three-level designs referred to as 'DSDs' where main effects are not biased by second-order effects and all quadratic effects are estimable. For $k \geq 6$, the DSD can project down to a full quadratic model in any three factors. It is this design we augment, adding runs to improve effects estimability under specified conditions.

Table 2 Nine-factor augmented definitive screening design (DSD+)

<i>A</i>	<i>B</i>	<i>C</i>	<i>D</i>	<i>E</i>	<i>F</i>	<i>G</i>	<i>H</i>	<i>J</i>
0	1	1	1	1	1	1	1	1
0	-1	-1	-1	-1	-1	-1	-1	-1
1	0	-1	-1	-1	-1	1	1	1
-1	0	1	1	1	1	-1	-1	-1
1	-1	0	-1	1	1	-1	-1	1
-1	1	0	1	-1	-1	1	1	-1
1	-1	-1	0	1	1	1	1	-1
-1	1	1	0	-1	-1	-1	-1	1
1	-1	1	1	0	-1	-1	1	-1
-1	1	-1	-1	0	1	1	-1	1
1	-1	1	1	-1	0	1	-1	1
-1	1	-1	-1	1	0	-1	1	-1
1	1	-1	1	-1	1	0	-1	-1
-1	-1	1	-1	1	-1	0	1	1
1	1	-1	1	1	-1	-1	0	1
-1	-1	1	-1	-1	1	1	0	-1
1	1	1	-1	-1	1	-1	1	0
-1	-1	-1	1	1	-1	1	-1	0
1	1	1	-1	1	-1	1	-1	-1
-1	-1	-1	1	-1	1	-1	1	1
0	0	0	0	0	0	0	0	0
1	-1	1	-1	-1	-1	-1	-1	-1
-1	1	1	1	1	-1	1	1	1
-1	-1	1	-1	-1	-1	-1	-1	1
-1	1	-1	-1	-1	-1	-1	1	-1
1	-1	1	1	1	1	-1	1	1
1	1	1	1	-1	1	1	1	-1
-1	-1	-1	1	1	-1	-1	-1	-1
1	1	1	-1	1	-1	1	1	1

The $2k + 1$ or $2k + 3$ runs for when k is even or odd, respectively, provide a sufficient number of degrees of freedom for estimates of the intercept, all k main effects, and all k pure quadratic effects. However, Dougherty et al. (2013) showed that when both two-factor interactions and pure-quadratic effects are active, regardless of heredity (strong or weak) or sparsity (factor or effect), the standard DSD may not have enough degrees of freedom to decouple the correlation between two-factor interactions and pure-quadratic effects. As a result, the DSD, when used as a single experimental design,

is susceptible to making Type-II errors particularly with regards to active pure-quadratic effects. Because the DSD is very run efficient when compared to other second-order screening designs, augmenting the original DSD to improve detection of active quadratic effects (both two-factor interactions and pure-quadratic) is desirable.

If the experimenter has *a priori* knowledge regarding the importance of a particular factor or factors second-order effects, augmentation of the DSD, hereafter referred to as DSD+, can reduce the correlation between a factors second-order effects without sacrificing too much in the way of design run efficiency while maintaining the requirement for a single design. Conversely, if the experimenter has *a posteriori* knowledge about a particular factor or factors second-order effects, augmenting the DSD demonstrates the feasibility of follow-up design runs for DSD.

Common approaches to design augmentation to clarify model ambiguity involves the augmentation of the design with runs specifically designed to de-alias a specific alias chain or using complete or fractional foldovers of the design. Since the DSD are basically already full foldover designs, using the foldover approach on DSD does not reduce aliasing between second-order effects. Additionally, the alias chains for DSD are very complex due to the nature of the design construction. Therefore, an alternative approach using a *D*-optimal strategy for selecting augmentation points is employed.

Similar to Jones and Nachtsheim (2011a), a computerised search algorithm is used to add $k - 1$ runs to the DSD. However, instead of the information matrix being based only a main effects model, our information matrix is based on the main effects and the $k - 1$ two-factor interactions involving a particular factor. The DSD+ were constructed using a variant of the coordinate exchange algorithm of Meyer and Nachtsheim (1995) to maximise the determinant of the updated information matrix. Multiple random starting designs for each k -factor design were explored to guard against local maxima; however, the generated designs were still not unique. Multiple designs were generated which were equivalent based upon both *D-optimal* and interestingly *I-efficient* criteria as well; although, as k increased the number of different designs decreased.

Table 2 shows the $k = 9$ factor DSD generated by JMP 10 plus $k - 1 = 8$ augmentation runs after updating the information matrix to include the 8 two-way interactions involving factor A .

4 Case comparison

Dougherty et al. (2013) conducted an empirical study of the nine-factor DSD generated using conference matrices based on Xiao et al. (2012) focusing on the design's robustness to detect important effects in models exhibiting different combinations of heredity and sparsity. Using Jones and Nachtsheim (2011a) recommended analysis methodology, the cases and scenarios studied are reexamined using the DSD+.

Jones and Nachtsheim (2011a) suggest performing a forward stepwise regression, which considers all terms in a second-order model of $k = 9$ factors. With a p -value of 0.1 to enter, effects are added into the second-order model while forcing a strong heredity model. As such, when either two-factor interactions or pure-quadratic effects are included in the model, the lower order terms must also be included.

Table 3 Nine-factor simulated response

Scenario	$\varepsilon \sim N(0, I)$				$\varepsilon \sim N(0, 2)$				$\varepsilon \sim N(0, 3)$			
	1	2	3	4	1	2	3	4	1	2	3	4
DSD	-6.5718	-2.0718	-1.0718	-6.0718	-5.0282	-0.5282	0.4718	-4.5282	-8.8568	-4.3568	-3.3568	-8.3568
	-8.9271	-6.4271	-6.4271	-8.4271	-6.3521	-3.8521	-3.8521	-5.8521	-8.4283	-5.9283	-5.9283	-7.9283
	6.7540	-0.2460	14.2540	-0.2460	8.5632	1.5632	16.0632	1.5632	5.3980	-1.6020	12.8980	-1.6020
	-5.3611	1.6389	13.1389	-12.3611	-7.5396	-0.5396	10.9604	-14.5396	-4.3540	2.6460	14.1460	-11.3540
	-1.0722	-4.0722	2.4278	-10.0722	-0.9806	-3.9806	2.5194	-9.9806	-1.5015	-4.5015	1.9985	-10.5015
	3.0372	-5.9628	-4.4628	-5.9628	-2.1549	-11.1549	-9.6549	-11.1549	-0.2920	-9.2920	-7.7920	-9.2920
	0.9647	2.9647	1.4647	2.9647	-2.2766	-0.2766	-1.7766	-0.2766	-0.9184	1.0816	-0.4184	1.0816
	-5.1812	10.8188	-7.6812	-3.1812	-7.7627	8.2373	-10.2627	-5.7627	-10.6842	5.3158	-13.1842	-8.6842
	-11.5682	8.9318	-4.5682	8.9318	-9.7422	10.7578	-2.7422	10.7578	-10.5137	9.9863	-3.5137	9.9863
	-11.6201	6.8799	-8.6201	8.8799	-11.1763	7.3237	-8.1763	9.3237	-7.5815	10.9185	-4.5815	12.9185
	5.9775	17.9775	13.4775	11.9775	5.9904	17.9904	13.4904	11.9904	1.9805	13.9805	9.4805	7.9805
	-6.1405	-8.1405	12.3595	-0.1405	-3.1020	15.3980	2.8980	2.8980	-3.1339	-5.1339	15.3661	2.8661
	-0.4898	9.0102	4.5102	3.0102	0.0662	9.5662	5.0662	3.5662	-3.6061	5.8939	1.3939	-0.1061
	-8.4915	3.0085	3.5085	-4.9915	-5.7396	5.7604	6.2604	-2.2396	-7.1792	4.3208	4.8208	-3.6792
	-0.3253	-7.8253	3.1747	-7.8253	-3.9942	-11.4942	-0.4942	-11.4942	0.6261	-6.8739	4.1261	-6.8739
	1.6734	2.1734	-5.8266	-5.8266	-0.9510	-0.4510	-8.4510	-8.4510	4.5618	5.0618	-2.9382	-2.9382
	-13.0033	12.9967	-2.5033	12.9967	-17.4189	8.5811	-6.9189	8.5811	-14.8327	11.1673	-4.3327	11.1673
	-17.0536	6.9464	-3.5536	8.9464	-15.4480	8.5520	-1.9480	10.5520	-24.6111	-0.6111	-11.1111	1.3889
	-0.3768	6.6232	0.1232	0.6232	1.1869	8.1869	1.6869	2.1869	-1.4119	5.5881	-0.9119	-0.4119
	-3.3919	-10.3919	-5.8919	-2.3919	-6.2247	-13.2247	-8.7247	-5.2247	-4.5994	-11.5994	-7.0994	-3.5994
	1.8669	1.8669	1.8669	1.8669	-1.1295	-1.1295	-1.1295	-1.1295	0.0071	0.0071	0.0071	0.0071
DSD+	-16.4003	14.5997	-5.9003	8.5997	-14.3990	16.6010	-3.8990	10.6010	-12.5880	18.4120	-2.0880	12.4120
	-18.5988	-3.5988	-5.0988	-11.5988	-15.7068	-0.7068	-2.2068	-8.7068	-10.7264	4.2736	2.7736	-3.7264
	-4.2611	11.7389	-6.7611	-2.2611	-2.9713	13.0287	-5.4713	-0.9713	-3.9842	12.0158	-6.4842	-1.9842
	-4.0588	-11.0588	-6.5588	-3.0588	-3.5441	-10.5441	-6.0441	-2.5441	-0.1862	-7.1862	-2.6862	0.8138
	-1.2761	13.7239	2.2239	13.7239	0.7377	15.7377	4.2377	15.7377	-1.8346	13.1654	1.6654	13.1654
	4.3426	-4.6574	11.8426	-4.6574	5.5804	-3.4196	13.0804	-3.4196	4.6927	-4.3073	12.1927	-4.3073
	-5.3180	-16.3180	13.1820	-14.3180	-3.7730	-14.7730	14.7270	-12.7730	-2.7244	-13.7244	15.7756	-11.7244
	0.9107	0.9107	1.4107	0.9107	1.0700	1.0700	1.5700	1.0700	0.8791	0.8791	1.3791	0.8791

Four cases were considered to represent different combinations of model heredity (strong or weak) and sparsity (factor or effect). In addition, each model was examined with four different noise levels scenarios; however, the noise level vector used for each scenario was identical across each model for each design. The 21 and 29 treatment combinations for the DSD and DSD+ designs are given in Tables 1 and 2, respectively. Table 3 shows the simulated response values for the 16 combinations of case and noise level scenario for the original DSD runs and the eight additional runs for the DSD+.

Case 1 data was simulated based on the model

$$y_i = 2A_i - 1.5E_i + 2G_i - 3A_i^2 + 2.5E_i^2 - 4G_i^2 + 4A_iE_i + 3.5A_iG_i - 5E_iG_i + \varepsilon_i, \quad (2)$$

thereby representing a response which exhibits factor sparsity and strong heredity between active two-factor interactions or pure quadratic effects and main effects. The model exhibits factor sparsity because only 3 of the 9 factors are active within the nine effects contained in the model.

Jones and Nachtsheim (2011a) perform forward stepwise regression with a p -value of 0.1 to enter while forcing a strong heredity model. Table 4 shows the forward stepwise regression steps for the Case 1 data for all four noise level scenarios of Table 3.

Table 4 Forward stepwise results: Case 1

Design	Scenario					
	$\varepsilon \sim N(0, 1)$		$\varepsilon \sim N(0, 2)$		$\varepsilon \sim N(0, 3)$	
	DSD	DSD+	DSD	DSD+	DSD	DSD+
Step	Effects added					
1	EG	EG	AG	AG	EG	EG
2	AG	AG	EG	EG	AG	AG
3	AE	AE	EJ	AE	AE	AE
4	G^2	G^2	AE	G^2	DF	H^2
5	AJ	AJ	–	DF	H^2	AH
6	DH	GJ	–	CJ	–	BG
7	AD	A^2	–	–	–	DE
8	F	AD	–	–	–	FH
9	C	CH	–	–	–	AF
10	–	–	–	–	–	B^2

Since the ‘combined’ option rule is used for the forward stepwise regression, the inclusion of two-way interaction or pure quadratic effects result in the inclusion of all the factors which comprise the two-way interaction or pure quadratic effects. For example, when considering the original DSD Scenario 3, where $\varepsilon_i \sim N(0, 3)$, the EG and H^2 effects, which entered the regression model in steps 1 and 5, respectively, would require the E, G, and H factors to also be in the model.

Case 2 data was simulated according to the model

$$y_i = 2A_i 0.15E_i + 2G_i + 4C_i - 3H_i + 2.5E_i^2 - 4G_iH_i + 3.5E_iH_i - 5C_iG_i + \varepsilon_i, \quad (3)$$

to represent a response exhibiting effect sparsity and strong heredity between active two-factor interactions or pure quadratic effects and their associated main effects. The model exhibits effect sparsity vice factor sparsity because although over 50% of the factors (5 of 9) are active only 9 of 54 total effects are active, not coincidentally the same number as Case 1.

Table 5 provides the forward stepwise regression results using the Case 2 response data associated with each design for all four noise level scenarios in Table 3.

Case 3 data was simulated according to the model

$$y_i = 2A_i + 2E_i - 1.5A_i^2 + 2.5E_i^2 - 3.5A_iE_i + 4A_iG_i - 5E_iG_i + \varepsilon_i, \tag{4}$$

thereby representing a response which exhibits factor sparsity and weak heredity between active two-factor interactions or pure quadratic effects and main effects. The model exhibits factor sparsity because only 3 of the 9 factors are active within the seven effects contained in the model. Since not all factors, which comprise the two-factor interactions, are present as a main effect, the model exhibits weak heredity. For instance, although factor *G* is significant within two two-factor interactions, factor *G* by itself is not significant.

Table 5 Forward stepwise results: Case 2

Design	Scenario					
	$\varepsilon \sim N(0, 1)$		$\varepsilon \sim N(0, 2)$		$\varepsilon \sim N(0, 3)$	
	DSD	DSD+	DSD	DSD+	DSD	DSD+
Step	Effects added					
1	CG	CG	C2	CG	C ²	CG
2	GH	GH	GH	GH	E ²	GH
3	EH	EH	CG	EH	DH	EH
4	A	A	CJ	AE	A ²	A ²
5	E ²	E ²	A	H ²	DG	DE
6	J ²	J ²	GJ	DF	AF	E ²
7	DH	DH	–	DE	–	AH
8	CF	CH	–	BJ	–	AE
9	–	CD	–	–	–	CF
10	–	CJ	–	–	–	–
11	–	D ²	–	–	–	–

Table 6 provides the forward stepwise regression results using the Case 3 response data associated with each design for all four noise level scenarios in Table 3.

Case 4 data was simulated according to the model

$$y_i = 2A_i - 1.5E_i + 2G_i - 3H_i^2 + 2.5E_i^2 + 4A_iC_i + 3.5E_iH_i - 5C_iG_i - 4G_iH_i + \varepsilon_i \tag{5}$$

to represent a response which exhibits effect sparsity and weak heredity between active two-factor interactions or pure quadratic effects and main effects.

Table 7 provides the forward stepwise regression results using the Case 4 response data associated with each design for all four noise level scenarios in Table 3.

Table 6 Forward stepwise results: Case 3

<i>Design</i>	<i>Scenario</i>					
	$\varepsilon \sim N(0, 1)$		$\varepsilon \sim N(0, 2)$		$\varepsilon \sim N(0, 3)$	
	<i>DSD</i>	<i>DSD+</i>	<i>DSD</i>	<i>DSD+</i>	<i>DSD</i>	<i>DSD+</i>
<i>Step</i>	<i>Effects added</i>					
1	AE	EG	AE	AE	EG	EG
2	BF	AG	CH	AG	AG	AG
3	J^2	AE	EJ	EG	AE	AE
4	A^2	E^2	J^2	D^2	DF	–
5	FH	J^2	E^2	AF	H	–
6	DJ	CE	–	DF	AF	–
7	E^2	–	–	BE	–	–

Table 7 Forward stepwise results: Case 4

<i>Design</i>	<i>Scenario</i>					
	$\varepsilon \sim N(0, 1)$		$\varepsilon \sim N(0, 2)$		$\varepsilon \sim N(0, 3)$	
	<i>DSD</i>	<i>DSD+</i>	<i>DSD</i>	<i>DSD+</i>	<i>DSD</i>	<i>DSD+</i>
<i>Step</i>	<i>Effects added</i>					
1	GH	GH	GH	AC	GH	GH
2	AH	CG	AE	CG	AH	CG
3	AF	AC	EG	EH	DE	AC
4	EF	EH	HJ	GH	AD	EH
5	G^2	J^2	E^2	AE	DG	DE
6	AC	E^2	J^2	DF	FH	A^2
7	DF	H^2	–	BH	A^2	E^2
8	J	EJ	–	–	–	AH
9	–	FH	–	–	–	FJ
10	–	CD	–	–	–	–
11	–	EF	–	–	–	–
12	–	DE	–	–	–	–

Tables 8, 9, 10, and 11 show which effects from Cases 1 through 4's four different noise level scenarios were properly identified, incorrectly identified (Type I error), and not identified (Type II error), for both the DSD and DSD+ based upon Jones and Nachtsheim (2011a) suggested analysis methodology.

In all four cases, regardless of noise level, the DSD+ performance in identifying active effects met or exceeded the DSD performance. However, similar to the DSD, the DSD+ was still susceptible to increased Type II errors as the noise level increased, even

with the increased design size. Fortunately, the DSD+ was more robust to the heredity (strong or weak) or sparsity (factor or effect) assumption than the DSD. When comparing strong heredity to weak heredity for DSD, the DSD performed better when strong heredity was exhibited, particularly when effect sparsity was present. In contrast, the DSD+ performed equally well under the heredity assumption. With regards to the sparsity assumption, the DSD+ showed better performance under effect sparsity than factor sparsity which was counter to the DSD. However, the DSD+ performance under factor sparsity assumption was still better than the DSD. Interestingly, all the Type II errors across all scenarios and cases made by the DSD+ involved not identifying active pure-quadratic effects.

Table 8 Second order screening design results: Case 1

		<i>Strong heredity, factor sparsity model:</i>		<i>Rep 1</i>
		$2A - 1.5E + 2G - 3A^2 + 2.5E^2 - 4G^2 + 4AE + 3.5AG - 5EG + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, G^2, AE, AG, EG	$A, E, G, A^2, G^2, AE, AG, EG$	
	Type I errors	$C, D, F, H, J, AD, AJ, DH$	$C, D, H, J, AD, AJ, CH, GJ$	
	Type II errors	A^2, E^2	E^2	
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, AE, AG, EG	A, E, G, G^2, AE, AG, EG	
	Type I errors	J, EJ	C, D, F, J, CJ, DF	
	Type II errors	A^2, E^2, G^2	A^2, E^2	
$\varepsilon \sim N(0, 3)$	Identified	A, E, G, AE, AG, EG	A, E, G, AE, AG, EG	
	Type I errors	D, F, H, H^2, DF	B^2, D^2, AH, BG, DG	
	Type II errors	A^2, E^2, G^2	A^2, E^2, G^2	

Table 9 Second order screening design results: Case 2

		<i>Strong heredity, effect sparsity model:</i>		<i>Rep 1</i>
		$2A - 1.5E + 2G + 4C - 3H + 2.5E^2 - 5CG + 3.5EH - 4GH + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	$A, E, C, G, H, E^2, CG, EH, GH$	$A, E, C, G, H, E^2, CG, EH, GH$	
	Type I errors	D, F, J, J^2, CF, DH	$D, J, D^2, J^2, CD, CH, CJ, DH$	
	Type II errors	None	None	
$\varepsilon \sim N(0, 2)$	Identified	A, C, G, H, CG, GH	$A, E, C, G, H, CG, EH, GH$	
	Type I errors	J, C^2, CJ, GJ	$B, D, F, J, H^2, AE, BJ, DE, DF$	
	Type II errors	E, E^2, EH	E^2	
$\varepsilon \sim N(0, 3)$	Identified	A, E, C, G, H, E^2	$A, E, C, G, H, E^2, CG, EH, GH$	
	Type I errors	$D, F, A^2, C^2, AF, DG, DH$	$D, F, A^2, AE, AH, CF, DE$	
	Type II errors	CG, EH, GH	None	

Table 10 Second order screening design results: Case 3

<i>Weak heredity, factor sparsity model:</i>		<i>Rep 1</i>	
$2A + 2E - 1.5A^2 + 2.5E^2 - 3.5AE + 4AG - 5EG + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	A, E, A^2, E^2, AE	A, E, E^2, AE, AG, EG
	Type I errors	$B, D, F, H, J, J^2, BF, DJ, F, H$	C, G, J, J^2, CE
	Type II errors	AG, EG	A^2
$\varepsilon \sim N(0, 2)$	Identified	A, E, E^2, AE	A, E, AE, AG, EG
	Type I errors	C, H, J, J^2, CH, EJ	$B, D, F, G, D^2, AF, BE, DF$
	Type II errors	A^2, AG, EG	A^2, E^2
$\varepsilon \sim N(0, 3)$	Identified	A, E, AE, AG, EG	A, E, AE, AG, EG
	Type I errors	D, F, G, H, AF, DF	G
	Type II errors	A^2, E^2	A^2, E^2

Table 11 Second order screening design results: Case 4

<i>Weak heredity, effect sparsity model:</i>		<i>Rep 1</i>	
$2A - 1.5E + 2G + 2.5E^2 - 3H^2 + 4AC - 5CG + 3.5EH - 4GH + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, AC, GH	$A, E, G, E^2, H^2, AC, CG, EH, GH$
	Type I errors	$C, D, F, H, J, G^2, AF, AH, DF, EF$	$C, D, F, H, J, J^2, CD, DE, EF, EJ, F, H$
	Type II errors	E^2, H^2, CG, EH	None
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, E^2, GH	A, E, G, AC, CG, EH, GH
	Type I errors	H, J, J^2, AE, EG, HJ	$B, C, D, F, H, AE, BH, DF$
	Type II errors	H^2, AC, CG, EH	E^2, H^2
$\varepsilon \sim N(0, 3)$	Identified	A, E, G, GH	$A, E, G, E^2, AC, CG, EH, GH$
	Type I errors	$D, F, H, A^2, AD, AH, DE, DG, FH$	$C, D, F, H, J, A^2, AH, DE, FJ$
	Type II errors	E^2, H^2, AC, CG, EH	H^2

5 Analysis replication results

In order to insure the improved performance in identifying active effects in the presence of heredity and sparsity assumption we note as exhibited by the DSD+ over the DSD was not limited to a single instance, the response data was replicated four additional times. Table 12 displays the average percentage of all active effects, second-order effects, and pure-quadratic effects correctly identified from five replications of all four cases and three scenarios. For instance, Case 3 (weak heredity, factor sparsity model), Scenario 1 ($\varepsilon \sim N(0, 1)$) shows on average the DSD correctly identified 80% of the active effects in

model, 72% of the active second-order effects (two-way interactions and pure-quadratic effects), and 50% of the active pure-quadratic effects. Additionally, Table 12 displays the average number of Type I errors made. Overall, the percentages show the DSD+ improves over the DSD with regards to identifying active effects and their various subsets across the board with little to no increase in Type I errors. However, when the noise level increases neither the DSD nor the DSD+ are consistently finding the active pure-quadratic effects. The individual replication results are found in Tables 13 to 28 in the Appendix.

Table 12 Second order screening design results: average

<i>Strong heredity, factor sparsity model:</i>			<i>5 Rep Avg</i>
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	67%, 50%, 20%	91%, 87%, 73%
	Type I errors	9.6	10.6
$\varepsilon \sim N(0, 2)$	Identified	58%, 37%, 20%	84%, 77%, 53%
	Type I errors	7.4	5.6
$\varepsilon \sim N(0, 3)$	Identified	51%, 33%, 27%	62%, 43%, 13%
	Type I errors	6.4	4.8
<i>Strong heredity, effect sparsity model:</i>			<i>5 Rep Avg</i>
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	98%, 95%, 80%	98%, 95%, 80%
	Type I errors	6.6	7.6
$\varepsilon \sim N(0, 2)$	Identified	78%, 55%, 20%	91%, 80%, 20%
	Type I errors	4.0	5.4
$\varepsilon \sim N(0, 3)$	Identified	84%, 70%, 40%	93%, 85%, 40%
	Type I errors	4.2	4.2
<i>Weak heredity, factor sparsity model:</i>			<i>5 Rep Avg</i>
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	80%, 72%, 50%	94%, 92%, 80%
	Type I errors	9.8	10
$\varepsilon \sim N(0, 2)$	Identified	60%, 44%, 20%	77%, 68%, 20%
	Type I errors	8.0	7.0
$\varepsilon \sim N(0, 3)$	Identified	51%, 32%, 0%	77%, 68%, 20%
	Type I errors	7.4	4.6
<i>Weak heredity, effect sparsity model:</i>			<i>5 Rep Avg</i>
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	49%, 23%, 0%	93%, 90%, 70%
	Type I errors	10.6	11.2
$\varepsilon \sim N(0, 2)$	Identified	47%, 23%, 10%	84%, 77%, 30%
	Type I errors	8.4	7.0
$\varepsilon \sim N(0, 3)$	Identified	44%, 20%, 10%	82%, 73%, 20%
	Type I errors	7.6	6.6

Note: Identified percentages correspond to percentage of active effects, second-order effects, and pure quadratic effects.

6 Conclusions

For a second-order polynomial model, if a factor screening design is not used, a design must contain enough degrees of freedom to estimate all effects. For k factors this equates to $\frac{(k+1)(k+2)}{2}$ design runs. As k increases, the number of required runs can quickly exceed the number of available runs provided to an experimenter, particularly within the DoD testing realm. As such, as k increases, a screening design must be employed while maintaining the ability to estimate a second-order polynomial model when constraints dictate a single experiment. Jones and Nachtsheim (2011a) proposed the economical three-level DSD for screening quantitative factors in the presence of active second-order effects. Dougherty et al. (2013) showed the DSD quite effective in identifying active main effects regardless of the heredity and sparsity assumption but lacked the power to differentiate between active second-order effects when both two-factor interactions and pure-quadratic effects are active. We introduce a way to augment the DSD, deemed DSD+, with $k - 1$ runs which increased the detection performance of active second-order effects involving a particular factor of interest. The $k - 1$ additional runs can be run as part of a single experiment with the original DSD if the experimenter has *a priori* knowledge or as part of a follow-on experiment based upon *a posteriori* knowledge. Furthermore, while the additional runs are optimised for two-factor interactions, the impact of adding additional centre point runs, or other design points, on identifying active pure-quadratic effects requires further investigation.

One might also consider potentially examining methods to build a DSD+-capability without necessarily relying on an initial DSD. Our approach took the run efficient DSD as a baseline and augmented it. It is worth looking at allocating the runs from a DSD+, again based on a presumed form of the underlying model, into a fully new design robust to model misspecification.

While the $k - 1$ runs are associated with the $k - 1$ two-factor interactions of a single factor of interest in a k factor experiment, the manner in which the DSD is augmented can easily be extended to additional factors. For instance, the DSD can be augmented with $k - 1 + k - 2 = 2k - 3$ runs for all the two-factor interactions of two factors and so on until a total of $\frac{(k)(k-1)}{2}$ runs are added for all the two-factor interactions in a k factor experiment. As such, the DSD can be tailored with augmentation runs which take the DSD from the standard $2k + 1$ runs all the way to $\frac{(k+1)(k+2)}{2}$ runs for a saturated second-order design.

Disclaimer

The views expressed in this article are those of the authors and do not reflect the official policy or position of the US Air Force, Department of Defense, or the US Government.

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Appendix

Table 13 Second order screening design results: Case 1

		<i>Strong heredity, factor sparsity model:</i>		<i>Rep 2</i>
		$2A - 1.5E + 2G - 3A^2 + 2.5E^2 - 4G^2 + 4AE + 3.5AG - 5EG + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, A^2, EG	$A, E, G, A^2, E^2, G^2, AE, AG, EG$	
	Type I errors	$B, C, D, F, B^2, D^2, BE, BF, CE, DF$	$B, C, F, H, F^2, BE, BF, CG, EH, FH$	
	Type II errors	E^2, G^2, AE, AG	None	
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, EG	$A, E, G, A^2, G^2, AE, AG, EG$	
	Type I errors	$B, D, F, J, F^2, J^2, AF, BD, BF, DJ, FG$	D, J, J^2, DG, DJ	
	Type II errors	A^2, E^2, G^2, AE, AG	E^2	
$\varepsilon \sim N(0, 3)$	Identified	E, E^2	A, E, G, AE, AG, EG	
	Type I errors	C, H, J, CH, EJ	B, F, BF	
	Type II errors	$A, G, A^2, G^2, AE, AG, EG$	A^2, E^2, G^2	

Table 14 Second order screening design results: Case 2

		<i>Strong heredity, effect sparsity model:</i>		<i>Rep 2</i>
		$2A - 1.5E + 2G + 4C - 3H + 2.5E^2 - 5CG + 3.5EH - 4GH + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	$A, E, C, G, H, E^2, CG, EH, GH, EH, GH$	$A, E, C, G, H, E^2, CG, EH, GH, EH, GH$	
	Type I errors	B, F, AF, BC, BG	$B, D, F, J, AH, BE, DJ, EG, FG$	
	Type II errors	None	None	
$\varepsilon \sim N(0, 2)$	Identified	A, E, C, G, H	$A, E, C, G, H, CG, EH, GH$	
	Type I errors	$B, D, J, AD, BE, CE, CH, DG, EJ$	B, D, AB, AD, BD, DG	
	Type II errors	E^2, CG, EH, GH	E^2	
$\varepsilon \sim N(0, 3)$	Identified	E, C, G, H, CG, EH, GH	$A, E, C, G, H, CG, EH, GH$	
	Type I errors	CH	A^2, CH	
	Type II errors	A, E^2	E^2	

Table 15 Second order screening design results: Case 3

		<i>Weak heredity, factor sparsity model:</i>		<i>Rep 2</i>
		$2A + 2E - 1.5A^2 + 2.5E^2 - 3.5AE + 4AG - 5EG + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	$A, E, A^2, E^2, AE, AG, EG$	$A, E, A^2, E^2, AE, AG, EG$	
	Type I errors	$B, C, F, G, BE, CE, CF, BE, BF, CG, FH$	B, C, F, G, H, J, J^2	
	Type II errors	None	None	
$\varepsilon \sim N(0, 2)$	Identified	A, E, A^2, AE, AG, EG	A, E, A^2, AE, AG, EG	
	Type I errors	B, D, G, J, B^2, BD, EJ	D, G, J, J^2, DG	
	Type II errors	E^2	E^2	
$\varepsilon \sim N(0, 3)$	Identified	A, E, AE, AG, EG	A, E, AE, AG, EG	
	Type I errors	C, G, H, CH	B, F, G, BF	
	Type II errors	A^2, E^2	A^2, E^2	

Table 16 Second order screening design results: Case 4

		<i>Weak heredity, effect sparsity model:</i>		<i>Rep 2</i>
		$2A - 1.5E + 2G + 2.5E^2 - 3H^2 + 4AC - 5CG + 3.5EH - 4GH + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, EH, GH	$A, E, G, E^2, H^2, AC, CG, EH, GH$	
	Type I errors	$B, C, F, H, G^2, AF, AH, BE, CF, EF$	$B, C, F, H, B^2, AB, BC, BE, BG, CF$	
	Type II errors	E^2, H^2, AC, CG	None	
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, GH	$A, E, G, E^2, AC, CG, EH, GH$	
	Type I errors	$B, C, D, F, H, J, D^2, AB, AJ, BF, CE$	$B, C, D, H, J, G^2, AB, AH, BD, BG, BH$	
	Type II errors	E^2, H^2, AC, CG, EH	H^2	
$\varepsilon \sim N(0, 3)$	Identified	A, E, G	A, E, G, AC, CG, EH, GH	
	Type I errors	B, D, AD, BD, BE	C, H, CH	
	Type II errors	E^2, H^2, AC, CG, EH, GH	E^2, H^2	

Table 17 Second order screening design results: Case 1

<i>Strong heredity, factor sparsity model:</i>			<i>Rep 3</i>
$2A - 1.5E + 2G - 3A^2 + 2.5E^2 - 4G^2 + 4AE + 3.5AG - 5EG + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, AE, AG, EG	A, E, G, G^2, AE, AG, EG
	Type I errors	$B, C, D, F, H, J, J^2, AB, DH, EJ$	C, D, F, H, J, AH, CF
	Type II errors	A^2, E^2, G^2	A^2, E^2
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, G^2, EG	A, E, G, G^2, AE, AG, EG
	Type I errors	$B, D, F, H, B^2, AH, BF, EF, EH$	$B, C, D, F, AF, BC, CD, CF$
	Type II errors	A^2, E^2, AE, AG	A^2, E^2
$\varepsilon \sim N(0, 3)$	Identified	A, E, G, A^2, G^2, EG	A, E, G
	Type I errors	$B, C, D, F, H, J, BF, CJ, DF, EH$	$B, F, H, J, J^2, BJ, EH, EJ, FG$
	Type II errors	E^2, AE, AG	$A^2, E^2, G^2, AE, AG, EG$

Table 18 Second order screening design results: Case 2

<i>Strong heredity, effect sparsity model:</i>			<i>Rep 3</i>
$2A - 1.5E + 2G + 4C - 3H + 2.5E^2 - 5CG + 3.5EH - 4GH + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	$A, E, C, G, H, E^2, CG, EH, GH$	$A, E, C, G, H, E^2, CG, EH, GH$
	Type I errors	B, D, F, BH, CD, FG	$B, D, F, J, G^2, AB, AJ, FG$
	Type II errors	None	None
$\varepsilon \sim N(0, 2)$	Identified	$A, E, C, G, H, CG, EH, GH$	$A, E, C, G, H, CG, EH, GH$
	Type I errors	F, AF	$B, D, F, G^2, AE, AF, AH, BF, DH$
	Type II errors	E^2	E^2
$\varepsilon \sim N(0, 3)$	Identified	$A, E, C, G, H, E^2, CG, EH, GH$	$A, E, C, G, H, E^2, CG, EH, GH$
	Type I errors	B, F, J, AB, CE, CF	A^2
	Type II errors	None	None

Table 19 Second order screening design results: Case 3

		<i>Weak heredity, factor sparsity model:</i>		<i>Rep 3</i>
		$2A + 2E - 1.5A^2 + 2.5E^2 - 3.5AE + 4AG - 5EG + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	A, E, AE, AG, EG	A, E, E^2, AE, AG, EG	
	Type I errors	$D, F, G, H, J, D^2, AJ, DH$	$B, C, D, F, G, H, J, B^2, D^2, AJ, CD, DG, FH, GJ$	
	Type II errors	A^2, E^2	A^2	
$\varepsilon \sim N(0, 2)$	Identified	A, E, AE	A, E, AE, AG, EG	
	Type I errors	$B, D, F, G, J, G^2, AD, BE, BF, DJ, EF$	$B, C, D, F, G, B^2, AC, AD, AF, BC, BF, DF$	
	Type II errors	A^2, E^2, AG, EG	A^2, E^2	
$\varepsilon \sim N(0, 3)$	Identified	A, E	A, E, E^2, AE, AG, EG	
	Type I errors	$B, C, D, F, G, H, J, B^2, F^2, J^2, AD, AJ, CE, DH$	G, H, EH	
	Type II errors	A^2, E^2, AE, AG, EG	A^2	

Table 20 Second order screening design results: Case 4

		<i>Weak heredity, effect sparsity model:</i>		<i>Rep 3</i>
		$2A - 1.5E + 2G + 2.5E^2 - 3H^2 + 4AC - 5CG + 3.5EH - 4GH + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, GH	A, E, G, AC, CG, EH, GH	
	Type I errors	$C, D, F, H, AD, AH, CE, DE, DG$	$B, C, D, F, H, J, G^2, AB, AG, AJ, DJ, FJ, GJ$	
	Type II errors	E^2, H^2, AC, CG, EH	E^2, H^2	
$\varepsilon \sim N(0, 2)$	Identified	A, E, G	A, E, G, AC, CG, EH, GH	
	Type I errors	$B, C, D, F, D^2, AG, BD, BF, CE, CF, FG$	C, H, J, J^2	
	Type II errors	E^2, H^2, AC, CG, EH, GH	E^2, H^2	
$\varepsilon \sim N(0, 3)$	Identified	A, E, G, AC, CG, EH, GH	A, E, G, AC, CG, EH, GH	
	Type I errors	$B, C, D, F, H, J, AF, CE, DJ$	$B, C, F, H, AB, AH, BF, CF, EF, FH$	
	Type II errors	E^2, H^2	E^2, H^2	

Table 21 Second order screening design results: case 1

<i>Strong heredity, factor sparsity model:</i>			<i>Rep 4</i>
$2A - 1.5E + 2G - 3A^2 + 2.5E^2 - 4G^2 + 4AE + 3.5AG - 5EG + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, E^2, AG, EG	$A, E, G, E^2, G^2, AE, AG, EG$
	Type I errors	$B, C, D, F, H, J, AD, BF, BG, CH, EJ, FJ$	$B, C, D, F, H, J, F^2, H^2, AC, BC, CD, CG, DE, EH$
	Type II errors	A^2, G^2, AE	A^2
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, G^2, AE, EG	A, E, G, G^2, AE, AG, EG
	Type I errors	B, D, F, AB, BF, DF	B, F, H, BF, FH, GH
	Type II errors	A^2, E^2, AG	A^2, E^2
$\varepsilon \sim N(0, 3)$	Identified	A, E, G, G^2, AG	A, E, G, E^2, AG, EG
	Type I errors	B, F, BE, BF	J, AJ, GJ
	Type II errors	A^2, E^2, AE, AG	A^2, G^2, AE

Table 22 Second order screening design results: Case 2

<i>Strong heredity, effect sparsity model:</i>			<i>Rep 4</i>
$2A - 1.5E + 2G + 4C - 3H + 2.5E^2 - 5CG + 3.5EH - 4GH + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	$A, E, C, G, H, CG, EH, GH$	$A, E, C, G, H, CG, EH, GH$
	Type I errors	$B, D, F, J, A^2, J^2, BG, EG, FG$	J, A^2, G^2, J^2, AC
	Type II errors	E^2	E^2
$\varepsilon \sim N(0, 2)$	Identified	$A, E, C, G, H, CG, EH, GH$	$A, E, C, G, H, CG, EH, GH$
	Type I errors	B	None
	Type II errors	E^2	E^2
$\varepsilon \sim N(0, 3)$	Identified	$A, E, C, G, H, CG, EH, GH$	$A, E, C, G, H, CG, EH, GH$
	Type I errors	F, AF, EF, FH	D, F, CD, FH
	Type II errors	E^2	E^2

Table 23 Second order screening design results: Case 3

<i>Weak heredity, factor sparsity model:</i>			<i>Rep 4</i>
$2A + 2E - 1.5A^2 + 2.5E^2 - 3.5AE + 4AG - 5EG + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	A, E, E^2, AE, AG, EG	$A, E, A^2, E^2, AE, AG, EG$
	Type I errors	$B, C, D, F, H, J, J^2, AC, BD, BJ$	$B, C, D, F, G, H, J, B^2, C^2, G^2, J^2, BG, CE, DF, EH, EJ, HJ$
	Type II errors	A^2	None
$\varepsilon \sim N(0, 2)$	Identified	A, E, AE	A, E, AE, AG, EG
	Type I errors	$B, F, H, J, B^2, J^2, AH, BF$	G, H, GH
	Type II errors	A^2, E^2, AG, EG	A^2, E^2
$\varepsilon \sim N(0, 3)$	Identified	A, E, AE	A, E, AE, AG, EG
	Type I errors	B, F, BE, BF	F, G, J, J^2, FJ, GJ
	Type II errors	A^2, E^2, AG, EG	A^2, E^2

Table 24 Second order screening design results: Case 4

		<i>Weak heredity, effect sparsity model:</i>		<i>Rep 4</i>
		$2A - 1.5E + 2G + 2.5E^2 - 3H^2 + 4AC - 5CG + 3.5EH - 4GH + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, GH	$A, E, G, H^2, AC, CG, EH, GH$	
	Type I errors	$B, C, D, F, H, J, B^2, AD, AH, CD, DE, DG, GJ$	$C, D, H, J, A^2, AD, AH, CE, CJ$	
	Type II errors	E^2, H^2, AC, CG, EH	E^2	
$\varepsilon \sim N(0, 2)$	Identified	A, G, CG, GH	A, E, G, AC, CG, EH, GH	
	Type I errors	B, C, H, J, A^2, AB, CJ	C, D, H, AD, CD	
	Type II errors	E, E^2, H^2, AC, EH	E^2, H^2	
$\varepsilon \sim N(0, 3)$	Identified	A, E, E^2	$A, E, G, H^2, AC, CG, EH, GH$	
	Type I errors	F, H, AF, AH, FH	C, D, F, H, CD, FH	
	Type II errors	G, H^2, AC, CG, EH, GH	E^2	

Table 25 Second order screening design results: Case 1

		<i>Strong heredity, factor sparsity model:</i>		<i>Rep 5</i>
		$2A - 1.5E + 2G - 3A^2 + 2.5E^2 - 4G^2 + 4AE + 3.5AG - 5EG + \varepsilon$		
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>	
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, AE, AG, EG	$A, E, G, A^2, E^2, G^2, AE, AG, EG$	
	Type I errors	$B, C, F, J, B^2, J^2, CE, EJ$	$B, C, D, F, H, J, C^2, D^2, AB, AC, BJ, DE, FJ, HJ$	
	Type II errors	A^2, E^2, G^2	None	
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, A^2, EG	$A, E, G, A^2, E^2, G^2, AE, AG, EG$	
	Type I errors	$B, C, D, F, J, F^2, BF, CJ, DF$	C, F, AF	
	Type II errors	E^2, G^2, AE, AG	None	
$\varepsilon \sim N(0, 3)$	Identified	A, E, G, EG	A, E, G, A^2, AE, AG, EG	
	Type I errors	$C, D, J, D^2, A^1, CE, CG, EJ$	D, J, J^2, EJ	
	Type II errors	A^2, E^2, G^2, AE, AG	E^2, G^2	

Table 26 Second order screening design results: Case 2

<i>Strong heredity, effect sparsity model:</i>			<i>Rep 5</i>
$2A - 1.5E + 2G + 4C - 3H + 2.5E^2 - 5CG + 3.5EH - 4GH + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	$A, E, C, G, H, E^2, CG, EH, GH$	$A, E, C, G, H, E^2, CG, EH, GH$
	Type I errors	B, D, F, J, BD, CH, FG	$B, F, J, A^2, AF, BC, BG, EJ$
	Type II errors	None	None
$\varepsilon \sim N(0, 2)$	Identified	$A, E, C, G, H, E^2, CG, EH$	$A, E, C, G, H, E^2, CG, EH, GH$
	Type I errors	F, AC, CE, EF	F, G^2, AF
	Type II errors	GH	None
$\varepsilon \sim N(0, 3)$	Identified	$A, E, C, G, H, CG, EH, GH$	$A, E, C, G, H, CG, EH, GH$
	Type I errors	J, J^2, AJ	B, D, J, J^2, AE, BG, CD
	Type II errors	E^2	E^2

Table 27 Second order screening design results: Case 3

<i>Weak heredity, factor sparsity model:</i>			<i>Rep 5</i>
$2A + 2E - 1.5A^2 + 2.5E^2 - 3.5AE + 4AG - 5EG + \varepsilon$			
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	A, E, A^2, AE, EG	$A, E, A^2, E^2, AE, AG, EG$
	Type I errors	$B, C, D, F, G, J, B^2, J^2, BD, BF, CE$	B, C, F, G, J, BJ, CF
	Type II errors	E^2, AG	None
$\varepsilon \sim N(0, 2)$	Identified	A, E, AE, AG, EG	A, E, E^2, AE, AG, EG
	Type I errors	$C, F, G, J, F^2, AC, AJ, CF$	C, F, G, H, AF, CF, GH
	Type II errors	A^2, E^2	A^2
$\varepsilon \sim N(0, 3)$	Identified	A, E, AE	A, E, A^2, AE, AG, EG
	Type I errors	$B, C, F, G, J, G^2, BF, EJ, GJ$	$B, C, G, J, J^2, AB, BC, BG, EJ$
	Type II errors	A^2, E^2, AG, EG	E^2

Table 28 Second order screening design results: Case 4

		<i>Weak heredity, effect sparsity model:</i>	
		$2A - 1.5E + 2G + 2.5E^2 - 3H^2 + 4AC - 5CG + 3.5EH - 4GH + \varepsilon$	
		<i>Rep 5</i>	
<i>Scenario</i>		<i>DSD</i>	<i>DSD+</i>
$\varepsilon \sim N(0, 1)$	Identified	A, E, G, GH	$A, E, G, E^2, H^2, AC, CG, EH, GH$
	Type I errors	$B, C, F, H, J, B^2, G^2, AE, AF, AH, EF$	$B, C, D, F, H, J, D_2, AF, BE, CE, DF, DH, FJ$
	Type II errors	E^2, H^2, AC, CG, EH	None
$\varepsilon \sim N(0, 2)$	Identified	A, E, G, AC, CG	$A, E, G, E^2, H^2, AC, CG, EH, GH$
	Type I errors	$C, F, C^2, G^2, AF, CE, FG$	$C, F, H, A^2, G^2, AF, CE$
	Type II errors	E^2, H^2, EH, GH	None
$\varepsilon \sim N(0, 3)$	Identified	A, E, G	A, E, G, AC, CG, EH, GH
	Type I errors	$B, C, D, F, J, G^2, AB, BD, BF, CE$	C, H, J, J^2, EG
	Type II errors	E^2, H^2, AC, CG, EH, GH	E^2, H^2