

Optimal design generation: an approach based on discovery probability

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Abstract Efficient algorithms for searching for optimal saturated designs for sampling experiments are widely available. They maximize a given efficiency measure (such as D-optimality) and provide an optimum design. Nevertheless, they do not guarantee a *global* optimal design. Indeed, they start from an initial random design and find a local optimal design. If the initial design is changed the optimum found will, in general, be different. A natural question arises. Should we stop at the design found or should we run the algorithm again in search of a better design? This paper uses very recent methods and software for discovery probability to support the decision to continue or stop the sampling. A software tool written in SAS has been developed.

Keywords (separated by '-') Design of experiments - Optimal designs - Unobserved species - Discovery probability

Footnote Information

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Abstract Efficient algorithms for searching for optimal saturated designs for sampling experiments are widely available. They maximize a given efficiency measure (such as D-optimality) and provide an optimum design. Nevertheless, they do not guarantee a *global* optimal design. Indeed, they start from an initial random design and find a local optimal design. If the initial design is changed the optimum found will, in general, be different. A natural question arises. Should we stop at the design found or should we run the algorithm again in search of a better design? This paper uses very recent methods and software for discovery probability to support the decision to continue or stop the sampling. A software tool written in SAS has been developed.

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1 Introduction

In the design of experiments, optimal designs, or optimum designs, are a class of experimental designs that are optimal with respect to a given statistical criterion.

In this paper we focus on saturated optimum designs for sampling experiments even if the methodology can also be applied to non-saturated designs without any modification. Saturated designs contain a number of points that is equal to the number of parameters of the model. It follows that saturated optimum designs are often used in place of standard designs, such as orthogonal fractional factorial designs, when

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21 the cost of each experimental run is high. Main references to optimal designs include
22 [Atkinson et al. \(2007\)](#), [Goos and Jones \(2011\)](#), [Pukelsheim \(2006\)](#), [Rasch et al. \(2011\)](#),
23 [Shah and Sinha \(1989\)](#) and [Wynn \(1970\)](#).

24 The optimality of a design depends on the statistical model that is assumed and is
25 assessed with respect to a statistical criterion, which, for information-based criteria,
26 is related to the variance-matrix of the model parameter estimators. Well-known and
27 commonly used criteria are A-optimality and D-optimality.

28 Widely used statistical systems like SAS and R have procedures for finding an
29 optimal design according to the user's specifications. In this paper we will refer to
30 Proc Optex of SAS/QC ([SAS Institute, Inc. 2010](#)), but the approach can be adopted
31 for other software.

32 The Optex procedure searches for optimal experimental designs. The user specifies
33 an efficiency criterion, a set of candidate design points, a model and the size of the
34 design to be found and the procedure generates a subset of the candidate set so that the
35 terms in the model can be estimated as efficiently as possible. By default, the standard
36 output of the procedure is a list of 10 designs that are found as the result of 10 runs of
37 the exchange search algorithm ([Mitchell and Miller 1970](#)) starting each time from an
38 initial completely randomly chosen design.

39 The number of times that we decide to run the search algorithm is crucial. Obviously,
40 if we increase it, in general we will explore different local optima with the possibility
41 to find better designs. On the other hand, sometimes, the extra time that we use to
42 explore other possibilities is wasted because new optima do not exist. This work aims
43 at developing a methodology based on a Bayesian updating methodology that could
44 support the user in making the decision whether to stop or continue the search.

45 Let us consider an example that will be described in more detail in Sect. 4.1. An
46 experimenter wants to study the influence on a response Y (e.g. the fuel consumption
47 of a given engine) of 7 factors (the type of fuel, the age of the engine, etc.) where
48 each factor has 2 levels. The full factorial design has $2^7 = 128$ runs. Let us suppose
49 that both the size of the full factorial design is too high with respect to the available
50 budget and the experimenter believes that a model with only the main effects and
51 2-factor interactions would be sufficiently rich to describe with a good accuracy the
52 phenomenon under study. A minimum size orthogonal fractional factorial design for
53 this case requires 64 runs, which is still a high value ([Fontana 2013](#)). The experimenter
54 decides to use a saturated D -optimal design (29 runs). The experimenter runs the Proc
55 Optex procedure of SAS/QC with the default settings and gets a saturated D -optimal
56 design with D -efficiency equal to 82.32. With the methodology described in this paper
57 the experimenter would have been able to find both a better design (D -efficiency equal
58 to 85.63) and a list of 103 D -optimal designs that could be further analysed with respect
59 to different criteria like space filling.

60 The paper is organized as follows. In Sect. 2 we state the problem of finding new
61 optimal designs as the problem of finding new species in a population. Then, in Sect. 3
62 we describe how our methodology, which is based on the estimator of the discovery
63 probability, could be used for optimal design generation. We also provide a detailed
64 description of the algorithm. In Sect. 4 we describe the results of a computational
65 study in which we ran our algorithm in different cases. Concluding remarks are made
66 in Sect. 5.

67 The software code that has been developed is written in SAS, is available on request
 68 and can be used for any choice of factors, levels and model. It is worth noting that the
 69 algorithm, being based on the Proc Optex procedure, can manage not only classical
 70 linear model but also nonstandard linear or nonlinear models, (SAS Institute, Inc.
 71 2010).

72 2 Optimal designs vs richness of species

73 We consider the following setting that is quite common in optimal design problems.

74 We have d factors, A_1, \dots, A_d . The factor A_i has s_i levels coded with the integer
 75 $0, \dots, s_i - 1, i = 1, \dots, d$. The full factorial design is $\mathcal{D} = \{0, \dots, s_1 - 1\} \times \dots \times$
 76 $\{0, \dots, s_d - 1\}$. For each point $\zeta = (\zeta_1, \dots, \zeta_d)$ of \mathcal{D} we consider a real-valued
 77 random variable $Y_{\zeta_1, \dots, \zeta_d}$. We make the hypothesis that the means of the responses,
 78 $E[Y]$ where Y is the column vector $[Y_\zeta; \zeta \in \mathcal{D}]$ can be modeled as

$$79 \quad E[Y] = X_{\mathcal{D}}\beta, \quad (1)$$

80 where $X_{\mathcal{D}}$ is the non-overparametrized design matrix, as it will be defined in Sect. 2.1,
 81 and β is the subset of all the effects (constant effect, main effects and interactions)
 82 that are supposed to affect the response Y . There is no restriction to the order of the
 83 interactions; polynomial effects (linear, quadratic, etc) can also be considered.

84 Given an efficiency criterion ϕ , a saturated optimal design is a subset of the full
 85 factorial design $\mathcal{D} = \{0, \dots, s_1 - 1\} \times \dots \times \{0, \dots, s_d - 1\}$, whose size is equal to the
 86 number of degrees of freedom of the model (1) and that maximizes this criterion ϕ . In
 87 this paper we focus on information-based criteria and, in particular, on D -optimality
 88 but other criteria can be chosen (like A -optimality and G -optimality). We denote
 89 this type of problem with the triple $(\mathcal{D}, \mathcal{M}, \phi)$ where \mathcal{D} is the full design, \mathcal{M} is the
 90 hypothesized model (see Eq. 1) and ϕ is the optimality criterion.

91 Given a subset \mathcal{F} of \mathcal{D} , the information matrix is defined as $X'_{\mathcal{F}}X_{\mathcal{F}}$ where $X_{\mathcal{F}}$ is
 92 the design matrix corresponding to \mathcal{F} and X' is the transpose of X . D -optimality aims
 93 at maximizing $D_{\mathcal{F}}$, the determinant of the information matrix

$$94 \quad D_{\mathcal{F}} = \det(X'_{\mathcal{F}}X_{\mathcal{F}}). \quad (2)$$

95 There are several algorithms for searching for D -optimal designs. They have a com-
 96 mon structure. They start from an initial design, randomly generated or user specified,
 97 and move, in a finite number of steps, to a better design. In general, if a different initial
 98 design is chosen, a different optimal design is found.

99 It follows that, given an algorithm α , a population \mathcal{A}_{α}^D of D -optimal designs can
 100 be defined. This population is made up of all the saturated designs that are the result
 101 of the execution of the algorithm α and is a subset of all the subsets of \mathcal{D} of size equal
 102 to the number of degrees of freedom of the model.

103 The elements of \mathcal{A}_{α}^D can be classified into species, according to the criterion for
 104 which $\mathcal{F}_1 \in \mathcal{A}_{\alpha}^D$ and $\mathcal{F}_2 \in \mathcal{A}_{\alpha}^D$ are of the same species if and only if they have the
 105 same value in terms of the D criterion, $D_{\mathcal{F}_1} = D_{\mathcal{F}_2}$.

106 Studying the species of \mathcal{A}_α^D or, in general, of \mathcal{A}_α^ϕ where ϕ is an optimal criterion,
 107 is interesting for optimal design generation. Let us consider the problem $(\mathcal{D}, \mathcal{M}, \phi)$
 108 and let us choose an algorithm α to search for ϕ -optimal saturated designs. If we run
 109 this algorithm n times, each time starting from a completely random initial design,
 110 we will get a sample of n elements of \mathcal{A}_α^ϕ . Such elements can be classified in $k_n \leq$
 111 n different species according to the value of the criterion ϕ . Recent methods for
 112 discovery probability estimation, Favaro et al. (2012), can be applied to the vector
 113 $(\ell_1, \ell_2, \dots, \ell_n)$ where ℓ_r is the number of species in the sample with frequency r ,
 114 $r = 1, \dots, n$. In particular, based on a sample of size n , for any additional unobserved
 115 sample size $m \geq 0$ and for any frequency $k = 0, \dots, n + m$, these methods provide,
 116 an explicit estimator for the probability $U_{n+m}(k)$ that the $(n + m + 1)$ -th observation
 117 coincides with a species whose frequency, within the sample size $n + m$, is exactly k .
 118 The case $m = k = 0$ corresponds to assessing the probability of finding a new species
 119 in the subsequent observation, that in the context of optimal designs, is the probability
 120 of finding a saturated design with a different value of the criterion ϕ in the subsequent
 121 run of the algorithm. If this probability $U_{n+0}(0)$ is sufficiently high (let us say greater
 122 than 0.1 or even 0.05) it would be convenient to run the algorithm again because it
 123 is quite likely that we could find a new optimal design. If we found a new design, it
 124 could have a greater value of ϕ and this obviously represents an improvement to our
 125 optimization process. Even if this new design did not have an higher value of ϕ than
 126 the existing ones, this would give the possibility to increase the known part of \mathcal{A}_α^ϕ .
 127 It is quite common, in practical applications, to choose a design where the optimal
 128 criterion has a slightly smaller value than the maximum obtained but which has other
 129 better characteristics, such as space filling properties.

130 In particular, for D -optimal designs, we know that designs with different values of
 131 $D_{\mathcal{F}}$ are non-isomorphic designs. Indeed we observe that, as proved in Proposition 1,
 132 see Angelopoulos et al. (2007), isomorphic designs belong to the same species. In
 133 general, the opposite is not true because there are designs with the same value of the
 134 D criterion but that are not isomorphic. As is known two designs are isomorphic if
 135 one can be obtained from the other by relabeling the factors, reordering the runs, and
 136 switching the levels of factors, e.g. Clark and Dean (2001).

137 **Proposition 1** *Let us consider $\mathcal{F}_1 \subseteq \mathcal{D}$ and $\mathcal{F}_2 \subseteq \mathcal{D}$. If \mathcal{F}_1 and \mathcal{F}_2 are isomorphic*
 138 *then $D_{\mathcal{F}_1} = D_{\mathcal{F}_2}$.*

139 *Proof* We separately analyse row/column permutations and the switching of the levels
 140 of some factors. If \mathcal{F}_2 is obtained permuting the rows and/or the columns of \mathcal{F}_1 it
 141 follows that

$$142 \quad X_{\mathcal{F}_2} = R X_{\mathcal{F}_1} C$$

143 where R and C are permutation matrices. Then

$$144 \quad \begin{aligned} D_{\mathcal{F}_2} &= \det((X'_{\mathcal{F}_2} X_{\mathcal{F}_2})) \\ 145 \quad &= (\det(R))^2 \det((X'_{\mathcal{F}_1} X_{\mathcal{F}_1})) (\det(C))^2 \\ 146 \quad &= D_{\mathcal{F}_1} \end{aligned}$$

147 being $\det(R) = \det(C) = 1$. A similar argument holds for switching the levels of
 148 some factors. \square

149 The knowledge of a set of non-isomorphic designs can also be used for non parametric
 150 testing procedures, [Giancristofaro et al. \(2012\)](#) and [Basso et al. \(2004\)](#).

151 In Sect. 2.1 and 2.2 we provide some details on how the design matrix is built and
 152 on how to compute the estimates of the discovery probabilities.

153 2.1 The design matrix

154 The design matrix $X_{\mathcal{D}}$ in Eq. 1 is built as follows.

155 The first column is equal to 1 and corresponds to the constant effect, denoted by μ .
 156 The constant effect is always considered as a term of the model.

157 If the main effect of the factor A_i is to be considered in the model, the corresponding
 158 $s_i - 1$ columns are computed as follows. For a design point with A_i at its k -th level if
 159 $1 \leq k \leq s_i - 1$ the columns are all 0 except for the k -th column that is 1; if $k = s_i$ the
 160 columns are all -1 .

161 If an interaction $A_{i_1} \star \dots \star A_{i_k}$ is to be considered in the model, the corresponding
 162 $(s_{i_1} - 1) \cdot \dots \cdot (s_{i_k} - 1)$ columns are computed by taking the horizontal direct product
 163 of the columns corresponding to the main effects of A_{i_1}, \dots, A_{i_k} .

164 This coding corresponds to modeling without over parametrization and $X_{\mathcal{D}}$ is full
 165 rank.

166 For a subset \mathcal{F} of \mathcal{D} , the design matrix $X_{\mathcal{F}}$ is simply built deleting from $X_{\mathcal{D}}$ the
 167 rows that correspond to the points of \mathcal{D} that are not in \mathcal{F} .

168 2.2 Discovery probability

169 We briefly summarize the main results that are used in this work, as in [Favaro et al.](#)
 170 [\(2012\)](#). The interested reader should refer to the original paper for a detailed descrip-
 171 tion of the methodology. We observe that the results in [Favaro et al. \(2012\)](#) are an
 172 improvement of those in [Lijoi et al. \(2007\)](#) concerning the evaluation of the probabil-
 173 ity that further sampling reveals new species.

174 Given a sample of size n , the vector (ℓ_1, \dots, ℓ_n) is built, where ℓ_r is the frequency
 175 of species that have been observed r -times in the sample, $r = 1, \dots, n$. We have
 176 $\sum_{i=1}^n i \ell_i = n$. We denote the number of different species that have been observed in
 177 the sample by j . We get $\sum_{i=1}^n \ell_i = j$.

178 Based on a sample of size n , for an additional unobserved sample size $m \geq 0$ and for
 179 any frequency $k = 0, \dots, n + m$, using a non parametric Bayesian approach, [Favaro](#)
 180 [et al. \(2012\)](#) provide an estimator for the probability $U_{n+m}(k)$ that the $(n + m + 1)$ -th
 181 observation coincides with a species whose frequency, within the sample of size $n + m$,
 182 is exactly k .

183 We are interested in discovering new species, that correspond to the case $k = 0$.

184 From Sect. 2, p.1,190 of [Favaro et al. \(2012\)](#) we obtain

$$185 \quad U_{n+0}(0) = \frac{V_{n+1,j+1}}{V_{n,j}}$$

186 where, for the two-parameter Poisson-Dirichlet process, we have $V_{n,j} = \prod_{i=1}^{j-1} (\theta +$
 187 $i\sigma)/(\theta + 1)_{n-1}$, $\sigma \in (0, 1)$, $\theta > -\sigma$. The symbol $(a)_n$ denotes the n -th ascending
 188 factorial of a , $(a)_n = a(a + 1) \dots (a + n - 1)$, $(a)_0 \equiv 1$. It follows that

$$189 \quad U_{n+0}(0) = \frac{\theta + j\sigma}{\theta + n}$$

190 and, for $m > 0$, we obtain

$$191 \quad U_{n+m}(0) = \frac{\theta + j\sigma}{\theta + n} \frac{(\theta + n + \sigma)_m}{(\theta + n + 1)_m}.$$

192 The estimates $\hat{\sigma}$, $\hat{\theta}$ of σ , θ are obtained as

$$193 \quad \arg \max_{(\sigma, \theta)} \frac{\prod_{i=1}^{j-1} (\theta + i\sigma)}{(\theta + 1)_{n-1}} n! \prod_{i=1}^n \left\{ \frac{(1 - \sigma)_{i-1}}{i!} \right\}^{\ell_i} \frac{1}{\ell_i!}. \quad (3)$$

194 Using $(\hat{\theta}, \hat{\sigma})$ we finally obtain the estimates of the discovery probability at the
 195 $(n + 1)$ -th observation

$$196 \quad \hat{U}_{n+0}(0) = \frac{\hat{\theta} + j\hat{\sigma}}{\hat{\theta} + n} \quad (4)$$

197 and at the $(n + m + 1)$ -th observation, $m > 0$,

$$198 \quad \hat{U}_{n+m}(0) = \frac{\hat{\theta} + j\hat{\sigma}}{\hat{\theta} + n} \frac{(\hat{\theta} + n + \hat{\sigma})_m}{(\hat{\theta} + n + 1)_m} \quad (5)$$

199 3 Methodology

200 We repeat the search for optimal designs to analyse the population \mathcal{A}_α^D of D -optimal
 201 designs that can be found for a given problem using a predefined algorithm α . Each
 202 time the algorithm starts from a randomly chosen initial design. We set a maximum
 203 (minimum) number of iterations equal to M_\star (m_\star). We continue the process until the
 204 minimum number m_\star of iterations is performed and the estimate of the discovery
 205 probability at the subsequent observation goes under a given threshold p_\star , or until the
 206 maximum number M_\star of iterations is reached.

207 The procedure can be described as follows. A problem $(\mathcal{D}, \mathcal{M}, \phi)$, with $\phi = D$
 208 in our examples, is defined and an algorithm α for ϕ -optimal design generation is
 209 chosen. For each iteration s , $s = 1, \dots, M_\star$,

- 210 1. using the algorithm α , a ϕ -optimal saturated design \mathcal{F}_s is obtained;
- 211 2. the value of the ϕ -criterion of \mathcal{F}_s is computed;
- 212 3. the vector (ℓ_1, \dots, ℓ_s) is built, where ℓ_r is the number of species with frequency
 213 r , $r = 1, \dots, s$;
- 214 4. an estimate $(\hat{\sigma}_s, \hat{\theta}_s)$ is obtained, see Eq. 3;
- 215 5. an estimate of $\hat{U}_{s+0}(0)$ is computed using Eq. 4;

216 6. if $\hat{U}_{s+0}(0) < p_*$ and $s \geq m_*$ the algorithm stops, otherwise the next iteration $s + 1$
 217 is performed (if $s + 1 > M_*$ the algorithm stops).

218 The main output of the algorithm is a set of designs, where each design belongs to
 219 a different species, i.e. has a different value of the ϕ -criterion.

220 We now provide a detailed description of each step of the algorithm.

221 3.1 Steps 1 and 2

222 At iteration s , with the chosen algorithm α , the Proc Optex procedure is used to
 223 generate a D -optimal design, \mathcal{F}_s . The species of \mathcal{F}_s is the value of its D -efficiency,
 224 $E_{\mathcal{F}_s}^D$. The D -efficiency of a \mathcal{F} , is defined as

225
$$E_{\mathcal{F}}^D = 100 \times \left(\frac{1}{\#\mathcal{F}} D_{\mathcal{F}}^{\frac{1}{\#\mathcal{F}}} \right)$$

226 where $\#\mathcal{F}$ is the number of runs of \mathcal{F} that coincides with the degrees of freedom of
 227 the model for saturated designs and $D_{\mathcal{F}}$ is the determinant of the information matrix.

228 The value of the efficiency is rounded to four decimal digits to avoid creating
 229 different species from numerical effects.

230 3.2 Step 3

231 Using all the designs $\mathcal{F}_1, \dots, \mathcal{F}_s$ with their corresponding D -efficiencies, $E_{\mathcal{F}_1}^D, \dots,$
 232 $E_{\mathcal{F}_s}^D$ the vector (ℓ_1, \dots, ℓ_s) is built, where ℓ_r is the number of species with frequency
 233 $r, r = 1, \dots, s$.

234 3.3 Step 4

235 An estimate $(\hat{\sigma}_s, \hat{\theta}_s)$ must be obtained searching for $(\sigma, \theta), \sigma \in (0, 1), \theta > -\sigma$ that
 236 maximizes $f(\sigma, \theta)$, (see Eq. 3),

237
$$f(\sigma, \theta) = \frac{\prod_{i=1}^{j-1} (\theta + i\sigma)}{(\theta + 1)_{n-1}} n! \prod_{i=1}^n \left\{ \frac{(1 - \sigma)_{i-1}}{i!} \right\}^{\ell_i} \frac{1}{\ell_i!}$$

238 The Genetic Algorithm module of SAS/IML has been used. In order to manage
 239 the constraints $\sigma \in (0, 1), \theta > -\sigma$ the search has been performed in the region
 240 $\mathcal{R} = [\delta, 1 - \delta] \times [-(1 - \delta), T_M]$ with $\delta = 0.01$ and $T_M = 1,000$. This region contains
 241 the non-feasible region made by the points inside the simplex $\mathcal{S} = \mathcal{R} \cap \{(\sigma, \theta) : \theta \leq$
 242 $-\sigma\}$ whose vertices are $(\delta, -(1 - \delta)), (\delta, -\delta)$ and $(1 - \delta, -(1 - \delta))$. We observe that
 243 the edges of \mathcal{S} contain non-feasible points.

244 We decided to manage this constraint with the penalty method, because this method
 245 usually works well when most of the points in the solution space do not violate the
 246 constraints, as in our problem. The way in which the penalty in the objective function
 247 for unsatisfied constraints has been imposed is described here.

248 From the point of view of the search of the point (σ_*, θ_*) that maximizes $f(\sigma, \theta)$,
 249 it is equivalent to consider $\log f(\sigma, \theta)$ instead of $f(\sigma, \theta)$

$$250 \quad \log f(\sigma, \theta) = \log \left(\prod_{i=1}^{j-1} (\theta + i\sigma) \right) + \log(n!) \\
 251 \quad - \log((\theta + 1)_{n-1}) + \log \left(\prod_{i=1}^n \left\{ \frac{(1-\sigma)_{i-1}}{i!} \right\}^{\ell_i} \right) - \log(\ell_i!).$$

252 Omitting the terms that do not depend on σ and θ and as $(a)_n = \frac{\Gamma(a+n)}{\Gamma(a)}$ where Γ is
 253 the gamma function, the previous equation becomes the function $f_*(\sigma, \theta)$ here

$$254 \quad f_*(\sigma, \theta) = f_*^{(1)}(\sigma, \theta) + f_*^{(2)}(\sigma, \theta),$$

255 where

$$256 \quad f_*^{(1)}(\sigma, \theta) = \sum_{i=1}^{j-1} f_*^{(1,i)}(\sigma, \theta)$$

257 with $f_*^{(1,i)}(\sigma, \theta) = \log(\theta + i\sigma)$ and

$$258 \quad f_*^{(2)}(\sigma, \theta) = -\log \Gamma(\theta + n) + \log \Gamma(\theta + 1) \\
 259 \quad + \sum_{i=1}^n \ell_i \log \Gamma(i - \sigma) - j \log \Gamma(1 - \sigma).$$

260 We observe that, when the point $(\sigma, \theta) \in \mathcal{R}$ does not satisfy the constraint $\theta > -\sigma$
 261 only $f_*^{(1)}(\sigma, \theta)$ becomes not defined. We apply a penalty value to $f_*^{(1)}(\sigma, \theta)$ and to
 262 $f_*^{(2)}(\sigma, \theta)$ as described below.

263 Given a point P_1 in the non-feasible region, $P_1 = (\sigma, \theta) \in \mathcal{S}$, \tilde{P}_1 , the closest
 264 point to P_1 with respect to the Euclidean distance that lies in the feasible region, is
 265 determined

$$266 \quad \tilde{P}_1 = (\tilde{\sigma}, \tilde{\theta}) = \left(\frac{1}{2}(\sigma - \theta + \epsilon), \frac{1}{2}(\theta - \sigma + \epsilon) \right)$$

267 where ϵ is a very small number to ensure that \tilde{P}_1 is feasible, i.e. $\tilde{P}_1 \in \mathcal{R} \cap \bar{\mathcal{S}}$. We
 268 used $\epsilon = 0.001$. The value of the function $f_*^{(1,1)}$ is computed in \tilde{P}_1 getting $\tilde{Y}_1 =$
 269 $f_*^{(1,1)}(\tilde{\sigma}, \tilde{\theta}) = \log \epsilon$. Then the value Y_1 of $f_*^{(1,1)}$ in P_1 is defined as $f_*^{(1,1)}(\sigma, \theta) = (1 +$
 270 $b_1)\tilde{Y}_1$ where b_1 is the Euclidean distance between P_1 and \tilde{P}_1 , $b_1 = \sqrt{\frac{1}{2}(\sigma + \theta - \epsilon)^2}$.
 271 In an analogous way, we apply this penalty method to all $P_i = (i\sigma, \theta)$ that even-
 272 tually fall in the non-feasible region \mathcal{S} getting $f_{*,p}^{(1)}(\sigma, \theta)$, the penalized version of
 273 $f_*^{(1)}(\sigma, \theta)$,

$$f_{\star, P}^{(1)}(\sigma, \theta) = \sum_{i=1}^{j-1} f_{\star, P}^{(1,i)}(\sigma, \theta)$$

where

$$f_{\star, P}^{(1,i)} = \begin{cases} \log(\theta + i\sigma) & \text{if } \theta + i\sigma > 0 \\ (1 + b_i) \log(\epsilon) & \text{if } \theta + i\sigma \leq 0 \end{cases}, i = 1, \dots, j - 1,$$

and b_i is the Euclidean distance between $P_i = (i\sigma, \theta)$ and $\tilde{P}_i = (\frac{1}{2}(i\sigma - \theta + \epsilon), \frac{1}{2}(\theta - i\sigma + \epsilon))$ determined as described above. The penalized version $f_{\star, P}^{(2)}(\sigma, \theta)$ of $f_{\star}^{(2)}(\sigma, \theta)$ is simply defined as

$$f_{\star, P}^{(2)}(\sigma, \theta) = \begin{cases} f_{\star}^{(2)}(\sigma, \theta) & \text{if } \theta + \sigma > 0 \\ (1 + b_1)f_{\star}^{(2)}(\sigma, \theta) & \text{if } \theta + \sigma \leq 0 \\ & \text{and } f_{\star}^{(2)}(\sigma, \theta) \leq 0 \\ (1 - b_1)f_{\star}^{(2)}(\sigma, \theta) & \text{if } \theta + \sigma \leq 0 \\ & \text{and } f_{\star}^{(2)}(\sigma, \theta) > 0 \end{cases}$$

We observe that

$$\begin{cases} p < q \Rightarrow b_p > b_q, p, q = 1, \dots, j - 1; \\ b_1 \leq \frac{\sqrt{2}}{2}(1 + \epsilon - 2\delta). \end{cases}$$

For $\delta = 0.01$ and $\epsilon = .001$ we get $b_1 < 0.694$.

Using the penalty method, an estimate $(\hat{\sigma}_s, \hat{\theta}_s)$ is obtained finding the maximum of $f_{\star, P}(\sigma, \theta) = f_{\star, P}^{(1)}(\sigma, \theta) + f_{\star, P}^{(2)}(\sigma, \theta)$.

Finally we point out that if $n = 1$ then $f_{\star}(\sigma, \theta) = 0 \forall \sigma, \theta$. It follows that n must be greater than 1 to obtain the estimates of σ and θ . If $j = 1$ then $\ell_1 = \dots = \ell_{n-1} = 0$, $\ell_n = 1$, $f_{\star}(\sigma, \theta) \equiv f_{\star}^{(2)}(\sigma, \theta)$ and

$$f_{\star}^{(2)}(\sigma, \theta) = -\log \Gamma(\theta + n) + \log \Gamma(\theta + 1) + \log \Gamma(n - \sigma) - \log \Gamma(1 - \sigma).$$

In this case we get $\hat{\sigma} = \delta$ and $\hat{\theta} = -\delta + \epsilon$.

3.4 Steps 5 and 6

The estimate of the discovery probability at the next iteration, $\hat{U}_{s+0}(0)$, is computed as described in Sect. 2, Eq 4. If its value is lower than p_{\star} and $s \geq m_{\star}$ the algorithm stops, otherwise the next iteration $s + 1$ is performed (if $s + 1 > M_{\star}$ the algorithm stops). The algorithm takes a decision only if $s \geq m_{\star}$ because we want to avoid that the estimates $(\hat{\sigma}_s, \hat{\theta}_s)$ and consequently $\hat{U}_{s+0}(0)$ be based on too small sample sizes. We suggest using m_{\star} at least equal to 50.

Table 1 Test cases description; ID is the test case number, d is the number of factors, p is the number of levels of each factor, \mathcal{M} is the model and Method is the algorithm that is used for D -optimal design generation. The notation $x_1 | \dots | x_d @ h$ means that all the k -factor interactions, $k \leq h$, are included in the model \mathcal{M} ; $k = 1$ refers to main effects

ID	d	p	\mathcal{M}	Method
1	7	2	$x_1 \dots x_7 @ 2$	Exchange
2	7	2	$x_1 \dots x_7 @ 2$	Fedorov
3	6	2	$x_1 \dots x_6 @ 1$	Exchange
4	6	2	$x_1 \dots x_6 @ 1$	Fedorov
5	5	3	$x_1 \dots x_5 @ 2$	Exchange

Table 2 Number ℓ_r of D optimal designs that have found r times, $r = 1, \dots, 487$; only $\ell_r \neq 0$ are shown

r	1	2	3	4	5	6	9	10	11	12	14	15	16	17	20	35	39	40	45	T
ℓ_r	48	17	8	10	1	4	1	1	1	1	2	2	1	1	1	1	1	1	1	103

4 Computational study

We show how the methodology works using the test cases summarized in Table 1. We point out that all the test cases consider the problem of finding saturated D -optimal designs.

4.1 Test cases 1 and 2

Let us consider 7 factors, each with 2 levels, and the model that contains the overall mean, the main effects and all the 2-factor interactions for a total of $1 + 7 + 21 = 29$ degrees of freedom. We search for *saturated* D -optimal designs, that is, D -optimal designs that contain 29 points.

In test case 1, we use Proc Optex [SAS Institute, Inc. \(2010\)](#) with the exchange method, which is its default search method. With the default setting, the algorithm starts from 10 initial randomly chosen designs providing 10 D -optimal designs. We consider the design with the highest value of the D -efficiency of the 10 optimal designs as the optimal design found by the algorithm.

Setting the seed that is used for the random generation of the initial designs at 6789, the best of the 10 optimal designs, that we denote by \mathcal{F}_1 , has $D_{\mathcal{F}_1} = 9.0911E39$ and $E_{\mathcal{F}_1}^D = 82.3162$.

Now we run the procedure above with $M_\star = 1,000$, $m_\star = 50$ and $p_\star = 0.10$. After 487 runs, the estimate of the discovery probability at the next observation becomes lower than $p_\star = 0.10$ and the algorithm stops ($\hat{U}_{487+0}(0) \approx 0.099$). We find 103 different species of local D -optimal designs. All these designs are not isomorphic (Proposition 1). The maximum (minimum) value of D -efficiency is 85.6265 (78.9605) and it has been found 9 times (1 time). The statistics ℓ_r , $r = 1, \dots, 487$ are shown in Table 2.

The estimates of the discovery probability at the next iteration $\hat{U}_{s+0}(0)$ as a function of the iteration s are plotted in Figure 1. The increase of the sample size seems clearly to stabilize the discovery probability estimates.

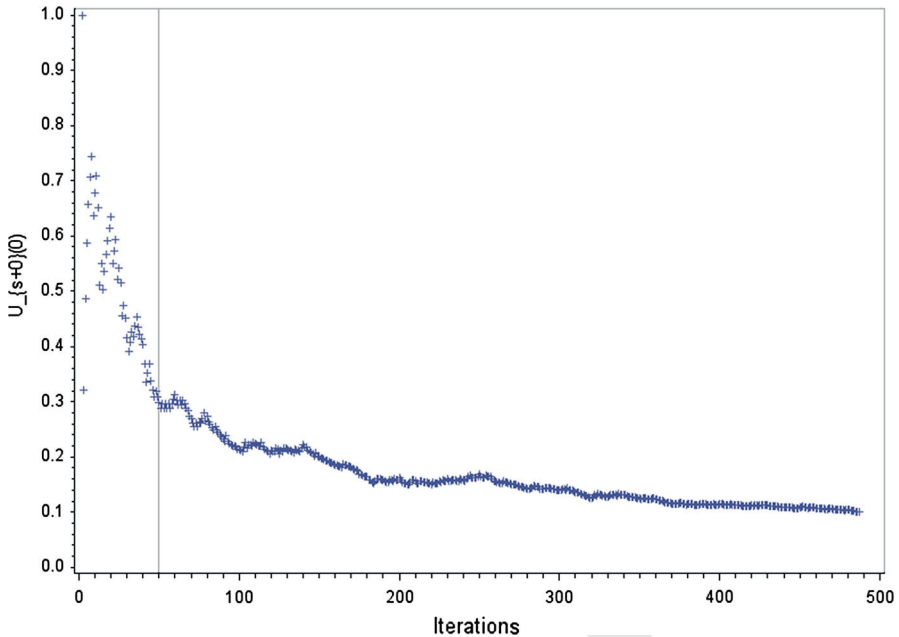


Fig. 1 Estimate of the discovery probability at the next iteration $\hat{U}_{s+0}(0)$ as a function of the iteration s . Test case 1, $M_\star = 1,000$, $m_\star = 50$ and $p_\star = 0.10$

325 We decide to continue the search for new species choosing $p_\star = 0.05$ and
 326 $M_\star = 2,000$. The latter value is chosen taking into account that using Eq. 5 we
 327 get $\hat{U}_{487+1000}(0) = 0.048$ and $\hat{U}_{487+2000}(0) = 0.034$. These supplementary runs are
 328 added to the previous ones.

329 After 1,252 supplementary runs the estimate of the discovery probability at the
 330 next observation becomes lower than 0.05, $\hat{U}_{1739+0}(0) \approx 0.0499$. After 1,252 +
 331 487 = 1,739 simulations we observe 191 different species of D -optimal designs. The
 332 maximum value of D -efficiency is still 85.6265, while the minimum is 78.1134.

333 In test case 2 we use the Fedorov algorithm, Fedorov (1972), that is considered more
 334 reliable, even if slower, than the exchange algorithm. We keep the standard setting for
 335 which, at each iteration, 10 local D -optimal designs are generated and the one among
 336 them that has the highest D -efficiency value is taken as the optimal design.

337 We choose 3456 as the initial seed. The first iteration provides an optimal design
 338 \mathcal{F}_1 with $E_{\mathcal{F}_1}^D = 82.7079$. Now we repeat the procedure with $M_\star = 1,000$ and $p_\star =$
 339 0.10. After only 18 iterations the estimate of the discovery probability at the next
 340 observation becomes less than 0.10, $\hat{U}_{18+0}(0) \approx 0.097$. But being $m_\star = 50$ the
 341 algorithm continues to iterate. It stops after 50 iterations, with the discovery probability
 342 approximately equal to 2% and with 4 designs. The maximum (minimum) value of
 343 D -efficiency is 83.9844 (82.4212). Thus we have empirical evidence that the Fedorov
 344 algorithm is more stable than the exchange algorithm. We observe that the best design
 345 found with the exchange algorithm, that has D -efficiency equal to 85.6265, is not
 346 found in this first sample. We were able to find it running the algorithm again with
 347 $M_\star = 1,000$ and $p_\star = 0.01$. In this case after 47 supplementary runs, 97 in total, we

348 find 5 designs and $\hat{U}_{97+0}(0) = 0.0099$. The maximum value of D -efficiency becomes
 349 85.6265. If we run the algorithm again with $M_\star = 2,000$ and $p_\star = 0.001$ after 1,009
 350 supplementary runs, 1,106 in total we find 8 designs and $\hat{U}_{1106+0}(0) = 0.00099$. The
 351 maximum (minimum) value of D -efficiency is 85.6265 (82.3622).

352 4.2 Test cases 3 and 4

353 Let us consider 6 factors, each with 2 levels, and the model that contains the overall
 354 mean and the main effects for a total of $1 + 6 = 7$ degrees of freedom. We search for
 355 D -optimal designs that contains 7 points.

356 In test case 3 we use the same D -optimal design generation method of test case 1
 357 (i.e. at each iteration the optimal design is the best design among ten optimal designs
 358 found using the exchange method starting from ten initial randomly chosen designs).
 359 We run our algorithm setting the initial seed to 6116 and with $M_\star = 1,000$, $m_\star = 50$
 360 and $p_\star = 0.10$. After 50 iterations the algorithm stops with $\hat{U}_{50+0}(0) \approx 0.005$ and
 361 has found two classes of designs with D -efficiency equal to 84.91 and 87.92.

362 After 50 iterations the estimate of the discovery probability at the next iteration is
 363 already quite small, around 0.5% but we decide to run a maximum of $M_\star = 1,000$
 364 supplementary runs setting $p_\star = 0.0001$. After a total of 1,050 runs the algorithm
 365 stops. No designs with different D -optimal efficiency are found. The estimate of the
 366 discovery probability at the next iteration is $\hat{U}_{1050+0}(0) \approx 0.00014$.

367 In test case 4 we replace the exchange algorithm with the Fedorov method. After 50
 368 iterations we find only one class of optimal designs with D -efficiency equal to 87.92.
 369 The estimate of the discovery probability at the next iteration is $\hat{U}_{51+0}(0) \approx 0.00002$.

370 4.3 Test case 5

371 Let us now consider 5 factors, each with 3 levels, and the model that contains the overall
 372 mean, the main effects and all the 2-factor interactions for a total of $1 + 5 \cdot 2 + 10 \cdot 4 = 51$
 373 degrees of freedom. We search for D -optimal designs that contain 51 points.

374 If we run the algorithm with the setting of test case 1 or 3 ($M_\star = 1,000$, $m_\star = 50$,
 375 $p_\star = 0.10$, method=exchange) after 1,000 iterations we find $\hat{U}_{1000+0}(0) \approx 95\%$
 376 and 978 different D -optimal designs with efficiencies ranging between 25.4333 and
 377 28.6677.

378 In this case it can be appropriate to round the efficiency values not to four decimal
 379 digits (as in all the previous test cases) but to one decimal digit. If we adopt this
 380 rounding, after 3,600 iterations we get 33 different designs with D -efficiencies ranging
 381 between a minimum of 25.2 to a maximum of 28.7. The estimate of the discovery
 382 probability at the next iteration is $\hat{U}_{3600+0}(0) \approx 0.0014$ ($\hat{U}_{3600+1000}(0) \approx 0.0011$).

383 4.4 Practical considerations and guidelines

384 After s iterations the algorithm provides $\hat{U}_{s+0}(0)$, an estimate of the probability of
 385 discovery of a new value of efficiency at the next iteration. This value is useful to assess
 386 how far the set of optimal designs that has been collected up to the iteration s is repre-

387 representative of *all* the optimal designs \mathcal{A}_α^ϕ . $1 - \hat{U}_{s+0}(0)$ estimates the *sample coverage*, that
 388 is the proportion of distinct species present in the sample observed with respect to the
 389 total population. If the probability of discovery is judged to be still too high or, equiv-
 390 alently, the sample coverage too low, the user can decide to run the algorithm again.

391 From a practical point of view, the ideal situation is when the computational budget
 392 of the user, M_\star , is large enough to reach a very high coverage, let us say of around
 393 99.9% (i.e. $\hat{U}_{s+0}(0) \approx 0.1\%$). In practice, in this ideal case, the algorithm can be run
 394 for the first time with $p_\star = 0.001$, $M_\star = 1,000$ and $m_\star = 50$. If after the first 1,000
 395 iterations the estimate of the discovery probability at the next iteration has not gone
 396 under p_\star the algorithm can be run again to obtain supplementary observations. The
 397 value of M_\star can be chosen computing the estimates of the discovery probability at
 398 the $(1000 + m + 1)$ -th observation with different values m of the size of an additional
 399 unobserved sample size.

400 In any case, even if M_\star is not large enough to make the estimate of the discovery
 401 probability at the next iteration as small as desired, the user has valuable information
 402 about the sample coverage that has been reached so far. Again, an estimate of the dis-
 403 covery probability at the next $(n + m + 1)$ -th observation can be computed. It is useful
 404 to consider this estimate for some values of m , let us say $m = 1,000$ and $m = 2,000$,
 405 to make the decision to continue or stop the sampling.

406 It is important that the number of simulations is not too small to make the estimates
 407 of the discovery probabilities sufficiently stable. We chose to work with $m_\star = 50$. To
 408 support the choice of m_\star the plot of the estimate of the discovery probability $\hat{U}_{s+0}(0)$
 409 as function of the iteration s is useful (see Fig. 1).

410 The values of the efficiency must be rounded to avoid creating different species from
 411 numerical effects. Different values of rounding allow us to reduce or to enlarge the
 412 number of species of the population under study. This reflects the user's opinion regard-
 413 ing the difference between efficiency values that must be considered significant from a
 414 practical point of view. For example, at the initial stage of our exploration we can round
 415 the values of the efficiency to one decimal digit just to know their approximate range.
 416 Then in the next stages we can decide to run the algorithm with more decimal digits.

417 We ran the simulation study on a standard laptop (CPU Intel Core i7-2620M CPU
 418 2.70 GHz 2.70 GHz, RAM 8 Gb). To give an idea of the computational times required
 419 we report that the first stage of test case 1 (487 iterations, exchange method) needed
 420 around 387 seconds (1.26 second per iteration) while the the first stage of test case 2
 421 (50 iterations, Fedorov method) needed around 27 seconds (1.85 second per iteration).

422 5 Conclusion

423 Given an optimality criterion ϕ , the problem of ϕ -optimal design generation has been
 424 addressed. A methodology to support the decision whether to continue or stop the
 425 search for optimal designs has been developed. It combines recent advances on dis-
 426 covery probability estimation, based on a Bayesian non parametric approach, Favaro
 427 et al. (2012), with well known methods for optimal design generation.

428 In principle, this methodology could be applied to any discrete optimisation prob-
 429 lem. This topic will be part of future research.

A software code, written in SAS, that makes use of the Proc Optex procedure, has been developed.

It should also be pointed out that the innovative side of this work lies in using sampling stopping rules to improve the generation process of optimal designs. In this paper we used the Bayesian updating of the discovery probability as proposed by Favaro et al. (2012) but other approaches could be adopted. For example Christen and Nakamura (2003) developed an algorithm based on backward induction. It makes use of a utility function based on the number of new species to be observed and the effort saved from the maximum horizon for accumulation. It could be part of future research using this algorithm in the context of optimal designs generation.

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