A KRIGING-HDMR COMBINED WITH ADAPTIVE PROPORTIONAL SAMPLING FOR MULTI-PARAMETER APPROXIMATE MODELING

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ABSTRACT

High-dimensional complex multi-parameter problems are commonly in engineering, while the traditional approximate modeling is limited to low or medium dimensional problems, which cannot overcome the dimensional disaster and greatly reduce the modelling accuracy with the increase of design parameter space. Therefore, this paper combined Kriging with Cut-HDMR, proposed a developed Kriging-HDMR method based on adaptive proportional sampling strategy, and made full use of Kriging's own interpolation prediction advantages and corresponding errors to improve modelling efficiency. Three numerical tests including coupling test, high-dimensional nonlinear test and calculation cost test were used to verify the effectiveness of the algorithm, and compared with the traditional Kriging-HDMR and RBF-HDMR in R^2, REEA and RMEA measuring the approximate accuracy, results show that the improved Kriging-HDMR greatly reduces the sampling cost and avoids falling into local optima. In addition, at the same calculation cost, when the scale coefficient is 1/2, Kriging-HDMR has higher global approximate accuracy and stronger algorithm robustness, while preserving the hierarchical characteristics of coupling between input variables.

KEYWORDS

Multiparameter decoupling, Kriging-HDMR, Surrogate model, Global approximation

1. INTRODUCTION

Approximate modelling technique is an integrated application of experimental design, mathematical statistics and optimization techniques. Its basic principle is to construct a mathematical model which meets the accuracy requirements to simulate the input-output relationship of problems to replace the complex and time-consuming original model, so as to realize the purpose of accelerating design and improving analysis efficiency [1]. It is precisely because of the excellent characteristics of approximate modeling, such as repeatability and foresight, that it has aroused strong research interest of researchers at home and abroad [2-3]. However, most of the existing approximation models, such as Radial Basis Function (RBF) and Kriging surrogate model, are limited to solve low or medium dimensional problems, and cannot overcome the "curse of dimensionality", that is, the amount of computation will increase exponentially with the increase of dimensionality [4]. As one of the methods to solve high-dimensional problems, High Dimensional Model Representation (HDMR) has a complete mathematical expression form, which can clarify the coupling characteristics between input variables, and can be used to construct a global surrogate model [5]. The model complexity is

reduced from exponential growth to polynomial growth, which has a very broad application prospect.

HDMR is a multi-parameter decoupling technique, which was first proposed by the Russian scholar Sobol [6] in 1993. Rabitz [7] and Li [8] subsequently perfected the theory: for any integrable function in the field, there is a unique HDMR expression. This lays the foundation for establishing approximate model methods in high-dimensional problems. Later Rabitz [7] elaborated on the basic composition principle and characteristics of HDMR and pointed out two variants of HDMR: ANOVA-HDMR and Cut-HDMR, and also pointed out that HDMR can be well applied to global uncertainty analysis and risk assessment. In other practical applications of HDMR, Omer and Rabitz [9] applied HDMR to sensitivity analysis and timing analysis. Banerjee [10] applied HDMR to the design optimization of black-box models with uncertain parameters. Shan and Wang [11] described the construction method of RBF-HDMR in detail and applied it to high-dimensional complex black-box problems. Based on RBF-HDMR, researchers have carried out a series of studies, most of which focus on replacing RBF with other surrogate models to construct the meta-model of Cut-HDMR. In 2011, H. Wang et al. [12-13] proposed a high-dimensional model representation method based on Moving Least Square (MLS-HDMR), and applied the DIRECT method to the sampling when constructing the meta-surrogate model. In the same year, L. Tang [14-15] proposed Kriging-HDMR to preliminary apply to nonlinear engineering problems. In 2013, L. Li [16] introduced Least Squares Support Vector Machine (LS-SVM) into Cut-HDMR, proposing SVM-HDMR, and gave the corresponding adaptive sampling and model construction algorithm. In 2015, H. Qiu et al. [17] enhanced AERBF-HDMR method, which can automatically explore the degree of linear/nonlinear relationship and correlation of design variables without prior information. Due to the completeness of the representation theory of high-dimensional models and the convenience of constructing models, the surrogate model method based on HDMR has attracted extensive attention from academic and engineering communities in recent years.

Up to now, HMDR multi-parameter decoupling technology is not mature to solve high-dimensional complex problems: a) Traditional surrogate models are often limited to medium or low dimensional problems, and it is difficult to achieve high-precision modeling and poor generalization in high-dimensional problems. b) The design variables of engineering optimization problems often have complex cross-coupling relationships. However, the existing approximate model techniques lack parameter decoupling mechanisms, and cannot well identify the coupling between design variables, which is difficult to reflect the essence of the problem. c)For problems with high nonlinearity, traditional surrogate models are easy to fall into local optimum, the efficiency and global search performance of this kind of methods depend heavily on the accuracy of the near-similar model, so it is difficult to find the true global optimal solution. In general, the key to the construction of the surrogate model-based Cut-HDMR method is the selection of the metamodel and the corresponding adaptive sequence sampling method. In order to achieve high precision global approximation for high-dimensional complex problems and use the minimum cost to construct sample points as much as possible, this paper developed Kriging-HDMR method which combining Kriging and Cut-HDMR based on adaptive proportional sampling strategy. Compared with original Kriging-HDMR and RBF-HDMR, it passed the coupling test and had the significant improvement in computational cost and approximation accuracy.

The reminder of this paper is organized as follows: In section 2, the basic principle of HDMR and the construction method of its derivative form Cut-HDMR are introduced. In section 3, A Kriging-HDMR combining with adaptive proportional sampling for multi-parameter approximate modeling was proposed. In section 4, numerical experiments are carried out, including three experiments of coupling test, high-dimensional nonlinear function test and computational cost test. The approximation accuracy was measured in R^2, REEA and RMEA with the traditional

Kriging and RBF-HDMR surrogate models. Finally, the conclusion and outlook of this paper are given in Section 5.

2. HDMR FOR MULTI-PARAMETER DECOUPLING TECHNOLOGY

2.1. High Dimensional Model Representation

High Dimensional Model Representation (HDMR) decomposes a multi-parameter function into the sum of several functions with fewer parameters according to the coupling between variables. Set $\Omega^p = \left\{ \left(x_1, x_2, \ldots, x_p \right) \mid 0 \leq x_i \leq 1, i = 1, 2, \ldots, p \right\}$ be a subset of the p dimensional Euclidean space R^p, and $X = \left\{ f \mid f(\mathbf{x}) = f\left(x_1, x_2, \ldots, x_p \right), \mathbf{x} \in \Omega^p \right\}$ is the linear space of all functions defined on Ω^p. Define a measure $\boldsymbol{\mu}$ on Ω^p such that:

$$
\begin{cases}
d\boldsymbol{\mu} = d\boldsymbol{\mu}\left(x_1, x_2, \ldots, x_p \right) = \prod_p^{i=1} d\mu_i\left(x_i \right) \\
\int_{\Omega^i} d\mu_i\left(x_i \right) = 1 (i = 1, 2, \ldots, p) \\
d\boldsymbol{\mu}(\mathbf{x}) = \mathbf{g}(\mathbf{x}) dx = \prod_p^{i=1} g_i\left(x_i \right) dx_i
\end{cases}
\tag{1}
$$

The inner product on the linear space X can be defined by the measure $\boldsymbol{\mu}$ as follows:

$$
\langle f, h \rangle = \int_{\Omega^p} f(\mathbf{x}) h(\mathbf{x}) d\boldsymbol{\mu}(\mathbf{x}), \quad f(\mathbf{x}), h(\mathbf{x}) \in X
\tag{2}
$$

It can be shown from [7-8] that X can be the direct sum of the specific subspaces, i.e.

$$
X = X_0 \oplus \sum_{1 \leq i \ll p} X_i \oplus \sum_{1 \leq i < j \leq p} X_{ij} \oplus \cdots \sum_{1 \leq i_1 < i_2 < \ldots, i_j \leq p} X_{i_1 i_2, \ldots, i_j} \oplus X_{12, \cdots, p}.
\tag{3}
$$

Based on the above theoretical, HDMR is described as follows: the output response corresponding to the input variable $\mathbf{x} = \left[x_1, x_2, \ldots, x_p \right]^T$ in the p dimensional design space is $f(\mathbf{x})$, and the mapping relationship between them is expressed as:

$$
\begin{aligned}
f(\mathbf{x}) = f_0 + \sum_{i=1}^{p} f_i\left(x_i \right) + \sum_{1 \leq i < j \leq p}^{p} f_{ij}\left(x_i, x_j \right) + \sum_{1 \leq i < j < k \leq p}^{p} f_{ijk}\left(x_i, x_j, x_k \right) + \cdots \\
+ \sum_{1 \leq i_1 < \cdots < i_l \leq p}^{p} f_{i_1 i_2 \cdots i_l}\left(x_{i_1}, x_{i_2}, \cdots, x_{i_l} \right) + \cdots + f_{12 \cdots p}\left(x_1, x_2, \cdots, x_p \right)
\end{aligned}
\tag{4}
$$

where, f_0 represents a zero-order tuple term and is a constant term; $f_i\left(x_i \right)$ is the influence of variable x_i on the output response $f(\mathbf{x})$ when acting alone, which is called a first-order tuple term, also called an uncoupled term. $f_{ij}\left(x_i, x_j \right)$ is the influence of x_i and x_j coupling on the output response, which is called the second-order coupling term. $f_{12 \cdots p}\left(x_1, x_2, \cdots, x_p \right)$ is the influence on the output response $f(\mathbf{x})$ when all input variables act together in coupling. HDMR

reveals a hierarchy of couplings between input variables, each of which has a specific mathematical meaning.

2.2. Cut-HDMR

There are two main forms of HDMR: ANOVA-HDMR and Cut-HDMR. The former is mainly used for sensitivity analysis and determination of key design variables, while the latter is widely used to predict high-dimensional valuable black-box problems due to its high computational efficiency and no need to calculate gradient information [17]. Cut-HDMR also comes in many forms, such as Kriging-HDMR, RBF-HDMR, SVR-HDMR and MLS-HDMR.

Cut-HDMR mainly includes three core technical which are test design method, construction basis function and Cut-HDMR decoupling models. The high-dimensional modal expression of $f(X)$ is written as the sum of a series of lines, planes and hyperplanes passing through the point cut-center point $x_0 = (c_1, c_2, c_3, ..., c_p)$. In Cut-HDMR, turn the measure μ in (1) into:

$$d\boldsymbol{\mu}(\mathbf{x}) = \prod_p^{i=1} \delta(x_i - x_0) dx_i \tag{5}$$

where $x_0 = (c_1, c_2, c_3, ..., c_p)$ is a specified point in Ω^p, also known as the cut-center point. $\delta(\bullet)$ is the Dirac function formed from:

$$\delta(x) = \begin{cases} 0 & (x \neq 0) \\ \infty & (x = 0) \end{cases} \text{ and } \int_{-\infty}^{\infty} \delta(x) \, dx = 1 \tag{6}$$

So, Cut-HDMR is expanded as follows:

$$f_0 = f(x_0)$$
$$f_i(x_i) = f(x_i, x_0^i) - f_0$$
$$f_{ij}(x_i, x_j) = f(x_i, x_j, x_0^{ij}) - f_i(x_i) - f_i(x_j) - f_0 \tag{7}$$
$$\cdots$$
$$f_{12...p}(x_1, x_2, ..., x_p) = f(x) - \sum_i f_i(x_i) - \sum_{ij} f_{ij}(x_i, x_j) - ... f_0$$

Where, f_0 is the output value of the cut-center point in the original model. (x_i, x_0^i) is $(c_1, c_2, ..., c_{i-1}, x_i, c_{i+1}, ..., c_p)$, whose entries are known and equal to the values corresponding to the x_0, except for the independent variable x_i. In this vein, the central basis of higher order terms has a similar meaning. Therefore, each first-order member function $f_i(x_i)$ is computed according to the cut-center point in the direction of the corresponding x_i line. Each second-order component $f_{ij}(x_i, x_j)$ is evaluated on the plane formed by the corresponding x_i and x_j according to the cut-center, as shown in Figure 1:
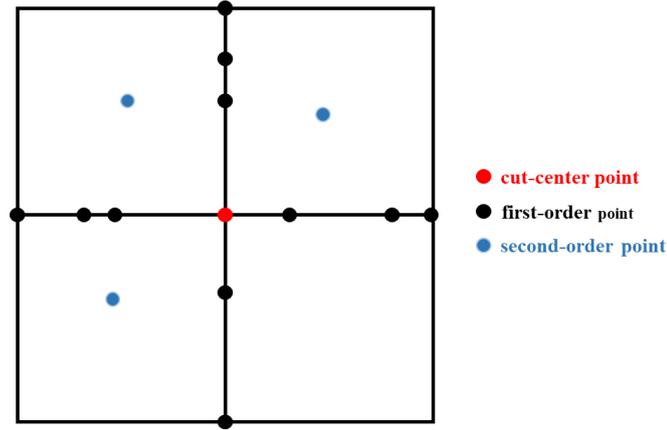
Figure 1. Cut-HDMR sampling distribution diagram

3. KRIGING-HDMR COMBINING WITH ADAPTIVE PROPORTIONAL SAMPLING

In this section, Kriging-HDMR is used as a technical framework to construct an approximate modeling method for high-dimensional nonlinear problems. The biggest advantage of Kriging-HDMR is that it can clarify the coupling characteristics of input parameters, and reduce the complexity of constructing the model from exponential growth to polynomial growth. For most practical engineering problems, the uncoupled term and the lower order coupling term are sensitive to the response function. Therefore, the developing Kriging-HDMR constructed in this paper takes into account the second-order coupling terms, and the form is as follows:

$$f(\boldsymbol{x}) \approx f_0 + \overbrace{\sum_{i=1}^{P}\left(\mathbf{f}^{i^T}(x_i)\boldsymbol{\beta}^i + z^i(x_i)\right)}^{fisrt-order\ uncoupled\ term} + \overbrace{\sum_{1\le i < j \le p}\left(\boldsymbol{f}^{ij^T}(x_i,x_j)\boldsymbol{\beta}^{ij} + z^{ij}(x_i,x_j)\right)}^{second-order\ coupling\ term} + ... + \qquad (8)$$
$$\underbrace{\phantom{\sum_{i=1}^{P}\left(\mathbf{f}^{i^T}(x_i)\boldsymbol{\beta}^i + z^i(x_i)\right) + \sum_{1\le i < j \le p}\left(\boldsymbol{f}^{ij^T}(x_i,x_j)\boldsymbol{\beta}^{ij} + z^{ij}(x_i,x_j)\right)}}_{Kriging\ surrogate\ model}$$

that is:

$$f(\boldsymbol{x}) \approx f_0 + \sum_{i=1}^{p}\hat{f}_i(x_i) + \sum_{1\le i < j \le p}^{p}\hat{f}_{ij}(x_i,x_j) \qquad (9)$$

Among it, the term representation with ^ is calculated by the Kriging-surrogate model.

The flow chart of Kriging-HDMR approximate modeling combined with adaptive proportional sampling is shown in Figure 2, and the construction process is as follows:
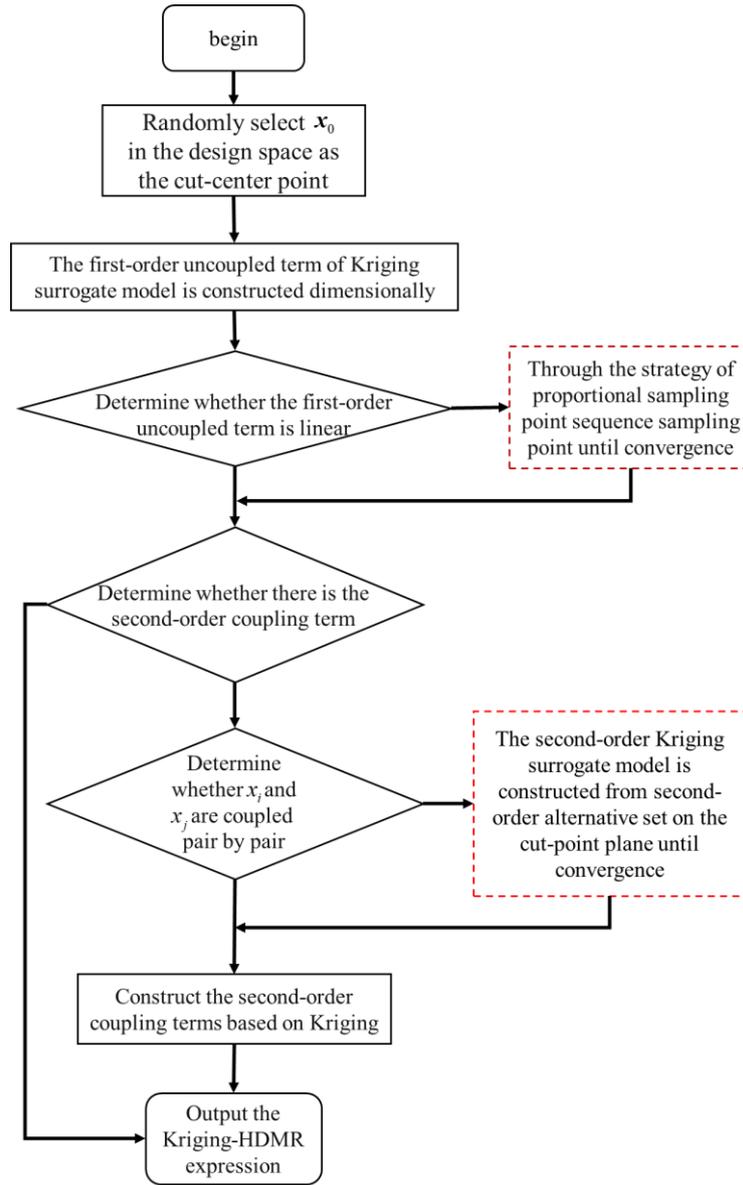
Figure 2. Flow chart of Kriging-HDMR based on adaptive proportional sampling

1) Take an arbitrary point $x_0 = (c_1, c_2, c_3, ..., c_p)$ as the cut-center point. We then compute the response of the true output function at x_0 to get f_0.

2) Construct Kriging models consisting of first-order uncoupled terms dimensionally. The points of the first-order uncoupled term $f_i(x_i) = f\left(\left[c_1, c_2, ..., c_{i-1}, x_i, c_{i+1}.., c_p\right]^T\right) - f_0$ are arranged on the value interval of the single variable $x_i\left(\left[c_1, c_2, ..., c_{i-1}, x_i, c_{i+1}.., c_p\right]^T\right)$. That is, two sample points are randomly generated in the upper and lower boundary neighborhood of the i-th dimension design variable, and their target response values are calculated:

$$f\left(x_{i\_lower}\right) = f\left(\left[c_1, c_2, ..., c_{i-1}, x_{i\_lower}, c_{i+1} .., c_p\right]^T\right) - f_0;$$

$$f\left(x_{i\_upper}\right) = f\left(\left[c_1, c_2, ..., c_{i-1}, x_{i\_upper}, c_{i+1} .., c_p\right]^T\right) - f_0.$$

Then $\hat{f}_i\left(x_i\right)$ is constructed by constructing the corresponding Kriging surrogate model using the above two sampling points.

3) Determine whether $f_i\left(x_i\right)$ is linear or non-linear. If the initial Kriging-surrogate model $\hat{f}_i\left(x_i\right)$ passes through the cut-center point x_0, it is regarded as a linear term and the construction terminates. Otherwise, $f_i\left(x_i\right)$ is a nonlinear term and proceed to the next step.

4) Construct nonlinear first-order terms based on adaptive proportional sampling strategy. The cut-center point x_0 is first added to the set of constructed sample set. Then the existing first-order constructed sample set $X_i = \left\{x_{i\_lower}, x_0, x_{i\_upper} ...\right\}$ is arranged in ascending order to obtain $\tilde{X}_i = \left\{r_{i1}, r_{i2}, ..., r_{in}\right\}$, where $r_{i1} = x_{i\_lower}$ and so on. Find two adjacent points r_{ik} and $r_{i(k+1)}$ so that their corresponding first-order Kriging corresponding deviation is the maximum interval: $\Delta f = \max\limits_{k=1,2,...,n}\left(\left|f_i\left(r_{i(k+1)}\right) - f_i\left(r_{ik}\right)\right|\right)$. Then a new sample point x_{inew} as:

$$x_{inew} = Cr_{ik} + (1-C)r_{i(k+1)}$$

is inserted in the above range. $C\left(0 < C < 1\right)$ is the scale coefficient in the scale sampling. By changing the value of the scale coefficient, a series of first-order structured sample points with different distributions can be obtained. If $\left|\dfrac{\hat{f}\left(x_i\right) - f\left(x_i\right)}{f\left(x_i\right)}\right| \leq \varepsilon$ is satisfied or the number of sample points constructed by the first-order term is greater than a given threshold, the construction of the first-order uncoupled term $\hat{f}_i\left(x_i\right)$ terminates. Otherwise, continue using the adaptive proportional sampling to construct $\hat{f}_i\left(x_i\right)$ until the convergence criterion is satisfied.

5) Iterate through steps (2) to (4) until all first-order uncoupled terms (for each $i = 1, 2, ..., p$) are constructed.

6) Determine whether there is a second-order coupling term in the model. Construct a new sample point $x_e = \left[x_{e_1}, x_{e_2}, ..., x_{e_i}, ..., x_{e_j}, ..., x_{e_p}\right]^T$ and without loss of generality, one of the sample point components x_{i_lower} and $(i = 1, ..., p)$ used in the construction of the first-order uncoupled term is randomly chosen as the i-th dimensional component x_{e_i} of the new sample point. Within the error range allowed by the accuracy criterion, if $f\left(x_e\right) = f_0 + \sum\limits_{i=1}^{p}\hat{f}_i\left(x_{e_i}\right)$ is satisfied, it is considered that there is no second-order

coupling term in the model, and the construction process is finished. Otherwise, proceed to step (7).

7) Construct the second-order coupling terms. Firstly, the existence of second-order terms on the cutting plane composed of each dimension variable is judged one by one. If so, the grid lattice formed by the sample points set of first-order construction on the corresponding cutting line on the two-dimensional plane is used for the construction of second-order terms. Specifically, the sample $\left(x_{e_i}, x_{e_j}, x_0^{ij}\right) = \left[c_1, c_2, ..., x_{e_i}, .., x_{e_j}, .., c_p\right]^T$ is randomly selected from the second-order alternative point set. Within the error range allowed by the precision criterion, if $f\left(x_{e_i}, x_{e_j}, x_0^{ij}\right) = f_0 + \hat{f}\left(x_{e_i}\right) + \hat{f}\left(x_{e_j}\right)$ $\left(1 \le i < j \le p\right)$, the input variables x_i and x_j are considered to be uncoupled or their coupling terms are invalid to the output response. Otherwise, it is considered that their coupling terms are valid for the output response, and Kriging second-order coupling terms are constructed with all the first-order constructed sample points $\left(x_i, x_0^i\right)$, $\left(x_j, x_0^j\right)$ and $\sum_{1 \le i < j \le p}^{p} \hat{f}_{ij}\left(x_i, x_j\right)$. Re-randomly select points from the second-order alternative set until all second-order variable combinations have been identified.

8) The high-order coupling function contributes little to the expression, thus Kriging-HDMR is constructed to the second-order coupling terms.

On one hand, Kriging-HDMR makes full use of the HDMR hierarchy to divide the problem domain into multiple subdomains and avoids the difficulty of high-dimensional modeling. On the other hand, it reveals the characteristics of design variables, including linearity and nonlinearity, coupling and global distribution, which can better reflect the global characteristics of the output function.

4. NUMERICAL COMPARISON TEST

4.1. Experimental Evaluation Index

In practical engineering application, the performance indexes of approximate models for high dimensional problems usually mainly consider the approximate accuracy and modeling efficiency of the models. In this paper, R^2, RAAE and RMAE are used to test the function approximation ability of the approximate model, and the computational efficiency was represented by sample points required for modeling.

Let $X_i \left(i = 1, 2, ..., s\right)$ be s test sample points in the design space. In order to obtain global and robust test results, s is set to a larger value, and all test sample points are randomly generated with uniform distribution on the design space.

a)   The judgment coefficient, R^2

$$R^2 = 1 - \frac{\sum_{i=1}^{s}\left(f\left(X_i\right) - \hat{f}\left(X_i\right)\right)^2}{\sum_{i=1}^{s}\left(f\left(X_i\right) - \bar{f}\right)^2}$$

Where, $f(X_i), \hat{f}(X_i), \overline{f}$ respectively represents the average value of the actual response value of the i-th test sample and the average value of s actual responses of the approximate model. The closer the value of R^2 is to 1, the more accurate the approximate model is.

b)   Relative Average Absolute Error, RAAE

$$RAAE = 1 - \frac{\sum_{s}^{i=1}\left|f(X_i) - \hat{f}(X_i)\right|}{s \cdot STD}$$

Where, $STD = \sqrt{\dfrac{1}{s-1}\sum_{s}^{i=1}\left(f(X_i) - \overline{f}\right)^2}$ is the standard deviation, and the higher the value of RAAE is, the higher the global accuracy of the approximate model will be.

c)   Relative Maximum Absolute Error, RMAE

$$RMAE = \frac{\max\left\{\left|f(f(X_i)) - \hat{f}(f(X_i))\right|, \ldots, \left|f(f(X_s)) - \hat{f}(f(X_s))\right|\right\}}{STD}$$

RMAE is a local index, which describes the error in a local domain where the accuracy of the approximate model is relatively poor. Therefore, the smaller the RMAE value, the better.

4.2. Three Numerical Tests and Results

4.2.1. Test for Coupling

As one of the strengths of Kriging-HDMR is that the coupling characteristic between input variables can be clearly defined, then the coupling test function of this time selected the non-convex Rosenbrock function proposed by Howard Harry Rosenbrock in 1960 to test the performance of the algorithm, and the form is selected by test function 1:

$$f(x) = \sum_{i=1}^{8}\left[100\left(x_{i+1} - x_i^2\right)^2 + (x_i - 1)^2\right], -2 \leq x \leq 2.$$

We used Kriging-HDMR based on adaptive proportional sampling to construct the approximate model. The scale coefficient $C = \{0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9\}$ were tested for several times to compare the accuracy results, so as to judge the quantization accuracy of three indexes, namely coefficient R^2, RAAE and RMAE. The coupling test results are shown in Table 1, and precision results are shown in Figure 3 and Table 2:
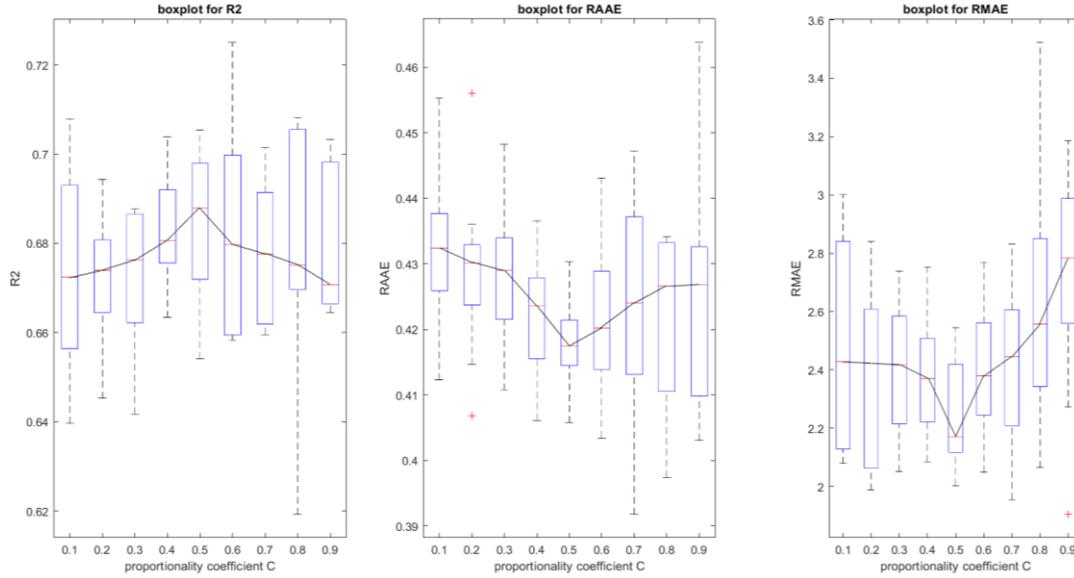
Figure 3. Box graph of precision results of 10 tests for Rosenbrock function

Table 1. Coupling test results   Table 2. The median results corresponding to figure 3

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9
x_1	1	1	0	0	0	0	0	0	0
x_2	1	1	1	0	0	0	0	0	0
x_3	0	1	1	1	0	0	0	0	0
x_4	0	0	1	1	1	0	0	0	0
x_5	0	0	0	1	1	1	0	0	0
x_6	0	0	0	0	1	1	1	0	0
x_7	0	0	0	0	0	1	1	1	0
x_8	0	0	0	0	0	0	1	1	1
x_9	0	0	0	0	0	0	0	1	1

C	R^2	RAAE	RMAE
0.1	0.67240	0.43240	2.42815
0.2	0.67390	0.43010	2.42060
0.3	0.67640	0.42895	2.41625
0.4	0.68065	0.42355	2.37005
0.5	**0.68785**	**0.41745**	**2.16925**
0.6	0.67975	0.42020	2.37945
0.7	0.67760	0.42405	2.44545
0.8	0.67515	0.42660	2.55645
0.9	0.67075	0.42685	2.78590

The results show that Kriging-HDMR based on the proportional sampling strategy passes the coupling test, and the coupling relationship between the variables of the Rosenbrock test function is correct. In addition, according to the box figure and corresponding result table of the accuracy results of 10 tests, it can be seen that when the proportion coefficient C=1/2, the performance is the best, and the closer the proportion coefficient is to the middle value 0.5, the better the approximate ability of the positive distribution trend. That is, the maximum R^2 is 0.68785, the RAAE and RMAE are 0.41745 and 2.16925 respectively, which are the smallest. Therefore, for the adaptive proportional sampling strategy, we default the maximum effect of the hyperparameter C=1/2, and there is no special explanation for the default value in the following tests.

4.2.2. Test for High-Dimensional Nonlinear Functions

This test mainly focuses on high-dimensional nonlinear functions, using Kriging-HDMR combined with Adaptive proportional sampling, which compares with similar algorithms as

Kriging, RBF-HDMR and Kriging-HDMR(unimproved using random sampling) by citing 4 test examples in literature [17]. The results are shown in Table 3:

i.   test fuction2: $f(X) = 100(x_1^2 - x_2)^2 + a_1^2 + a_3^2 + 90(x_3^2 - x_4) + 10.1(a_2^2 + a_4^2) + 19.8a_2a_4,$
$$where \ a_i = x_i - 1, i = 1,2,3,4$$

ii.   test fuction3: $f(X) = \sum_{i=1}^{10} x_i \left(c_i + \ln\left(\dfrac{x_i}{\sum_{k=1}^{10}(x_k)} \right) \right),$ where $\left(\begin{array}{l} c_{i=1,...,10} = -6.089, -17.164, -34.054, -5.914, -24.721, \\ -14.986, -24.100, -10.708, -26.662, -22.179. \end{array} \right)$;

iii.   test fuction4: $f(X) = x_1^2 + x_2^2 + x_1x_2 - 14x_1 - 16x_2 + (x_3 - 10)^2 + 4(x_4 - 5)^2 + (x_5 - 3)^2$
$$+ 2(x_6 - 1)^2 + 5x_7^2 + 7(x_8 - 11)^2 + +2(x_9 - 10)^2 + (x_{10} - 7)^2 + 45$$

iv.   test fuction5: $f(X) = (x_1 - 1)^2 + \sum_{16}^{i=2} i(2x_i^2 - x_{i-1})^2$

Table 3. High-dimensional nonlinear test results table

Test Function	Method	R^2	RAAE	RMAE
test fuction2(p=4) $x_i \in [-10,10], i = 1,2,3,4$	Kriging	0.8994	0.5007	0.6765
	RBF-HDMR	0.9937	0.0501	0.2766
	Kriging-HDMR-1	0.9967	0.0397	0.1997
	Kriging-HDMR-2	**0.9998**	**0.0255**	**0.1005**
test fuction3(p=10) $x_i \in [-5,5], i = 1,...,10$	Kriging	0.8665	0.1003	0.9980
	RBF-HDMR	0.9901	0.0740	0.5033
	Kriging-HDMR-1	0.9975	0.0344	0.3310
	Kriging-HDMR-2	**0.9999**	**0.0137**	**0.2563**
test fuction4(p=10) $x_i \in [-10,11], i = 1,...,10$	Kriging	0.8779	0.1024	0.9445
	RBF-HDMR	0.9935	0.0723	0.1974
	[a]Kriging-HDMR-1	0.9928	0.0708	0.2570
	[b]**Kriging-HDMR-2**	**0.9987**	**0.0473**	**0.1010**
test fuction5(p=16) $x_i \in [-5,5], i = 1,...,16$	Kriging	0.8340	0.3466	1.7890
	RBF-HDMR	0.9496	0.1714	1.3368
	Kriging-HDMR-1	0.9635	0.1457	1.0097
	Kriging-HDMR-2	**0.9778**	**0.1012**	**0.9887**

Note: [a]Kriging-HDMR-1 represents the original Kriging-HDMR approximate modeling method using the original random sampling; [b]Kriging-HDMR-2 represents the improved Kriging-HDMR modeling method using adaptive proportional sampling in this paper.

The results show that the performance of Kriging in high-dimensional nonlinear problems is obviously the worst of the combination methods. For RBF-HDMR and Kriging-HDMR, the performance in R^2 index is almost 1, and Kriging-HDMR is more prominent. The developed Kriging-HDMR global approximation error in RAAE and RMAE is also relatively small. This indicates that Kriging-HDMR based on adaptive proportional sampling strategy makes full use of the predictive response value difference information of the component Kriging surrogate models, which have wider applicability and stronger approximation ability to high-dimensional complex problems.

4.2.3. Test for Computational Cost

The test function4: $f(\boldsymbol{x}) = \sum_{i=1}^{p-1}\left[\left(x_i^2\right)^{\left(x_{i+1}^2+1\right)} + \left(x_{i+1}^2\right)^{\left(x_i^2+1\right)}\right], 0 \le x_i \le 1$ is used to prove the optimized performance of the improved Kriging-HDMR on the calculation cost. $p = 15, 25, 35$ and 8 sampling points were taken for each dimension in the test (meeting the expected error requirements). Table 4 lists the comparison of calculation costs of different levels.

Table 4. Test results for calculating cost

Dimension	Kriging-HDMR	Full second-order expansion of HDMR $1 + p(s-1) + \dfrac{p(p-1)}{2}(s-1)^2$ (polynomial)	Full factorial design s^p (exponential)
10	144	2276	$1.07*10^9$
15	234	5251	$3.52*10^{13}$
20	376	9451	$1.15*10^{18}$
25	534	14876	$3.78*10^{22}$
30	722	21526	$1.24*10^{27}$
35	997	29401	$4.01*10^{31}$

From the experimental results, it is proved that the number of samples required by Kriging-HDMR modeling increases polynomially with the increase of the dimension of the objective function, rather than the exponential increase of the traditional method, which greatly reduces the calculation cost.

5. CONCLUSIONS AND OUTLOOKS

Multi-parameter nonlinear optimization is a common problem in engineering. The bottleneck of traditional approximate model technology is that with the increase of design parameters, the number of sample points required for modeling will increase on a large scale, resulting in very low modeling efficiency. In this paper, the approximate modeling of high-dimensional complex multi-parameter problems is studied, and a Kriging-HDMR approximate modeling method based on adaptive proportional sampling is proposed, which greatly reduces the sampling cost and avoids falling into local optimal. In addition, at the same calculation cost, when the scale coefficient is 1/2, Kriging-HDMR has higher global approximate accuracy and stronger algorithm robustness, while preserving the hierarchical characteristics of coupling between input variables. The work done in this paper is only preliminary exploration and research, and there are still a lot of problems to be further studied. For example, the Kriging-HDMR approximate model technology proposed in this paper is mainly aimed at the case of low parameter coupling order. When the high- order coupling term is completely ignored, which may cause large errors. How to estimate the above errors correctly and add appropriate correction items to further improve the accuracy of the model is a problem that needs to be solved in the future.

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