Handling Ambiguous Inverse Problems by the Adaptive Genetic Strategy *hp*-HGS

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Abstract. We propose the new multi-deme, adaptive genetic strategy *hp*-HGS that allow solving ill posed parametric inverse problems that may posses multiple solutions. The strategy was obtained by combining *hp*-adaptive Finite Element Method with the Hierarchic Genetic Strategy. Its efficiency results from the coupled adaptation of the accuracy of solving optimization problem and the accuracy of *hp*-FEM direct problem solver. We present the simple L-shape domain benchmark that posses exactly two solutions. Test results show how the tuning of *hp*-HGS may affect on the number of solutions to be found. Moreover we discuss the artifacts that may appear by the particular setting of genetic operations.

1 Ambiguity of the Parametric Inverse Problems Solution

The inverse problems under consideration base on the particular class of direct problems:

$$\text{ess min}_{u \in u_V} \{E(d; u)\}, \quad (1)$$

where $E(d; u) = \frac{1}{2}b(d; u, u) - l(u)$ stands for the total energy of the modeled physical system, V is the proper Sobolev space shifted by the Dirichlet boundary condition. The form of functionals b, l depend of the physical phenomena (e.g. linear elasticity, heat conduction) and of their parameters $d \in \mathcal{D}$, where $\mathcal{D}$ is the regular compact in $\mathbb{R}^N$, $N < +\infty$. We assume, that the above problem is well posed in the sense of Hadamard and its solution $u \in V$ can be obtained as the limit of the sequence $\{u_{h,p}\} \subset V$ of solutions of finite dimensional problems obtained by the *hp*-adaptive Finite Element Method (*hp*-FEM) assuming $h \rightarrow 0$ and $p \rightarrow +\infty$ (see Demkowicz [5]).

The inverse problem under consideration leads to encountering the unknown parameter $\hat{d} \in \mathcal{D}$ while the energy $J(\hat{d}) = E(\hat{d}; u)$ of the exact solution $u \in V$ to (1) is known (e.g. it is measured during the laboratory test). Because the exact energy $J(d)$ is impossible to compute effectively for each $d \in \mathcal{D}$, we can only find the approximation $\hat{g} \in \mathcal{D}$ of the exact parameter $\hat{d} \in \mathcal{D}$ such that:

$$\lim_{h \rightarrow 0, p \rightarrow +\infty} |J_{h,p}(\hat{g}) - J(\hat{d})| \leq \lim_{h \rightarrow 0, p \rightarrow +\infty} |J_{h,p}(g) - J(\hat{d})| \quad \forall g \in \mathcal{D} \quad (2)$$

where $J_{h,p}(d) = E(d; u_{h,p})$ stands for the energy of the approximate solution $u_{h,p}$ obtained for the parameter d .

The inverse problem presented above is a kind of the global optimization one with the very costly objective $|J_{h,p}(g) - J(\hat{d})|$. The most frequent difficulty is caused by the ambiguity of its solution (multiple solutions) manifested as the objective multimodality. Moreover, the uncertainty of the mathematical model as well as the errors in the numerical objective evaluation caused, that not only the global minimizers, but also the local ones with the sufficiently low objective value may represent the solutions. A large variety of such problems in mechanics and other branches may be found in the literature. The good example was published by Cabib, Davini and Chong-Quing Ru [3] where the ambiguity of the global minimizer was mathematically proved.

The only way to solve such kind of problems is to find all local minimizers that satisfies the additional criterion (e.g. objective is lower then the assumed threshold). Niching genetic algorithms as well as multi start strategies were often applied as the robust methods for finding multiple minimizers (see e.g. [8], [9]). The adaptive strategies that can significantly decrease the number of objective calls are also highly appreciated (see e.g. [4]).

We propose the new strategy called *hp*-HGS composed of the adaptive numerical method *hp*-FEM (see Demkowicz [5], [6]) that allow very effective direct problem solving up to the assumed accuracy expressed by the energy error of the physical phenomenon and the multi-deme, Hierarchic Genetic Strategy HGS (see Schaefer, Kołodziej [10]) that allow economic global search with the adaptive accuracy in the parameters domain. The nature of HGS allow finding many local minimizers in parallel. The proper rule of scaling the error of solving direct problem vs. inverse problem error decreases the computational cost of the single objective call. The computational example show the *hp*-HGS behavior by solving the simple bimodal problem of heat conductivity identification. The parameter tuning as well as appearing of dangerous artifacts are discussed.

2 *hp*-HGS

The HGS introduced by Kołodziej and Schaefer (see e.g. [10], [11]) proceeds tree-structured, dynamically changing set of dependent demes. The depth of HGS tree is limited by $m < +\infty$. All demes work asynchronously and are synchronized by the message-passing mechanism if necessary. The evolution of each deme is governed by the separate instance of the Simple Genetic Algorithm (SGA) (see Vose [15]).

The low-order demes (closer to the root) perform more chaotic search with the lower accuracy, while the demes of higher order perform the more accurate, local search. The various search accuracy is obtained by the various encoding precision and by the different length binary strings as the genotypes in demes of different order. The unique deme of the first order (root) utilizes the shortest genotypes, while the leafs utilizes the longest ones. To obtain the search coherency for demes of different order the special kind of hierarchical, nested encoding is used. First

the densest mesh of phenotypes in $\mathcal{D}$ for the demes of m -th order is defined. Next the meshes for the lower order demes are recursively defined by selecting some nodes from the previous ones. The maximum diameter of the mesh δ_j associated with the demes of the order j determines the search accuracy at this level of the HGS tree. Of course $\delta_1 > \dots > \delta_m$.

Each deme expecting leaf-demes sprouts the new child-deme after the constant number of genetic epochs K called the *metaepoch*. The child-deme is activated in the promising region of the evolutionary landscape surrounding the best fitted individual distinguished from the parental deme at the end of the metaepoch.

HGS implements also two mechanisms that allow to reduce the search redundancy. The first one called *conditional sprouting* disable to sprout new deme in the region already occupied or explored by the brother-deme (another child-deme of the same order sprouted by the same parent). The second mechanism called *branch reduction* reduces the branches of the same order that perform the search in the common landscape region or in the region already explored.

Let us apply HGS for solving the inverse problem (2). The fitness function for the particular deme should be based on the energy error

$$e_{h,p}(g) = \left| J_{h,p}(g) - J(\hat{d}) \right| \quad (3)$$

computed by using hp -FEM which approximate the objective function of the global optimization problem (2) for the particular values of h and p . As previously, $\hat{d} \in \mathcal{D}$ denotes the exact parameter value and $J(\hat{d})$ the known, exact energy of the exact solution while $J_{h,p}(g)$ the approximated value of energy computed by hp -FEM with respect to the parameter value $g \in \mathcal{D}$ obtained from the HGS individuals' genotype.

Let us assume for a while that g represents the parameter value decoded from the genotype that appears in the HGS deme of the j -th order, $j \in \{1, \dots, m\}$. Using the Lemma 2 in [14] and the formula (8) in [12] that follow the regression of the error (3) while improving the hp -FEM approximation we obtain

$$e_{\frac{h}{2},p+1}(g) \leq \|u_{\frac{h}{2},p+1}(g) - u_{h,p}(g)\|_E^2 + \|u(g) - u_{h,p}(g)\|_E^2 + L|g - \hat{d}|. \quad (4)$$

The left-hand-side $e_{\frac{h}{2},p+1}(g) = \left| J_{\frac{h}{2},p+1}(g) - J(\hat{d}) \right|$ stands for the energy error while the first right-hand-side component $err_{FEM}(g) = \|u_{\frac{h}{2},p+1}(g) - u_{h,p}(g)\|_E^2$ is the relative error decrement in the single hp -FEM step (see Demkowicz [5]). Moreover L stands for the Lipschitz constants of the functional J and $|g - \hat{d}|$ is the error of the inverse problem solution that characterizes the individuals belonging to the HGS demes of the j -th order. It is easy to observe, that $|g - \hat{d}|$ corresponds to δ_j . The above formula shows, that the error of the energy evaluation over the fine FEM mesh is restricted by the relative FEM error on the coarse FEM mesh solution with respect to the fine mesh solution plus the absolute FEM error over the coarse FEM mesh plus the accuracy of the proper HGS branch.

The main idea of hp -HGS is to adjust dynamically the accuracy of the objective computation to the particular value of the parameter g encoded in the

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1. if ( $j = 1$ ) then
2.   initialize the root deme;
3. end if
4.  $t \leftarrow 0$ ;
5. repeat
6.   if (global_stop_condition received) then
7.     STOP;
8.   end if
9.   for ( $i \in P^t$ ) do
10.    solve the direct problem for  $g = \text{code}(i)$  on the coarse and fine FEM meshes;
11.    compute  $\text{err}_{FEM}(g)$ ;
12.    while ( $\text{err}_{FEM}(g) > \text{Ratio} * \delta_j$ ) do
13.      execute one step of hp adaptivity;
14.      solve the problem on the new coarse and fine FEM meshes;
15.      compute  $\text{err}_{FEM}(g)$ ;
16.    end while;
17.    compute fitness  $f_j(i)$  using the FEM mesh finally established;
18.  end for
19.  if ( $j > 1$ ) then
20.    compute the phenotypes' average and send it to the parental deme;
21.    if (branch_stop_condition( $P^t$ )) then
22.      STOP;
23.    end if
24.  end if
25.  if ( $((t \bmod K) = 0) \wedge (j < m)$ ) then
26.    distinguish the best fitted individual  $x$  from deme  $P^t$ ;
27.    if ( $\neg \text{children\_comparison}(x)$ ) then
28.      sprout;
29.    end if
30.  end if
31.  perform proportional selection, obtaining multiset of parents;
32.  perform SGA genetic operations on the multiset of parents;
33.   $t \leftarrow t + 1$ ;
34. until (false)

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Algorithm 1. Pseudo-code of the j -th order deme P in the *hp*-HGS tree

individuals' genotype as well as for the inverse problem error that characterizes the current HGS branch. It may be obtained by balancing the components of the FEM error given by the right hand side of the formula (4), assuming δ_j as the accuracy of inverse problem solving by the branch of j -th order. We will perform then the *hp*-adaptation of the FEM solution of the direct problem while the quantity $\text{err}_{FEM}/\delta_j$ is greater then the assumed *Ratio*, which stands for the parameter of this strategy. The value of the parameter *Ratio* corresponds to the Lipschitz constant L , because two first components of the right-hand-side of (4) asymptotically vanish as a consequence of the *hp*-FEM convergence.

Notice, that no matter how the fitness of the individual i is computed by iterative process of the hp -FEM adaptation, the fitness function f_j is well defined for all individuals in branches of j -th order (it is not a random variable).

The draft of the single hp -HGS deme activity is stressed in the pseudo-code Algorithm 2. The function *branch_stop_condition*(P) returns *true* if it detects the lack of evolution progress of the current deme P . The separate module continuously checks whether the satisfactory solution was found or hp -HGS could not find more local extremes. If yes, the *global_stop_condition* signal is send to all computing demes. The *conditional sprouting* mechanism is implemented as follows. Each branch excepting root computes the average of its phenotypes and send it to its parental deme. These values are analyzed by the *children_comparison*(x) procedure and compared with the phenotype of the best fitted individual x distinguished from the parental deme. This procedure returns *true* if x is sufficiently close to the existing child-demes. The *branch reduction* mechanism is omitted in Algorithm 2 for the sake of simplicity.

3 Sample Bimodal Inverse Problem

The inverse problem under consideration is originated from the classical L-shape domain direct problem, a model academic problem formulated in [1], [2], to test the convergence of the p and hp adaptive algorithms. The direct L-shape domain problem consists in computing the temperature distribution over the L-shape domain, presented in Figure 1 with fixed zero temperature in the internal part of the boundary, and the Neumann boundary condition prescribing the heat transfer on the external boundary. There is a single singularity in the central point of the domain, where the gradient of temperature $\|\nabla u\|$ goes to infinity, so the accurate numerical solution requires a sequence of adaptations in the direction of the central point.

The strong formulation of the direct problem consists in finding the temperature distribution $u \in C^2(\mathbb{R}^2)$ such that

$$\nabla \cdot K \nabla u = 0 \quad \text{in } \Omega \subset \mathbb{R}^2 \quad (5)$$

Fig. 1. The L-shape domain problem

with boundary conditions

$$u = 0 \text{ on } \Gamma_D, \quad \frac{\partial u}{\partial n} = \chi = r^{\frac{3}{2}} \sin^{\frac{3}{2}} \left(\theta + \frac{\pi}{2} \right) \text{ on } \Gamma_N \quad (6)$$

with n being the unit normal outward to $\partial\Omega$ vector, and (r, θ) the radial system of coordinates with the origin point O (see Figure 1). K is the heat transfer coefficient, that takes the constant values K_1, K_2, K_3 over three parts of the domain, as illustrated in Figure 1.

The strong formulation (5) – (6) is transformed to the weak one: Find $u \in V = \{v \in L^2(\Omega); \int_{\Omega} \|v\|^2 + \|\nabla v\|^2 dx < +\infty, tr(v) = 0 \text{ on } \Gamma_D\}$ such that:

$$b(d; u, v) = l(v) \quad \forall v \in V; \quad b(d; u, v) = \int_{\Omega} K uv dx, \quad l(v) = \int_{\Gamma_N} \chi v dS \quad (7)$$

where $d = (K_1, K_2, K_3) \in \mathcal{D} = [0, 3]^3 \subset \mathbb{R}^3$ is the vector of parameters.

The benchmark inverse problem is formulated in the following way: Find values of the heat transfer coefficients $\hat{g} \in \mathcal{D}$ that satisfy (2). The energy of the "exact" solution, was computed as $J_{h,p}(\hat{d})$, where $\hat{d} = (0.1, 1.5, 2.9)$ are the assumed values of the heat transfer coefficients. In order to obtain the energy $J_{h,p}(\hat{d}) = \int_{\Omega} \|u\|^2 + \|\nabla u\|^2 dx$ close to the $J(\hat{d})$ the L-shape domain problem was computed once with the very high relative accuracy 10^{-5} by using the self-adaptive hp -FEM code.

Because both boundary conditions are symmetric with respect to the domain geometry (e.g. with respect to the axis $\theta = \pi/4$) then the parameter vector $\hat{d}' = (2.9, 1.5, 0.1)$ gives the same energy as $\hat{d}$, so the inverse problem (2) has two solutions in this case.

4 Test Results

We applied the three level's hp -HGS algorithm for solving inverse problem described in previous section. Because of the high computational cost of the accurate fitness evaluation, we decide to set *Ratio* to 900. Each metaepoch contains only three epochs. The next step of tuning the algorithm was to choose the mutation and crossing rates on each level. In order to do it properly we analyze the standard deviation of phenotypes for different values of the binary mutation rate (see Table 1). The mutation rate should decrease from the root to the leafs in order to increase the search locality in higher tree levels. From the other side, the standard deviation of the phenotypes obtained by the mutation has to be greater then the search accuracy δ_j on each level j in the hp -HGS tree in order to assure the enough search efficiency. The first choice was 0.3 for the crossing rate on each level of hp -HGS tree, and the mutation rates 0.05, 0.035, 0.005 for the root, the branches and leafs respectively. Many tests show that such setting allow to find only one solution to the inverse problem, mostly because of the small diversity of the root and the branches. The corrected setting of the mutation and crossing rates as well as other hp -HGS parameters are contained in Table 2. We pre-define the number of meataepoch as the stopping condition of our algorithm.

Table 1. Standard deviations of phenotypes for various mutation rates tested for all levels of the *hp*-HGS tree

Mutation rate	level 1	leve 2	level 3
0.5	1.54	1.51	1.51
0.2	1.29	1.19	1.21
0.1	0.85	0.91	0.83
0.035	0.49	0.55	0.56
0.025	0.4	0.53	0.55
0.01	0.31	0.23	0.25
0.005	0.24	0.18	0.11

Table 2. Final parameters of the *hp*-HGS tree applied by solving the sample inverse problem

	level 1	level 2	level 3
Code length	9	18	27
δ_j	0.375	0.047	0.006
Population size	50	12	8
Crossing rate	0.7	0.5	0.2
Mutation rate	0.5	0.1	0.01

Table 3. Leaves statistics obtained for the 5 selected *hp*-HGS settings

	test 1	test 2	test 3	test 4	test 5
number of leafs	21	21	10	21	21
err_{fit}	1.29	3.67	0.74	0.29	0.71
min $eucl_1$	0.65	0.62	2.02	0.22	0.89
min $eucl_2$	1.42	0.93	0.21	1.29	0.68
aver err_{fit}	30,38	98,63	230,81	179,33	66,48
aver $eucl_1$	0,98	1,28	2,02	1,16	1,6
aver $eucl_2$	2,03	1,69	0,9	1,33	0,89

The Table 3 shows the result of five selected runs of *hp*-HGS algorithm with the final parameters. The $\min eucl_1$ and $\min eucl_2$ mean the smallest euclidean distance between the computed solutions and the first exact solution $\hat{d} = (0.1, 1.5, 2.9)$ and the second exact solution $\hat{d}' = (2.9, 1.5, 0.1)$ respectively. The values $\text{aver } eucl_1$, $\text{aver } eucl_2$ are the averages of the euclidean distance between the best solutions found by leafs, which are in the attractor of the proper exact solution.

Perhaps the best result gave tests number two and five. In these cases both extremes were found by the separate leafs. In the test number one there are also both solutions found, but the second with much worst accuracy. It is also visible in the average distance between computed and real solutions. The same situation appears in the test number four. Because of the shorter assumed computational period in the third test, there were only about the half leafs than in others runs. It would be a reason, why the algorithm detected only one solution in this case.

In the case of multimodal problems the culmination of individuals may be located not only in the basins of attractions of global or local extremes. It may appear out of them when two solutions are linked to each other through mountain ridges with shallow saddle and the expected distance of the offspring from the parent is above half of the distance between these solutions. Such artifact looking like the optimum found was described by Karcz-Duleba [7] and called *evolutionary channel*. Such phenomenon appears in about 15% of our tests. In these tests at least two leafs found both exact solution with the accuracy comparable to those presented in tests number two and five. Moreover, the point laying in the half way between two solutions were encountered as the solution by the other single leaf. This was probably caused by the unfortunate setting of the mixing parameters that results in the standard deviation of the phenotypes 1.6, almost the half of the distance between exact solutions, which is equal to 3.96. The flat shape of the fitness between two solutions and the assumed (by setting large *Ratio*) moderate accuracy of the *hp*-FEM caused that the fitness value at the artifacts could not be used to discard them from the set of potential solutions. The only way to eliminate the artifacts is to take into account their rare appearance in comparison to the right solutions of the inverse problem.

5 Conclusions

- The main difficulties in solving inverse parametric problems are caused by their ill posedness, in particular by the solution ambiguity, the low stability (sensitivity for the numerical errors) and high computational cost of the objective evaluation. The sophisticated global optimization strategies can be applied in order to find multiple solutions, keeping the memory and computational costs at the acceptable level.
- The proposed *hp*-HGS strategy is well suited for solving ambiguous inverse problems, because of its global search possibilities (local, parallel search controlled by the deme hierarchy). It is confirmed by the test results for the simple bimodal benchmark. Its well asymptotic properties can be also verified mathematically (see [13]).

- The *hp*-HGS strategy offers two ways to decrease the computational and memory costs. Firstly it is obtained by decreasing of the number of the objective calls by using the adaptation of the inverse problem accuracy (HGS strategy). Secondly, the cost of the direct problem solution which is necessary for fitness evaluation is decreased by the proper scaling of the FEM error using the *hp* adaptation technique.
- The parameters of *hp*-HGS have to be carefully tuned. The genetic mixing (mutation with crossover) has to be intensive enough in the higher levels in order to ensure the sufficient diversity of the root and high order branches. The standard deviation of mixing in leafs has to be correlated with the maximum search accuracy. Moreover, it needs to be "desynchronized" with the fitness periodicity (it should be significantly less than the half of the distance between each pair of solutions) in order to avoid artifacts that may be recognized as a solutions.
- No matter how SGA with the binary encoding is sometimes criticized as a tool for solving optimization problems in the continuous domains, it is used in each branch of the first version of *hp*-HGS mainly because the theoretical results that characterize its asymptotic behavior are available. We plan to design the next version of *hp*-HGS which will be based on the hierarchic genetic strategy with the real number encoding (see [11], [16]). Moreover the much broader testing program will be performed in order to evaluate the *hp*-HGS particular behaviors statistics and in order to confirm its advantages in solving inverse problems of the considered type.

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