

Hierarchic Genetic Search with α -Stable Mutation

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Abstract. The paper analyzes the performance improvement imposed by the application of α -stable probability distributions to the mutation operator of the Hierarchic Genetic Strategy (HGS), in solving ill-conditioned, multimodal global optimization problems in continuous domains. The performed experiments range from standard benchmarks (Rastrigin and multi-peak Gaussian) to an advanced inverse parametric problem of the logging measurement inversion, associated with the oil and gas resource investigation. The obtained results show that the application of α -stable mutation can first of all decrease the total computational cost. The second advantage over the HGS with the standard, normal mutation consists in finding much more well-fitted individuals at the highest-accuracy HGS level located in attraction basins of local and global fitness minimizers. It might allow us to find more minimizers by performing local convex searches started from that points. It also delivers more information about the attraction basins of the minimizers, which can be helpful in their stability analysis.

Keywords: Multi-deme genetic search · α -stable mutation · Hierarchic genetic strategy · Inverse problems

1 Motivation

A simplified and general definition of a class of parametric inverse problems for Partial Differential Equations (PDEs) can be formulated as follows.

Find parameter vector $\hat{\omega} \in \mathcal{D} \subset \mathbb{R}^n, n \geq 1$, being a solution to a global optimization problem

$$\arg \min_{\omega \in \mathcal{D}} \{f(u_o, u(\omega)) : A(u(\omega)) = 0\}, \quad (1)$$

where A is a *forward problem operator*, $u(\omega) \in U$ is the forward solution corresponding to ω , $u_o \in \mathcal{O}$ is an observation (typically a measured quantity related somehow to the forward solution) and $f(\mathcal{O}, U) \rightarrow \mathbb{R}_+$ is a *misfit functional*.

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Typically, U is a Sobolev space and $A : U \rightarrow U'$ is a differential operator between U and its conjugate space (see for details *e.g.* [1] and references therein).

Solving inverse parametric problems plays a crucial role in many branches of science and technology, such as the Structural Health Monitoring [2,3], the oil and gas resource investigation [4], the tumor diagnosis [5], etc.

Problems (1) are usually ill-conditioned: unstable (small changes in parameters or observations result in huge misfit variations) or otherwise almost insensitive in some parameters, multimodal with a misfit valleys or plateaus or/and non-smooth in some subdomains. One of possible ways to overcome this obstacles is the misfit regularization (see *e.g.* [6]) typically making the problem smooth, unimodal and globally convex. This approach is often very effective, but its usefulness decreases when the misfit is inherently multimodal (see *e.g.* [7]) and has vast, almost flat regions (plateaus). In such cases the careless regularization may result in locating artifacts instead of true solutions.

Another, more advanced way is to find all “essential” minimizers to (1) and to evaluate roughly their stability. Such results give more information to the experts in the area allowing them to make right further decisions. Among methods of this type you can find stochastic [8] or multi-start [9] ones. Unfortunately, standard approaches of this kind exhibit unacceptable computational cost, mainly because of the high complexity of the forward problem numerical solution necessary for each misfit evaluation. All the above argument is a motivation to look for new, exceptionally economical strategies, skilfully joining the exhaustive exploration of large domains with the detailed investigation of the central parts of local minimizer attraction basins.

Such a combination is a fundamental idea of the *Hierarchic Genetic Strategy* (HGS). The strategy develops dynamically a tree of demes (sub-populations), among which the root deme performs the most broad, superficial search, while the demes located deeper in the tree search more locally and more accurately (see [10,11] for details). The strategy is further extended in *hp*-HGS and *hp*-HMS (see [4,7,12–15] and references therein) which combine hierarchic evolutionary search with the *hp*-adaptive Finite Element Method (*hp*-FEM) [16] for the misfit evaluation. They offer the advantageous, additional computational cost reduction, by the common scaling of *hp*-FEM error according to the accuracy of the inverse search at various branches of the deme tree.

A crucial role in each genetic strategy is played by the mutation operator, that influences greatly the structure of offspring populations. The heart of the operator is a selected probability distribution used to sample new individuals. A common choice for real number encoded individuals is the normal (Gaussian) distribution. However, it has recently been criticized because of its strong non-isotropy (dependence on the coordinate system setting), a pathological behavior near the parental individual (the “wall effect”) as well as the lack of flexibility in density configuration in large domains (see *e.g.* [17]). An advantageous alternative for the normal mutation is the *stable mutation*, which uses various types of stable probability distributions [18] for an offspring sampling. The first study of applying stable distributions in genetic computations was performed by Rudolph [19]. An extended concept of applying α -stable distributions, their

isotropic and non-isotropic instances and the flexible adaptation to the necessary exploration/exploitation ratio was studied by A. Obuchowicz (see e.g. [17, 20]).

The authors apply the α -stable distributions in the HGS strategy as the mutation and sprouting operators. We show the additional speedup obtained by the improved mutation at the various levels of the deme tree. Benchmark tests were used to study the influence of α -stable distribution configuration on the HGS performance. A computational example of DC logging measurement inversion by *hp*-HGS shows the impact of the α -stable mutation in solving a real-life engineering inverse problem.

2 Hierarchic Genetic Strategy with Adaptive Misfit Evaluation

The Hierarchic Genetic Strategy (HGS) was introduced by Kołodziej and Schaefer in [10]. It produces a tree-structured set of concurrently evolving demes (see Fig. 1). The structure of the tree may be dynamically changed, while its depth is bounded by $m < +\infty$. First, the *root deme* is created which performs a chaotic search with low accuracy. Demes at consecutive levels search with higher and higher accuracy. The maximum, target accuracy is used by leaves. After K genetic epochs (a *metaepoch*), each non-leaf deme selects its best fitted individual and *sprouts* a child-deme in the neighboring region of this individual in the admissible domain \mathcal{D} . Sprouting new demes is repeated concurrently after each metaepoch. Two important mechanisms are applied in order to avoid the search redundancy: *conditional sprouting* and *branch reduction*. Roughly saying, they both prevent multiple demes from exploring the same region (see [14] for details).

We use the real-number encoding version of HGS [11], in which a genotype is a vector of floating point numbers. In order to introduce a sequence of increasing genetic spaces for subsequent orders of branches, we use scaling coefficients $+\infty > \eta_1 \geq \eta_2 \geq \dots \geq \eta_m = 1$, so that the genetic space at i -th level is defined as $\prod_{i=1}^N [0, \frac{b_i - a_i}{\eta_i}] \subset \mathbb{R}^N$, where $a_i, b_i; a_i < b_i$ are the lower and upper bounds for i -th decision variable. The genetic space for leaves is of the same size as the admissible domain $\mathcal{D} = \prod_{i=1}^N [a_i, b_i] \subset \mathbb{R}^N$ allowing for most accurate search.

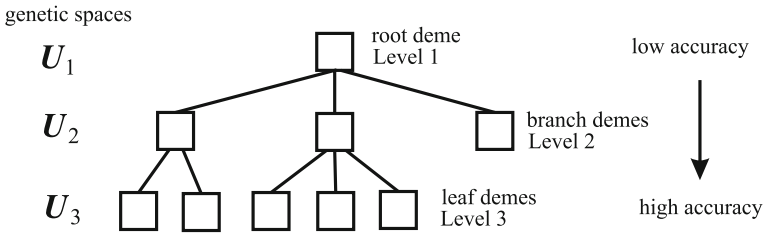


Fig. 1. HGS evolutionary population tree

If a search accuracy in leaves equals δ_m , then the accuracy in higher order demes will be reduced to $\delta_j = \eta_j \delta_m$, for $j = 1, \dots, m - 1$.

The evolution in demes (except for the root) is stopped when the search progress is unsatisfactory (mean misfit does not decrease). The whole strategy is stopped when the satisfactory number of well fitted individuals has already been found by HGS leaves.

Asymptotic analysis of HGS was studied in [10]. In particular, the asymptotic guarantee of success was proved as well as the cost decrement ratio with respect to the single population algorithm with the finest encoding, represented in HGS leaves. Analogous features of *hp*-HGS were studied in [21].

3 Stable Phenotypic Mutation

A random variable X has stable distribution [22], if it satisfies the following condition:

$$\forall a, b > 0 \quad \exists c > 0 \quad \exists d \in \mathbb{R} \quad aX_1 + bX_2 \stackrel{d}{=} cX + d, \quad (2)$$

where X_1 and X_2 are independent copies of X and $\stackrel{d}{=}$ means that the random variables on both sides are identically distributed. We will use later a more convenient observation on characteristic functions of stable random variables (see *e.g.* [22]).

$$\varphi(k) = \begin{cases} \exp(-\sigma^\alpha |k|^\alpha \{1 - i\beta \text{sign}(k) \tan(-\frac{\pi\alpha}{2})\} + i\mu k), & \alpha \neq 1, \\ \exp(-\sigma |k| \{1 + i\frac{2}{\pi} \beta \text{sign}(k) \ln |k|\} + i\mu k), & \alpha = 1. \end{cases} \quad (3)$$

Parameter $\alpha \in (0, 2]$, called the *stability index*, defines the distribution concentration and influences the existence of moments in the following way [22]:

$$E(X) < +\infty \text{ for } \alpha > 1 \text{ and } \text{Var}(X) = +\infty \text{ for } 0 < \alpha < 2. \quad (4)$$

$\mu \in \mathbb{R}$ is the shift parameter, whereas β , called the skewness parameter, is a measure of the distribution's asymmetry. We will denote by $S_\alpha(\sigma, \beta, \mu)$ the probability distribution with the characteristic function (3). Unfortunately, the density function of $S_\alpha(\sigma, \beta, \mu)$ is not explicitly given except for three cases: Gaussian ($\alpha = 2, \beta = 0$), Cauchy ($\alpha = 1, \beta = 0$), and Lévy ($\alpha = \frac{1}{2}, \beta = 1$) distributions. Nevertheless, there is a possibility to simulate α -stable distribution using algorithms described in *e.g.* [20].

The mutation operation in floating-point phenotypic Evolutionary Algorithms (EAs) is performed by the addition of a random vector to current attributes of an individual. In order to define the mutation with a stable distribution we may replace the multivariate normally-distributed random vector $\mathcal{N}(\mathbf{0}, \sigma^2 \mathbf{I}_n)$ with the following random vector:

$$\mathbf{X} = [X_i \sim S_\alpha(\sigma, 0, 0) | i = 1, 2, \dots, n]^T. \quad (5)$$

A big disadvantage of the obtained multivariate distribution is the lack of the spherical symmetry in case $\alpha < 2$ [22]. New individuals prefer directions along axes of Cartesian coordinate system, which is highly undesired. To avoid it, we may use sub-Gaussian stable random vector defined in [22]. In that paper it was also proved that this vector has multivariate isotropic stable distribution

$$\mathbf{X} = A^{1/2}\mathbf{G} \quad (6)$$

where $A \sim S_{\alpha/2}((\cos(\frac{\pi\alpha}{4}))^{2/\alpha}, 1, 0)$ and $\mathbf{G} \sim \mathcal{N}(\mathbf{0}, \sigma^2 \mathbf{I}_n)$ are independent.

The lack of moments' existence is of great significance in evolutionary process. If we take into consideration a numerical representation of real numbers, the normal mutation ($\alpha = 2$) has strict boundaries, where the mutated successor may be generated. Obviously this fact imposes a restriction on the explored area. For $\alpha \leq 1$ distribution $S_{\alpha}(\sigma, 0, 0)$ does not have the expected value. As a consequence one can observe a significant rise in the probability of macro-mutations, i.e. the creation of children far away from parents. This can be a desirable feature, because the exploratory abilities of the strategy become enormous. On the other hand, there is a danger that the algorithm gets too chaotic. In the sequel we shall always take $\mu = \beta = 0$, hence using symmetric stable distribution $S_{\alpha}(\sigma, 0, 0)$ in the mutation operator.

Let us consider λ realizations of the random variable X with probability distribution $S_{\alpha}(\sigma, 0, 0)$ ordered in the sequence $X_{1:\lambda} < X_{2:\lambda} < \dots < X_{\lambda:\lambda}$. The following condition is satisfied (see Theorem 2 in [23]):

$$X_{i:\lambda} \text{ has } k^{\text{th}} \text{ moment} \Leftrightarrow k - \alpha(\lambda - i + 1) < 0. \quad (7)$$

Condition (7) implies that the random variable $X_{1:\lambda}$ has the expected value if $\lambda > \frac{1}{\alpha}$. It means that the local convergence of an evolutionary algorithm endowed with α -stable mutation can be quite effective provided the number of the best parent's descendants is large enough (i.e. greater than $\frac{1}{\alpha}$).

Another problem is that the most probable distance from the mutated point to the its offspring grows with the number of dimensions. This effect known as "dead surrounding" is limited for the isotropic stable mutation with lower α [24].

4 Benchmark Tests

First, we have compared the behavior of HGS with the stable mutation for different values of α and σ . That includes normal mutation cases for $\alpha = 2$. Both performed tests represent typical difficulties (multimodality, large plateaus) appearing in solving inverse parametric problems. In each test the computation was stopped when a given budget was reached. As far, as each fitness call has the same computational cost, we can accept the simplest budget definition as a number of benchmark function evaluations.

We have set the depth of the HGS tree to two levels. Leaves always use normal distribution with $\sigma = 0.1$ to perform mutation. The root applies different stable mutations with all combinations of $\alpha \in \{0.5, 1, 1.5, 2.0\}$ ($\alpha = 2$ means normal

Table 1. Parameters of HGS for all benchmark tests

	3 dimensions	10 dimensions
Root population	30	100
Leaf population	6	20
Budget (fitness evaluations no.)	3000	10000
Metaepoch length	2	2
Mutation rate	0.5	0.5

mutation), and $\sigma \in \{0.4, 0.7, 1.4\}$. The HGS parameters collected in Table 1 were set according to our best experience (see e.g. [7, 10–12, 25]). In order to highlight the mutation impact we did not use the crossover.

We have compared the best fitness values obtained in tests for the three-dimensional Rastrigin function translated upwards by 1 in domain $[-5, 5]^3$, with the global minimum value 1.0. Each test was performed 80 times, and the averages of best fitness found are presented in Table 2. The distributions of best fitness found for $\sigma = 0.4$ are presented in Fig. 2. The distributions for other values of σ are similar.

Table 2. Average best fitness result in tests on Rastrigin function.

	$\sigma = 0.4$	$\sigma = 0.7$	$\sigma = 1.4$
$\alpha = 2.0$ (normal mutation)	1.179	1.225	1.254
$\alpha = 1.5$	1.178	1.204	1.236
$\alpha = 1.0$	1.197	1.220	1.250
$\alpha = 0.5$	1.213	1.191	1.214

Another desired property of a global optimization search is the exploration ability, which can be measured as a number of global and local minimizers found by the strategy. A series of tests was performed for the following benchmark functions:

1. three-dimensional sum of three Gaussian functions,
2. three-dimensional sum of three Gaussian functions and the Rastrigin function,
3. as above, 10-dimensional case with ten Gaussian functions.

The search domain was set to $[-5, 5]^N$. In the second and third benchmark of this group, each Gaussian function has minima much smaller than the Rastrigin component. The tests were executed 80 times for 3-dimensional cases and 40 times for 10-dimensional case. In every run we counted the number of Gaussians' extrema reached by HGS. The average results are presented in Table 3.

Results of both series of tests (see Tables 2 and 3) show that the stable mutation with $\alpha = 1.5$ or 1.0 applied to the HGS root delivers a good compromise between exploration and exploitation performance, and it is slightly better than the normal mutation ($\alpha = 2.0$). Applying stable mutation in HGS leaves does not improve its performance (results of such tests are not presented in this paper).

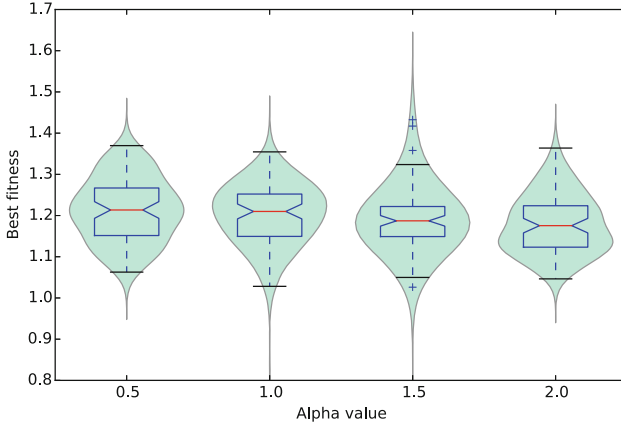


Fig. 2. Violin plot of best fitness obtained in Rastrigin test for $\sigma = 0.4$.

5 Applying *hp*-HGS with Stable Mutation for DC Logging Measurement Inversion

The hydrocarbon (oil and gas) exploration might be performed by the estimation of subsurface electrical properties. Logging instruments equipped with several transmitter electrodes move along a borehole axis emitting and receiving signals. We consider two types of problems: forward and inverse. The former consists of finding the voltage for a certain position of transmitter and receiver electrodes knowing resistivities of formation layers. A series of forward problems for consecutive positions of electrodes provides a vector of solutions called *logging curve*. The inverse problem consists in searching resistivities of formation layers for a

Table 3. Average number of extremes found in benchmark tests: A - sum of three Gaussian functions; B - as A with addition of Rastrigin function; C - as B, 10-dimensional case

A				B			
	$\sigma = 0.4$	$\sigma = 0.7$	$\sigma = 1.4$		$\sigma = 0.4$	$\sigma = 0.7$	$\sigma = 1.4$
$\alpha = 2.0$ (normal)	0.1375	0.2625	0.325	$\alpha = 2.0$ (normal)	0.1375	0.2625	0.325
$\alpha = 1.5$	0.1	0.3	0.425	$\alpha = 1.5$	0.1	0.3	0.425
$\alpha = 1.0$	0.1375	0.3	0.4	$\alpha = 1.0$	0.1375	0.3	0.4
$\alpha = 0.5$	0.2	0.25	0.35	$\alpha = 0.5$	0.2	0.25	0.35

C			
	$\sigma = 0.4$	$\sigma = 0.7$	$\sigma = 1.4$
$\alpha = 2.0$ (normal)	0.65	1.8	3.075
$\alpha = 1.5$	0.9	1.475	2.425
$\alpha = 1.0$	0.95	1.2	1.825
$\alpha = 0.5$	0.575	1.1	1.375

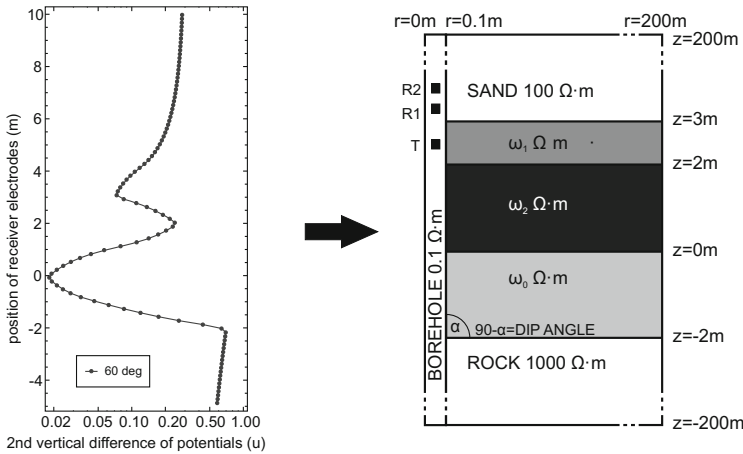


Fig. 3. Finding resistivities of formation layers from a given logging curve. T, R1 and R2 are the position of transmitter and two receivers respectively, z - depth of a consecutive layers and r - the radial coordinate.

given reference logging curve. It was formulated as a global optimization problem with the misfit computed as the square of the Euclidean distance between the computed logging curve and the reference one, usually obtained from the measurements. In our case, logging devices operate at very low frequencies (close to zero), which can be modeled as zero-frequency, direct current (DC).

We refer to [14] for details of direct and inverse DC problems, goal oriented hp -FEM application and proof of the dependency between the inverse error and the relative hp -FEM error, necessary for their economic scaling in the hp -HGS strategy.

We have searched for the values of three ground layer resistivities $\omega_0, \omega_1, \omega_2$ belonging to the cube $[0.1, 10^3]^3$ in our case study (see Fig. 3). The reference values are $\omega_0 = 1 \Omega \cdot m$, $\omega_1 = 5 \Omega \cdot m$ and $\omega_2 = 20 \Omega \cdot m$. As in [14], to provide a more thorough search for the parameter values around 1 we transformed the original domain with the following mapping $\mathbb{R}^3 \ni x \mapsto [\log_{10}(x_i) + 1]_{i=1,2,3} \in \mathbb{R}^3$, which resulted in the cube $[0, 6]^3$.

The parameters of HGS with the normal as well as with the α -stable mutation are summarized in Table 4. These are the same values as in [14], except for α and σ parameters for stable distribution. For the root population, the mutation with $\alpha = 0.5$ was used, because its heavy tail was supposed to enhance the exploration ability. For the intermediate level $\alpha = 1.5$ was chosen, which provided the best results in the benchmark tests. The leaves are focused on the exploitation, so the normal mutation with a small σ was applied.

The HGS with the normal mutation found 5 well-fitted points with the misfit value below 0.1 (see Table 5), while the HGS with α -stable mutation performed in the root deme found 16 points of the same quality (see Table 6).

Table 4. Parameters of HGS with the normal and stable mutation.

	Root	Intermediate level	Leaves
Population size	12	6	4
Mutation probability	0.1	0.01	0.001
Mutation σ	Normal: 1.0, stable: 0.7	0.2	0.01
Mutation α	Normal: 2.0, stable: 0.5	Normal: 2.0, stable: 1.5	2.0
Crossover probability	0.5	0.5	0.5
Crossover mean	0.5	0.5	0.5
Crossover std. dev.	0.01	0.01	0.01
Sprout std. dev.	0.1	0.01	
Sprout min. distance	0.5	0.2	
Sprout max. value	2	0.5	
Encoding scale (η)	16384	128	1
Ratio	265	13557	694136

Table 5. Results of the HGS with the normal mutation.

	ω_0	ω_1	ω_2	<i>misfit</i>
Point 1	1.436	5.081	64.404	0.0123941038654
Point 2	0.955	7.895	33995.309	0.0155211450748
Point 3	1.003	2.287	491.275	0.0309955725861
Point 4	0.410	9.422	409.705	0.0788856673271
Point 5	0.429	1.441	13317.938	0.0998952955352

The logging curves corresponding to the seven best found points with misfits below 0.03 are presented in Fig. 4. The curves have been also compared to the exact logging curve, drawn with the shade line.

By analyzing the log files we have estimated computational budget T_b of *hp*-HGS with the normal and the stable mutation. Now fitness evaluation has a different computational cost at each *hp*-HGS level because the variable accuracy, so it is most convenient to define budget as the total serial execution time. For the normal mutation the budget is equal to 6206 min, while for stable mutation it is equal to 4597 min. It is the amount of time spent on solving the DC problem on a single workstation with quad cores, where all the calls of *hp*-FEM were serial, but the *hp*-FEM code itself utilized four cores for each computation. It can be estimated by means of the following formula: $T_b = t_0 * N_0 + t_1 * N_1 + t_2 * N_2$, where $t_0 = 2.2, t_1 = 2.7, t_2 = 10.0$ min are the average times of calling *hp*-FEM with the accuracy of the root, branch and leaf levels respectively, whereas N_0, N_1, N_2 are the numbers of such calls.

Table 6. Results of the HGS with the stable mutation.

	ω_0	ω_1	ω_2	<i>misfit</i>
Point 1	0.762	3.045	23.769	0.013620991
Point 2	0.714	6.552	34.347	0.013657428
Point 3	1.118	8.149	37.615	0.016489642
Point 4	0.912	4.092	215.083	0.025547867
Point 5	0.748	4.181	715.807	0.029160002
Point 6	0.624	2.360	21.728	0.032128412
Point 7	0.654	4.141	6374.512	0.033704187
Point 8	0.584	4.796	1454.993	0.037422516
Point 9	1.199	5.640	14847.693	0.04148432
Point 10	0.757	1.643	15.940	0.046510098
Point 11	0.535	2.953	3348.759	0.0506232
Point 12	1.734	6.780	68.596	0.057612481
Point 13	1.144	2.998	3.476	0.085280937
Point 14	0.788	15.403	306.036	0.09455748
Point 15	0.417	1.625	2219.693	0.097377075
Point 16	0.508	12.401	18735.271	0.09922374

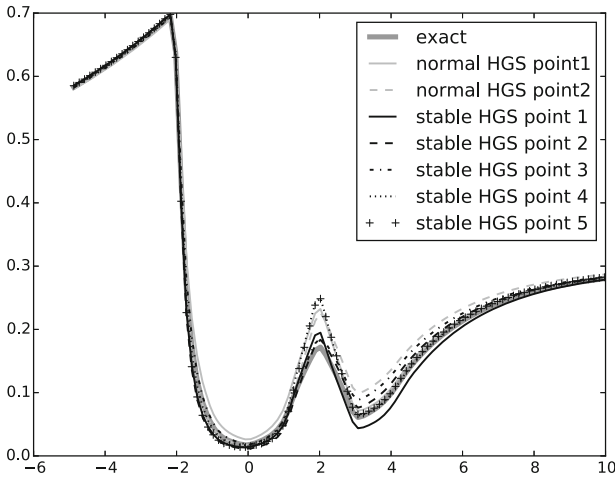


Fig. 4. The logging curves corresponding to the best solutions found. The labels of charts correspond to Tables 5 and 6. The bold green curve corresponds to the exact logging curve.

6 Conclusions

The selection of a global optimization strategy for solving parametric inverse problems should be performed very carefully, satisfying several contradictory criteria, such as good exploratory skills together with a relatively high accuracy, because of the usual ill conditioning, and the extremely tough economics, because of the huge computational cost of the forward problem computation.

The HGS with the stable mutation with $\alpha < 2$ applied in higher order demes (root demes and branches) significantly improves the exploratory skills of the composite strategy. In particular, the number of well-fitted individuals is more than three times greater in the case of DC logging measurements inversion. Moreover, this result was obtained within a smaller computational budget, about 2/3 of the budget spent in the normal mutation case.

The obtained computational experience makes an advantageous perspective of including the stable mutation in more advanced hierarchic stochastic searches combined with a convex, gradient-based optimization methods, such as the Hierarchic Memetic Search [25, 26].

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