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3

Electromagnetic Device Optimization with Stochastic Methods

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1. Introduction

Device optimization using metaheuristic methods has been successfully applied to electromagnetic devices since their development in the early 1980s. Some recent examples of the application of metaheuristics in electromagnetic device design include, among others, genetic algorithms [Zaoui2007], evolution strategies [Coelho2007], Tabu search [Cogotti2000], artificial immune systems [Campelo2006], particle swarm optimization (PSO) [Ciuprina2002].
In this chapter the author summarizes some of his experiences in the use of two stochastic optimization techniques which are very suitable to typical electromagnetic devices and systems. First the algorithms are briefly introduced and then their application to typical challenging problems, including Polymer Exchange Membrane Fuel Cells (PEMFC), high-field-uniformity solenoids and Superconducting Magnetic Energy Storage (SMES) systems, is presented.

2. Algorithm 1: differential evolution

Evolutionary algorithms (EAs) are a class of nonlinear optimization approaches which somehow mimic features of biological systems and Darwin's principle of the survival of the fittest. EAs have some particular advantages such as robustness, parallelism, and global search capability, which make them applicable and attractive within a wide range of engineering problems including electromagnetic optimization.
DE is a powerful and simple EA which improves a population of individuals over several generations through the operators of mutation, crossover and selection. DE presents good convergence characteristics and requires few control parameters. The most important operation in DE is its offspring-generating scheme, namely, each offspring is generated by differential mutation and probabilistic crossover from the current population.
In the context of EAs, an attractive and repulsive (AR) approach was introduced in [Ursem2002], [Ursem2003] within the framework of particle swarm optimization. AR uses a diversity measure to control the population and the result is a powerful algorithm which alternates between phases of attraction (exploitation) and repulsion (exploration).
Such a diversity measure can be applied within the framework of Differential Evolution (DE) in order to improve both the global convergence as well as the local search performance. The DE approach showed here uses an attractive-repulsive, diversity-guided

operator (ARDGDE) prevents the fluctuation of the estimated parameters during the evolution procedure. ARDGDE will be applied on the well-known TEAM workshop problem 22 which has been solved with a number of different techniques in the past [Magele1993], [Alotto1998], [Saldanha1999], [Magele 2007]. The benchmark consists in determining the optimal design of a superconducting magnetic energy storage (SMES) device in order to store a significant amount of energy in the magnetic field with a fairly simple and economical coil arrangement which can be rather easily scaled up in size.

2.1 Classical DE

The fundamental idea behind DE is the scheme which generates the trial parameter vectors. DE, at each time step, mutates vectors by adding weighted, random difference vectors to them. If the cost (objective function value) of the trial vector is better than that of the target, the target vector is replaced by trial vector in the next generation. This greedy behavior lies at the heart of the efficiency of DE.

In 1995 Storn and Price [Storn1995] proposed several variants of the basic DE which are identified by the notation DE/*ind*/*num*/*mode*, where *vec* indicates the individual to be mutated (i.e. either a randomly chosen individual, *rand*, or the best individual of the current generation, *best*), *num* is the number of difference vectors used in the mutation (i.e. either 1 or 2) and *mode* is the method of crossover used. For independent binomial experiments of the degrees of freedom, this is set to *bin*, whereas independent exponential experiments are indicated by *exp*.

Studies have shown that for general problems two of the most effective strategies are DE/*rand*/1/*bin* and DE/*best*/2/*bin*. The variant implemented here is the DE/*rand*/1/*bin* given by the following steps:

i. Initialize a population of M individuals (real-valued solution vectors) $\boldsymbol{x}_i(t)$, i=1,…,M, with random values generated according to a uniform probability distribution in the n dimensional problem space. In this step, t = 0.
ii. For each individual, evaluate its fitness (objective function value), F.
iii. Mutate individuals according to following equation:

$$\mathbf{z}_i(t+1) = \mathbf{x}_{r_1}(t) + f_m \cdot [\mathbf{x}_{r_2}(t) - \mathbf{x}_{r_3}(t)] \tag{I.1}$$

where r_1, r_2 and r_3 are three mutually different random integers in [1,M], and $f_m > 0$ is a real parameter, called *mutation factor*, which controls the amplification of the difference between two individuals and is usually taken in the range [0.1, 1]. Practically, each mutant individual irradiates from a current individual by addition of a vector depending on the weighted difference between randomly chosen population members (Fig. I.1).

iv. Following the mutation operation, crossover is applied to the population. For each mutant vector, $z_i(t+1)$, an index $r_i \in [1, M]$ is randomly chosen using a uniform distribution, and a *trial vector*, $\mathbf{u}_i(t+1)$, is generated (component by component) by

$$u_{i_j}(t+1) = \begin{cases} z_{i_j}(t+1), & \text{if } (r_j \le CR) \text{ or } (j = r_i), \\ x_{i_j}(t), & \text{otherwise} \end{cases} \tag{I.2}$$

where r_j is the j-th evaluation of a uniform random number generation within [0, 1] and CR is a *recombination* or *crossover rate* in the range [0, 1]. It has been shown that the

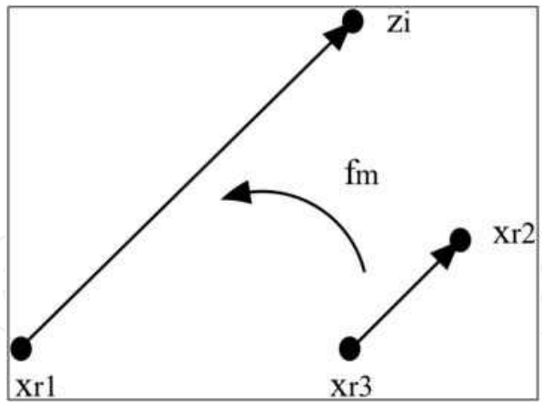

Fig. I.1. Generation of mutants according to the DE/best/1/exp approach.

performance of DE does not depend very critically upon the choice of *CR*. To decide whether or not the vector $\boldsymbol{u}_i(t+1)$ should be a member of the population comprising the next generation, it is compared to the corresponding vector $\boldsymbol{x}_i(t)$. In this context, if *F* is the objective function subject to minimization, then

$$\mathbf{x}_i(t+1) = \begin{cases} \mathbf{u}_i(t+1), \text{ if } F(\mathbf{u}_i(t+1)) < F(\mathbf{x}_i(t)), \\ \mathbf{x}_i(t), \text{ otherwise} \end{cases} \tag{I.3}$$

v. Update $t = t + 1$. Loop to step (ii) until a stopping criterion is met, usually a maximum number of iterations (generations), t_{max}.

Usually, the performance of a DE algorithm depends on the population size *M*, the mutation factor f_m, and the crossover rate *CR*. Various studies have shown that the mutation factor is the parameter which most critically influences the performance and robustness of DE.

2.2 DE using diversity-guided operator

Population diversity is a key issue in the performance of evolutionary algorithms. A common hypothesis is that high diversity is important to avoid premature convergence and to escape local optima. Various diversity measures have been used to analyze algorithms, but so far few algorithms have used a measure to *guide the search*.

To improve the control over the population diversity, Ursem introduced a diversity guided evolutionary algorithm (DGEA) [Ursem2002], [Ursem2003]. The idea behind DGEA is simple. Unlike most other evolutionary algorithms DGEA uses a diversity measure to alternate between exploiting and exploring behaviors. These behaviors are also called attraction and repulsion, hence the acronym AR. To use a measure for this purpose it has to be robust with respect to the population size, the dimensionality of the problem, and the search range of each of the variables. An immediate measure for *N*-dimensional numerical problems is the "distance-to-midpoint" measure, which is defined as:

$$diversity(P) = \frac{1}{|D| \cdot M} \cdot \sum_{i=1}^{M} \sqrt{\sum_{j=1}^{n} \left(x_{ij} - \overline{x}_j \right)^2} \tag{I.4}$$

where $|D|$ is the length of the diagonal (assuming that each design variable is in a finite range) in the search space $X \in \Re^n$, P is the population, M is the population size, n is the dimensionality of the problem, x_{ij} is the j-th component of the i-th individual, and $\bar{x}_j$ is the j-th component of the midpoint $\bar{x}$.
Based on this diversity concept, a modified attractive-repulsive diversity guided DE (ARDGDE) is used here. The pseudocode for ARDGDE based on DE/*rand*/1/*bin* is listed in Fig. I.2. The diversity measure is given by

$$diversity(P_i) = \frac{1}{D_i \cdot M} \cdot \sum_{i=1}^{M} \sqrt{\sum_{j=1}^{n} \left(x_{ij} - \bar{x}_j \right)^2} \tag{I.5}$$

where

$$D_i = \max\left\{ \sum_{j=1}^{n} \left(x_{ij} - \bar{x}_j \right)^2 \right\} \tag{I.6}$$

The ARDGDE algorithm has an adaptive mutation factor which alternates between phases of attraction and repulsion. The diversity analysis of $x_{i,r_2}(t)$ and $x_{i,r_3}(t)$ determines which phase ARDGDE is currently in, simply by setting sign-variables, d_1 and d_2, either to 1 or -1 depending on the diversity. Here the lower and higher bounds of diversity measure, d_{low} and d_{high}, are set to 0.05 and 0.25, respectively.

3. Algorithm 2: Tribes

3.1 Motivation

As will be shown in the sections devoted to typical electromagnetic applications, most realistic problems have a rather high number of parameters and highly non-linear objective functions. In some cases appropriate models of modest computational cost can be built and in these cases robust and possibly parameter free (self-adapting) stochastic optimizers can be used.
The *Tribes* algorithm, proposed in [Clerc2006][Cooren2006], and which has attracted attention from researchers in different application areas such as the optimization of milling operations [Onwubolu2005], flow shop scheduling [Onwubolu2005], and molecular docking [Chen2006], seems to be the particularly suitable for solving this kind of problems.

3.2 Particles

The population in *Tribes* is called *swarm* and each individual is called *particle*. Each particle flies around in a multi-dimensional problem search space. In other words, a swarm consists of N particles moving around in a D-dimensional search space.

3.3 Informers

An informer for a given particle P is a particle Q that can pass some information to P. Typically this information includes the best position ever found by Q and the function value at this best position. The informer Q, therefore, influences the behavior of P.

ARDGDE main
{
Generation t = 0;
Initialize the direction variables d_1=1 and d_2=1;
Initialize the population $P(t)$ of individuals;
While (stopping criterion is not met),
Evaluate the fitness of population;
Update the generation number, $t = t + 1$;
Apply mutation operator given by:
Select the indices r_1, r_2 and r_3
Update the adaptive mutation factor using $f_m(t) = 0.5 \cdot (t / t_{\max}) + 0.3$
If rand > 0.5 (where rand is a random number generated using uniform probability distribution function)
If *diversity* ($P_{i,r_2}(t)$) < d_{low}
$d_1 = 1$;
Else if *diversity*($P_{i,r_2}(t)$) > d_{high}
$d_1 = -1$;
Endif
$z_i(t+1) = x_{i,r_1}(t) + d_1 \cdot f_m(t) \cdot \left| x_{i,r_2}(t) - x_{i,r_3}(t) \right|$
Else if
If *diversity* ($P_{i,r_3}(t)$) < d_{low}
$d_2 = 1$;
Else if *diversity*($P_{i,r_3}(t)$) > d_{high}
$d_2 = -1$;
End if
$z_i(t+1) = x_{i,r_1}(t) + d_2 \cdot f_m(t) \cdot \left| x_{i,r_2}(t) - x_{i,r_3}(t) \right|$
End if
Apply crossover operator
End while
}

Fig. I.2. Pseudocode of ARDGDE with adaptive mutation factor.

3.4 Tribes

A tribe is a sub-swarm formed by particles which have the property that all particles inform all others belonging to the tribe (a symmetrical clique in graph theoretical language). The concept is therefore related to the "cultural vicinity" (information neighborhood) and not on "spatial vicinity" (parameter-space neighborhood). It should be noted that, due to the above definition, the set of informers of a particle (its so-called *i-group*) contains the whole of its tribe but is not limited to it. This is shown in Fig. II.1 where the *i-group* of particle B1 contains all particles of its tribe (black) and particle W1 belonging to the white tribe.

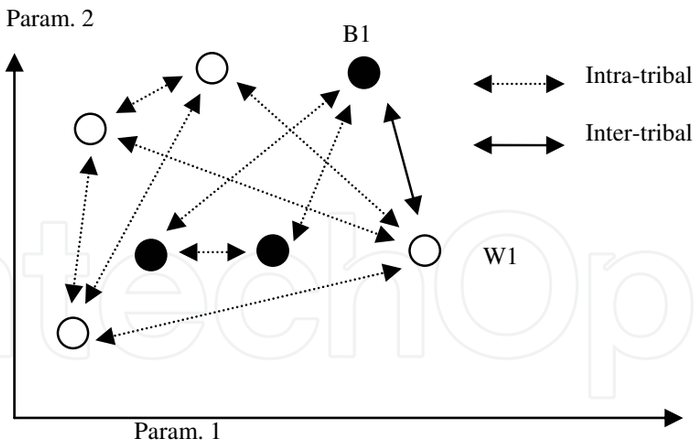

Fig. II.1. Tribal relationships

3.5 Optimization procedure

The Tribes mechanism is auto-parametrising. The principles of Tribes are: i) the swarm is divided in tribes; ii) at the beginning, the swarm is composed of only one particle; iii) according to tribes' behaviors, particles are added or removed; and iv) according to the performances of the particles, their displacement strategies are adapted. The so-called structural adaptation rules describe when a particle is created or removed and when a particle becomes the informer of another, whereas so-called moving strategies indicate how particles modify their positions.

3.6 Structural adaption rules

The most important structural adaption rule is that "good" tribes may benefit from the removal of their weakest member, since they already possess good problem solutions and thus may afford to reduce their population; "bad" tribes, on the other hand, may benefit from the addition of a new member, increasing the possibility of improvement. In Tribes, for each "bad" tribe, the best particle generates a new particle using uniform probability distribution and becomes its informer. Particles generated in one iteration step are interconnected into a tribe and provide inter-tribe exchange of information.

Crucial for the above steps is the definition of "good" and "bad" tribes: the more "good" particles a tribe has, the more "good" the tribe is. This behavior is obtained by generating a random number between 1 and N_{tribe}–the number of particles in a tribe–, and checking if it is less than or equal to G_{tribe}–the number of "good" particles in the tribe.

In contrast to most standard PSO approaches, particles keep memory of their last two previous cost function values. The particle is said to be "good" if the last movement produces an improvement of the objective function, "excellent" if both the last two movements produce an improvement, otherwise the particle is "neutral".

Structural adaptation should not take place after each iteration since some time (iterations) are necessary for information to propagate throughout the swarm.

In his original algorithm Clerc proposes to reevaluate and modify the population structure every $L/2$ iterations, where L is the dynamically changing number of links in the population. In fact, a more sophisticated approach would be to compute the length of all shortest paths between all couples of particles and the longest of such paths would indicate the number of

iterations it would take to propagate information through the whole swarm. Since such algorithm could quickly become expensive in the case of large swarms the above heuristic, which has been tested to give similar results to the more complex one, is implemented instead.
As a result, Fig. II.2 shows the dynamics of tribe and particle creation/deletion for the μ-DMFC optimization problem described later.

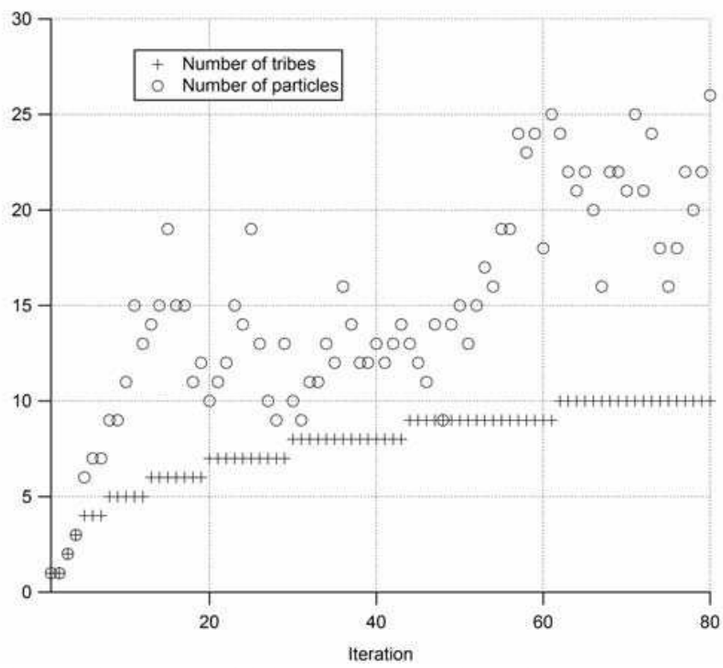

Fig. II.2. Tribe and particle creation/deletions vs. number of iterations.

3.7 Moving strategies

In contrast with standard PSO algorithms particles do not have explicit associated velocities: their position is updated according to history only. "Excellent" particles are updated according to the "simple pivot" strategy [Serra1997], whereas "good" and "neutral" particles evolve according to the "noisy pivot" method.
In the "simple pivot" method two positions are used: the best position p of a given particle P and the best position q of its informer Q. Then two hyperspheres of radius $|p\text{-}q|$ are created around p and q and the new position is generated inside the intersection of the two hyperspheres in such a way that the newly generated point is most likely to be nearer to the best between p and q. In order to obtain such behavior two weights w_1 and w_2 proportional to the relative fatnesses of P and Q are generated and the new position is obtained by $w_1h_p+w_2h_q$., where h_p and h_e are two randomly generated points in the hyperspheres surrounding p and q respectively.
In the "noisy pivot" method the same procedure is applied but random noise is added to the obtained position in such a way that exploration beyond the hyperspheres becomes possible.
The combined use of these strategies has a twofold effect: very good particles search in their close neighborhood (exploitation) whereas all other sample wider regions of parameter space (exploration).

3.8 Brief description of the algorithm

Summarizing, the Tribes algorithm consists of following steps:

Initialization of swarm

Set iteration t=1. Initialize a population of 1 particle (real-valued D-dimensional vector) and 1 tribe with random values generated according to a uniform probability distribution within given upper and lower bounds.

Evaluation of each particle in the swarm

Evaluate the fitness (objective function) value of each particle.

Swarm moves

Apply the moving strategies ("simple pivot" or "noisy pivot") according to the quality of particles ("excellent", "good" or "bad").

Adaptation scheme

After every $L/2$ iterations, where L is the number of links in the population, adapt the structure of the swarm by applying the above described structural adaptation rules.

Stopping criterion

Set the generation number for $t = t + 1$. Proceed to step *Evaluation of each particle in the swarm* until a stopping criterion is met, usually a maximum number of iterations or a maximum number of objective function evaluations.

4. Application 1: fuel cells

Recently, small-scale direct methanol fuel cells (μ-DMFCs) have gained considerable attention as power sources with potentially higher energy density compared to traditional Li-ion batteries [Larminie2003]. This feature, together with the low operating temperature and low weight, makes μ-DMFCs particularly suited for supplying low-power portable devices such as laptops, PDAs, or mobile phones.

Several factors contribute to the overall cell performance, e.g., methanol concentration, load current, room humidity and temperature, membrane conductivity and permeability, catalyst loadings. Modeling and optimizing the cell performance becomes particularly complex since electro-chemical coupled problems are fully non-linear.

To date design procedures have been developed mainly for polymer electrolyte fuel cells (PEMFC) [Katykatoglu2007][Cheng2006]. Here a one-dimensional analytical model of a μ-DMFC that accounts for current generation, mass transport, electronic and protonic electrical conduction, and electrochemical reactions is shown.

4.1 Direct methanol fuel cell modeling

A small-scale direct methanol fuel cell consists of a proton exchange membrane (PEM) sandwiched between the anode and cathode electrodes (Fig. III.1). In passive fuel cells methanol is stored in a tank, while oxygen is taken from the atmosphere. Reactants are distributed through diffusion layers to catalyst layers, where the electro-chemical energy conversion occurs. Electrons generated at the anode catalyst layer flow to the external circuit by means of a current collector.

The model takes into account the following physical phenomena: electrochemical reactions, electronic and protonic conduction, methanol crossover through the PEM, diffusion of reactants inside the substrates, and electric current generation.
In the following sections the static and dynamic modeling of the μ-DMFC are treated separately.

4.2 Static modeling of a μ-DMFC

The electric steady-state external characteristic of the fuel cell is obtained from mass transport and electro-chemical relations under the assumption of a one-dimensional geometry.

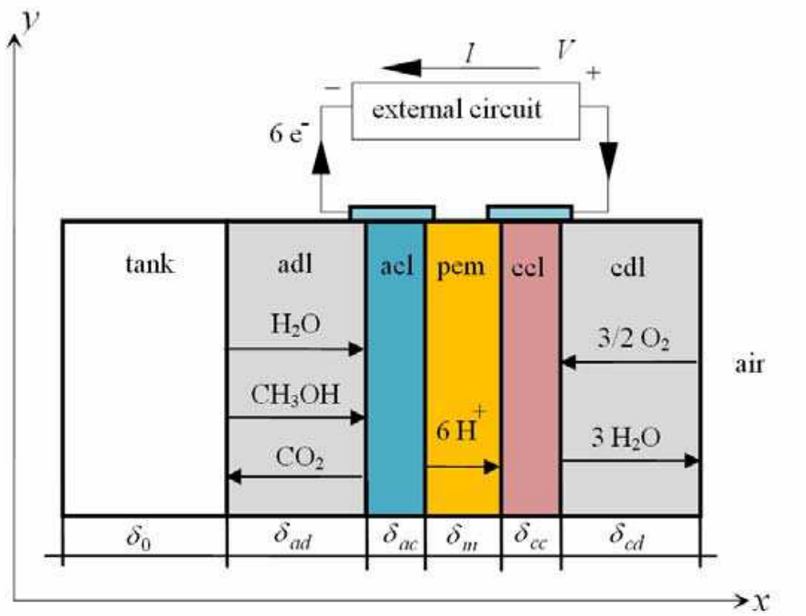

Fig. III.1. DMFC schematic (a=anode, c=cathode, pem=proton exchange membrane, dl=diffusion layer, cl=catalyst layer).

The external circuit is coupled to the cell by the following generalized continuity equations that apply at catalyst layers:

$$\begin{aligned} \nabla \cdot \mathbf{J}^{+} + \partial_t \rho^{+} &= \partial_t \rho_g^{+} \\ \nabla \cdot \mathbf{J}^{-} + \partial_t \rho^{-} &= \partial_t \rho_g^{-} \end{aligned} \tag{III.1}$$

where superscripts indicate protons and electrons, ρ, ρ_g the stored/ generated charge densities, and $\mathbf{J}$ the current density.
Current densities at the anode and cathode are computed by Butler-Volmer's equation, neglecting the concentrations of reduced (anode) and oxidized species (cathode), as [Bard2001]:

$$\begin{aligned} J_a &= J_a^{*} (C_a / C_a^{*})^{\gamma} \exp(\alpha_a f v_a) \\ J_c &= J_c^{*} (C_c / C_c^{*})^{\gamma} \exp(\alpha_c f v_c) \end{aligned} \tag{III.2}$$

where concentrations C_a, C_c and over-voltages v_a, v_c are independent variables, and the other quantities are constant.
Reactant concentrations at both catalyst layers depend on the diffusion rate across diffusion layers by Fick's law:

$$\mathbf{N} = -D\nabla C \tag{III.3}$$

where $\boldsymbol{N}$ is the reactant molar flow, and D is the diffusivity. Using (3) methanol flow from the tank can be expressed as:

$$N_{ad} = K_a(C_{0,a} - C_{ac}) \tag{III.4}$$

assuming very thin layers and a one-dimensional mass flow. In the same way, oxygen flow at the cathode can be expressed as:

$$N_{cd} = K_c(C_{0,c} - C_{cc}) \tag{III.5}$$

where K_a, K_c are the mass transfer coefficients, $C_{0,a}$ and $C_{0,c}$ the methanol and oxygen concentrations in the tank and in the ambient, and C_{ac}, C_{cc} those at catalyst layers.
Due to electro-osmosis and concentration gradient effects, part of the methanol does not react completely at the anode and flows through the membrane. This effect is the so-called *crossover*, causing significant voltage loss and waste of fuel. The anode current density J_a is related to crossover N_m, as:

$$J_a = 6F(N_{ad} - N_m) \tag{III.6}$$

where F is the Faraday's constant (96.485 C mol^{-1}). At the cathode side, current density J_c can be derived as:

$$J_c = 4F(N_{ad} - \tfrac{3}{2}N_m) \tag{III.7}$$

The methanol crossover in (III.6) and (III.7) can be computed by means of the following mass balance equation:

$$\mathbf{N}_m = -D_m\nabla C + n_d\mathbf{J}_a / F \tag{III.8}$$

where D_m is the methanol diffusivity on the membrane, and n_d the electro-osmotic drag coefficient.
The anode activation over-voltage is obtained by combining (III.4) and (III.6) with (III.2), as:

$$v_a(J) = \frac{1}{f\alpha_a}\log\frac{C_a^* J_a / J_a^*}{C_{eq,a}(1 - J / J_{\lim,a})} \tag{III.9}$$

where the anode equivalent concentration and limiting current values are:

$$C_{eq,a} = \frac{K_a\delta_m}{K_a\delta_m + D_m}C_{0,a}\ ,\quad J_{\lim,a} = \frac{K_a C_{0,a}}{\frac{1}{6F} + \frac{n_d}{F}}$$

where thickness δ_m is defined in Fig. III.1.

Similarly, the cathode over-voltage can be computed by combining (III.5) and (III.7) as:

$$v_c(J) = \frac{1}{f\alpha_c} \log \frac{C_c^* J_c / J_c^*}{C_{eq,c}(1 - J / J_{\lim,c})} \tag{III.10}$$

where the equivalent cathode concentration and limiting current values are:

$$C_{eq,c} = C_{0,c} - \frac{3}{2} \frac{D_m}{K_a \delta_m + D_m} \frac{K_a}{K_c} C_{0,a}, \quad J_{\lim,c} = \frac{K_c (C_{eq,c} / C_{eq,a}) C_{0,a}}{\frac{1}{4F} + \frac{3}{2F} n_d}$$

Anode and cathode current densities in (III.9) and (III.10) can be related to load current density J on the external circuit, as:

$$\begin{aligned} J_a &= J \\ J_c &= J + 6FN_m \end{aligned} \tag{III.11}$$

which states that the electron flow at the anode equates the proton flow, while at the cathode the electron flow from methanol crossover oxidation must be considered as well.
Finally, the fuel cell voltage at the collector is obtained from anode and cathode over-voltages in (III.9) and (III.10), as

$$V(J) = E_{eq}(J) - R_{eq} J \tag{III.12}$$

where $E_{eq}(J) = E^0 - v_a(J) - v_c(J)$ is the equivalent fem, E^0 the standard cell voltage, $R_{eq} = \delta_m / \sigma_m + R_c$ the equivalent resistance, σ_m the PEM non-linear conductivity, and R_c the contact resistance between collectors and diffusion layers.

4.3 Dynamic modeling of a μ-DMFC

The fuel cell dynamics on the long time scale is dominated by the consumption of the methanol in the reservoir, which can be computed by using the mass conservation law [Bard2001]:

$$\nabla \cdot \mathbf{N} + \partial_t C = 0 \tag{III.13}$$

where ∂_t is the time derivative. The voltage discharge of the DMFC is evaluated for a constant load current density.
The state variable model is obtained by assembling (III.4), (III.6) and (III.13) into the following ODE system:

$$\mathbf{M}_1 \mathbf{x} + \mathbf{M}_2 \dot{\mathbf{x}} = \mathbf{g} \tag{III.14}$$

where:

$$\mathbf{M}_1 = \begin{pmatrix} K_a & -K_a - D_m / \delta_m \\ K_a & -K_a \end{pmatrix} \quad \mathbf{M}_2 = \begin{pmatrix} 0 & 0 \\ \delta_0 & 0 \end{pmatrix}$$

$$\mathbf{g} = \begin{pmatrix} J / 6F + n_d J / F \\ 0 \end{pmatrix} \qquad \mathbf{x} = \begin{pmatrix} C_{0,a} \\ C_{ac} \end{pmatrix}$$

and δ_0 is the tank thickness indicated in Fig. III.1. This system is solved numerically by the so-called *θ-method*, which consists in the following iterative scheme:

$$\left(\theta\mathbf{M}_1+\frac{\mathbf{M}_2}{\tau}\right)\mathbf{x}_{k+1}=\left[(\theta-1)\mathbf{M}_1+\frac{\mathbf{M}_2}{\tau}\right]\mathbf{x}_k+\mathbf{g} \tag{III.15}$$

where τ is the time integration step, and the parameter θ is set to 2/3 in order to ensure unconditional stability.
As an example, Fig. III.2 shows the voltage discharge profiles computed at different load current densities and for an initial methanol concentration in the reservoir of 3 M.

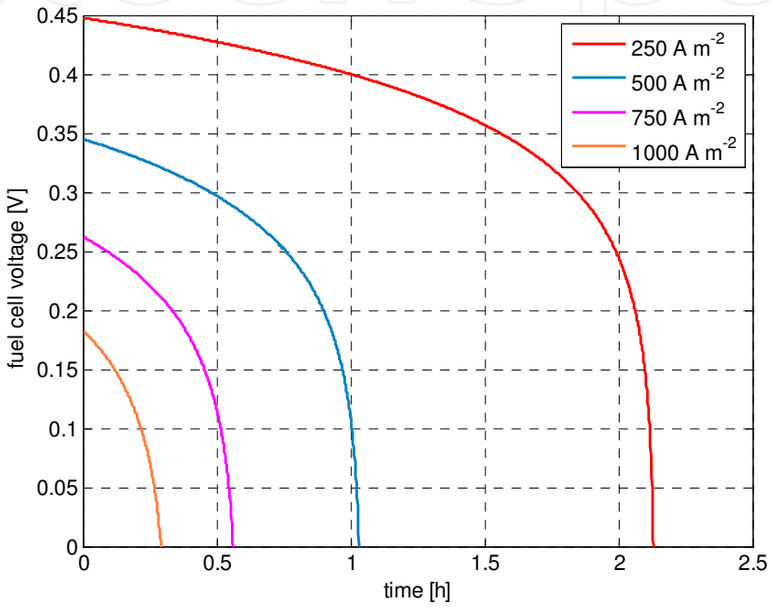

Fig. III.2. Voltage discharge profiles at constant current densities.

4.4 Particle swarm optimization

In order to optimize the cell performance two conflicting objectives were considered, i.e., the maximization of the cell duration between two consecutive fuel recharges – obtained from (15) – and the minimization of the methanol crossover. The importance of the second objective is twofold: on one hand crossover is obviously a waste of (limited) fuel, on the other hand fuel cell life-time is shortened by catalyst poisoning due to the carbon monoxide produced at the cathode from crossover methanol oxidation.
Both the objectives depend on the following parameters: methanol concentration in the tank, diffusion/catalyst layer thicknesses, membrane thickness, current density, and room temperature.
The above-described Tribes algorithm was applied to the μ-DMFC model with a maximum number of 5000 objective function evaluations as a stopping criterion.
It was observed that the optimization procedure identifies quite rapidly the shape of the Pareto front, and then further refines it. Fig. III.3 shows that the Pareto front is coarsely identified when number of individuals on the front first reaches one hundred (triangular markers). This happens after roughly 300 function evaluations. In the remaining iterations the algorithm spreads out individuals along the front.

Fig. III.4 shows that particles are very well distributed on the front. The corresponding positions in parameter space, i.e., the *Pareto set*, show that the solutions forming the Pareto front lie in completely different positions. These correspond to really different design solutions. For instance, Fig. III.5 shows the Pareto set in the three-dimensional subspace ($C_{0,a}$, δ_{ad}, δ_{ac}).

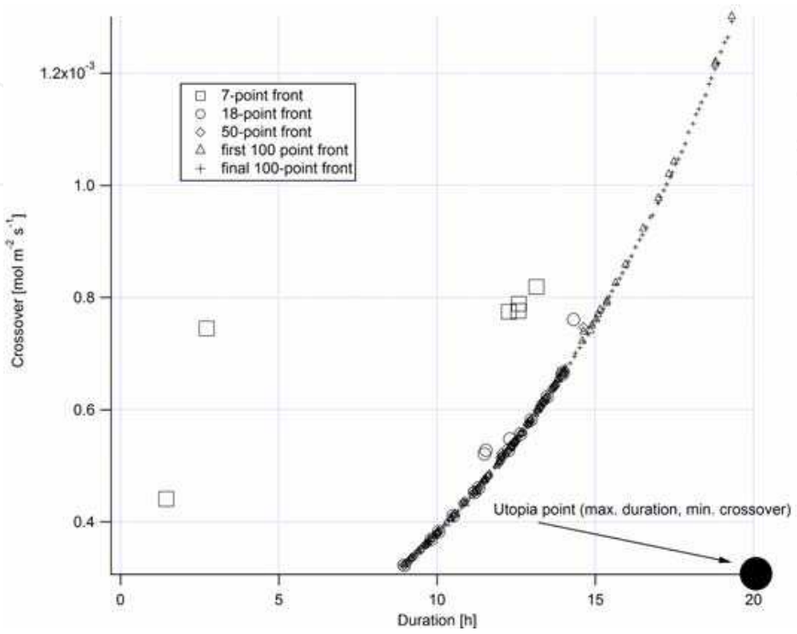

Fig. III.3. Evolution of the Pareto front during iteration.

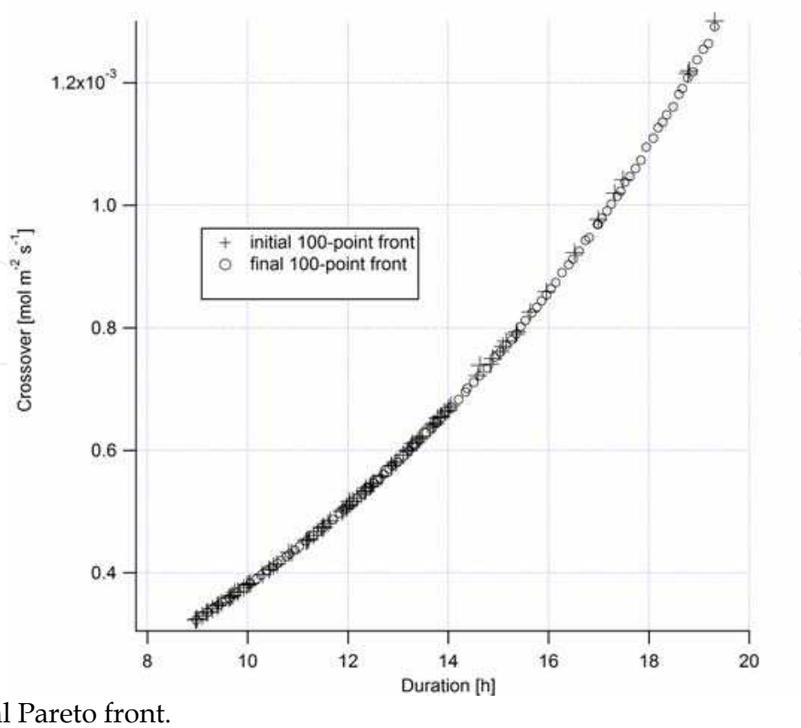

Fig. III.4. Final Pareto front.

Once the front has been identified it is the responsibility of a decision-maker to choose one or more particular designs which emphasize one of the two objectives with respect to the other depending on the specific application field of the DMFC.

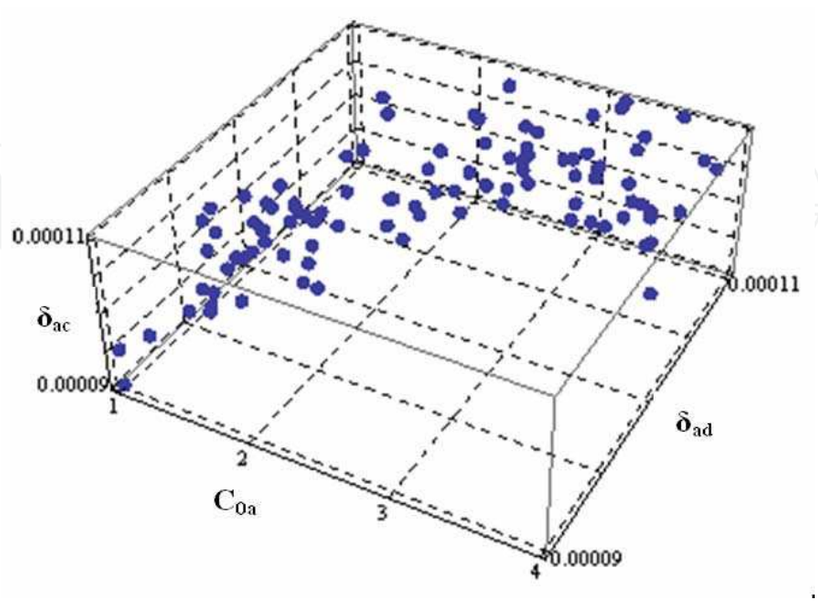

Fig. III.5. Pareto set (three parameters only)

5. Application 2: solenoid design

The electrical engineering literature has several references to optimization approaches which have been used to solve Loney's solenoid design problem [Cogotti2000], [Ciuprina2000].

Appropriately stated, Loney's solenoid design problem consists in determining the position and size of two correcting coils in order to generate a uniform magnetic flux density B within a given interval on the axis of a main solenoid.

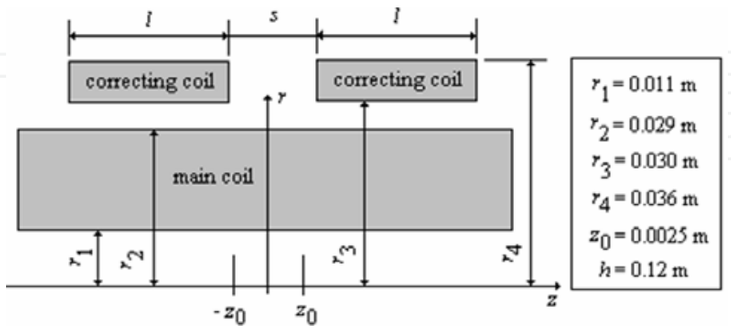

Fig. IV.1. Axial cross-section of Loney's solenoid

The upper half plane of the axial cross-section of the system is presented in Fig. IV.1. The interval of the axis, where the magnetic flux density B must be as uniform as possible is ($-z_o$, z_o). The separation s and the length l of the correcting coils are to be determined while all other dimensions are given. Both s and l are bounded in [*0,0.2*] according to the problem definition.

The field behavior along the axis can in principle be computed by several means, but in order to allow for a fair comparison between different methods we chose to follow the same route followed by other research groups, namely to represent each coil by four coaxial current sheets.
The optimization problem to be solved is:

$$\min F(s,l) \tag{IV.1}$$

where the objective function F is given by:

$$F = \frac{B_{max} - B_{min}}{B_0} \tag{IV.2}$$

where B_{max} and B_{min} are the maximum and minimum values of the magnetic flux density in the interval $(-z_o, z_o)$ and B_0 is the flux density at $z=0$.
Due to the peculiar way in which the field is computed (coils are represented by four current sheets) and due to the way B_{max} and B_{min} are evaluated (five uniformly spaced points in $[-z_0,0]$) the objective function is very noisy.
Three different basins of attraction of local minima can be recognized in the domain of F with values of $F > 4 \cdot 10^{-8}$ (high level region: HL), $3 \cdot 10^{-8} < F < 4 \cdot 10^{-8}$ (low level region: LL), and $F < 3 \cdot 10^{-8}$ (very low level region - global minimum region: VL). The very low level region is a small ellipsoidally shaped area within the thin low-level valley. In both VL and LL small changes in one of the parameters can give rise to changes in objective function values of several orders of magnitude.
Tribes was run with a stopping criterion of either 1000 or 2000 objective function evaluations.
Table IV.1 summarizes the behavior of the swarm size and number of tribes at convergence. It is interesting to note that the adaptive mechanism practically always generates the same number of tribes for a given number of function calls. The overall swarm size is also quite stable.

F calls	*S=Swarm Size, T=Number of tribes*							
	S_{min}	S_{avg}	S_{max}	S_{stdev}	T_{min}	T_{avg}	T_{max}	T_{stdev}
2000	22	34,9	56	6,2	9	9,7	10	0,48
1000	13	27,8	43	5,8	8	8,1	9	0,29

Table IV.1 Simulation Results of F in 100 runs

Table IV.2 summarizes the behavior of the algorithm in terms of the best objective function value found in 100 independent runs of the algorithm. The last three columns show the number of optima lying in the above-defined basins of attraction.
Results are very good also in the case of just 1000 function evaluations. A more detailed representation of the distribution of optima for both convergence criteria can be seen in Fig. IV.1, while Fig. IV.2 shows the location of the 100 optima for the case of 2000 function evaluations.
Tribes, like all stochastic optimizers, can be successfully coupled to a deterministic optimizer, like the derivative-free SolvOpt [Kappel2000] method which is based on Shor's method and is very well suited to noisy objective functions. Furthermore, SolvoOpt was chosen because lack of derivative information was hypothesizes also for the stochastic optimizer.

F calls	HL=High Level, LL=Low Level, VL=Very Low Level						
	F_{min} 10^{-8}	F_{avg} 10^{-8}	F_{max} 10^{-8}	F_{stdev} 10^{-9}	N VL	N LL	N HL
2000	2,0574	3,4870	3,9526	5,23	18	82	0
1000	2,2732	3,6450	4,5052	4,18	9	88	3

Table IV.2 Simulation Results of *F* in 100 runs

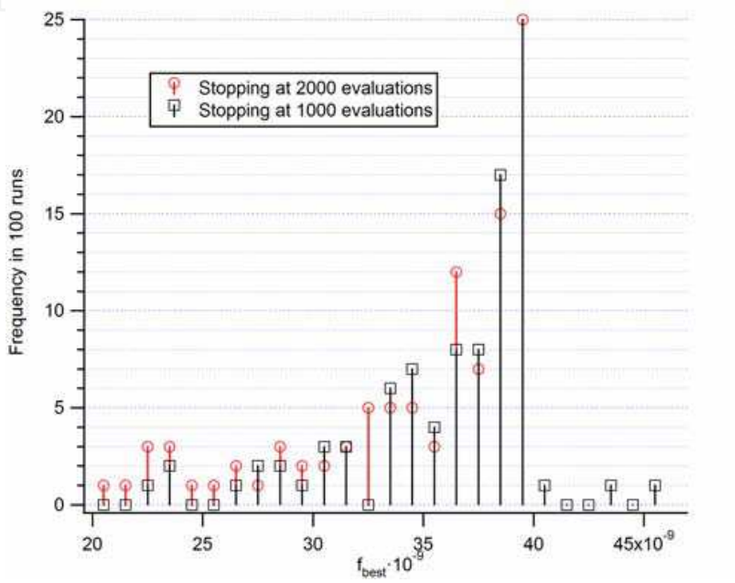

Fig. IV.1. Distribution of optima in 100 runs

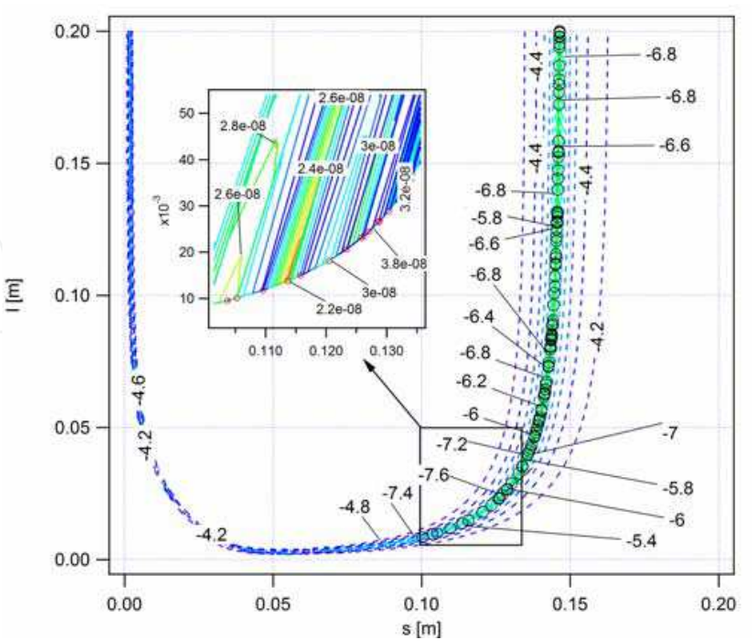

Fig. IV.2. Location of optimal solutions in 100 runs

Results of this coupling are shown in Fig. 5. Tribes was run with increasingly high numbers of function evaluations as stopping criterion (20, 40, 80, 160, 320, 640, 1200, 2400) and the best, average and worst optimal solutions are shown in Fig. IV.3. The algorithm improves only minimally after about 1200 function evaluations.

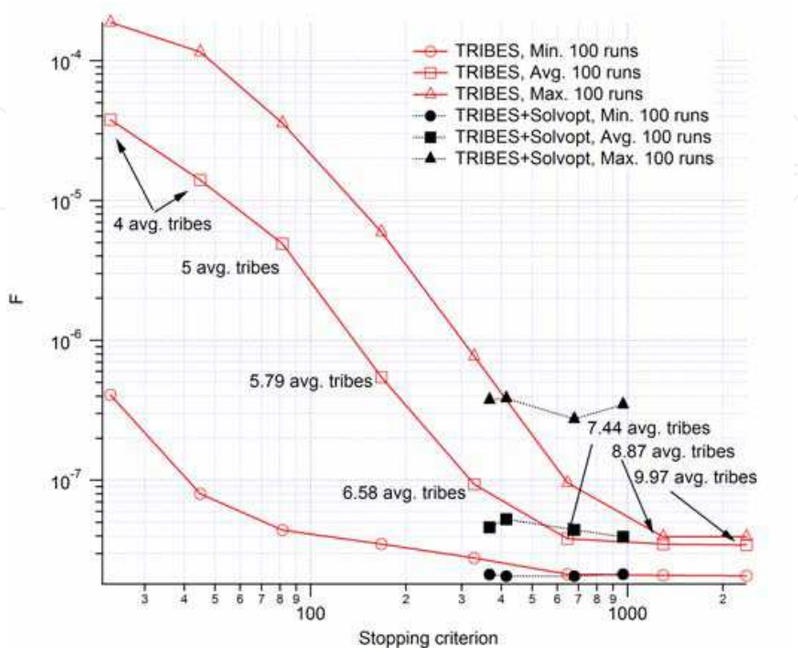

Fig. IV.3. Convergence of TRIBES and TRIBES+Solvopt

Tribes was then coupled to Solvopt and the deterministic optimizer was executed after the convergence of Tribes with stopping criteria of 20, 40, 320, 640 evaluations, respectively.
It can be seen that, for a given number of evaluations, the coupling of the two optimizers gives improvements for the first three cases but becomes practically useless afterwards (in fact the coupled optimizer becomes worse since it increases evaluations without improving the objective). It should also be noted that while the best and average optimal values improve, the worst values are almost always much worse, indicating misconvergence (remaining trapped in a local minimum) of the deterministic optimizer in some cases.

6. Application 3: superconducting magnetic energy storage

TEAM workshop problem 22 is a continuous, eight-parameter benchmark. Mathematically, this optimization problem has an objective function consisting of the weighted average of two conflicting goals (energy and stray field requirements). The optimization problem to be solved is the following:

$$\min \; OF = \frac{B_{stray}^2}{B_{normal}^2} + w \cdot \frac{\left| Energy - E_{ref} \right|}{E_{ref}} \tag{V.1}$$

where OF is the objective function to be minimized; the reference stored energy and stray field are E_{ref}= 180 MJ, B_{normal} = 200 μT, and w is a penalty factor with value equals to 100. The

introduction of the penalty factor w is a deviation from the problem definition in which w=1.0. The penalty factor was introduced to make the stray field and energy error terms of roughly the same magnitude in order to achieve better convergence of the algorithm (failure to introduce w slightly worsen the average results). It should be noted, however, that results reported in Table 3 include reference to the original problem definition for ease of comparison with other approaches.

B^2_{stray} is defined as

$$B^2_{stray} = \frac{\sum_{i=1}^{22} \left| B_{stray,i} \right|^2}{22} \tag{V.2}$$

where $B_{stray,i}$ is evaluated along 22 equidistant points along *line a* and *line b* in Fig V.1. Both the energy and the stray field are calculated using an integral formulation for the solution of the forward problem (*Biot-Savart law*). The bounds of the optimization parameters are shown in Table V.1.

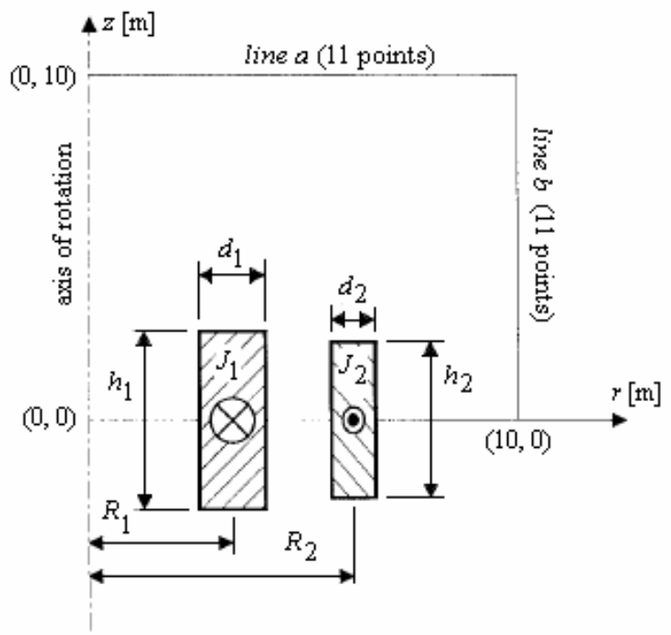

Fig. V.1. Setup of the SMES device (TEAM workshop problem 22).

Variables	R_1 [m]	R_2 [m]	$h_1/2$ [m]	$h_2/2$ [m]
Minimum	1.00	1.80	0.10	0.10
Maximum	4.00	5.00	1.80	1.80
Variables	d_1 [m]	d_2 [m]	J_1 [A/mm²]	J_2 [A/mm²]
Minimum	0.10	0.10	10.0	-30.0
Maximum	0.80	0.80	30.0	10.0

Table V.1. Limits of the optimization Parameters for the SMES Device.

Finding the optimal design is not an easy task because, besides usual geometrical constraints, there is a material related constraint: the given current density and the maximum magnetic flux density value on the coil must not violate the superconducting quench condition which can be well represented by a linear relationship shown in Fig. V.2.
In the TEAM 22 workshop study used to investigate the performance of the classical DE and ARDGDE approaches, the population size M was 15 and the stopping criterion t_{max} was 100.

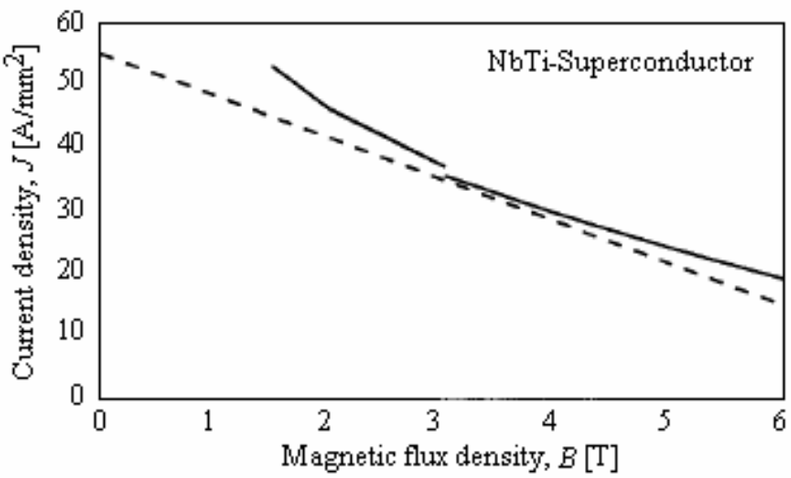

Fig. V.2. Critical curve of the superconductor.

Table V.2 reveals that ARDGDE2 provides better solutions than the DE1, DE2, and ARDGDE1 for the TEAM 22 workshop problem, particularly in terms of mean and best *OF* values. In Table 3 the best results of each tested approach (mentioned with statistical details in Table V.2) are shown (OF_{std} refers to OF with w=1).
It should also be noted that the "2" variants (adaptive f_m) always beat the respective "1" variants (constant f_m) and that the ARDG variants (attractive/repulsive diversity guided) always beat the respective standard non-ARDG variants.

DE approach	Description	Objective Function *OF* in 30 Runs			
		Max (Worst)	Mean	Min (Best)	Standard Deviation
DE1	classical DE with f_m = 0.4	69.4793	38.7011	2.9292	24.5652
DE2	classical DE with adaptive mutation factor	19.5515	5.4716	0.3967	6.4238
ARDGDE1	ARDGDE with f_m = 0.4	105.1539	46.0814	2.2359	35.1500
ARDGDE2	ARDGDE with adaptive mutation factor	**8.1377**	**2.2967**	**0.2296**	**2.5668**

Table V.2. Best Results (30 runs) for TEAM Workshop Problem 22.

Parameter	DE1	DE2	ARDGDE1	ARDGDE2
R_1 [m]	3.1339	1.2387	1.3248	1.2173
R_2 [m]	3.5174	1.8000	1.8080	1.8424
$h_1/2$[m]	0.4174	0.9366	0.3185	0.4367
$h_2/2$ [m]	1.1600	1.1986	1.7944	0.9577
d_1 [m]	0.5912	0.4303	0.7919	0.7999
d_2 [m]	0.2627	0.3801	0.1377	0.4184
J_1 (A/mm²)	20.8337	23.8491	29.9255	24.5171
J_2 (A/mm²)	-13.461	-10.079	-16.4139	-9.6477
Energy [MJ]	180.017	179.831	180.012	179.847
B_{Stray} [mT]	341.762	110.069	298.607	76.107
OF	2.9292	0.3967	2.2359	0.2296
OFstd	2.9201	0.3038	2.2292	0.1457

Table V.3. Best Results (30 runs) for TEAM Workshop Problem 22.

7. Acknowledgements

The author whishes to express his gratitude to his colleagues and friends F. Moro, Massimo Guarnieri and A. Stella from the Dipartimento di Ingegneria Elettrica, Università di Padova, Padova, Italy for sharing their expertise in the joint work on fuel cell modeling and to L. dos Santos Coelho from the Industrial and Systems Engineering Graduate Program, Pontifical Catholic University of Paraná, Curitiba, Paraná, Brazil for the cooperation on the development of optimization algorithms over the years.

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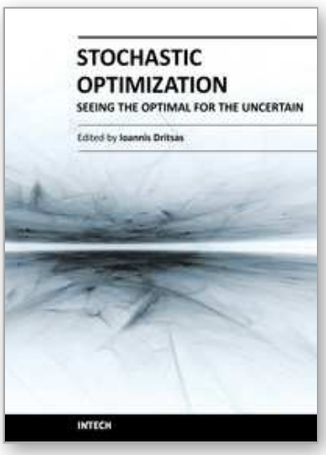

Stochastic Optimization - Seeing the Optimal for the Uncertain
Edited by Dr. Ioannis Dritsas

ISBN 978-953-307-829-8
Hard cover, 476 pages
Publisher InTech
Published online 28, February, 2011
Published in print edition February, 2011

Stochastic Optimization Algorithms have become essential tools in solving a wide range of difficult and critical optimization problems. Such methods are able to find the optimum solution of a problem with uncertain elements or to algorithmically incorporate uncertainty to solve a deterministic problem. They even succeed in â€œfighting uncertainty with uncertaintyâ€. This book discusses theoretical aspects of many such algorithms and covers their application in various scientific fields.

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