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Harmonic Distortion State Estimation Using an Evolutionary Strategy

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Harmonic Distortion State Estimation Using an Evolutionary Strategy

Elcio F. de Arruda, Member, IEEE, Nelson Kagan, Senior Member, IEEE, and Paulo F. Ribeiro, Fellow, IEEE

Abstract—This paper presents a new methodology to estimate harmonic distortions in a power system, based on measurements of a limited number of given sites. The algorithm utilizes evolutionary strategies (ES), a development branch of evolutionary algorithms. The main advantage in using such a technique relies upon its modeling facilities as well as its potential to solve fairly complex problems. The problem-solving algorithm herein proposed makes use of data from various power-quality (PQ) meters, which can either be synchronized by high technology global positioning system devices or by using information from a fundamental frequency load flow. This second approach makes the overall PQ monitoring system much less costly. The algorithm is applied to an IEEE test network, for which sensitivity analysis is performed to determine how the parameters of the ES can be selected so that the algorithm performs in an effective way. Case studies show fairly promising results and the robustness of the proposed method.

Index Terms—Evolutionary algorithms, evolutionary strategy, harmonic distortion, power quality (PQ), state estimation.

I. INTRODUCTION

A SSESSING the impact of harmonic sources to the performance and behavior of electric power systems is a relevant and complex aspect concerning power quality (PQ).

When one admits harmonic injections to the power system as known parameters, actions can be devised in order to mitigate the impact of the harmonic distortions throughout the network. This is generally carried out by the design and utilization of passive or active harmonic filters. However, one should realize that in most cases the sources of harmonic distortions are not known [1].

Although PQ meters are becoming less costly, it is still economically unviable to design PQ monitoring systems where meters are to be installed in all network buses.

In such a condition, when a few sites are selected for the installation of PQ meters, the use of a harmonic distortion state estimation algorithm is highly recommended.

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Color versions of one or more of the figures in this paper are available online at http://ieeexplore.ieee.org.

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The harmonic distortion state estimation (HDSE) consists of a process which is the reverse of a simulation process. Simulators determine the power system response to harmonic injection in one or more locations, whereas estimators evaluate the harmonic injections when the power system responses are given by a set of measurements [2].

The HDSE methodology consists in an efficient and economic tool to be used in PQ monitoring systems, so that harmonic distortions can be estimated throughout the network. The HDSE algorithm is based on the network topology and the corresponding harmonic frequency admittance matrices, passive (linear) loads and PQ meter locations and measurements [3].

Intelligent computation can be used as a good hand to evaluate harmonic sources, as it is herein proposed. Evolutionary strategies (ES) are interesting options due to their easy implementation, especially when simulation algorithms for the specific problem are well known. The implementation and speed of ES are important aspects when comparing to conventional techniques.

Estimation of the network harmonic distortion states is a complex problem since one should base its formulation on minimum and reliable data coming from a few PQ meters. Many aspects might result in discrepancies between the real and simulated systems. Besides meter calibration, important issues such as data communication and network data fidelity are really important. Another important aspect though is related to the synchronization data from different PQ meters, which is dealt with in this paper in an innovative and viable manner.

Harmonic Estimation is generally considered as two classes of problems. The first one concerns the estimation of the harmonic content in a measured waveform whereas the second one regards the estimation of harmonic distortions in non monitored buses of an electric power system by using information from PQ meters in monitored buses as reference (harmonic propagation). Several works concerning the first class of problems are addressed by using tools like genetic algorithms (GAs) [4]. As for the second class of problems, which is herein dealt with, a number of HDSE methods can be found in the scientific literature. One of the earlier methods [2] identifies sources of harmonic signals in electric power systems by using the least square (LS) method to calculate the frequency spectra at buses suspected as harmonic sources. Reference [5] shows the relevance of PQ meters specification as well as the equipment used in the process of HDSE. Reference [6] shows a HDSE method based on global positioning systems (GPS) to synchronize data from different meters. Other research works in harmonic state estimation can be seen in [7]–[10]. All of these methods use traditional

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Fig. 1. Flowchart of the proposed harmonic distortion state estimation algorithm.

techniques that demand a total observability from the measurement system or a mathematical method like Least Square to find a harmonic response in a wide solution space.

This paper considers evolutionary strategy (ES) to find the harmonic injections in the non monitored buses.

Waveforms stored in PQ meters as well as power flow information (in steady state—fundamental frequency conditions) can be used to synchronize data from the meters. This consideration is a valuable alternative to reduce costs in solutions that integrate innovative HDSE algorithms to PQ monitoring systems.

II. FORMULATION OF THE HARMONIC DISTORTION STATE ESTIMATION PROBLEM

The HDSE problem consists in evaluating the system state for each harmonic order, using the voltage and current measurement data. The system state is defined by the voltage values in all buses. The voltage and possibly current harmonic values in monitored buses are usually available from a PQ measurement system. As PQ meters costs are considerably high, a few measurement points are generally available.

When the proposed algorithm is processed for all relevant harmonic orders, the total harmonic distortion (THD) can be estimated in any network bus. The flowchart in Fig. 1 illustrates the proposed methodology. Its main steps are described in detail in the following items.

A. Fundamental Frequency System State Estimation

The fundamental frequency system state, represented by the stage (i) in Fig. 1, can be obtained in two ways:

 load flow using the active and reactive power load measurements and the generators state; conventional state estimators, where power flow and voltage measurements compose a redundant measurement set.

In this work, the fundamental frequency system state is obtained by using a conventional load flow model. Active and reactive power in load buses and voltage in generation buses are assumed to be known. In particular, for this specific application, a simple Gauss Method load flow algorithm determines the fundamental frequency system state based on the following matrix relation:

$$[\mathbf{I}_1] = \begin{bmatrix} \mathbf{I}_{1S} \\ \mathbf{I}_{1C} \end{bmatrix} = [\mathbf{Y}_1][\mathbf{V}_1] = \begin{bmatrix} \mathbf{Y}_1^{SS} & \mathbf{Y}_1^{SC} \\ \mathbf{Y}_1^{CS} & \mathbf{Y}_1^{CC} \end{bmatrix} \begin{bmatrix} \mathbf{V}_{1S} \\ \mathbf{V}_{1C} \end{bmatrix}$$
(1)

where

 $[I_1], [I_{1S}], [I_{1C}]$ are the vectors of injected currents, respectively, in all buses, supply buses, and load buses;

 $[V_1], [V_{1S}], [V_{1C}]$ are the vectors of nodal voltages, respectively, in all buses, supply buses, and load buses;

[Y₁] is the nodal admittance matrix for the fundamental frequency, partitioned according to supply and load buses.

From (1), one can derive the voltage vector at load buses as a function of the known supply voltages and load injected currents

$$[\mathbf{V}_{1C}] = \left[\mathbf{Y}_{1}^{CC}\right]^{-1} \left\{ \left[\mathbf{I}_{1C}\right] - \left[\mathbf{Y}_{1}^{CS}\right] \cdot \left[\mathbf{V}_{1S}\right] \right\}.$$
 (2)

In the case that the elements of the vector $[I_{1C}]$, which are injected currents, are functions of the corresponding load bus voltages $[V_{1C}]$, as it is the case of well known load models (e.g., constant power or constant impedance), (2) can be solved in an iterative way.

B. Offline Synchronization for each Harmonic Order

The voltage or current measured values in a network bus, for a harmonic order, are available in magnitude and angle. As the PQ meters also provide the fundamental frequency data, the harmonic angles can be referenced to the fundamental frequency values.

By taking as reference the bus angles obtained by the load flow algorithm stated in Section II.A, the harmonic angles, for each harmonic order, are able to be synchronized. This step is represented by the stage (ii) of Fig. 1. The phasor \dot{V}_1^i regarding the voltage at bus i, determined as the solution of (2), can be written as

$$\dot{V}_1^i = V_1^i e^{j\theta_1^i}.$$
(3)

In PQ monitoring systems where information regarding the phasor of harmonic voltages are not known, the phasors in (3) that correspond to the system state at the fundamental frequency, and especially the phase angles θ_1^i , $i = 1, \dots, nb$, are used by the algorithm to adjust the phasor angles for the different harmonic frequencies which are measured by the PQ meter. In this fashion, a given measured harmonic voltage at bus *i*, which is an output from the meter as

$$\dot{V}_{hM}^i = V_{hM}^i e^{j\phi_{hM}^i} \tag{4}$$

can be adjusted to

$$\dot{V}_{hM}^{i} = V_{hM}^{i} e^{j\left(\phi_{hM}^{i} + h\theta_{1}^{i}\right)} = V_{hM}^{i} e^{j\theta_{hM}^{i}}.$$
(5)

The aforementioned procedure promotes the synchronization of measurement information according to the variations of the harmonic voltage angles with respect to the fundamental frequency voltage, at each system bus. This method provides a simple technique to compensate a possible unavailability of more sophisticated GPS based PQ meters that would provide synchronized phasors at different sites.

C. Individual Harmonic Distortion State Estimation

As shown in Fig. 1, the procedure makes use of the selected or available harmonic frequency measurements as input for the HDSE. This selection might be defined as the most significant harmonic frequencies, or all available harmonic frequencies captured by the PQ meter or still those ones defined by the HDSE user. The selected harmonic orders are organized in a vector **h**, which is given by $[h_1 \cdots h_n]^t$, where *n* is the number of selected harmonic frequencies. The ES algorithm, corresponding to stage (iii) of Fig. 1, is then run for each harmonic order in **h**.

The HDSE model assumes measurements in some given buses and the presence of harmonic distortion due to harmonic injected currents in some customers located in the network.

At this way, the problem to be solved is to find, for a specific harmonic order, the network harmonic injected currents. Once the injected harmonic currents are found, the evaluation of the harmonic voltages at any system bus is straightforward. The HDSE can be formulated as follows:

Determine the injected harmonic currents in (n_c) load buses, $\dot{I}_h^j = I_h^j e^{j\delta_h^j}$, $j = 1, ..., n_c$, in order to minimize the sum of squared errors between the measured and calculated voltage values, given by

$$\min \sum_{k=1}^{n_{\text{meas}}} |\mathbf{ee}_{h}^{k}|^{2} = \sum_{k=1}^{n_{\text{meas}}} \left| \dot{V}_{\text{hM}}^{k} - \dot{V}_{\text{hCalc}}^{k} \right|^{2}$$
(6)

where the calculated voltages in the monitored buses $(k = 1, ..., n_{\text{meas}})$ are evaluated by

$$\dot{V}_{\rm hCalc}^k = \sum_{j=1}^{n_c} \bar{Z}_h^{\rm kj} \cdot \dot{I}_h^j \tag{7}$$

where

| ee_{h}^{k} | estimation error for bus k , for the harmonic order |
|--------------|---|
| 11 | h; |

 \dot{V}_{hCalc}^k calculated voltage at bus k, which is related to the injected currents for the harmonic order in analysis;

 $\dot{V}_{\rm hM}^k$ measured harmonic voltage at bus k;

 Z_h^{kj} impedance matrix element (kj) for the harmonic order h, given by the inverse of the admittance matrix $[\mathbf{Z}_h] = [\mathbf{Y}_h]^{-1}$.

The stated problem formulation (6-7) can be solved by many heuristic search algorithms. In an exhaustive search algorithm,

for example, one must vary the injected harmonic current values (magnitude and angle) and assess the mean squared error for each combination. Another technique uses the Monte Carlo method, randomly simulating a large number of possible solutions (injected current values), and then, using an adequate evaluation criterion to choose the best solution (or solutions).

This paper however uses Evolutionary Strategy, as detailed in Section III, to evaluate the injected currents that generate the least sum of the squared errors in the harmonic estimated voltages for the monitored buses. Once the harmonic injected currents are determined, the system state for any harmonic order is estimated by (7).

After assessing the harmonic state for all harmonic orders, the total harmonic distortion in a given bus k, can then be defined, as

$$\text{THD}_k = \frac{\sqrt{\left(\sum_{i=2}^{\infty} V_i^{k^2}\right)}}{V_1^k}.$$
(8)

III. EVOLUTIONARY STRATEGIES APPLIED TO THE HARMONIC DISTORTION STATE ESTIMATION

A. First Considerations

Evolutionary strategies were developed by Rechenberg and Schwefel [11], [12], who developed research works in these topics in the 1960s at the Technical University of Berlin, Germany.

Such an approach makes use of evolution concepts that apply to a population of individuals, each one representing a possible solution to the given problem. Mutation and recombination processes, that base the main ES operators, do not rely upon each real problem. Rather, only the individual codification and the fitness evaluation method are very much related to the specific problem to be dealt with and must be consistently adapted and designed by the problem formulator.

In a general way, an ES algorithm can be simply described as follows:

t = 0;initialize P(t);evaluate P(t);while (stopping criterion) do P'(t) = variation P(t);evaluate P'(t); Q(t) = f[P(t)] $P(t+1) = \text{selection } [P'(t) \ U \ Q(t)];$ t = t + 1End

In this algorithm, P(t) denotes a population of μ individuals in a given generation t. Q(t) represents a set of individuals that can be considered for selection, according to the function $f[\cdot]$. As illustrative examples, Q(t) can be made equal to the P(t)or Q(t) can be made equal to the null set. A new population P'(t) of λ individuals is then generated through the recombination and mutation operators. New individuals from P'(t) are then evaluated by measuring their "distance" to the "target" or optimal solution of the given problem. As a result, a specific fitness function is established for each one individual. A new population is then formed at generation t + 1, by selecting the most fitted individuals.

After a given number of generations, a stopping criterion is to be met, that usually presupposes that a given individual in the population represents the most acceptable solution to the problem. When such criterion is difficult to be previously established, the number of generations is used as an input parameter [11], [12] to determine the end of the process.

In the following sections the ES operators will be detailed with considerations regarding the HDSE formulation.

B. Codification of Individuals in the HDSE-ES Formulation

The codified individual must represent an alternative solution for the problem, i.e., it should lead to a given harmonic distortion state of the system. Furthermore, the ES formulation considers each harmonic frequency at a time, that is, the general problem is decomposed into a number of harmonic orders selected for the analysis.

In steady state estimation methods, the problem state is generally given by the voltage variables. In the HDSE problem herein stated, for a given network topology and linear load composition, such voltage variables are directly dependent upon harmonic current injections, as shown in (7).

In this manner, the authors proposed an individual codification that consists of variables representing the specific harmonic currents, in terms of their magnitude and angle, given, respectively as a percentage of the magnitude and the angle variation with respect to the fundamental frequency load currents. In such strategy, it is easier to set up limiting values regarding the harmonic components for non linear loads, needed for the ES algorithm, i.e., a "per unit" value is more representative and readily available in PQ meters that provide harmonic components as a percentage of the fundamental frequency value. Thus, for nbuses where injection harmonic currents are to be determined, the individual dimension will be 2n, which corresponds to nmagnitude value percentages and n angle variations, related to the injected fundamental frequency currents.

In ES one also considers for each variable in the individual codification, a mutation step, named σ . It represents the distance that a generated descendent might occupy in the solution space in relation to the current individual location. Thus each parameter, corresponding to the magnitude value percentage or to the angle variation, is given an associated mutation step.

For illustration sake, the representation of the individual codification for the network in Fig. 2, where one is to determine the harmonic currents injected to the 3 bus network, can be designed as follows:

Individual =
$$\begin{cases} k_h^1 & \sigma_{k,h}^1 & \phi_h^1 & \sigma_{\phi,h}^1 \\ k_h^2 & \sigma_{k,h}^2 & \phi_h^2 & \sigma_{\phi,h}^2 \\ k_h^3 & \sigma_{k,h}^3 & \phi_h^3 & \sigma_{\phi,h}^3 \end{cases}$$
(9)



Fig. 2. Representing an individual for harmonic order h.

where

 k_h^i percentage (multiplying factor) with respect to the magnitude value of the fundamental frequency current at the load bus *i* for the harmonic order *h*;

$$\varphi_h^{\circ}$$
 angle variation with respect to the angle of the fundamental frequency load current at bus *i*, harmonic order *h*;

$$\sigma_{k,h}^{i}$$
 mutation step regarding the parameter k, at bus i,
harmonic order h;

- $\sigma^{i}_{\phi,h}$ mutation step regarding the parameter ϕ , at bus *i*, harmonic order *h*;
- I_1^i and fundamental frequency current parameters

 $\theta_1^{\tilde{i}}$ (magnitude value and angle) at bus *i*.

The number of individuals in a given population is empirically determined and must be adjusted according to each application.

C. Mutation Operator

As described in [12], Evolutionary Strategies regard the mutation process as a central role in directing the evolution of a single individual. In this respect, each individual generates a subset of $n_{\rm mut}$ individuals. The variations imposed by the mutation process correspond to small steps around the original individual position.

In order to dynamically assign values to the mutation steps, a self-adaptation method was introduced, as defined in [13] and [14]. This method optimizes the parameters σ (the mutation steps) as the generations evolve. This is carried out in such a way that their absolute values gradually decrease as the solutions move towards better regions.

The mutation operator changes each parameter value x_i of the individual and the corresponding mutation step σ_i according to the following equations:

$$\sigma'_i = \sigma_i \cdot \exp(\tau' \cdot N(0, 1) + \tau \cdot N_i(0, 1)) \tag{10}$$

$$x_i' = x_i + \sigma_i' \cdot N_i(0, 1) \tag{11}$$

where

 σ_i mutation step, index *i*; σ'_i variation of the mutation step σ_i ;

- $N_i(0,1)$ randomly generated value at each generation, with a Gauss probability distribution of 0 (zero) mean value and 1 (unitary) standard deviation value;
- N(0,1) randomly generated value at each generation, with a Gauss probability distribution of 0 (zero) mean value and 1 (unitary) standard deviation value; this is kept constant for each individual;
- τ' learning rate ($\propto (\sqrt{2\beta})^{-1}$);
- τ learning rate ($\propto (\sqrt{2\sqrt{\beta}})^{-1}$).

In ES algorithms, the parameter β , which is a constant that controls the mutation variability, and the initial mutation steps σ must be adjusted for each application.

D. Recombination

The recombination operator, which is associated to the mutation operator, provides variability to the random search towards the problem solution. It is based on the fact the "genetic" information exchanges amongst individuals of a given species might result in better individuals as far as the fitness function is concerned. Also, the recombination operator helps the algorithm in not converging to local optima.

This operator is also called crossover, since it consists in creating new individuals that are formed by genetic information from two original individuals.

The parameters of the new individual are generated by a reproduction process, for instance by the average of each parameter and mutation steps of a pair of original individuals or still by exchanging parameter information from each locus of the pair of original individuals.

E. Fitness Function

The evaluation of the individuals in each population is a process that assesses, through a given fitness function, how close each alternative solution is from the best possible and attainable solution.

The algorithm assumes that harmonic voltage distortions are measured in specific sites of the network. Based on that, the fitness function determines how close the computed voltage harmonic distortions are from the measured ones. The computation of voltage values is based on the injected harmonic currents, which are given by the individual codification, namely its parameters related to the magnitude value and angle of injected harmonic currents.

As for the HDSE problem, the fitness function is based on a vector formed by the absolute values of the differences between the measured and computed estimated harmonic voltage values, which are applied for each individual. This vector provides the required information for the formation of the fitness function. The lower the difference between measured and computed values, the better is the individual under evaluation.

The fitness function or the grade of a given individual in estimating harmonic distortions for harmonic order h, is based on the aggregation of bus estimation errors, given by (6). For a PQ monitoring system comprising n_{meas} measurements, an



Fig. 3. Selection method type $(\mu + \lambda)$.

individual grade was adopted as being the inverse of the sum of the squared errors as show in (6) for harmonic order h, that is, the algorithm must determine the least mean squared estimation error

$$\operatorname{Grade}_{h} = \frac{1}{\sum_{i=1}^{n_{\text{meas}}} (\operatorname{ee}_{h}^{i})^{2}}.$$
 (12)

The fitness function also incorporates a rule that penalizes individuals in which estimation errors are not within an expected range (i.e., such individuals are forced very low grades).

F. Selection

The selection operator is responsible for choosing individuals from generation t to form generation t + 1. In this work, this operator is assumed deterministic, since it strictly selects, for a generation t, the best individuals in the Universe comprising the population P(t)—or alternatively Q(t) which is a subset of P(t), and P'(t), which comprises the descendents of P(t), by mutation and recombination operators. The selection operator is generally of type $(\mu + \lambda)$, which applies the selection to the union of Q(t) and P'(t), or type (μ, λ) , which applies the selection for P'(t) only [13]. Fig. 3 illustrates the $(\mu + \lambda)$ selection operator.

IV. SETTING THE ALGORITHM PARAMETERS

Before starting the HDSE using the ES-based algorithm, one needs to better understand the sensitivity of the method with respect to the variation of the parameters mentioned in the previous section.

Such sensitivity analysis is carried out at the 14-bus network presented in Fig. 4, whose topology and data were extracted from the IEEE site [15]. The analysis is based on the simulation of the third harmonic distortion estimation and a number of PQ meters installed in 6 buses of the network, namely, buses #2, #4, #8, #9, #12, and #14, as shown in Fig. 4.



Fig. 4. Network for HDSE case studies.



Fig. 5. Average estimation error as a function of the number of individuals in the initial population.

A. Setting the Number of Individuals for the ES Initial Population

A first parameter to be analyzed corresponds to the number of individuals used in the initial population of the evolutionary strategy.

The base case considers as fixed the following parameters:

- simulation of 100 generations;
- five mutation operations per individual;
- recombination rate equal to 10%;
- initial mutation step for voltage amplitudes $\sigma_{k,h}^i = 1$;
- initial mutation step for voltage angle variations $\sigma_{\phi,h}^i = \pi$;
- self-adaptation parameter $\beta = 2$;
- selection procedure type $(\mu + \lambda)$;
- recombination operator takes the average between parameters of the two original individuals.

In these conditions, a number of 30 simulations were carried out for alternatives of [2 5 20 40 100 400] individuals in the initial population. The results in Fig. 5 show the average relative bus estimation errors.

One can readily notice that as the number of individuals in the population increases, the estimation errors tend to decrease.



Fig. 6. Evolution for different pairs of initial mutation steps.

However, from 20 individuals per population upwards, the variation on errors is not significant, which shows that this limit ensures a good HDSE.

B. Setting the Mutation Step

The mutation step determines the distance from the original to the generated individual, which sets the possible positions of new individuals in the solution space. A very large mutation step will produce too large variations on the population, what does not characterize the concept of mutation in ES. On the other hand, too small of a step implies in too slow variations, reducing the convergence speed of the algorithm.

For the parameters k (percentage of the magnitude value of the fundamental frequency current) of the individuals the [0.1 0.5 1 2 5] initial mutation steps were considered. As for the parameters ϕ (angle variation with respect to the angle of the fundamental frequency current), the $[\pi/10\pi/4\pi/2\pi 2\pi]$ initial mutation steps were considered.

The same base case was used, considering 20 individuals per population and 30 cases for each of the initial mutation steps considered.

Fig. 6 shows the evolution of pairs of mutation steps starting from the given initial considered values. One can notice that too large initial mutation steps imply in convergence difficulties since the mutation process does not proceed properly. Too low initial mutation steps tend rapidly to zero, which eliminate the evolution variability and, therefore, jeopardize the determination of the global optimal solution. The pair of mutation steps $\sigma_k = 1$ and $\sigma_{\phi} = \pi/2$ have proven a good configuration for the HDSE requirements.

C. Setting the Number of Mutations per Individual

Another important ES parameter is the number of mutations for which each original individual is submitted to.

This parameter is related to the characteristics of the solution region, since it increases the covering of the search space.

The number of mutations per individual were set to [1 5 10 50 100]. During these simulations, the number of individuals in the population was fixed to 20, initial mutation steps $\sigma_k = 1$ and $\sigma_{\phi} = \pi/2$ and 30 simulations in each case.

| DUC | 1 | NUMBER OF MUTATIONS PER INDIVIDUAL | | | | | |
|-----|--------|------------------------------------|--------|--------|--------|--|--|
| BUS | 1 | 5 | 10 | 50 | 100 | | |
| 1 | 1.3526 | 0.6649 | 0.5273 | 0.4022 | 0.4516 | | |
| 2 | 1.3817 | 0.4989 | 0.4346 | 0.2562 | 0.1543 | | |
| 3 | 1.2358 | 0.3120 | 0.1531 | 0.0842 | 0.0589 | | |
| 4 | 1.1489 | 0.5558 | 0.5385 | 0.3228 | 0.2269 | | |
| 5 | 1.1660 | 0.6300 | 0.6175 | 0.3720 | 0.3776 | | |
| 6 | 1.4802 | 1.1147 | 0.9023 | 0.8349 | 0.9120 | | |
| 7 | 0.8732 | 0.2931 | 0.2621 | 0.0993 | 0.0688 | | |
| 8 | 1.2676 | 0.4537 | 0.3389 | 0.2006 | 0.1239 | | |
| 9 | 1.2049 | 0.6523 | 0.5334 | 0.2726 | 0.1551 | | |
| 10 | 1.3017 | 1.0191 | 0.7979 | 0.5766 | 0.8354 | | |
| 11 | 1.1962 | 0.9638 | 1.0658 | 0.9433 | 1.2052 | | |
| 12 | 1.5128 | 0.4517 | 0.2922 | 0.0942 | 0.0514 | | |
| 13 | 1.7985 | 0.9765 | 0.6746 | 0.7539 | 0.9224 | | |
| 14 | 1.5170 | 0.5370 | 0.4112 | 0.1886 | 0.0953 | | |

TABLE I Average Percentual Error as a Function of the Number of Mutations Per Individual in a Population

As shown in Table I, the estimation error tends to be reduced as the number of mutation per individual increases, though this is the case until a certain limit, where the results are no longer dependent on this parameter. One can perceive that varying from 50 to 100 mutations per individual, the estimation errors in the monitored buses are reduced but they can worsen in other system buses. Another very important aspect in selecting this parameter concerns its direct relation to the computation time. That is, the higher the number of mutations per individual, the higher the computation time.

D. Setting Self-Adaptation Parameters

As shown in [12], self-adaptation aims at varying the mutation steps along the evolution of an individual. Thus the mutation step must be reduced as the individual directs towards the optimal solution. The behavior of the mutation process due to changes in self-adaptation parameters might vary the evolution form and speed.

The use of a mutation step for each parameter in the individual provides more evolution diversity, allowing for the individuals to evolve in elliptical regions around the original individual [12].

The parameter β is related to the speed of the mutation step variation in each generation. This parameter was varied at the values [0.1 1 2 10 100] and 30 cases were simulated for each analysis.

Although expressive speed variations were noticed when altering parameter β , benefits were not perceived for values of β greater than 1. For values lower than 1, the evolution of the mutation steps really changes, as can be seen in Fig. 7. Larger variations occur when β is equal to 0.1. As for the other values of β , the evolution of mutation steps followed a similar trajectory.

Although one can notice huge variations in the evolution, as shown in Fig. 7, the estimation errors do not vary substantially with the variation of the parameter β .

Table II shows the estimation errors in each network bus for each value of the self-adaptation parameter. By verifying such errors, one can infer that the sensitivity analysis does not show a suggestive value for this parameter.



Fig. 7. Mutation steps evolution as a function of the β parameter.

 TABLE II

 ESTIMATION ERRORS AS A FUNCTION OF THE SELF-ADAPTATION PARAMETER

| BUS | | Self-adap | PTATION PARA | AMETER eta | |
|-----|--------|-----------|--------------|--------------|--------|
| 000 | 0.1 | 1 | 2 | 10 | 100 |
| 1 | 0.5085 | 0.5952 | 0.7417 | 0.5734 | 0.7430 |
| 2 | 0.4007 | 0.3644 | 0.5359 | 0.4019 | 0.4455 |
| 3 | 0.3340 | 0.2444 | 0.3433 | 0.2259 | 0.2638 |
| 4 | 0.5242 | 0.4556 | 0.5093 | 0.5000 | 0.5638 |
| 5 | 0.5556 | 0.4913 | 0.5639 | 0.5547 | 0.5550 |
| 6 | 1.1131 | 1.3904 | 1.1678 | 1.4486 | 1.1684 |
| 7 | 0.3571 | 0.3140 | 0.2545 | 0.2709 | 0.2964 |
| 8 | 0.6394 | 0.5066 | 0.5088 | 0.5951 | 0.4053 |
| 9 | 0.6866 | 0.7909 | 0.6228 | 0.5632 | 0.5148 |
| 10 | 1.0471 | 1.3505 | 1.0594 | 1.0291 | 0.8784 |
| 11 | 0.9901 | 1.3673 | 1.1234 | 1.3224 | 1.0632 |
| 12 | 0.4204 | 0.4734 | 0.5121 | 0.4150 | 0.5011 |
| 13 | 1.0604 | 0.9386 | 0.8408 | 0.9563 | 1.0008 |
| 14 | 0.6008 | 0.6326 | 0.5012 | 0.4886 | 0.5825 |

E. Setting the Recombination Operator

Besides mutation, variations in populations can be achieved by recombination. This can be carried out by either creating a new individual for which each parameter and mutation step is determined by the average of the parameters of the pair of original individuals or by exchanging the parameters of the two original individuals. Recombination is a powerful genetic operator that tends to create individuals that completely redirect the search, thus avoiding convergence to local optima.

The two alternatives for the recombination were tested for the base case. A total of 100 cases were simulated for each alternative.

As shown in Fig. 8, the alternative of averaging the parameters shows a behavior where larger variations are noticed when comparing with the exchange of parameters between the two original individuals. This variation on the mutation steps does not affect substantially the estimation errors, as shown in Table III. Nevertheless, one is to expect that convergence to local optimal solutions when using the average of parameters is more easily avoided.

F. Setting the Selection Operator

As shown in [11], there is no consensus on the selection type. This paper compares the two selection types for the HSE,



Fig. 8. Mutation steps evolution related to the alternatives of recombination.

| | ERROR FOR THE TWO RECOMBINATION | | | | |
|-----|---------------------------------|----------------------|--|--|--|
| BUS | | OPTIONS | | | |
| | AVERAGE | EXCHANGE INFORMATION | | | |
| 1 | 0.8319 | 0.8144 | | | |
| 2 | 0.6432 | 0.5845 | | | |
| 3 | 0.3528 | 0.3748 | | | |
| 4 | 0.6327 | 0.5827 | | | |
| 5 | 0.6430 | 0.6139 | | | |
| 6 | 1.1738 | 1.3238 | | | |
| 7 | 0.4024 | 0.3380 | | | |
| 8 | 0.5437 | 0.6643 | | | |
| 9 | 0.7770 | 0.6815 | | | |
| 10 | 1.2743 | 1.1689 | | | |
| 11 | 1.1813 | 1.0825 | | | |
| 12 | 0.5382 | 0.6244 | | | |
| 13 | 0.8523 | 0.9375 | | | |

 TABLE III

 BUS ESTIMATION ERRORS FOR THE RECOMBINATION OPTIONS

namely $(\mu + \lambda)$ and (μ, λ) , by simulating 100 cases for each selection procedure.

0.6687

0.6936

Fig. 9 shows the evolution of mutation steps for the two selection types. The (μ, λ) type, which does not consider elitism, led to large variations on the mutation steps and did not converge to a solution. One can also notice that the algorithm does not converge for the (μ, λ) selection type, by analyzing the estimation errors in Table IV.

V. RESULTS

The total harmonic distortion (THD) is determined for each bus in the IEEE test network shown in Fig. 4. The THD is determined by (8), that considers the estimation results obtained at each harmonic order h.

PQ meters are considered at buses #2, #4, #8, #9, #12, and #14 and the simulation includes harmonic orders 3, 5, 7, 9, 11, and 13 for the THD composition in each network bus.

As previously mentioned, the algorithm carries out the estimation for each harmonic order in an independent way. Following that, the total harmonic distortion is readily computed.



Fig. 9. Mutation steps evolution related to the selection type.

| Duc | SELECTIO | n Type |
|-------------|----------|-------------------|
| B 03 | (μ,λ) | $(\mu + \lambda)$ |
| 1 | 14.7769 | 0.8454 |
| 2 | 14.6325 | 0.6937 |
| 3 | 14.4508 | 0.4865 |
| 4 | 13.4392 | 0.7645 |
| 5 | 13.6969 | 0.7716 |
| 6 | 11.8724 | 1.2729 |
| 7 | 11.4144 | 0.4601 |
| 8 | 11.2406 | 0.5736 |
| 9 | 10.6349 | 0.7973 |
| 10 | 10.3667 | 1.1879 |
| 11 | 10.5926 | 1.2099 |
| 12 | 10.8155 | 0.6366 |
| 13 | 10.5179 | 1.1006 |
| 14 | 9.4858 | 0.7107 |

TABLE IV ESTIMATION ERROR FOR THE SELECTION TYPES

The following algorithm parameters were considered for the first case study, namely case #1:

- number of generations: 500;
- initial population size: 40;
- number of mutations per individual: 5;
- recombination rate per generation: 10%;
- initial mutation steps: $\sigma_k = 1$ and $\sigma_{\phi} = \pi$;
- self-adaptation parameter: $\beta = 2$;
- selection type $(\mu + \lambda)$;
- recombination method: average of parameters.

Table V shows estimation errors for each harmonic order. These results actually show the average error for 30 simulation cases in each harmonic order. Similar results were found in [16], though focusing on the estimation of specific harmonic order distortions. This table shows fairly small estimation errors. The outlined lines in the table show the monitored buses. Fig. 10 shows the evolution speed at the solution space, by plotting the average grade for the best individuals in each harmonic order along the generations. This grade is obtained according to (6), representing the inverse of the squared deviations between measured and computed harmonic voltage distortions. Although for some harmonic orders the best individuals are not so well



Fig. 10. Average grade of best individuals (vertical axis) in each harmonic order along the generations (horizontal axis).

 TABLE V

 Estimation Error (%) for Each Harmonic Order

| | HARMONIC ORDER | | | | | |
|-----|----------------|--------|--------|--------|--------|--------|
| BUS | 3 | 5 | 7 | 9 | 11 | 13 |
| 1 | 0.3011 | 1.4361 | 0.9143 | 0.2239 | 0.0416 | 0.5515 |
| 2 | 0.2087 | 1.4178 | 0.2884 | 0.0352 | 0.0265 | 0.4715 |
| 3 | 0.1155 | 1.3434 | 0.1728 | 0.0205 | 0.0213 | 0.4600 |
| 4 | 0.2059 | 1.0616 | 0.0411 | 0.0053 | 0.0017 | 0.0734 |
| 5 | 0.3408 | 1.1694 | 0.2054 | 0.2230 | 0.0404 | 0.4252 |
| 6 | 0.9816 | 0.7969 | 0.1441 | 0.6052 | 0.5011 | 0.5294 |
| 7 | 0.0782 | 0.6707 | 0.0535 | 0.0125 | 0.0875 | 0.2008 |
| 8 | 0.1786 | 1.1199 | 0.1492 | 0.0124 | 0.0810 | 0.1084 |
| 9 | 0.2241 | 0.5227 | 0.1913 | 0.0304 | 0.1671 | 0.4033 |
| 10 | 0.1606 | 0.5286 | 0.5390 | 0.2800 | 0.5236 | 1.0011 |
| 11 | 0.8894 | 0.5185 | 0.2987 | 0.3013 | 0.4648 | 0.7420 |
| 12 | 0.0750 | 0.2000 | 0.0556 | 0.0250 | 0.0414 | 0.2551 |
| 13 | 0.7392 | 0.2835 | 0.1388 | 0.2131 | 0.1332 | 0.7624 |
| 14 | 0.0842 | 0.3115 | 0.3637 | 0.0717 | 0.1189 | 0.6046 |

graded, the estimation errors are satisfactory, as can be seen inTable V.

The continuous growth of individual grades for each harmonic order confirms the elitism of the proposed algorithm and its capacity in finding solutions for the HDSE. Due to the complexity of the solution space, the monotonous growth of the best individual grades might represent some difficulty in the recombination operator to input variability to the evolution, taking individuals more quickly to better solution regions.

Fig. 11 shows the evolution of mutation steps for each harmonic order considered. One can perceive that mutation steps can vary along the generations but tend to values close to zero. Those variations are mainly due the recombination process that determines variability to the evolution.

Figs. 12 and 13 show the magnitude and angle, respectively, related to the calculated and the reference third harmonic currents in each network bus. Although errors in third harmonic currents are considerably high, voltage estimation is adequate.



Fig. 11. Evolution of mutation steps (vertical axis) for each harmonic order (H) during the generations (horizontal axis).



Fig. 12. Third harmonic current magnitude in each bus.



Fig. 13. Third harmonic current angle in each bus.

This can be explained by (6) and (7), since in this case, different combinations of injected currents might produce very small voltage estimation errors (suboptimal solutions), due to the relative positions of PQ meters and injected currents. Nevertheless the method still works in an appropriate way in estimating harmonic voltage distortions. This could be improved by a different allocation of PQ meters in the network. The voltage magnitude and angle values are shown in Figs. 14 and 15. Since the fitness function is based on voltage values obtained from the individuals, the resulting calculated and reference voltage



Fig. 14. Third harmonic voltage magnitude in each bus.



Fig. 15. Third harmonic voltage angle in each bus.

values were very close. Similar behavior was verified for other harmonic orders.

Once harmonic voltage distortions are obtained for each harmonic order and network bus, THD values can be straightforwardly obtained. The reference and estimated THD values are shown in Table VI, alongside with relative and absolute estimation errors. The reference THD values simulate the values to be determined.

The absolute error shown in Table VI represents the deviation with respect to the rated voltage. It is expected therefore that relative THD errors are to be much higher. The algorithm though determined fairly small relative errors, not greater than 5%.

In order to check the robustness of the proposed methodology, a second case study, case #2, is considered, with PQ meters at network buses #2, #8, and #12 only. Table VII shows estimation errors and THD values when considering these three PQ meters installed in the system. The much higher estimation errors in nonmonitored buses are due to the low visibility of the PQ meters associated with the network topology and their installation sites, even though (i.e., with low visibility PQ meters) the results are satisfactory, especially when one considers absolute errors.

A simple way to improve the estimation results is by considering other known information or system measurements, for instance, harmonic currents. Since the proposed methodology considers the variation of angles and percentage of magnitude of fundamental currents as parameters of the individuals codified in the HDSE, the inclusion of a measured current limits the

TABLE VI REFERENCE AND ESTIMATED THD VALUES AND ESTIMATION ERRORS FOR CASE #1

| | THD | | ERROR (%) | |
|-----|-----------|-----------|-----------|----------|
| Bus | Reference | ESTIMATED | RELATIVE | ABSOLUTE |
| 1 | 0.0545 | 0.0548 | 0.5468 | 0.0298 |
| 2 | 0.0528 | 0.0529 | 0.1370 | 0.0072 |
| 3 | 0.0502 | 0.0496 | 1.1816 | 0.0593 |
| 4 | 0.0405 | 0.0395 | 2.4706 | 0.1001 |
| 5 | 0.0421 | 0.0410 | 2.7515 | 0.1159 |
| 6 | 0.0378 | 0.0379 | 0.3151 | 0.0119 |
| 7 | 0.0394 | 0.0391 | 0.7450 | 0.0294 |
| 8 | 0.0426 | 0.0424 | 0.2744 | 0.0117 |
| 9 | 0.0409 | 0.0407 | 0.6056 | 0.0248 |
| 10 | 0.0407 | 0.0425 | 4.4646 | 0.1818 |
| 11 | 0.0398 | 0.0406 | 1.8083 | 0.0721 |
| 12 | 0.0387 | 0.0388 | 0.2835 | 0.0110 |
| 13 | 0.1952 | 0.2009 | 2.8884 | 0.5639 |
| 14 | 0.2082 | 0.2085 | 0.1322 | 0.0275 |

 TABLE VII

 REFERENCE AND ESTIMATED THD VALUES

 AND ESTIMATION ERRORS FOR CASE #2

| | THD | | Error (%) | |
|-----|-----------|-----------|-----------|----------|
| BUS | REFERENCE | ESTIMATED | RELATIVE | ABSOLUTE |
| 1 | 0.0545 | 0.0560 | 2.7401 | 0.1493 |
| 2 | 0.0528 | 0.0532 | 0.6888 | 0.0364 |
| 3 | 0.0502 | 0.0481 | 4.0441 | 0.2028 |
| 4 | 0.0405 | 0.0390 | 3.8868 | 0.1576 |
| 5 | 0.0421 | 0.0431 | 2.2602 | 0.0952 |
| 6 | 0.0378 | 0.0428 | 13.3189 | 0.5035 |
| 7 | 0.0394 | 0.0396 | 0.4340 | 0.0171 |
| 8 | 0.0426 | 0.0408 | 4.1465 | 0.1765 |
| 9 | 0.0409 | 0.0438 | 7.1387 | 0.2921 |
| 10 | 0.0407 | 0.0461 | 13.1931 | 0.5372 |
| 11 | 0.0398 | 0.0449 | 12.5873 | 0.5016 |
| 12 | 0.0387 | 0.0370 | 4.4007 | 0.1705 |
| 13 | 0.0390 | 0.0401 | 2.5793 | 0.1007 |
| 14 | 0.0416 | 0.0573 | 3.,6589 | 1.5682 |

search space, which obviously helps the algorithm to take the solution to the global optimal solution. Table VIII shows the estimation errors for a third case study, case #3, in which the same three PQ meters are installed in the system, though one of the meters also outputs the injected harmonic currents at network bus #8. One can notice a significant reduction in estimation errors for most network buses.

VI. CONCLUSION

This paper dealt with a new method for the estimation of individual and total harmonic distortions in network buses based on the measurement of voltage distortions in a limited number

| | THD (%) | | Error (%) | |
|-----|-----------|-----------|-----------|----------|
| BUS | REFERENCE | ESTIMATED | RELATIVE | ABSOLUTE |
| 1 | 0.0545 | 0.0542 | 0.4897 | 0.0267 |
| 2 | 0.0528 | 0.0527 | 0.2176 | 0.0115 |
| 3 | 0.0502 | 0.0486 | 3.1340 | 0.1572 |
| 4 | 0.0405 | 0.0384 | 5.3272 | 0.2159 |
| 5 | 0.0421 | 0.0403 | 4.3416 | 0.1830 |
| 6 | 0.0378 | 0.0381 | 0.7013 | 0.0265 |
| 7 | 0.0394 | 0.0380 | 3.4948 | 0.1378 |
| 8 | 0.0426 | 0.0426 | 0.0602 | 0.0026 |
| 9 | 0.0409 | 0.0404 | 1.2209 | 0.0500 |
| 10 | 0.0407 | 0.0404 | 0.7511 | 0.0306 |
| 11 | 0.0398 | 0.0386 | 3.1834 | 0.1268 |
| 12 | 0.0387 | 0.0390 | 0.7811 | 0.0303 |
| 13 | 0.0390 | 0.0443 | 13.5514 | 0.5291 |
| 14 | 0.0416 | 0.0499 | 19.8447 | 0.8264 |

TABLE VIII REFERENCE AND ESTIMATED THD VALUES AND ESTIMATION ERRORS FOR CASE #3

of buses of the power system. Evolutionary strategy was considered as a tool to determine the best possible solution in a vast search space. The main advantage in using such a technique relies upon its modeling facilities as well as its potential to solve fairly complex problems.

The Evolutionary Strategy shown in this paper is a promissing tool to deal with the HDSE problem, where individuals in a population representing possible solutions are submitted to evolutionary operators and evaluated in each generation. During the evolution, only the best individuals (best problem solutions) survive. Another benefit is that the proposed approach requires fewer simulations to find a viable solution when compared to the Monte Carlo statistical method.

The 14-bus IEEE test network [15] was taken as basis for the case studies to estimate 3rd, 5th, 7th, 9th, 11th, and 13th harmonic voltages. A total of 30 cases for each harmonic order have shown the robustness of the algorithm and promising estimation results. Harmonic voltage distortions for each harmonic order were used to compose the THD for each network bus. For all simulations, estimation errors do not exceed 1%.

In low visibility conditions of the PQ monitoring system, some possible actions to reduce estimation errors include the consideration of few additional measurements, such as harmonic currents at lines or buses. Case study #3 utilized only three PQ meters with information of harmonic voltage distortions and the injection of harmonic current in one single bus. The algorithm was then able to reduce estimation errors by more than 50% in some specific buses when compared to case study #2 that did not consider the measurement of the injected harmonic current.

The authors have considered decoupled harmonic sources modeled as constant current injections and network elements as linear components. Moreover, nonlinear characteristics with frequency couplings were not dealt with in this paper. This decision was mainly for simplicity reasons, though more detailed network and load representation could be implemented on future modeling and simulations. Computation time can be further reduced by using techniques such as parallel processing:

- estimation of different harmonic orders can be computed in different processors;
- groups of individuals created during the ES can be evaluated in different processors.

These characteristics show that one can envisage online or quasi online applications. Also, when considering time-varying harmonics, the authors believe that previously evolved populations, stored in a database and prepared in offline mode, could be used to speed up processing.

The results obtained in this paper, though in a small size network, show promising future research with respect to HDSE.

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