

## A GENETIC BASED TECHNIQUE FOR THE DETERMINATION OF POWER SYSTEM TOPOLOGICAL OBSERVABILITY

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The management of a large electric power system requires detailed knowledge of what is happening in each one of its nodes (power sources, power drains) and branches (power lines connecting nodes) in any given instant of time so that efficient use of the resources can be made and incidences detected. The knowledge about the networks is obtained by means of state estimation techniques based on statistical inference using a set of redundant measurements. The measurements that are usually considered are voltages in the nodes, active and reactive power flow in the branches and injection in the nodes. There is a non linear relationship between the measurements obtained ( $\mathbf{z}$ ) and the state of the system ( $\mathbf{x}$ ). This relationship is affected by the inherent errors of the measurement equipment ( $\mathbf{e}$ )

$$\mathbf{z}=h(\mathbf{x})+\mathbf{e}$$

Obviously, for the system to have a solution for  $\mathbf{x}$  the set of measurements must be large enough and their locations appropriate for the system to be solved (rank of  $h$  must be at least as large as the size of  $\mathbf{x}$ ). When these conditions are met the system is said to be observable.

Determining the observability of a system is not a simple task in large power systems. Two main approaches have been followed in the literature in order to address it. On One hand, some authors have resorted to numerical methods trying to determine the range of the Jacobian matrix corresponding to  $h(x)$ . Within this group we may find [1][2][3]. Due to the precision problems of numerical methods some authors have proposed approaches based on graphs of the power systems [4][5][6][7]. These methods have been called topological methods. The basic idea of topological methods for determining observability is based on the seminal result by Krumpholz and col [4] whereby a system can be said to be topologically observable with respect to a measurement set consisting of one voltage magnitude measurement and paired P, Q measurements if and only if there exists a spanning tree of the system of full rank. In practical terms, we need to find a spanning tree that contains all the nodes in the network and where the branches have measurements assigned to them. To this end, the measurements that are available in the network are assigned to branches following two criteria: The power measurements in the branches of the graph are assigned to the branches of the tree corresponding to their location. The node power measurements are assigned to one (and only one) of the branches that converge in the node. It is important to take into account that a measurement can only be used once in the construction of the tree.

To address the problem of finding this spanning tree many heuristic solutions have been proposed such as [1][2][3], they usually differ in the algorithm they use for assigning node measurements to branches when constructing the tree, but their basic procedure is very similar in terms of reading the network sequentially and constructing a tree in a stepwise fashion. As with most tree construction techniques, these approaches are very

prone to getting stuck, that is, running out of possible paths before achieving a full rank tree due to previous inadequate selections of branches to follow in the power system graph. As a consequence, backtracking is usually required, which in the extreme case leads to a random search. This problem becomes even more poignant due to the quasiexponential growth of possible trees as the size and/or connections of the power system grow.

In this paper we have chosen a different approach by using evolutionary techniques for the determination of the spanning tree of full rank. Some authors have already made some inroads in the use of this approach [8][9]. There are three hurdles to overcome in the use of a genetic algorithm based solution to determine topological observability: the encoding of the trees, defining the appropriate genetic operators and fitness function, reigning in sufficient computing power to be able to solve large problems. In this paper we will concentrate on the first two.

Encoding valid trees that correspond to the power system we are considering is a difficult problem as there are many restrictions to the way in which they can be constructed. Consequently, if the encoding is not carefully handled, most of the chromosomes would represent invalid solutions, that is, trees that do not represent the network and/or trees that do not correspond to an observable solution, especially after mutations or crossovers. To verify all the constraints and generate trees that are always valid, in this work we have chosen an indirect representation of the phenotype in the chromosome. Our chromosomes do not represent the tree, but rather the way in which we construct the tree from the information on the real power system. Thus, when constructing a tree from the system we first obtain a connectivity matrix where we represent the connections between the nodes of the power system and whether these connections or the corresponding nodes have measurements. Once this matrix is constructed we can define the maximum connectivity  $C_{max}$  as the number of connections of the node with maximum number of real connections. The chromosome that encodes the possible trees representing the power system will have a length of  $2n$  integers, the first one between 1 and  $n$  and the rest with values between 0 and  $C_{max}$  where  $n$  is the number of nodes in the power system. The chromosome may be written as  $P_1, F_1, P_2, F_2, \dots, P_n, F_n$ . where  $P_i$  represents the relative number of the node and  $F_i$  the fan out of this node (number of branches departing from it). Thus, if we want to construct a tree from the chromosome we take  $P_1$  and go to the corresponding line in the connection matrix. We take a  $F_1$  (fan out value) and it will tell us the fan out of this node (number of branches originating in it). If this number is larger than  $C_i$  (number of possible connections for this node at this time), we take as effective fan out  $F_i^{eff} = F_i \bmod C_i$  otherwise  $F_i^{eff} = F_i$ . The following  $F_i^{eff}$  pairs in the chromosome will correspond to the nodes connected to node  $i$ . Whenever we use a node or a measurement it is eliminated from the connection table. This process is carried out recursively until the whole tree is constructed or a situation where no more nodes are available in the connection matrix lines corresponding to the leaf nodes of the tree.

This strategy for encoding trees in chromosomes provides a way to use a very simple genotype ( $2n$  integer values for a power system with  $n$  nodes) that always results in valid trees. Thus, now all the genetic algorithm has to do is to find one of these chromosomes that produces a whole tree, that is, a tree that contains all of the nodes in the power system. To do this we will define a very simple fitness function that increases with the number of nodes in the resulting tree with a modulating term that increases with the percentage of nodes outside the tree that contain node measurements.

As a result of the simplicity of the genotypic encoding, the genetic operators that are used are quite straightforward. Take into account that we are handling integer value

strings. Thus, crossover is a classical two point crossover and mutation is a simple random mutation. The only element we must take into account is the significance of mutations, a mutation in a gene in the left part of the chromosome produces more drastic changes in the resulting phenotype than one in the right part of the chromosome and this is taken into account through a positional weight term for the mutation.

The preliminary results of applying this approach to the standard 14 and 24 node problems are very promising and complete results to these and larger problems will be presented as well as a comparison to the results of other authors.

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