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ANT-BASED SEARCH STRATEGY FOR INDUSTRIAL MULTIPLE-FAULT DIAGNOSTICS

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Abstract – A swarm-intelligence solution to industrial problems of automatic multiple-faults diagnostics is proposed. In particular, drawbacks of swarm-based algorithms in heuristic search strategy related to the mutual dependence of solutions are overcome by a likelihood-based trail intensity modification of ant-colony optimization. Experimental results of comparison tests with an evolutionary state-of-the-art solution of a case study on an advanced industrial system for remote monitoring, diagnostics, and maintenance are reported.

Keywords: Artificial Intelligence, Industrial Diagnostics, Multiple Faults Diagnosis.

1. INTRODUCTION

Swarm intelligence is a biologically-inspired soft computing technique based upon the study of collective behaviour in decentralized and self-organized systems [1]. These systems typically consist of numerous autonomous simple agents whose movements through a continuous space are governed by various local forces exerted by other nearby agents or by the environment. Although normally a centralized control structure dictating how individual agents should behave is missing, local interactions among such agents often lead to the emergence of an interesting global behavior.

The vast majority of applications of swarm intelligence have involved modelling movements in a 2D or 3D physical space, especially in the simulation of biological populations, computer graphics, and robotic control [1]-[4]. Inspired by successes in these applications, recently several efforts have been carried out to generalize swarm methods to higher dimensional abstract spaces. In particular, particle swarms [5] and bacteria-inspired chemotaxis algorithms [6] have shown their applicability as general-purpose numerical optimization methods.

Among high-dimensional numerical problem, Multiple Faults Diagnosis (MFD) problem [7] is a formidable task. However, MFD features cannot be easily faced by a classical swarm intelligence approach [3]. In particular, MFD defines a solution composed by a set of possible faults, where the occurrence of each fault is not conditioned to other faults. Conversely, most promising swarm intelligence methods, such as classical Ant Colony Optimization (ACO) algorithms [3], resolve numerical optimization problems (e.g. the traveling salesman problem), with optimal solutions composed by a set of mutually-conditioned choices influencing the final solution.

In this paper, a novel swarm intelligence method, inspired to a likelihood-based trail intensity modification of the classical algorithm ACO aimed at overcoming the above drawback, is proposed for MFD problems (and similar) of industrial diagnostics. In particular, after stating analytically the MFD problem in Section2, the state of the art of the proposed solutions is analyzed in Section 3. In Sections 4 and 5, the and the implementation of the proposed method are outlined, respectively. Finally, in Section 6, the preliminary experimental results of the proposed approach application to a case study of industrial diagnostics, with performance comparison to a classical evolutionary solution, are reported.

2. MULTIPLE-FAULTS DIAGNOSIS PROBLEM

Multiple Fault Diagnosis problems are characterized as the 4-tuple [7]: $<D, M, C, M^+>$ where:

- D is a finite nonempty set of faults,
- M is a finite set of symptoms,
- C is a relation, which is a subset of DxM, pairing faults with associated symptoms such that $(d,m) \in C$ means that the fault d may cause the symptom m,
- M^+ is a subset of M identifying the observed manifestations.

A diagnosis DI (i.e. a subset of D) identifies the disorders eventually responsible for the symptoms in M^+. A prior probability p_j is associated to each fault d_j in D. Values are assumed to exist and faults in D are assumed to be independents each other. Associated with each "causal association" in the matrix C is a causal strength c_{ij} representing how frequently a fault d_j causes the symptom m_i. The causal strength represents the conditional probability $P(d_j$ causes $m_i|d_j)$. An example of prior probability and C matrix 3x3 one-half dense is reported in Tab. 1.

Table 1. Prior Probability and C Matrix: 3x3 One-Half dense.

	d_1	d_2	d_3
p_i	0,58	0,21	0,14
m_1	0,91	0,38	0,50
m_2	0,02	0,25	0,17
m_3	0,13	0,56	0,16

Using this approach, a relationship for calculating the "relative likelihood", denoted $L(DI, M^+)$, of a diagnosis DI, given the observable symptoms M^+, can be derived. The likelihood is the product of three factors:

$$L(DI, M^+) = L_1 L_2 L_3 \tag{1}$$

where the first factor,

$$L_1 = \prod_{m_i \in M^+} (1 - \prod_{d_j \in DI} (1 - c_{ij})) \tag{2}$$

is the likelihood that faults in DI cause the manifestations in M^+, the second factor,

$$L_2 = \prod_{d_j \in DI} \prod_{m_l \in effects(d_j) - M^+} (1 - c_{ij}) \tag{3}$$

is the likelihood that faults in DI do not cause the manifestations outside of M^+, and finally, the third factor,

$$L_3 = \prod_{d_j \in DI} \frac{p_j}{(1 - p_j)} \tag{4}$$

is the likelihood that a highly probable fault d_j contributes significantly in the overall likelihood of a diagnosis DI containing d_j.

The quantity L in (1) has to be maximized in order to find the most probable cause (fault) determining the observable symptoms.

3. STATE OF THE ART

Many methods for finding the optimal solution of problem (1) have been proposed [8]-[18]. Some of these can be derived from the exact approaches for deriving the marginal a-posteriori probabilities, such as clique-tree propagation algorithms [8]-[9], by replacing the summation by maximization. Dawid [10] developed an efficient algorithm to calculate the solution in a junction tree by using max-marginalization. The max-marginalization can be employed also to eliminate variables.

However, if the number of configurations is large, the maximization itself will be very costly. A message-passing scheme derived by Pearl [11], the "belief revision" is guaranteed to converge and find the optimal solution for cases of cycle-free graphs. Confronted with the intractability of exact inference, many researchers have resorted to approximate inference algorithm.

Among the proposed approximate inference algorithms, search-based optimization methods, such as genetic algorithms (GAs), can be employed to find an approximate solution of the problem (1). Several authors have used GAs to find approximate solutions [14]-[16]. The performance of GAs is highly dependent on their parameter settings. Kask and Dechter [17] showed how their combination with other methods, such as stochastic simulation, achieves better performance than individual application. Yuan et al. [18] developed the annealed algorithm, using Monte Carlo methods for sampling the target distribution, applied to the simulation of a non homogeneous Markov chain. However, its performance is to be improved by fine adjustments of the annealing speed and the number of iterations.

4. THE PROPOSED METHOD

The issue stated by eq. (1) can be classified as a hard combinatorial optimization problem. This kind of problem is defined as [19]: given a graph with N nodes numbered from 1 to N, an accurate permutation of N elements among 2^n - in the worst case –verifying a specified rule has to be found.

Owing its powerful performance in combinatorial optimization problems [3], ACO approach is an excellent candidate. The main idea is to adapt the classical Ant-Colony system to the search of optimal diagnosis in industrial MFD by modifying its strategy of conditioning potential solutions suitably.

The feasibility of this approach was analyzed by checking the problem representation of the set of definitions provided by Dorigo *et al* in [3], [12]-[13]. Therefore, the following considerations must be taken into account:

- The number of the admissible states of the problem are 2^n;
- The objective function f and the cost function J overlap ($f = J = L$ the likelihood function) ;
- The cost function, evaluated upon a current node during the search, depends on the occurred symptoms and previous ant's path;
- Specifying a set of visited node (a tour) the ants associated to several permutations of such nodes show the same value of f (redundant paths);
- Several sub-paths lead to a probability of null transition.

The above points point out the need of the MFD problem for a different formulation of the ant colony algorithm with respect the common one.

In the classical ACO, at each iteration, a number of artificial ants are considered [3]. Each of them builds a solution by walking from vertex to vertex on the graph with the constraint of not visiting any vertex already visited in her walk. At each step of the solution construction, an ant selects the following vertex to be visited according to a stochastic mechanism biased by the pheromone: when in vertex i, the following vertex is selected stochastically among the unvisited ones. In particular, if vertex j was not visited, it can be selected with a probability proportional to the pheromone associated with edge (i, j).

At the end of an iteration, on the basis of the quality of the solutions constructed by the ants, the pheromone values are modified in order to bias ants in future iterations to construct
solutions similar to the best ones previously constructed.

However, in state-of-the-art versions [3], [12]-[13], pheromone is associated with the edge (*i,j*), by constraining to its current position the choice of a single ant when has to visit the next vertex. In this way, the final solution depends on the order the ants visit the vertexes. However, in the definition of MFD problem, the presence or the absence of a specific fault d_i can not be affected by all other faults [7]. In other words, the final solution must not be dependent on the order of the choices d_i but only on their presence (or absence).

Consequently, the classical ant-based approach of [3], [12]-[13] can not be applied to MFD problem straightforwardly.

Then, in the present paper, a different approach is proposed: the fully-connected graph (where the vertexes are the possible faults) is considered. In particular, the vertex to be considered are the faults d_j (the presence of fault) and also the associated $\neg d_j$ (absence of the fault d_j). Again, the graph is weighted on the vertex (and not on the edge (*i.j*) such as in the classical approach). The graph in Fig. 1 is an example for a multiple diagnosis problem with only 3 faults.
At each iteration, the variable pheromone (deposited by the ants) is associated at each vertex and not on the edge (i.e. at choice presence/absence of fault d_i). In this way, the next ant choice is not conditioned by the current one and the final solution does not depends on the order by which the ants visited every vertex (such as in MFD problem).

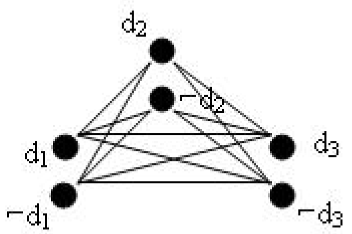

Fig. 1. Example of a fully connected graph for a multiple diagnosis problem of 3 faults.

At this point, let be $d_j \in D$ of the matrix C in the multiple faults diagnosis problem are the towns of weighted graph, the problem of finding best *DI* for an observable symptoms can solved with ant based strategy.
Indeed, let $\tau_i(t)$ be the intensity of trail on the vertex d_i at time *t*. At each iteration of the algorithm trail intensity becomes:

$$\tau_i(t+1) = \rho \cdot \tau_i(t) + \Delta\tau_i(t,t+1) \qquad (5)$$

where ρ is a coefficient such that (1-ρ) represents the evaporation of trail,

$$\Delta\tau_i(t,t+1) = \sum_{k=1}^{m} \Delta\tau_i^k(t,t+1) \qquad (6)$$

m is the number of ants, $\Delta\tau_i^k(t,t+1)$ is the quantity of trail laid on the vertex d_i by k-th ant between time *t* and *t+1*.

The ant is constrained to visit *n* different towns by associating to it a data structure called *tabu list*, storing the visited towns up to time 5t and forbidding the ant to visit them again before a tour has been completed.

In the proposed approach, when the ant visits a specific vertex d_i (i.e. the fault d_i is considered in the solution), the tabu list has to contain both the specific vertex d_i and the associated $\neg d_j$ (because if the presence of a specific fault d_i is considered, the absence of the same fault in that solution must be excluded).

Again, the "visibility" η_i is the quantity L_i (L_i is the weight associated to the vertex d_i), and the transition probability from the vertex d_i to the next vertex for the *k-th* ant is:

$$p_i(t) = \frac{[\tau_i(t)]^\alpha \cdot [\eta_i]^\beta}{\sum_{i \in allowed} [\tau_i(t)]^\alpha \cdot [\eta_i]^\beta} \qquad (7)$$

where "allowed" are the vertexes not in the *tabu* list, and α and β are parameters for controlling the relative importance of trail versus visibility.

Different choices for computing $\Delta\tau_i(t,t+1)$ for the *k-th* ant causes different instantiations of the ant algorithm.
In particular, in the proposed method, the quantity (1) acts as weight L_i for the generic vertex d_i. Thus, the relative likelihood in (1) allows the trail intensity in (6) to be chosen.

5. IMPLEMENTATION

According to the previous definition, an Ant Colony algorithm with vertex trail update for the solution of the MFD problem is defined. A phase of initialization, before the starting of search, takes place, i.e. the algorithm parameters are set: a binary string representing the occurred symptoms is filled out, the tendency matrix and prior probability are loaded, and each element of the vertex trail matrix is set to a default value too. Afterward, the ants on a single fault presence/absence (a node) are placed randomly. Then the *tabu* list, the initial diagnosis (coded as symptoms), and the list of the visited nodes are associated to each ant. Such a phase is repeated at the beginning of each colony tour. Thereafter, each ant in the colony carries out a complete search on the graph, pointing out a diagnosis as a whole. The probability of the ant to move from a current node to a next one (updating of the ant diagnosis) can be set as either the value reported in eq. (7), or with uniform distribution (when the likelihood function is 0 for all the accessible nodes [7]). Obviously, during the ant journey, all the quantity associated to the ant are updated at each visited node. Then, the founded solution for each ant is used in order to update the vertex trail matrix for the next colony tour and the solution with maximum value is stored. The algorithm ends after a predetermined number of set cycles.

6. EXPERIMENTAL RESULTS

The proposed approach has been tested and compared with a GA approach on MFD problem reported in [16]. In [16], a GAs approach to the MFD problem has been applied to the tendency matrix with 15 faults and 10 anomalies. The authors found the best solution for a value of goodness (likelihood) L = $7.70 * 10^{-2}$ of the equation (1).

With this aim, the proposed ant-based diagnostic algorithm was implemented in Matlab 7.0, and applied on the same tendency matrix in [16]. The parameter setting of ant-based diagnostic algorithm was:

- *m = 100;*
- $\alpha = 1$;
- $\beta = 30$

where *m* is number of ants, α and β are the weighted trail coefficient and the visibility weighted coefficient defined in (7), respectively.

In Fig. 2, the average likelihood is represented as a function of the number of cycles. After only 200 iterations the ant-based diagnostic algorithm found the best solution for a value of goodness $L = 7.77 * 10^{-2}$ of the equation (1), corresponding to the same solution of GAs approach reported in [16].

Hence, the two approaches are very similar in the performance and results, although the ant-based diagnostic approach is simpler in parameter setting than the GAs approach and requires a lower number of iterations (only 200 in this case).

7. CONCLUSIONS

In this paper, a novel approach to the Multiple Faults Diagnosis problem based on swam intelligence, has been proposed.

The proposed method has been compared to the GAs approach on MFD problem [16]. Preliminary performance tests showed encouraging results. They constitutes a sound basis for a possible more effective alternative to classical MFD solutions, in particular where a complexity of the problem is high. However, the study is currently ongoing, and a final conclusion can not be drawn yet.

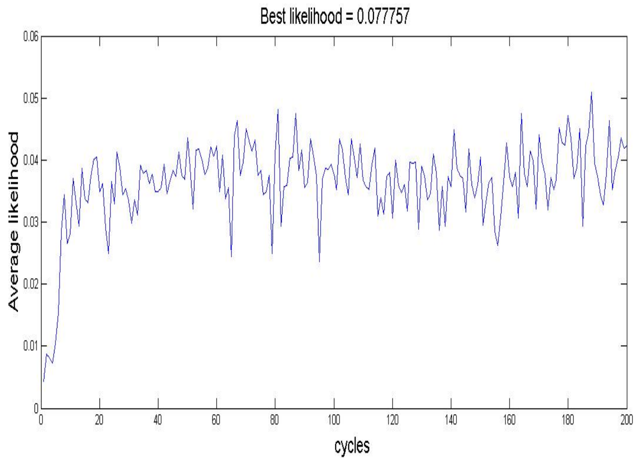

Fig. 2. Experimental average likelihood vs number of cycles.

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