COUPLING OF THE BOUNDARY ELEMENT METHOD WITH A HYBRID METHOD FOR INVERSE STRESS ANALYSIS OF PIPELINES

CIBELE CORNEJO JACINTO PORTELA[1,2], AMANDA JAREK[3,4] & LUIZ ALKIMIN DE LACERDA[2,3,4]
[1]ITeCons – Institute for Research and Technological Development in Construction,
Energy, Environment and Sustainability, Portugal
[2]Postgraduate Program in Numerical Methods in Engineering, UFPR – Federal University of Paraná, Brazil
[3]LACTEC – Institute of Technology for Development, Civil Engineering, Brazil
[4]Department of Civil Engineering, UFPR – Federal University of Paraná, Brazil

ABSTRACT

The aim of this work is to develop a numerical tool for structural inverse analysis to obtain boundary conditions and their location. The inverse analysis is performed through an optimization process having as restrictions the information obtained from a direct analysis, representing data which could be obtained from surface monitoring of pipelines. Thus, the numerical models comprehend the solution of two problems: the direct one in which the boundary element method (BEM) is used to obtain the displacements and tractions in the structure, and the inverse problem, in which two optimization models were implemented. The first approach uses the genetic algorithm (GA) method associated with the BEM (GA-BEM), minimizing the residuals between the calculated and the "monitored" relative surface displacements. The second approach is a hybrid method (HM) in which the GA is associated with the Newton–Raphson method for performing the inverse analysis with the BEM (HM-BEM). All tests demonstrated the efficiency of the numerical tools for structural inverse analysis, with the HM approach showing lower computational cost and better accuracy.

Keywords: boundary element method, inverse analysis, genetic algorithm, Newton–Raphson method, elasticity, hybrid method.

1 INTRODUCTION

Transportation of oil and gas is an important issue in the oil industry where the main means of transportation are the pipelines. With the increase of demand and the use of oil and its derivatives, there has been a significant increase in pipeline projects requiring larger diameters and smaller wall thicknesses operating under high pressure. Due to the variable geotechnical conditions, the risks of rupture cannot be neglected. It is ideal to minimize these risks with structural or geotechnical improvements in order to prevent accidents while obtaining lower cost of production. Therefore, it is very important to provide proper tools to the maintenance engineers to detect and avoid conditions which can potentially result in structural failure, and consequently, generating environmental damages and/or economic and human losses. For this reason, analyses of pipelines were performed by many researchers up to present days and a wide range of analytical and numerical models can be found in literature [1]–[3], characterized by different assumptions for pipelines behaviour.

In this context, the present work aimed the development of two computational codes, in Fortran 95 programming language, for the analysis of three dimensional linear elastic problems. The purpose of these tools is the application of structural inverse analysis in deformed ducts to retrieve their boundary conditions. Inverse problems constitute a large field of research in science and engineering, since in many applications it is necessary to identify parameters such as boundary unknown conditions, geometry or material properties from experimental measurements.

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In this work, a first numerical tool was built employing the boundary element method (BEM) to obtain the displacements and stresses distributed in the structure. This initial implementation was used for direct analyses and production of synthetic data and also as an auxiliary program for the inverse algorithms.

The first inverse analysis was performed with BEM and a genetic algorithm (GA). This numerical tool was called GA-BEM. There are many works in the technical literature, in several areas of application that have been successful in solving optimization problems using this combination [4]–[6]. For instance, Katsifarakis and Petala [4] presented numerical results for the maximization of the rate of extraction of underground water without saline intrusion for management in coastal aquifers. Miltiadou and Wrobel [5] used this coupling technique for the identification of polarization curves in cathodic protection systems. Another reference is the work of Kita and Tanie [6] for shape optimization of structures.

The GA's tools have the disadvantage of generally requiring a high computational effort when compared to gradient methods. Thus, a second numerical tool for inverse analysis was elaborated, using the same BEM code with a hybrid method (HM), which conjugates GA with the Newton–Raphson gradient method (NR). This numerical tool was called HM-BEM. It is known that the NR method implies in lower computational cost, but requires a good initial value to ensure convergence. The work of Feliz [7] is an example that used the proposal of a hybrid system to study power flux convergence problem in energy systems. The system was composed by GA method responsible to provide an initial solution from a group of possibilities, followed by the NR method to achieve the final result. In this work, a combination of GA and NR is evaluated for the inverse analysis of deformed structures searching the identification of load boundary condition magnitude and location.

2 BOUNDARY ELEMENT METHOD FOR ELASTICITY

Most of the physical phenomena occurring in nature can be described by differential equations where initial conditions or boundary conditions are imposed. There are different methods for solving these problems.

Analytical solutions to mathematical problems that satisfy both differential equations and boundary conditions can be obtained only for some very simple problems. Therefore, numerical methods are essential if complex problems are under investigation. The BEM is one possible approach for the solution of three-dimensional problems [8]–[9].

2.1 Fundamental solution

For the BEM, a solution to the governing equation is required, and is called the fundamental solution. Considering a homogenous three-dimensional linear elastic infinite domain under a concentrated unit load, the fundamental Kelvin displacement and traction solutions in 3D domains are [9]:

$$U_{ij}(X',x) = \frac{1}{16\pi G(1-\upsilon)r}\left[(3-4\upsilon)\delta_{ij} + r_i r_j\right], \tag{1}$$

$$T_{ij}(X',x) = \frac{-1}{8\pi(1-\upsilon)r^2}\left[\frac{\partial r}{\partial n}\left[(1-2\upsilon)\delta_{ij} + 3r_i r_j\right] + (1-2\upsilon)\left(n_i r_j - n_j r_i\right)\right], \tag{2}$$

where $U_{ij}(X',x)$: displacement at any field point x, in the direction j, when the unit load is applied in a collocation point X' in the direction i; $T_{ij}(X',x)$: traction at any field point x, in the direction j, when the unit load is applied in a collocation point X' in the direction i; r: distance from collocation point X' to field point x; n: normal direction at x, in the boundary; G: Shear modulus; υ: Poisson's ratio; δ: Kronecker delta.

2.2 Boundary integral equation

The Somigliana's identity brings the displacement value at an internal point X' in terms of the values of displacements u_j and tractions t_j on the boundary surface Γ, and of the body forces b_j. Considering $x \in \Gamma$, $X \in \Omega$ and $X' \in \Omega$. Somigliana's identity is expressed by:

$$u_i(X') = \int_{\Gamma} U_{ij}(X',x)t_j(x)d\Gamma - \int_{\Gamma} T_{ij}(X',x)\; u_j(x)d\Gamma + \\ + \int_{\Omega} U_{ij}(X',X)\; b_j(X)\; d\Omega. \tag{3}$$

The direct boundary element formulation relating boundary tractions and displacements can be obtained from eqn (3) by considering a limiting process as the internal point X' approaches the boundary, becoming x'. The resulting expression is the displacement boundary integral equation, written as:

$$C_{ij}(x')u_j(x') + \int_{\Gamma} T_{ij}(x',x)u_j(x)d\Gamma = \int_{\Gamma} U_{ij}(x',x)t_j(x)d\Gamma + \\ + \int_{\Omega} U_{ij}(x',X)\; b_j(X)\; d\Omega, \tag{4}$$

where the free term coefficient Cij(x') depends on the boundary geometry at the collocation point x'.

Discretizing eqn (4), neglecting body forces and applying it to all nodal points in the boundary, one can assemble a system of equations in the format [10]:

$$\boldsymbol{Hu} = \boldsymbol{Gt}, \tag{5}$$

where $\boldsymbol{H}$ and $\boldsymbol{G}$ are coefficient matrices, which depend on the discretized geometry and material properties, and $\boldsymbol{u}$ and $\boldsymbol{t}$ are the vectors of nodal values of displacements and tractions in the boundary, respectively.

If there is only one unknown value at each nodal point, the system can be rearranged by placing all the unknowns on the left-hand side and all known variables to the right-hand side, forming:

$$\boldsymbol{Ax} = \boldsymbol{F}, \tag{6}$$

where all unknown nodal values are located in vector $\boldsymbol{x}$ and $\boldsymbol{F}$ is found by multiplying the corresponding $\boldsymbol{H}$ and $\boldsymbol{G}$ columns by the known boundary data.

Once this solution is complete, all boundary variables are known and the solution at any domain point can be calculated.

3 INVERSE PROBLEMS

When solving a direct problem in elasticity, the boundary conditions, the geometry and the material properties are all known. Stresses, strains and displacements along the body are the usual results. On the other hand, in an inverse problem, boundary parameters, geometry and material characteristics, may not be known explicitly. One way to solve an inverse problem is to consider it as an optimization problem, searching to maximize or minimize an objective function.

Genetic algorithms and the Newton–Raphson method are examples of techniques which can be used to solve an optimization problem. Each technique is briefly described in this section pointing out how they are coupled to the BEM. Moreover, a strategy for their combination as a hybrid method is also shown, bringing their advantages into a single solution method.

3.1 Genetic algorithms

Genetic algorithms are numerical optimization algorithms based on the natural process of biological evolution (Darwinism) [11]. From the theory of Darwin, the principle of selection privileges the individuals who are more apt, with more possibility of survival and, therefore, with higher probability of reproduction. The larger the number of descendants, the bigger the chances of their genetic codes remain for the next generations. These genetic codes constitute the identity of each individual and are represented in the chromosomes. These are the principles that inspire the construction of GA's, which seek a better solution to a given problem through the evolution of populations of solutions encoded by means of artificial chromosomes [12].

In GA's, a chromosome is a structure that can be seen as a solution point in the search space of the problem to be optimized. These chromosomes are then subjected to an evolutionary process. After several generations, the population evolves in order to obtain more fit individuals.

According to Coley [12], GA's are initialized with a population of possible solutions that are usually randomly scattered in the search space and are converted to real variables. After obtaining the first population, the value of an objective function for each generated variable is calculated. Through this function, also called the fitness function, it is possible to evaluate the quality of each solution for the maximum or minimum problem.

In the present work, GA is implemented to determine the minimizers of the objective function that is represented by:

$$Z_k = \sum_{i=1}^{N_v} \left(\frac{x_{expi} - x_{calci}}{x_{calci}}\right)^2, k = 1,2 \dots N_p \ , \tag{7}$$

where Z_k: value of the objective function for each individual; x_{expi}: experimentally measured relative displacement between two points of the structure under analysis. x_{calci}: numerically calculated relative displacement between two points, with the BEM; N_v: number of measurements; N_p: number of individuals.

These chromosomes are then subjected to an evolutionary process with the application of Selection and Genetic Operators. A typical genetic algorithm uses two operators to "guide" the population over a series of generations to the overall optimum: crossover and mutation [13].

Selection is applied on the population in a manner similar to the natural selection found in biological systems. Using the fitness function, weaker individuals are eliminated, and the more fit individuals have higher chance of promoting the information they have for the next generation. This process does not totally exclude individuals less able to maintain the diversity of the population.

The crossover allows the exchange of information from the solutions in a manner similar to that used by natural organisms submitted to reproduction. This operator promotes a blend of the characteristics of the "parents", who were previously selected based on their fitness.

The mutation randomly changes the bit value of an individual. Its purpose is to maintain the genetic diversity of the population by ensuring that the probability of reaching any point in the search space will not be zero. Its application creates new characteristic values that does not exist or that appeared in small numbers in the population.

After selection, crossover and mutation have been applied in the initial population, a new population is formed, and the generation counter is increased by one. These processes of selection, crossover and mutation continue until a certain number of generations or until some form of convergence criterion is fulfilled.

3.2 Newton–Raphson method

The Newton–Raphson method consists of a procedure for calculating the root of a function $f(x)$. The basic idea is to successively apply a formula starting from an initial approximation x_0 and generating a sequence of approximations that will converge to the root of the function [14]. Generally, for a single function, one has:

$$x_{i+1} = x_i - \frac{f(x_i)}{f'(x_i)} \,. \tag{8}$$

But this method can also be applied to a function that represents a system of equations as:

$$\boldsymbol{F}(\boldsymbol{x}) = 0, \tag{9}$$

where $\boldsymbol{x} = [x_1, x_2, \ldots, x_n]^T$.

Using the Taylor Series of $\boldsymbol{F}(\boldsymbol{x})$ about the point $\boldsymbol{x}_0$, where $\boldsymbol{x}_0$ is an approximation for the solution of $\boldsymbol{F}(\boldsymbol{x})=0$ and keeping only the first order terms:

$$\boldsymbol{F}(\boldsymbol{x}) \approx \boldsymbol{F}(\boldsymbol{x}_0) + (\boldsymbol{x} - \boldsymbol{x}_0)\boldsymbol{F}'(\boldsymbol{x}_0). \tag{10}$$

The Jacobian Matrix is formed by the partial derivatives of $\boldsymbol{F}$ components:

$$\boldsymbol{J_F} = \begin{pmatrix} \frac{\partial f_1}{\partial x_1} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \vdots & \cdots & \vdots \\ \frac{\partial f_m}{\partial x_1} & \cdots & \frac{\partial f_m}{\partial x_n} \end{pmatrix}. \tag{11}$$

And it is possible to rewrite eqn (10) as:

$$\boldsymbol{F}(\boldsymbol{x}) = \boldsymbol{F}(\boldsymbol{x}_0) + (\boldsymbol{x} - \boldsymbol{x}_0)\boldsymbol{J}_F(\boldsymbol{x}_0). \tag{12}$$

Finally, the NR formula for iteratively solving problems involving systems of equations is:

$$\boldsymbol{x}_{i+1} = \boldsymbol{x}_i - \boldsymbol{J}_F^{-1}\boldsymbol{F}(\boldsymbol{x}_\mathrm{i}). \tag{13}$$

3.3 Model formed by the hybrid method and the boundary element method (HM-BEM)

The scheme in Fig. 1 briefly illustrates the operation of the HM for inverse analysis with the BEM. First, an initial population (possible solutions of the problem) is created and represented by binary vectors. Then, these binary vectors are transformed into real numbers. For each generation, all individuals are submitted to the BEM. According to the results, each individual of this population is evaluated by the fitness function and classified according to its quality.

The best individual of this population is used as the starting point for the NR and the new individual is created and converted to a binary vector. The previous population along with this new individual are subjected to genetic operators and a new population is created. This cycle is repeated until a stopping criterion is satisfied.

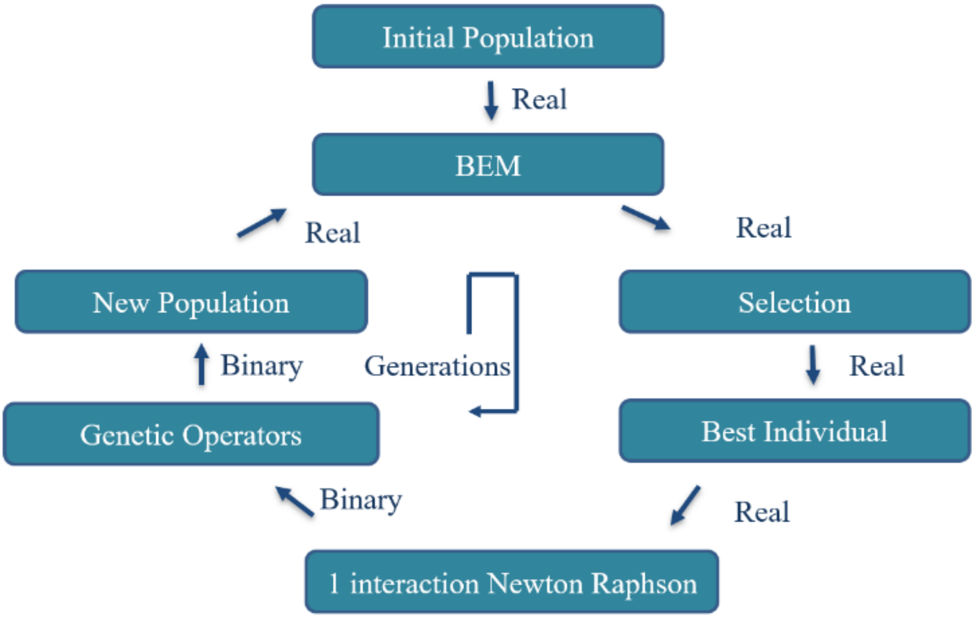


Figure 1: Diagram of the hybrid method associated with the BEM.

4 NUMERICAL ANALYSES

Two problems are proposed in order to test the hybrid strategy. In both cases body forces are neglected and a steel duct is modelled in 3D with the following material properties and geometry:

- Young's modulus: 200 GPa;
- Poisson's ratio: 0.32;
- Length: 7.0 m;
- External diameter: 0.3 m;
- Internal diameter: 0.26 m.

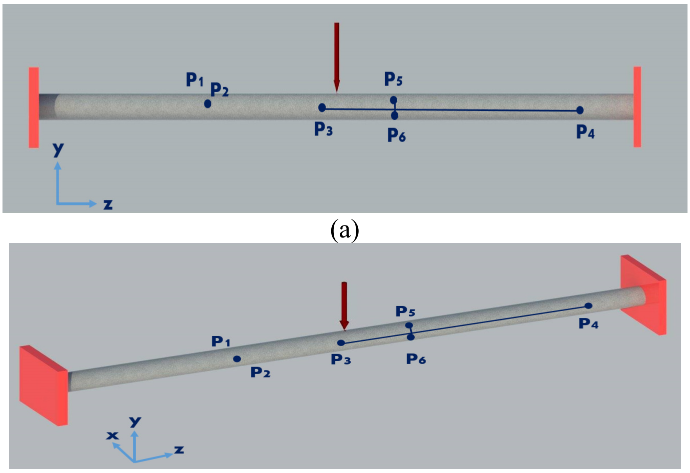
In each example, a direct analysis is initially performed in order to obtain synthetic experimental data. Afterwards, an inverse analysis is conducted for obtaining unknown parameters.

The inverse analysis is performed twice using the GA-BEM and the HM-BEM optimization techniques for comparative purposes.

4.1 First numerical test

This example consists of a fixed ended duct with a central vertical load represented by traction on an element in the central region, as shown in Fig. 2. Two parameters are selected to be unknowns in the inverse analysis:

- The magnitude of the central vertical traction (t_y);
- The traction t_y location (n).



(a)

(b)

Figure 2: Model study of the first numerical example. (a) Front view; (b) Perspective view.

For searching the traction location parameter (n), a matrix $\boldsymbol{M}$(16x32) is defined representing all elements of the external surface of the duct. In this sense, searching for this location (n) requires identifying, two variables of matrix $\boldsymbol{M}$: column (k_1) and row (k_2).

4.1.1 Direct analysis

As mentioned previously, the direct problem is initially solved. The boundary was discretized into 1056 constant quadrilateral boundary elements. The problem is solved by assuming a vertical $t_{y\,=}$ -900kPa; located at the element n = 529, corresponding to k_1 = 2 and k_2 = 19.

The values of displacements at points P_1 to P_6 located on the boundary, depicted in Fig. 2, are used to calculate their relative distances. These distances represent the experimental data, which are necessary to solve the inverse problems.

4.1.2 Inverse analysis

The following value intervals are assumed for the unknown parameters t_y, k_1, k_2: [-2MPa, 0MPa] [1, 32] and [1, 16], respectively. They constitute the GA searching limits, in which its GA operators and parameters are shown in Table 1.

Table 1: Genetic parameters.

Population Size	200
Number of generations	100
Selection scheme	Tournament selection
Crossover scheme	Segmented crossover
Mutation scheme	Bit-flipping mutation
Other operators	Elitism
Crossover probability	90%
Mutation probability	1%
Binary chromosomes	23 bits

Table 2 shows the best individual result obtained by the GA-BEM inverse analysis formulation in each generation, including its magnitude, location and fitness function value (FFV) calculated from eqn (7).

Table 2: Best individual of each generation of first example (GA-BEM).

Generation	t_y(MPa)	location (n)	FFV
1	-1.2871	563	2.37E-013
2	-1.2884	1009	3.78E-015
3	-1.2884	1009	3.78E-015
4	-1.2884	1009	3.78E-015
5	-1.2884	1011	3.67E-015
6	-1.2884	1011	3.67E-015
7	-1.3096	1009	1.36E-015
8	-1.3096	1009	1.36E-015
9	-1.3323	1011	8.21E-017
10	-1.3323	1011	8.21E-017
11	-0.9043	529	6.26E-017
12	-0.9043	529	6.26E-017
13	-0.8965	529	3.95E-017
14	-0.8965	529	3.95E-017
15	-0.8965	529	3.95E-017
16	-0.8965	529	3.95E-017
17	-0.8965	529	3.95E-017
18	-0.8965	529	3.95E-017
19	-0.8965	529	3.95E-017
20	-0.9004	529	6.56E-019
:	:	:	:
81	-0.8999	529	6.03E-019
:	:	:	:
100	-0.8999	529	6.03E-019

A stopping criterion for fitness function value from eqn (7), of the best individual was adopted with tolerance 10^{-26}.

Table 3 shows the results obtained with the HM-BEM inverse approach. Once again, the best individual data parameter of each generation is presented. It must be emphasized that the NR is only applied for searching the traction and not its location on the boundary. Clearly, generation after generation the best result either remains the same or improves. This is due to the process called elitism employed in the algorithms, where the best individual is kept in the new population of the next generation. Fig. 3 shows the fitness function values of the best individual along the generations, with both GA-BEM and HM-BEM inverse analysis formulations. Clearly, both results converge towards the correct solution. In the GA-BEM analysis, the boundary traction magnitude relative error was 4.74E-03% in the last generation, while in the MH-BEM analysis it was 2.22E-06% in the 11th generation. In both cases the correct loading element was found.

Table 3: Best individual of each generation of first example (HM-BEM).

Generation	t_y(MPa)	location (n)	FFV
1	-1.2871	563	2.37E-013
2	-1.2884	1009	3.78E-015
3	-1.2884	1009	3.78E-015
4	-1.2884	1009	3.78E-015
5	-1.2884	1011	3.67E-015
6	-1.2884	1011	3.67E-015
7	-1.3096	1009	1.36E-015
8	-1.3096	1009	1.36E-015
9	-1.3323	1011	8.21E-017
10	-1.3323	1011	8.21E-017
11	-0.9000	529	1.78E-027

Fig. 3 shows the fitness function values of the best individual along the generations, with both GA-BEM and HM-BEM inverse analysis formulations. Clearly, both results converge towards the correct solution. In the GA-BEM analysis, the boundary traction magnitude relative error was 4.74E-03% in the last generation, while in the MH-BEM analysis it was 2.22E-06% in the 11th generation. In both cases the correct loading element was found.

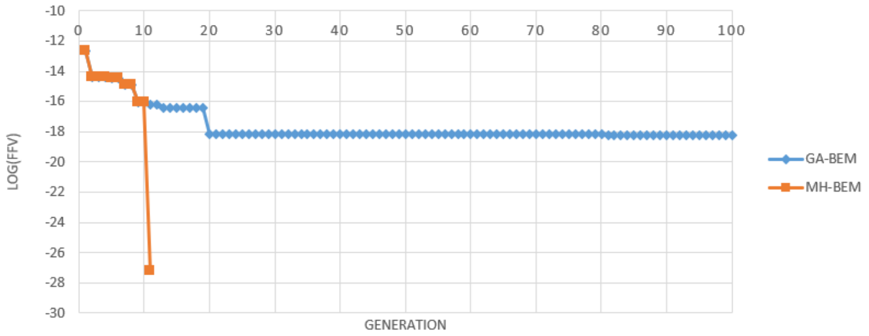


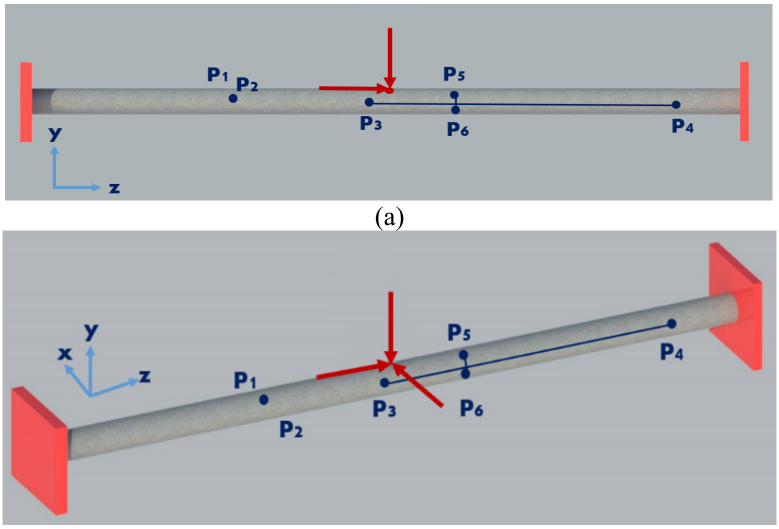
Figure 3: Variation of the function fitness value of the best individual in log 10 of each generation with the use of the GA-BEM and HM-BEM in the first example.

4.2 Second numerical test

This second numerical test, illustrated in Fig. 4 consists of a fixed ended steel duct, loaded with the action of three orthogonal concentrated forces at one point, represented by 3 tractions (t_x, t_y, t_z) applied on one element.

This example had as its objective the search of four unknown parameters:

- The magnitude of t_x;
- The magnitude of t_y;
- The magnitude of t_z;
- The location which (t_x, t_y, t_z) are acting (n).



(a)

(b)

Figure 4: Model study of the second numerical example. (a) Front view; (b) Perspective view.

In the HM-BEM analysis, once the correct loading element location was found, the NR method lead the iterative process towards the expected result.

4.2.1 Direct analysis

The direct problem for 3D domain has been solved for this problem with the same mesh with 1056 constant quadrilateral boundary elements of the previous example. The direct problem is solved by assuming the parameters boundary tractions as t_x = 3MPa, t_y= -9MPa and t_z = 14MPa, located at the element number n=529, corresponding to $k_1 = 2$ and $k_2 = 19$.

4.2.2 Inverse analysis

The genetic operators and parameters to GA of both program (GA-BEM and HM-BEM) are shown in Table 4. Table 5 presents the result of the best individual for each generation using GA-BEM.

Table 4: Genetic parameters.

Population size	200
Number of generations	200
Selection scheme	Tournament selection
Crossover scheme	Segmented crossover
Mutation scheme	Bit-flipping mutation
Other operators	Elitism
Crossover probability	90%
Mutation probability	1%
Binary chromosomes	51 bits

Table 5: Best individual of each generation of second example (GA-BEM).

Generation	t_x(MPa)	t_y(MPa)	t_z(MPa)	location (n)	FFV
1	3.6037	-6.9511	13.5237	529	1.37E-011
2	3.6037	-6.9511	13.5237	529	1.37E-011
3	3.6037	-6.9511	13.5237	529	1.37E-011
4	3.6037	-6.9511	13.5237	529	1.37E-011
5	3.2960	-7.2636	13.5201	529	9.04E-012
6	3.6476	-9.7637	13.5201	529	2.53E-012
7	3.6476	-9.7637	13.5201	529	2.53E-012
:	:	:	:	:	:
200	2.9994	-8.9957	13.9998	529	5.21E-019

The search space is made up of 2^{51} possibilities of answers, for these 4 search variables. It is verified, by the analysis of the results, a convergence to the expected result over the generations even for 4 variables, demonstrating the validation of the algorithm GA-BEM. The program generated a result with relative errors of 1.83E-02%, 4.74E-03% and 8.72E-04% for the three tractions parameters t_x, t_y and t_z respectively, and found the exact location of these tractions action.

For the HM a stopping criterion was chosen for the fitness value of the best individual with tolerance 10^{-26}, as in the previous example. The results generated are shown in Table 6.

Table 6: Best individual of each generation of second example (HM-BEM).

Generation	t_x(MPa)	t_y(MPa)	t_z(MPa)	location (n)	FFV
1	3.0000	-9.0000	14.0000	529	1.37E-028

It is verified that in the first generation the stop criterion was satisfied, generating results with relative errors of 1E-06%, 7.77E-07% and 8.57E-08% to tx, ty and tz, respectively. This is because the GA found in the first generation the correct actuation element and, with the application of the NR, with only one iteration, generated results with a good precision. It was found, then, that in this example too, the inverse analysis with the HM-BEM was more efficient and accurate than with the use of the GA-BEM.

5 CONCLUSION

The contribution of this work is the association of the BEM with optimization formulations obtaining robust and efficient techniques for the search of unknown parameters applied to elasticity problems. More specifically, BEM was combined with genetic algorithms and the Newton-–Raphson method to produce such formulations. Two numerical tests were carried out and the developed tools, GA-BEM and MH-BEM showed good approximations in their results. However, the use of MH-BEM presented better results with a lower computational cost, showing a good potential for use in structural analysis.

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