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UNDERWATER TARGET LOCALISATION AND ESTIMATION OF OCEAN ENVIRONMENTAL PARAMETERS USING A GENETIC ALGORITHM

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Summary: In the field of underwater acoustics the signal processing technique "Matched Field Inversion" (MFI) is an important research topic. This technique can be used for determining both target location and parameters describing the ocean environment. For example, these parameters are needed as input into models that are used on board Dutch navy vessels and for mine hunting operations. When using MFI, the acoustic field that is measured with a sonar array is compared with the acoustic field that is predicted by an acoustic propagation model for a certain set of the unknown model parameters, such as target location and geo-acoustic ocean bottom parameters. An energy function providing a measure for the similarity between the two acoustic fields is defined. By minimising this energy function, the set of input parameters corresponding to the maximum similarity between both acoustic fields, i.e. the solution, is found. Due to the extremely large number of possible parameter value combinations and the occurrence of local minima, global optimisation methods are required to solve this inverse problem.
The developed MFI techniques are applied to shallow water experimental data. A genetic algorithm is used for the global optimisation.

1 INTRODUCTION

During the last decade the "Matched Field Processing" (MFP) technique has become an important research item in underwater acoustics. The main application of MFP is localisation of underwater acoustic sources. When applying MFP, an acoustic field that is measured using an array of hydrophones, is correlated with acoustic fields that are calculated on the hydrophone positions for different possible (or candidate) source ranges and depths using an appropriate acoustic propagation model. This correlation as a function of source depth and source range is called a range-depth ambiguity surface. The source range and depth combination that results in the highest correlation should correspond to the true range and depth of the source.

With MFP it is assumed that all ocean environmental (and other) parameters that are needed as input into the acoustic propagation model are accurately known. However, in practical conditions this is generally not the case, thereby prohibiting a successful source location estimation. This problem is referred to as mismatch. In [1] the so-called focalisation approach is described. With this approach not only the source position, but also the environmental (and other) parameters are the unknowns that have to be determined. In this way the problem has become an optimisation problem where the function that has to be optimised depends on many variables. This function is called the energy function and represents a measure for the correlation between measured and modelled acoustic field. The number of possible parameter value combinations is extremely large as the number of unknown parameters is in the order of ten. In addition, the parameter search space can have a large number of local optima. Finding the global optimum of such an energy function requires modern global optimisation methods, such as simulated annealing ([1], [4]) or genetic algorithms ([2], [5]). This process of finding the parameter value combination that provides the maximum correlation is denoted by Matched Field Inversion (MFI). Matched Field Inversion has been applied to experimental data acquired in a shallow water ocean area.

A brief description of the experimental setup and the acoustic problem is given in section 2. We have used a genetic algorithm as the global optimisation method. Section 3 provides a description of the basic principles of a genetic algorithm. It also provides the specific setting of the algorithm for the current inversion, including the type of energy function used. Results are presented and discussed in section 4.

2 THE ACOUSTIC PROBLEM

The data used in the inversion were obtained during an experiment in a virtually range-independent shallow water area north of the island of Elba (October 1993) ([3]). Here, range-independent means that the environmental parameters are independent of the distance to the sound source and the only variation is the variation with depth. The water depth H_w amounts to approximately 127 m. We assume that the bottom in this ocean area consists of a single homogeneous medium described by the following three geo-acoustic parameters: the sound attenuation constant α_b, the density ρ_b and the sound speed c_b. From previous experiments in the area rough estimates for these parameters were obtained: 0.15 dB/λ, 1.8 kg/m^3 and 1600 m/s, respectively. These values are referred to as the baseline values.

The receiving system is a vertical array consisting of 48 hydrophones with 2 meter spacing between the succeeding hydrophones. The depth of the receiving array (d_R) is defined as the depth of the deepest hydrophone, being 112.7 m. The source is deployed at a range r_s of 5.5 km from the receiving array at a depth z_s of 75 m.

Figure 1 shows the assumed ocean environment. The sound speed profile, i.e. the sound speed as a function of depth in the water column, used for calculating the modelled acoustic fields is the sound speed profile as measured at the array site and is schematically depicted in the figure. The water column mainly consists of two layers: a warm upper layer having a sound speed of about 1525 m/s, on top of a colder layer with a sound speed of 1510 m/s.

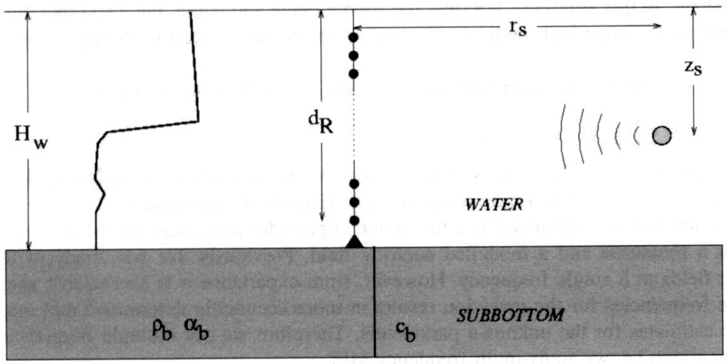

Figure 1 The assumed ocean environment.

Figure 2 shows the range-depth ambiguity surface when use is made of the baseline model input parameter values as given above. Notice we have chosen a dB scale for the correlation. It is clear that there are many peaks and that the source is not localised, as the highest peak does not occur close to the true source position of 5.5 km range and 75 m depth. From this it can be concluded that there is a lot of mismatch.

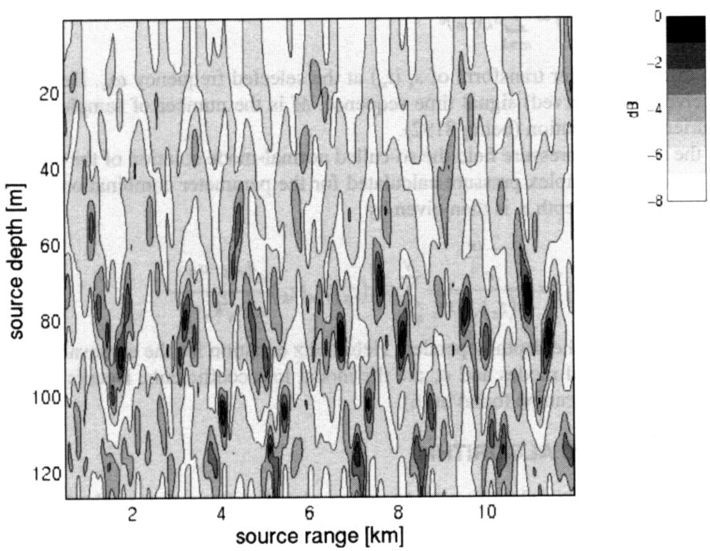

Figure 2 The range-depth ambiguity surface as obtained using the baseline values for the model input parameters.

It has already been mentioned that for mismatch conditions the focalisation approach has to be applied. In this approach, not only the source range and depth, but also other environmental and geometrical model input parameters are determined in the optimisation process.

The vector containing the parameters for which the inversion is performed is

$$\vec{m} = \left[\alpha_b \;\; \rho_b \;\; c_b \;\; r_s \;\; z_s \;\; H_w \;\; d_R\right]$$

Due to array tilt and/or imprecise measurement of the water depth, the actual array depth is not known exactly and therefore has to be determined in the optimisation.

The function that is optimised is a function that provides a measure for the difference between a measured and a modelled acoustic field. Previously use was made of the acoustic fields at a single frequency. However, from experience it is known that using multiple frequencies for the inversion results in more accurately determined and more realistic estimates for the unknown parameters. Therefore we use multiple frequencies for the analysis, i.e. we apply multi-frequency MFI.

During the experiment the source transmitted broadband signals. The signal used in our MFI analysis has a frequency band of 160-180 Hz. From the spectrum that is obtained after Fourier transformation of 8.192 seconds of the data, six frequency bins are selected for the analysis, i.e. the Fourier coefficients at 164.43, 166.87, 168.95, 171.14, 172.85 and 174.44 Hz. These Fourier coefficients as a function of depth give the complex pressure fields. The 6 frequencies were selected such that the differences in the pressure fields at six frequencies in the 160-180 Hz band are maximal. The expression for the complex pressure on the kth hydrophone in the frequency domain is

$$p_{obs,k}\left(\omega_{m'}\right) = \sum_{m=1}^{M} s_k\left(t_m\right) e^{2\pi i(m'-1)(m-1)/M}$$

i.e. the discrete Fourier transform of $s_k\ (t_m)$ at the selected frequency $\omega_{m'}$. Here $s_k\ (t_m)$ is the received (or observed) signal time sequence. M is the number of samples taken for the Fourier transformation (being 8192).

For the modelled pressure field the so-called normal-mode solution of the wave equation is used. The complex pressure calculated for the parameter combination $\vec{m}_j$ at the kth hydrophone at a depth z_k is then given by

$$p_{calc,k}\left(\vec{m}_j\right) = \frac{e^{\frac{i\pi}{4}}}{\rho\left(z_s\right)\sqrt{8\pi r_s}} \sum_{n=1}^{N} \psi_n\left(z_s\right)\psi_n\left(z_k\right) \frac{e^{ik_n r_s - \alpha_n r_s}}{\sqrt{k_n}}$$

with ψ_n solutions of the depth-dependent Helmholtz equation for the eigenvalues k_n. N is the number of normal modes and α_n are the modal loss coefficients. Details of the normal-mode technique can be found in [6].

3 THE GENETIC ALGORITHM

We have used a genetic algorithm (GA) as the global optimisation method. The algorithm is described below and is based on genetic processes of biological organisms, i.e. it is an analogy with nature.

The first step in a GA is to create an initial *population* consisting of q members. Each member represents a possible parameter value combination $\vec{m}_j$, i.e. a possible solution to the optimisation problem. This first *generation* is created randomly. The population size q should be large enough to ensure that the problem space can be searched thoroughly. On the other hand the population size should be not too large, thereby limiting the amount of energy function evaluations (i.e. the number of forward acoustic model calculations). At this creation stage the members are in their binary encoded form, i.e. the parameter value combinations are represented by a string of zeros and ones. In the following these strings are denoted as *chromosomes*. Each parameter is represented by a certain part of the chromosome. These parts are called *genes*. The encoded form of the parameter value combinations is needed when applying certain operators as will be explained later. After decoding, the values for the energy function can be calculated for all members of this first population. This is also referred to as assigning a *fitness* score to each member. When the energy function E is normalised ($0<E<1$), the fitness φ is given by

$$\varphi = 1 - E$$

i.e. a low value for the energy function means a high value for the fitness.
The energy function we have selected is based on the incoherent multi-frequency linear or Bartlett processor and is given by ([5])

$$E(\vec{m}) = 1 - \frac{1}{K}\sum_{k=1}^{K}\left|\vec{p}_{obs}(f_k)\cdot\vec{p}^{\,*}_{calc}(f_k,\vec{m})\right|^2$$

with $\vec{m}$ the vector containing the parameters for which the inversion is performed, K the number of frequencies (being 6 in this study), $\vec{p}_{obs}(f_k)$ the measured (normalised) pressure field at frequency f_k and $\vec{p}_{calc}(f_k,\vec{m})$ the (normalised) pressure field at frequency f_k calculated by the normal-mode model.

For the creation of the next generation, first a *parental population* is selected from the initial population. This selection is based on the fitness values obtained for the different chromosomes: a higher fitness implies a larger probability of being selected, thus resulting in a parental population with a higher proportion of fit members. The selection criterion should be such that, on the whole, more opportunities to reproduce are given to the population members that are the most fit. However, at the beginning the selection criterion should not be chosen too strict as that would force the algorithm to converge to a local minimum. On the other hand a criterion that allows nearly all members to reproduce will result in slow convergence. In our application the probability p_j for the member $\vec{m}_j$ to be selected is given by the Boltzmann distribution ([2])

$$p_j = \frac{e^{\frac{-E(\vec{m}_j)}{T}}}{\sum_{i=1}^{q} e^{\frac{-E(\vec{m}_i)}{T}}}$$

The *temperature* T is chosen equal to the lowest value of the energy function found in the entire current population. This choice results in a flat probability distribution at the beginning, but as the optimisation process continues, the temperature will decrease, resulting in a more peaked probability distribution and therefore more emphasis will be put on the most fit members in later generations.

The following step is to create a population of q *children*. This is done by applying different operators to the members of the parental population. These operators are *crossover* and *mutation*, and they are applied to the members when they are in encoded form.

In order to apply crossover the members of the parental population are paired randomly. Crossover results in the exchange of corresponding chromosome parts between the two chromosomes of each pair of parents. We have applied multiple point crossover: a crossover point is selected at each gene, i.e. the number of crossover points is equal to the number of parameters for which the optimisation is performed. Crossover is applied with crossover probability p_c. Using a value of p_c less than one will allow genes to be passed on to the next generation without the disruption of crossover (usually $0.6 < p_c < 1.0$). The crossover point, i.e. the location on the gene at which it is cut, is selected at random. After crossover another operator called mutation is applied to the chromosomes. Mutation changes each bit of the chromosome with a probability p_m.

Crossover is considered to be a mechanism for rapid exploration of the search space. More crossover points or a higher crossover probability imply a more thorough search, but also more disruption. On the other hand, mutation is a process that provides a small amount of random search, ensuring that no point in the search space has zero probability of being explored. However, the mutation probability should not be chosen too high as then the search becomes effectively random (in general $p_m < 0.1$).

A new population (again consisting of q members) is established by taking at random $f.q$ $(0 < f \leq 1)$ members of the children population and the $(1\text{-}f)q$ most fit members of the original population. f is called the *reproduction size*. For values of f close to one, or even equal to one (called generational replacement), convergence of the algorithm to the global minimum might be slow. On the other hand, low values of f might promote the algorithm to converge rapidly to a local minimum.

The new population is used as the next generation onto which the same procedure is applied as described above. This process is continued for a certain amount of generations, which should be chosen large enough to allow convergence of the optimisation process.

Most of the values for the GA parameters were taken equal to those used in [2], i.e. a population size q of 64, a crossover probability p_c of 0.8, a mutation probability p_m of 0.05 and a reproduction size f of 0.5. The number of generations is taken to be 400, hence the number of forward model calculations per GA run amounts to approximately 13000 per frequency.

A genetic algorithm is a very powerful and robust technique as it can be applied to a wide range of problems. However, the difficulty comes from finding the best setting for the genetic algorithm for each specific optimisation problem, i.e. finding the best values for the different GA parameters (q, p_c, p_m and f).

4 RESULTS

The search bounds for the parameters, $[B_l, B_u]$, can be found in table 1.
Estimates for the final values of the unknown parameters have to be derived from the members of the final GA population. Several independent GA runs (in our case 5) have been performed in order to increase the probability on finding the global optimum. At the same time the parameter space close to the global optimum is explored more thoroughly, thereby improving the accuracy of the parameter estimates.
The energy function values corresponding to the parameter value combinations of all final populations are shown in Figure 3.

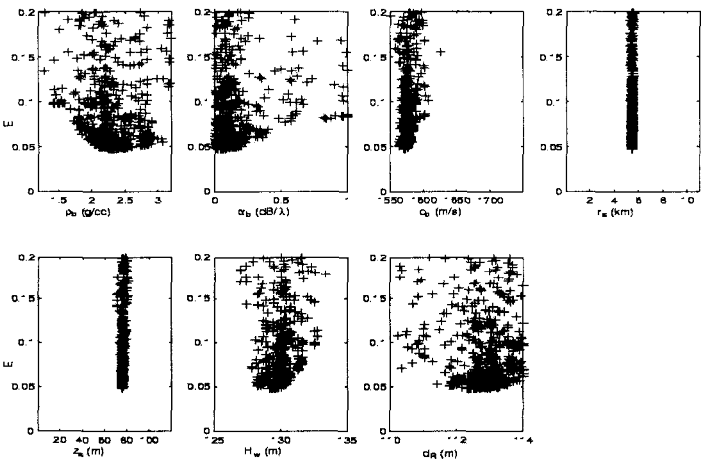

Figure 3 Energy versus parameter values in the final populations.

Estimates for the unknown parameters can be obtained by simply taking the parameter combination with the lowest energy function value. This solution to the inverse problem is referred to as GA_{best}.

An alternative method to obtain estimates for the unknown parameters from the final populations is to calculate the so-called a posteriori mean values ([2]). This solution to the inverse problem is referred to as GA_{mean} and is given by

$$GA_{mean} = \sum_{j=1}^{nq} \vec{m}_j \sigma(\vec{m}_j)$$

with

$$\sigma(\vec{m}_j) = \frac{e^{\frac{-E(\vec{m}_j)}{T}}}{\sum_{i=1}^{nq} e^{\frac{-E(\vec{m}_i)}{T}}}$$

with n the number of independent GA runs for the inversion. Here the temperature parameter T is taken equal to the lowest value of E in the final population ([2]).

Generally, it is useful to calculate both the GA_{best} and GA_{mean} solution, since a significant difference between the two solutions for a particular parameter indicates that the acoustic field is hardly sensitive to corresponding changes in that parameter. This corresponds to a flat or at least ambiguous distribution of energy function values for this parameter, see Figure 3. This is only valid for a temperature T that is not too low as then both solutions will coincide automatically.

Table 1 The search bounds, the baseline values and the values for the best and the mean.

m_i	B_l	B_u	Baseline	Best	mean
ρ_b (kg/m^3)	1.2	3.2	1.8	2.33	2.30
α_b(dB/λ)	0.0	1.0	0.15	0.05	0.11
c_b (m/s)	1550	1750	1600	1570	1575
r_s (km)	0	11	5.4	5.441	5.451
z_s (m)	1	120	75	76.0	75.9
H_w (m)	125	135	127	129.5	129.9
d_R (m)	110	114	112.7	112.5	112.9

Figure 4 shows for the different frequencies the absolute values for the measured pressure fields and the pressure fields calculated for the parameter combination corresponding to the lowest E, i.e. the GA_{best} solution. It is clear that the optimisation has been performed successfully as the measured and optimised fields are very similar. Finally, Figure 5 shows the range-depth ambiguity surface when use is made of the optimised parameter values. It is clear that now there is one clear peak that is at the correct source position. This also indicates that the optimisation has been successful.

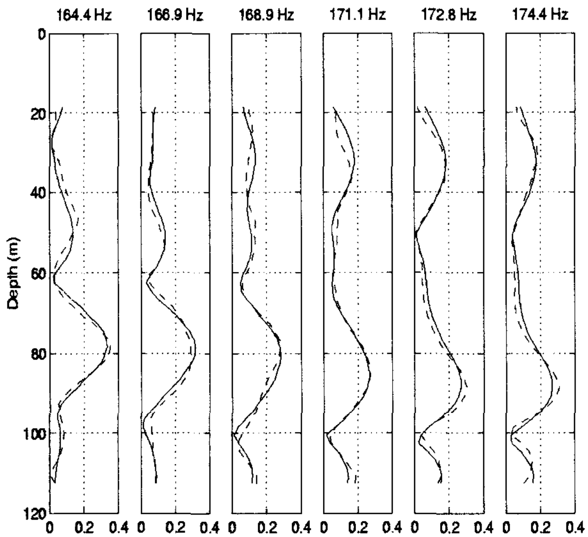

Figure 4 Absolute values of the measured pressure fields (solid line) and calculated pressure fields (dashed line) for the frequencies that were used for the optimisation.

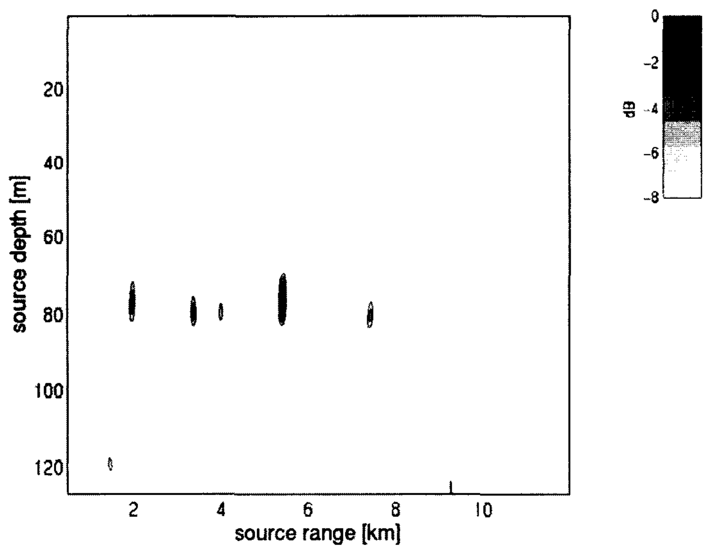

Figure 5 Range-depth ambiguity surface obtained when use is made of the optimised parameter values.

5 SUMMARY AND CONCLUSION

It can be concluded that realistic estimates for the unknown parameters have been found. The source range and depth in particular were accurately determined and are in excellent agreement with the true source position. The GA_{mean} and GA_{best} values do not differ significantly for all parameters (except for α_b) indicating that these parameter values are well determined. The attenuation constant in the bottom, α_b, is less well determined. This is due to the fact that this parameter has the least effect on the acoustic propagation.

6 REFERENCES

[1] M.D. Collins and W.A. Kuperman, 1991. Focalization: environmental focussing and source localization, J. Acoust. Soc. Am., **90**, 1410.

[2] P. Gerstoft, 1994. Inversion of seismoacoustic data using genetic algorithms and a posteriori probability distributions, J. Acoust. Soc. Am., **95**, 770.

[3] D.F. Gingras and P. Gerstoft, 1995. Inversion for geometric and geo-acoustic parameters in shallow water: experimental results, J. Acoust. Soc. Am., **97**, 3589.

[4] D.G. Simons, 1995. Source localization and estimation of geo-acoustic bottom parameters by matched field inversion of real acoustic data, TNO-report FEL-95-A260, December.

[5] D.G. Simons & M. Snellen, 1998. Multi-frequency matched field inversion of benchmark data using a genetic algorithm, Journal of Computational Acoustics, Vol. **6**, Nos. 1 & 2, 135-150.

[6] F.B. Jensen, W.A. Kuperman, M.B. Porter and H. Schmidt, 1994. Computational ocean acoustics, American Institute of Physics, Inc., New York.