Sea bottom parameter estimation by inversion of underwater acoustic sonar data

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Citation for published version (APA):
Appendix C

Global optimization of a test function

In this appendix the performance of the GA as a function of its setting is assessed through the use of a test function. It should be noted that to perform a similar study for the real acoustic problem is not feasible, since in this case the function evaluation is too slow.

The test function used has the following form

\[
z = [4.8 + x_1^2 + 5x_2^2 + 0.1x_3^2 + 0.05x_4^2 + x_5^2 + x_6^2 + ... - 0.3\cos(\pi(x_1 - x_2)) - 1.4\cos(\pi(x_1 + x_2)) - 0.5\cos(10\pi(0.05x_4 - 0.1x_3)) + ... - 1.0\cos(10\pi(0.05x_4 + 0.1x_3)) - 0.25\cos(2\pi(x_5 - x_6)) - 1.35\cos(2\pi(x_5 + x_6))]/20
\]

The features of this function include: a reasonable number of parameters (6 in total), local minima, parameter correlations and varying sensitivity of \(z\). The minimum of this function is at \(x_i = 0, (i = 1,..,6)\). Figure 1 shows 1-D and 2-D cross-sections of \(z\). Parameters that are not varied are kept at their value at the global minimum, i.e., zero.
This function is very suitable for investigating the performance of the genetic algorithm in finding the global optimum of the function $z$, since the computational effort for calculating $z$ is small. In the following we will consider the influence of several of the GA-parameters on the performance of the genetic algorithm to find the global optimum of $z$.

### C.1 GA performance as a function of its setting

For investigating the performance of the GA, 1000 independent GA runs have been carried out for various settings of the genetic algorithm, i.e., for various values of the different GA-parameters. The GA-parameters and their default settings are:

- Number of generations: 601;
- The number of bits used for the coding of the parameters: 10 for each parameter. Together with the search bounds of $[-3, 3]$, this results in steps of $\frac{3 + 3}{2^{10} - 1} = 0.0059$;
- Reproduction size, i.e., the fraction of the population that is replaced by randomly selected children each generation $f_r$: 0.5;
- Population size $q$: 64;
- Crossover rate $p_c$: 0.8;
- Mutation rate $p_m$: 0.05.

When considering the performance of the GA, two measures can be considered. These are 1) the percentage of the runs that have located the global optimum, and 2) the time that was

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**Fig. 1** 1-D and 2-D cross-sections of $z$. 
needed to accomplish this. Some preliminary runs were carried out to estimate a criterion for determining whether the global optimum has been located. The requirement that all six unknown parameters should be in between -0.2 and +0.2, was found to be a suitable criterion, since it excludes all surrounding local minima.

To determine the percentage of converged runs, for each run the parameter set that corresponds to the lowest energy function found in the final population was considered. The run is converged if this parameter set satisfies the above-mentioned requirement. In order to allow for comparison of the GA performance for different setting, also the uncertainty on the percentage of converged runs has to be taken into account. The situation considered here, comprising a set of independent events, each with a certain probability on success, typically corresponds to a binomial distribution. Then, denoting the amount of converged runs by $N_c$, the fraction of the total amount of runs ($N_r$) that has converged by $f_c$, and assuming this fraction to be the probability on convergence, the standard deviation of the amount of converged runs, $\sigma_{N_c}$, is

$$\sigma_{N_c} = \sqrt{f_c(1-f_c)N_r}$$

For determining the rate of convergence one approach would be to estimate for each converged GA the amount of calculations that were carried out up to the point at which the convergence criterion was satisfied. However, another approach was selected, since it was found to give a good overview of the general convergence behavior of the GA run. For this approach, the lowest energy found in each population was considered as a function of generation. By now taking the mean of all these curves that correspond to converged runs, an idea of the rate of convergence is obtained.

In the following the influence of the different GA-parameters is considered. No significant difference in GA performance was found when varying the amount of bits used for encoding the parameters, and therefore this GA-parameter is not considered in the following. This is also the case for the amount of generations.

### C.1.1 Influence of reproduction size

To ensure that good solutions do not get lost during the GA run, part of a current population is put directly into the succeeding population. The parameter controlling this process is called the reproduction size. The reproduction size, $f_r$, is defined here as that fraction of the population that is renewed when creating the population of a new generation. Thus, for low values of $f_r$, only a few elements of the populations corresponding to two succeeding generations are different. For high values of $f_r$, the populations of two succeeding generations will differ a lot. Employing higher $f_r$ values is thought to result in a higher percentage of converged runs, since there is more exploration of the search space. Lower $f_r$ values should result in a faster convergence, since there is more exploitation of promising solutions.

Figure 2 shows the percentage of converged runs as a function of $f_r$. The remaining parameters were kept at their default values. Employing a value of zero for $f_r$ is not considered here, since for this situation all populations of succeeding generations are equal to the initial population. The standard deviations are plotted as dashed lines in Fig. 2. As expected, the amount of converged runs increases with increasing $f_r$, although there seems to be an area of $f_r$ values (0.2-0.7), where there is no significant influence of $f_r$ on the percentage of converged GA runs. Note also the large decrease in converged runs when employing a value of 1 for $f_r$. This setting is denoted by generational replacement, i.e., no elements of a current population are put directly into the next population. For this setting one of the mechanisms that guide the search towards good solutions is excluded. The result is that good results can get lost during the optimization. The remaining mechanism forcing the algorithm towards good solutions is
the selection of elements for the parental population. This selection is such that good solutions have a larger probability to get selected.

Figure 3 shows the curves representing the mean rate of convergence. Increasing \( f_r \) results in an increase in the amount of forward runs needed for obtaining a certain level of the mean energy, but also, in general, in an increase of the amount of converged runs as shown in Fig. 2. Also with regards to the rate of convergence, employing a value of 1 for \( f_r \), shows a clearly different behavior. For this setting, the decrease in the energy for succeeding populations is caused solely by the mechanism of selecting elements for the parental population based on their fitness.

![Fig. 2](image1.png)  
**Fig. 2** Percentage of converged runs as a function of \( f_r \).

![Fig. 3](image2.png)  
**Fig. 3** Curves representing the mean rate of convergence for different \( f_r \) values.

The cause for the change in the slope of the curves shown in Fig. 3 is illustrated in Fig. 4, showing the distribution of the energy of all converged runs as a function of generation, and results from solutions going from some local to the global minimum.
It can be concluded that the influence of \( f_r \) is limited. For values \( f_r \) values from 0.2-0.7, employing different values of \( f_r \) does not result in a statistically significant change in the percentage of converged runs. For values of 0.8, 0.9 the percentage of converged runs increases from 64.9 ±1.5 % for \( f_r = 0.7 \), to 76.7 ± 1.3 % for \( f_r = 0.9 \), i.e., about 10 %. Up to 2000/3000 forward calculations the rate of convergence is hardly influenced a lot by \( f_r \). Beyond this point, the curves corresponding to different values of \( f_r \) start to deviate, such that for higher values of \( f_r \) the amount of forward calculations to obtain a certain value for the mean energy is much larger than for low \( f_r \) values.

C.1.2 Influence of population size

To investigate the influence of the population size, population sizes of 32 and 128 have been employed. Fig. 5 shows the percentage of converged runs as a function of \( f_r \) for the three population sizes \( q \). Clearly the amount of converged runs increases with increasing \( q \), due to the increased exploration of the search space. Figure 6 shows the mean energy of all converged runs as a function of the amount of forward calculations for the three population sizes and for the different \( f_r \). At an equal amount of forward calculations, the mean energy decreases with decreasing population size (at the cost of a smaller percentage of converged runs, see Fig. 5).
Fig. 5 Percentage of converged runs as a function of \( f \), for the three population sizes (\( q \)) of 32, 64 and 128, respectively.

Fig. 6 Mean energy as a function of the amount of forward calculations for the three population sizes and for the different \( f \).

Making the population size twice as large is seen to result in a (statistically significant) increase of about 15% in the increase of the amount of converged runs. However, this increase is obtained at the cost of slower convergence.

C.1.3 Influence of the crossover rate and mutation rate

In this section the influence of the mutation and the crossover rates are considered. Mutation and crossover are the two mechanisms through which children are created from the parental population. If for both a value of zero is selected, the populations of each succeeding generation are equal to the initial population.

Figures 7 and 8 show the percentage of converged runs and the mean rate of convergence for four values of \( p_m \). Employing values for the mutation rate of zero and 0.2 is seen to result in a small percentage of converged runs. Employing a value of 0.1 gives in general the best results with respect to the amount of converged runs. The sudden decrease in the percentage of converged runs for \( f_c = 0.1 \) probably will disappear when more generations, i.e., more forward calculations are considered. Similarly it is expected that by increasing the amount of forward calculations, the amount of runs that converge for \( p_m = 0.2 \) will increase.

Increasing the mutation rate is seen to result in slower convergence. This is expected since increasing \( p_m \) introduces more and more randomness in the search. The plateau in the rate of convergence that is reached for \( p_m = 0 \), corresponds to that part of the search where the population has converged. At that stage mutation is the only mechanism that results in children that are different from their parents.
The influence of the crossover rate $p_c$ on the behavior of the GA is much less pronounced than that of the mutation probability. Employing a value of zero for the crossover rate, i.e., the children are created from the parental distribution through mutation only, results in less exploitation of promising solutions. Consequently, this setting was found to result in a statistically significant lower percentage of converged runs for the lower values of $f_r$ (<0.4) and slower convergence. Also a value of 0.5 and one for $p_c$ has been considered. No significant change in behavior compared to the default setting was found for these two settings. It can be concluded that the influence of the crossover rate is limited.

\section*{C.2 The optimal setting}

In the previous section, a large number of settings for the GA have been assessed with regards to the amount of the converged runs, and the rate of convergence. It is found that when selecting a setting, a trade-off needs to be made between the probability on convergence, and the amount of forward calculations. The percentage of converged runs increased with increasing reproduction size $f_r$, increasing population size $q$, and increasing mutation probability $p_m$. However, this desirable result is obtained at the cost of a slower rate of convergence, i.e., more forward calculations are needed. The highest percentage of converged runs of all settings considered, was obtained for a population size of 128, a reproduction size of 0.9, and default values for the remaining GA parameters. For this setting 90 ± 1 % of the runs had converged. From the results presented in Figs. 7 and 8, it is expected that a similar result can be obtained for a mutation rate of 0.1, a population size of 128, a reproduction size of 0.5, and all remaining GA parameters at their default values. This setting was found to result in 92 ± 1 % converged runs, which indeed is comparable to the 90 ± 1 % converged runs. Figure 9 shows the mean energy.
Fig. 9 Mean energy as a function of the amount of forward calculations the two settings corresponding to the highest percentage of converged runs.
References

