Towards Evolutionary Optimisation for High Resolution Bathymetry from SideScan Sonars

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Abstract: The main objective of this paper is to use genetic algorithms in order to improve the quality of the bathymetry derived from sidescan raw data. The optimisation sequence starts with inverse modelling of the phase data, which uniquely coresponds to the characteristics of the coupled system of the sidescan vehicle and the seafloor terrain. These phase data are then compared with phase data actually collected by the sonar, to produce a correlation coefficient as an objective function. Simulation results are reported for the algorithm showing robust convergence towards the optimum value of the objective function.

The results indicate that this new approach can be used to avoid difficulties widely encountered during forward processing of phase data to derive bathymetry.

INTRODUCTION

Optical and radar methods, vastly used in other environments, are not appropriate underwater investigations for and communications. The rapid attenuation of electromagnetic energy in marine environments restricts remote sensing of such terrains acoustic to frequencies (Voght et al., 1986). Sonars (SOund NAvigation and Ranging). operating at frequencies of a few Hz to several MHz (Blondel et al., 1997), are used nearly exclusively in submarine remote sensing. This exclusivity, coupled with the fact that almost 50% of earth's surface is under water at depths over 3000 m (Fowler, 1990), has stirred the research interest of developers, such as engineers and software designers, as well as end-users. such as geologists, geophysicists, geographers and oceanographers. The greatest issue, as in most cases of remote sensing, is the costeffective increase of resolution.

Sonars transmit acoustic waves through the water column and receive their echoes off the seafloor, which return information about the local morphology. The end products may be qualitative tools, describing the structure of the seabed (e.g. imagery), or quantitative tools, measuring geographic and topographic parameters (e.g. bathymetric charts). While imagery looks essentially as satellite or aerial photographs and is the predominant tool in geomorphological, structural and tectonic studies and assessments, bathymetric charts represent the topography of the seafloor, similar to topographic maps, and are used primarily for navigation and positioning.

A rough categorisation of sonar systems would distinguish echosounders, sidescan sonars and multibeam sonars. In broad terms, echosounders transmit a single, vertically oriented, sound beam; sidescan sonars, such as TOBI (Flewellen et al., 1990) (Fig. 1), DSL-120 and GLORIA (Blondel et al., 1994), transmit two broad beams, one per side; while multibeam sonars, such as EM12 and SeaBeam (Blondel et al., 1994), transmit several tens of beams on each side. In general, echo-sounders and multibeam systems are hull-mounted and sidescan systems may be autonomous, shallow- or deep-towed. Originally, echo-sounders and multibeam systems were designed to acquire bathymetry in big scale surveys (tens to hundreds of km²) and side-scan systems to acquire imagery in smaller scales (up to tens of km²). However, the latest generation of multibeam sonars are capable of acquiring imagery and sidescan sonars may derive high-resolution bathymetry.

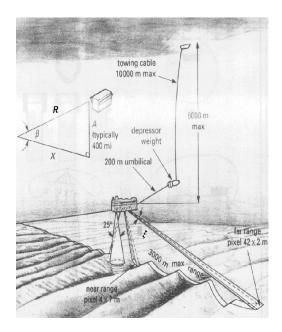


FIG. 1: Operational principles of TOBI, a deep-towed sidescan, adapted from (Flewellen et al., 1990)

IMPROVING BATHYMETRY QUALITY USING GENETIC ALGORITHMS

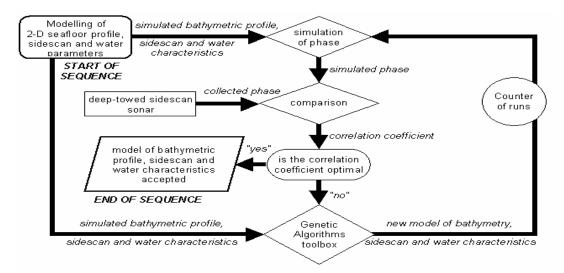
This paper concerns the capability of deep-towed sidescan sonars to acquire using high-resolution bathymetry interferometric techniques (Fig. 1). The raw data in this method consist of phase differences of the acoustic echoes received by two transducers. The mathematical inversion of this phase data derives bathymetry (Fig. 4). The main objective of this work is to use genetic algorithms (GA's) in order to improve the quality of the bathymetry derived from the sidescan raw data. Factors such as insruments' inherent noise and frequency interference, are in most of the cases difficult to assess or quantify when deriving bathymetry from such phase data. Furthermore, assumptions introduced by uncertainties in the coupled system of the sidescan vehicle and the seafloor terrain (henceforth referred to as "model"), may not hold at all times (e.g. flat bottom assumption, horizontal as opposed to inclined seafloor, evaluations of the vehicle attitude with respect to the seafloor etc). By using evolutionary optimisation techniques, and through inverse modelling, we aim to eliminate these factors which may harm the information content of the phase data. For this study we used the specifications of the deep-towed sidescan sonar TOBI (Towed Ocean Bottom Instrument) (Flewellen et al., 1990), although our findings hold for all sidescan sonars.

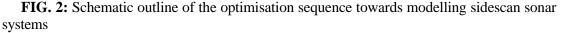
The general practice in producing bathymetry from sidescan phase data is to process the data with algorithms which the mathematical perform inversion (Avgerinos, 2000). These techniques processing mav be computationally time-consuming, costly to repeat for different parameter values, and are based on assumptions such as the ones mentioned above, affecting in this way the quality of the resulting bathymetry (Avgerinos, 2000). In most cases of submarine surveys, on the other hand, there is a fair knowledge of the bathymetric terrain, as well as the operational specifications of the sidescan sonar and the parameters controlled by the marine environment, such as sound velocity. This knowledge may be used in the inverse modelling of phase data.

Our approach, as illustrated in Figure 2, is based on well-established knowledge to model a 2-D bathymetric profile, as well as the rest of the model characteristics (sidescan specifications and environment parameters) (Fig. 3a). The optimisation sequence starts with inverse modelling of the phase data which uniquely correspond to these characteristics (Fig. 3b). This phase data is then compared with phase data actually collected by the sonar, to produce a correlation coefficient. The correlation coefficient is the objective function which we want to optimise by using GA's.

The new genes produced by GA techniques are used to simulate new phase

data through the inverse modelling. The comparison of the new phase data with the collected phase and the processing of the individuals by GA's continue until the correlation coefficient, i.e. the objective function, is optimal, although there is no way to ensure a global optimum as opposed to a local one. The individual which generated the phase data is accepted then as the optimum solution and the sequence is terminated. In this way, the resulting bathymetry is improved without the need to make assumptions (such as the assumption of a flat and horizontal seafloor) or evaluate all sources of noise and other harmful effects which affect the quality of phase data and consequently of the bathymetry because of assumptions during forward processing.





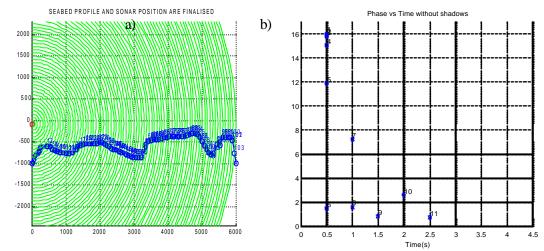


FIG. 3: Graphic representation of a 2-D bathymetric profile, modelled to comprise a gene (a). The position of the sidescan is at (0,0). The circle sectors correspond to the time intervals at which phase is calculated. The y-axis measures depth in m and the x-axis measures distance from the sidescan in m. Inverse modelling simulates the phase data (b). The y-axis measures phase in rads (multiples of p) and the x-axis measures time in seconds.

THEORY OF SIDESCAN BATHYMETRY

Sonars in general measure the amplitude of the acoustic returns as a function of signal travel time elapsed since

the acoustic transmission. In order to produce bathymetry by evaluating x and d, i.e. the horizontal and vertical distance of the target from the deep-towed sonar respectively (Fig. 4), we need to know the

slant range to the target, R, and the arrival angle of the acoustic returns, q. The slant range R is provided by the signal travel time. The arrival angle may be calculated by using a pair of receivers to measure the phase difference of he reception signal between the two receivers (Fig. 4). The geometry shown in Figure 4 indicates that the arrival angle of the acoustic return q is the same as the angle of incidence of the wavefront of the acoustic return to the vehicle (also shown as q in the blow up insert of Figure 4). Then d and x are:

$$d = R\sin \boldsymbol{q} \quad (1)$$
$$x = R\cos \boldsymbol{q} = R\sqrt{1 - \sin^2 \boldsymbol{q}} \quad (2)$$

Equations (1) and (2) are the trigonometric transformations of the polar coordinates R and q to the Cartesian coordinates d and x. The slant range R is proportional to the sound velocity in water, c, and the TWTT (two-way travel time) of the signal, t. Therefore equations (1) and (2) from above may be written as:

$$d = c \frac{t}{2} \sin \boldsymbol{q} \quad (3)$$
$$\mathbf{x} = c \frac{t}{2} \sqrt{1 - \sin^2 \boldsymbol{q}} \quad (4)$$

The phase difference j of the backscattered signal received by two sensors separated by s is proportional to the extra distance d covered by the signal wavefront in between its reception by the two receivers and in radians is given by

$$\boldsymbol{j} = \frac{2\boldsymbol{p}}{\boldsymbol{l}}\boldsymbol{d} \quad (5)$$

where l is the wavelength of the signal. The phase j demonstrates the extra number of wavelengths the returning signal travels before it reaches the receiver, which is further away. The ratio d/l represents this number and is multiplied by 2p in order for the phase angle to be expressed in radians. The relation of the distance d to the angle of arrival of the acoustic echo q is given by

$$\boldsymbol{d} = s \sin \boldsymbol{q} \quad (6)$$

where s is the separation between the transducers (Fig. 4). Hence:

$$(5) \land (6) \Rightarrow \sin \boldsymbol{q} = \frac{\boldsymbol{H}}{2\boldsymbol{p}} \quad (7)$$
$$(3) \land (7) \Rightarrow d = \frac{ct\boldsymbol{H}}{4\boldsymbol{p}} \quad (8)$$
$$(4) \land (7) \Rightarrow x = c \frac{t}{2} \sqrt{1 - \left(\frac{\boldsymbol{H}}{2\boldsymbol{p}}\right)^2} \quad (9)$$

The last two equations express the principles of interferometry. They use the information of the phase difference \ddot{o} between the two sensors against time in order to calculate the position of the point from which the received signal is coming. In other words, equations (8) and (9) illustrate how bathymetry is calculated from phase data.

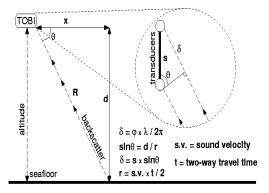


FIG. 4: The geometry of sidescan and seafloor for acquiring bathymetry (out of scale, adapted from (Avgerinos, 2000)

Equation (7) may be rewritten with respect to phase j as:

$$\boldsymbol{f} = 2\boldsymbol{p} \frac{s}{l} \sin \boldsymbol{q} \quad (10)$$

Equation (10) demonstrates that the ratio s/l, or the distance between the two receiving transducers over the signal wavelength, is the controlling factor of the quality of sampling of $\sin q$ by phase j. Consequently, we may increase the sampling of $\sin q$, therefore also the resolution of bathymetry, by increasing s. However, there is a trade-off in increasing the separation of the two receivers. Equation (10) shows that the maximum

value of phase is controlled by the ratio s/Iand in rads is equal to as many times as sis greater than I. Since phase may be uniquely counted only in the 0-2p interval, when s is greater than the wavelength I, phase wraps back to the 0-2p interval. These phase wraps introduce an extra problem when these data are processed, since they have to be identified in order to unwrap the phase data before deriving bathymetry from them. In the case of TOBI, as many as 8 phase wraps are typically present per profile, complicating the processing even more.

Another complication in deriving bathymetry from phase data is due to the presence of acoustic shadows in the phase data. These shadow zones occur when elevated morphological features block the acoustic energy transmitted by the sidescan and have to be identified and omitted during forward processing of phase data to derive bathymetry.

SONAR MODELLING AND OPTIMISATION

This project concerns with modelling of a sidescan sonar in order to examine what the output of the sonar looks like for a given underwater terrain. For this we have developed the automated sequence outlined in Figure 2.

By using the interferometric method we obtain the phase difference j of the backscattered signal received by two sensors separated by distance s (Fig. 4). The user has the ability to set up the characteristics of the model as a whole, as well as to set up the parameters which control the optimisation procedure. The sonar model returns the phase differences of points of seafloor profile which correspond to time sample steps set by the user (Fig. 3a).

The optimisation procedure aims to pick up the phase returns from a seabed profile randomly chosen by the user and compare them with a given phase record. The optimisation is considered complete if the phase data of the user profile are approximately the same as the given phase data. In this case, if the given phase is the result of experimental measurements and the user phase the outcome from the model for the same profile, then the optimisation determines as the optimum settings of the model the required parameter values in order to achieve a high quality solution in the resulting bathymetry.

The two initial assumptions of the model are: (i) it is a two-dimensional system, and (ii) the position of the sonar is a steady one (the sonar is motionless).

THE OPTIMISATION PROCEDURE

Once a profile is set up, the model runs once and returns the total number of points (i.e. including points within the shadow zones) on the bathymetric profile for which phase is calculated, depending on the time sampling rate, with the corresponding phase differences, as well as the phase differences of points excluding those within the shadow zones.

The total number of points together with the speed of sound, the separation transducers between the and the transmission frequency constitute some of the inputs to the optimisation procedure. matrix containing the The phase differences of the total number of points is compared with the matrix of the phase differences given by the user and the comparison factor (i.e. the objective function) is the correlation coefficient.

Each individual consists of a number of characteristics or variables. In the model design process, the variables are the XY coordinates of the intersection points of seafloor, the speed of sound (*sv*), the separation between the transducers (*separ*) and the frequency of transmission (*freq*). In this study, the following values are fixed: sv = 1500m/s, separ = 0.8m, and freq = 30KHz.

X_1	Y1	X _n	Y _n	Sv	separ	Freq

The creation of the testing population follows the run of the model for each individual member of the population. The outcome of each run (i.e. a matrix containing the phase differences produced by the elements of each individual corresponding to x- and y- coordinates) is compared with the given phase and the result will be the value of the correlation coefficient.

Hence, matrix of correlation а coefficient values is created as large as the number of individuals which comprise the population. From that matrix the mean value of all correlation coefficients is calculated and plotted in graphs of mean value of correlation coefficients vs. the number of runs/generations.

The evolutionary process applied to each generation is summarised in the following. Each individual is assigned a reproduction probability according to its own objective value and the objective value of the other individuals within the Selection is based upon population. stochastic universal sampling and multipoint crossover is performed. The offspring are mutated by the addition of small random values (size of the mutation step) with low probability.

The optimisation cycle is repeated for a number of generations with final target the stabilisation of the mean correlation coefficient of the population as close as possible to the unit value. This approximation means that even continuing recombination of the members of the population and performing mutation, any further improvements will be negligible to justify the time and effort.

In practical terms the user sets up a profile and the aim of the optimisation is to transform it, together with the model parameters, in such a way that from a certain point on (i.e. after a number of

generations) is closely similar to the given one. For example, if a real seabed profile is given, it is compared with the analogous product of the model and the result of the optimisation procedure is the optimum values of the model characteristics (i.e. variables like frequency transmission and separation of transducers) in order to get the best possible resolution.

As the optimisation is concluded, the transformation of phase differences of the optimised model to bathymetry is the last stage of the modelling. This part of the development considers the phase data to output x- and y- coordinates, i.e. the horizontal and vertical distance of the target points on the bathymetric profile from the sonar.

SIMULATION RESULTS

All variables and settings are shown in Table I, while Figures 5-T1 to 5-T8 show the optimisation history for each of the tests. Tests 12 are performed with the default mutation rate (1/number of variables), while tests 36 are performed with no mutation, and tests 7-8 are performed with a low mutation rate (MutR = 0.001). High boundary limits for the individual's variables are selected, with the chromosome having 40 genes (37 bathymetry points and three sonar parameters which are sound velocity (sv), separation of transducers (separ) and frequency of transmission (*freq*)).

1

0 2 1

2 0 0

Table I	
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Table I								
Parameter Values in various simulation	on test	5						
Gene	Т	Т	Т	Т	Т	Т	Т	
Maximum listening time of sonar (s)	4	4	4	4	4	4	4	
Unit sampling time (s)	0	0	0	0	0	0	0	
Upper and lower limits of the profile	1	1	1	0	1	0	1	
Upper and lower limits of the speed of	1	2	1	5	1	1	1	
Upper and lower limits of the	0	0	0	0	0	0	0	
Upper and lower limits of the	3	3	3	5	3	1	3	
Number of times the optimisation	1	1	1	1	1	1	1	
Size of population	1	1	1	1	1	2	2	
Crossover rate	0	0	0	0	0	0	0	
Population gap	0	0	0	0	0	0	0	

Test 1 shows the model is unstable. In Test 2, we lower the variable boundaries significantly and reduce the size of the chromosome (18 genes per chromosome instead of 40) by considering less coordinates leading to less fluctuations but the mean correlation coefficient is low to start with. Hence, Test 3 returns to using high limits for the variables boundaries but omitting the mutation function. Also the size of the population is kept the same as in the second test. By comparison with previous tests, the instability is reduced and the model starts to stabilise at high values of the mean correlation coefficient. In Test 4, the mutation factor is still omitted, the boundaries of the variables are set to low, and the size of the chromosome is the same as in the previous two experiments. The crossover rate is slightly lowered in order to check its influence on the behaviour of the model. The fluctuations of the mean correlation coefficient are limited to the first ten generations but the coefficient is still not close enough to the desired optimum (i.e. 1.0).

During Test 5, the boundaries of the variables are kept high and the size of the

population maintained. The result is improved. Test 6 sets the limits of the variables low but the size of the population is doubled to twenty members from the ten used before. The size of the chromosome is retained as before. The model obtains high values for the mean correlation coefficient faster than in the previous cases. In other words the instability period is much shortened when the size of the population is increased.

Tests 7 and 8 are conducted with a low mutation rate. The population size and chromosome size remain the same, but the difference is in setting the variables limits between the two tests. The results of Test 7 is very much the same as in the previous test (i.e. without mutation and population of 20). The range of instability is much shorter than with half the above population (i.e. the mean correlation coefficient starts to stabilise after the 60th generation and the approximation can be considered close enough to the optimum.) The range of instability is even shorter in Test 8. The variations of the mean correlation coefficient are very limited after the 30th generation, and after the 90th generation the approximation is above 99%.

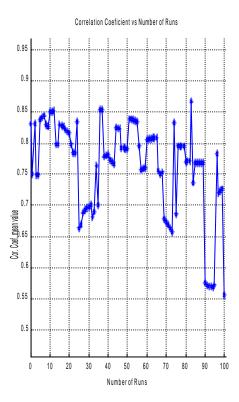


Figure 5-T1

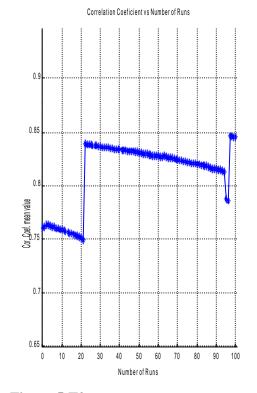


Figure 5-T2

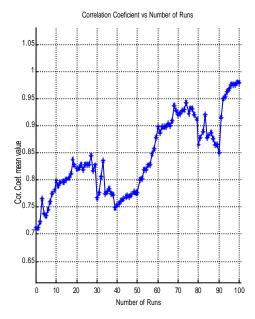


Figure 5-T3

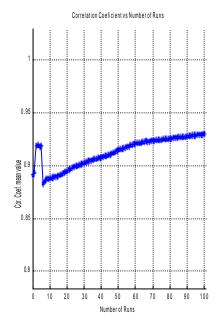


Figure 5-T4

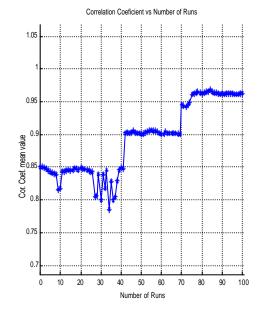


Figure 5-T5

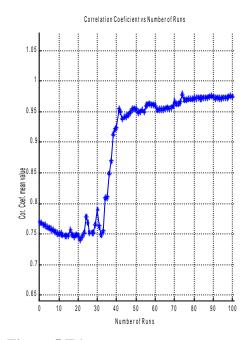


Figure 5-T6

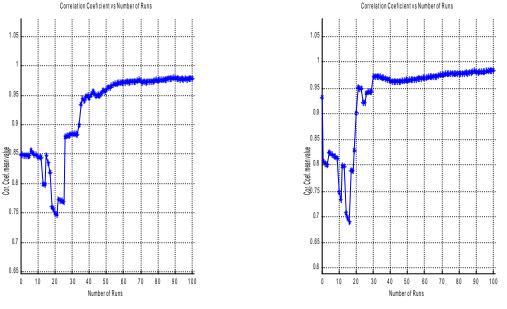


Figure 5-T7

Figure 5-T8

FIGS. 5-T1 5-T8: Test results showing the correlation coefficient vs. number of generations.

CONCLUSIONS

This paper presents a new direction towards increasing the quality of sidescan bathymetry, that has not been investigated before bv the sonar engineering community. While research in the field focuses in general in improving the forward processing of phase data in order to derive bathymetry, we consider the inverse modelling approach. This latter approach utilises an evolutionary technique to optimise the extraction of bathymetry from phase data.

In this work, the evolution of chromosome only included the bathymetric profile coordinates to get a basic understanding of the optimisation outcome. However, the specifications of the sidescan characteristics of the water environment – usually set as constants by the sonar operators – do vary and may be taken into consideration in further research.

The testing was conducted with chromosomes with size from 15 to 25. If we can apply a much smaller sampling rate (i.e. the size of the chromosome will be in the range of a few thousands) the model will probably perform better and the outcome is going to be closer to a realistic one. However, computational power will pose a difficulty.

Having a low mutation rate gave better performance than not having the mutation. Increasing the size of the population achieve improved results in shorter time (i.e. smaller number of generations).

The upper and lower limits of the boundaries of the variables play a role in the behaviour of the model. High limits destabilise the model behaviour. On the other hand, very small limits bring the opposite result since the transition is extremely lengthy and the optimisation may achieve efficient results after hundreds of generations. The best way is to keep the limits in a balanced range and to manage the best performance through it.

By using the inverse modelling approach and optimising the chromosome using GAs, we overcome factors such as inherent noise and frequency interference, as well as phase wraps and acoustic shadows, which deteriorate the quality of the bathymetry. In forward processing of phase data in order to derive bathymetry, these factors need to be accounted for, properly quantified and corrected. Using our approach though, there is no need for assessment of these parameters anymore.

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