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Study of the Locating Capability of Genetic Algorithms

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Abstract

A modern locating method based on global optimization with genetic algorithms (GAs) has been used to locate seismic events at distances up to 1500 kilometres in Fennoscandia and the surrounding territories. Of special interest were some well-known mining sites, publicized depth charge explosions carried out by the Finnish Navy and precisely located explosions set off as part of deep seismic sounding studies. Also, regional seismic events were examined by relocating them and comparing the results with those of the Helsinki bulletins. GAs seem to compare well with the more traditional least squares approach as a locating method. The median location discrepancy between genetic algorithms and least squares optimization of the Helsinki bulletins have been found to be approximately 21 kilometres, and 90 % of the events located within 63.4 kilometres from the epicentres reported by the Helsinki bulletins. The main reason for location discrepancies was evidently poorly associated later phases which gave large travel time residuals.

The behaviour of GAs have been studied by applying different travel time models. Complex crustal models tend to produce more local minima so avoiding monotonous convergence toward the global minimum.

The theories of evolutionary programming in general are presented and their benefits and possible drawbacks are discussed.

Key words: genetic algorithms, locating seismic events, crustal models

1. *Introduction*

Locations of seismic events are of great importance to seismological analysis. Exact locations require adequate velocity model and accurate readings of specific phase arrival times (*Gomberg*, 1990). Modern locating methods are based on *Geiger*'s (1910) least squares method and its extensions. Those methods involve calculation of partial derivatives of travel time parameters to some position. This is followed by a matrix inversion is performed an updated epicentre. If an event is poorly constrained some numerical damping is needed to avoid problem instabilities, such as matrix singularity.

Evolution programming, such as genetic algorithms (*Holland*, 1975), are a class of computation methods which obtain their behaviour from a metaphor of evolutionary processes. These algorithms encode a potential solution to a specific problem on a simple chromosome-like data structure and apply recombination operators to these structures so

as to preserve critical information. Genetic algorithms are often viewed as multidimensional optimizers, although the range of problems to which genetic algorithms have been applied is quite broad.

Genetic algorithms do not need a priori information about the objective function other than its actual value. The aim is to set the various parameters so as to optimize some output. Consequently, some function $f(x_1,x_2,...,f_m)$ should be minimized (or maximized). In other words, they use no predetermined internal model of the objective function. Unlike local, deterministic techniques, such as the least squares method, genetic algorithms do not require partial derivative information, but only evaluate the misfit function. Consequently, the problem of non-linearization is avoided. Another property of genetic algorithms is the collective learning process within a population of individuals parameters sets, each of which presents a search point in the space of potential solutions of the problem.

Genetic algorithms start at an arbitrarily chosen initial population of parameter set of a model, and use probabilistic transition rules to guide the optimization search, while conventional methods are based on deterministic search. Offspring of smaller misfit are further reproduced and mated by the genetic operations, e.g. mutations and crossovers of higher probability. The poorer models in turn die off. Since these algorithms evaluate the objective function from many parts of the search space, it is not likely that their execution will be trapped in some local minimum, but they tend to define the near optimal solutions. Finally, the averaged results of the repeated runs of the algorithm provide near optimal solutions. The working principle of genetic algorithms is given in the Appendix.

Genetic algorithms are widely tested and used in geophysics. *Stoffa* and *Sen* (1992) used them for seismic velocity inversion on synthetic data and *Sambridge* and *Drijkoningen* (1992) on real data. Also, genetic algorithms have been used for seismic locating optimization. *Kennett* and *Sambridge* (1992) used them on teleseismic events, while *Bondar* (1994) located events at local distances. In this study genetic algorithms are used to locate different type of seismic events at local and regional distances. The velocity model used by genetic algorithms was the same which is used to compile the Helsinki bulletins (Table 1). Also, a velocity model used by *Saastamoinen* and *Tarvainen* (1984) was used to compare results and examine the behaviour of genetic algorithms. This velocity model is given in Table 2 and it was used on explosions carried out during deep seismic sounding studies. The latter model is quite complex and differs from the crustal model used to compile the *Helsinki bulletins*.

Table 1. The crustal model used for comparison and initial calculation of locations with genetic algorithms.

Layer thickness	P-velocity	S-velocity
15.00	6.07	3.51
25.00	6.64	3.84
40.00	8.03	4.64
-	8.50	4.75

Table 2. The complex crustal model used for locating calculations of some deep seismic sounding explosions.

Layer thickness	P-velocity	S-velocity
2.00	5.90	3.33
3.00	6.00	3.40
13.50	6.20	3.71
12.00	6.50	3.54
3.00	7.00	3.54
4.00	6.95	4.09
8.00	7.10	4.10
10.00	7.60	4.39
13.00	8.00	4.70
25.00	8.30	4.80
25.00	8.40	4.85
-	8.50	4.90

Table 3. Depth charge locations according to Helsinki bulletin and as provided by genetic algorithms.

#	year	mm-dd	hh-mm-ss.s	lat	lon	#	year	mm-dd	hh-mm-ss.s	lat	lon
1	1993	1116	13:06:06.8	59.69	22.77	11	1993	1117	13:06:41.6	59.69	22.77
			13:06:05.6	59.68	22.65				13:06:41.1	59.65	22.71
Δ			1.2	0.01	0.12	Δ			0.5	0.04	0.06
2	1993	1116	13:25:48.3	59.73	22.58	12	1993	1118	06:59:50.4	59.75	22.35
			13:25:50.8	59.84	22.77				06:59:53.9	59.84	22.65
Δ			-2.5	-0.09	-0.19	Δ			-3.5	-0.09	-0.30
3	1993	1116	13:28:40.4	59.75	22.62	13	1993	1118	07:22:44.6	59.58	22.66
			13:28:43.0	59.79	22.87				07:22:47.4	59.73	22.87
Δ			-2.6	-0.04	-0.25	Δ			-2.8	-0.15	-0.21
4	1993	1116	13:58:51.0	59.83	22.37	14	1993	1118	07:25:46.7	59.49	22.74
			13:58:54.8	59.70	22.93				07:25:48.8	59.57	22.87
Δ			-3.8	-0.13	-0.56	Δ			-2.1	-0.08	-0.13
5	1993	1116	14:01:13.7	59.59	22.75	15	1993	1118	07:25:42.0	59.69	22.48
			14:01:15.4	59.65	22.93				07:25:44.9	59.79	22.71
Δ			-1.7	-0.06	-0.18	Δ			-2.9	-0.10	-0.23
6	1993	1117	09:14:40.5	59.69	22.65	16	1993	1118	07:54:47.7	59.62	22.52
			09:14:39.8	59.79	22.39				07:54:48.8	59.73	22.49
Δ			0.7	-0.10	0.26	Δ				-0.11	0.03
7	1993	1117	10:51:42.0	59.63	22.66	17	1993	1118	07:57:00.3	59.79	22.36
			10:51:45.4	59.76	22.90				07:57:02.8	59.87	22.61
Δ			-2.6	-0.13	-0.24	Δ			-2.5	-0.08	-0.25
8	1993	1117	11:24:41.8	59.63	22.61	18	1993	1118	08:03:41.4	59.71	22.65
			11:24:44.8	59.68	22.90				08:03:44.5	59.82	22.90
Δ			-3.0	-0.05	-0.29	Δ			-3.1	-0.11	-0.25
9	1993	1117	11:27:22.1	59.70	22.69	19	1993	1118	08:32:34.5	59.68	22.66
			11:27:20.0	59.59	22.39				08:32:36.6	59.62	22.96
Δ			1.9	0.11	0.30	Δ			-2.1	0.06	-0.30
10	1993	1117	11:27:33.3	59.81	22.53						
			11:27:36.6	59.90	22.80	Median difference			-2.6s	-0.09°	-0.25°
Δ			-3.3	-0.09	-0.27						

As mentioned by *Sambridge* and *Gallagher* (1992) and *Bondar* (1994) in the locating problem solution genetic algorithms try to minimize the root-mean-square of the weighted travel time residual over stations namely:

$$\phi = \frac{\sum_{i=1}^{N} \left(w_i T_{res_i} \right)^2}{\sum_{i=1}^{N} w_i^2} \qquad (1)$$

where N is the number of stations w_i is the weight and T_{res} is the travel time residual at the ith station. The station weights are determined during the search in the same manner as for the least squares approach to epicentre and focus location (*Lee* and *Lahr*, 1972; *Klein*, 1978).

2. *Locating well-defined explosions at local distances*

First we studied the locating capability of genetic algorithms at local distances (Δ<200 km) from the detecting network and compared the results with the actual epicentres. The events selected for this set are shown in Figure 1. The first set are mining explosions in the Siilinjärvi mine, and the second set consists of depth charge explosions carried out by the Finnish Navy.

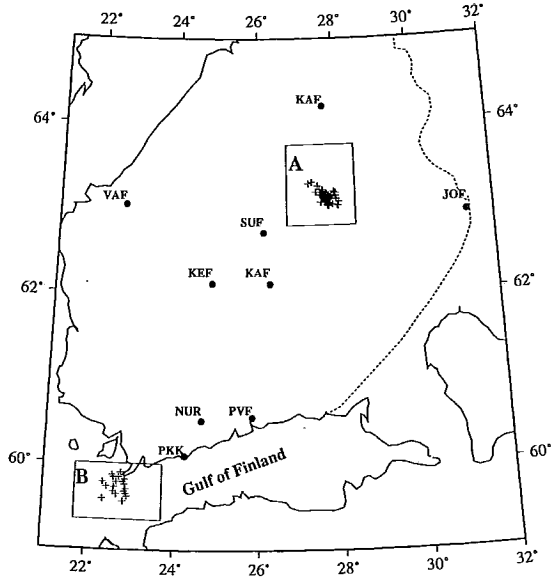

Fig. 1. Events used in this study and listed in the Helsinki bulletins. The cluster in central Finland, denoted by "A" presents explosions in the Siilinjärvi mining area. In Gulf of Finland the events are depth charge explosions carried out by the Finnish navy within the area marked by "B".

The Siilinjärvi mine is a well-known phosphate mine in Finland. Explosions take place 2-3 times a week at 11-12 GMT (1-2 PM local time). Seismic signals from these explosions, reaching yields up to eighty tonnes have very strong onsets (*Tarvainen*, 1992) and are detonated in two separate fields. Blasts in the nearby Nilsiä mine ($\Delta \approx 20$ km) are sometimes erroneously associated with the Siilinjärvi mine, but the respective shooting practices are different. Also, the corresponding seismic wave forms are different. In 1994 altogether 107 explosions in the Siilinjärvi mine and its vicinity were located using the GA approach using the recordings of the three stations in central Finland (SUF, KEF and KAF). The locating clusters are shown in Figure 2. Events are plotted according to their distance from the nearest station SUF (62.7191°N, 26.1506°E, h=185 m). They locate either at distances less than or equal to 90 kilometres or more than 90 kilometres from the station, respectively. The "coded" explosion site deviates to some extend from both of these fields. Some over spread events can be associated with any of these fields or with the mine in Nilsiä.

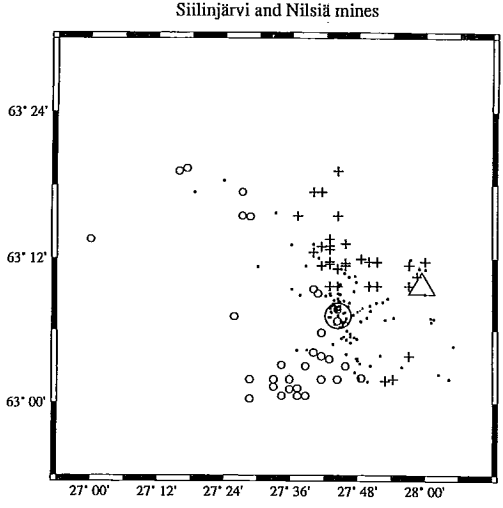

Fig. 2. The close-up examination of epicentres near the Siilinjärvi mine. The open circles and crosses are events, for which the SUF epicentral distances are below and beyond 90 km, respectively. The epicentres found in Helsinki bulletins are shown by dots. The big circle denotes the Siilinjärvi "code site" while the triangle is the location of Nilsiä mine, used in the Helsinki bulletin location template procedure.

The Finnish Navy has a well defined practice areas both in the Gulf of Bothnia and the Gulf of Finland. The explosions are detected at many of the Finnish seismograph stations even beyond 250 kilometres. Further, the location can be confirmed from bulletins. In Figure 1 nineteen clustered depth charge explosions close to the town Hanko (denoted by "B" in the map), in November 1993 are located by GAs. The eight explosions carried out on 18th November have a rough line spacing as a function of time, so the locations obtained via GAs can be interpreted as a naval ship tracking operation (Fig. 3). The best locating capability was found using stations in southern Finland at distances less than 200 kilometres, but seismic signals as far as $\Delta \approx 400$ km (station JOF), were also utilized.

3. *Comparing the locating capability of genetic algorithms with the Helsinki bulletins*

The *Helsinki bulletins* (also cited as *Seismic events in northern Europe*) are widely used as a reference data base to examine the capability of seismic monitoring systems. This bulletin and also, the analysis data of other Nordic authorities are archived at the Institute of Seismology, University of Helsinki.

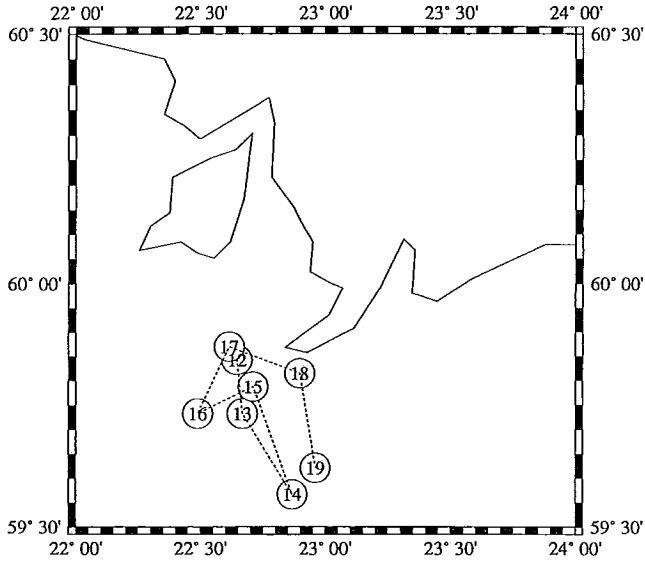

Fig. 3. A detailed plot of the depth charge explosions on 18th November 1993 near the town Hanko, just above shot-point 18. The movements of the vessel are clearly indicated by the dispersion of epicentres as a function of time, reflecting the standard manoeuvre practice during this kind of naval operations.

The genetic algorithms are tested on that data, using readings of Finnish seismograph stations only. The results provided by the genetic algorithms and Helsinki bulletins are shown in Figures 4a and 4b. The distribution of epicentres obtained by the both methods are very similar. The well-known mining sites which used to be applied as "code" sites, show more stable solutions in Helsinki bulletins than provided by genetic algorithms which did not utilize any predetermined knowledge apart from phase readings.

The events showed a strong concentration in eastern Estonia and Russian Karelia. Also, some areas in Finland showed strong concentrated epicentres. Events in those regions are mainly ripple fired mining explosions which are detected only at three stations in southern Finland. Events at the brink of the search area or far from the detecting network seem to be hard to locate adequately with GAs. A reason for this may be the applied velocity model, which evidently is not valid at longer distances.

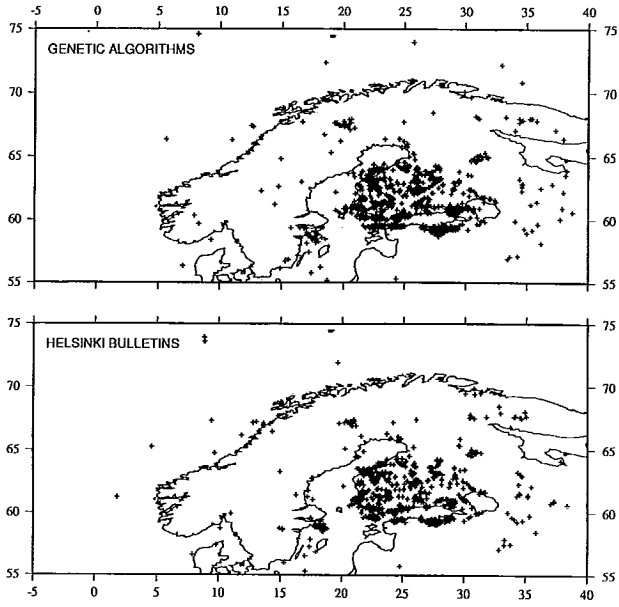

Fig. 4. Epicentres provided by genetic algorithms (a) and Helsinki bulletins (b). The oil shale area in Estonia is clearly visible. Also, some mining sites in Russian Karelia and Sweden have great activity. Most of events in Finland are construction work explosions and events along the coast are often depth charge explosions.

The locating differences were compared by selecting the corresponding events. This was done by assuming an event to be common when origin times were within 30 seconds so allowing quite a big origin time deviations. Consequently, 2384 common events were found, and are analyzed. The location difference was computed as a distance between epicentres obtained via two different methods. The cumulative location errors are shown in Figure 5. The median location error was found to be 21.3 kilometres. Consequently, the error is roughly half of the error obtained from 3C studies (*Tarvainen*, 1992). Further, 90 % of the events were located within 63 kilometres a result which can be taken to be very satisfactory, while no other information than phase readings were in hand for genetic algorithms. No kind of ground truth, like prior knowldge of waveforms from known code sites were available to steer the solutions as is the case in routine analyses.

Next we examined possible systematic distribution of those events having greater location errors. This was done by selecting events having a location error at least 63.4 kilometres from the epicentre reported by the Helsinki bulletins. Consequently, we analyzed 239 events. The origin was set at the barycentre of the tripartite network in central Finland, and the relative location errors were computed from this point. The ten degrees' bins represent the relative amount of events having location error of 63.4 kilometres or more. This means that in any analyzed direction number of events exceeding the location error of 63.4 kilometres were compared with the total number of events in that direction. The

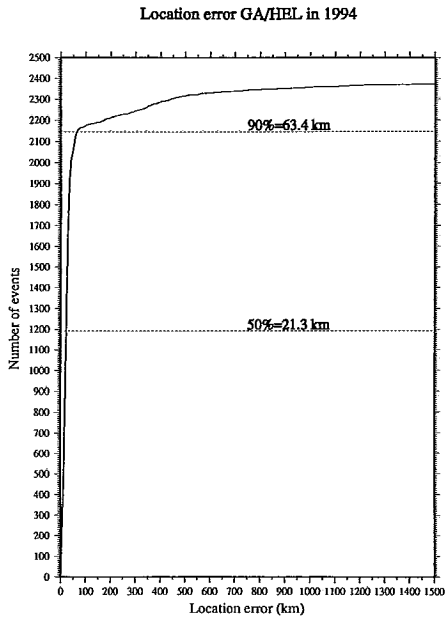

Fig. 5. The cumulative error function. Altogether 2384 events were analyzed and they had 21.3 kilometres median error and 90 % of events were located within 63.4 kilometres.

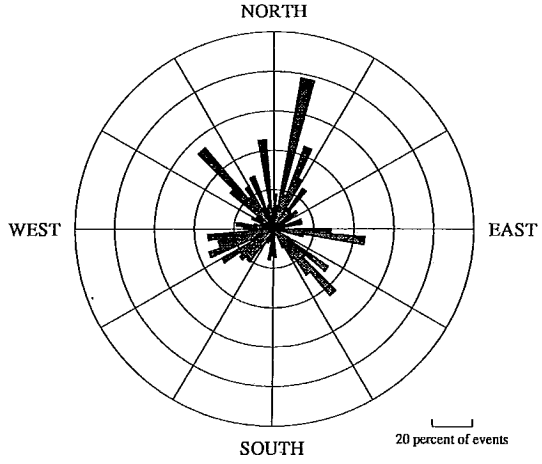

Fig. 6. Relative distribution of errors equal to or greater than 63.4 kilometres. The strongest bin pointing to direction 20° means that 77 % of events detected in that direction had the error of the size mentioned.

percentage distribution is shown in Figure 6. The greatest relative number of events having location errors at least 63.4 kilometres were found at a direction of approximately 20°. In that direction 77 % of analyzed events had errors of the size mentioned. Because, most of the detecting seismograph stations in Finland are located south of the thicker crust (H≈60 km) in central Finland and the Lake Ladoga-Bothnian Bay fracture zone, the seismic signals arriving from the directions of azimuth ≈20° are distorted by the crustal effects which in turn affect the seismic wavetrain and phases.

4. *Re-locating earthquakes in Fennoscandia in 1993*

The number of earthquakes in Fennoscandia is approximately one hundred per annum. The most active zones in Finland and Sweden are around the Gulf of Bothnia. Events there may be connected to land uplift, also indicating some tectonic push effect from the North Atlantic ridge. In Norway, earthquakes occur along the western coast. Events in southern Norway are connected with the coastal areas and to the Viking graben. From northern North Sea up to Svaldbard regions the earthquakes locate along the continental margin zones (*Bungum* et al., 1991). Earthquakes in Fennoscandia are small, seldom having magnitudes over 4. In this study all the seismograph stations in Fennoscandia have been taken into account which meant that up to 25 separate stations might have contributed phase readings

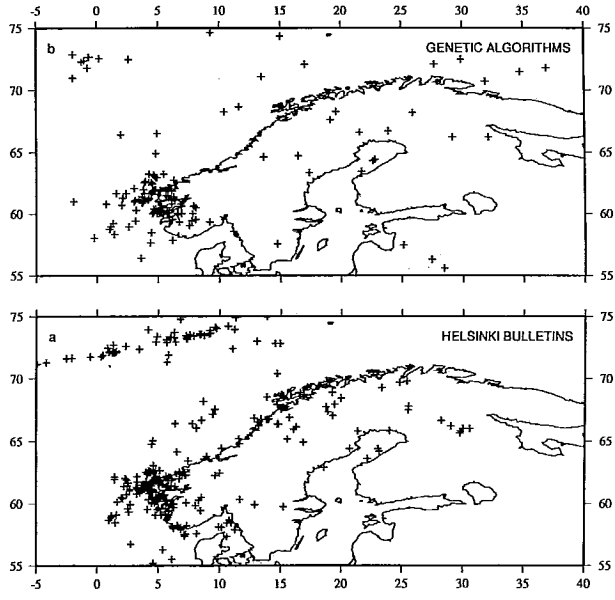

Fig. 7. Earthquake epicentres in northern Europe in 1993. The western Norway epicentre concentration is very similar regardless of method while events along the north-Atlantic ridge are almost missing when located with genetic algorithms. This evidently is due to the crustal model which was used. Events there locate close to the teleseismic window and would be easier to locate with some local crustal model such as used by the university of Bergen in their bulletin production (Sørnes and Navrestad 1975).

for analysis. For the study 164 earthquakes were selected as shown shown in Figure 7, together Helsinki bulletin epicentres.

More detailed analysis was done on earthquakes which occurred along the western coast of southern Norway which is the most active seismic zone in the entire Fennoscandia. Figure 8 depicts the epicentres computed by genetic algorithms and those reported by the Helsinki bulletins. The epicentres obtained via genetic algorithms showed systematic eastward bias which clearly is due the to crustal model used to compute them.

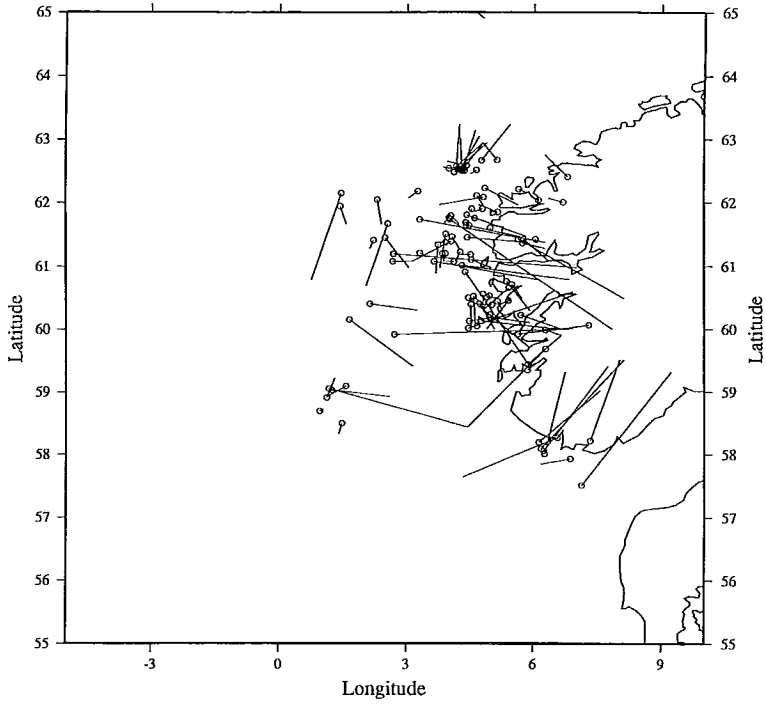

Fig. 8. Epicentres provided by genetic algorithms and compared with Helsinki bulletin epicentres. The Helsinki epicentres are shown by small circles and the heads of the lines point to the epicetres of genetic algorithms. Epicentres of genetic algorithms show systematic eastward bias which evidently is caused by the crustal model used by the genetic algorithms.

5. *Comparing results of two different velocity models using exactly defined explosions*

Next we studied the behaviour of genetic algorithms with two different velocity models and using locations of exactly defined shots carried out during the fieldwork of FENNIA deep seismic sounding study in 1994. The shot points used in this study were five small lakes, excluding the shot point in the Gulf of Finland. Explosions up to 1200 kilograms in size were detonated on three nights in these lakes .

Genetic algorithms can be used to search over a very large initial parameter space. Consequently, we selected a very large search area spanning from 5° western longitude up to 45° eastern longitude and from 50° northern latitude up to 80° northern latitude, respectively. The depth constrains were limited to 35 kilometres. These produced a combined chromosome of 41 bits so totalling as many as $2.2*10^{12}$ individual epicentres in the parameter space with the simpler velocity model and 47 bits chromosome and $1.4*10^{14}$ individual epicentres with the complex velocity model.

Figure 9 shows the epicentres obtained via genetic algorithms using two different crustal model. The event which is analyzed is a shot exploded on 6th June 1994 at 22:40 GMT at the point 62.28976°N; 24.49871°E. The event which occurred during the most silent hours of the day had a good signal-to-noise ratio and it was detected well at all the stations used to compute the location. The misfit surfaces are very similar and the final solutions locate very close to each other. The simpler crustal model showed weak east-west oriented distortion on misfit surfaces while the complex model produced more circular misfit surfaces. Also, the final solution with the complex crustal model occurred somewhat at the edge of the minimum misfit layer.

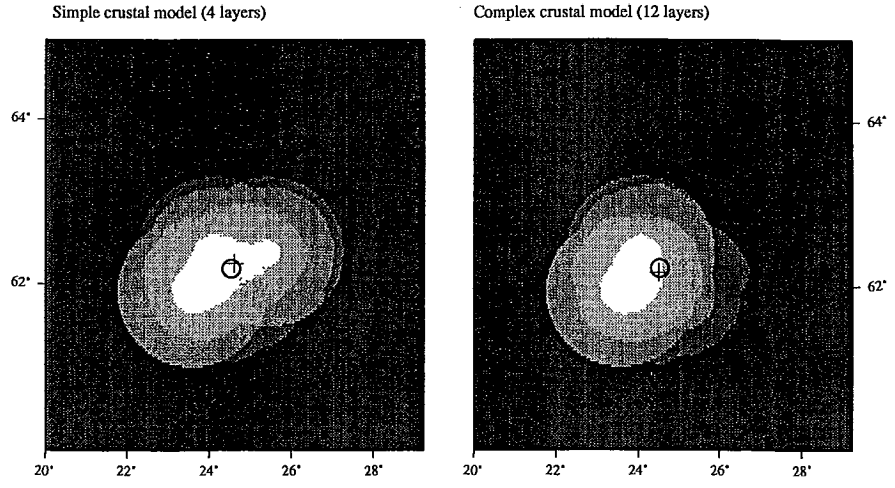

Fig. 9. The misfit layers of two different crustal models. The smallest misfit values (white areas) have travel time errors less than 0.2 seconds according to the model used. The greatest misfit (the dark gray shaded areas) value is 1 second.

In Figure 10 all the FENNIA shots which were located with two different crustal models are shown. The precise epicentre is assumed to locate at the origin and the errors were computed in x- and y-directions. When the simpler crustal model was used the error

circle had a radius of 11 kilometres and two events were located close to 15 km way off from the correct location. When the complex crustal model was applied to genetic algorithms the epicentres fell within 6 kilometres from the correct location. Consequently, when more complex crustal models are used the accuracy is notably increased.

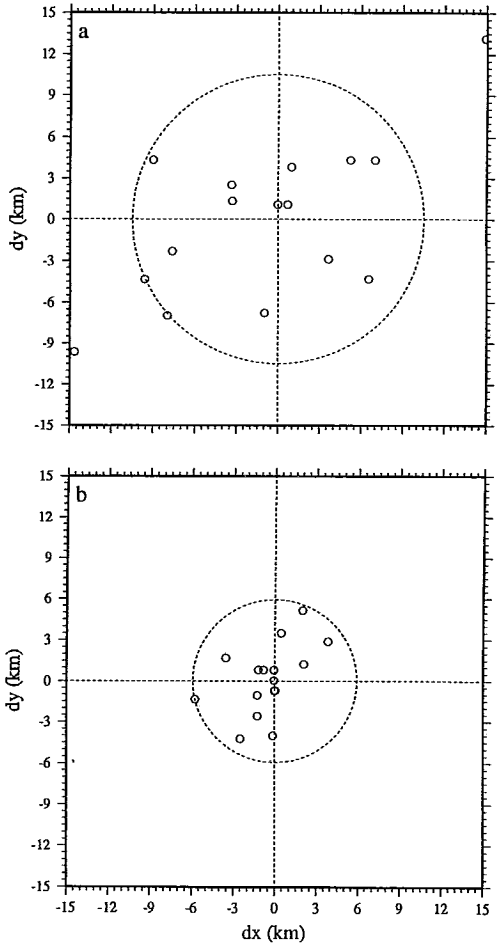

Fig. 10. Location errors of two different crustal models. In the simpler model (10a), which is also used in the Helsinki bulletins' production, the error circle has a radius of 11 kilometres. Still, there were two events which were outside of this circle. Their location errors were more than 14 kilometres. The complex crustal model (10b) formed an error circle having a radius of 6 kilometres, and all the events located within this area.

6. *Discussion and conclusions*

Genetic algorithms have received much attention over the last few years. They have proven to be useful in a variety of constrained problem optimization. The genetic operators (e.g. crossovers) combine the features of two parent structures to form two similar off springs. Crossovers work by swapping corresponding binary strings representing the parent solutions.

When the GAs start, the values of the genes for different members of population are randomly distributed. So, there is a wide spread of individual fitnesses. During the progress, particular values for each gene begin to dominate and as the population converges, the range of fitnesses in the population reduces. This variation of fitness range throughout the run often leads to the problem of premature convergence or slow finishing.

Premature convergence occurs, when there are genes from a moderate highly fit individuals, which may fast begin to dominate the population, causing it to converge toward some local minimum and once the population has converged, the ability of the GAs to continue the search toward a better solutions is effectively eliminated. Crossovers of almost identical chromosomes do not produce any remarkably improvements. These problems can be overcome by mutations of higher probability, but one must remember that they produce only a slow random search.

Slow finishing may take place, if the fitness function has many local minima, the algorithms may fall into these "fox holes", without producing good optimization result. Also, in some cases, after many generations, the populations may have converged well, but may still not have precisely located the global minimum. The average fitness will be good, and there may be little difference between the best and the average individuals. Consequently, there can be an insufficient gradient in the fitness function to steer the algorithms toward the global minimum.

To make GAs work efficiently on finite populations, one can modify the way of selecting the individuals to be reproduced. Several methods can be chosen e.g.

- selecting parents according to fitness
- selecting according to ranked fitness score
- explicit fitness remapping by dividing each individuals' fitness by average fitness of the population
- generation gaps, which is the proportion of individuals in the population, which are replaced in each generation

In this study genetic algorithms were tested and used to locate seismic events at regional distances. They were found to be effective for event location problems. They have the benefit of not to having to compute partial derivatives of parameter function. Consequently, they are very flexible for applying any velocity (travel time) model without modifying algorithms themselves. Genetic algorithms are very similar to another direct search method called a grid search. Also, genetic algorithms are independent of the misfit

function. Genetic algorithms are effective for global optimization because they handle information globally, i.e. each solution is a potential candidate in the search space to fulfill the search criteria.

They worked well at any distances, but the best coinciding results with Helsinki bulletins were found at distances less than 400 kilometres from the detecting network. At longer distances the effects of crustal model must be taken into account. When using more complex crustal models and perhaps allowing them to vary within larger constrains it was found that genetic algorithms could produce epicentres which were equally or better matched than bulletin epicentres. This in turn, as it involves a more complicated optimization task, resulted in increased computing time. The events locating close to the teleseismic window produced some unsatisfactory solutions which can be solved by some training methods. In general those distances can be seen as a remarkable challenge for event locating optimization tasks.

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APPENDIX

A genetic algorithm $\mathcal{G}$ can be expressed by a 8-tuple like:

$$\mathcal{G} = \left(P^o, \lambda, l, s, \rho, \Omega, f, t\right) \tag{A.1}$$

where $P_o = \left(a_1^o, \ldots, a_\lambda^o\right) \in I^\lambda$ is a randomly selected initial population, $\lambda \in N$ is the number of population, $l \in N$ is the length of the presentation of each individual, s is the selection operator, ρ the operator determination function, Ω is a genetic recombination operator set as explained below, f the fitness function to be optimized $f: IR^n \rightarrow$ ^IR and t is the termination criterion, respectively. The recombination operator set $\Omega \subseteq \left\{\omega : I \times I^\lambda \rightarrow \wp \rightarrow I\right\}$ includes genetic operators, such as mutations and crossovers (*Holland*, 1975). The statistical elements of these operators are included in some manner in the probability function $p \in \wp$. Consequently, to an individual $a_i'' \in P''$ the operator selects the mating partners out of the P^t if needed and determines the new offspring individual. Operators leading to more than one offspring at first select one of the offsprings randomly to be a resulting generation and the rest of the offsprings will be deleted.

The conventional recombination operator used in GAs is the crossover operator $\omega_c \in \Omega$, which is applied with some predetermined probability p_c and yields a result $a = \omega_c\left(a_1, P^t\right), \left\{a_1 = \left(\alpha_{1,1} \ldots \alpha_{1,l}\right)\right\}$. Further, there is a schemata H of elements from a set $\{0,1\}^l$, and for a given schemata $H \in \{0,1\}^1$ a string $a \in I$ is called an instance of H. Whenever H is defined $H = (0,1)$, this bit is identical to a corresponding bit in string a. The GAs can be evaluated as

- Random selection of mating partners $a_2 = \left(\alpha_{2,1} \cdots \alpha_{2.1}\right)$ from P^t
- Random definition of crossover position $x \in \{1, \ldots, l-1\}$
- Forming two new individuals $a_1' = \left(\alpha_{1,1} \cdots \alpha_{1,x}\alpha_{2,x+1} \cdots \alpha_{2,l}\right)$ and $a_2' = \left(\alpha_{2,1} \cdots \alpha_{2,x}\alpha_{1,x+1} \cdots \alpha_{1,l}\right)$
- Random selection of $\in \left\{a_1', a_2'\right\}$

Since, there are l-1 possible crossover split points (e.g.), the probability $\mathcal{P}$ of that a schema $H \in \{0,1\}^l$ is destroyed by crossover is given by

$$\mathcal{P} = \delta(H) / (l-1) \tag{A.2}$$

where $\delta(H)$ defines the distance between the first and the last fixed position of the *chromosome* schema; i.e.

$$\delta:\{0,1\}^l \rightarrow \{0,\ldots,l-1\}$$
$$\delta\left(H=\left(\gamma_1\cdots\gamma_l\right)\right)=\max\left\{i\,|\,\gamma_i\in\{0,1\}\right\}-\min\left\{i|\gamma_i\in\{0,1\}\right\}. \tag{A.3}$$

Since, crossover is applied probabilistically, the expression (A.2) must be multiplied by the crossover probability p_c.

Further, in GAs there are (as in nature) also mutations, which play collateral roles. They prevent the populations from the total premature loss of alleles at some particular positions, which may not be recoverable by crossovers alone. To allow this, mutations are simply occasional random changes in bit-string positions and the probability of bit-mutations p_m is very small. If $a=\omega_m\left(a_1,P^t\right)$ then bit-mutation operator $\omega_m\in\Omega$ works as

- Random selection of positions $\{x_1,\ldots,x_h\}\subseteq\{1,\ldots,l\}$ to present mutations
- $a=\left(\alpha_{1,1}\cdots\alpha_{1,x_1-1}\alpha'_{x1}\,\alpha_{1,x_1+1}\cdots\alpha_{1,x_h-1}\alpha'_{xh}\alpha_{1,x_h+1}\cdots\alpha 1,l\right)$ where $\alpha'_{x_i}\in\{0,1\}\ \forall i=1,\ldots,h$ are selected randomly. For the mutation operator the probability that a schema $\delta(H)$ is destroyed is

$$1-\left(1-p_m\right)^{\sigma(H)} \tag{A.4}$$

where order $\sigma(H)$ of a schema $H\in\{0,1\}^l$ is given by the number of fixed positions of the schema.

$$\sigma:\{0,1\}^l \rightarrow \{0,\ldots,l-1\}$$
$$\sigma\left(H=\left(\gamma_1\cdots\gamma_l\right)\right)=\left\{i\,|\,\gamma_i\in\{0,1\}\right\} \tag{A.5}$$

For small mutation probability $p_m\approx 0.001$, it will be close to $\sigma(H)p_m$. The applications allow more than one operator to be applied sequentially to one individual. Consequently mutation is often applied to the offspring created by crossovers, and this might be included in the scheme H.

Genetic algorithms start with a set of randomly chosen initial population models and the model parameters are coded as binary strings (can also be strings of real numbers) and the resulting bit-strings are concatenated to build up "chromosomes", which are considered as an instantaneous model space. A genetic algorithm in this study was intended to work using the following steps:

- Start with a randomly generated population of chromosomes (e.g. candidate solutions of the problem ≈ rough epicentre parameters; geographical limits and depth maximum)
- Calculate the fitness of each chromosome in the population

- Apply the selection and genetic operator (mutation or crossover) to the population to create a new population.

These steps are then iterated several times, and these iterations are called "generations". After several generations, the result is often one or more highly fit chromosomes in the population. The selection can be used in different ways. It can arbitrarily eliminate the least fit of the population and replicate every other individual once. Also, it can replicate individuals in direct proportion to their fitness, or it can scale the fitness and replicate individuals in direct proportion to their scaled fitnesses.

7. *References*

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