RESOLUTION OF SHALLOW SHEAR STRUCTURE USING REGIONAL SURFACE WAVES FROM MINING EXPLOSIONS AND GENETIC ALGORITHMS

ABSTRACT

Surface-wave dispersion analysis of regional seismograms from mining explosion is used to extract shallow subsurface structural models. Seismograms along a number of azimuths were recorded at near-regional distances from mining explosions in Northeast Wyoming. The group velocities of fundamental mode Rayleigh wave were determined by using the Multiple Filter Analysis (MFA) and refined by Phase Matched Filtering (PMF) technique. The surface wave dispersion curves covered the period range of 2 to 12 sec and the group-velocities range from 1.3 to 2.9 km/sec. A genetic algorithm (GA) was used for crustal shear-wave velocity inversion. As a global optimization method, this algorithm consists of selection, crossover, and mutation of individuals in a population of models. A fitness function was chosen based upon the inverse of the square of the difference between the predicted and observed group-velocity. This fitness function in combination with the genetic algorithm provided improved model determination, allowing an efficient search of the model space and convergence to a global optimal solution. The procedure is not dependent upon the starting model. The average velocity model resulting from the GA consists of 8 thin layers in the upper 10 km of the crust. Lateral variations in the resulting models are consistent with the regional structure that includes the Powder River Basin aligned NS, Wind River Basin and Mountains to the SW, and stable continental craton of North America to the east. As a final check, synthetic seismograms based on these models using an explosion source function with same source duration as the blast were calculated. Comparisons between observation and synthetic data were good for the fundamental mode.

STUDY GOALS

- Extract regional Rayleigh wave from mining explosion data
- Obtain fundamental surface-wave dispersion curves
- Invert crustal shear-wave velocity structure
- Introduce Genetic Algorithms for inversion

















GENETIC ALGORITHMS

- Genetic Algorithms are nonlinear optimization methods for moving from one population of "chromosomes" (e.g..., strings of ones and zeros, or "bits") to a new population by using a kind of "natural selection" together with the genetics-inspired operators of selection, crossover and mutation. Genetic Algorithms (GA's) are different from other optimization and search procedures in four ways: (1) GA's work with a coding of the parameter set, not the parameters themselves.
- (2) GA's search from a population of points, not a single point.
- (3) GA's use payoff (objective function) information, not derivatives or other auxiliary knowledge. (4) GA's use probabilistic transition rules, not deterministic rule
- GA's allow the efficient search of the model space and converge towards a global minimum. Fitness function provides the criteria to compare observed data and synthetic values:

$$f_{j} = \frac{1}{\sum_{i=1}^{N} (x_{i}(j) - y_{i}(j))}$$

where $x_i(j)$ (i = 1, ..., N; N= total data points) are the observed data at component j (j = 1, ..., Ns) and $y_i(j)$ are the synthetic data.

Binary Coding

Lower bound (Vmin): 0.46 0.99 1.72 1.95 2.45 2.62 3.03 3.10 3.30 3.50 Upper bound (Vmax): 1.46 1.99 2.72 2.95 3.45 3.62 4.03 4.10 4.30 4.50 Binary coding scheme (3-bits) for model parameter :

	0	0	0	Vmin
	0	0	1	Vmin + ΔV
	0	1	0	Vmin + 2 ΔV
	0	1	1	Vmin + 3 ΔV
ole [†]	Pare	nt: 1.0	03 1.4	2 2.72 2.52 3.3

Chromosome: 100011111100110011100011111110

The classical GA's are composed of three operators, i.e., selection, crossover and mutation, which involve random number generation, string copies and some partial string exchanges. They must be specified for a particular application. This includes the parametrization of the model space and the probabilities associated with the processes of crossover, mutation and the reliance on fit models from previous generations. The three processes perform different roles in the performance of GA's. The selection affects the survival of the fittest between generations while the crossover controls the degree of mixing and sharing of information between the models. The purpose of the mutation is to keep a certain amount of diversity or randomness in the population. When creating a new population, there is a finite chance that the best chromosomes (models) may be lost by crossover and mutation. Elitism allows the best chromosome (or a few chromosomes) to be copied to the new generation first and remaining members produced in the classical way. Elitism can very rapidly increase performance of GA's because it prevents the lose of the best solution. The flow chart of the GA's is presented at right.



Crossover occurs at No.23 point and total Mutated genes are 9

The procedure of crossover and mutation from two individual paired parents. The total length of binary string (chromosome) is 30 and the red represents bit 1 and green represents bit 0. The crossover site is selected by random number which is located at cyan line. And the yellow bits are the mutated bits. Resulting new model (offspring) shown to right.

Fundamental Rayleigh wave group velocity dispersion curves from MFA (Multiple Filter Analysis)

Explosion data (Blue) and fundamental Rayleigh waves (Red) extracted by PMF (Phase Matched Filtering) technique

Data Characteristics

- Group velocities exhibit normal dispersion
- Group velocities range from 1.3 to 2.9 km/sec over period 2 to 12 sec Dispersion curve is a non-linear function of medium properties

1 0 0 Vmin + 4 ΔV 1 0 1 $Vmin + 5 \Delta V$ 1 1 0 $\operatorname{Vmin} + 6 \Delta V$ 1 1 1 $Vmin + 7 \Delta V = Vmax$ 1 3.05 3.60 3.53 4.30 4.40





Synthetic tests have been carried out to test the program and investigate the effect of parameters. Upper panel is the 3-D map of fitness vs. generations illustrating the rapid increase in fitness in later generations. Lower-left panel presents shear-wave velocity profiles and lower-right presents the Rayleigh wave dispersion curves. The input model consists of 9 layers (blue), the thick-red lines show the search space. Three models with greatest fitness functions were presented as green, cyan and nagenta line, respectively. Their fundamental Rayleigh wave dispersion curved were presented at lower-right panel as corresponding color. The parameters used for synthetic test are:

Number of population: Number of elitism models: 2 Number of generation: 50 Probability of crossover: 0.9 Probability of mutation: 0.05 Length of chromosome: 27

From the inversion results, those parameters could give inversion result with reasonable convergence. And it shows that the GA's are robust and effective and it can be used to interpret surface wave dispersion data for inverting crustal shear wave velocity structure. We use the same parameters for the inversion of observed data.



Inversion results of all stations in study area. For each station, the left panel presents the dispersion curves (black is observation data and other three colored curves corresponding to inverted models with greatest fitness function at right panel). The thick red is presented as the model search space, resulting models are magenta, cyan and green. Models verlap resulting in dominance of magenta.

This study shows that:

- ★ Mining explosions yield strong mid period (2~12 sec) surface wave

- ***** Narrow range of models for each path
- are able to model fundamental mode Rayleigh waves in time domain

SYNTHETIC TEST

RESULTS

The outlined procedure is now applied to the observational dispersion from a mining explosion in the Powder River Basin.





Comparison of observation (blue) fundamental Rayleigh waves extracted from PMF and synthetic (red) seismograms calculated from average model of three inverted models with greatest fitness function. An explosion source function with same source duration as the blast were used for synthetic data.

CONCLUSION

★ Group velocities of fundamental Rayleigh wave range from 1.3 to 2.9 km/sec over period 2 to 12 sec \star Genetic Algorithms are robust and effective and can be used to interpret surface wave dispersion ***** The inverted structure models dependent on azimuth and are consistent with the regional structure

***** Dispersion analysis in combination with explosion source model constrained to match explosions duration