EVOLVING THE REGOLITH FROM GRAVITY AND MAGNETICS TENSOR DATA: THEORY AND PRELIMINARY RESULTS

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INTRODUCTION

The Australian regolith is a largely unexplored area of geology. The development of mechanisms to measure the potential field tensor provides detailed data that may be suitable for regolith exploration, should the data be collected on a suitable scale (e.g., in the order of metres). This may soon be possible, with work being carried out at the Oak Ridge National Laboratories in Canada (Gamey *et al.* 2002), The Bell Geospace Full Tensor Gradient (FTG) system (Doll *et al.* 2003), and work being carried out by the CSIRO in Brisbane, Australia (http://www.tip.csiro.au/IMP/SmartMeasure/GETMAG.htm).

The potential field tensor is defined by Heath *et al.* (2003). For a continuous vector field, **F**, there exists a potential field, ϕ (Blakely 1995) (1). The tensor is a 3 by 3 matrix, each component representing a vector gradient of the total field (2),

$$\mathbf{F} = \nabla\phi \qquad (1)$$

$$\mathbf{F}_{tensor} = \begin{bmatrix} \frac{\partial\phi_x}{\partial x} & \frac{\partial\phi_x}{\partial y} & \frac{\partial\phi_x}{\partial z} \\ \frac{\partial\phi_y}{\partial x} & \frac{\partial\phi_y}{\partial y} & \frac{\partial\phi_y}{\partial z} \\ \frac{\partial\phi_z}{\partial x} & \frac{\partial\phi_z}{\partial y} & \frac{\partial\phi_z}{\partial z} \end{bmatrix} \qquad (2)$$

where

$$\phi_x = F_x = \frac{\partial\phi}{\partial x}, \phi_y = F_y = \frac{\partial\phi}{\partial y}, \phi_z = F_z = \frac{\partial\phi}{\partial z}.$$

Some advantages of measuring the potential field tensor are described by Schmidt\ & Clark (2000). Some of these benefits include the increased resolution of shallow features and structural features, the rejection of geomagnetic variations, and the constraining of data between flight lines.

With the improvements in data acquisition and quality comes the chance of improved interpretation from inversion. I am using Genetic Algorithms (GAs) to undertake these inversions. As a global search technique, they provide a search of a large solution space. The process is based on the evolutionary theory, where DNA strands contain information that gets passed onto future generations.

METHODOLOGY

The application of GAs as a non-linear inversion technique has been described by Bäck (1996). The technique can be applied to potential field data (Boschetti *et al.* 1997) to determine the appropriate physical properties (e.g., density, magnetic susceptibility, direction of magnetisation) of the subsurface. A flow chart showing the steps of the GA used is shown in Figure 1. The process is based on Gallagher *et al.* (1991) and is described below.

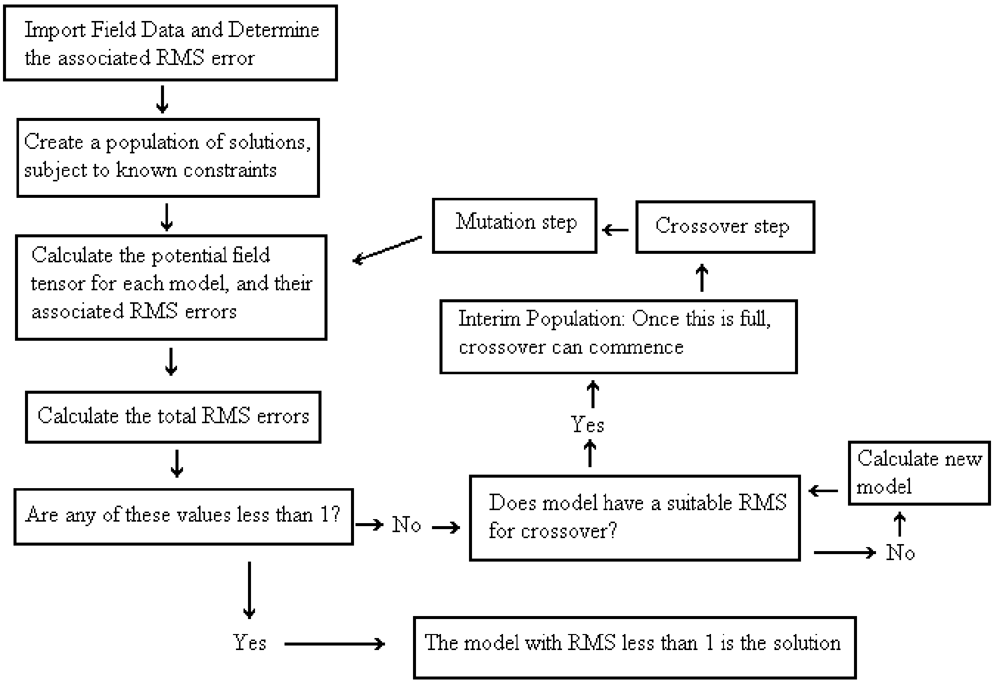

Figure 1: Flow chart showing the steps taken in a GA, based on Gallagher *et al.* (1991).

Importing data
This step simply loads the data onto the computer, making sure that the data is in a suitable reference frame. The computer then calculates the RMS error of this data. Equation (3) is used to determine this error.

$$RMS_{field} = \sum \frac{(Z - Z_{average})^2}{N} \tag{3}$$

where Z is the value at the measured point, $Z_{average}$ is the average value of the measured data, and N is the number of measured points. The value of RMS_{field} remains constant throughout the inversion process.

Creating a population of solutions and finding their responses
A matrix array is created, such that each matrix represents a depth slice, and the value is equal to the physical property that you wish to invert for. In order to constrain values for the inversion, the constrained values are simply typed in, and all other spaces are allocated a random number. The array is repeatedly stored into the computer memory, creating new random numbers each time. For each model, the tensor response is calculated, and their associated RMS errors given by equation (4),

$$RMS_{mismatch} = \sum \frac{(G - Z)^2}{N} \tag{4}$$

where G is the calculated tensor value. The total RMS is then calculated via equation (5),

$$RMS_{total} = \frac{RMS_{mismatch}}{RMS_{field}} \times 100\% \tag{5}$$

If RMS_{total} is less than 1%, then we consider the problem solved. However, if not, it must still have a suitable value to be considered for crossover. If the model is still not good enough, it is discarded and a new model takes its place. This continues until an interim population has been created that is to be used for crossover. The models are randomly paired off and converted to strings. The strings represent DNA strands that are the fundamental elements of genetic inversions. Figure 2 shows the process of converting a block of data (e.g. a section of subsurface) to a string of data.

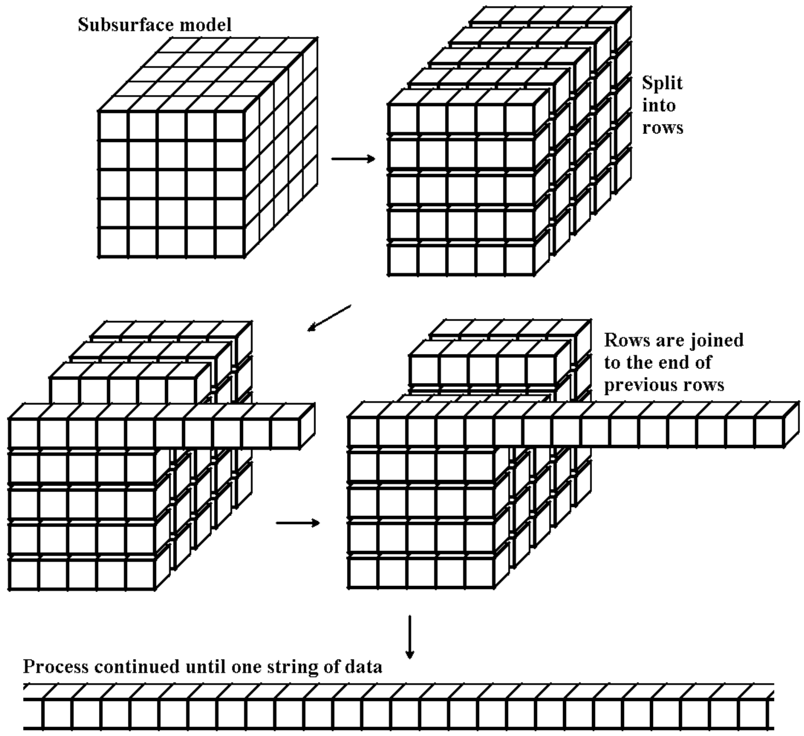

Figure 2: Simply taking each row of data and pasting it on the end of the previous row creates a string of data from a three-dimensional block of data. The result of this is a string of data that can be used to simulate a DNA strand.

Crossover

Once all the models are paired off, a random number is generated for each pair. If the number is above a chosen limit, then the pair is allowed to crossover. If not, the pair passes onto the next generation unaffected. Crossover is illustrated in Figure 3. It simply involves taking the two strings and swapping over a portion of their data. The point at which crossover occurs is randomly chosen, and can occur at any point along the string.

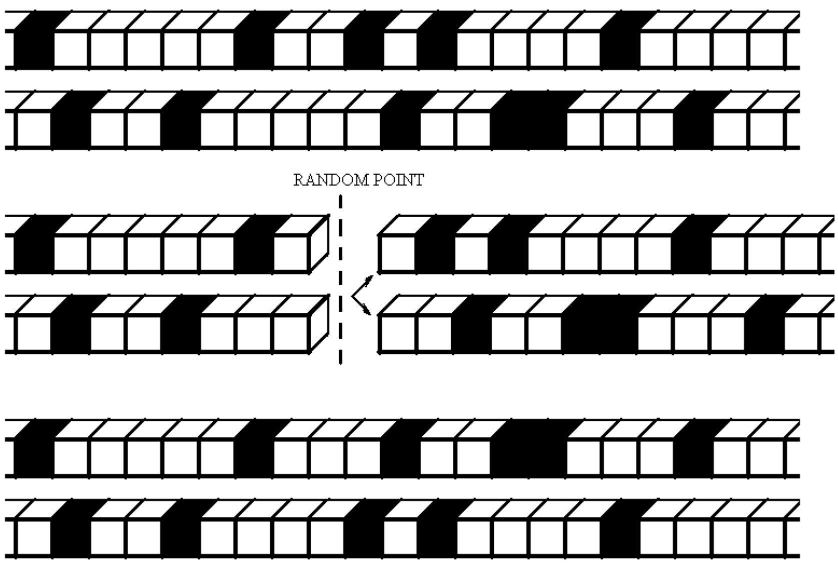

Figure 3: A random point is selected along the strings, and the remaining string segments are swapped over.

Mutation

There is a small probability that a mutation can occur, i.e., a point of data gets replaced by a defined opposite (e.g., 9 gets replaced by 10-9, 1, and 4 gets replaced by 10-4, 6). The probability of mutation occurring is usually very small, however, if the chance is high enough, all the points get mutated, and the inversion becomes a Monte Carlo style inversion, where an exhaustive search of the solution space is performed (Press *et al.* 1992).

PRELIMINARY RESULTS

Algorithms have been constructed in Matlab in order to invert potential field tensor data via a GA. While a full inversion has not yet been completed, figures 4 and 5 show a distinct decrease in RMS over time. This means that the inversion technique is working, but until a supercomputer is used, it will take a while to complete.

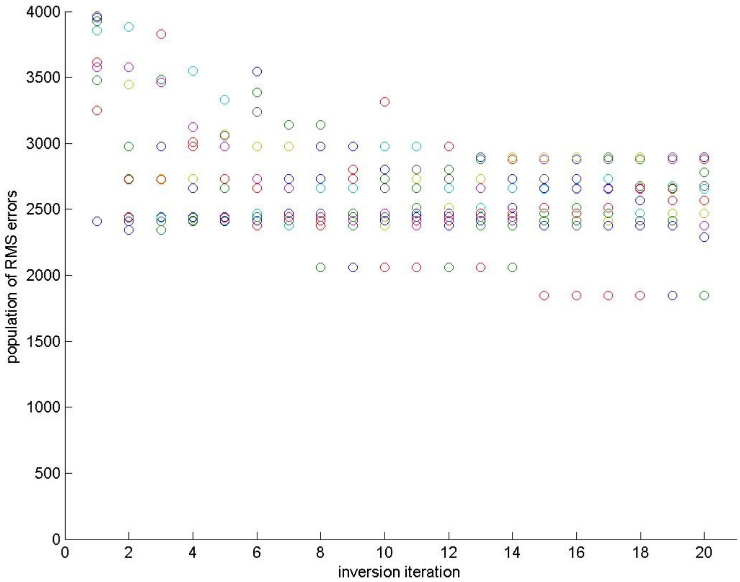

Figure 4: Plots of RMS errors against inversion iteration numbers. For each inversion iteration there exists 10 RMS errors, one for each of the models, represented here as a small circle. The inversion selects models with smaller RMS errors, and allows them to continue into further generations

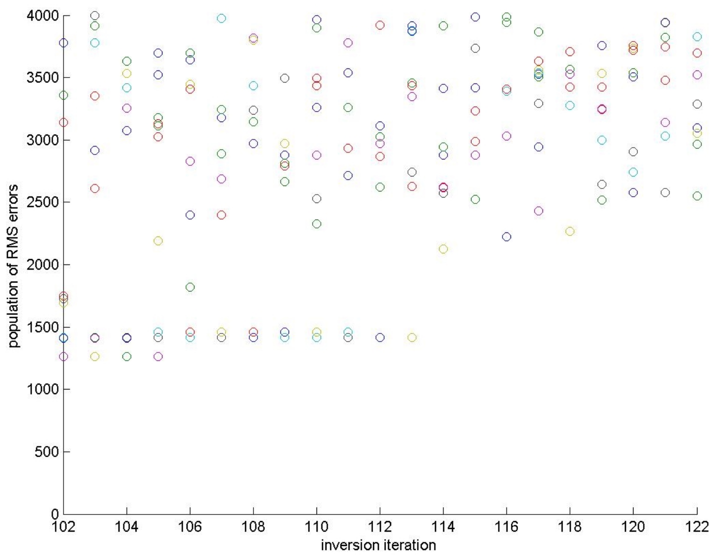

Figure 5: Plots of RMS error against inversion iteration numbers for the same inversion, but later on. The graph covers RMS values calculated for iterations 102 to122. The best models have been overwhelmed by the large number of random models, and have therefore died away. In this case, the final best model is seen at inversion iteration 112 before all the models are randomly chosen.

DISCUSSION

The results show that the process of minimisation is being carried out, although the best models are lost after about 112 inversion iterations. The main reason for this is as there were not enough starting models. Ten models do not provide a wide range of values that can crossover randomly to provide significant changes in the RMS. Time constraints have not allowed me to run full inversions with a larger population, although this will be happening in the very near future.

Once the algorithm has been run and a final model has been selected, it can easily be visualised on a computer. Software exists that can take a multi-dimensional array and convert it into a three-dimensional graphic. I plan to use the freeware program "Sliceomatic," as it provides excellent visualisation for three-dimensional information (Carey 2003).

CONCLUSIONS

GAs can be used for three-dimensional inversion of potential field tensor data for regolith exploration. The results presented are for a case where a starting population of 10 models was used. A larger population is required to better explore the solution space. Future processing will utilise a 1.2 Teraflop Supercomputer at the University of Adelaide, speeding up the inversion immensely.

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