Measuring and Visualizing Convergence using Cell Weighted Relative Residuals

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ABSTRACT

Seismic travel time tomography is used to create velocity models for determining the velocity structure of the crust of the Earth. One method to generate these models is the execution of an iterative tomography algorithm, developed by J. E. Vidale and J. A. Hole. This algorithm is applied repetitively until an acceptable solution is found.

To reach an acceptable solution, a model must show convergence by a constant reduction of the RMS error that approaches a predefined threshold. However, it is possible that a model lacks convergence, hence retuning incorrect or no results at all.

Previously there was no way to visualize the convergence property of a model. This left researchers blindfolded, only able to apply trial and error techniques to correct the models and force convergence. This is a very tedious and time consuming process, and although an acceptable solution can be found with this process, not all acceptable solutions are an accurate representation of the experimental area.

We created a new visualization based on the residuals of the actual travel time and the expected travel time of seismic waves. The residuals can then be visualized as a 3D model for areas with a lack of convergence.

Residual visualization for model convergence can be used by geologists to determine where intermediate and final tomographic velocity model areas have the greatest average residual time, pinpointing the problematic sections that reduce the overall accuracy of the model.

KEYWORDS

Seismic, tomography, residual, visualization, convergence, error

INTRODUCTION

Seismic travel time tomography is a technique used to investigate the velocity structure of the Earth's crust. The algorithm that generates these models is an iterative application of forward modeling and non-linear inversion designed and implemented by J. E. Vidale [1] and J. A. Hole [2], respectively. Forward modeling uses the eikonal equation to compute a discrete three-dimensional first arrival time model for each seismic wave source included in a tomographic experiment. The inversion procedure uses the forward modeling output to compute the source-to receiver wave propagation path and the first arrival time for each source and receiver pair of an experiment. The algorithm concludes when experimentally measured first arrival times and propagation times calculated during inversion agree within RMS values of measurement error.

As Hole's code executes, it generates a set of models before the final outputs. These intermediate models, which are also visualized, include the travel times of each separate shot point through each receiver, and two smoothing passes. For the models to converge, the experimentally measured first arrival times and propagation times calculated must be less than the RMS values of measurement error. Convergence is measured in every pair of shot point and geophone.

If the models converge and the initial pick times are accurate, every iteration of Hole's code will reduce the error between the actual pick times and the estimated pick times and the process will converge to a stable result. However if the process does not converge, then scientists must revise the initial model and parameters and start over. One problem with this process is that once the input has been provided, there is no way to determine if the process is converging or if the models being produced match other domain constraints not included in the model. On the other hand, when there is no convergence between a pair of shot point and geophone, and the iterations of Hole's code have finished, the ray path is ignored and never calculated or visualized.

The final outputs of the tomographic algorithm include a three-dimensional velocity model and seismic ray coverage of the model.

There is no convergence check or visualization other than the RMS value check, which returns a single number and no geospatial information about its position and distribution throughout the model. The individual residuals of the travel times of each ray path are not an output of the algorithm either. The lack of convergence visualizations complicates the assessment of the accuracy of the models. Moreover, errors contained in a model are propagated through all the

following iterations of the algorithm, making them difficult to trace and locate, and impossible to distinguish them from initial input errors, or a divergence started after the computation of an iteration.

Average residual visualization helps scientists understand and correct data collected during their investigations and process it in an improved, efficient manner. In a practical example, if convergence is achieved during the first iterations of Hole's code, then no other iterations are needed, since the errors are already within an acceptable range. Currently a fixed number of iterations is applied regardless of the convergence, and convergence is defined solely on the RMS value at the final iteration.

BACKGROUND

The basic idea of tomography in all of its uses is to obtain a cross-section of an object which will then be used to infer various facts regarding the particular object's internal structure. In processing seismic data the earth internal parameters of velocity and density play a critical role. Seismic imaging methods all require an accurate parameter estimation process. [3]

Travel time tomography is another way of referring to seismic tomography, one that puts the emphasis on the key aspect used to investigate the subsurface: travel time. The term refers to the time it takes a seismic wave to travel into the subsurface, reach a reflecting boundary and return to the surface. [3]

The seismic waves we are dealing with here are artificial and caused during experiments involving the detonation of certain explosives or other source mechanisms.

Seismic tomography is a relatively new method of determining the velocity structure of the Earth. In this method, an image of an object (a heterogeneity), is formed by analyzing the travel times of many waves that have passed through the target area for which the image is sought. Some reference Earth model (a velocity structure) is assumed; variations from this model are determined and are typically expressed as percentage of changes in velocity.[5]

The Vidale-Hole algorithm for first-arrival travel-time seismic tomography is used to create velocity models of the Earth's crust.

The only way to visualize these models with the original algorithm was through a non-interactive bi-dimensional image representation.

Although the experiment data produced was three-dimensional, the visual output was generated by smashing this data and overlapping all the depth information. In addition, the geologists were unable to do any manipulation on the 2D image file and there was no visualization for intermediate steps.

With the optimizations applied to Hole's code, and the new visualization algorithms that permit full 3D interactive displays of the result and intermediate steps, additional computational resources and new visualization possibilities emerged.

One such new potential visualization is related to the residual data that defines if a model is correct or not, which is now available and the focus of this paper.

There are two types of residuals that can be calculated and used to enhance the seismic models. The residual velocity, and the residual travel time.

The residual velocity attribute has been used in seismic tomography for exploration of fractures, natural gas deposits and oil wells. Residual velocity has also been used as a seismic risk reduction tool parameter for tight gas sand exploration in over-pressed environments.

The residual velocity for these purposes has been calculated by subtracting the regional compaction trend from the seismic interval velocity. On previous experiments, residual velocity has been used in an effort to visualize "traps" of over-pressured tight gas. [4]

While 2D and 3D seismic data can be used for calculating the residual velocity, 3D provides a better model by representing the actual structure of the earth without smashing the layers into a single 2D model or image, or by taking a single slice of the model which lacks information of the surrounding areas, which, through smoothing can reveal additional information for the subsurface of the experiment area, or the accuracy of the model.

This paper focuses on the other type of residual, the travel time residual.

If the travel time for an individual seismic wave is different from what we expect from the reference Earth model, we say that there is a travel-time residual.

At this stage we would know only that there was a velocity anomaly somewhere along the ray path that the wave had travelled.

The essence of seismic tomography is to employ a large number of such observations for waves that have travelled by a variety of ray paths and to locate the position of the velocity anomaly.

There are many mathematical approaches to this complex problem, but the most commonly employed one that is to approximate the Earth by a 3-dimensional mesh of blocks.

The travel-time integral in the equation then becomes the summation of the travel times through each block intersected by the ray path. Many observations lead to a large system of equations in which the unknowns are the

velocities of the blocks. The quality of the solution depends on the number of observations and their accuracy, the distribution of ray paths, and the degree to which the block model actually approximates to the true velocity structure. [5]

The travel-time error can be characterized in terms of an individual travel-time misfit for each shot-receiver pair and an overall root mean square (RMS) for all travel-time residuals.

For the Soutehr Rio Grande Rift, which is the model used for this experiment, the overall RMS for the model is 70 ms, however, individual misfits are locally much higher. A plot of calculated and observed travel times combined with the travel-time residuals provides a qualitative understanding of the reliability of different regions of the model. In general, the highest misfits (> 200 ms) are observed at short source-receiver offsets (< 10 km) corresponding to a lack of reversing coverage caused by sparse source coverage and to ray paths traveling thru low velocity basins. In addition, high residuals between 175 and 200 km in the model are the result of low signal to noise ratio for arrivals in urban El Paso. [7]

Although it is known that there are local residuals that exceed by far the RMS values, and that there is a general understanding of where these anomalies might be, previous to this experiment, there was no way of visualizing them and pinpointing their exact location.

For this experiment, we use one of the key intermediate steps to generate the velocity perturbation final model, and to visualize convergence, which is the check for ray coverage.

The coverage file is an existing and essential step of Hole's code that is generated during a step of every iteration. The coverage step outputs an integer file containing the amount of ray paths that pass through each individual cell. Coverage only includes ray paths that can be back traced successfully from the geophone to the shot point, in other words, only complete and convergent rays generate coverage output.

METHODOLOGY

To create the residual files and visualizations, we modified the original coverage file so that it outputs the residual averages per cell as well. Recall that residuals are the difference between the actual travel time and the expected travel time of a convergent ray path that can be traced from its shot point and geophone or vice versa.

It is unlikely that a ray path generated by Hole's code is exact, meaning that it has no residual. Because the nature of Hole's code, which in addition contains several smoothers,

even convergent ray paths generate a residual between the expected arrival time and the actual pick time.

These errors measured in seconds are evenly distributed through all the cells that the ray path traverses, based in addition to the ray's length within the cell.

The error file is a model with the same dimensions as the velocity model with a propagated value of the error for each cell based on the given error assigned to the model.
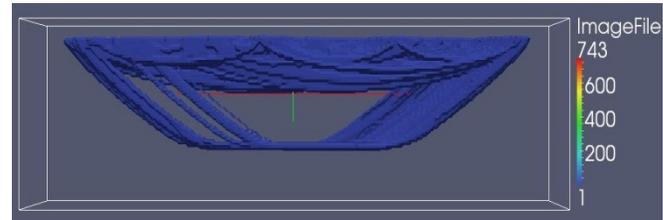

Figure 1. Coverage Visualization

Throughout every Hole's code iteration, the residual error per cell should diminish until it is under the predetermined acceptable RMS threshold, which indicates that the model is accurate enough and no further iterations are required.

These distributed residual times eventually lead to the verification of the convergence of the model that Hole's code can now process and generate a velocity perturbation model revealing the structure of the area of the experiment.

The modified version of cover produces two other three dimensional models that represent the propagated RMS residual value throughout the model and the propagated error value.

The residual value per cell has been accumulated inside cover using the following formula:

Residual in the Cell = Previous Residual Value + Travel Time Residual*(Length of the Ray in the Cell/Total Length of the Ray)

The distributed error model is calculated inside cover using the following:

Error Value in the Cell = Previous Error Value + (Picking Error for the Model *(Length of the Ray in the Cell/Total Length of the Ray)).

To produce the RMS propagated residual value throughout the model the following formula is applied using the final accumulated residual value model and the final coverage file:

Residual RMS Value of the Cell= SQRT(Accumulated Residual Value of the Cell /Ray Coverage of the Cell)

The final distributed error model is also divided by the final coverage file for the model iterating through each cell and dividing de value buy the ray coverage count of the cell.

Finally, to produce the weighted cell relative residual we implement the following formula using the RMS

propagated residual value throughout the model, the distributed error model, and the final coverage model.

Weighted Residual of the Cell = ((Residual Value – Error Value)/Error Value) *100

VISUALIZATION

The original Hole's code algorithm outputs have been optimized so that they now output files for every intermediate operation throughout each iteration, which makes it possible to visualize intermediate residual steps.

On every visualization a scale representing the error is provided. This scale is truncated to avoid a color spectrum that is too large to allow a more detailed visualization of the interest areas. The truncation occurs only on the topmost outliers. If the error exceeds 1000%, then everything above it is assigned the 1000% error color. These anomalies are usually contained within a single cell only, which is impossible to see when visualizing the whole model.

The percentages indicate the error percentage exceeding the allowed RMS value.

Residuals can be difficult to analyze on a 3D representation, since important information can often be found only on very specific slices of the model. An alternative approach would be generating all slices of the model, but without seeing the whole model, it rises the problem of identifying the space location around the axis it's being sliced. An additional problem with this approach is the computing time and the amount of visualized slices, which for this experiment can be as much as 25, but for other experiments an even greater number.

To solve this problems we created a 2.5D representation, where the user can see the info in several 2D planes which represent the whole 3D structure. This is done by creating a max/min box, where the minimum values are smashed n the top and left faces, and the maximum residual values are smashed to the right and bottom faces. These surface views are 2D layers of the model, one viewed from the top of the while the other one is viewed from the side. The normal frontal view remains.

In this case, we use smashing of the data and avoid the usual and generally better 3D representation for two reasons. First, the shot points are not on a single plane, they are on 3D space. If iso-contours or other 3D volume is used to represent the area around the shot points, the lower residuals envelop the higher residuals, which are normally located close to the shot points. This can be solved by slicing or clipping, however, at least one slice is required per shot point, and it has to be adjusted manually, which can be a long and inexact process. Second, even while doing the slicing and clipping, there is no guarantee that

one will be able to see the maximum errors location, as it can require a lot of precision to slice or clip in the correct area. Second, since the shot points don't overlap on the top or front views, even when smashing the maximum values on a 2D surface, there can be no doubt as to which shot point they belong to.

Smashing also avoids the often complicated task to those unfamiliar with 3D applications of navigating through a 3D model with data that by the final iterations, if the model converges, is often reduced to just small, barely visible colored areas in a large space.

In addition, being able to see the maximum and minimum values from top, bottom, left, and right, and the whole frontal model at the same time makes it a more efficient representation for still images, and greatly reduces the need of additional manipulations on a 3D space, which can make it complicated to achieve the desired angle and position to view the relevant information.

[FIGURES WHERE HERE… NEW FIGURES HERE MAYBE?]

RESULTS

The new method was applied successfully to a converging model, and a non-converging model with a 20%error through several iterations.

Both models converge faster at lower depths and areas with less coverage, and slower close to the shot points.

On one hand, the converging model, the error percentage decreases per iteration until most percentages are below the RMS value. We can also see that around certain shot points, the residuals sometimes increase per iteration. This demonstrates that residuals do not decrease linearly throughout the model, but rather increase on certain areas while they decrease on the rest of the model.

These changes are now visible, and allow scientists to see whether a model will ever converge, or fluctuate infinitively throughout any amount of iterations.

On the other hand, the non-converging model clearly shows an almost complete model with unacceptable residual values, that even when they improve throughout the iterations, convergence is less likely to happen, and if it does, it would require a significantly greater amount of iterations. This is a clear visual warning that the model is defective and needs additional changes to represent the initial model more accurately for it to converge.

For models that don't converge, the residual visualization can help by making it simple to identify visually a shot point or a geophone with noise. It also shows if an entire

layer of the model has a convergence problem (e.g. from depth 10km to depth 20km throughout the whole model), leading the scientist to modify the initial one dimensional velocity input, in which moving the layers of the initial velocity input can fix convergence in an entire zone, rather than having to go through thousands of pick times.

The residual visualization also allows the scientist to view the areas that don't converge, and disregard them if that is not an area of interest at the time, or simply lower the computing time of a model by stopping those calculations when it doesn't converge after a reasonable amount of Hole's code iterations, if it turns out to be a model that although does not fully converge, a great percentage of the ray paths do converge, and the non converging areas are not critical to the study.

CONCLUSIONS

On both, the converging and non-converging visualizations, residuals were always present. The greatest residual magnitudes were located close to the shot points. Due to the nature of the emitters, the ray path density, ray path length, and angle diversity is greater the closer it is from the shot point.

We have developed an algorithm with its respective visualization that renders the average distribution of errors of all rays per cell.

With a clearer understanding of the errors location, the total area to be modified to justify convergence is reduced, making it a less daunting task identify and fix defective shot points and geophones with incorrect readings due to noise, malfunction or other extraneous or erroneous information, reducing the scientists' work from months to days.

FUTURE WORK

There are several options for visualizing convergence. A possible future development would be to visualize convergence per ray path with vectors, as opposed to convergence per cell, which is unable to pin the location of a specific defective ray path on a cell with multiple rays passing through it.

An extension to the residuals visualization is the weighted version. Models tend to accumulate higher residuals on densely populated cells and shorter ray paths, than on long ray paths traveling through lower density cells. Although convergence wise this holds true, it is also true that the quality of the information on each cell differs, the denser

ones possessing higher quality. In addition there are other means of calculating a cell's reliability, such as an angular diversity measure. These new cell quality attributes, treated as weights on a regular version of the convergence models, can contribute additional information that help pinpoint prone to error areas.

The algorithm also makes possible the creation of faster convergent models. Instead of using Hole's code with a fixed number of iterations, the code can be stopped earlier if convergence is acceptable at early stages of the iterative process. It is also a useful solution that can allow more accurate models, by letting the scientist reduce the RMS threshold on models with fast convergence.

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