

# Operating Manual v. 1.1

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# 1 Introduction

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WinTomo is a tomographic processing software developed for RAMAC/GPR/BH data. The program runs under WIN95/98/ME/2000/XP and is delivered as one file, WinTomo.EXE.

WinTomo runs in Project mode where a project is created for processing data. This project contains different information files, which can be read from disk or created directly in WinTomo by the user.

Access to traces or palettes are often made by Right clicking on the mouse.

Project files containing first arrivals, borehole co-ordinates, scan list can be saved to be used later.

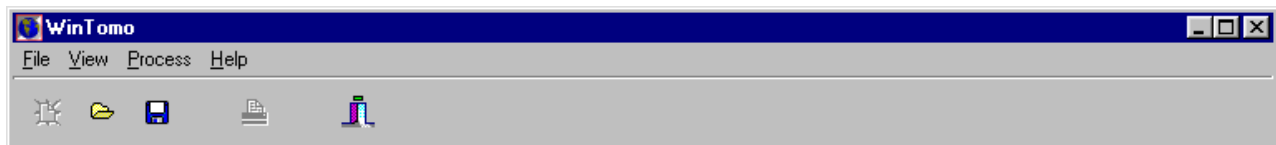


Figure 1. Main menu of WinTomo

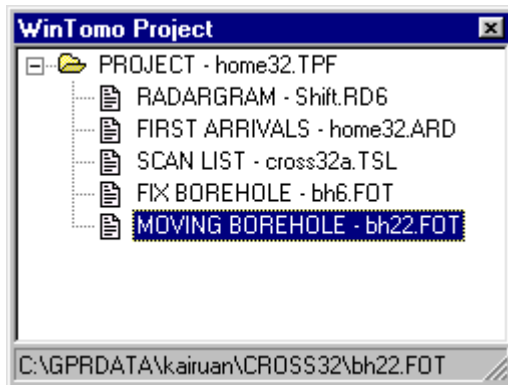


Figure 2. Project window

For information about tomography in general we refer to appropriate literature on the subject.

We recommend reading previous version of **RAMAC Tomography manual** or **CROSSHOLE INVESTIGATIONS**. Both these reports can be obtained from MALA GeoScience Marketing Department.

## 2 Installing the software

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WinTomo is copy protected through the use of a combination of serial number and password; both of which should be provided with your copy of the software (generally printed on the CD-cover).

### 2.1 System requirements

The WinTomo software is designed to run on a PC with the following minimum specifications:

- 133 MHz Pentium
- 32 Mb RAM
- Window 95/98/NT

It is recommended that the system have at least 100 Mb free hard disk space available for processing data.

The amount of available RAM memory to a certain degree determines the speed of running RadInter. A minimum of 32 Mbyte is needed but we recommend 64 Mbyte to be able to operate the software smoothly.

### 2.2 Running the software

The shortcut to start WinTomo is found in the MALA GeoScience folder on the Start-Programs menu in Windows.

The main window is the only window that is displayed when "WinTomo" is started. Here we find the main menu as well as the common speed buttons (New-Open-Save-Print-Exit). On the main menu bar there are four drop-down menus:

"File" contains functions to load and save data files, creating new files, printing and closing the program.

"View" is used to select which windows should be visible.

"Process" contains command to start the more involved processing functions, find first arrivals and calculate tomogram.

"Help" is opens the on-line help system containing information about WinTomo. Help pages for the active window can also be accessed by pressing the F1 function button..

If a menu selection is unavailable it is either because it would make no sense in the present context or that it might have harmful side effects. When they are needed the appropriate menu selections are always available.

## **2.3 Description of windows**

The project window shows the status of the five data files in the project. All five are needed to perform a tomographic inversion. If no data of a certain type exists within the project, the <empty> marker to the right of the data type name indicates this. When a new data file is created this marker changes to <unnamed>, to indicate that data are available but has not yet been saved. Once the data have been saved the marker changes to reflect the chosen filename (<filename>). Opening an existing file also changes the marker to this state (<filename>).

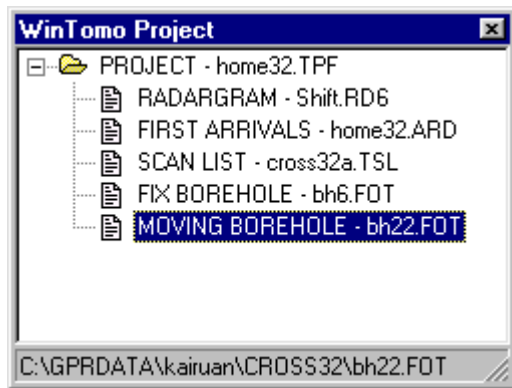


Figure 3. Project window

The project window co-operates with main menu when creating and opening data files. To create a new instance of a data type, simply mark this in the project window and select File-New from the menu in the main window. The resulting dialog lets the user choose which type of data should be created. To open an existing data file mark the appropriate type in the project window and select File-Open. This activates the open file dialog and lets the users select the file to be opened. A short cut to opening a file is to double click on the corresponding data type in the project window. This also opens the open file dialog.

### Radargram window

The radargram window is quite self-explanatory. It is a simple display of the contents of the open data file. The horizontal axis represents the position of the trace in the data file and the vertical axis represents time. If there are first arrival data these can also be shown, superimposed on the radargram. The first arrival data can be adjusted by dragging the first arrival marker to a new position. Double clicking on any trace will open this trace in the trace window for closer inspection or a more detailed adjustment of the first arrival. Traces marked as bad are displayed in a contrasting solid colour (colour settings are available under the Colours tab in the Settings window).

Window is used to display a single trace. It is well suited to make fine adjustments to the first arrivals or to judge the effect of applying a band pass filter. The data quality of some traces is also inevitably so low that the traces should be removed from further interpretation. This is most easily done in the trace window. To mark a displayed trace as bad simply press the Mark as bad speed button in the upper part of the window. To remove the bad mark, simply press the speed button again. No data is thrown away; a trace marked as bad remains in the data file, it is simply not being used in the calculations.

## **Borehole Coordinate and Scan List windows**

This window contains all information about the measuring geometry, i.e., the fix and moving borehole definitions, as well as the scan-list. Each data set is found under a separate tab, and is displayed in a table where it can be edited if necessary. The four thumbnail images in the right-hand part of the window shows the three projections of the presently active borehole, together with the ray geometry display. Clicking on any of these thumbnails will open the full size window for closer inspection.

## **Borehole Geometry window**

The borehole geometry window has a very simple task. It displays the projection of the selected borehole on the coordinate planes.

## **Ray Pattern window**

The ray pattern window displays the position of the boreholes together with the ray geometry, as defined by the scan-list. This display is especially useful to locate errors in the scan-list or the borehole definition files. The view perpendicular to the tomography plane can give the user an idea of the deviations from the basic assumption that all rays lie in the same plane. The user can choose to display only selected scans to enhance the readability of the display.

The ray pattern window can also display the grid geometry chosen for the tomographic inversion. This can be an aid in finding the optimum grid geometry (the grid geometry settings are available under the Grid tab in the Settings window).

## **Residual Data window**

The residual data window displays the residual data as a function of ray. The main purpose of this window is to allow the user to adjust the background parameters (velocity and time zero, attenuation and transmitted power) in a convenient way. The residual data plot looks like a cluster of points. If the assumption that the features in the tomogram are deviations from a constant background velocity (or attenuation) is correct, then this cluster is centred on the background velocity (or attenuation) which form a straight line in the plot.

The background velocity and time zero (attenuation and transmitted power) are correctly chosen when the cluster lies horizontally centred on the length-axis.

If they are not it will result in errors in the inverted tomogram like stripes and irregularities or other artifacts that will mask the useful information.



## Ray Check plot window

The ray check plot displays the residual data in a second form. The residual value is plotted as the grey level of a pixel in the plot. The position of the pixel is determined by considering the depth of the start and endpoints of a ray as rectangular coordinates in the plot. This plot is especially useful to locate bad rays and scans. The plot should be fairly smooth. If it is not, then there is probably something amiss, either with the radar data or the geometry.

## Tomogram window

The tomogram window is used to display the resulting tomogram. This window is naturally not available before an inversion has been performed.

# 3 Entering Data

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## 3.1 Data file

WinTomo reads data files created by GPR.EXE for RAMAC/GPR. They should be named \*.RD3 and accompanied by a header file, \*.RAD. These files are automatically output by GPR.EXE.

Once the data file is imported **Right click** on the mouse gives access to a menu for zooming data, viewing traces or changing colours.

Bad traces can also be marked here. These are given another colour and will not be used further in the processing. They can however be included again.

In the data window the first arrivals can be calculated as in the "Process" menu.

First arrivals are stored with data in a new file, \*.RD6.

## 3.2 Borehole files

Borehole coordinates can either be read from existing files or be created within the program.

Borehole co-ordinates should be read from files named \*.FOT. Format for these files should be:

Text files with data in the following order:

<b>Depth</b>	<b>X-coordinate</b>	<b>Y-coordinate</b>	<b>Z-coordinate</b>
--------------	---------------------	---------------------	---------------------

Commas, space or TAB may separate data.

Data should be referred to in a right-handed co-ordinate system with the positive Z-axis downwards.

Once data is read or created it can be viewed with the scan list. By clicking on one of the four vertical right windows there are enhanced enlarged.

To create a coordinate file simply left click in the project list on either "Fix borehole" or "Moving borehole". Thereafter right click on the same. By using the "New" command a coordinate file can be created.

The file name will be "unnamed" until you right click again on the "Fix borehole" or "Moving borehole" and save the file.

### **3.3 Scan list**

The scan list may either be read from the data directory as \*.LST, or \*.TSL if it has been created by GPR.EXE by selecting the TOMOGRAPHY option. Or, a scan list can be created within WinTomo.

Once a scan list is read into the project individual numbers in it may be changed or deleted as desired.

Whole scans can be excluded from the processing by high lightening the scan no and thereafter clicking on the "√" button. They can be included again by clicking on the same button.

To create a scan simply right click on the "Scan list" option in the project list and select the "New" option. By using the "Insert row" marker in the upper left corner new rows can be entered manually.

In the Scan list there is also the option of entering the "Antenna offset". This is the distance from the referred 0-point during the survey to the antenna centre.

The correct number to be entered here for the different antenna frequencies are;

100 MHz	0.66 m
250 MHz	0.33 m

### 3.4 Settings

Settings option contains parameters filtering raw data by bandpass filter, setting of template length for first arrival picking, grid parameters, inversion parameters and general colour setting. Colour scale settings for data and results can be made separately for each colour palette.

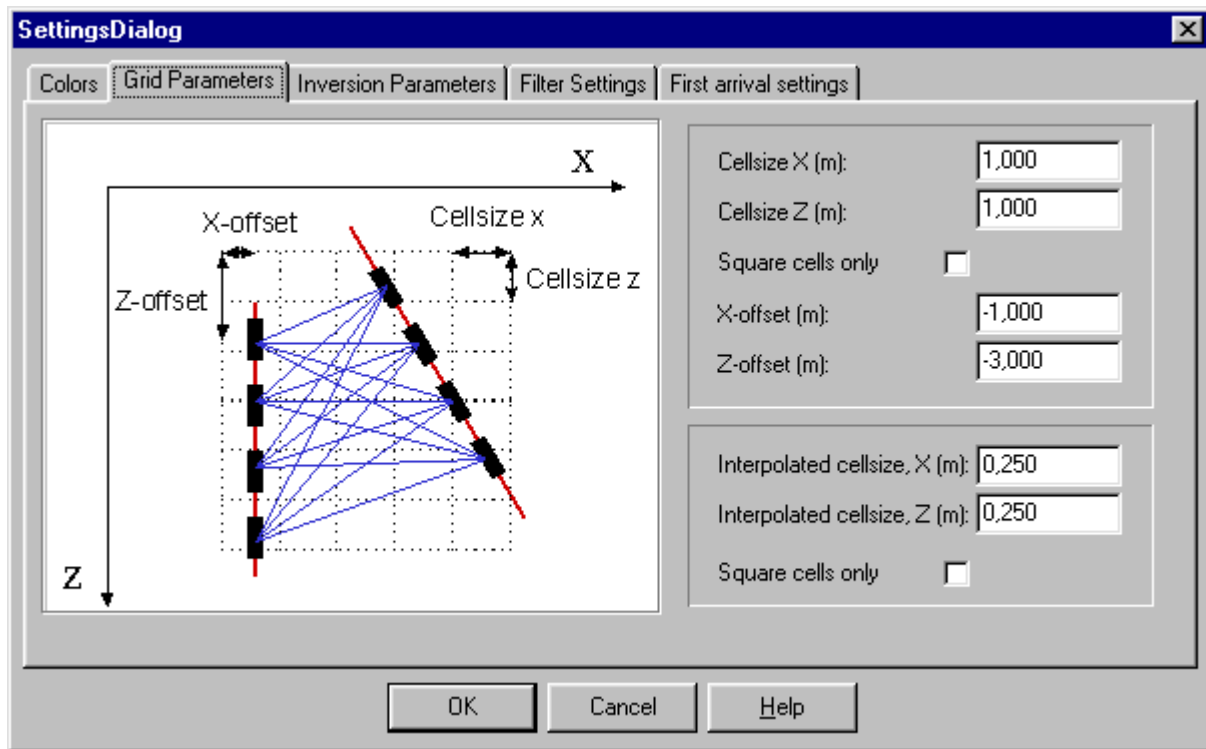


Figure 4. Grid Parameters menu in the Settings menu.

## 4 Running WinTomo

### 4.1 Setting Parameters

In the "View> Settings" window you can enter parameters for the different routines in the processing as well as the screen colours.

The parameters that should be adjusted besides screen colours are those for;

- Band-pass Filter frequencies

- First Arrival Picking window length
- Grid Size for Inversion
- General Inversion parameters

## **4.2 Band-pass filter**

A band-pass filter can be applied on the raw data. This should be applied in cases where the signal amplitudes are very low or noisy causing bad first arrival pickings. The filter parameters should be set according to the antenna centre frequency. E.g. when a 100 MHz antenna has been used 100 MHz can be used as a centre point. The upper and lower break points can be set around 75 and 125 MHz respectively. Trial and error will show which break points will give the best result. If the break points are chosen too close to each other the result is generally an introduced ringing in the data.

By clicking on the square marked "Apply BP-filter" the data will be filtered. Numerous filters can be applied by changing the filter parameters and thereafter on the "OK" square.

## **4.3 First arrival picking**

After importing a data file a first arrival picking can be made direct or after filtering of the data.

The first arrival window length can be selected in number of samples. The length depends on the selection of the sampling frequency versus antenna frequency. The total length should exceed the pulse length.

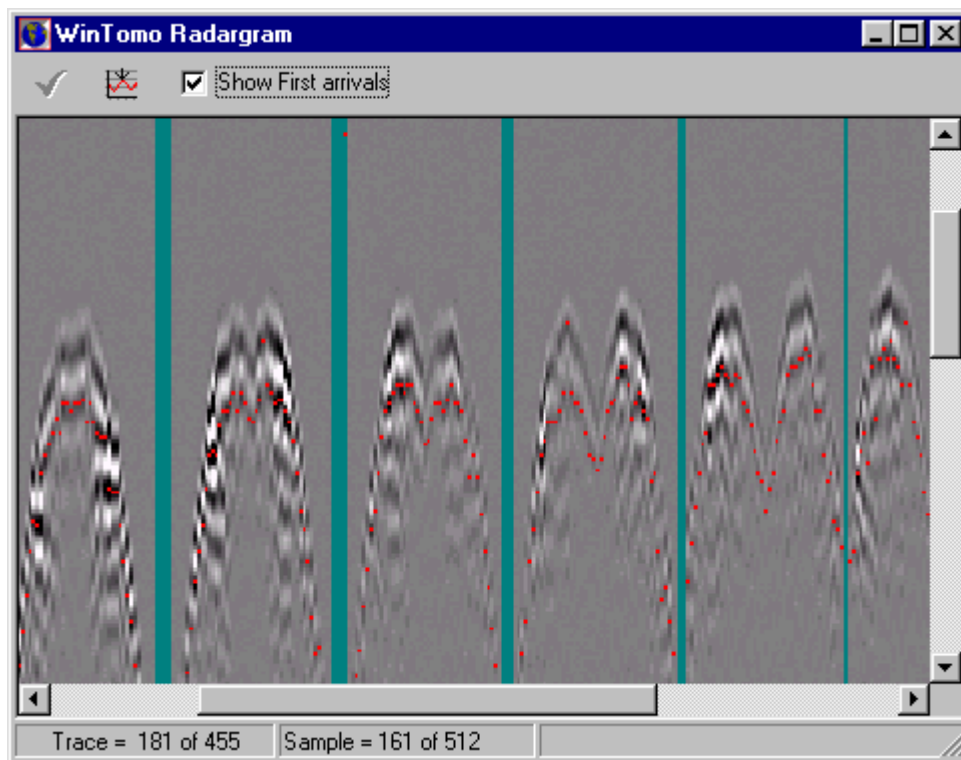


Figure 5. First arrival picking with "bad traces" marked in green.

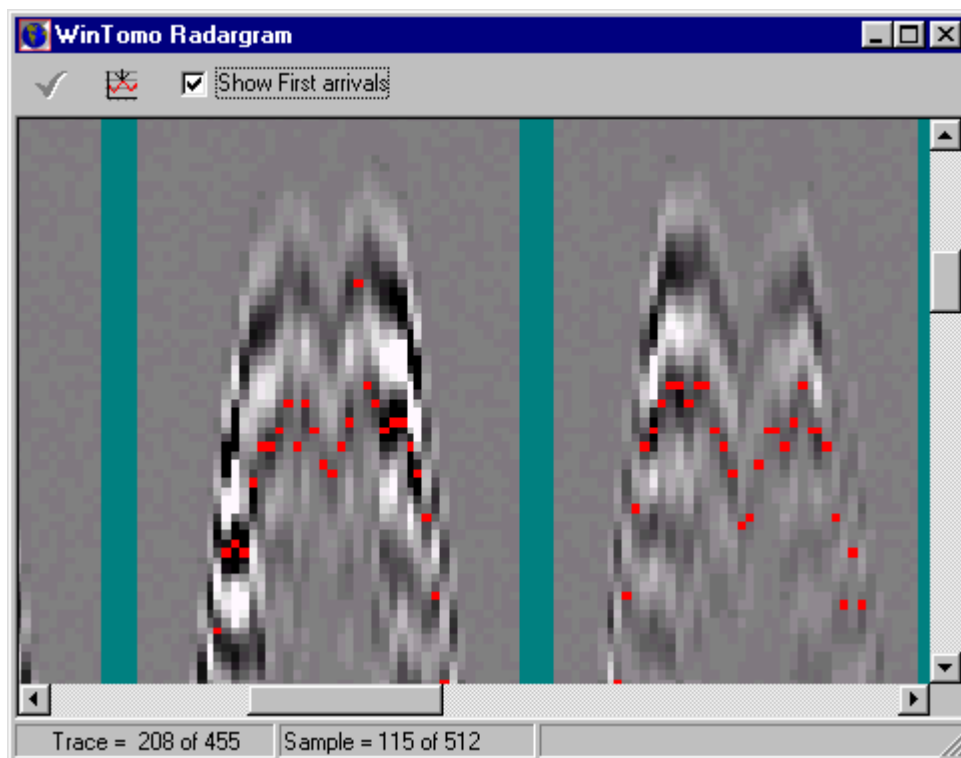


Figure 6. Zoomed part of the first arrival picking.

Viewing the first arrivals and by right clicking on the mouse brings you to a menu where you can zoom the data, re-pick the arrivals by viewing individual traces or change colour settings. You can zoom desired area by left clicking on the mouse and drawing a desired square area on the screen.

In zoom mode you can "drag" the red squares marking first arrival if you wish to change the picking.

Clicking on the "√" sign will mark each trace as "BAD", shown by a red colouring. This indicates that the trace will not be used in the inversion process.

If a whole section of data should be marked as "BAD" you can do this by placing the cursor at the desired starting point, while holding down the "SHIFT" key on the keyboard and left clicking on the mouse and dragging the cursor to the desired end point. There after click on the red marker for "√". Such areas will receive the colour specified in the "View>Settings>Colours>Bad Trace". They traces can be reset by performing the same procedure again. The result should be that the colour is reset to the original one.

To change the colour palette of the radargram you should double click on the desired interval to select appropriate colour.

To perform an interpolated scale between selected intervals proceed as follows:

- Left click on the first colour box in the interpolation range. Note that you can perform interpolation between numerous intervals at one instance. This box will then become lightened. Double click on the same box to select suitable colour.
- Left double click on the next box to select suitable colour. Then left click on the same box to have it lightened. Continue with next box if you chose to have many interpolated intervals.
- Left click on the box marked "Interpolate". The colour area between the selected boxes will now be interpolated.

Palettes can be saved on the working directory or at any desired directory for future use.

## 4.4 Grid size

The "Grid size" option is used to define the inversion area as well as pixel sizes for inversion and interpolation.

Normally the inversion areas need to be defined with a certain offset in order to include the all rays in the transformed coordinate system. This system where the inversion is performed uses the FIXED borehole as the Z-axis and the direction vector the second borehole as the X-axis.

The pixel size is recommended to be set according to the antenna wavelength, e.g. 1 m for the 100 MHz and 0.5 m for the 250 MHz antennas. If the inversion is interrupted by e.g. too little RAM memory in the computer the pixel size can be increased some to save memory.

## 4.5 Data quality checking

Data quality checking consists of two separate steps where parameters are determined depending on whether amplitude or time data are studied.

Residual/distance plot and Ray Check Plot are the two plots top be studied. From these the **Background Attenuation/Velocity** and **Transmitter Power/Start Time** of the pulse should be determined.

The determination of these parameters is carried out in such way to align the residual data points on a horizontal line centred around a zero-background value.

Velocity and attenuation are calculated as the quotient between distance/time and amplitude/distance respectively. Therefor these parameters mainly determine the slope of the data sets. By adjusting these parameters the slope of the data sets can be changed.

Start time and Transmitter Power represent offset values that determine the level of the data on the vertical axis.

However, Start Time in the arrival data affects both the level and the slope of data so regarding the velocity inversion the data reduction process might turn out to be some more "tricky" compared to the attenuation data.

Individual data or scans can be viewed and re-picked by clicking on the data cross

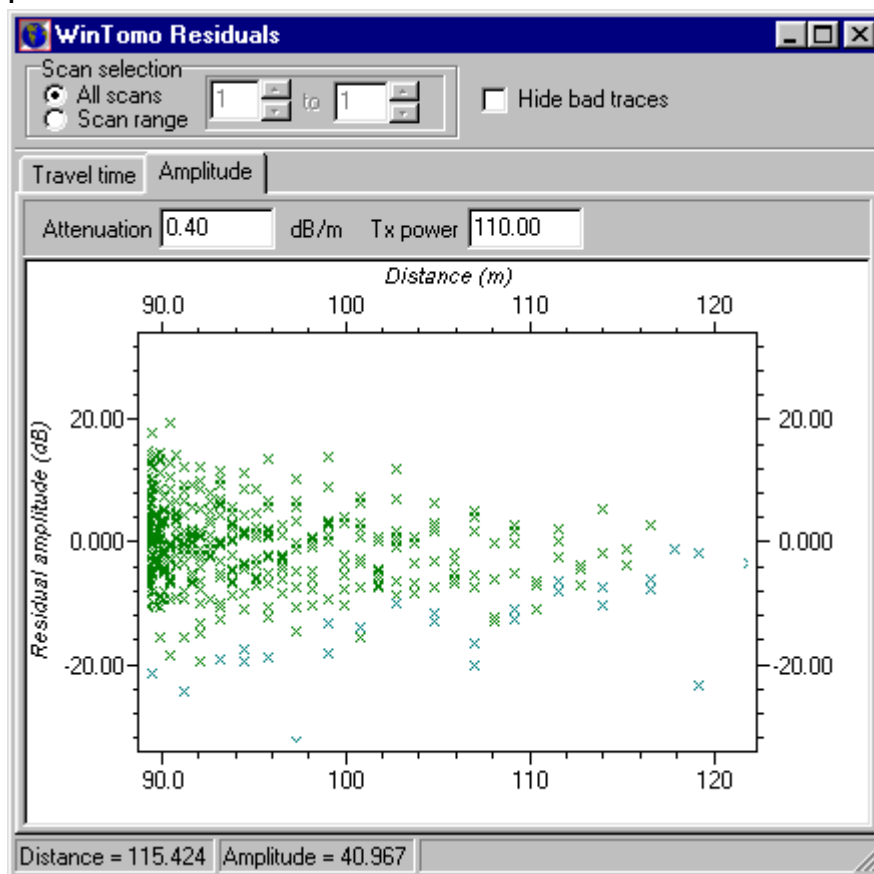


Figure 7. Residual time window.



The ray check plot shows graphically each measured trace residual value after background removal.

It shows each scan horizontally with the option to disclose all traces regarded as "bad" and not given as input to the inversion process.

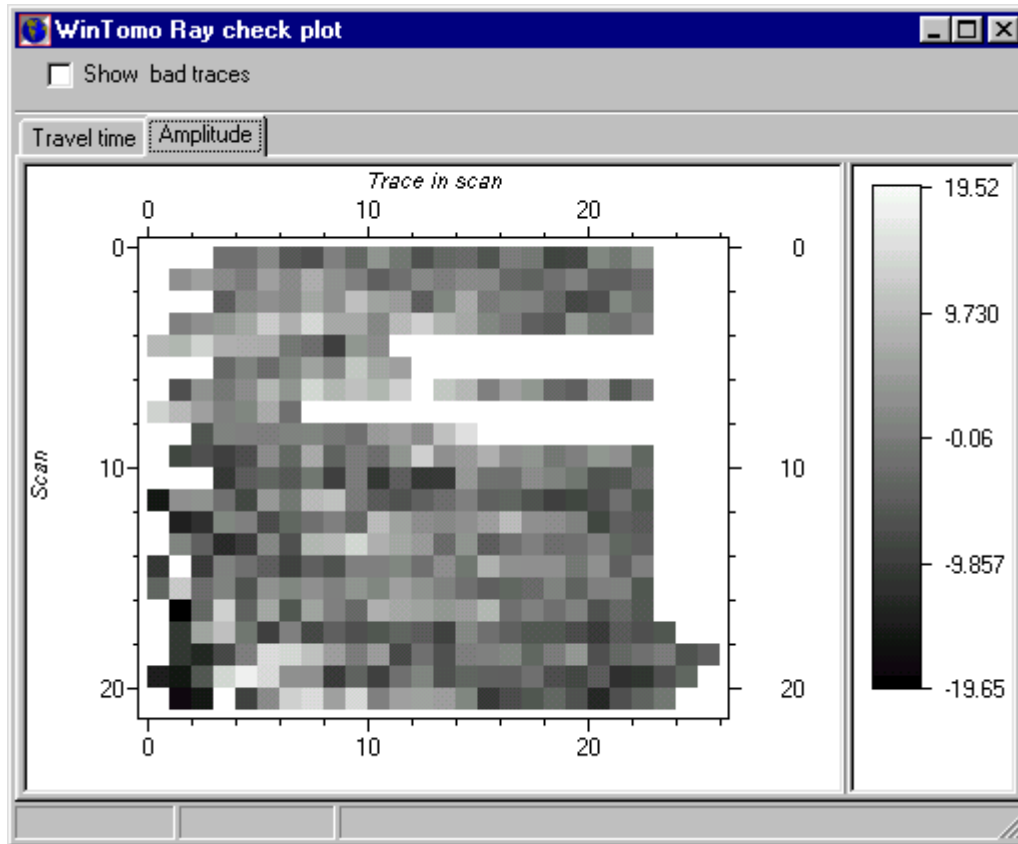


Figure 8. Ray Check plot

Once this is achieved the residual data are ready for tomographic inversion.

By clicking on a selected square representing one trace that trace is brought up on the screen. The arrival can be re-picked manually by hand for that trace by moving the arrival marker. Or, the arrival data for the whole data set can be re-picked by clicking on the coordinate system marker at the top.

**NOTE:** If you have been re-picking data manually you should be careful to perform a new pick on the whole data set as this will erase your manual picking.

## 4.6 Inversion of data

Inversion parameters are set in the "Settings" menu. The min and max values can be changed from the pre-set values if desired. Generally speaking these values set constraints to the inversion result. Therefore any predetermined value of these parameters can be entered as aid. If no pre-information is available the min and max values should be set to cover a maximum interval, e.g. 20-200 for velocity and 0.1-50 for attenuation.

The inversion routing used is a modified Conjugate Gradient method, which is an iterative method. It converges fast and therefor the necessary number of iterations can be set generally as low as 5.

The damping factor is a wavelength damping factor set on the inversion to smooth it. Generally values between 0.1 and 5 give the best results.

Inversion can be made on both velocity and attenuation. The resulting values are expressed in either **m/μs** or **dB/m** respectively.

After finished inversion the data can be interpolated by setting the desired pixel size.

By right clicking on the mouse the tomogram can be zoomed, boreholes can be shown and the colour palette be changed by clicking on the colour bar and setting the desired colours.

Intermediate colours can be inserted at the desired value point and dragged up or down along the colour scale.

The scale can be selected to be viewed as "Automatic" or as "Manual".

"Automatic" in this case means that the minimum and maximum values appearing in the resulting pixel values will be set as limits to the colour scale.

"Manual" means that the operator can insert values as limits to the colour scale.

In case the operation of setting manual scales does not function the operation should be repeated once again by insert the values again.

The tomograms can be printed on the selected printer entered in the "File>Printer Setup" menu.

The tomogram is automatically scaled to the full-page version on to the paper that is selected in the print menu.

In this delivered version the tomogram is displayed with the Z-axis along the "FIX" borehole. The zero point along that axis is set to the first ray point in the scan list, adjusted for any offset set in the scan list.

The velocity or attenuation data behind the tomographic images can be exported into a text file for further processing or presentation using additional software. To export the data make the tomogram window active and select Save As from the file menu. The default file extension is TOM. One truncated example of such exported data is shown below:

```
Tomogram type : amplitude
Background attenuation = 3.00 dB/m
Transmitted power = 115.00 dB
Damping factor = 50.000
Number of iterations = 10
```

```
0.400000, 0.200000, 2.049647
0.400000, 1.200000, 1.972682
0.400000, 2.200000, 3.473368
0.400000, 3.200000, 2.949587
0.400000, 4.200000, 2.403549
0.400000, 5.200000, 2.823905
```

The first six lines contain information about the processing performed to realize the tomogram plus a blank line. Following this header is the actual data in the format: X-coordinate, Z-coordinate, velocity or attenuation. The coordinates given are the coordinates for the centre of each cell in the tomogram.

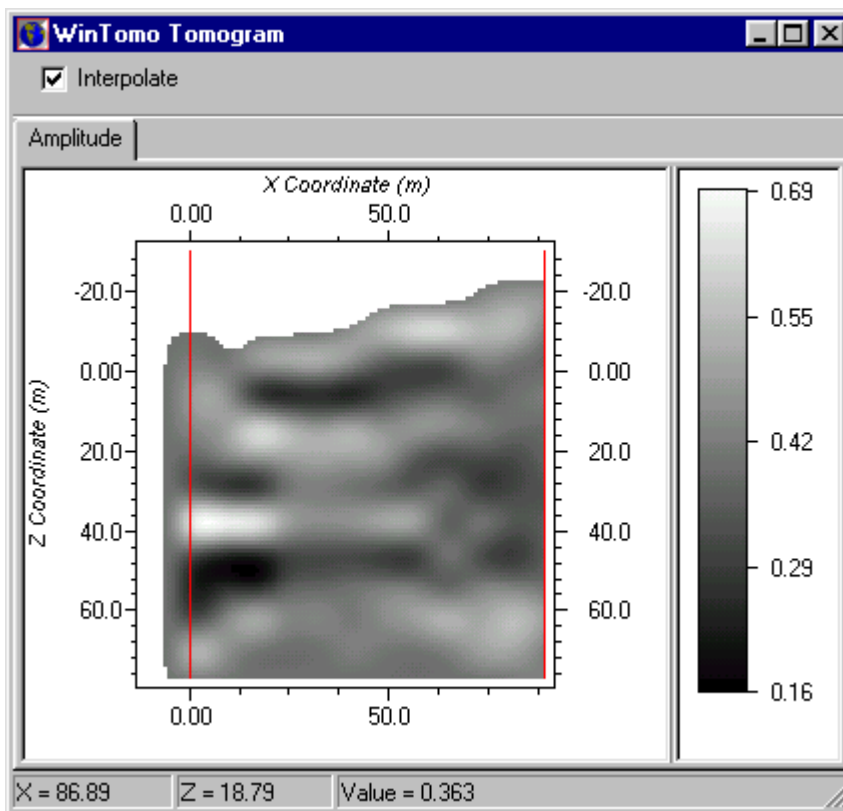


Figure 8. Tomogram output.

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