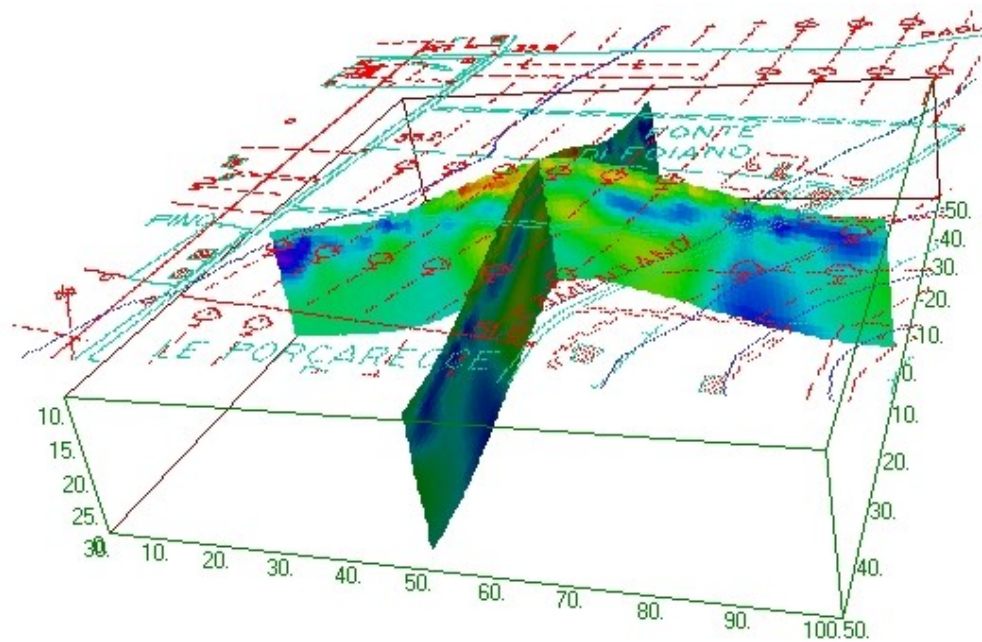




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# TomoLAB User Manual



June 2009

# Summary

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## Introduction

The present software comes out from different experiences in geophysics (Electrical Resistivity Tomography) and from the development of specific software application in data management.

Many tools for data analysis and manipulation have been added to the inversion module INV\_2D.EXE. Such facilities have been thought and tested by the same group of geophysicists involved in carrying out field measurements. So we hope to have prepared a tools truly related with field activities.

It's beyond the scope of this manual to introduce the user to the ERT technique, for this purpose relevant books and articles would be easily find.

Moreover the number of different configuration is not high, vertical sounding is not concerned, and the software will recognize only five different array configuration:

Array	Id. number
Pole – pole	2
Dipole – dipole	3
Pole – dipole	5
Wenner	6
Wenner - Shlumberger	7
Gradient Array	8

In order to help user in a better understanding of the logic of the software, the data structure will be sketched.

Electrodes	
N.	Electrode number
X	X coordinate
Y	Y coordinate
Z	Z coordinate
zt	z topography
Zb	z exploration depth
Chk	Flag. The electrode is used in topography calculation.
Skip	Flag. The electrode is skipped (quadrupoles with this electrode will be ignored)

Sequence	
A	Current electrode
B	Current electrode
M	Potential electrode
N	Potential electrode
K	Geometrical factor

Measurements	
I	Current flowing between A and B
V	d.d.p. between M and N
q	Error on $v_{MN}$
rho	Apparent resistivity ( $k * v/i$ )
m	Chargeability
M1	Chargeability in interval 1
M2	Chargeability in interval 2
M3	Chargeability in interval 3
x	Quadrupole x position in pseudosection
z	Quadrupole z position in pseudosection
at	Array type, Wenner, Dipole-Dipole etc
n	Quadrupole order
a	Aperture

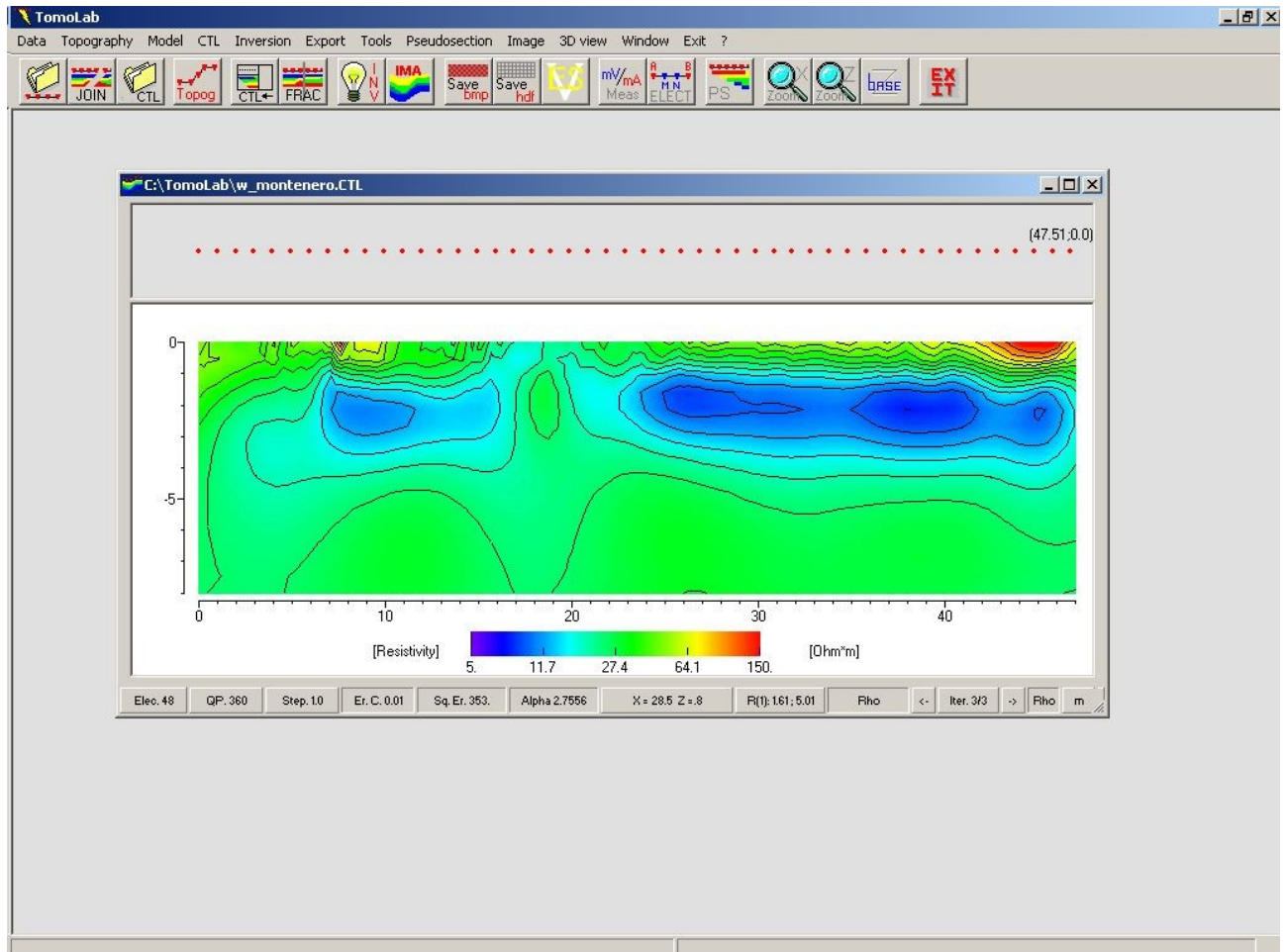
Data structure of electrodes and measurements have been kept separated, for compatibility with older formats and because ensure high flexibility..

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## Sections

TomoLab acts as container of field data arrays, each file is related to a structured form as sketched below:



For a better understanding of the TomoLab structure we need to look inside some issues:

Data Files were collected in single form, data value and electrodes positions can be shown by a proper function. Measurements should be viewed as "pseudosection". Data inversion run over a control file that collects information on:

- 1 – electrodes position and topography
- 2 – mesh
- 3 – measurements

An external module (INV\_2D.EXE) could perform the "data inversion" (batch mode) using the control file .CTL. Inversion results were collect in ASCII file with .IMA extension, such files should be loaded in TomoLab environment.

## The mesh grid: cells and nodes

In order to perform data inversion, the underground should be modelled as finite dimension half-space (domain). Boundary condition should be set in order to resolve many differential equation for the electrical potential function (Poisson equation). Domain can be viewed as an internal region where electrodes are placed (the **foreground region**) and a frame that span from the foreground to the boundaries (the **background region**).

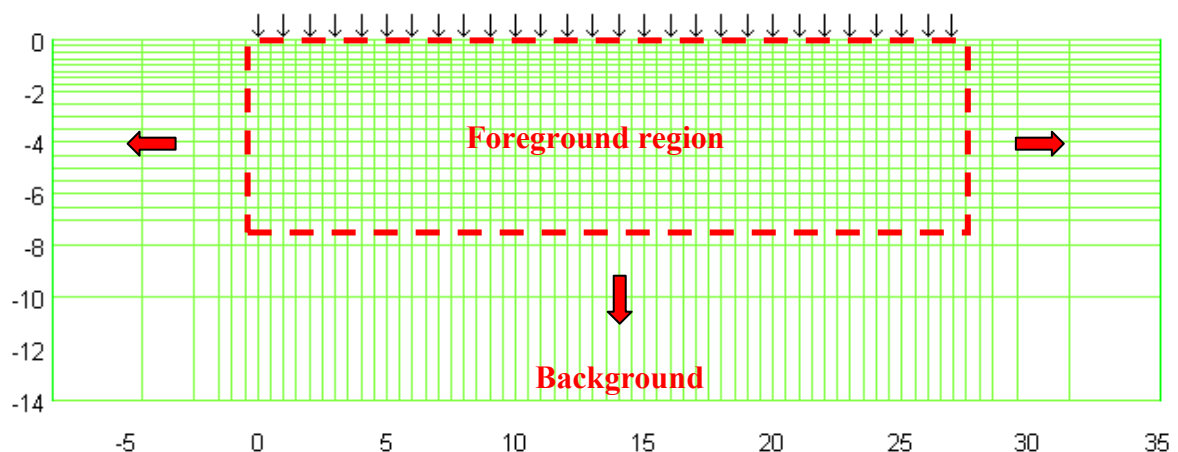
The half space is divided in cells, each cell define a finite region with constant resistivity. Cells dimension grow towards the boundaries, just because the resolution goes down far from the electrodes. Cell's vertex are named "nodes", they represent points where the electrical potential should be truly calculated for each current source. In TomoLab domain is divided in cells with four nodes.

Sampling in X direction: reasons related to numerical accuracy in solving differential equation suggest to define cells dimension in the foreground region as half of electrodes mean distance.

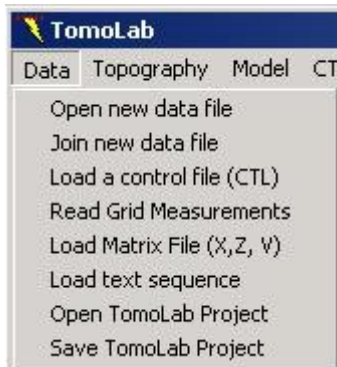
Background region is sampled in 8 cells (9 nodes), so the first electrode lay on the 10<sup>th</sup> node. Distance between 9<sup>th</sup> and 8<sup>th</sup> nodes, 8<sup>th</sup> and 7<sup>th</sup>, and so on, follow a geometric progression.

The same criteria define nodes spacing at the right side of the last electrode.

Sampling in Z direction: the depth is sampled with nodes at half of electrodes distance until the investigation depth is reached (foreground region); in the background region distance between two adjacent nodes grow as geometric progression.



## Menu Data



### Open new data file:

the program automatically detect many data formats, among them, the ones from IRIS - Instruments (done with Electre or Prosys). The internal data structure of TomoLab require the electrodes position and number, unfortunately files from ProSys (.bin extension) have lost information on cable and electrode number. In order to recover such data, when a .bin file is loaded, TomoLab asks user to specifies the mean electrodes spacing defined in the sequence (not n the real data acquisition!).



### Join new data file:

It is possible to append a data file to the active one and shift both the numerical order of the electrodes and the x coordinate, the program will ask the user to specify the number of roll electrodes and the distance of the first electrode in the new data file from the first in the old one. The two information could differ in special case, in standard application



### Load a control file (CTL):

the native data file format has the .CTL extension. Such files contain information on the electrodes position, the mesh and the measurements. The inversion process works over these files

### Read Grid Measurements:

measurements could be saved as datasheet. This function allow to reload data previously saved as datasheet. The file format is very simple and resemble the structure of the data grid.

### Load a Matrix file (X, Z, v):

data disposed as matrix column should be loaded in TomoLab and plotted. The data should respect some constraints: columns must have the same numbers of rows,

value in Z should be in ascendant order. TomoLab makes a virtual set of electrodes that fit the matrix structure. The 0 ("zero") value in the third column is detected as filling symbol.

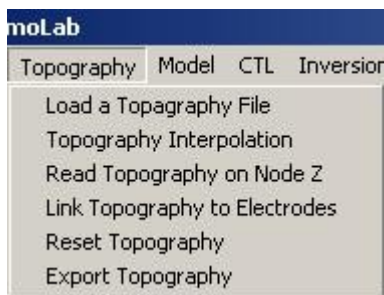
### Open TomoLab Project:

read a script file (.tmlb) within the details of CTL file, IMA file, iteration, labels, colours scale.

### Save TomoLab Project:

save a script file (.tmlb) within the details of the current CTL file, IMA file, selected iteration, labels, colours scale.

## Menu Topography



There are many ways to insert topography in ERT profile, the topography information should be known before carrying out field measurements and TomoLab recover it from the .BIN file, in general the topography is an external information that user has to link to field measurements. TomoLab allows user to insert topography in three ways:

- 1 – direct: drag the electrode on the picture
- 2 – datasheet: modify the z coordinate of electrodes (all or a part) and interpolate
- 3 – file: load an ASCII file with the topography information (Electrode; Z).

### Load Topography File:

TomoLab can load topography information from a two columns ASCII file. The first column is the electrode's number, the second is the electrodes elevation [m] with respect to an arbitrary reference. In case the file doesn't define all the electrodes, TomoLab makes linear interpolation for the undefined electrodes. In this case the first and the last electrodes should be defined.



### Topography Interpolation

Perform linear interpolation of the Z coordinate for the electrodes undefined in the topography file or in the direct mode.

## Read Topography on node Z

In special case (floating electrodes, borehole) topography information saved in the .CTL file isn't on the first node of the mesh. TomoLab asks user to specify the node Z which define the topography.

## Link Topography to Electrodes

Topography information got with the previous menu function should be used as standard topography: related to electrodes

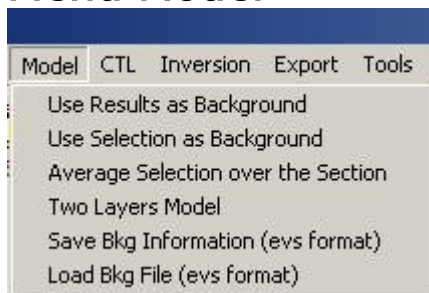
## Reset Topography

Set the Z coordinate to zero for all electrodes

## Export Topography

Save topography information in a two columns ASCII file. The topography file has the root name of the current window and the extension .TPG

## Menu Model



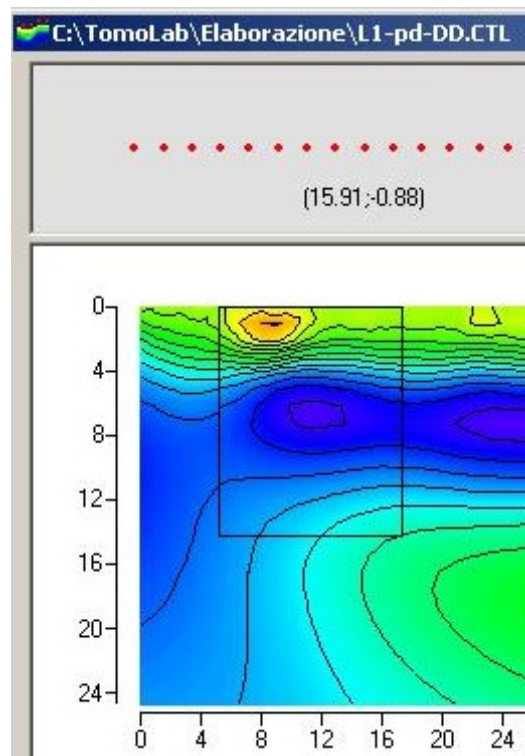
## Use Results as Background

In special situation would be necessary modelling data with respect to a non-homogeneous background. This function tells TomoLab to use the current results (iteration) as starting and reference model in further inversion process.

## Use Selection as Background

The starting and reference model would be defined only for a part of the foreground region, this function tells TomoLab to use the selected region of the current results (iteration) as starting and reference model in further inversion process.

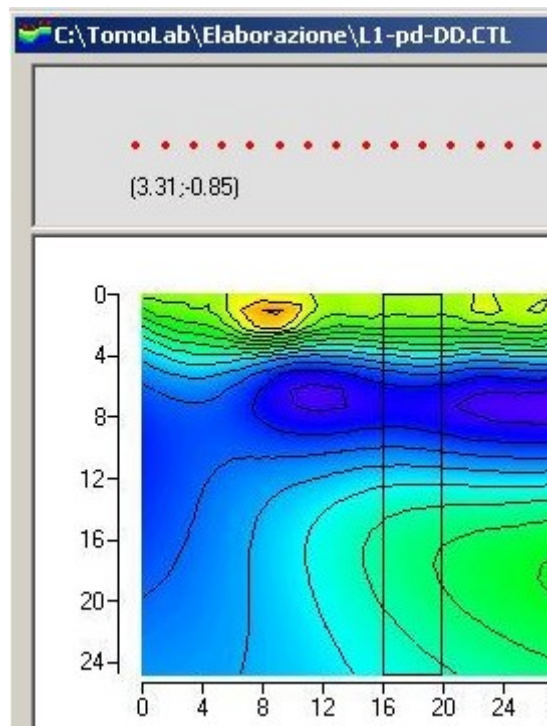




**Pic. 1** - Select a region (Ctrl + RgtMouse)

## Average Selection over the Section

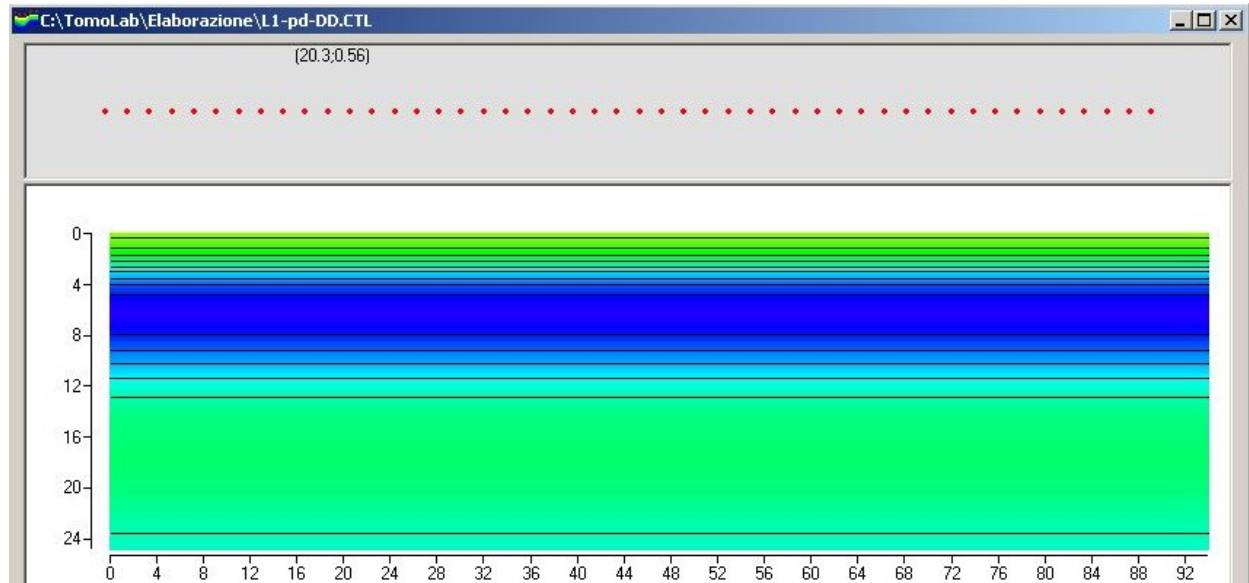
It is possible to select a region of a result iteration and then average along the profile in order to create a stratified model. User should follow these steps:



**Pic. 2** - Step 1: Select e region

Step 2 : Use Selection as Background

### Step 3: Average Selection over the Section



**Pic. 3** Step 4: View Background

### Two Layers Model

In special case would be useful define a two layer model. User has to feed the depth of the interface and the resistivity of the two layers.

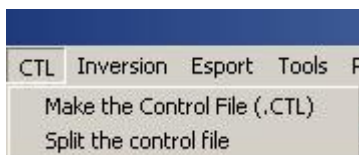
### Save Bkg Information (EVS format)

The background model defined for a profile would be useful for other profile. It is possible to save the background definition in an ASCII file with the EVS format.

### Load Bkg Information (EVS format)

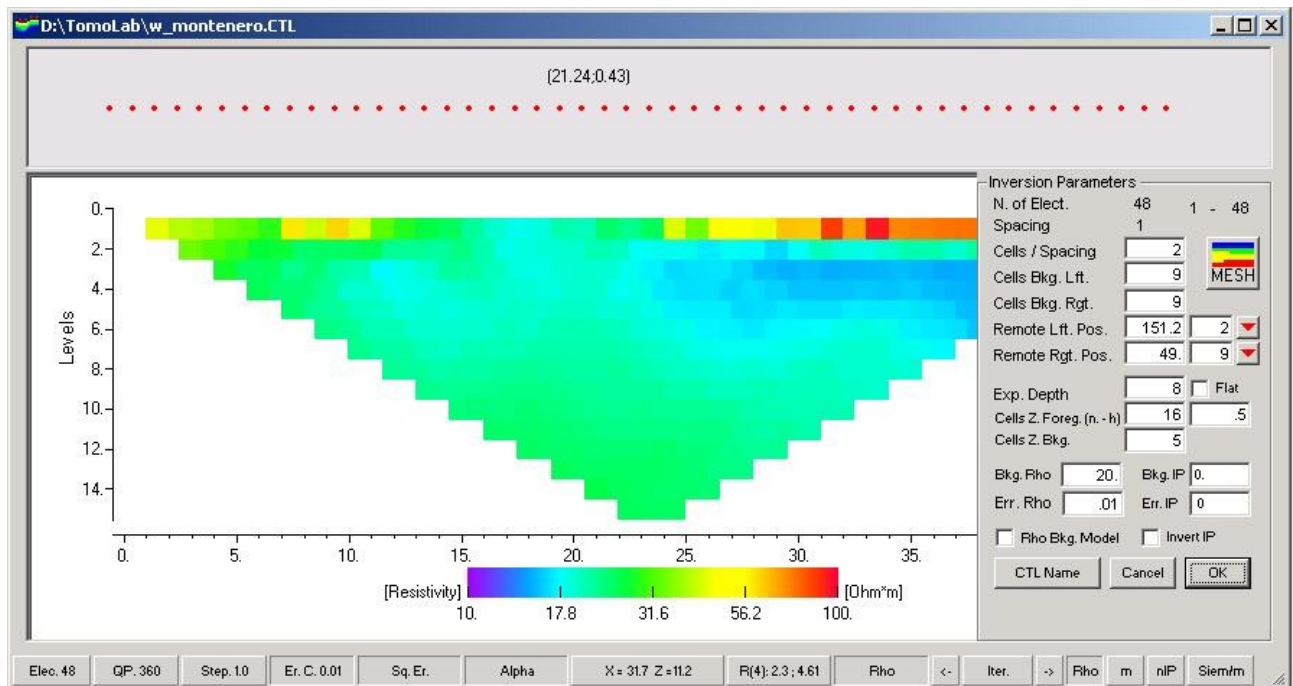
It is possible to load the background definition from an ASCII file in the EVS format.

## Menu CTL



### Make the Control File (.CTL)

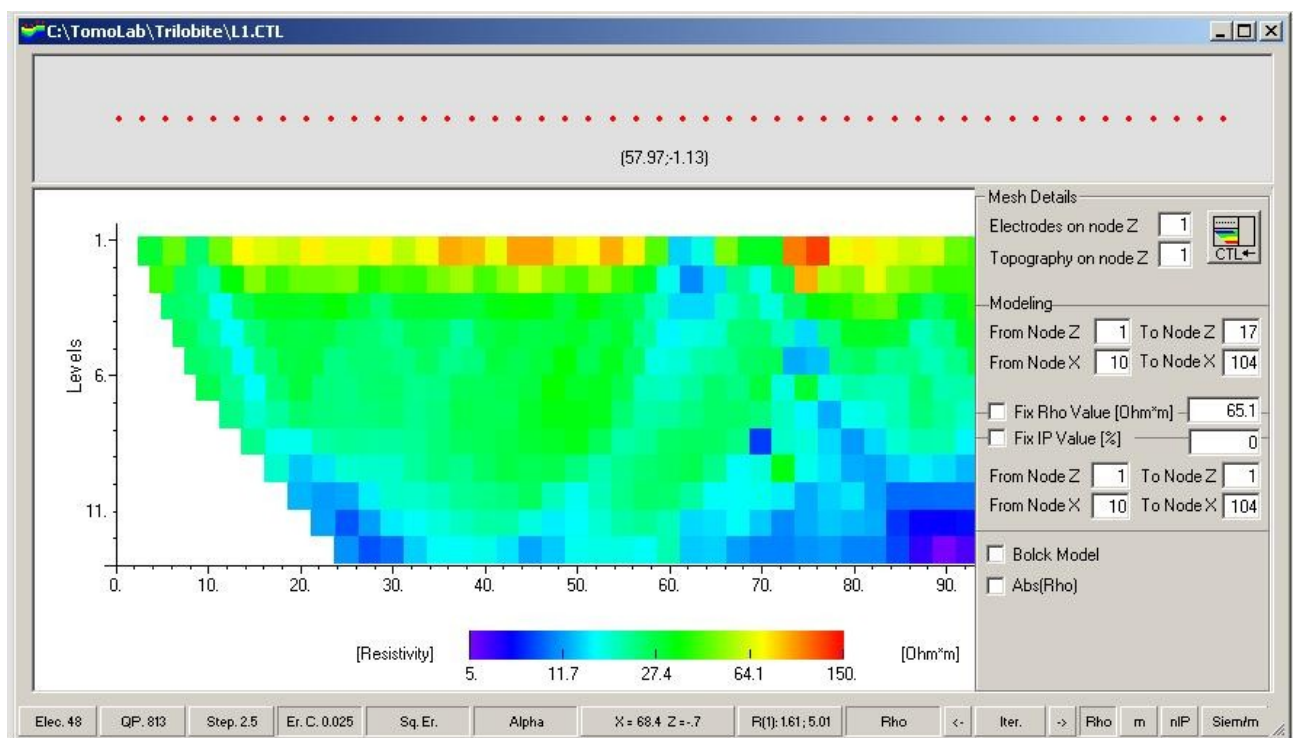
The inversion module process a file that contain data on electrodes position, the mesh and the data. In order to create the CTL file user must feed some (many) information filling a form on the array window.



Pic 4 - CTL Form 1

- [N. Of Elect.]** specify the number of electrodes of the array. The two number on the right should define a sub set of the array. The CTL file will contain only quadrupoles with electrodes greater than or equal to the first number and less than or equal to the second one.
- [Cells/Spacing]** number of cells in foreground region between adjacent electrodes;
- [Cells Bkg. Lft.]** number of cells in the background region before (on the left of) the first electrode;
- [Cells Bkg. Rgt.]** number of cells in the background region after (on the right of) the last electrode;
- [Remote Lft. Pos]** x distance in [m] of the remote electrode from the first electrode; node of the mesh of the remote electrode; add remote to the CTL file;
- [Remote Rgt. Pos]** x distance [m] of the remote electrode from the last electrode; node of the mesh of the remote electrode; add remote to the CTL file;
- [Exp. Depth]** exploration depth, define the Z limit of the foreground region for the mesh, Exp. Depth should be equal to [Cells Z Foreg. ] (cells number x cells height);
- [Flat]** the exploration depth follows the electrodes elevation. If this option is on, the exploration is a fix value along the profile;
- [Cells Z Foreg.]** number of cells in Z within the foreground region;

[Cells Z Bkg.]	number of cells in Z in the background region;
[Bkg. Rho]	model resistivity value at the beginning of the inversion;
[Bkg. IP]	model chargeability value at the beginning of the inversion;
[Err. Rho]	error coefficient in resistivity modelling;
[Err. IP]	error coefficient in chargeability modelling;
[Rho Bkg. Model]	add the background model into the CTL file;
[Invert IP]	invert chargeability data;
[CTL Name]	change file name of CTL;
[Cancel]	return to section view;
[OK]	confirm data and write the CTL file;



Pic 5 CTL Form 2



## MESH - Mesh details

[Electrodes on node Z]	set the node z of the forward mesh which define the position of the electrodes. For surface survey electrodes should be on node 1, for floating electrodes the node should be 1, 2 or more;
------------------------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

**[Topography on node Z]** set the node z of the forward mesh which define the topography. In case of floating electrodes can be at the sea level and the topography represent the water depth measured with an echo sounder;

- Modelling

**[From node Z]** set the starting node z in the inversion mesh;

**[To node Z]** set the ending node z in the inversion mesh ;

**[From node X]** set the starting node x in the inversion mesh;

**[To node X]** set the ending node x in inversion mesh;

(the inversion mesh should be a subset of the forward mesh)

- Fix Value

If the inversion mesh and the forward mesh are different, a subset of the forward mesh can assume a fix value different form the one specified in the background

**[Fix Rho value]** set the Rho value;

**[Fix IP value]** set the chargeability value;

**[From node Z]** set the starting node z of the subset in the inversion mesh;

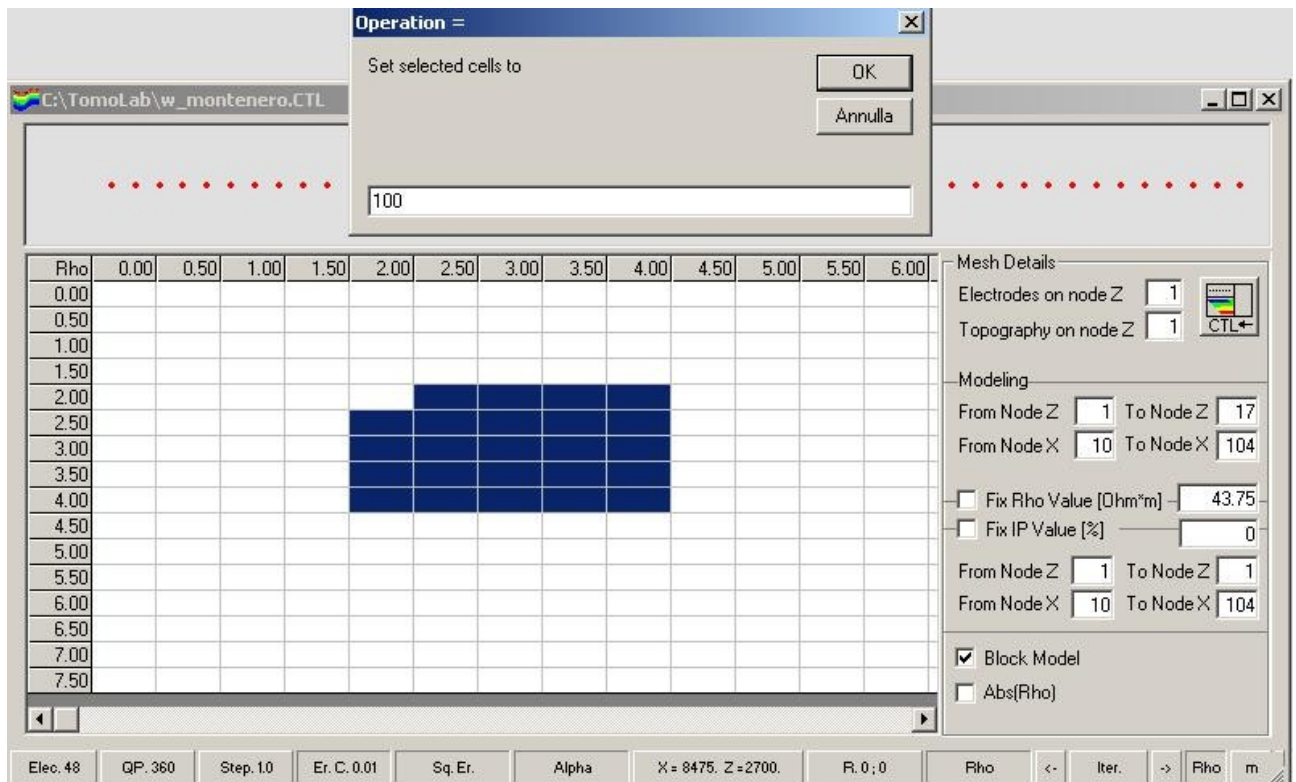
**[To node Z]** set the ending node z of the subset in the inversion mesh;

**[From node X]** set the starting node x of the subset in the inversion mesh;

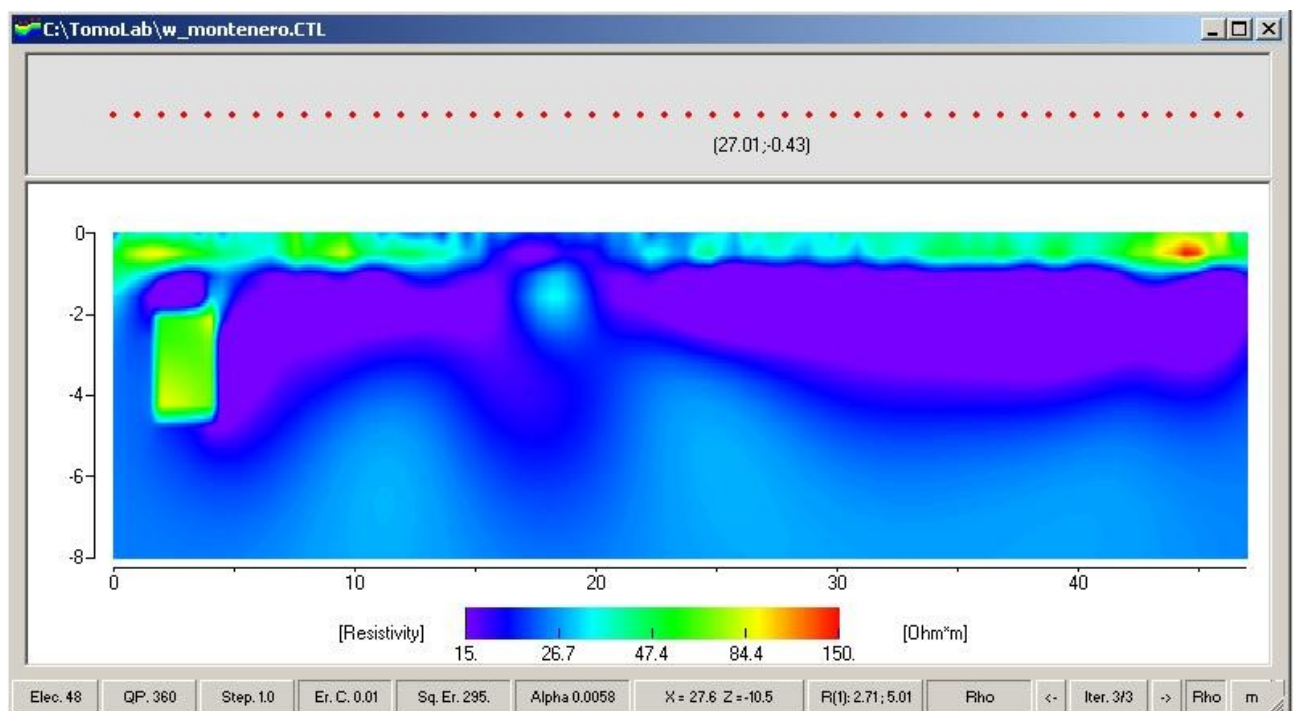
**[To node X]** set the ending node x of the subset in the inversion mesh;

**[Block Model]** show/hide data grid to edit block rho value;

**[Abs(Rho)]** modelling the absolute value of the resistivity. In this case, writing the CTL, TomoLab correct the sign of the  $V_{MN}$  in order to get always positive value resistivity



**Pic 6** Select a cells group and assign the value of 100 Ohm\*m



**Pic 7** Results with a model as reference

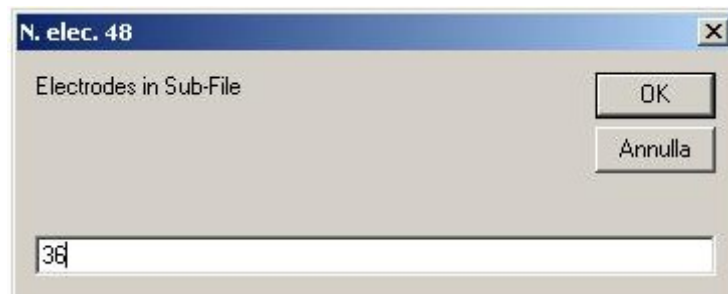


### Split the Control File (.CTL)

The inversion process would take several minutes. Time consuming is strictly related to the electrodes number and exploration depth. So would be necessary to split the



control file in two or more file smaller than the initial one, invert each file and, then, if it is necessary, link the results into a single image.  
The splitting operation ask user for number of electrodes in each sub-file and number of electrodes of overlapping.

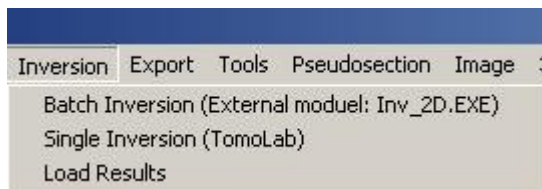


**Pic 8** Set number of electrodes for each sub file



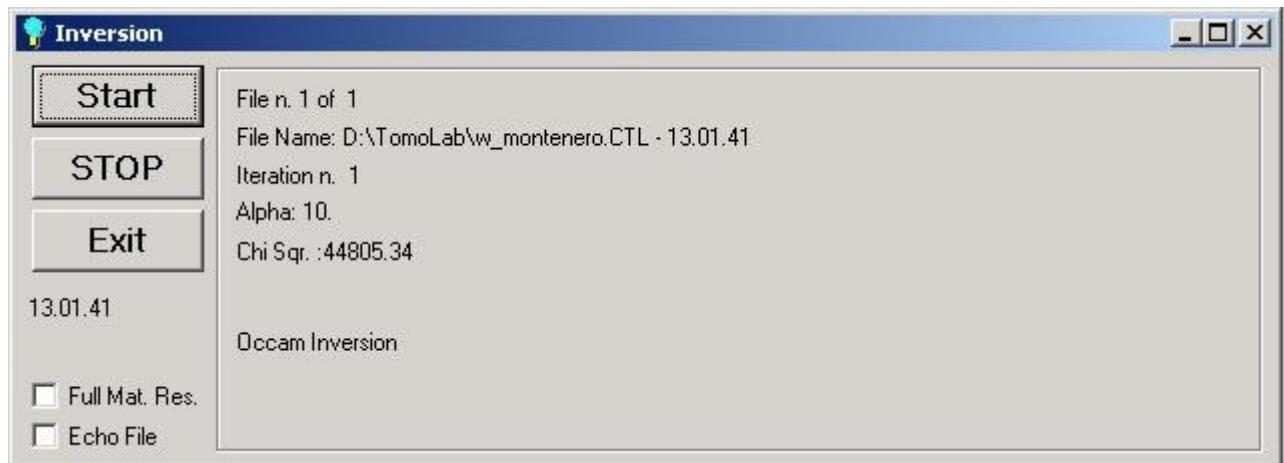
**Pic 9** Set the number of overlapping electrodes between files

## Menu Inversion



### Batch Inversion

The inversion process act on the .CTL files. Since the intense time and machine resources consuming, seems good to do this operation alone. The Batch Inversion create an ASCII file with the names of the .CTL windows active in TomoLab, then pass the focus to an external module that will operate all the calculus of the inversion for each file writing, in the end, an ASCII file with the real resistivity (.IMA). Inv\_2D.exe runs also without TomoLab.

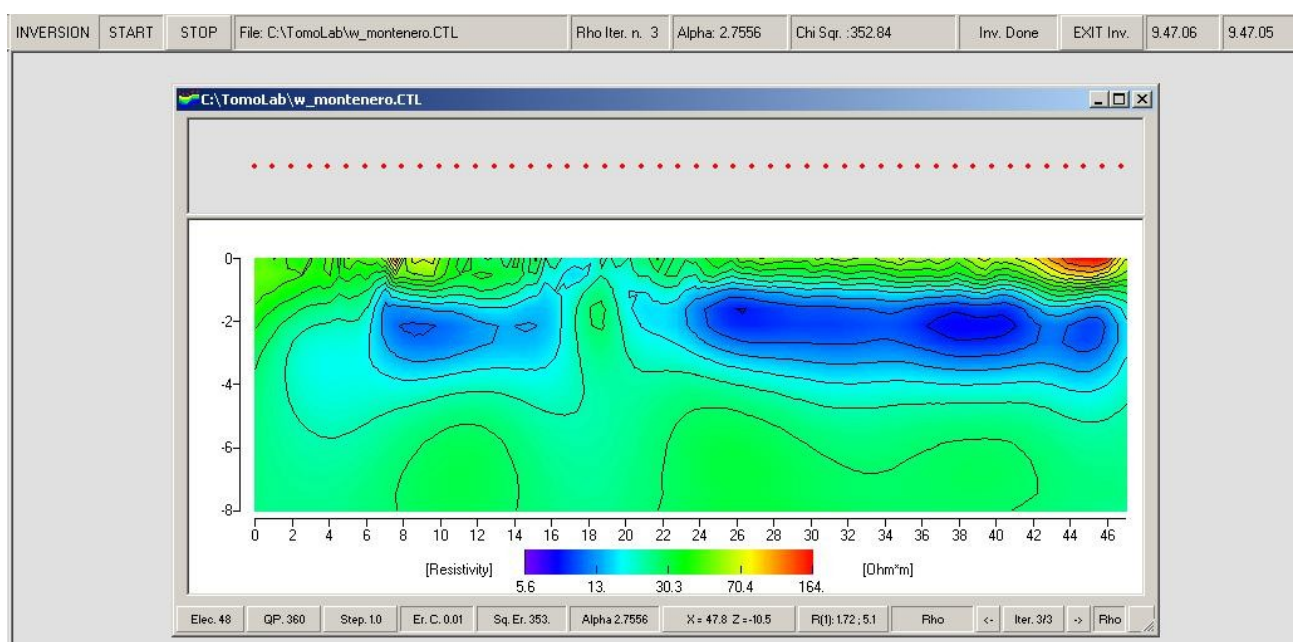


**Pic 10** Inv\_2D.exe window.

- [Start] the inversion process begins, the four label in the right panel tell the file name under inversion, time start and stop about the file, the current iteration, the Alpha parameter and the Chi Squared calculated over the direct model.
- [Stop] allows user to interrupt the inversion, this command doesn't act immediately and user should wait the end of the iteration.
- [Exit] quit the program.
- [Full Mat. Res.] set the matrix inversion algorithm to full. I.e. that no approximate procedure. This option will slow the program, use carefully.
- [Echo File] save an echo file (.ECH) with the forward model at each iteration

## Single Inversion

Activating this option TomoLab show an Inversion Bar just under the toolbar. Command on this toolbar act only on the active window, and update it dynamically at each iteration.



**Pic 11** Inversion bar and data window with results



The information on the Inversion Bar are the same in the data window:

[Sq. Er.] squared error (should be of the order of measurements)  
 [Alpha] smoothness parameter (should be between 0.5 and 5)



## Load Results

In the end of the inversion process results, stored in ASCII file (.IMA) can be loaded into TomoLab. TomoLab load the last Rho iteration as default.

## Menu Export



## Export Image as Bitmap

Save a bitmap image of the section or pseudosection. The file name is the root of the form caption with the extension .BMP



## Export Image Results as Matrix

Save the value of current iteration or pseudosection in an ASCII file as bi-dimensional array. The file name is the root of the form caption with the extension .HDF

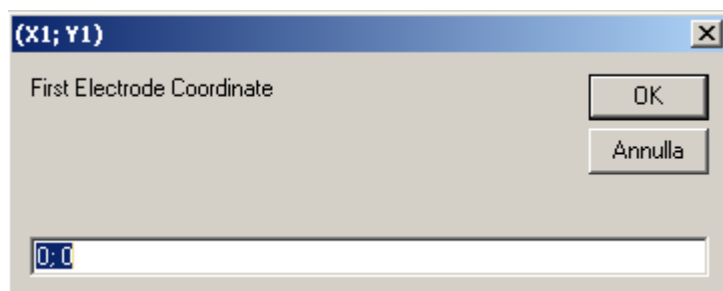


## Export Image Results in EVS format

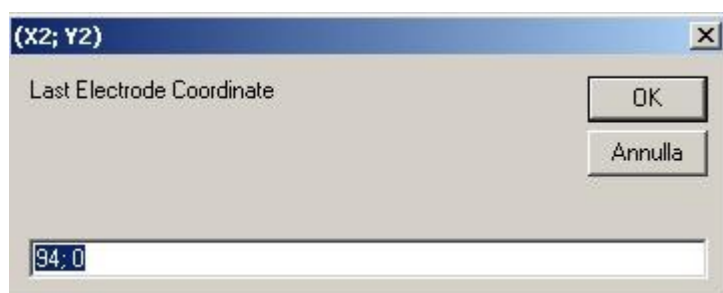
Save the value of current iteration or pseudosection in an ASCII file as column matrix following the format of EVS (Environmental Visualization System). This format allow user to assign to each rho value a set of three coordinate. The file name is the root of the form caption with the extension .EVS



**Pic 12** Offset Z to add to each electrode's quote



**Pic 13** (X; Y) coordinate of the first electrode, the default is (0; 0)



**Pic 14** (X; Y) coordinate of the last electrode, the default is ((nel-1)\*step; 0)

**L1-pd-DD.EVS - Blocco note**

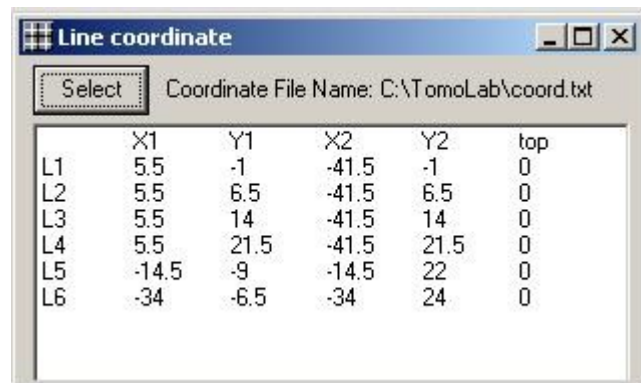
File Modifica Formato Visualizza ?

0.5	0.0	-0.52	68.9502	A1B1	0
0.5	0.0	0.52	55.8403	A1B2	0
0.5	0.0	1.55	42.7402	A1B3	0
0.5	0.0	2.58	34.6007	A1B4	0
0.5	0.0	3.62	29.701	A1B5	0
0.5	0.0	4.65	26.6702	A1B6	0
0.5	0.0	5.68	24.7609	A1B7	0
0.5	0.0	6.72	23.5806	A1B8	0
0.5	0.0	7.75	22.9101	A1B9	0
0.5	0.0	8.78	22.5704	A1B10	0
0.5	0.0	9.82	22.4801	A1B11	0
0.5	0.0	10.85	22.5505	A1B12	0
0.5	0.0	11.88	22.7401	A1B13	0
0.5	0.0	12.92	23.0006	A1B14	0
0.5	0.0	13.95	23.3203	A1B15	0
0.5	0.0	14.98	23.6801	A1B16	0
0.5	0.0	16.02	24.0601	A1B17	0
0.5	0.0	17.05	24.4703	A1B18	0

Linea 6, colonna 1

**Pic 15** An ASCII file in the EVS format with Notepad.exe

It is possible to use coordinates stored in an external ASCII file. User should append X Y Z coordinate to each resistivity element using data stored in an external ASCII file with the coordinate and the elevation of the extreme of a set of data files



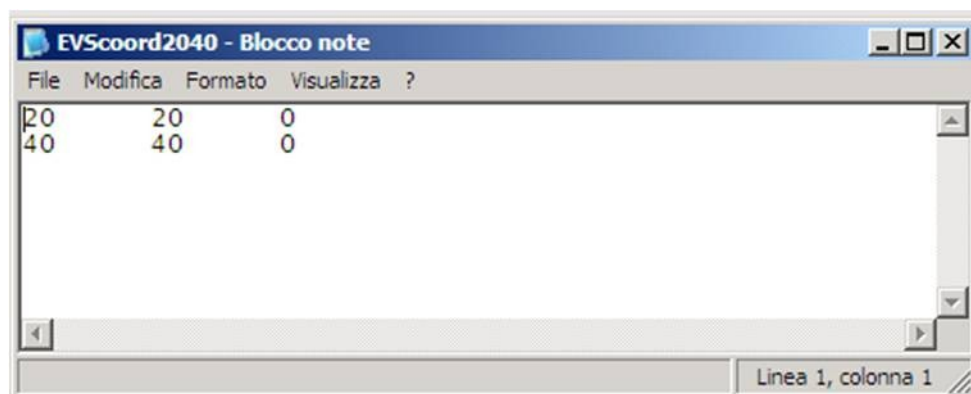
The dialog box titled "Line coordinate" has a "Select" button and a text field for "Coordinate File Name: C:\TomoLab\coord.txt". Below is a table with 6 rows (L1 to L6) and 6 columns (X1, Y1, X2, Y2, top).

	X1	Y1	X2	Y2	top
L1	5.5	-1	-41.5	-1	0
L2	5.5	6.5	-41.5	6.5	0
L3	5.5	14	-41.5	14	0
L4	5.5	21.5	-41.5	21.5	0
L5	-14.5	-9	-14.5	22	0
L6	-34	-6.5	-34	24	0

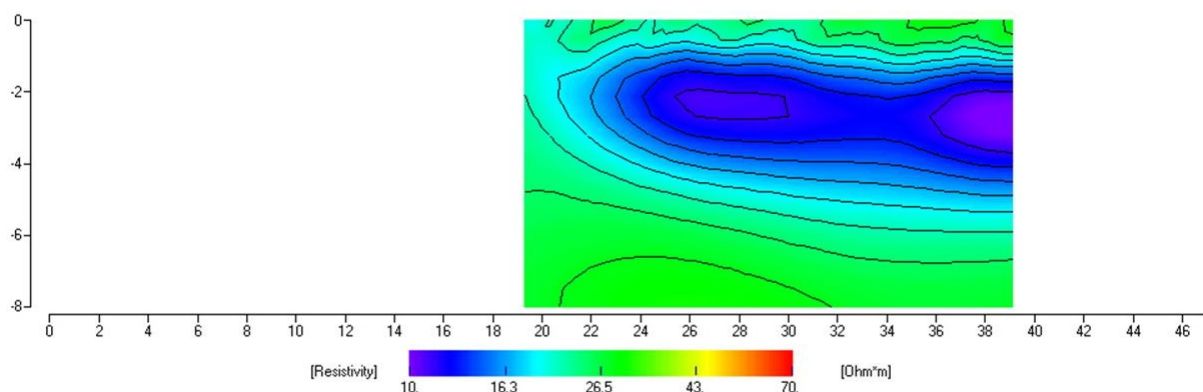
**Pic 16** Coordinate Form

### Export Image Results in EVS format (coord file req.)

It is possible to export results image in EVS format using coordinate information specified for each electrode. In this case, user have to select the ASCII file with the coordinate information (three columns ASCII file: electrode number; X coord; Y coord). By this option user can export only a selected part of the image result and, if reloaded, view only a selection of the inversion.



**Pic 17** Format for export in EVS format (save image results from electrode 20 to electrode 40)



**Pic 18** Image results from electrode 20 to electrode 40 (form X 19 to X 39)

## Export Image Results and Mesh

This function allows user to save an ASCII file with the extension .MSH, in this file the current image (pseudosection or inversion) will be saved as multi columns file (X, Z1, V1 .... Zn, Vn).

## Export Image Results as Column Matrix

This function allows user to save an ASCII file with the extension .DAT, in this file the current image (pseudosection or inversion) will be saved as three columns file (X, Z, value).

## Export Measurements for Res2DInv (.dat)

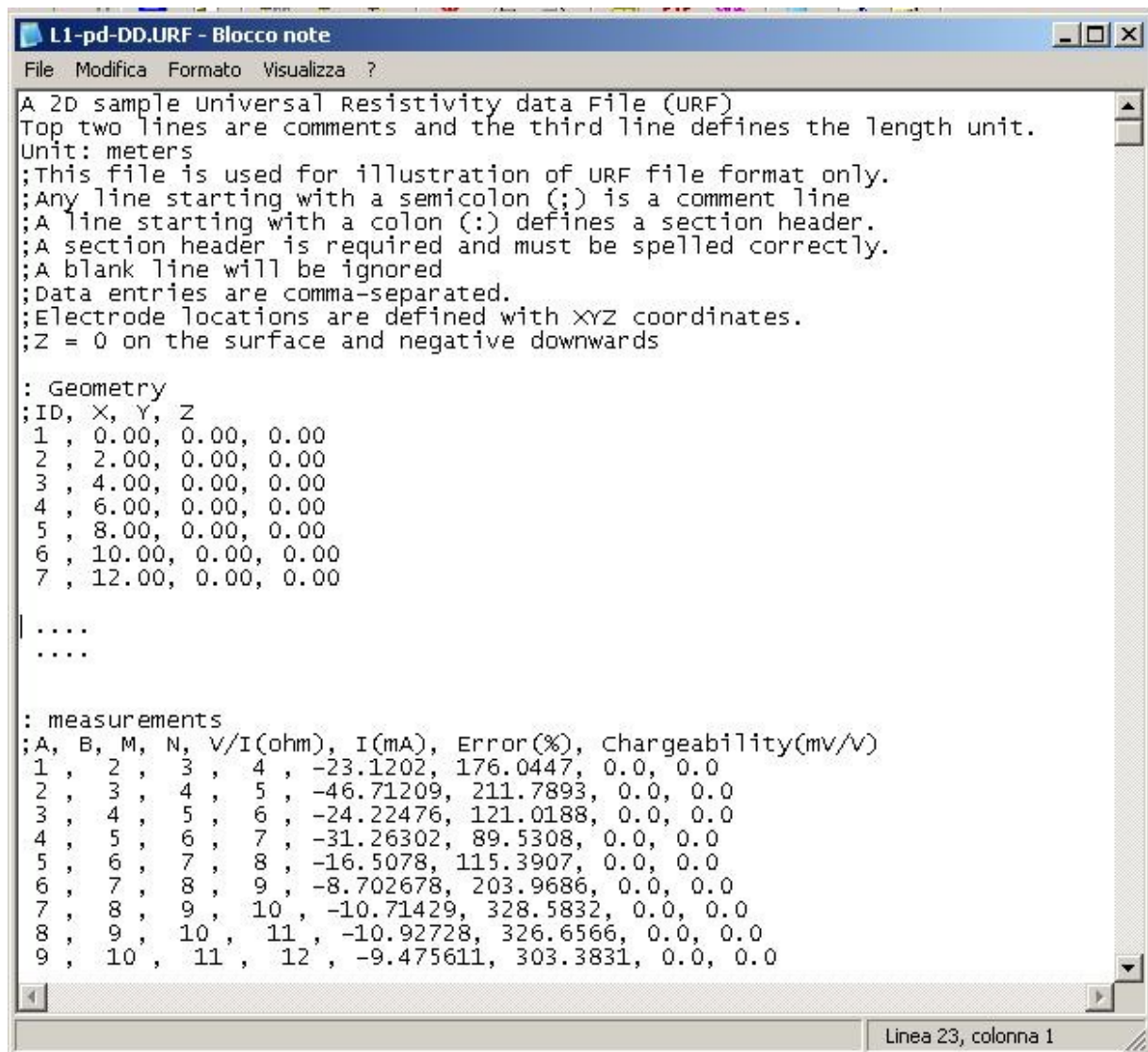
This function allows user to save an ASCII file with the extension .dat using the format of Res2DInv. This option support only file without topography information.

## Export Measurements in IRIS format (.bin)

This function allows user to save measurements into a binary file with the extension .bin using the format of IRIS. This option allow user to process file with the Prosys software from IRIS Instruments.

## Export Measurements in URF format (.urf)

This function allows user to save measurements into an ASCII file with the extension .urf using the Universal Resistivity Format.



```

L1-pd-DD.URF - Blocco note
File Modifica Formato Visualizza ?

A 2D sample Universal Resistivity data File (URF)
Top two lines are comments and the third line defines the length unit.
Unit: meters
;This file is used for illustration of URF file format only.
;Any line starting with a semicolon (;) is a comment line
;A line starting with a colon (:) defines a section header.
;A section header is required and must be spelled correctly.
;A blank line will be ignored
;Data entries are comma-separated.
;Electrode locations are defined with XYZ coordinates.
;Z = 0 on the surface and negative downwards

: Geometry
;ID, X, Y, Z
1 , 0.00, 0.00, 0.00
2 , 2.00, 0.00, 0.00
3 , 4.00, 0.00, 0.00
4 , 6.00, 0.00, 0.00
5 , 8.00, 0.00, 0.00
6 , 10.00, 0.00, 0.00
7 , 12.00, 0.00, 0.00

....
....

: measurements
;A, B, M, N, V/I(ohm), I(mA), Error(%), Chargeability(mv/v)
1 , 2 , 3 , 4 , -23.1202, 176.0447, 0.0, 0.0
2 , 3 , 4 , 5 , -46.71209, 211.7893, 0.0, 0.0
3 , 4 , 5 , 6 , -24.22476, 121.0188, 0.0, 0.0
4 , 5 , 6 , 7 , -31.26302, 89.5308, 0.0, 0.0
5 , 6 , 7 , 8 , -16.5078, 115.3907, 0.0, 0.0
6 , 7 , 8 , 9 , -8.702678, 203.9686, 0.0, 0.0
7 , 8 , 9 , 10 , -10.71429, 328.5832, 0.0, 0.0
8 , 9 , 10 , 11 , -10.92728, 326.6566, 0.0, 0.0
9 , 10 , 11 , 12 , -9.475611, 303.3831, 0.0, 0.0

```

Pic 19 Sample of URF format

## Export Measurements in STG format (.stg)

This function allows user to save measurements into an ASCII file with the extension .stg using the STG format.

## Export Measurements Grid

This function allows user to save measurements into an ASCII file with the extension .grd. This format should be loaded by Excel.

## Copy Image to Clipboard

This function copy the image (inversion or pseudosection) to clipboard memory area (CTRL+C) and allows user to paste image into another software.

## Menu Tools





## Edit Measurements

This function shows measurements in a data grid. User can edit the single field and save it by press carriage return, it's possible to remove a data record by selecting the whole row and the press cancel, it is also possible to do simple arithmetic operation over a group of cells by pressing [=] (assign value), [+] (add value) or [\*] multiply. Change will be saved at next click on menu item or toolbar.

D:\TomoLab\w48.bin

Num.	A	B	M	N	V [mV]	I [mA]	V/I	K	Rho [ohm*m]	m	q	Array	Skip
1	1	4	2	3	3492.431	492.9092	7.0853	6.283	44.5186	.	0.028	6	0
2	2	5	3	4	3371.376	531.473	6.3435	6.283	39.8572	.	0.031	6	0
3	3	6	4	5	3312.761	540.8838	6.1247	6.283	38.4828	.	0.032	6	0
4	4	7	5	6	3164.253	567.8767	5.5721	6.283	35.0105	.	0.043	6	0
5	5	8	6	7	2122.797	402.1288	5.2789	6.283	33.1684	.	0.026	6	0
6	6	9	7	8	1713.349	365.6913	4.6852	6.283	29.4383	.	0.051	6	0
7	7	10	8	9	3488.936	368.1426	9.4771	6.283	59.5467	.	0.05	6	0
8	8	11	9	10	1279.269	190.2846	6.7229	6.283	42.2415	.	0.082	6	0
9	9	12	10	11	3621.39	366.0873	9.8921	6.283	62.1543	.	0.028	6	0
10	10	13	11	12	2626.634	376.1519	6.9829	6.283	43.875	.	0.04	6	0
11	11	14	12	13	1180.541	223.8584	5.2736	6.283	33.1351	.	0.074	6	0
12	12	15	13	14	2790.55	606.3617	4.6021	6.283	28.9161	.	0.03	6	0
13	13	16	14	15	2949.254	693.3843	4.2534	6.283	26.7251	.	0.032	6	0
14	14	17	15	16	2187.57	538.0819	4.0655	6.283	25.5443	.	0.034	6	0
15	15	18	16	17	1664.787	478.6637	3.478	6.283	21.8529	.	0.028	6	0
16	16	19	17	18	1918.323	611.2899	3.1382	6.283	19.7177	.	0.	6	0
17	17	20	18	19	463.6238	158.4842	2.9254	6.283	18.3806	.	0.088	6	0
18	18	21	19	20	875.8931	291.5161	3.0046	6.283	18.8786	.	0.033	6	0
19	19	22	20	21	538.837	161.045	3.3459	6.283	21.0228	.	0.041	6	0
20	20	23	21	22	287.4485	88.6899	3.2411	6.283	20.3642	.	0.03	6	0
21	21	24	22	23	704.8876	180.457	3.9061	6.283	24.543	.	0.043	6	0
22	22	25	23	24	406.4836	112.7222	3.6061	6.283	22.6576	.	0.054	6	0
23	23	26	24	25	283.2668	69.79262	4.0587	6.283	25.5016	.	0.034	6	0
24	24	27	25	26	811.8788	116.9298	6.9433	6.283	43.6261	.	0.049	6	0
25	25	28	26	27	584.091	105.8731	5.5169	6.283	34.6638	.	0.061	6	0

Elec. 48   QP. 360   Step. 10   ErC. 0.01   Sq. Er.   Alpha   X = 10635, Z = 15.   R. 0 : 0   Rho   <-   Iter.   ->   Rho

Pic 20 Data Grid of wenner measurements



## Edit Electrodes

This function shows electrodes position in a data grid. User can edit the single field and save it by press carriage return, it's possible to remove a data record by selecting the whole row and the press cancel, it is also possible to do simple arithmetic operation over a group of cells by pressing [=] (assign value), [+] (add value) or [\*] multiply.

Change will be saved at next click on menu item or toolbar.

Num.	X [m]	Y [m]	Z [m]	Z(b)	Z(t)	Mark	Skip
1	0	0	0	-24.8	0	1	0
2	2	0	0	-24.8	0	1	0
3	4	0	0	-24.8	0	1	0
4	6	0	0	-24.8	0	1	0
5	8	0	0	-24.8	0	1	0
6	10	0	0	-24.8	0	1	0
7	12	0	0	-24.8	0	1	0
8	14	0	0	-24.8	0	1	0
9	16	0	0	-24.8	0	1	0
10	18	0	0	-24.8	0	1	0
11	20	0	0	-24.8	0	1	0
12	22	0	0	-24.8	0	1	0
13	24	0	0	-24.8	0	1	0
14	26	0	0	-24.8	0	1	0
15	28	0	0	-24.8	0	1	0
16	30	0	0	-24.8	0	1	0
17	32	0	0	-24.8	0	1	0
18	34	0	0	-24.8	0	1	0
19	36	0	0	-24.8	0	1	0
20	38	0	0	-24.8	0	1	0

Elec. 48    QP. 1217    Step. 2.0    Er. C. 0.01    Sq. Er. 1766    Alpha 0.0001    X = 5070, Z = 1275

**Pic 21** Data Grid of non remote electrodes;

X[m], Y[m], Z[m] are the surface coordinates,

Z(b) is the exploration depth,

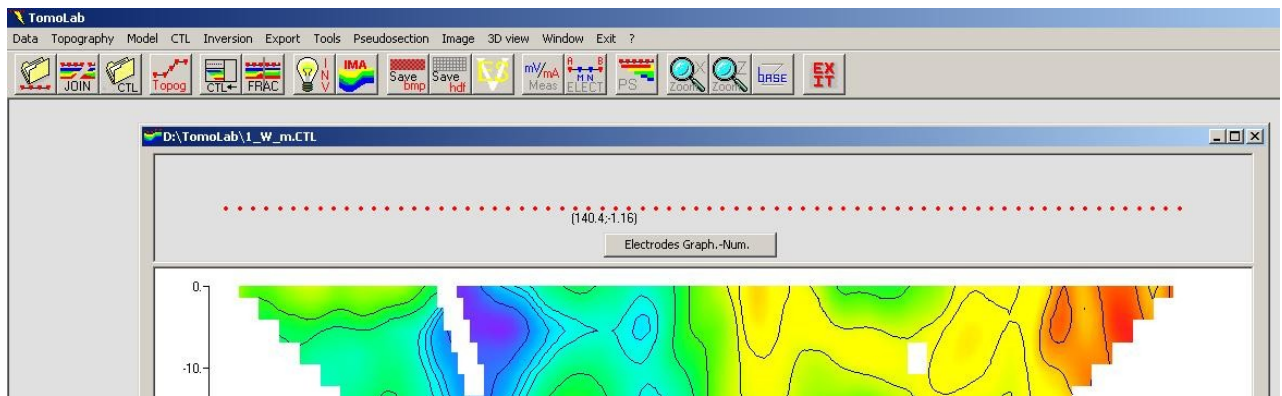
Z(t) is the quote of the topography (in case of floating electrodes Z[m] should be different from Z(t),

Mark = 1 means that electrode should be used as reference in interpolation, first and last electrodes must have Mark = 1,

Skip = 1 means that all the measurements involving the electrode will non included in the CTL

## Flip Electrodes

Swap the positions of an electrode's subset. In case the user has to reverse cable position (i.e. electrodes 1- 24) this function set the first electrode in the position of the 24<sup>th</sup> and the 24<sup>th</sup> in the first (swap 1 and 24), the 2<sup>nd</sup> in the 23<sup>th</sup> and vice versa, the 3<sup>rd</sup> in the 22<sup>th</sup> and so on. In order to view the effect of the flip operation, user can switch between two visualization option of the electrodes window by clicking the right mouse button.



**Pic. 22** Show popupmenu to change electrodes visualization



**Pic. 23** Electrodes as number 12 -18 are x position reversed

## Sort Electrodes by position

In case user needs to invert two or more sets of measurements carried out in the same area but not with the same set of electrodes, it is possible to join them by loading as roll along and specify the distance of the electrodes set. In order to view data as pseudosection user has to sort electrodes by position and the electrodes will be renamed following the x coordinate, also the k factor of each measurement will be recomputed.

## Load Results (.IMA) Rho

Load Rho results form an .IMA file selected by the user (non the default name space)

## Load Results (.IMA) IP

Load IP results form an .IMA file selected by the user (non the default name space)

## Load Results (.EVS)

Load results (Rho or IP) form an .EVS file saved with the default name space.

## Set Image Dimension (pixels)

In order to use TomoLab images in a report, user have to save it in bitmap format and manage images with any image processor software. TomoLab allows user to set the pixels dimension of the saved bitmap.

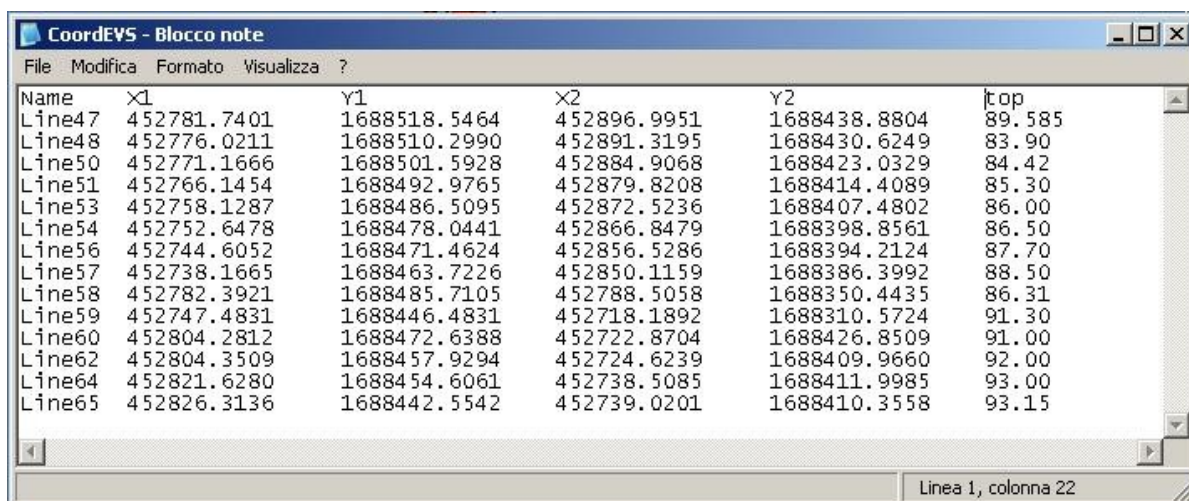
## Set Section Dimension (pixels)

The as Image Dimension, but the pixel specification acts only on the section (a sort of scale).



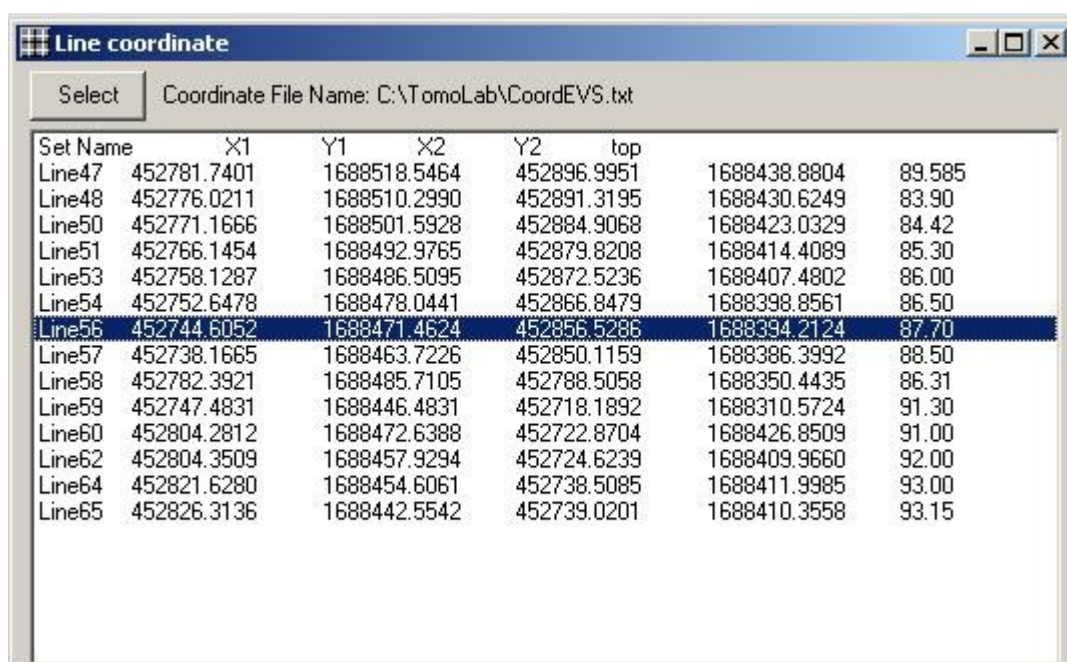
## Show Coordinate List

In order to append X, Y coordinate to the data user should load them from an ASCII file ordered in columns, space or tab separated.



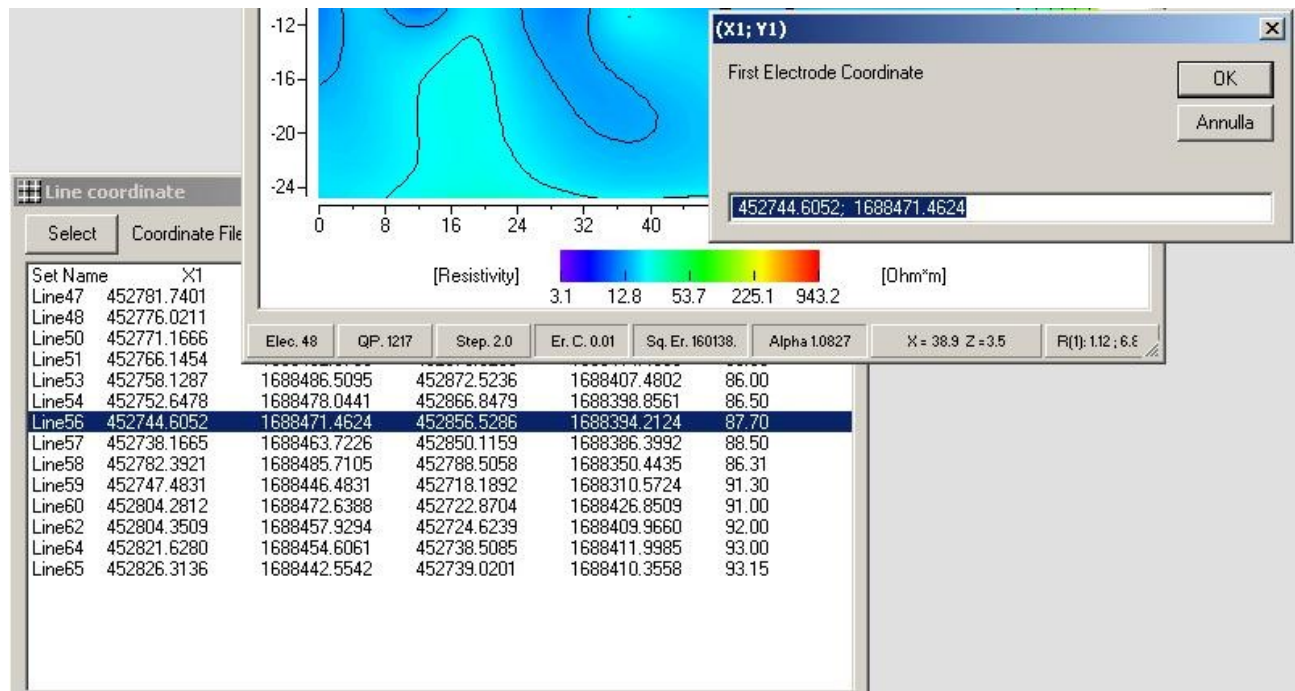
Name	X1	Y1	X2	Y2	top
Line47	452781.7401	1688518.5464	452896.9951	1688438.8804	89.585
Line48	452776.0211	1688510.2990	452891.3195	1688430.6249	83.90
Line50	452771.1666	1688501.5928	452884.9068	1688423.0329	84.42
Line51	452766.1454	1688492.9765	452879.8208	1688414.4089	85.30
Line53	452758.1287	1688486.5095	452872.5236	1688407.4802	86.00
Line54	452752.6478	1688478.0441	452866.8479	1688398.8561	86.50
Line56	452744.6052	1688471.4624	452856.5286	1688394.2124	87.70
Line57	452738.1665	1688463.7226	452850.1159	1688386.3992	88.50
Line58	452782.3921	1688485.7105	452788.5058	1688350.4435	86.31
Line59	452747.4831	1688446.4831	452718.1892	1688310.5724	91.30
Line60	452804.2812	1688472.6388	452722.8704	1688426.8509	91.00
Line62	452804.3509	1688457.9294	452724.6239	1688409.9660	92.00
Line64	452821.6280	1688454.6061	452738.5085	1688411.9985	93.00
Line65	452826.3136	1688442.5542	452739.0201	1688410.3558	93.15

**Pic 24** Longitude, Latitude Coordinate with Notepad.exe



Set Name	X1	Y1	X2	Y2	top
Line47	452781.7401	1688518.5464	452896.9951	1688438.8804	89.585
Line48	452776.0211	1688510.2990	452891.3195	1688430.6249	83.90
Line50	452771.1666	1688501.5928	452884.9068	1688423.0329	84.42
Line51	452766.1454	1688492.9765	452879.8208	1688414.4089	85.30
Line53	452758.1287	1688486.5095	452872.5236	1688407.4802	86.00
Line54	452752.6478	1688478.0441	452866.8479	1688398.8561	86.50
Line56	452744.6052	1688471.4624	452856.5286	1688394.2124	87.70
Line57	452738.1665	1688463.7226	452850.1159	1688386.3992	88.50
Line58	452782.3921	1688485.7105	452788.5058	1688350.4435	86.31
Line59	452747.4831	1688446.4831	452718.1892	1688310.5724	91.30
Line60	452804.2812	1688472.6388	452722.8704	1688426.8509	91.00
Line62	452804.3509	1688457.9294	452724.6239	1688409.9660	92.00
Line64	452821.6280	1688454.6061	452738.5085	1688411.9985	93.00
Line65	452826.3136	1688442.5542	452739.0201	1688410.3558	93.15

**Pic 25** coordinate file in TomoLab, item n. 7 selected



**Pic 26** Export results: use the coordinate of the selected item

## View Background

Display the background in the graph window

## Configuration

Show the configuration form

Pic 27 The configuration form

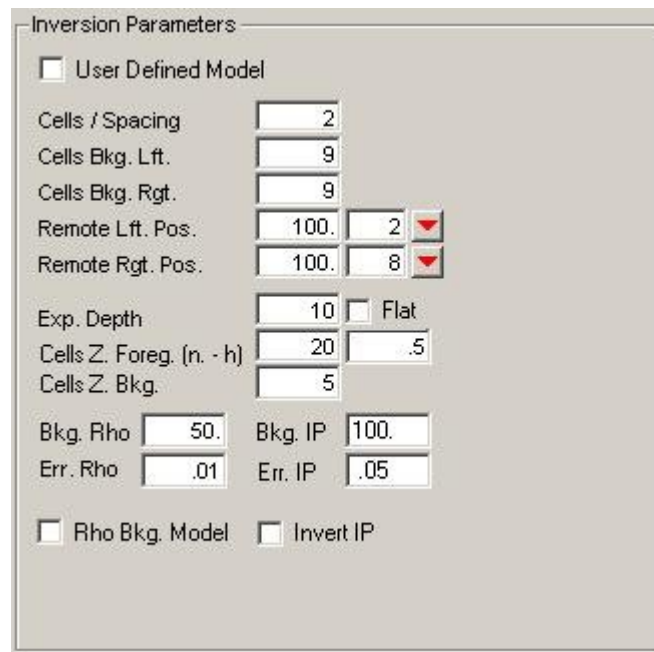
Pic 28 Data Filter Criteria

User can accept or refuse a measurement by using different criteria depending on the instrument, the site geology, the mean noise. In order to set an automatic filter to remove bad data from the CTL file user should determine many threshold limits. The current intensity  $I_{AB}$  is usually positive, the potential  $V_{MN}$  should have different signs depending on the quadrupole configuration, also the geometrical factor  $K$ . The constraint is that  $\rho = V_{MN}/I_{AB} \cdot K$  should be positive.

A measure should pass the filter if the following criteria are satisfied:

$ABS(V_{MN}) \geq V_{min}$	AND	$ABS(V_{MN}) \leq V_{max}$	AND
$ABS(I_{AB}) > I_{min}$	AND	$ABS(I_{AB}) \leq I_{max}$	AND
$q \geq q_{min}$	AND	$q \leq q_{max}$	AND
$\rho > \rho_{min}$	AND	$\rho \leq \rho_{max}$	AND
$m \geq m_{min}$	AND	$m \leq m_{max}$	AND
$K \geq K_{min}$	AND	$K \leq K_{max}$	

**Note:**  $ABS(I_{AB}) > I_{min}$  to ensure  $I_{AB} > 0$ ,  $\rho > \rho_{min}$  to have positive  $\rho$

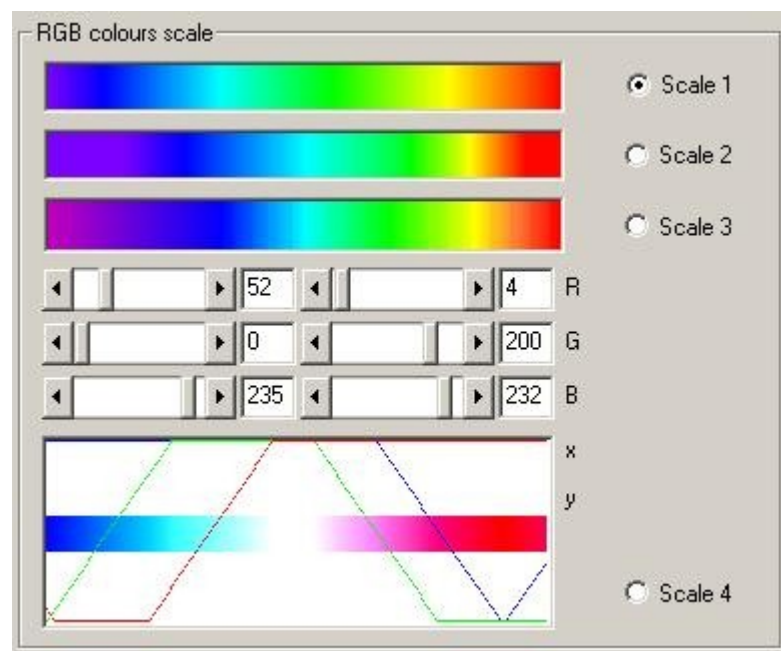


The 'Inversion Parameters' dialog box contains the following settings:

- ☐ User Defined Model
- Cells / Spacing: 2
- Cells Bkg. Lft.: 9
- Cells Bkg. Rgt.: 9
- Remote Lft. Pos.: 100. 2 (dropdown)
- Remote Rgt. Pos.: 100. 8 (dropdown)
- Exp. Depth: 10 ☐ Flat
- Cells Z. Foreg. (n. - h): 20 .5
- Cells Z. Bkg.: 5
- Bkg. Rho: 50. Bkg. IP: 100.
- Err. Rho: .01 Err. IP: .05
- ☐ Rho Bkg. Model ☐ Invert IP

**Pic 29** Inversion Fix Parameters

In order to invert a set of arrays with the same inversion parameters, it is possible to define the base parameter in the configuration form and check the User Defined Model. If this option is true, when creating the CTL, TomoLab will not ask for parameters and create the CTL file with the parameters defined in the configuration form. The meaning of each field has been already given.



The 'RGB colours scale' dialog box shows four color scales and their corresponding RGB values:

- ☒ Scale 1: Standard rainbow scale.
- ☐ Scale 2: Inverted rainbow scale.
- ☐ Scale 3: Another variation of the rainbow scale.
- ☐ Scale 4: User-defined scale.

For Scale 4, the RGB components are defined by scroll bars with the following values:

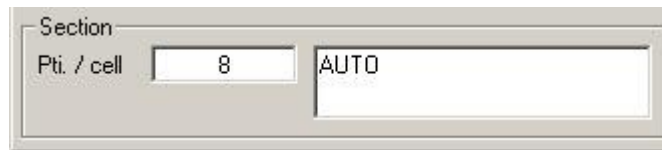
- R: 52 (range 0 to 255)
- G: 0 (range 0 to 255)
- B: 235 (range 0 to 255)

A preview window shows the resulting color gradient across a rectangular area.

**Pic 30** Colours scale

It is possible to choose among four rainbow scale. Scale 1, 2, 3 are fixed. The scale 4 is user defined. Moving the scroll bars of the RGB components a custom scale is created in the picture.

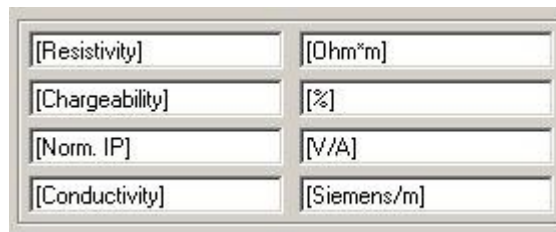
When TomoLab display an inversion result or a pseudosection the colour scale is automatically set on the data limits, in case of user defined limits, value below the minimum of the scale are plotted with the same colour, so for data over the maximum of colour scale.



**Pic 31** Section options

Few options could be set from the configuration form:

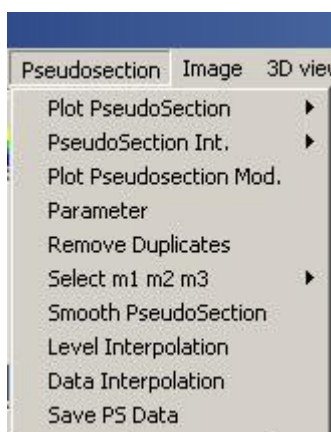
- Pti./cell (Points per cell): the default plot fine interpolate between adjacent cells using a number of points specified in this frame
- AUTO: means that the contour plot range automatically from min and max of data values, this option draw 15 level lines. Other option are allowed, "AUTOR" means that level lines range between limits of colour scale, otherwise it is possible to specify min, max and step of contour plot by a control string ("50:10:150;", means first level line at 50 ohm\*m, last level line at 150 ohm\*m, spacing of the other lines is 10 ohm\*m). The AUTO option range over a logarithmic scale, the string option range over a linear scale



**Pic. 32** Section Labels

Picture results use default labels defined at configuration form. User can change them. Each couple of label are associated to [resistivity], [chargeability], [norm. Inductively Polarization ], [conductivity]

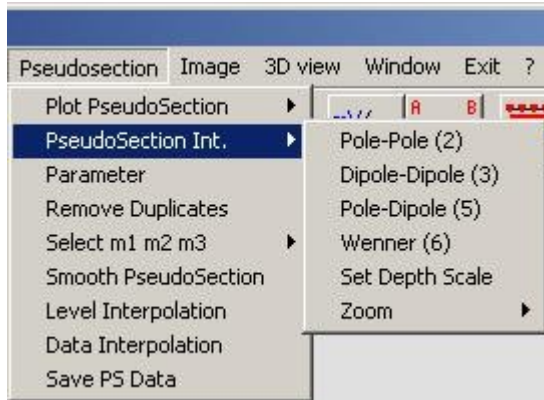
## Menu Pseudosection



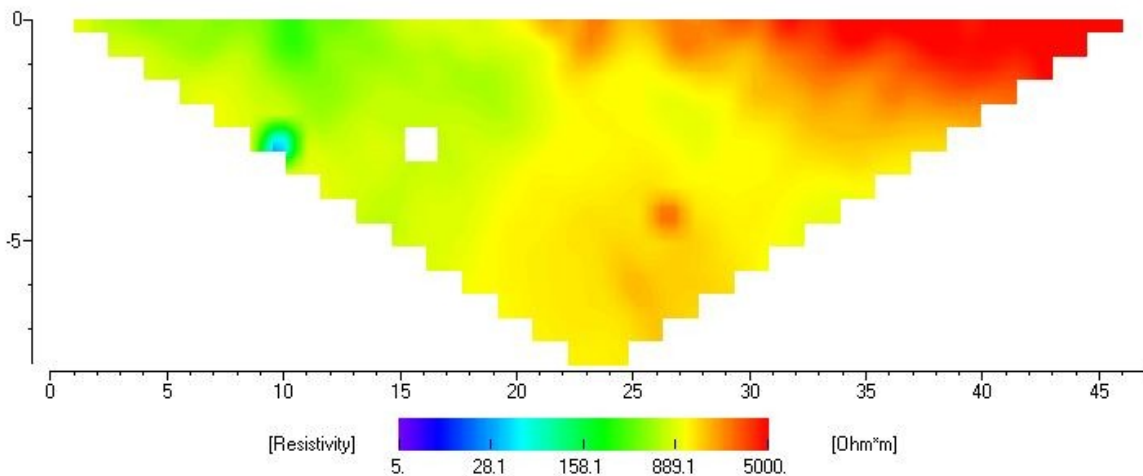


The Pseudosection is conventional way to plot measurements as far each data would be representative of about a cell with a definite X and Z coordinate.

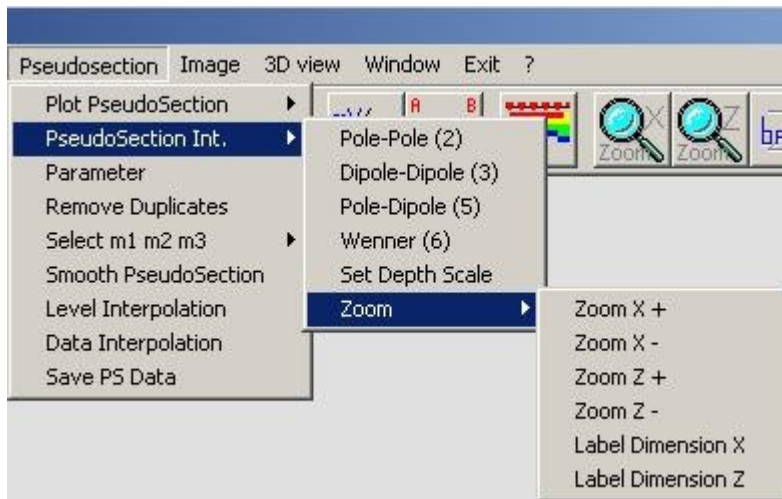
TomoLab allow user to plot data as pseudosection in two different ways. The first one is a normal plot, a couple of coordinate (X, Z) are assigned to each quadrupole, the X coordinate is the average of X coordinate of the non remote electrodes in the quadrupole, the Z is a function of the quadrupole aperture  $a$ , the order  $n$  and a specific coefficient  $k$  depending on  $a$ ,  $n$  and quadrupole array, this coefficient has been calculates from sensitivity maps and has been tabulated by Locke.



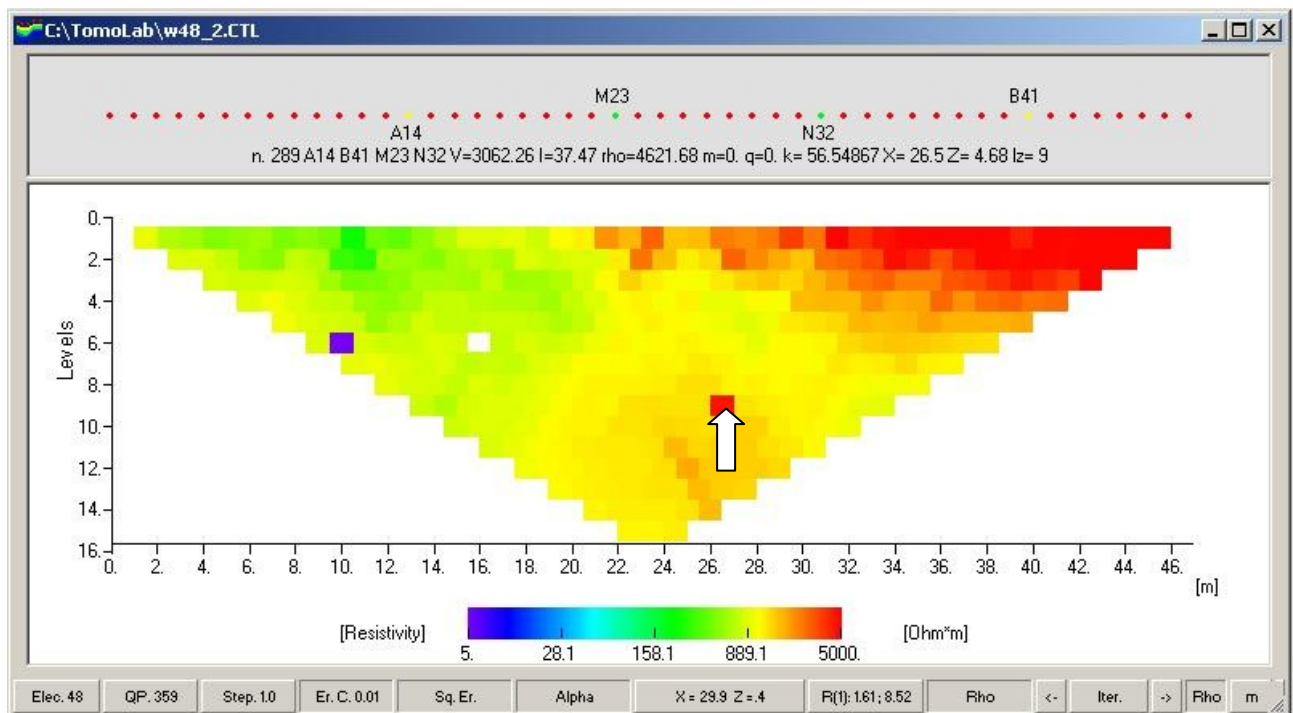
As far that data sets should include different array types, user have to choose the one has to be plotted



**Pic 33** Wenner array – pseudosection plot



The second way to plot a pseudosection is the "Pseudosection Interactive". Each measurement is shown as a label ordered by level. As you RgtClick over a label the quadrupole will be highlighted. Double-click on a label remove the measurements from the pseudosection. This action set the skip value to a progressive non zero integer number, user can undo skip with the CTRL+Z keys combination. When creating the CTL file the measurements with the skip flag major than zero will be discarded.

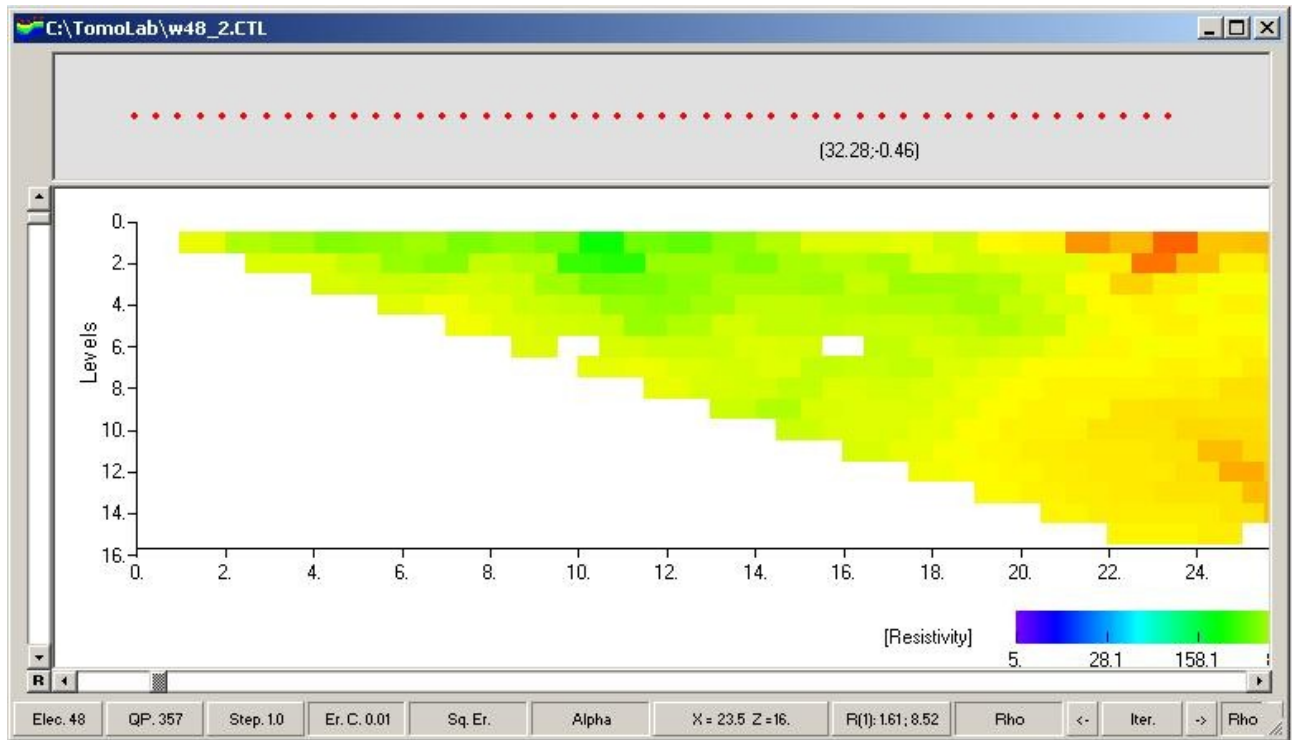


**Pic 34** Rgt. mouse down (arrow), highlight electrodes



## Zoom X+

Large data set cannot be analyzed in a standard window, this function double the x dimension of graph window and allow user to scroll image with a bar. This function act also on inversion results



**Pic 35** graph window doubled n X

## Zoom X-

This function divide by two the x dimension of graph window, if the graph window is still wider than the container, user can scroll image with a bar. This function act also on inversion results



## Zoom Z+

As for as Zoom X+.

## Zoom Z-

As for as Zoom X-.



## Reset Zoom

Reset image to standard window and remove the scroll bars.



## Label Dimension X

Double the x dimension of the label representing measurements in pseudosection, useful when a level is not complete

## Label Dimension Z

Double the z dimension of the label representing measurements in pseudosection, useful when many levels are not complete

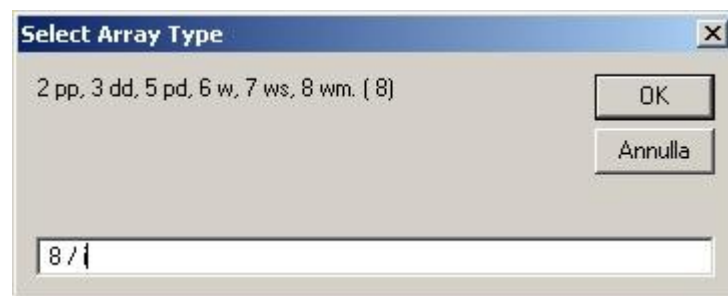
## Plot PseudoSection Mod.

It is possible to plot the modeled measurements as pseudosection (if only the specific option have been selected in the inversion). The modeled data are used to calculate the objective function (chi-square).

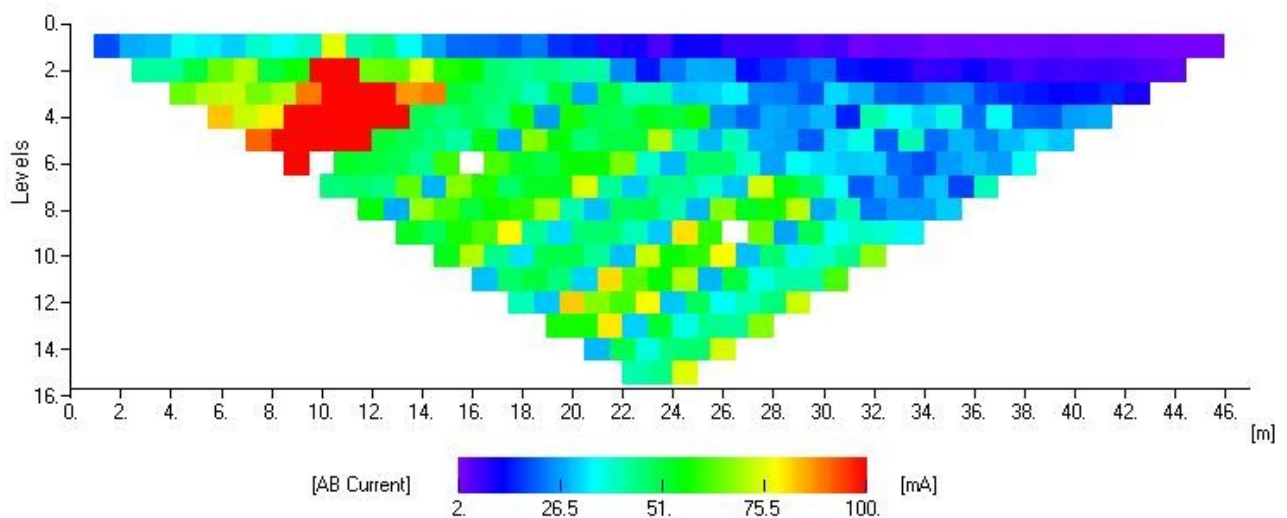


### Parameter

TomoLab can plot as pseudosection many parameters other than the Rho. User can select a parameter by the dialog box.



**Pic 36** Pseudo Section - select the current AB as parameter



**Pic 37** AB current as pseudosection

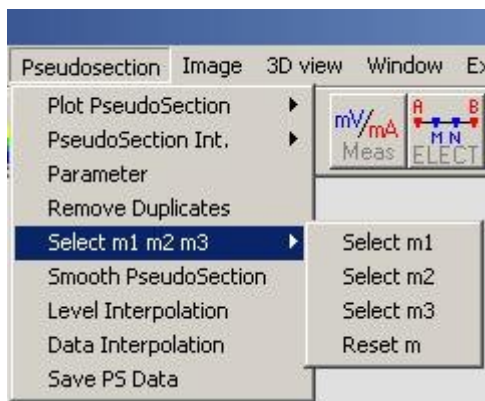
Following the list of the parameters allowed in pseudosection Plot:

Parameter	string	color scale
-----------	--------	-------------

- resistivity	/ RHO	logarithmic
- abs(resistivity)	/ ABSRHO	linear
- AB current	/ I	linear
- MN potential	/ V	linear
- Self Potential	/ SP	linear
- V/I ratio	/ VI	linear
- error	/ Q	linear
- chargeability	/ MM	linear
- chargeability window 1	/ M1	linear
- chargeability window 2	/ M2	linear
- chargeability window 3	/ M3	linear
- Inductively Polarization	/ IP	linear
- IP window 1 ( $m1*v/i$ )*100	/ IP1	linear
- IP window 2 ( $m2*v/i$ )*100	/ IP2	linear
- IP window 3 ( $m3*v/i$ )*100	/ IP3	linear
- Conductivity ( $1/RHO$ )	/ COND	logarithmic
- Electrode A	/ A	linear
- Electrode B	/ B	linear
- Electrode M	/ M	linear
- Electrode N	/ N	linear

## Remove Duplicates

Some measurements set may have measurements duplicate. In order to speed up the inversion process it's necessary to remove one or more duplicates. Before this operation data would be sorted by levels and x position

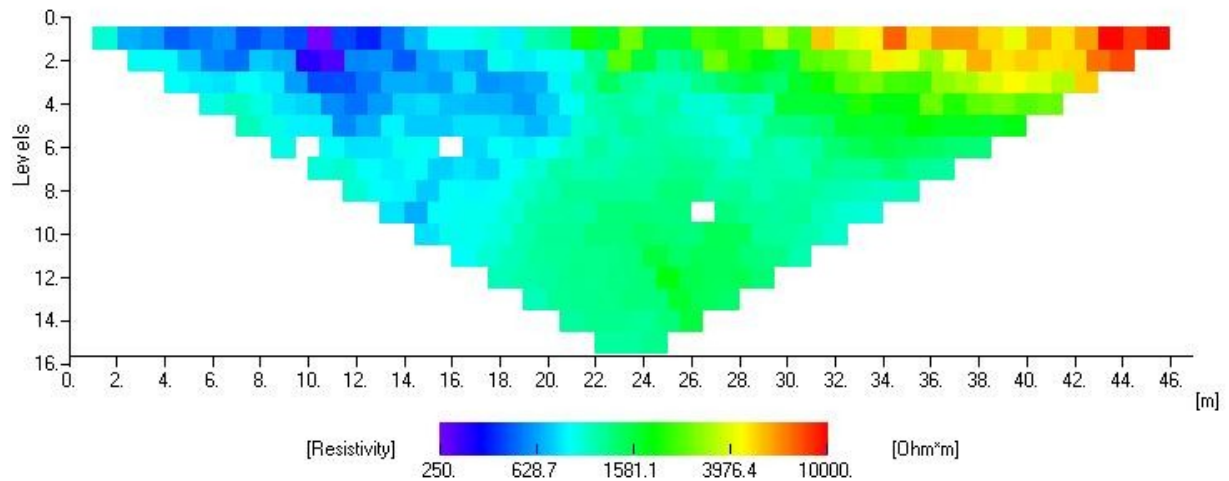


## Select m1 m2 m3

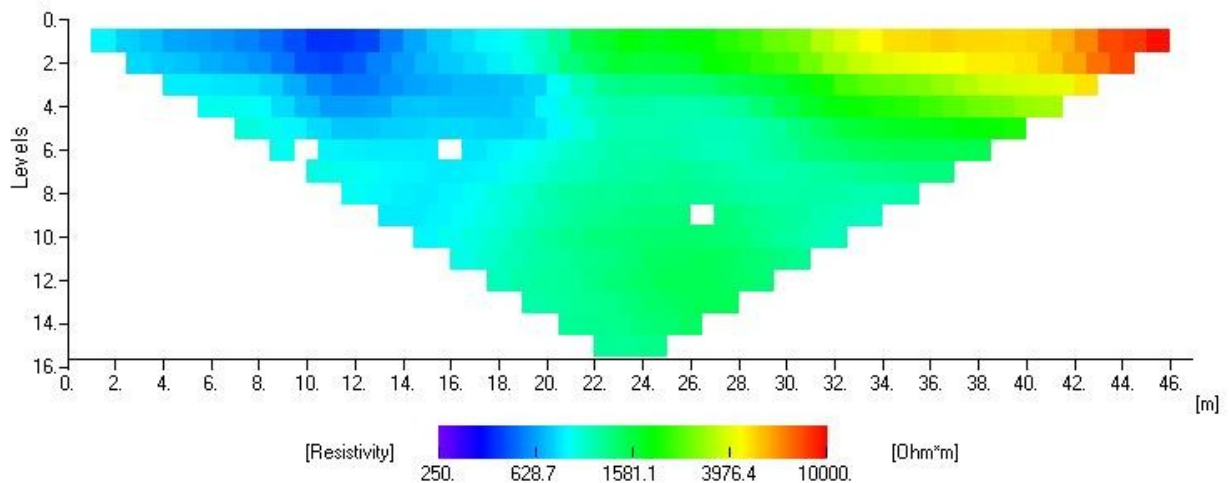
The chargeability value used by is the a data averaged over three time windows got by the Syscal. Sometimes happens that data from a single window seems better than the averaged one. This function allows user to select a time window and use the specific chargeability value in CTL and IP calculation.

## Smooth Pseudosection

Some data sets may need a smooth process in order to reduce noise. This process acts on the rho value and recalculate the  $v_{MN}$  value.



**Pic 38** Pseudosection before smooth process

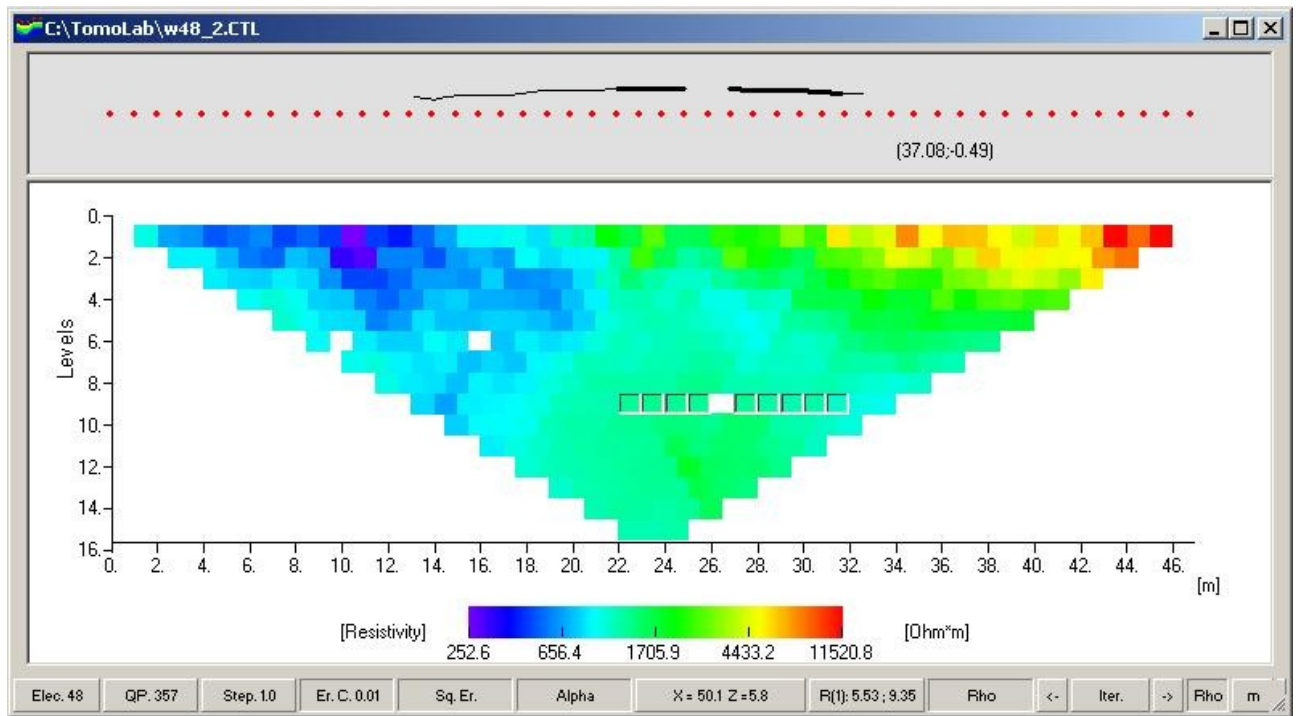


**Pic 39** Pseudosection after smooth process

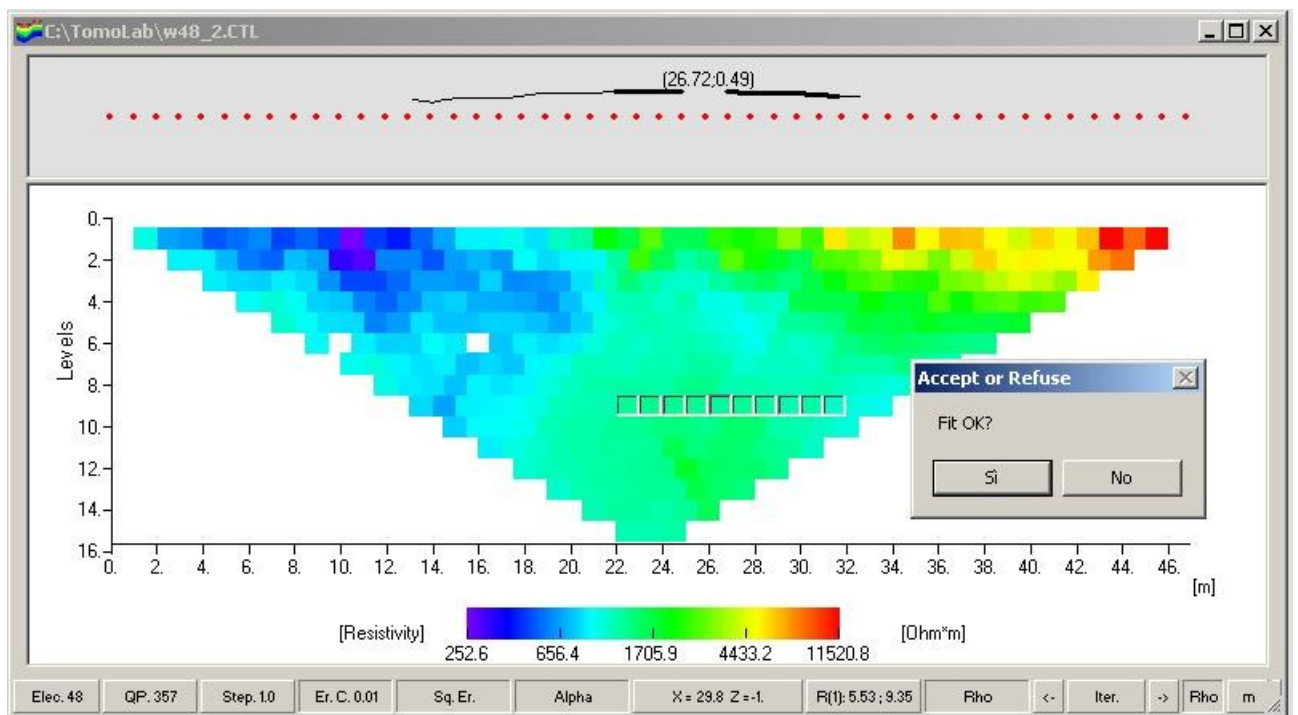
## Level Interpolation

For study purpose it is possible to fill/correct bad pseudosection data points.

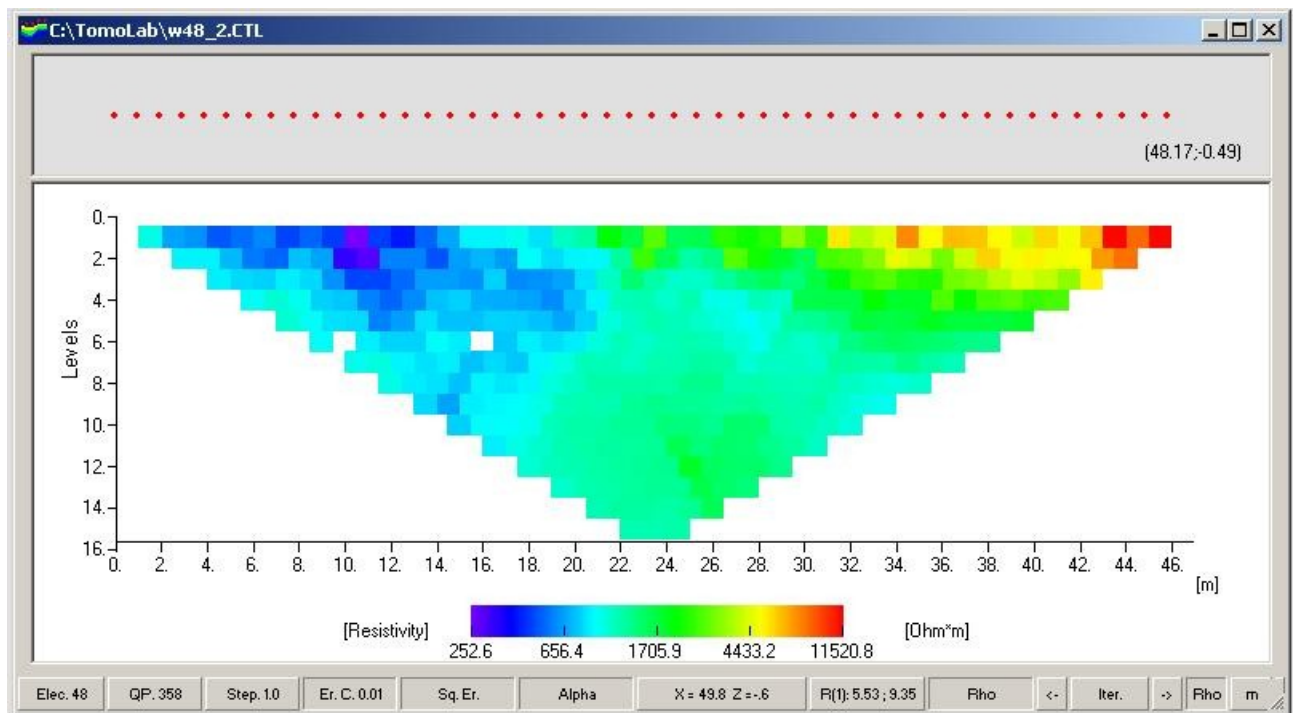
- Combine Alt key with LeftMouse to select two group of data around the measurement you want to correct (or generate if it's missing), data will be 3D highlighted;
- Select the level interpolation, TomoLab interpolate the region between the selected data with a polynomial function ( $3^{\circ}$ )
- Accept or refuse results. If accept measurements between the selected regions are modified/generate according to fit results (modify  $\rho$ , recalculate  $v$  according the  $i$  value).



**Pic 40** Pseudosection with two group of data highlighted (357 quadrupoles)



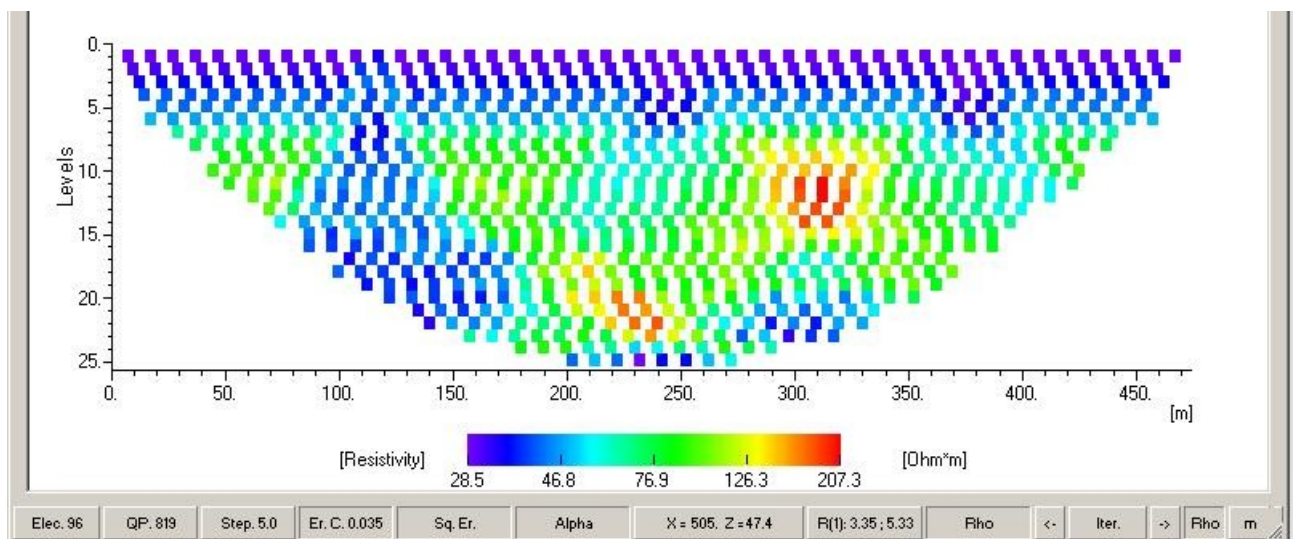
**Pic 41** Pseudosection with the fit results and dialog box



**Pic 42** Pseudosection with the "new" measures (358 quadrupoles)

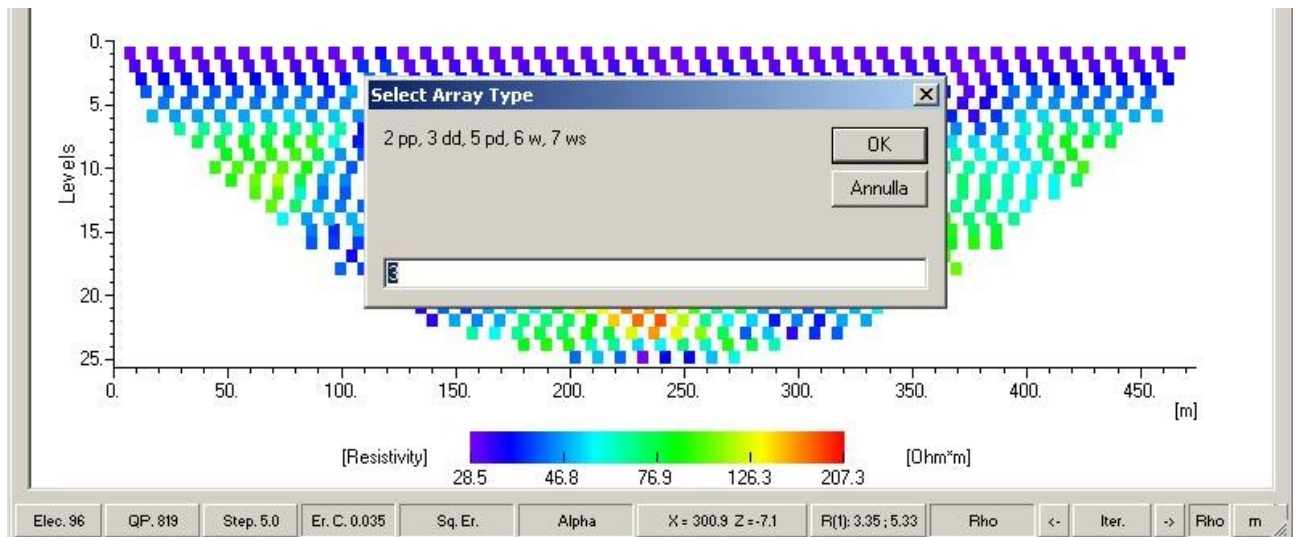
## Data Interpolation

The procedure described above should be used also for the entire pseudosection. To do this it's important to feed TomoLab with the information about the data set

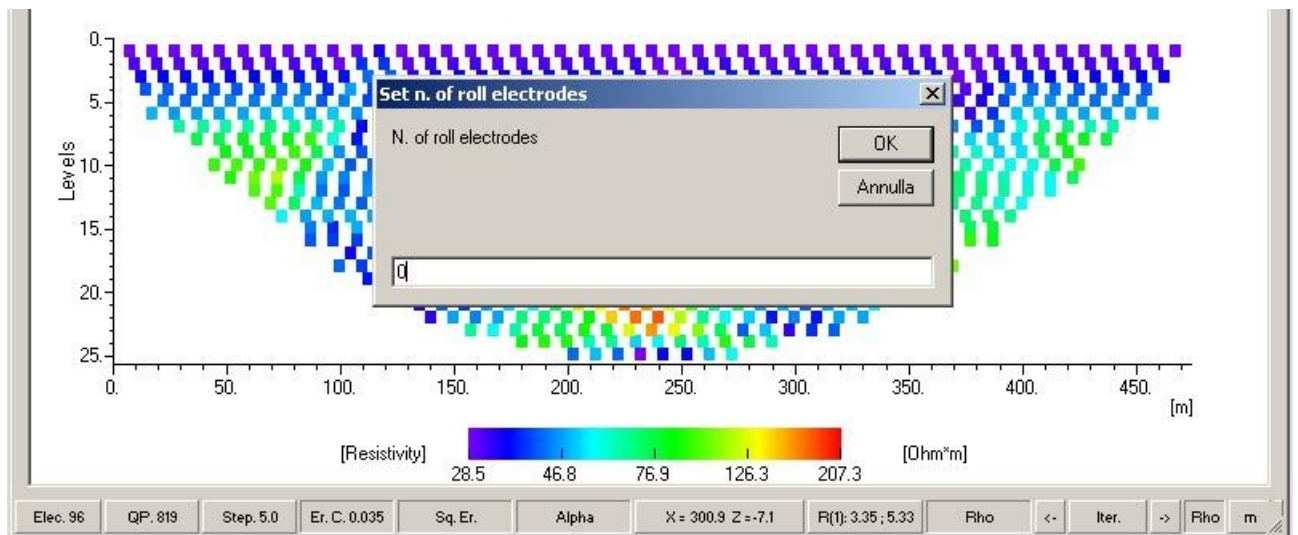


**Pic 43** Dipole-Dipole pseudosection - 819 quadrupoles

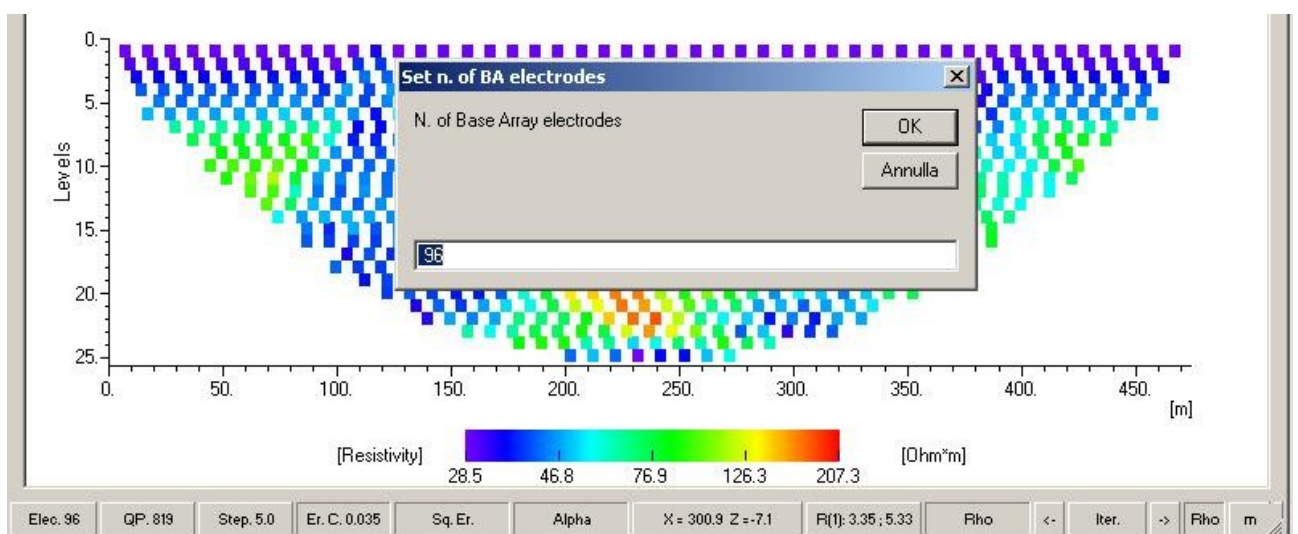




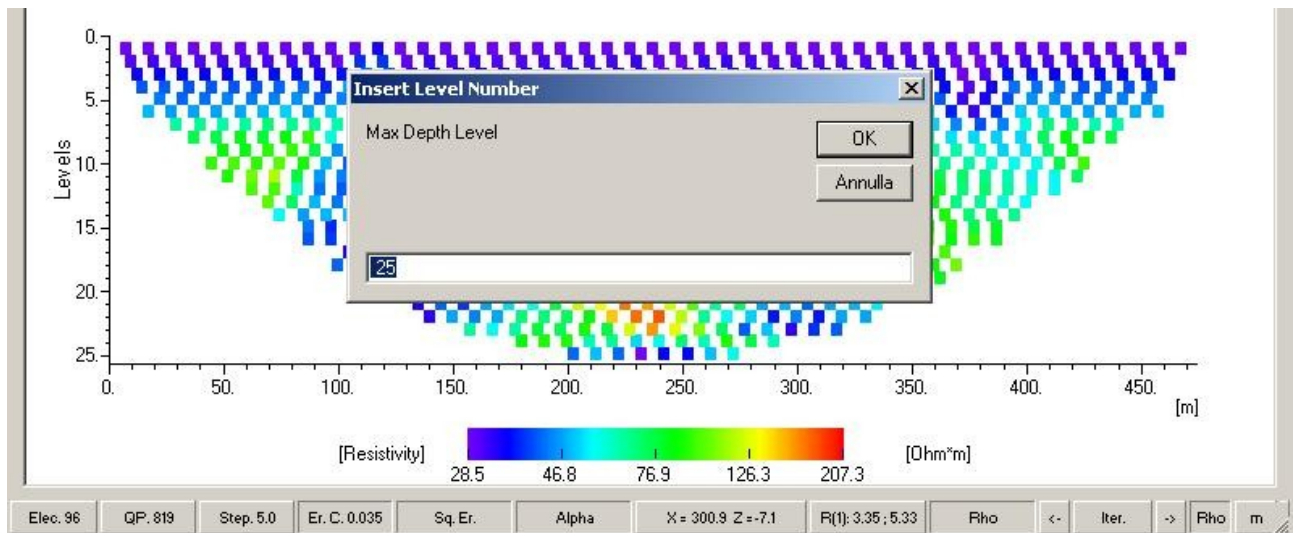
Pic 44 Select Array type to interpolate (3 dd)



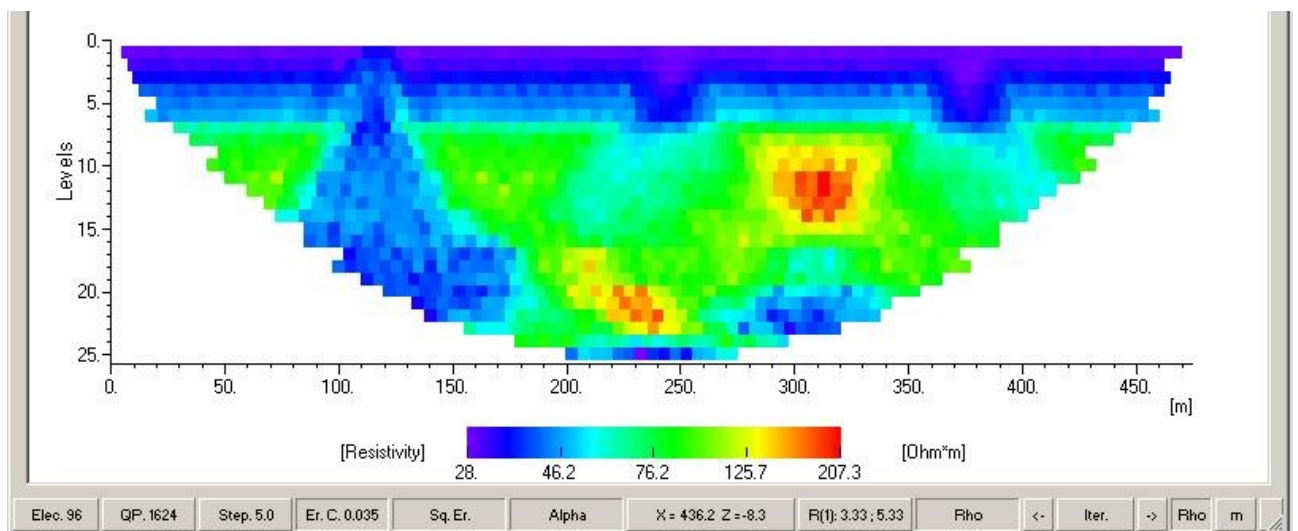
Pic 45 Set the number of roll electrodes



Pic 46 Set the number of electrodes in base array (before roll)



**Pic 47** Set the number of levels have to be interpolated

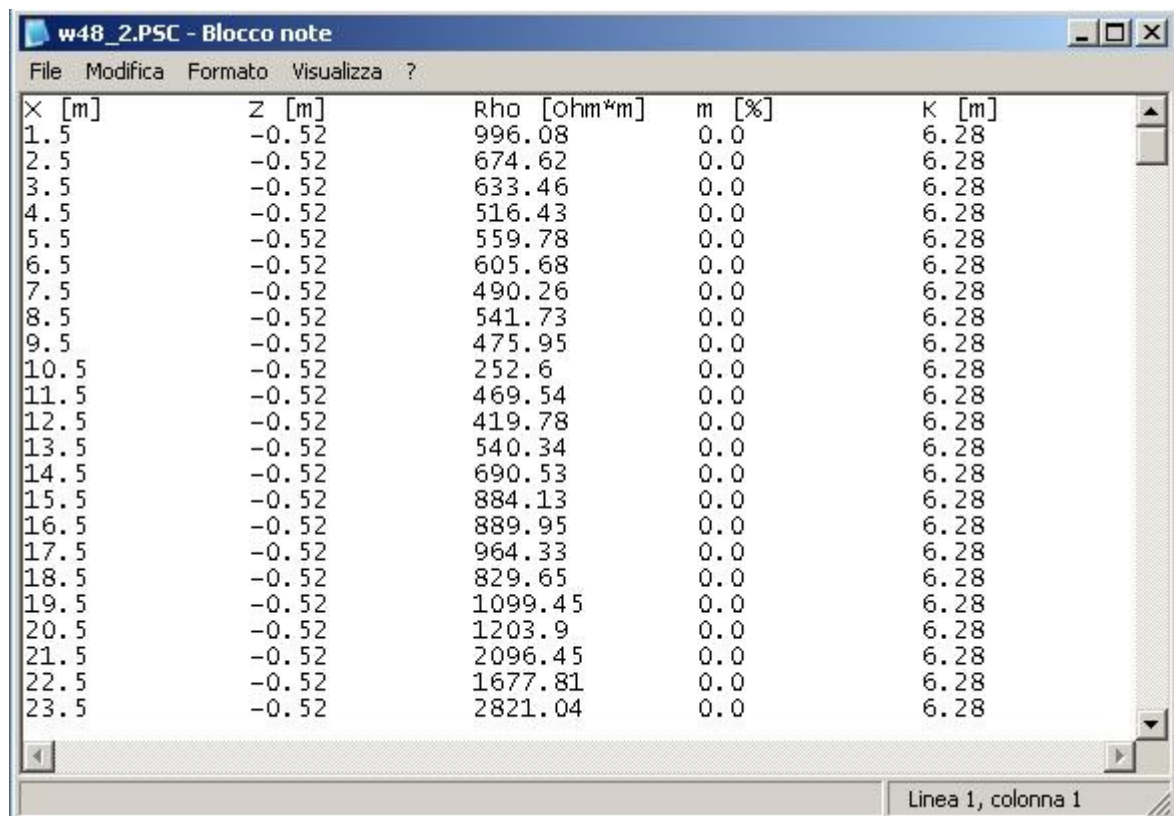


**Pic 48** Pseudosection after the interpolation 1624 quadrupoles

## Save PS data

Pseudosection data should be used in other software. This function create an ASCII file with the extension .PSC with the data of the pseudosection ordered in columns.

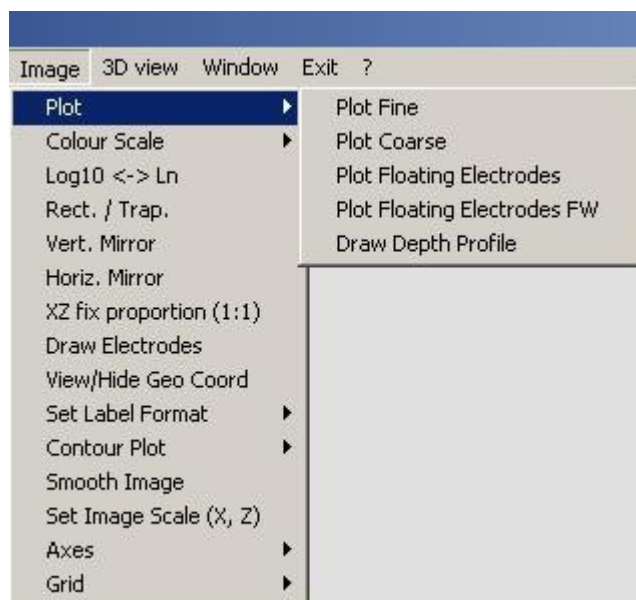




X [m]	Z [m]	Rho [Ohm*m]	m [%]	K [m]
1.5	-0.52	996.08	0.0	6.28
2.5	-0.52	674.62	0.0	6.28
3.5	-0.52	633.46	0.0	6.28
4.5	-0.52	516.43	0.0	6.28
5.5	-0.52	559.78	0.0	6.28
6.5	-0.52	605.68	0.0	6.28
7.5	-0.52	490.26	0.0	6.28
8.5	-0.52	541.73	0.0	6.28
9.5	-0.52	475.95	0.0	6.28
10.5	-0.52	252.6	0.0	6.28
11.5	-0.52	469.54	0.0	6.28
12.5	-0.52	419.78	0.0	6.28
13.5	-0.52	540.34	0.0	6.28
14.5	-0.52	690.53	0.0	6.28
15.5	-0.52	884.13	0.0	6.28
16.5	-0.52	889.95	0.0	6.28
17.5	-0.52	964.33	0.0	6.28
18.5	-0.52	829.65	0.0	6.28
19.5	-0.52	1099.45	0.0	6.28
20.5	-0.52	1203.9	0.0	6.28
21.5	-0.52	2096.45	0.0	6.28
22.5	-0.52	1677.81	0.0	6.28
23.5	-0.52	2821.04	0.0	6.28

Pic 49 File .PSC

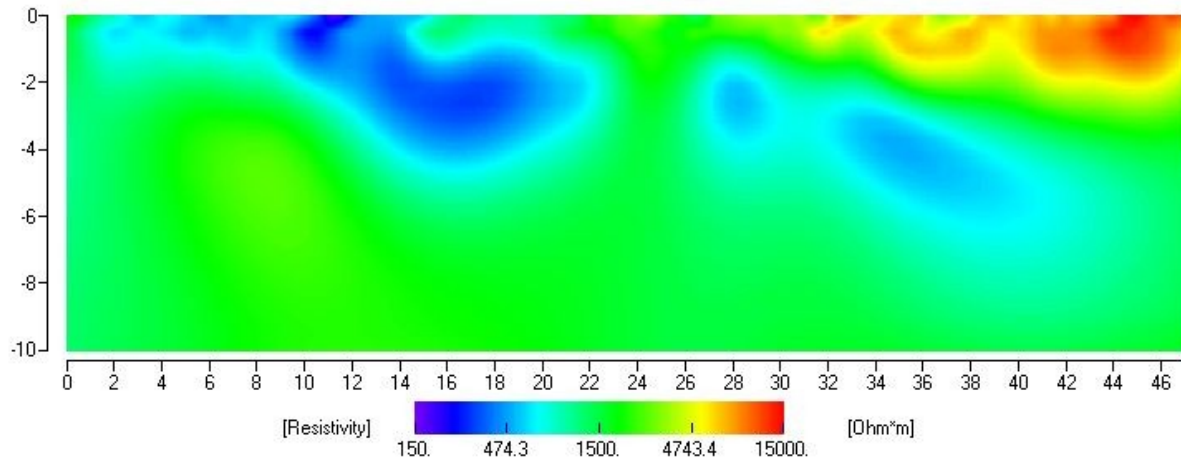
## Menu Image



There are four ways of drawing the inversion results, each mode seems to be appropriate in different situation.

## Plot Fine

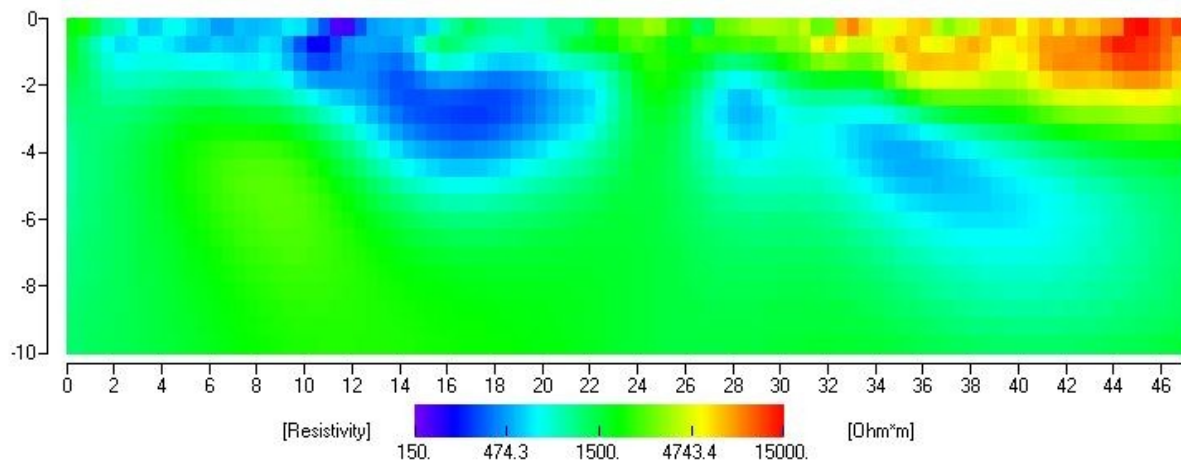
This is the standard mode to draw the inversion results (or pseudosection), each resistivity cell is linear interpolated at plot time with the first neighbouring.



**Pic 50** Plot Fine (default, graphic interpolation between adjacent cells, no contour line)

## Plot Coarse

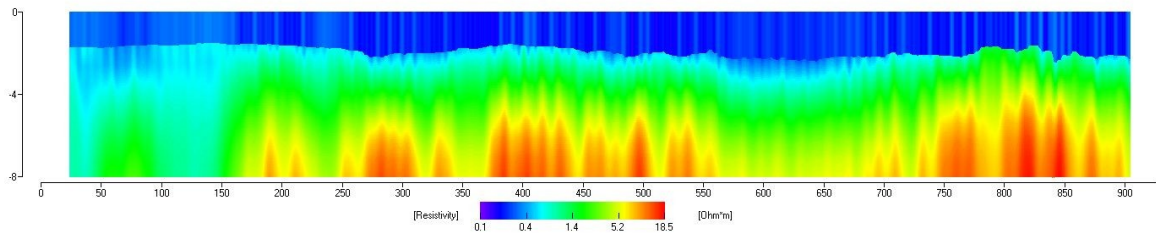
Allow to plot results or pseudosection) without interpolation. TomoLab draw each cell a block with uniform colour



**Pic 51** Plot Coarse (no graph interpolation between adjacent cells)

## Plot Floating Electrodes

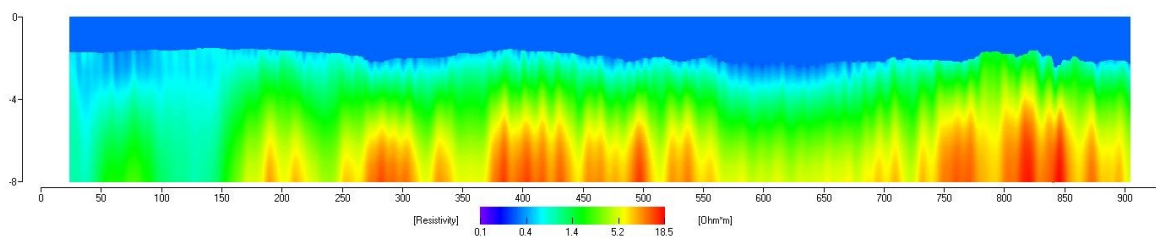
The same as Plot Fine, in this case the mesh definition should take into account that the topography information is related to water depth and, in general, the water should be modelled with a single cell.



**Pic 52** - Plot floating electrodes, the first cell is not interpolated

## Plot Floating Electrodes FW

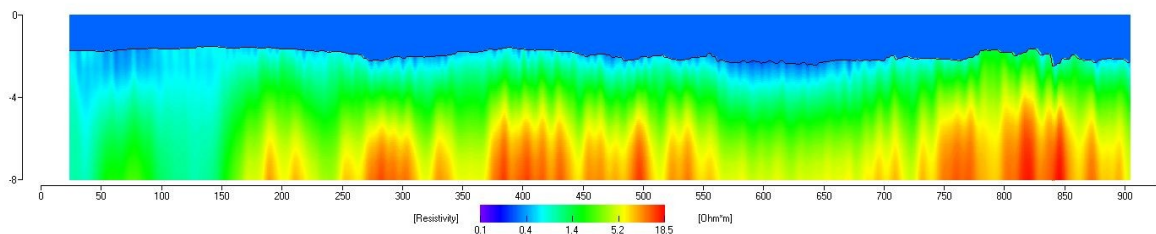
The same as Plot Floating Electrodes, in this case, cells representing the water have been plotted as uniform value (the level median value).



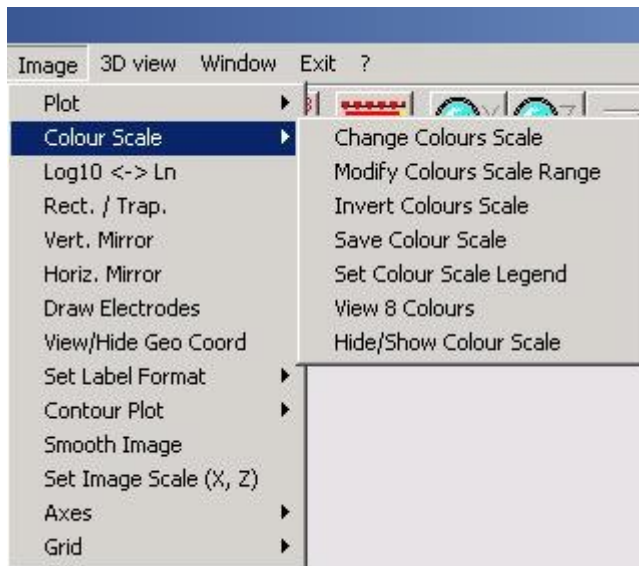
**Pic 53** Plot Floating Electrodes, the first cell is fixed

## Draw Depth

Add to the image a line of the water depth profile acquired with echo sounder and stored as quote Z of the electrodes.



**Pic 54** Add a line at the water-soil interface

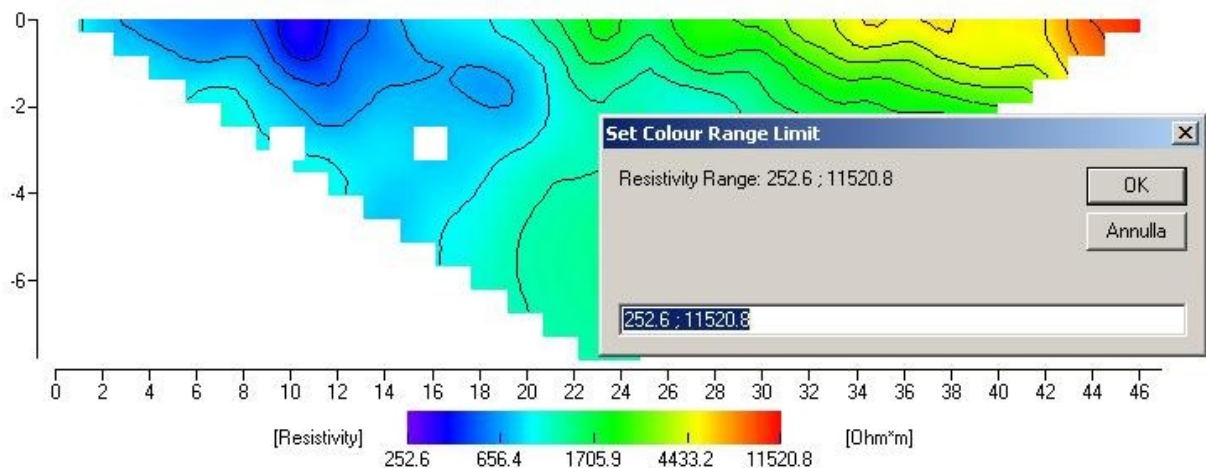


## Change Colour Scale

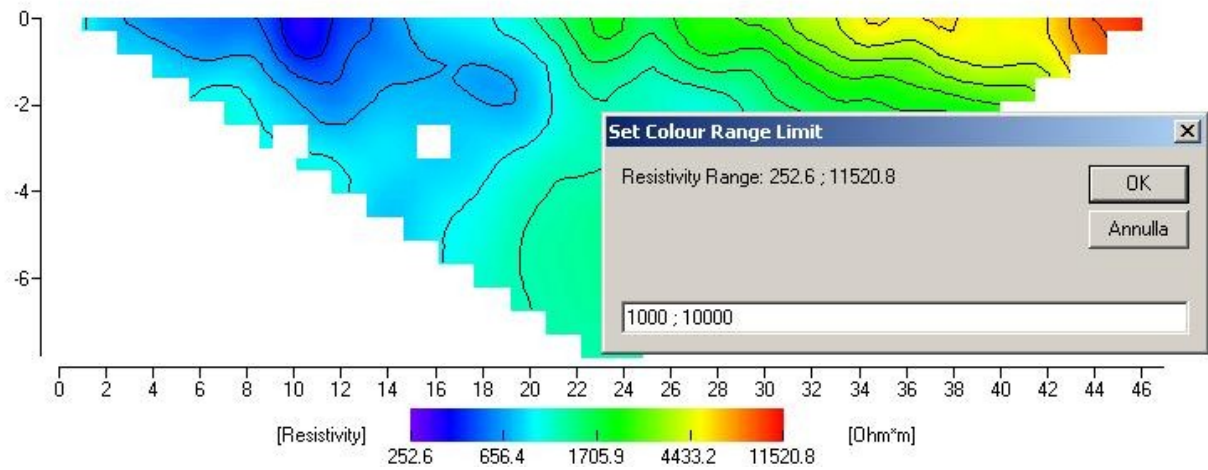
Turn the current colour scale from the four available

## Modify Colours Scale Range

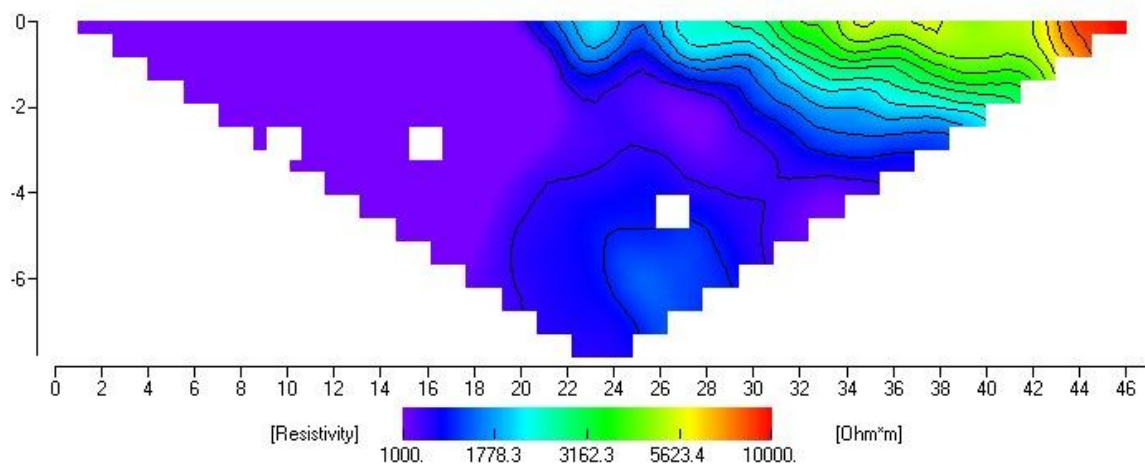
The current colour scale range automatically on the data minimum and maximum, so it's possible to set limits and rescale image colours. Measurements greater than the upper limit of the colour scale will be represented with the same colour of the upper value, the ones lower than the low limit will be plotted as the limit.



**Pic 55** - Default pseudosection plot ad colour scale limits



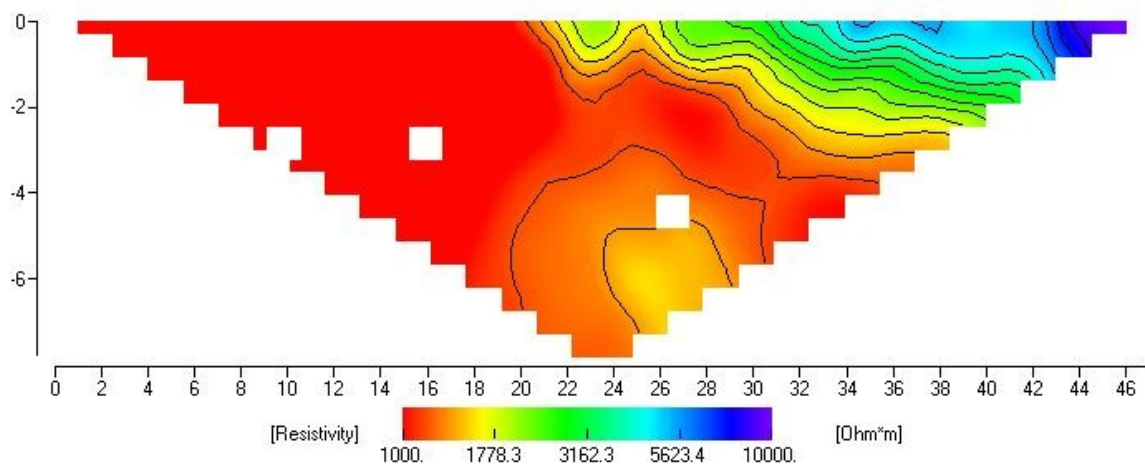
**Pic 56** Pseudosection Plot and new colour scale limits



**Pic 57** Pseudosection Plot using the new colour scale limits

## Invert Colour Scale

Reverse the colour scale



**Pic 58** Pseudosection plot with a reverse colour scale



## Save Colour Scale

Export the 250 colour value into an ASCII file named rainbow.dat

## Set Colour Scale Legend

Following the convention of VB or VBA it's possible to set a format string for colour scale legend

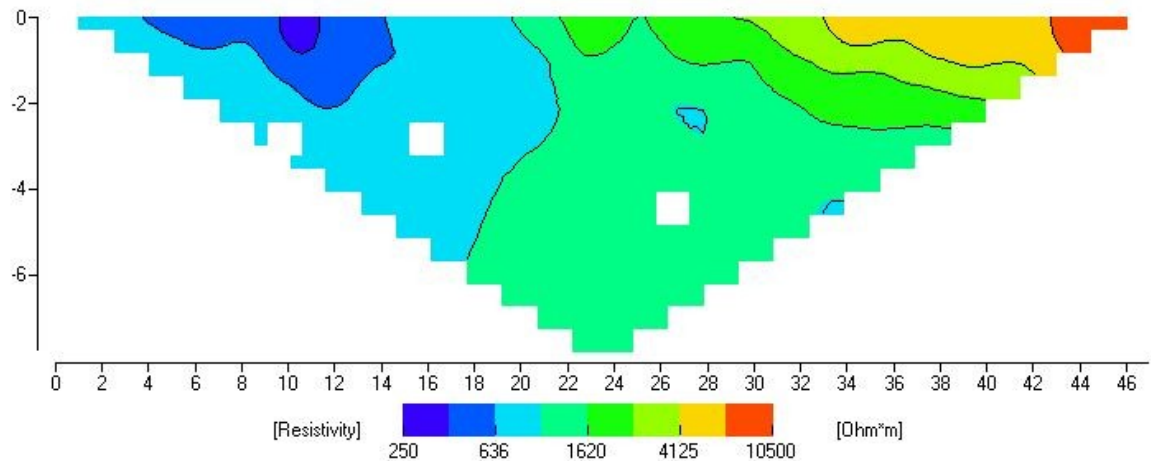
<i>Format</i>	<b>Positiv 5</b>	<b>Negativ 5</b>	<b>Decimal 0,5</b>	<u>Null</u>
Zero lenght string ("")	5	-5	0.5	
0	5	-5	1	
0.00	5.00	-5.00	0.50	
#,##0	5	-5	1	
#,##0.00;;;None	5.00	-5.00	0.50	None
\$#,##0;(\$#,##0)	\$5	(\$5)	\$1	
\$#,##0.00;(\$#,##0.00)	\$5.00	(\$5.00)	\$0.50	
0%	500%	-500%	50%	
0.00%	500.00%	-500.00%	50.00%	
0.00E+00	5.00E+00	-5.00E+00	5.00E-01	
0.00E-00	5.00E00	-5.00E00	5.00E-01	



**Pic 59** Colours Scale Legend Format String

## View 8 Colours

Set an eight colour scale based on the current colour scale



**Pic 60** Pseudosection plot using the 8 colours scale

### Hide/Show Colour Scale

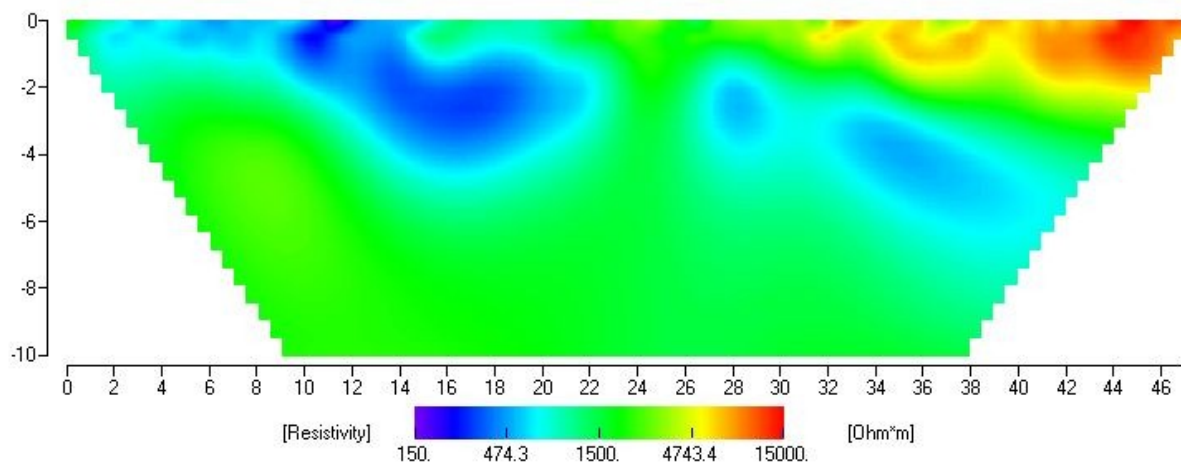
The default plot include the colour scale. With this function user should include or remove the colour scale from the image

### Log10 <-> Ln

Switch from base 10 logarithm and natural logarithm

### Rect / Trap

Switch from the default plot of the results (entire mesh) as a rectangle and different level of trapezoid

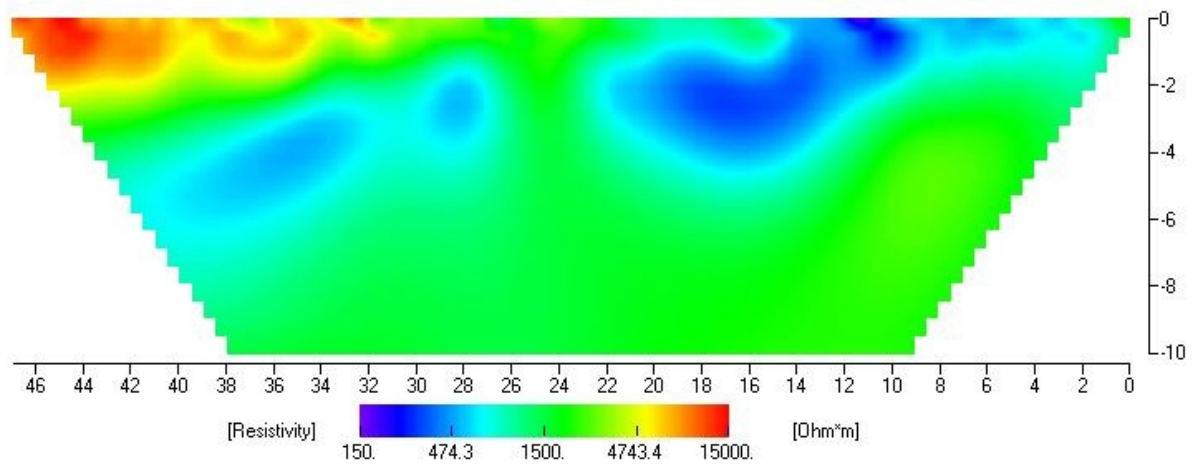


**Pic 61** Image Results (trapezoid 2)

### Vert. Mirror

Flip the image vertically





**Pic 62** Results Image flipped vertically

### Horiz. Mirror

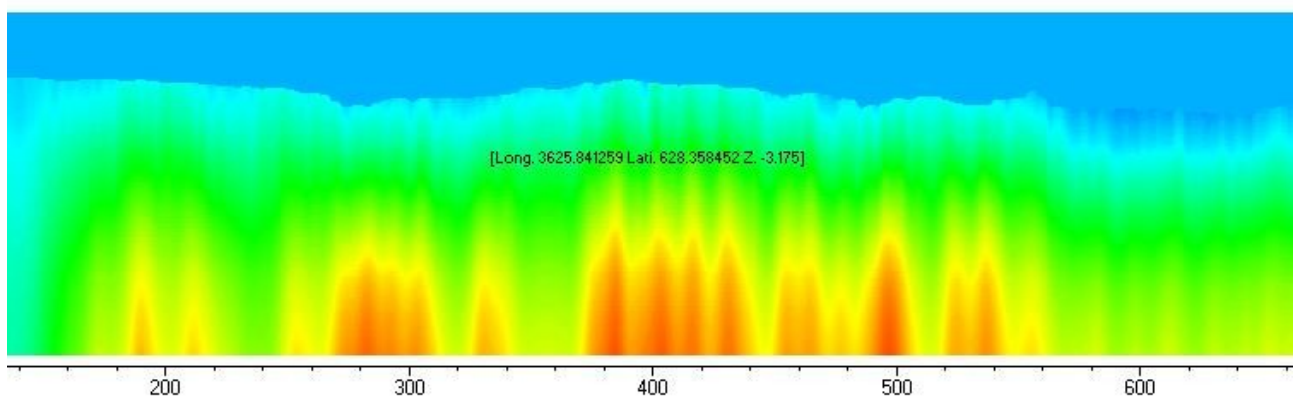
Flip image data horizontally. This option is quite different from the Vert. Mirror command because if the Vert. Mirror just rotate the point of view of 180°, the Horiz. Mirror flip data along Z axis. This option is useful when different data have to be collected inside TomoLab (the tomlab Z standard axis is a quote, so position under the ground level would be negative. In case position under the ground level were represented as depth, i.e. z positive, this option reset to the standard mode)

### XY Fix proportion

Set the ratio between scale x and y to 1.

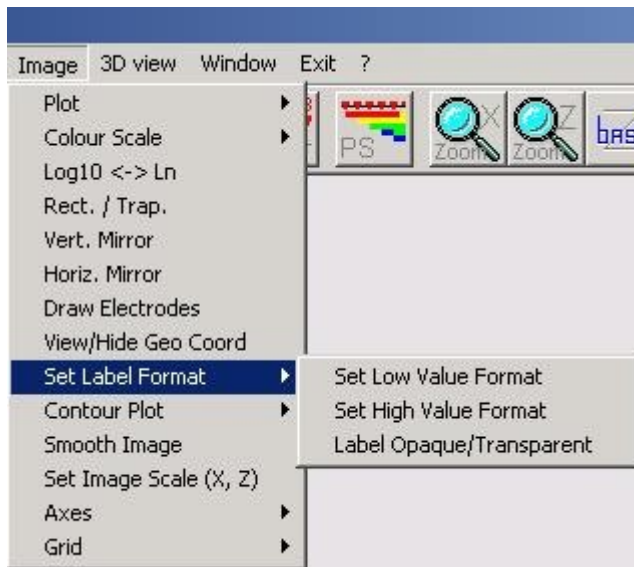
### View/Hide Geo Coord

In case of georef measurements it is possible to display the Lat. Long. data at the mouse move.



**Pic 63** Floating Electrodes Image with geo coord.

## Set Label Format



The combination of Shift + RgtMouse add a label to image (Shift + RgtMouse over the label just remove it). The label caption is the value of rho under the mouse pointer. The caption format follows these rules:

Value $\leq 1$	→ format as "Low Value format"
$1 < \text{value} \leq 10$	→ 1-2 digits
$10 < \text{value} \leq 100$	→ 2-3 digits round 5
$100 < \text{value} \leq 500$	→ 3 digits round 50
Value $> 500$	→ round 50, format as "High Value Format"

### Set Low Value Format

Set the caption format for value less than 1.

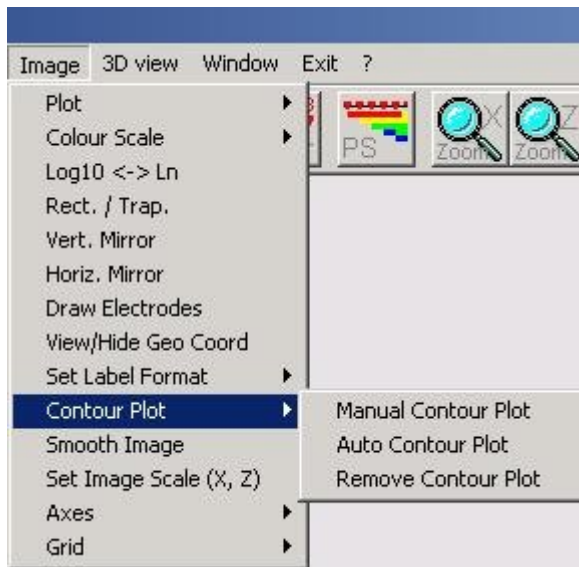
### Set High Value Format

Set the caption format for value greater than 500.

### Label Opaque/Transparent

TomoLab default set the caption background to opaque white, this function set the label background to transparent.

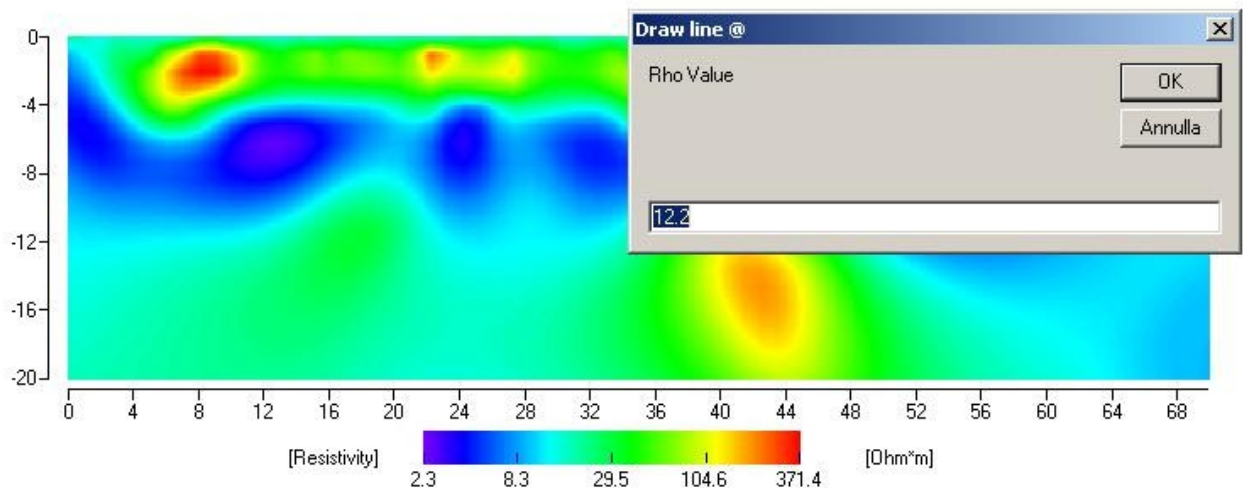
## Contour Plot



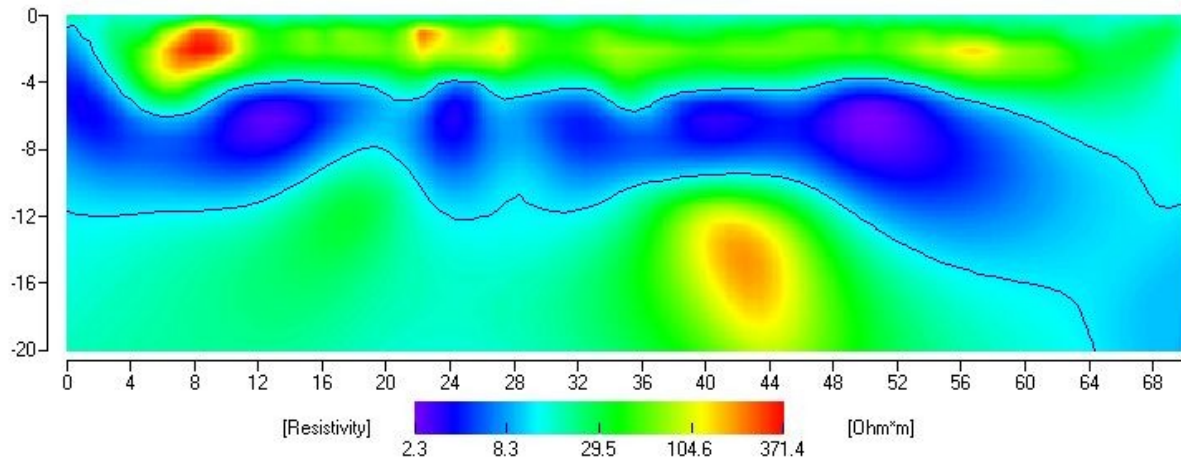
### Manual Contour Plot

Activate the option to add single level line to current image. This function works with combination of keys and mouse:

- Shift+LeftMouse* draw a level line over the entire image at the value under the mouse pointer.
- Ctrl+Shift+LeftMouse* open a dialog box to set the level of the line to plot



**Pic 64** Set the level (12.2) to draw a contour line



**Pic 65** Contour line at 12.2  $\Omega \cdot m$

### Auto Contour Plot

Add contour plot to image. The contour mode is defined in the configuration form. The default is 15 lines ranging over image value limits

### Remove Contour Plot

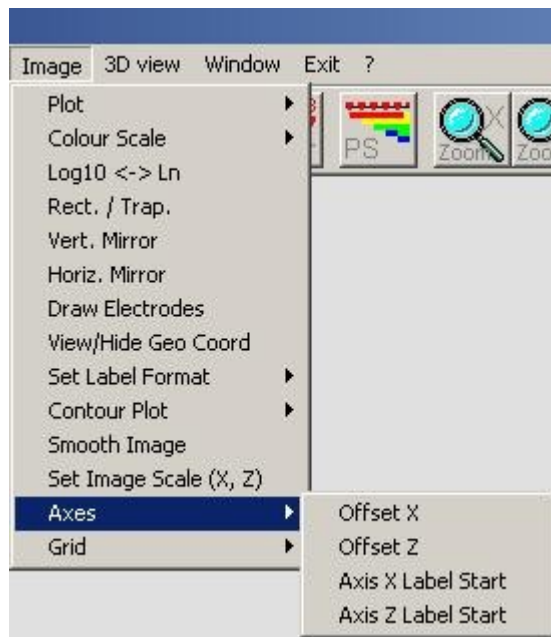
Draw image without the contour plot

### Smooth Image

Smooth image through a moving average. User should set the width of the moving window by set the x and z point. These value can range from 0 (no smooth) to half of section points. This operation works at graphics level and doesn't alter the measurements.

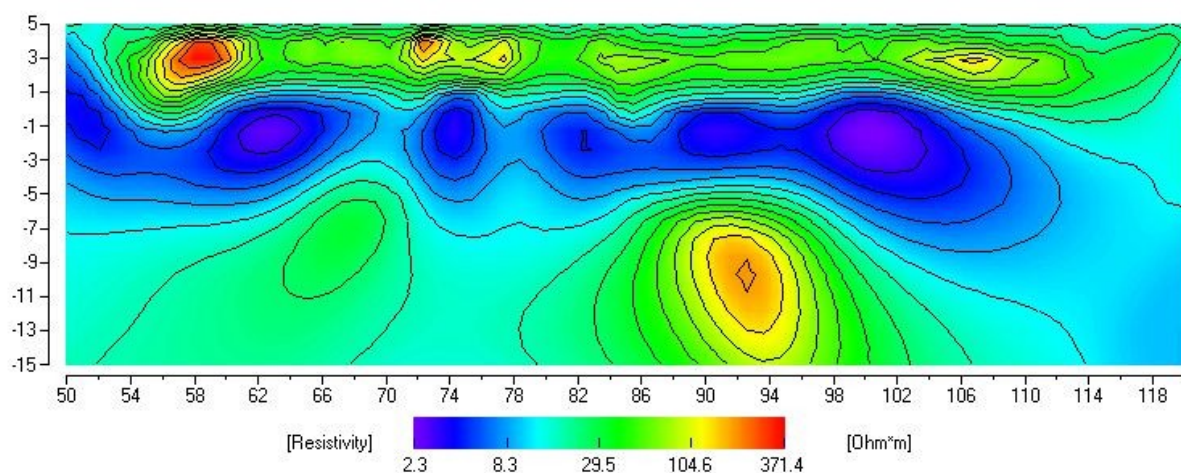
### Set Image Scale (X, Z)

Set the scale size one to nnnn and TomoLab create an image with the scale specified. Example: Setting "200" for X scale, means that the saved bitmap form the image will have a scale 1 to 200, each cm of the image represent 2 m of the reality. Set both scales to 1, reset the scale to the default: image fit to window, no scale.



## Offset X, Offset Z

Add an offset to axes coordinate at image result level.

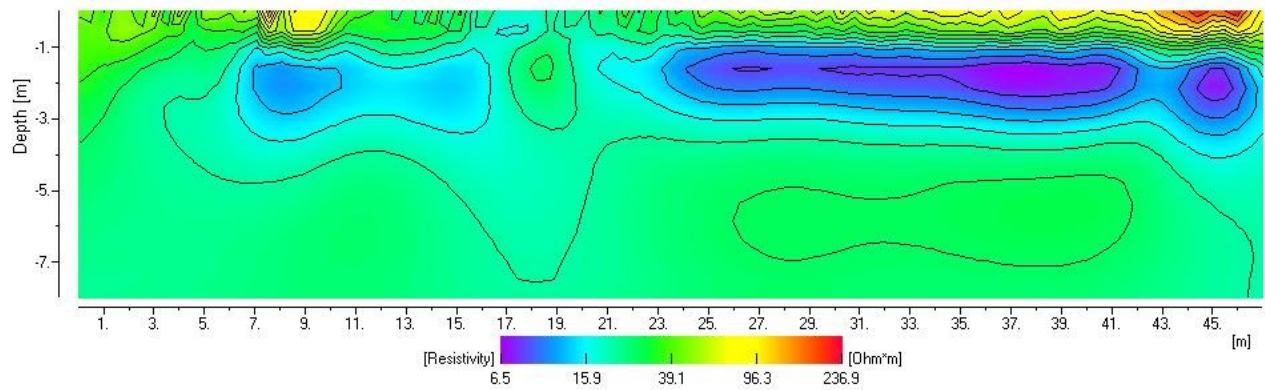


**Pic 66** Image, axes with offsets, 50 for X and 5 for Z

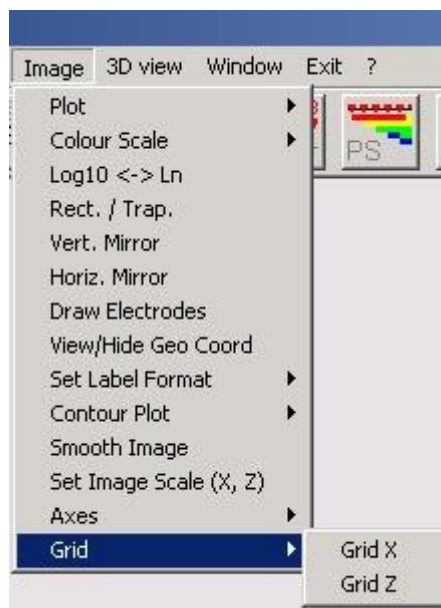
## Axis X Label Start (Axis Z Label Start)

Allow user to set first label value that will be plot in the axis (user can set label step and minor tick by using the command in the status bar).



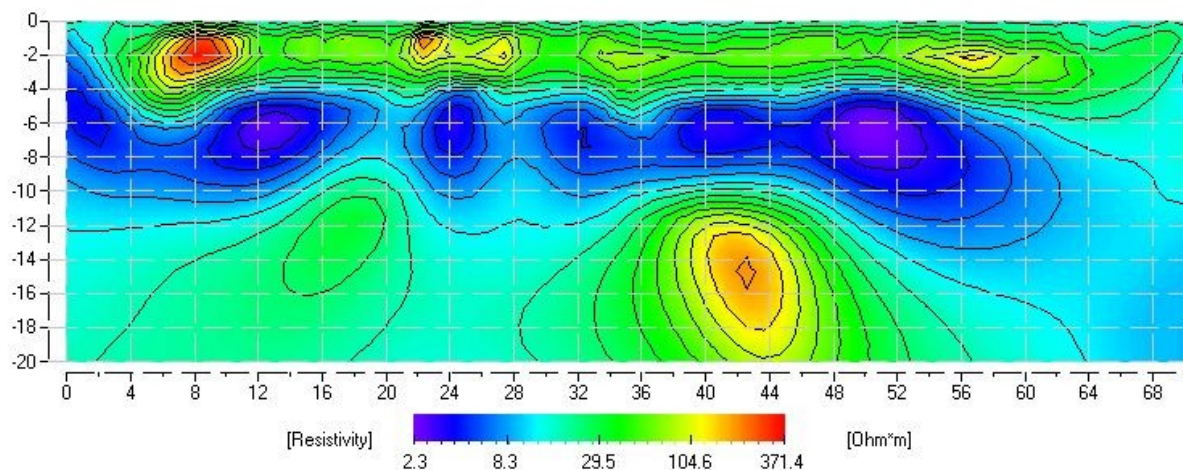


**Pic 67** Image, axes with X labels starting at 1, Z labels starting at -1



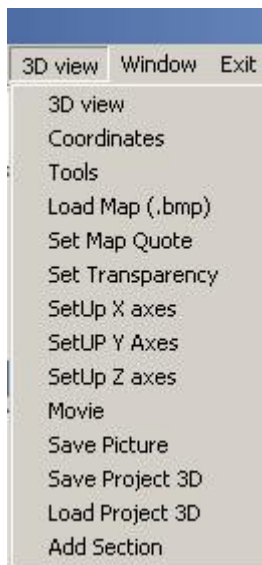
## Grid X, Grid Z

Add horizontal and/or vertical line to image results at value of major tick in both axes

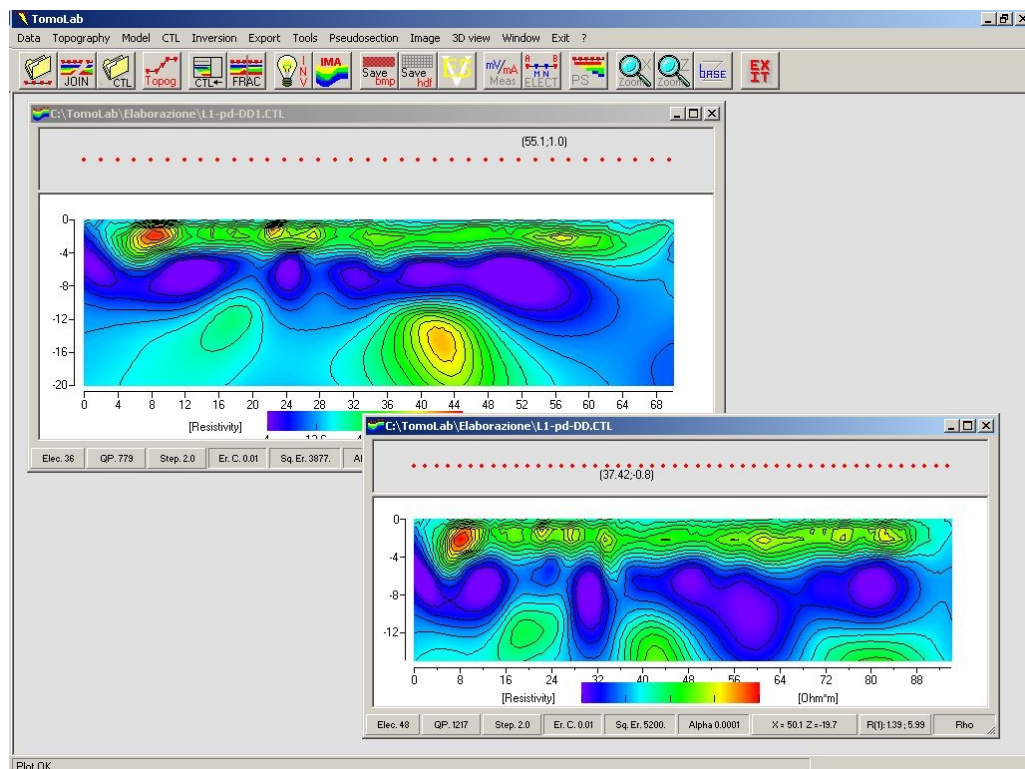


**Pic 68** Grid X and Grid Z

## Menu 3D view

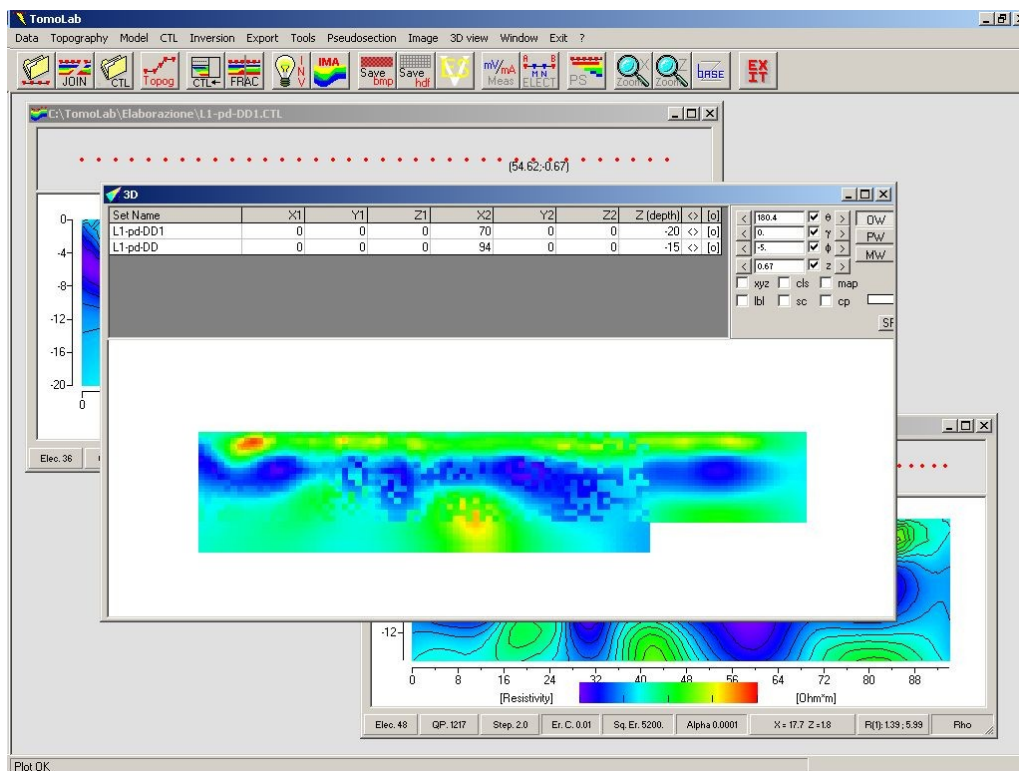


The function of menu 3D allows user to display image results (or pseudo sections) of about more than one in a three-dimensional environment. Data from every active windows in TomoLab were collect into a single data structure and plot in 3D (orthographic view or perspective view). Information of about relative coordinates should be insert at design time or loaded from an external ASCII file. Using these functions it is possible to verify the agreement between sections that cross each other and create image of the results in 3D

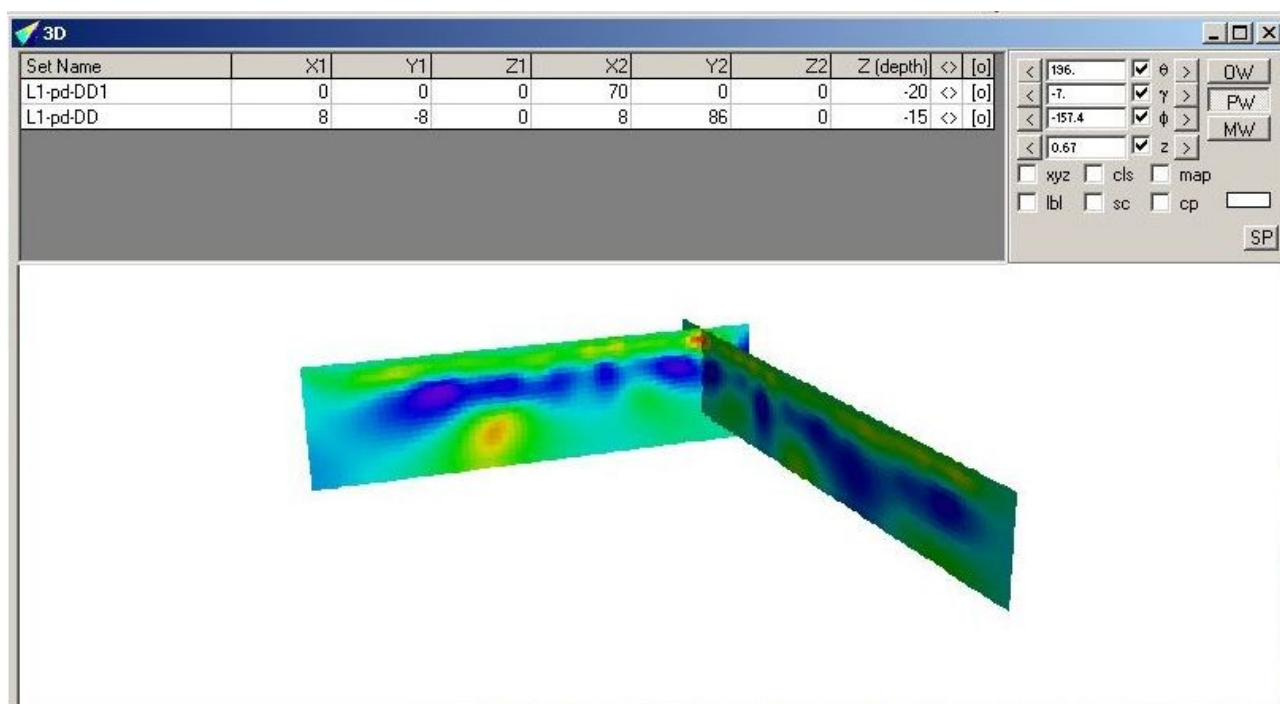


**Pic 69** Step 1 - Results in TomoLab

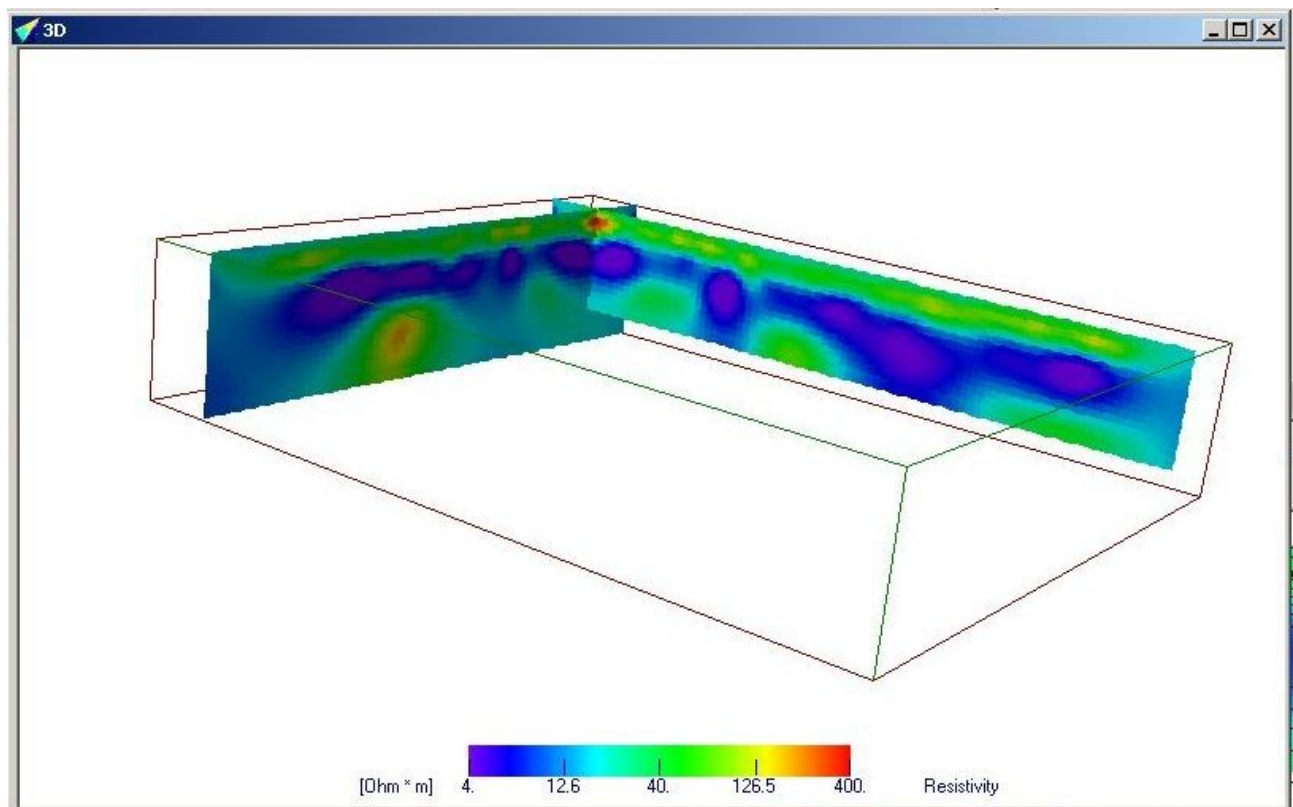




**Pic 70** Step 2 - Results collected in the 3D form by activating the 3D view



**Pic 71** Step 3 - Adjust the (X; Y) coordinate of both extremes of the sections, click on the graph window and the section will be plotted in 3D.  
Click the perspective option [PW] to see a better 3D



**Pic 72** Step 4 – 3D view of two sections crossing each other. Box option [xyz] and colour scale option [cls] are activated

Set Name	X1	Y1	Z1	X2	Y2	Z2	Z (depth)	<>	[o]
L1-pd-DD1	0	0	0	70	0	0	-20	<>	[o]
L1-pd-DD	8	-8	0	8	86	0	-15	<>	[o]

**Pic 73** 3D coordinate panel

Double click on a coordinate cell to change the coordinate of the image limits, the cell will be re-scaled in order to fit the coordinate points. Quote Z1 and Z2 shouldn't vary separately, so only changes in Z1 will produce vertical translation of the section. Also the depth cannot be changed at the 3D time.

[<>] load into the panel the coordinate specified in the coord-file

[O] remove/plot the section from/into the 3D image set

<	130.6	<input checked="" type="checkbox"/>	$\theta$	>	OW
<	-2.	<input checked="" type="checkbox"/>	$\gamma$	>	PW
<	-159.3	<input checked="" type="checkbox"/>	$\phi$	>	MW
<	0.67	<input checked="" type="checkbox"/>	z	>	
<input checked="" type="checkbox"/> xyz	<input checked="" type="checkbox"/> cls	<input type="checkbox"/> map			
<input type="checkbox"/> lbl	<input type="checkbox"/> sc	<input type="checkbox"/> cp			
					SP

**Pic 74** View panel

**[theta]** is the angle around X axis (Horizontal axis, from the left to the right of the screen). Click [ $<$ ] or [ $>$ ] rotate the image of about "one" degree around the X axis. The mouse vertical movement with the LftMouseDown cause rotation around X axis. The value of the rotation depends on the mouse movement. If the checkbox if not selected rotation generated by the mouse are forbidden. By setting the theta value into the text box and press carriage return the image will set at the angle specified.

**[gamma]** is the angle around Y axis (Horizontal axis, from user to the screen). Click [ $<$ ] or [ $>$ ] rotate the image of about "one" degree around the Y axis. The mouse vertical movement with the combination of Alt+LftMouseDown cause rotation around Y axis. The value of the rotation depends on the mouse movement. If the checkbox if not selected rotation generated by the mouse are forbidden. By setting the gamma value into the text box and press carriage return the image will set at the angle specified.

**[phi]** is the angle around Z axis (Vertical axis, from down to up). Click [ $<$ ] or [ $>$ ] rotate the image of about "one" degree around the Z axis. The mouse horizontal movement with LftMouseDown cause rotation around Z axis. The value of the rotation depends on the mouse movement. If the checkbox if not selected rotation generated by the mouse are forbidden. By setting the phi value into the text box and press carriage return the image will set at the angle specified.

**[zoom]** Mouse moving up and down with the right button pressed determine the zoom of the image. Move up: zoom in, move down: zoom out

**[OW]** Orthographic view. No visual information about the third dimension

**[PW]** Perspective view. Graph distortion to simulate the third dimension

**[MW]** Map view. Show the map to add to the sections

**[xyz]** Show a box around the image determined by the X, Y, Z, extremes value

**[cls]** Show the colour scale. Colours scale limits can be set with the function in menu Image

**[map]** Show the map (if loaded)

**[lbl]** Show the (x, y, z) coordinate at each corner of the [xyz] box

**[sc]** Show the scale close to three adjacent axes

**[cp]** Add the standard contour plot to the sections

**[SP]** Save a bitmap file of the current image

## 3D view

Collect data from the active windows in TomoLab into an unique data structure, otherwise ask for a 3D file

## Coordinates

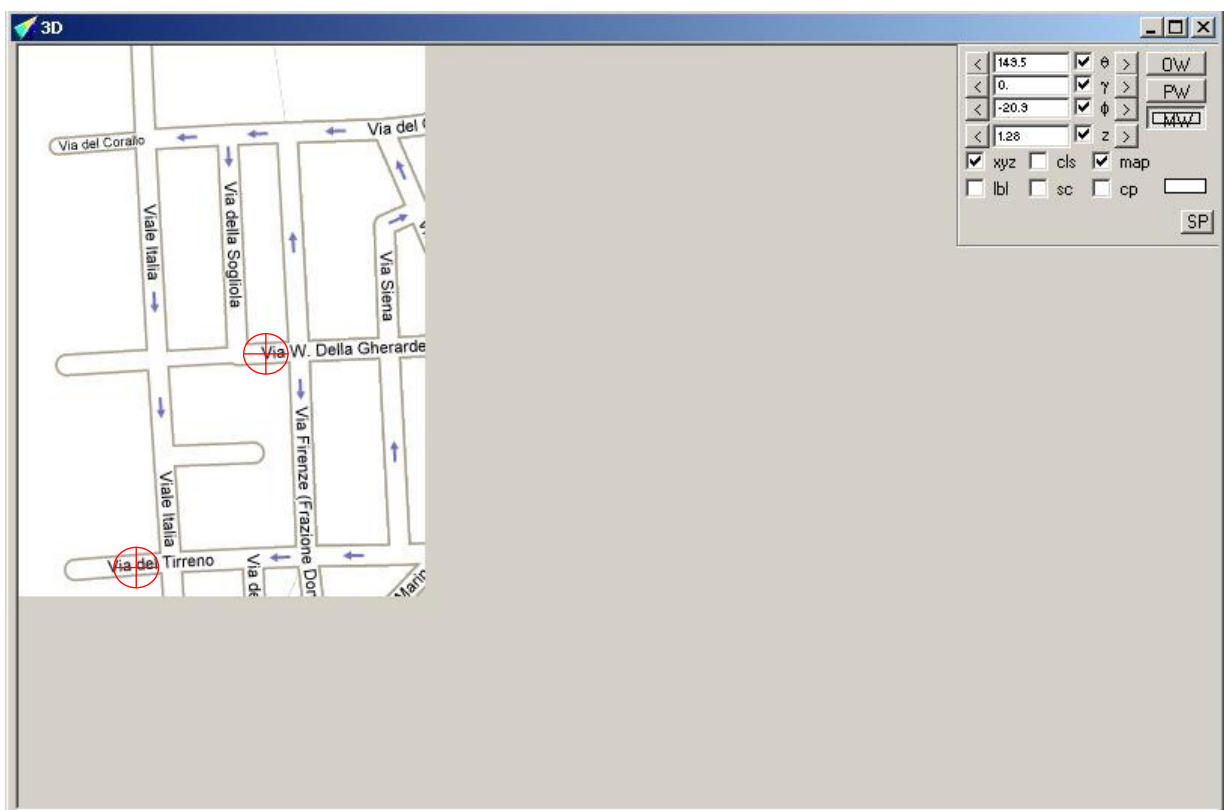
Show the section file coordinates panel over the image, the panel is automatically displayed when the mouse cross over the upper part of the image

## Tools

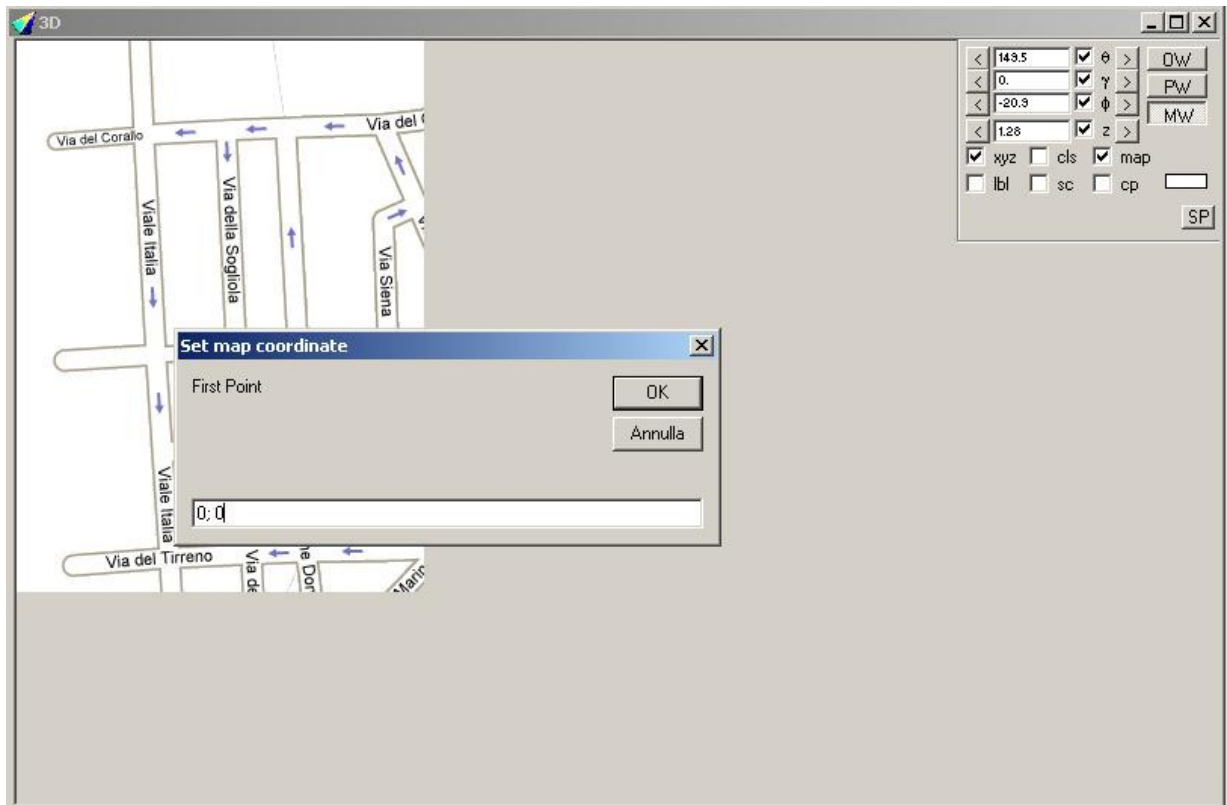
Show the tools frame, this frame is automatically displayed when mouse cross over the upper part of the image

## Load Map (.bmp)

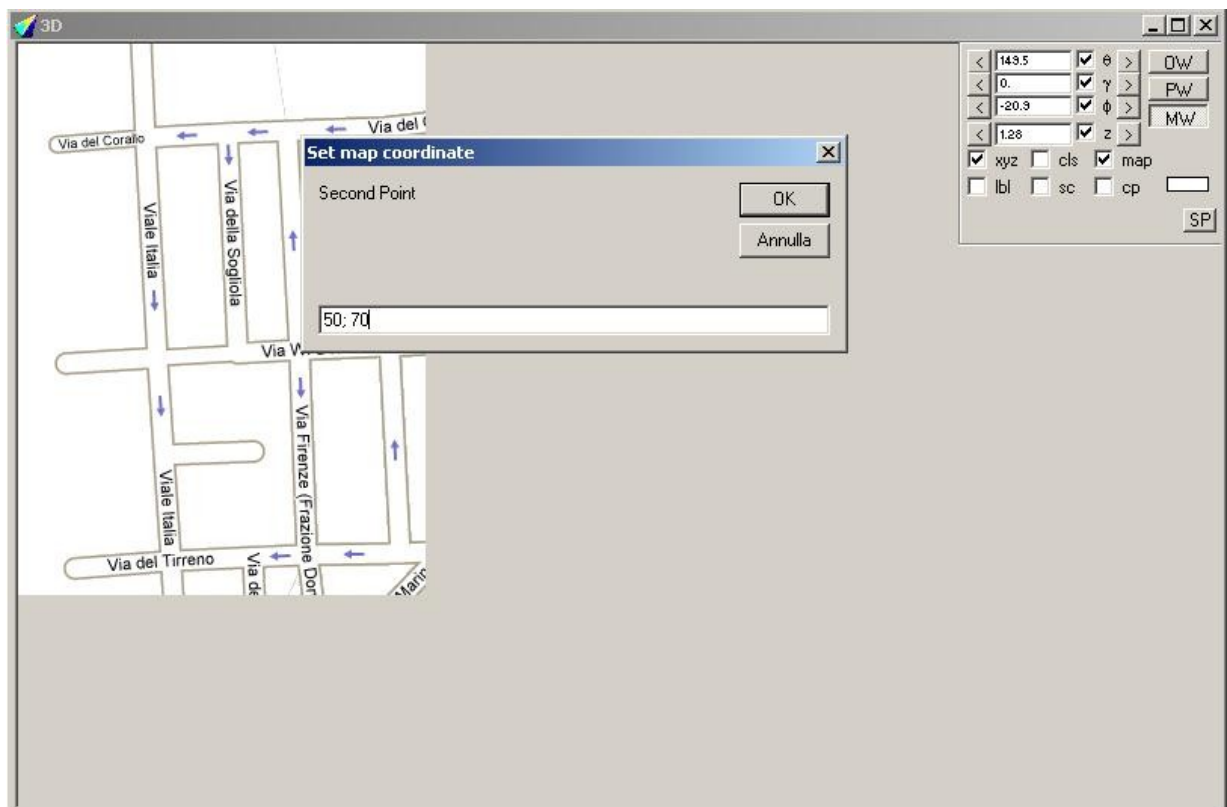
It is possible to add a map the current 3D image set. TomoLab accept only bitmap file. User should know relative coordinate of the sections to the map in order to rescale the map data points into the sections reference system



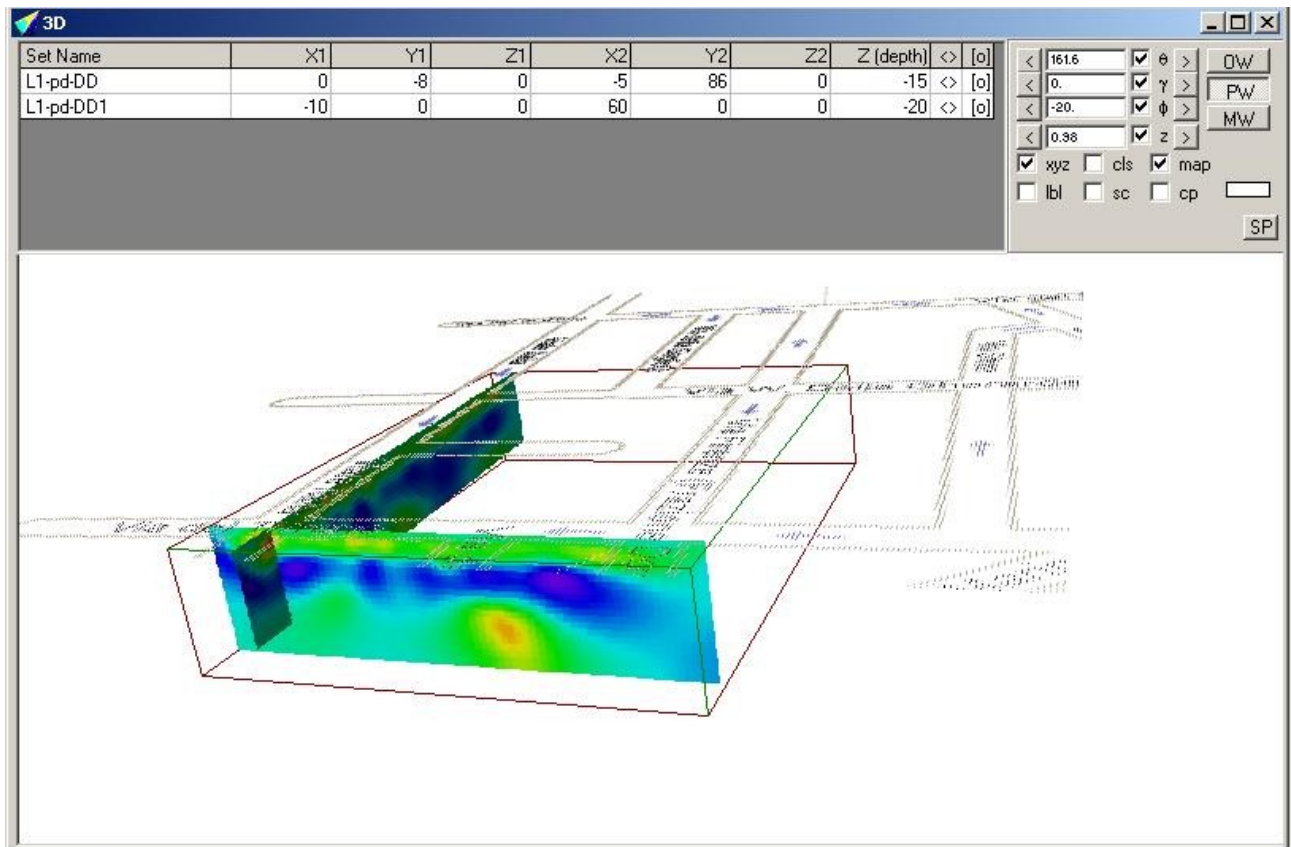
**Pic 75** BitMap file loaded into the form. Use map file with white background. Red circles are the points used to link the map scale to the sections scale



**Pic 76** DoubleClick over the first point (red circle). A dialog box appear. Set in the dialog box the (X, Y) coordinate of the map point in the reference system of sections (defined in the coordinate panel)



**Pic 77** DoubleClick over the second point (red circle). A dialog box appear. Set in the dialog box the (X, Y) coordinate of the map point in the reference system of sections (defined in the coordinate panel). The map points will be rescaled into the reference frame of the sections



**Pic 78** After the rescaling process it is possible to display the map into the 3D environment

## Set Map Quote

The default Map quote is "Zero". User can make a z translation of the map by setting the Z quote

## Set Transparency

When TomoLab rescale the map image into the reference frame of the sections, TomoLab scan the bitmap file for the non-white pixel. The white pixel were ignored (transparent in 3D environment). User can set another colour as transparent by Shift+LeftClick on the select colour (the rectangle shape will appear of the same colour under the muse pointer) then run Set Transparency. When TomoLab will rescale the image, pixels of the selected colour will be ignored.

## Set Up X axis

The X axis range over the minimum and maximum value of the x coordinate of the sections. User should set minimum, step and maximum value of the labels on the axis.

## Set Up Y axis

The Y axis range over the minimum and maximum value of the y coordinate of the sections. User should set minimum, step and maximum value of the labels on the axis.

## Set Up Z axis

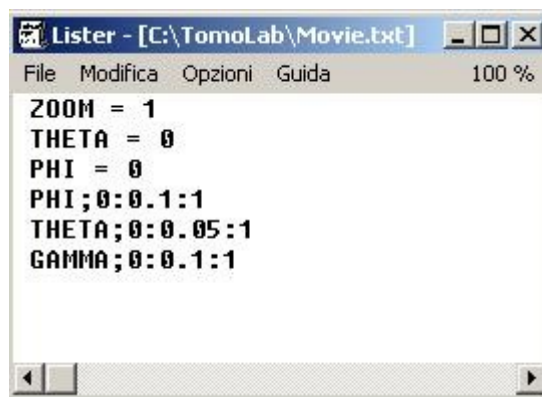
The Z axis range over the minimum and maximum value of the z coordinate of the sections. User should set minimum, step and maximum value of the labels on the axis.

## Movie

By activating this option a text box and two buttons are displayed into the view panel.



**Pic 79** Create a movie varying Phi from zero to pi stepping 0.05 radian, movie start clicking [M]



**Pic 80** More articulate movie should be create using a text file "Movie.txt" in the TomoLab directory. movie start clicking [MP]

With this option TomoLab save a bitmap for each view. The entire sequence can be joined into a movie by Microsoft Movie Maker released with Windows XP

## Save Picture

Save a bitmap file of the current 3D view

## Add Section

It is possible to add a section saved in EVS format



## Save Project 3D

Sections with relative coordinate and rescaled map can be saved into a single project file.

## Load Project 3D

Load a 3D project file saved with TomoLab

## A – Invert Rho Data

In this section it is possible to follow the procedure from .bin data file to a reliable inversion.

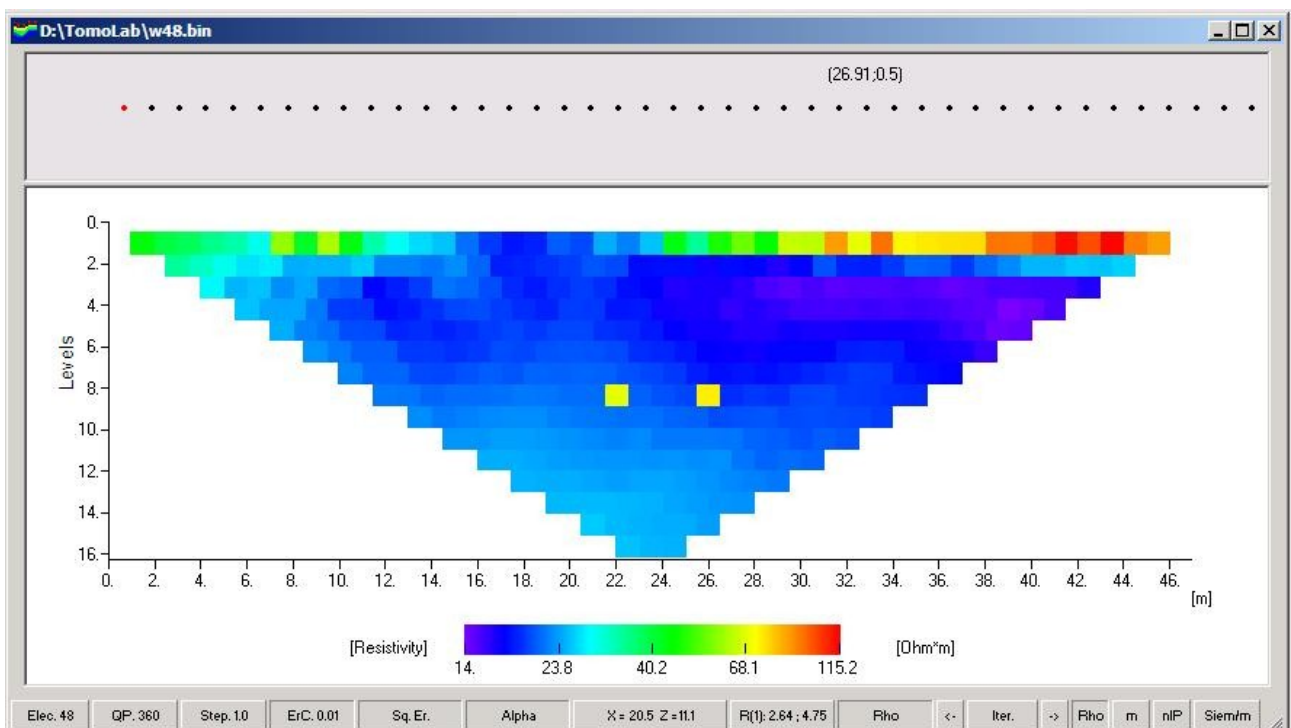
User can follow the example using the w48.bin file enclosed to the setup file of TomoLab



- 1 - open the “\TomoLab\w48.bin” file and set the spacing between adjacent electrodes to 1.

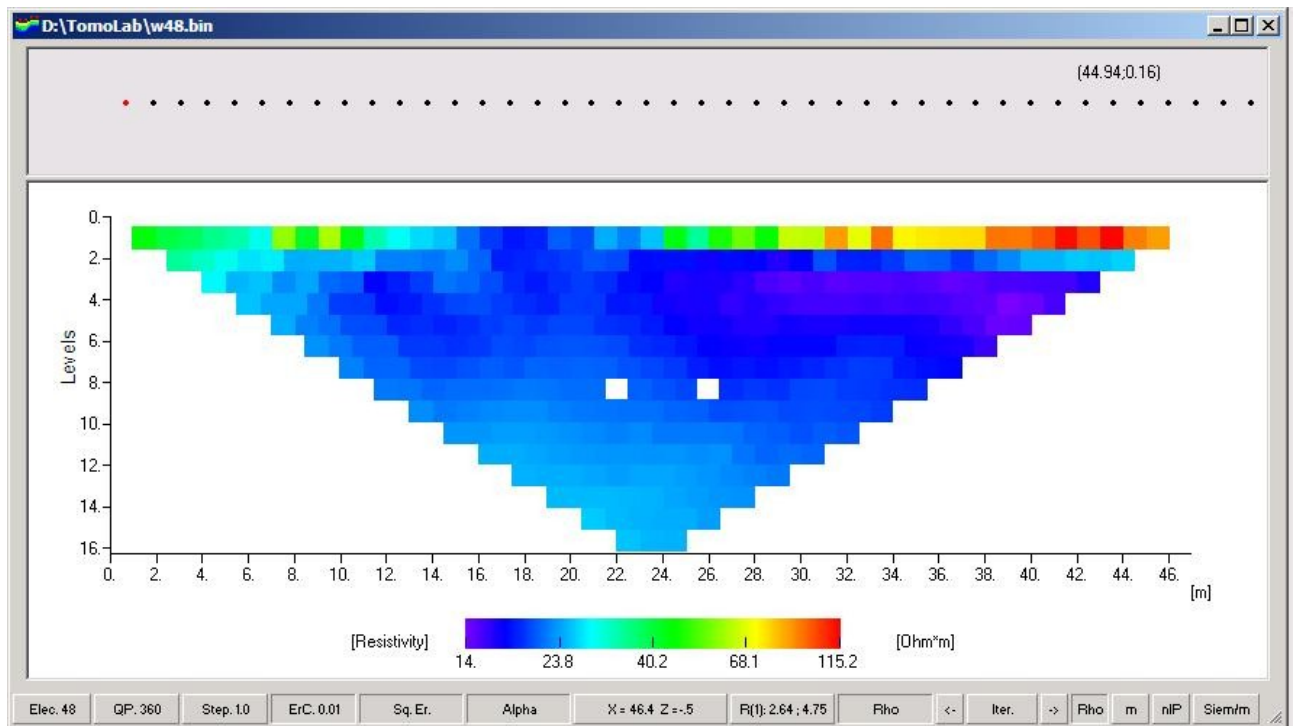


- 2 - plot the “Interactive Pseudosection”, n. 6 (Wenner data)



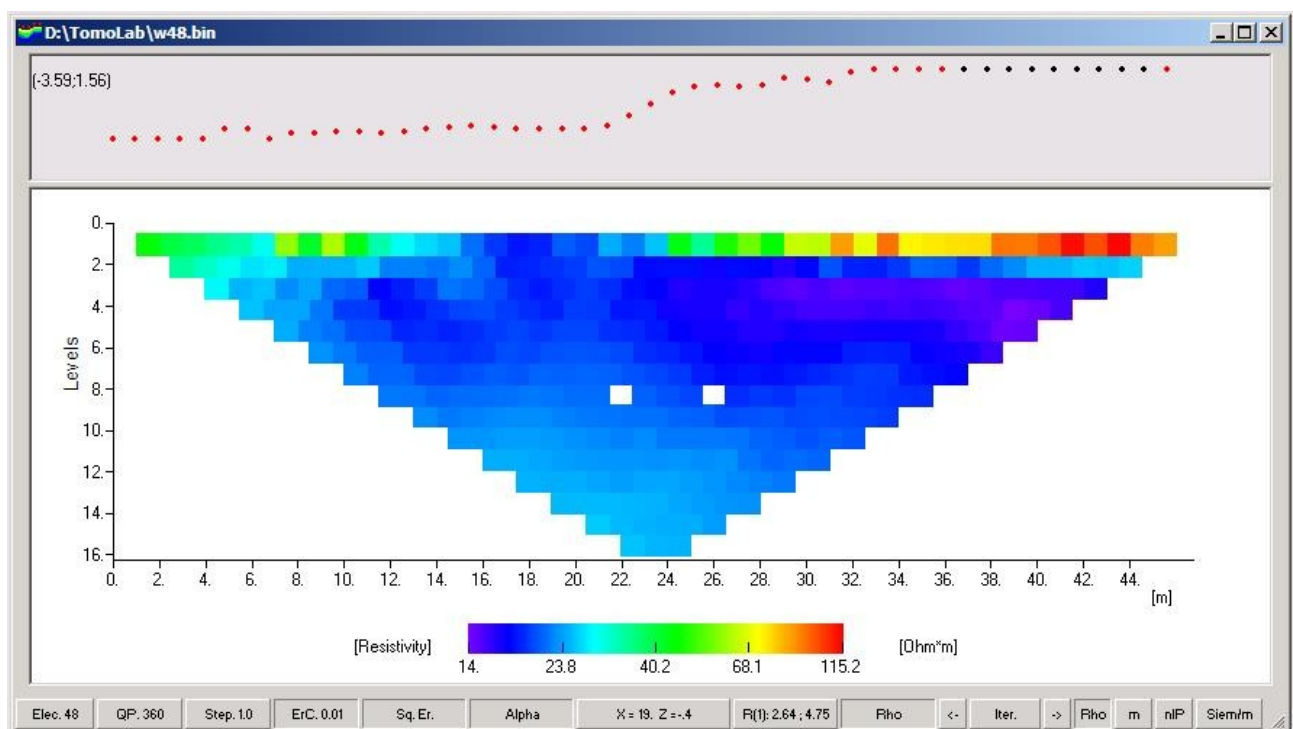
**Pic 81** Wenner pseudosection (6), two data looks bad

- 3 - Remove bad data point by double clicking over the two “yellow” measure. This is an “heuristic” approach to data filter. The two measures looks different from their neighbours (around  $50 \Omega \cdot m$ ), other criteria as (injection current more than a specific value, and potential across M and N electrodes more than the noise level) should be set in the configuration form.




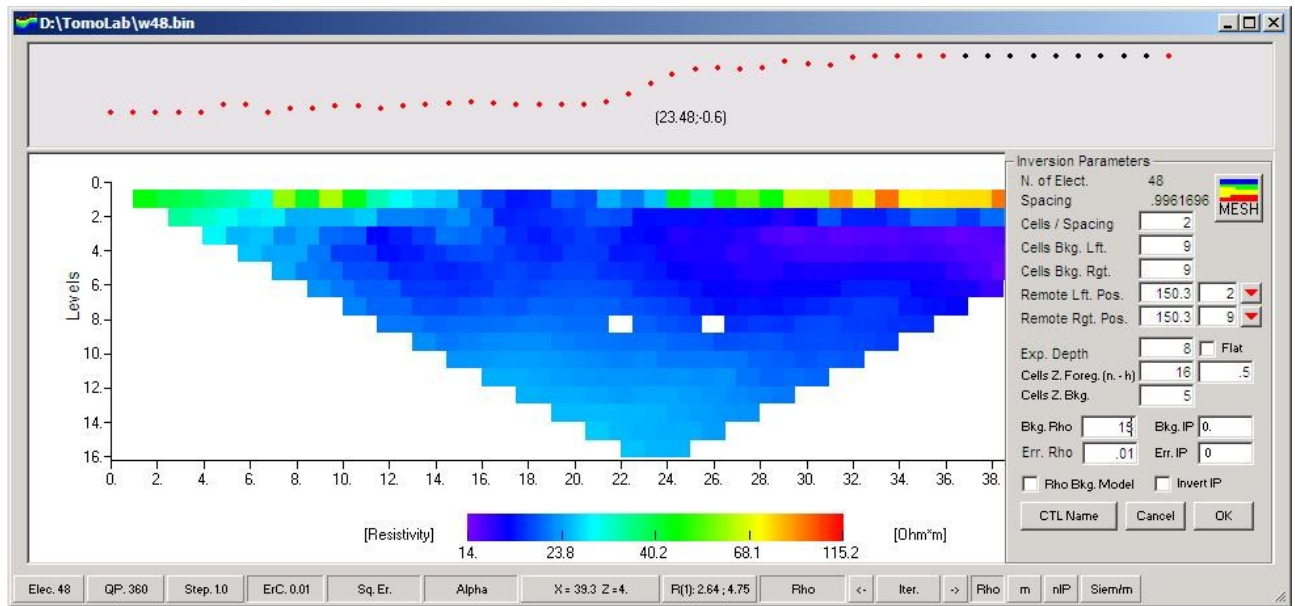
**Pic 82** Wenner pseudosection after data filter (manual)

4 - Add topography form data file (two columns [electrodes number, Z elevation]) .  
Open the "\\TomoLab\\w48\_topo.txt"



**Pic 83** Electrodes with topography information

5 - Click the icon  and set the inversion parameters:



**Pic 84** CTL panel. Set exploration depth, cell's height, background Rho

## 6 - Set the parameters as in the picture

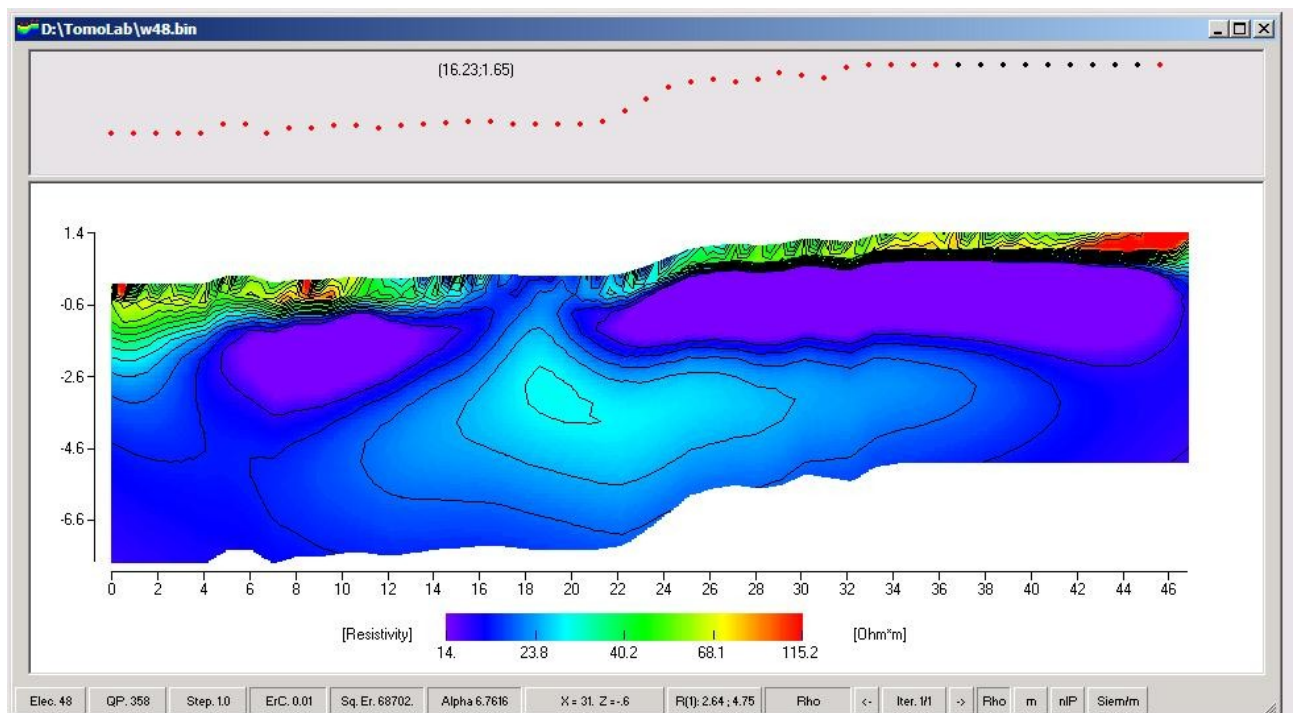
Exp. Depth: 8 m (in Wenner configuration the exploration depth is around 1/6 of the AB maximum, or 1/6 the length of the section)

Flat : none (the depth profile will follow the electrodes topography)

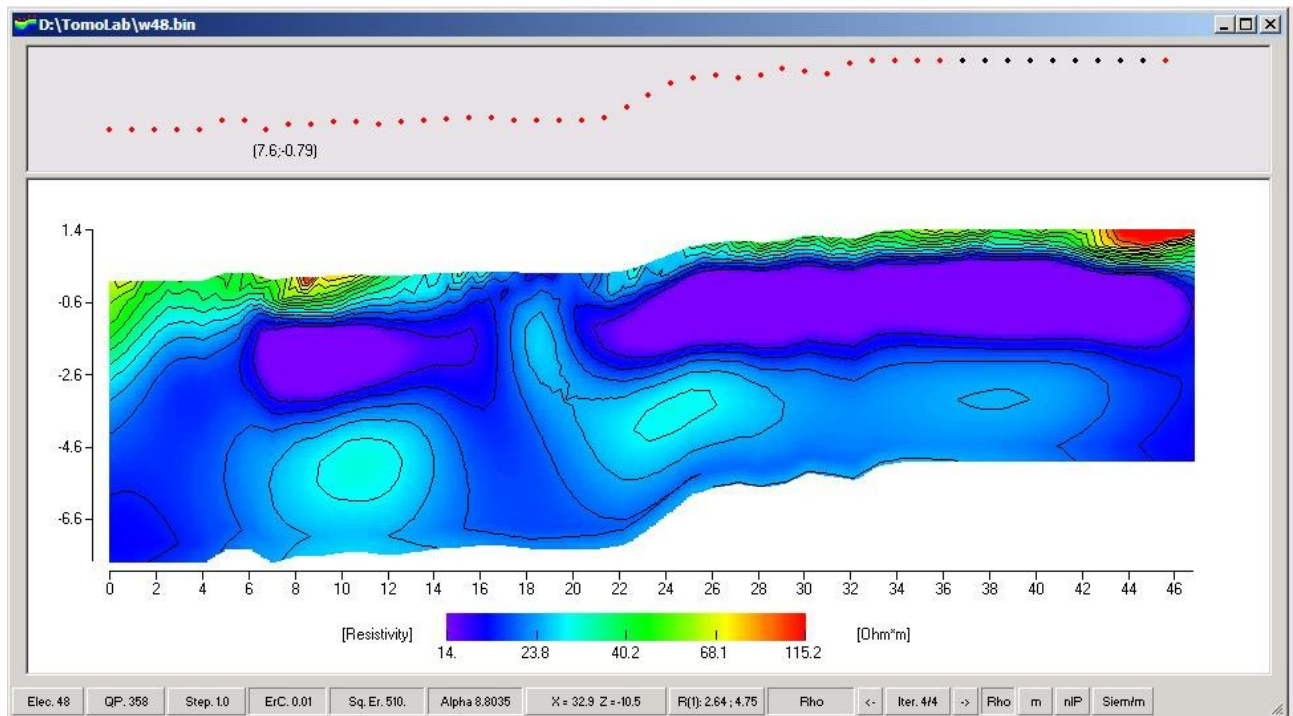
Cells Z. Foreg.: 16 (16 x 0.5 = 8)

Bkg. Rho: 15 (rho value of the blue colour in pseudosection)

Click [OK] button and run the "Single Inversion" from menu "Inversion"



**Pic 85** Iteration n. 1



**Pic 86** Iteration n. 4 - Inversion OK

7 - The program stop after the fourth iteration (max 10 iteration) lasting 60'' (dual core 2.2 GHz, 1GByte). The results looks good. The image is quite smooth but the resistivity range is wide enough, the Squared Error is 510, the same order of number of quadrupoles ( $360 - 2 = 258$ ), the alpha parameter is  $\alpha = 8.8$ , a bit high (better  $0.5 < \alpha < 5$ ), but is ok.

User must pay attention to few parameters:

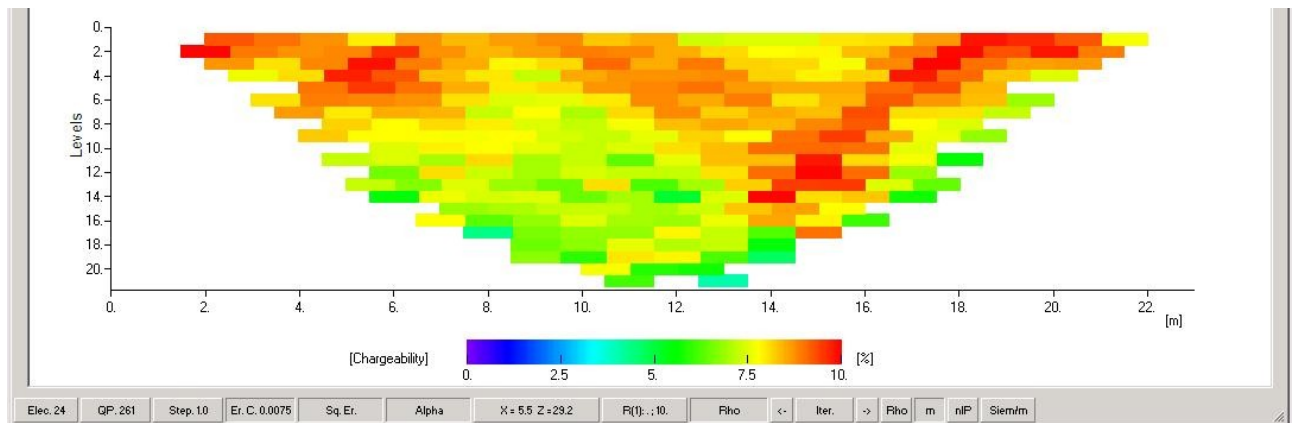
- Background Rho: TomoLab use the average apparent resistivity as default, an average over deep levels should be better.
- Error Coefficient: TomoLab use 0.01 as default (means 1%). If the inversion stop with a squared error greater than number of quadrupoles and alpha less than one (Sq. Err. > NQp AND Alpha << 1) it can be suggest to try another inversion loop with Error Coefficient 0.015 or more, in case of squared error less than number of quadrupoles and alpha greater than one (Sq. Err. < NQp AND Alpha >> 1, section over smoothed) it can be suggested to try with a smaller Error Coefficient
- Remove from data set all the measure that look "anomalous" within their neighbouring



## B – Invert IP Data

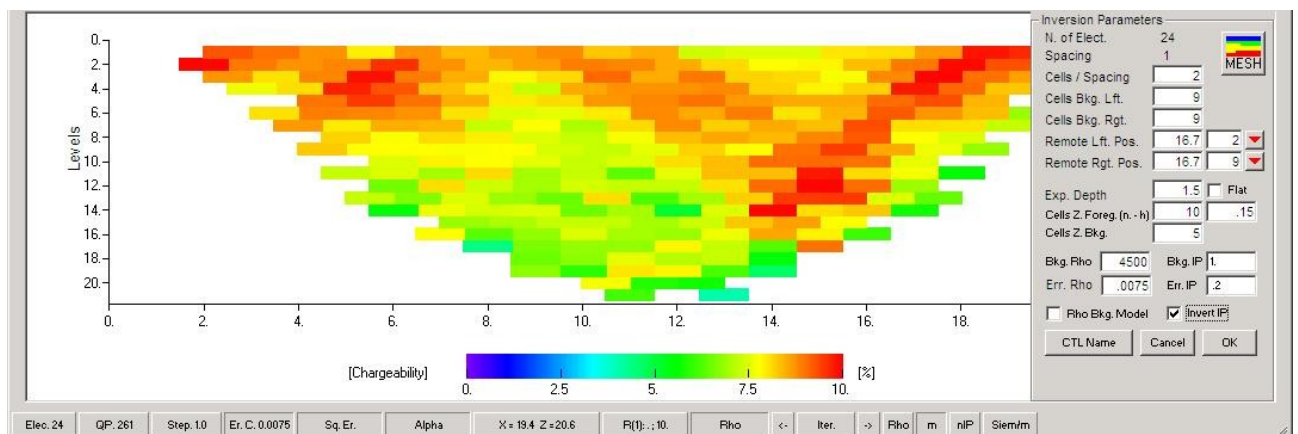
IP means "Inductively Polarization", many circumstances should create electrical capacity in soil, so after the current injection time, the potential difference between electrodes doesn't vanish immediately but show a decay curve. Usually the chargeability signal is measured as a percentage of the  $V_{MN}$  during the injection time. The way of carrying out the chargeability should vary among different instruments.

TomoLab can display the chargeability



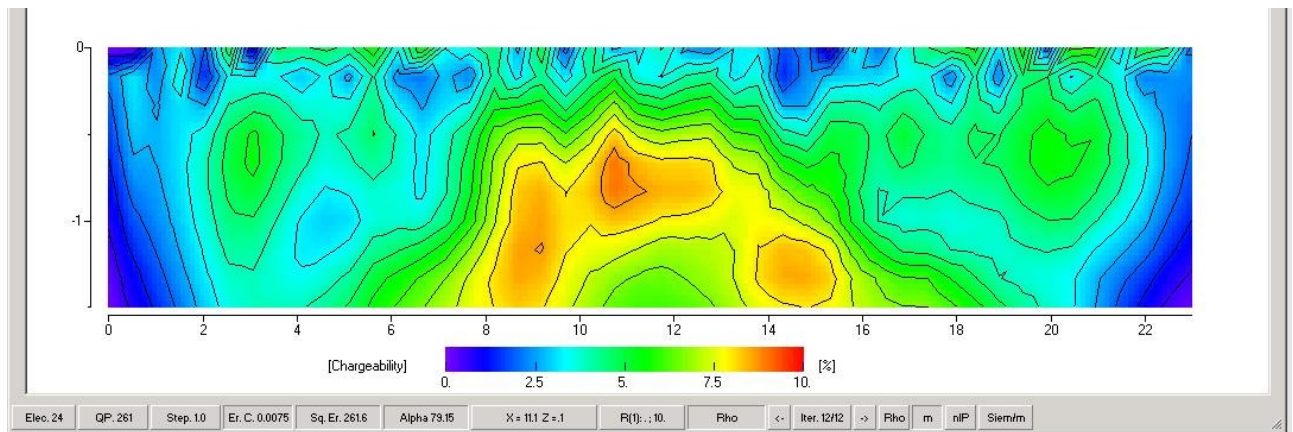
**Pic 87** Chargeability Pseudosection

TomoLab invert IP data only if request. User must set the box as in the picture below. The inversion routines start with rho inversion and perform the IP inversion after the rho one.



**Pic 88** CTL panel: check box "Invert IP"



**Pic 89** IP inversion results

The IP inversion follow the same rules as the ones for resistivity. The IP iteration use the last Rho iteration as reference.

## C - Invert long section

The inversion process would take a lot of time (several minutes) and it's very machine consuming. In order to reduce computational time TomoLab allow user to divide the section into two or more sub-file (with some electrodes overlapped each other), invert each sub-file and then collect all together into a single file with an unique result image.

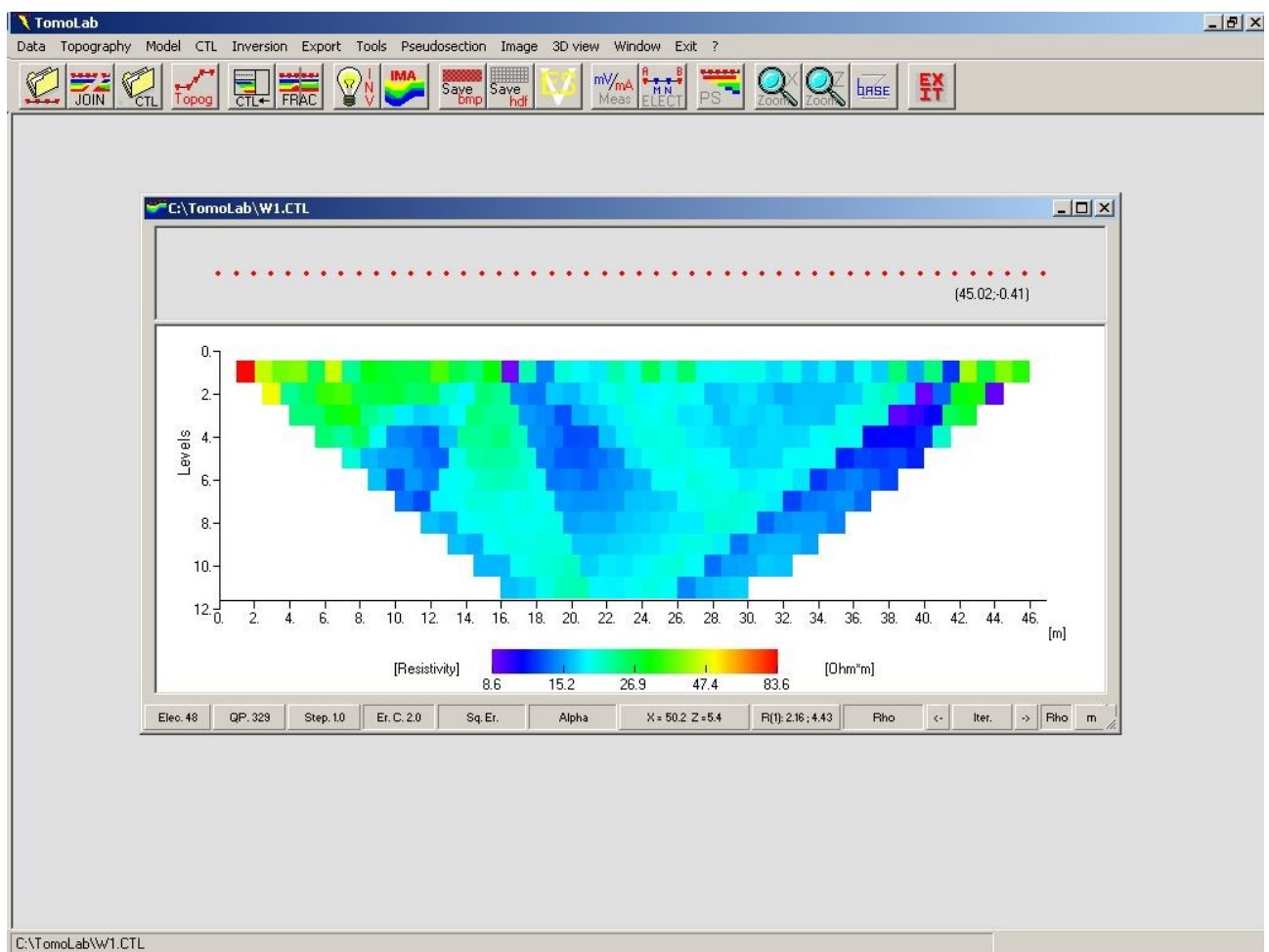
### Step 1 – Split the main section



Load a CTL file and



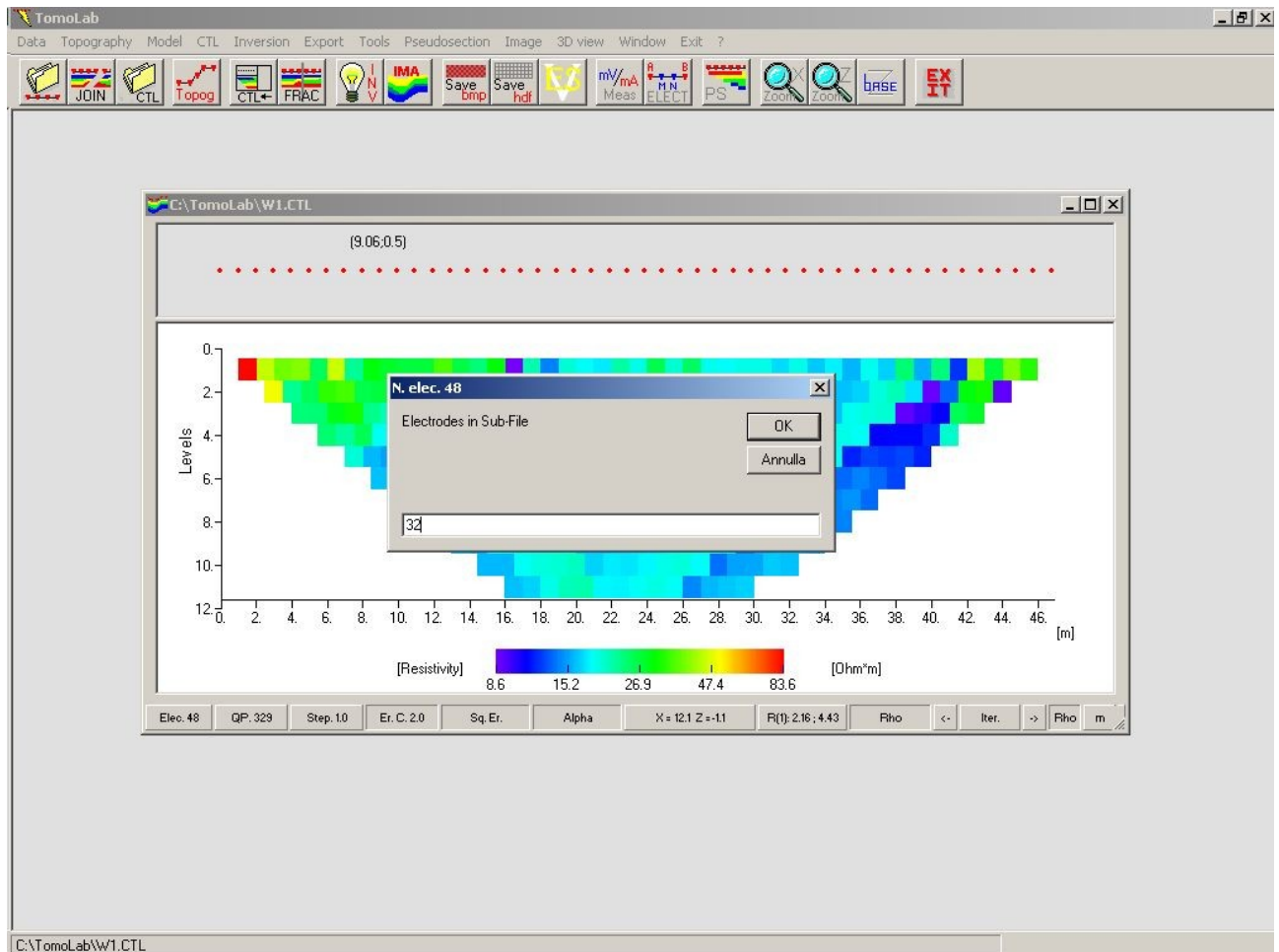
plot the Int. Pseudosection



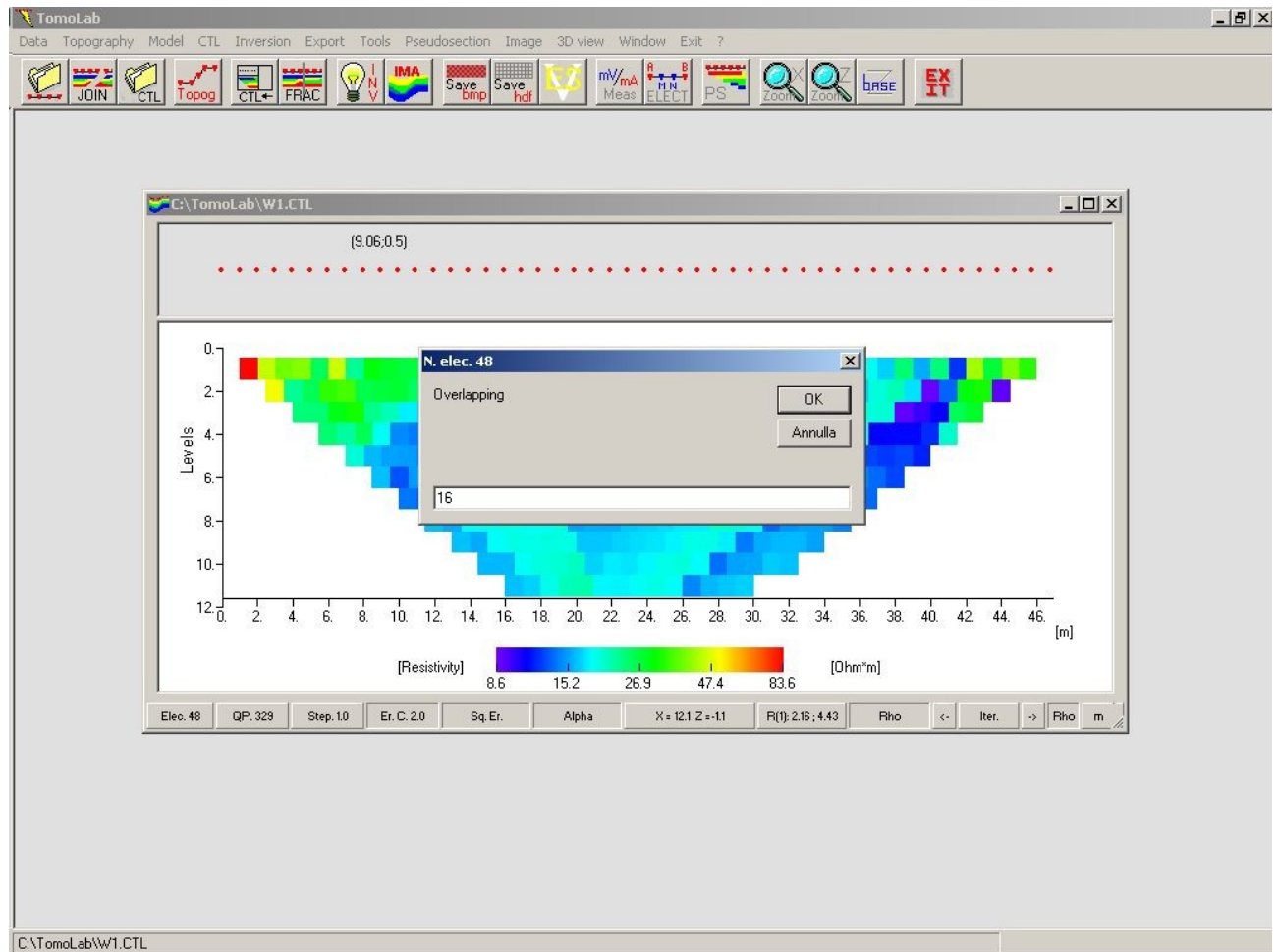
**Pic 90** Load the "long" CTL file and plot the pseudosection



Split the CTL file into two sub files, define 32 electrodes in each sub-file with 16 electrodes of overlapping.

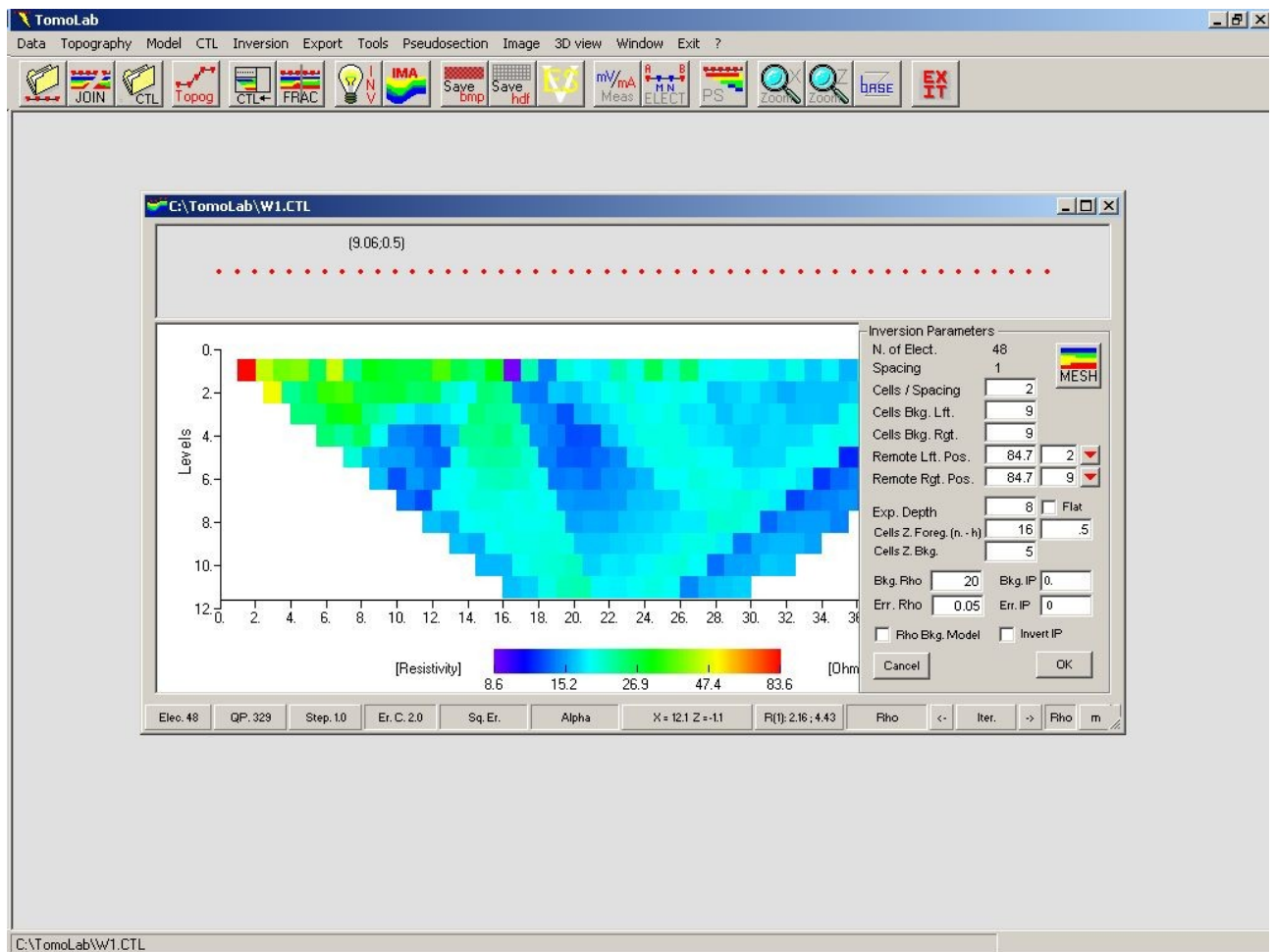


**Pic 91** Split the CTL into two sub file with 32 electrodes each one ( $32 + 32 - 16 = 48$ )



**Pic 92** Set an overlapping zone of 16 electrodes ( $32 + 32 - 16 = 48$ )

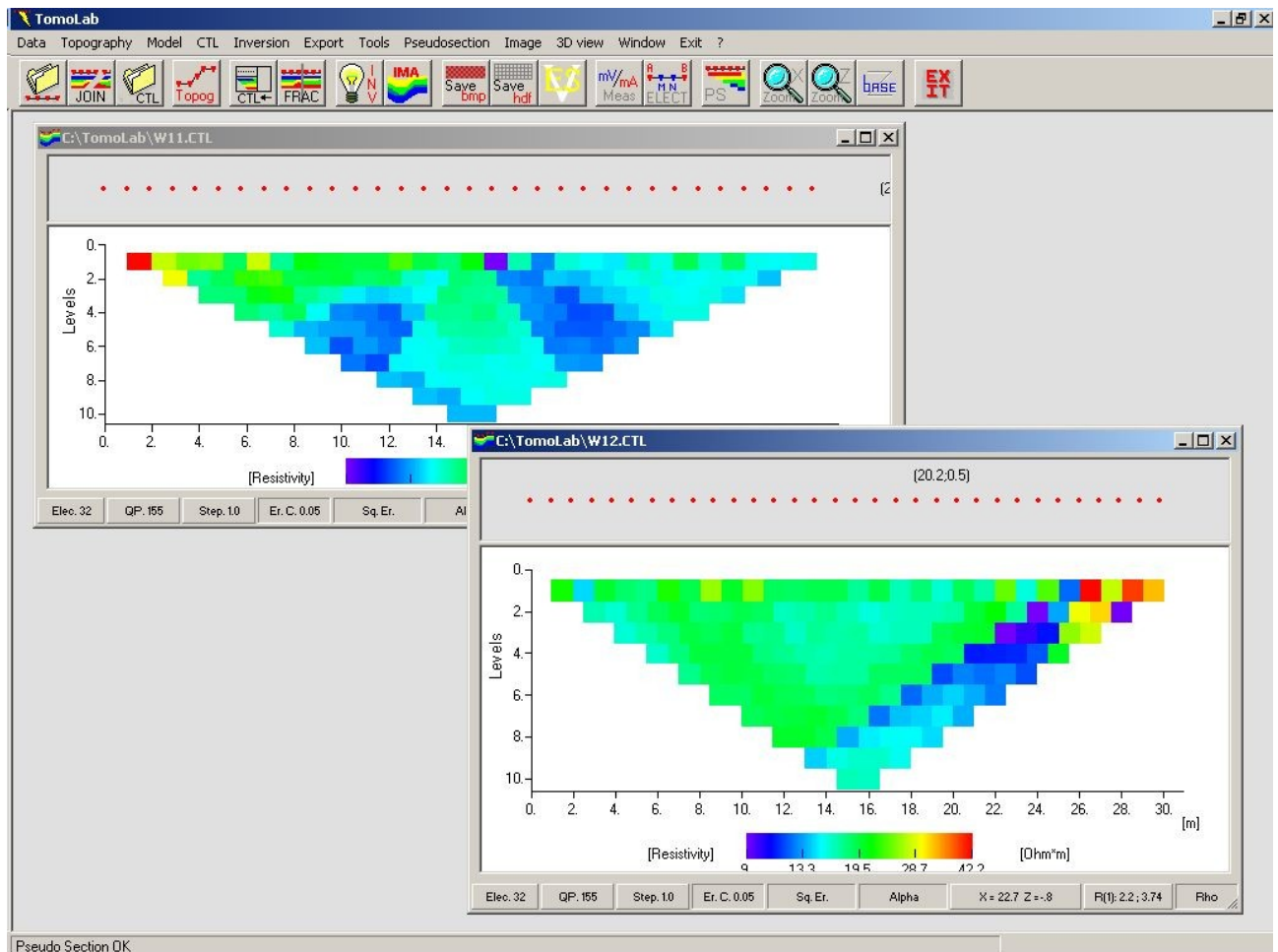
Fill the CTL form with the appropriate parameters (Exp. Depth, Cells, Rho). Use the same mesh specifications for each file and, if it's possible, the same inversion parameters (Rho, Err., etc)



**Pic 93** Create the two sub CTL (use the same mesh in every CTL)



Plot the PseudoInt to ensure that the splitting procedure is correct

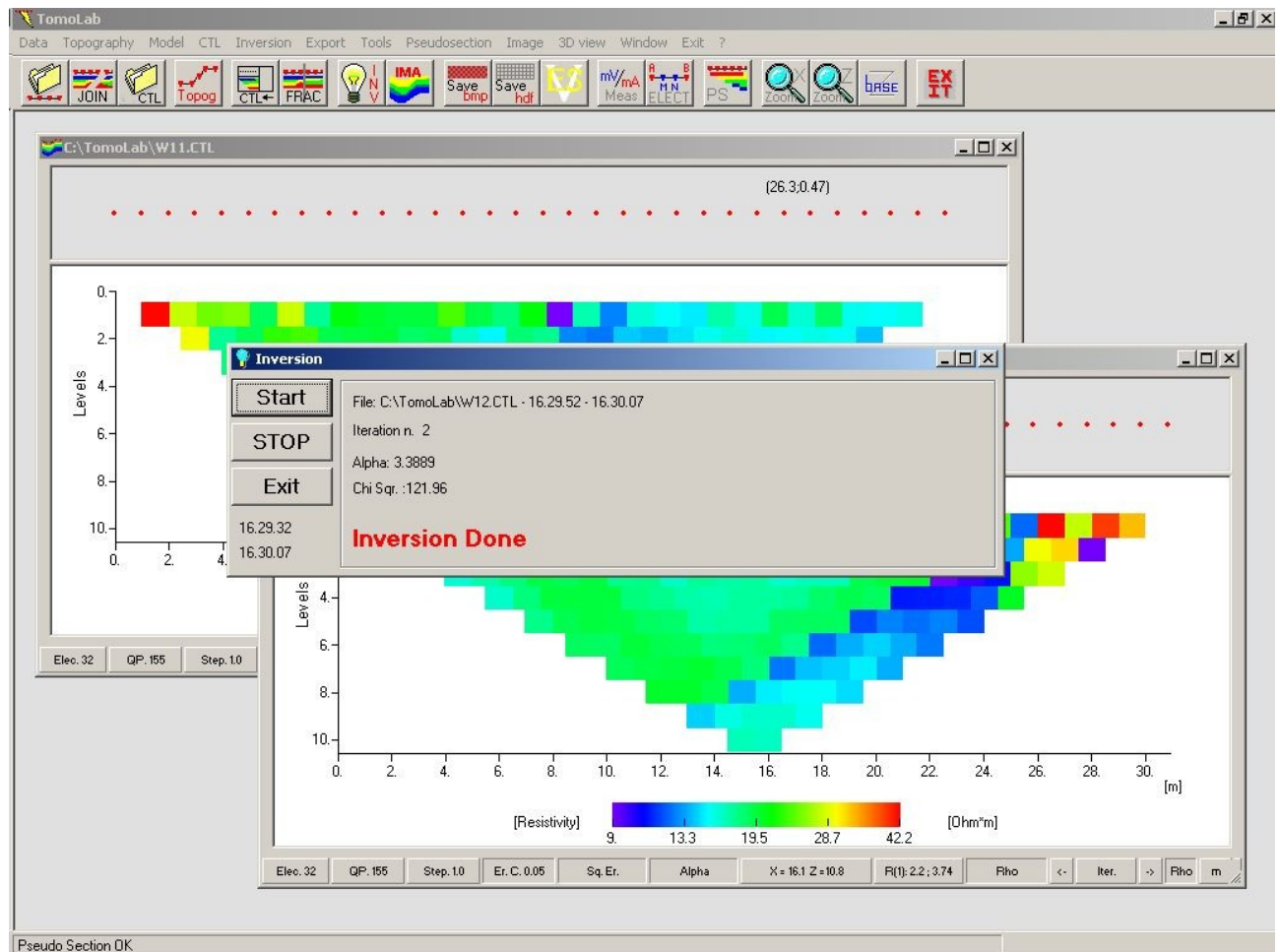


**Pic 94** The two sub files and pseudo sections



Remove the main data file and proceed with the inversion of the sub-files using the

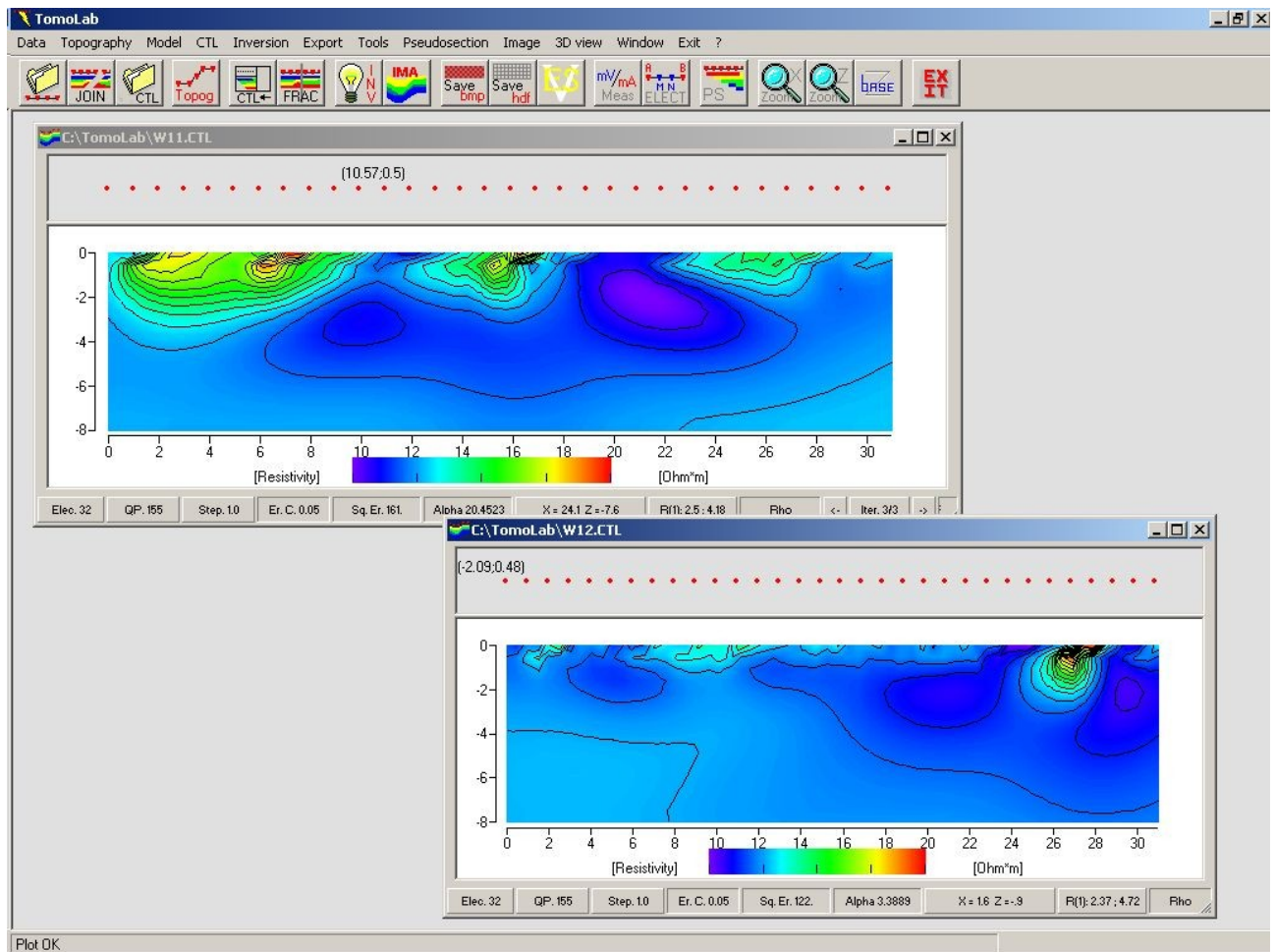
Batch Inversion



Pic 95 The batch inversion on the two CTL ended

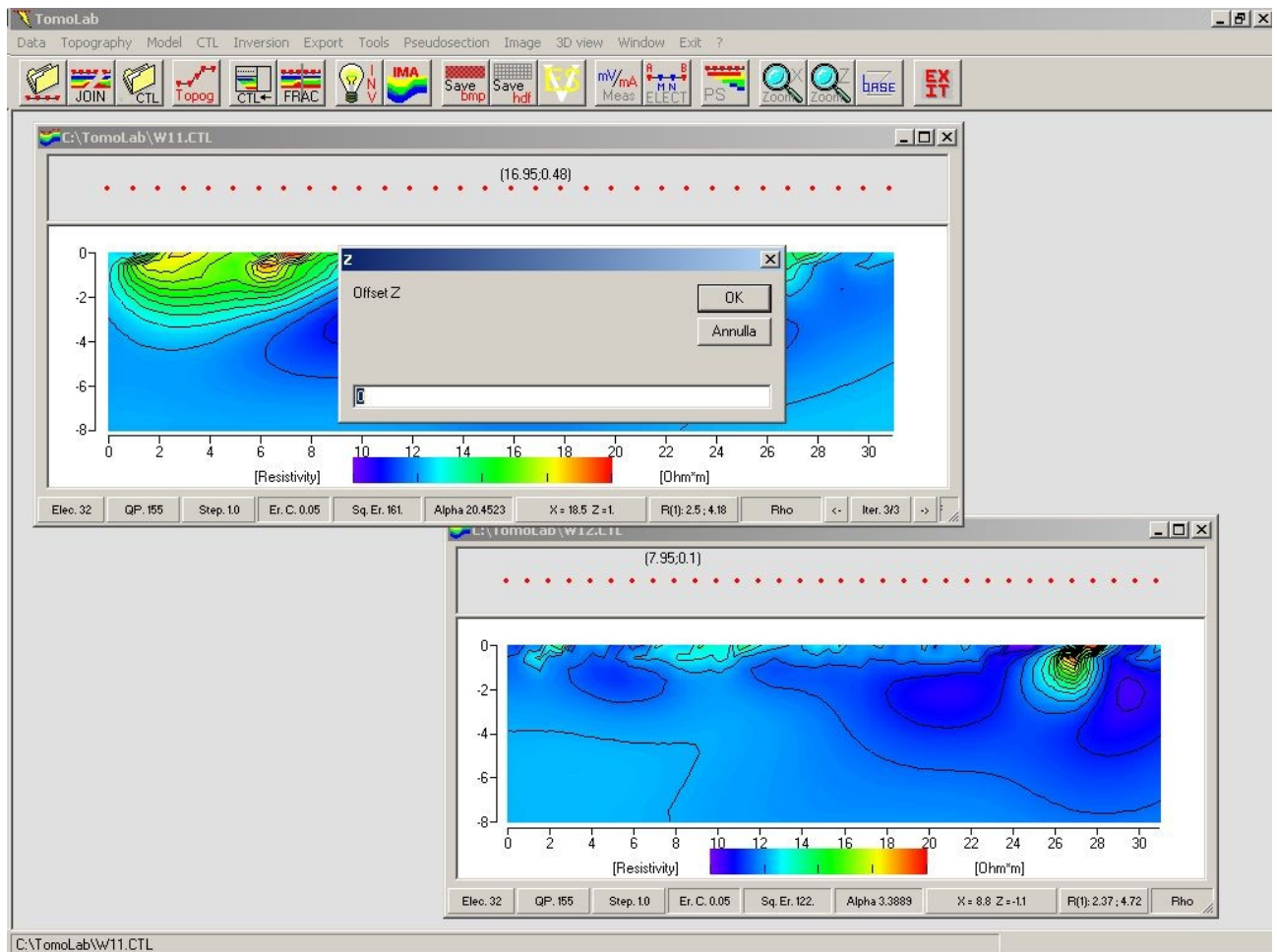


Load the results (.IMA) file and select the proper iteration





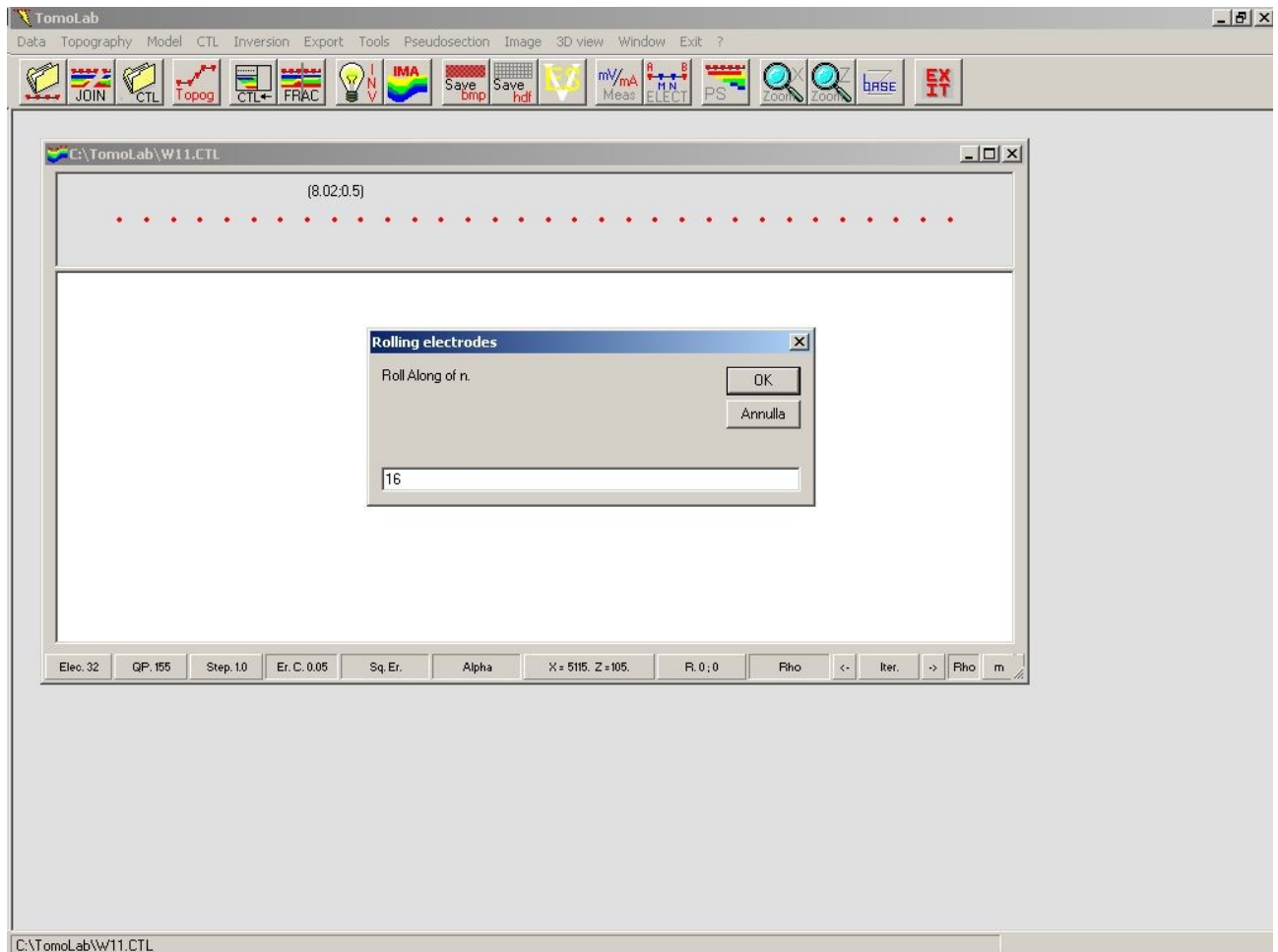
**Pic 96** Load results in each file and select the best iteration

Export the best iteration in .EVS format using the default options

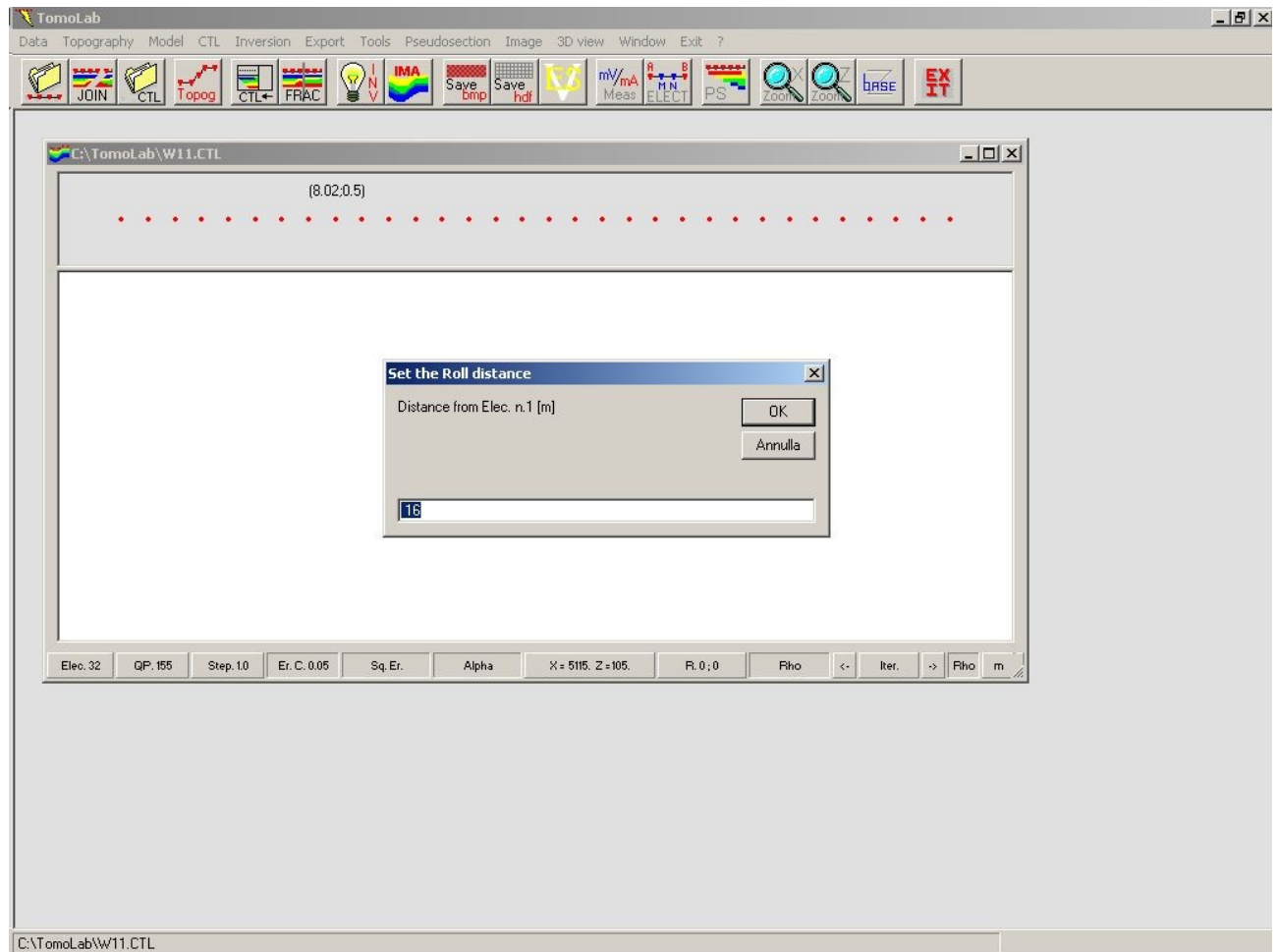


**Pic 97** Export in EVS format the selected iteration for each file

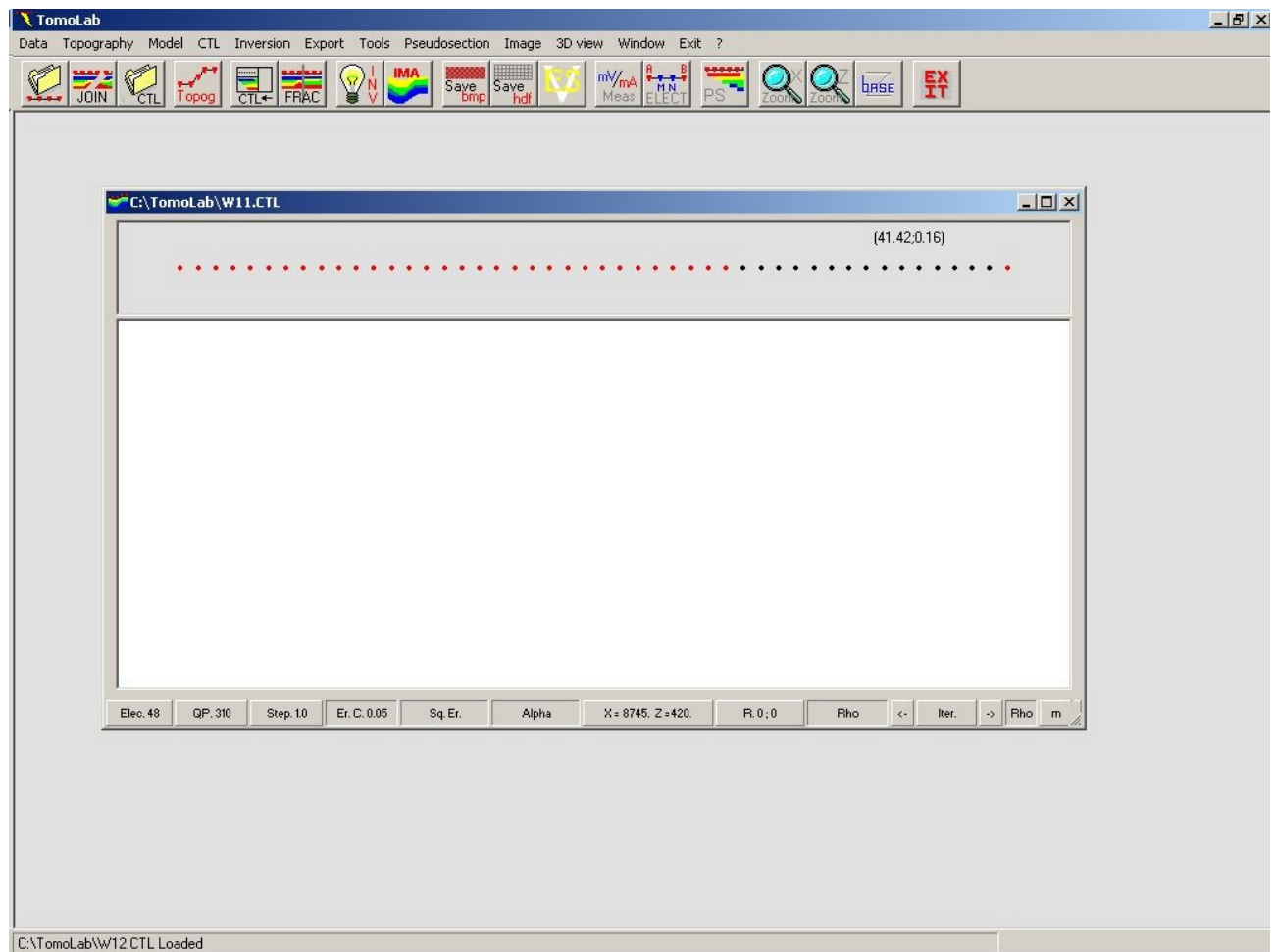
Now start to merge results into a single array.  Open the first sub-files and  join the following as for a roll-along measure. Use the appropriate value for electrodes of roll-along, in our example 16



**Pic 98** Reload the first sub-file and start the joining chain (Roll Along of  $n = 16$  electrodes)



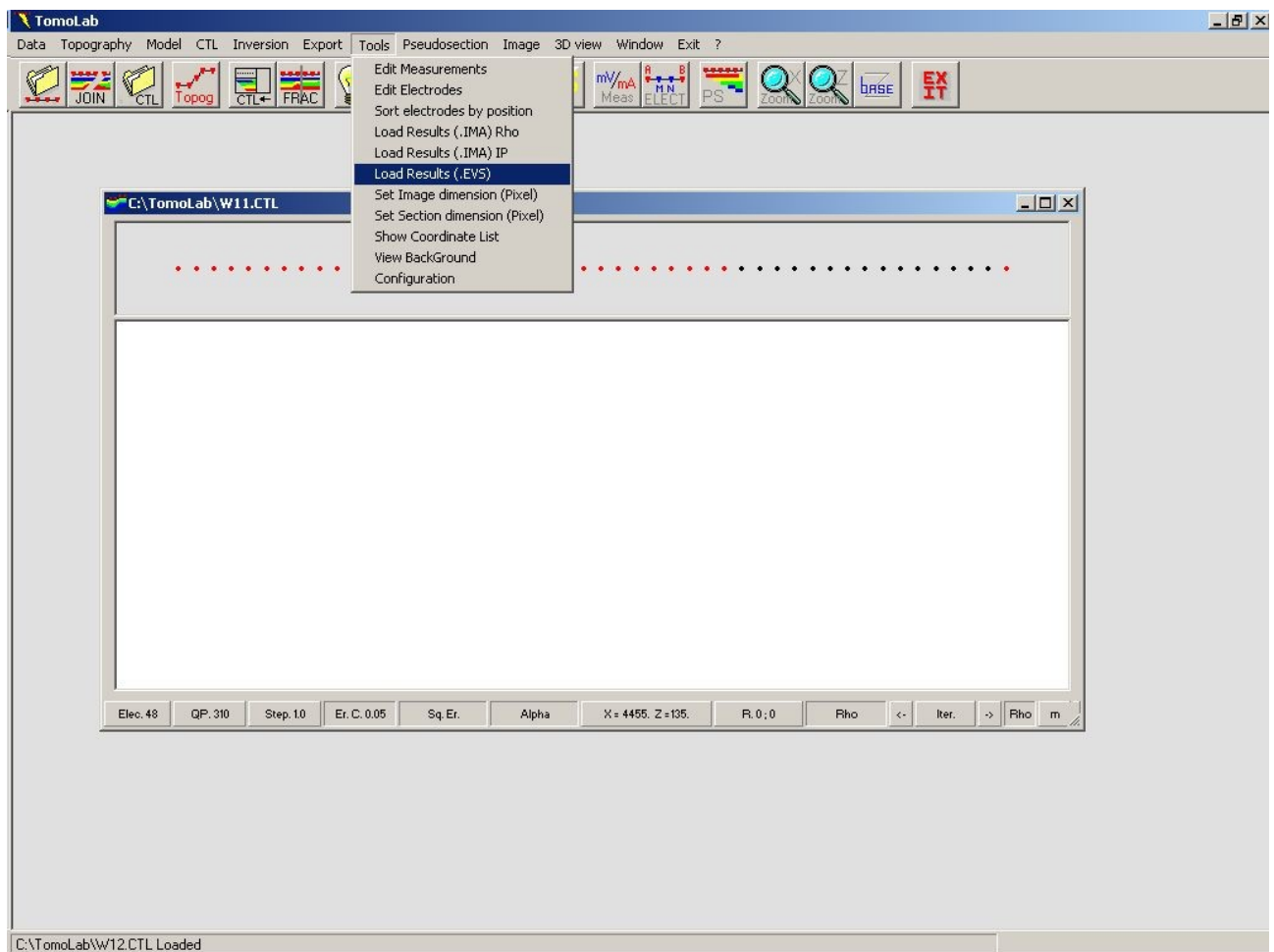
**Pic 99** Roll Along of n. = 16 meters



**Pic 100** The two sub-files are now chained

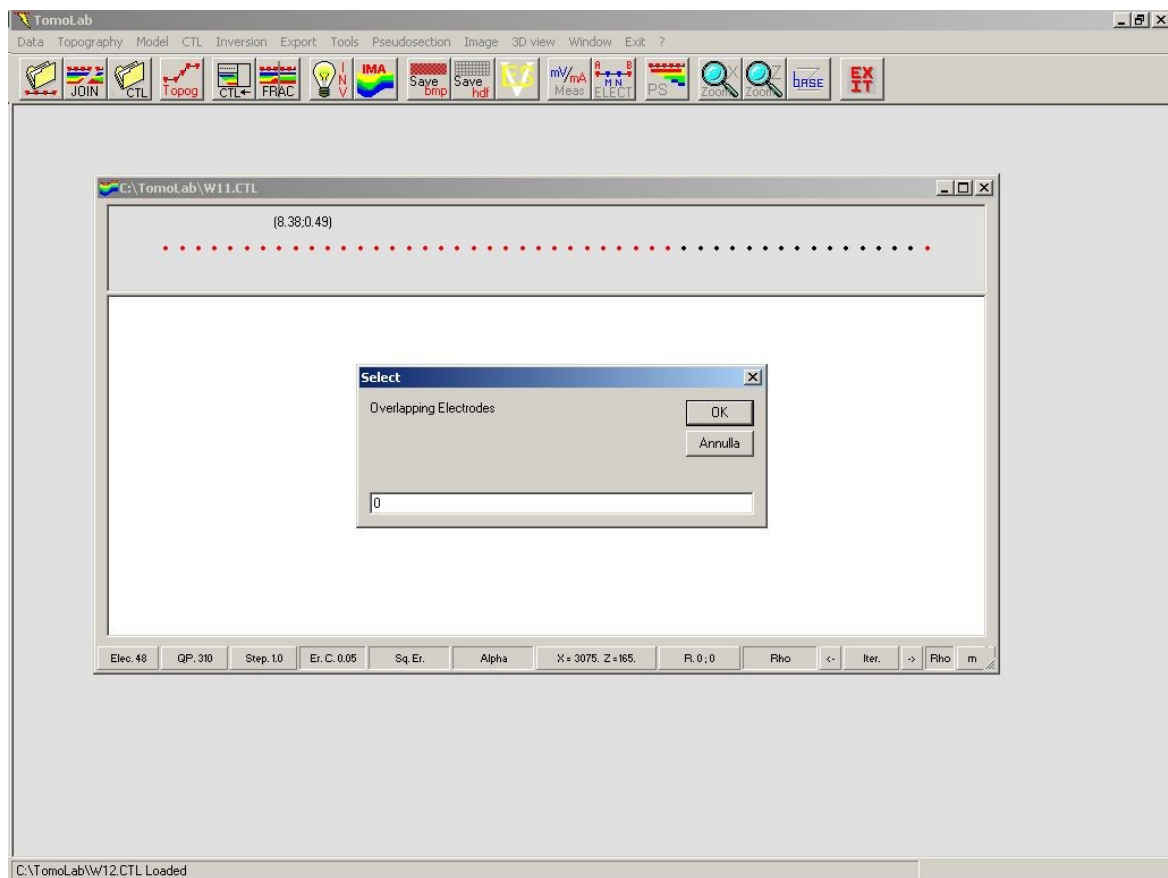


Start loading results in EVS format using the menu function

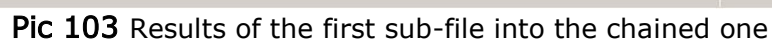


**Pic 101** Load the EVS results of the first sub file

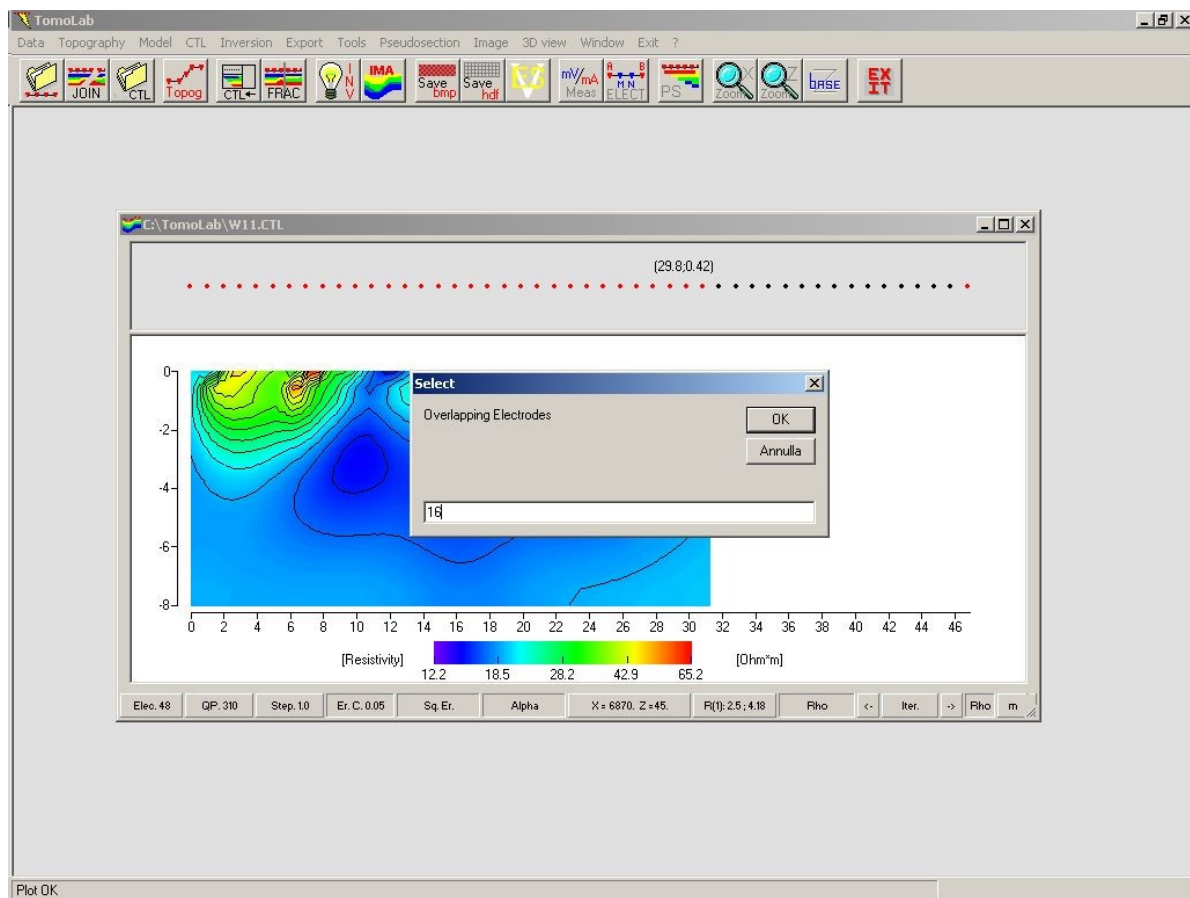
For the first result file use zero as overlapping electrodes



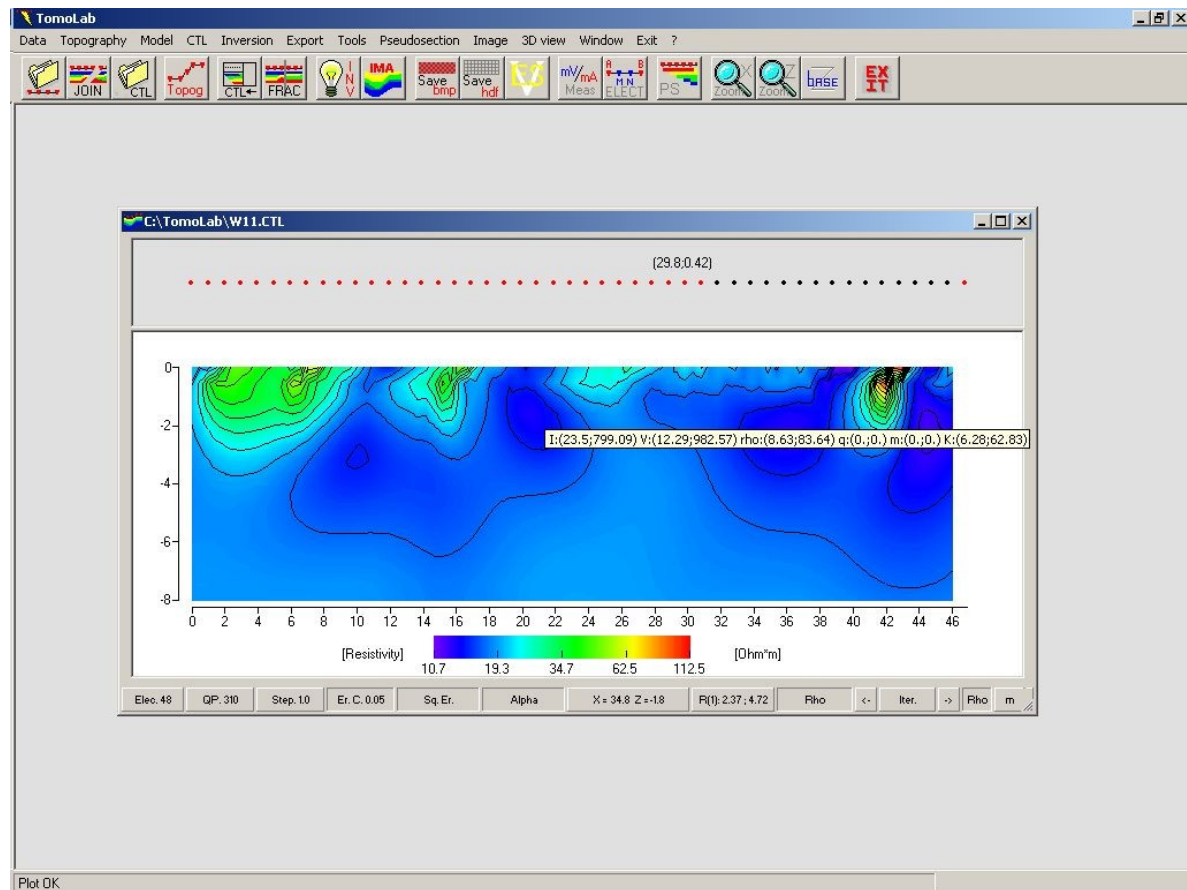
**Pic 102** The results file of the first sub-file has zero offset X



For the second file use the value used in the split operation



**Pic 104** Load results of the second sub-file: n = 16 electrodes of overlapping

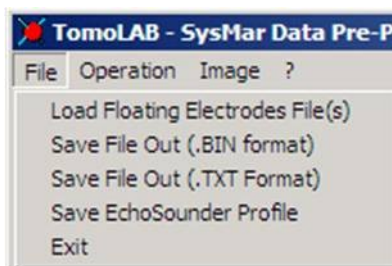


**Pic 105** Results chained. The overlapped region is the average of the two

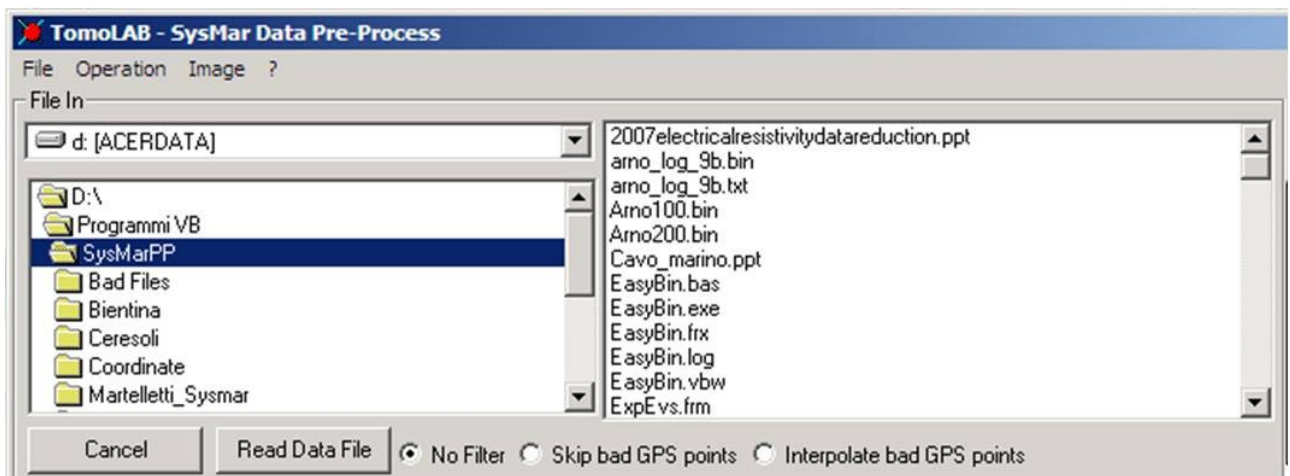
## D – Manage Floating Electrodes

The introduction of multichannel resistivimeters has been reliable a continuous acquisition by dragging a cable. Measurements carried out on shallow water environment have a peculiar role. The water layer ensure electrical contact and continuity, the simultaneous acquisition of both the position with a GPS and the water depth with an echo sounder system, create a consistent set of data.

TomoLab can perform 2D data inversion, so the very first operation is to check if data have been acquired along a straight line, otherwise data files have to be split into straight subsets. To do this data must be viewed into a 3D environment. A simple application named Sysmar Pre-Process have been added to TomoLab setup package to allow user to look at data into 3D space and split file into linear subsets.



Select "Load Floating Electrodes File" (multiple selection allowed). The .bin and .txt file formats form IRIS SysMar are supported.



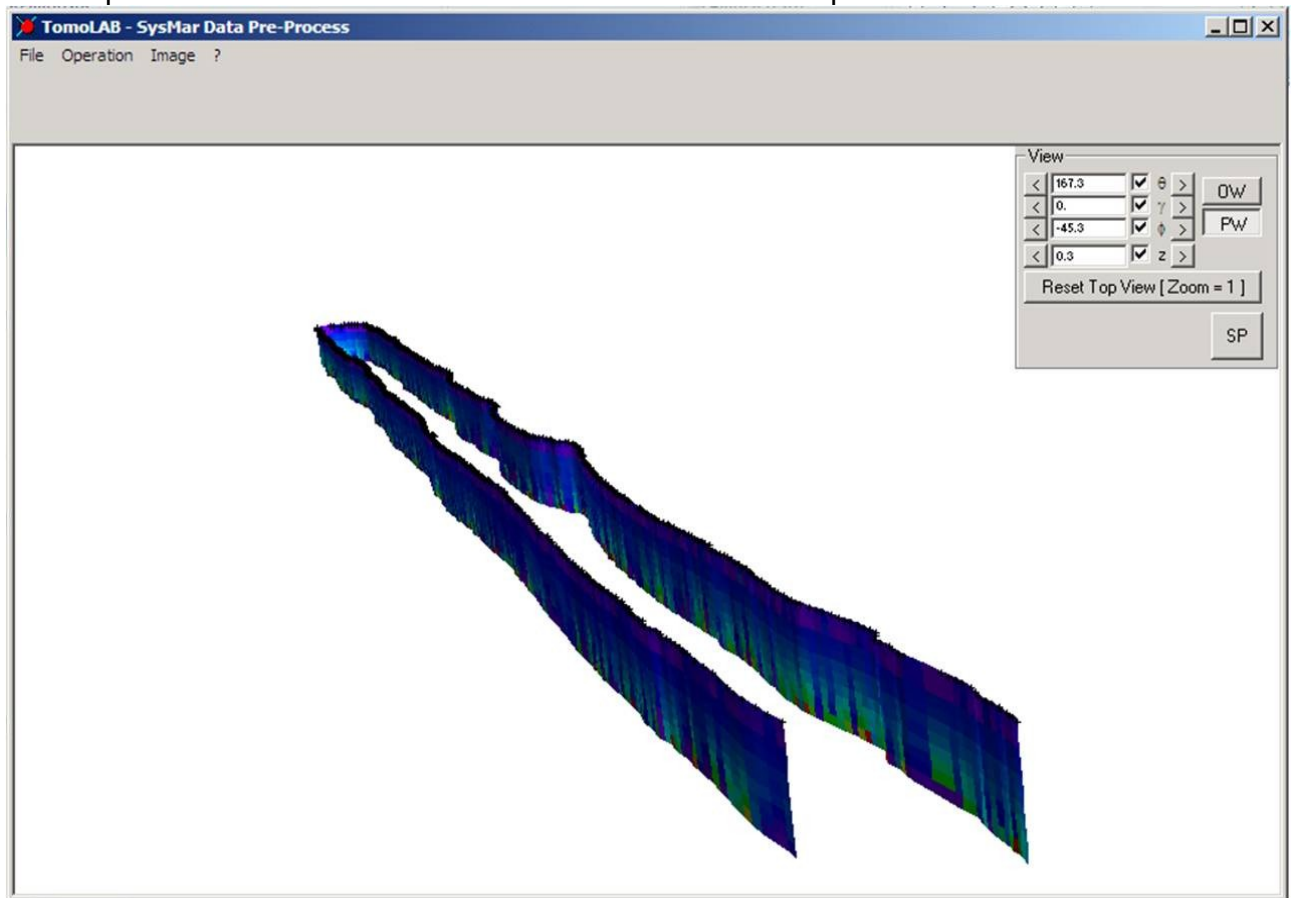
**Pic 106** Load File Panel

Browse the directory and select the file(s). The default option button is "No Filter", file will be read with no action on data. In case of some stations don't have the correct GPS string (null value) user should select "Skip bad GPS point" (bad data will be removed from data set) or "Interpolate bad GPS points" (bad data will be replaced with linear interpolation between the two nearest good points, distance, rho value will be recomputed too).

Data are plotted as pseudosection, ten channels are ten levels, levels are vertically spaced as the distance between current electrodes as defined in the Sysmar configuration. Image can be rotated and zoomed as in the 3D viewer environment of TomoLab. Orthographic and perspective view are also possible.



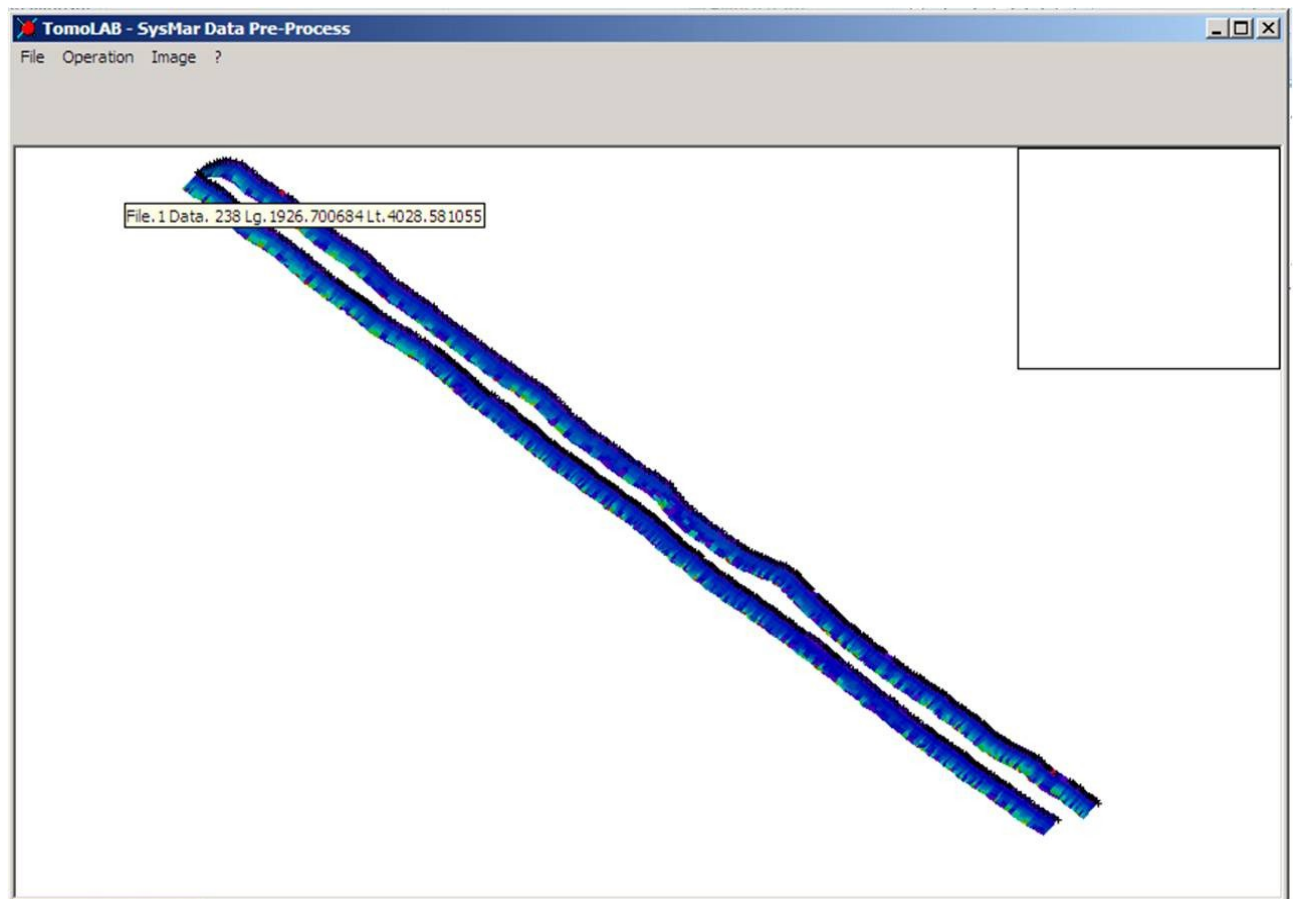
In the picture below there is a data set that should be split in almost two subsets.



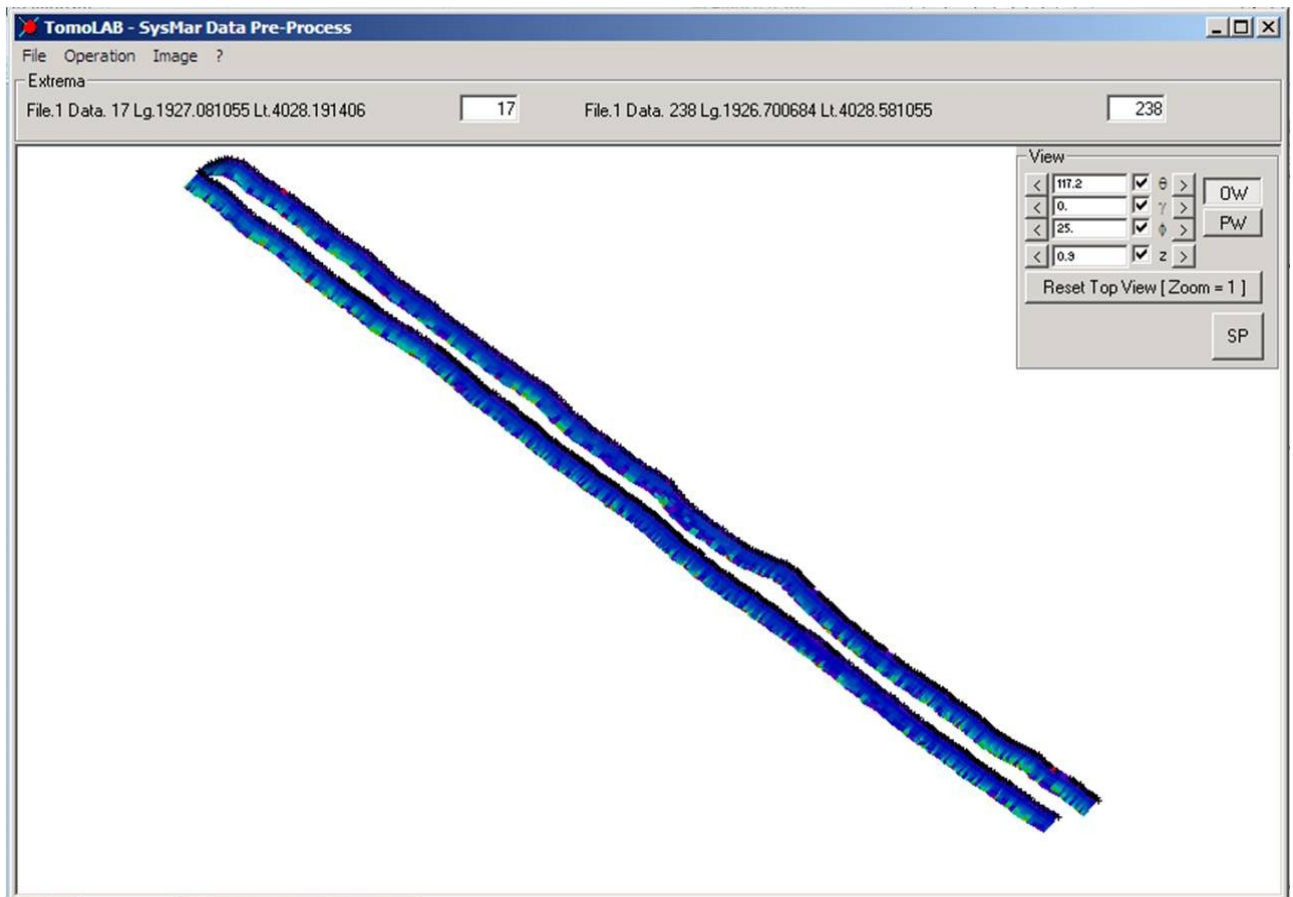
**Pic 107** Perspective view of the data. Small black cross represent the centre of the quadrupoles array



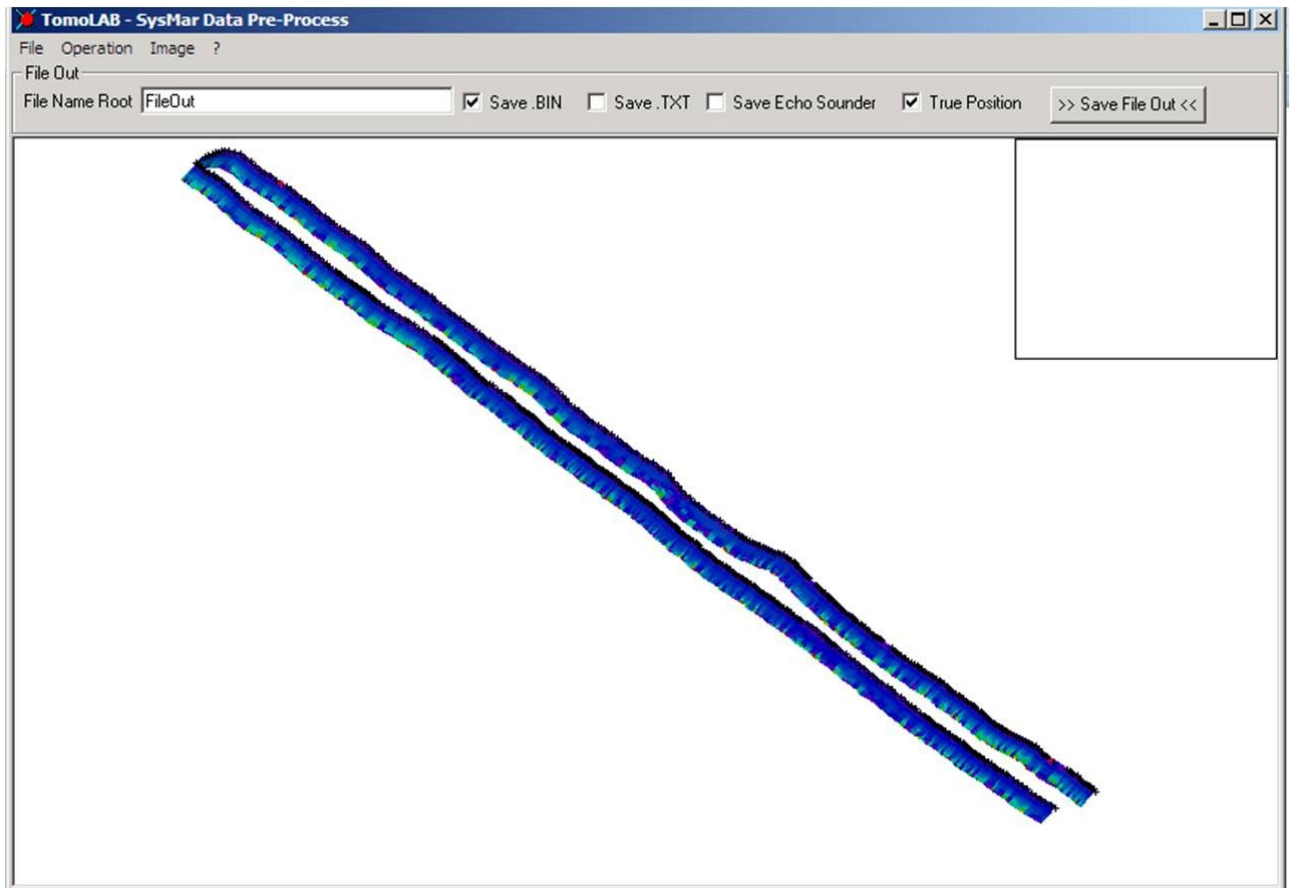
**Pic 108** Orthographic view. First position for the straight extraction is selected with a mouse click (Data n. 16, red cross)



**Pic 109** Orthographic view. Second position for the straight extraction is selected with a mouse click (Data n. 238, red cross)



**Pic 110** The two extremes can be set by a couple of text box activated with the menu operation (Select First Data, Select Second Data)



**Pic. 111** From menu File, select the option "Save File Out" and choose the output file name and format. The extensions ".BIN", ".TXT" or ".ECS" for the echo-sounder tracks are automatically added.

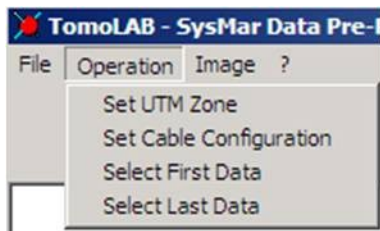
It is possible to save extracted straight line as standard .bin format and manage it with TomoLab or Prosys, or in a ASCII format (.TXT). It also possible to extract the echo-sounder tracks (three columns ASCII file, Lat, Lon from GPS and water depth from the echo-sounder) in a text file with the extension .ECS.

The couple of coordinates saved into the .bin o .txt file are not the Lat Lon from the original but follow UTM (Universal Transverse of Mercatore) scheme in order to make easier to report data into a map. So if you look at the extract .bin file with Prosys you will find UTM value instead of Lat Lon (the field names are still Longitude and Latitude).

Within the approximation of "straight line" it is possible to "correct" ("True Position" check box) the measure coordinate for the distance between Syscal (and GPS) and current electrodes that are, in general, several meters far from the resistivimeter.

The correction shift depends on the distance between the middle of current electrodes and the nearest electrode plus an offset value determined by the fields conditions.

Few other functions have been added to this software tool

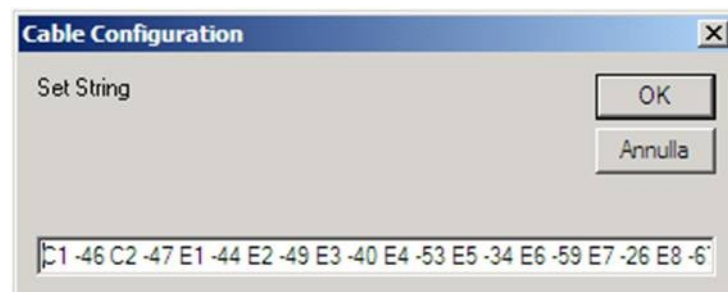


Set UTM zone: the UTM zone is automatically detected from longitude value of the first good data point. In some specific case would be need to set a different UTM zone number.



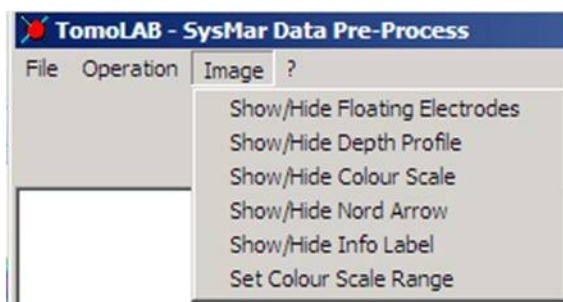
**Pic. 112** The UTMx coordinate will be calculated with the central meridian derived from the zone number set in this dialog box

The cable layout and the geometry of the acquisition system must be set into the Sysmar software before the measurements start. In case of a bad configuration it is possible to reset the cable configuration to the right one, recomputed the geometrical factors and the apparent rho values



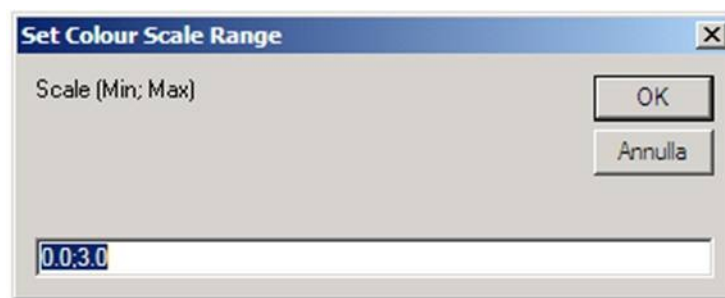
**Pic. 113** The string show the electrodes position as derived from data. User can modify the string pay attention to keep the electrodes order and tags.

The menu image offer few tools to adjust the current image plot.





[Show/Hide Floating Electrodes]	Show or Hide the black crosses represent the current electrodes midpoint;
[Show/Hide Depth Profile]	Show or Hide the line of the echo-sounder data. Z scales of echo-sounder and rho pseudo-sections are different. Remember that echo sounder data are referred to GPS position (the Syscal) and the rho data are referred to the cable midpoint, several meters from Syscal;
[Show/Hide Colour Scale]	Show or Hide the colour scale at the bottom of the graph window;
[Show/Hide Nord Arrow]	Show or Hide an Arrow to the geographic Nord;
[Show/Hide Info Label]	Show or Hide a label with info on current operation or error
[Set Colour Scale Range]	Adjust the colour scale limits, for marine environment $0 \Omega \cdot m$ and $3 \Omega \cdot m$ looks ok;



**Pic. 114** Dialog box of the color scale limits. Rho value less than the minimum will be plot as the minimum and Rho greater than the maximum will be plot as the maximum. The color scale is logarithmic

## E - Array status bar



Each window in TomoLab is a data-file. At the bottom a status bar collect some info and allow basic operation

- [Elec.]      Number of electrodes in the data-file. Left click activate the electrodes data grid;
- [QP.]        Number of quadrupoles in the data-file. Left click activate the measurements data grid;
- [Step]       Average distance between adjacent electrodes. Left click activate a dialog box that allow to reset this parameters. With the new "Step" TomoLab compute distances, geometrical factors and apparent resistivity;
- [Er. C.]      Error coefficient of the current iteration;
- [Sq. Er.]     Squared error of the current iteration;
- [Alpha]      Alpha parameter of the current iteration;
- [X = ; Z =] (X;Z) position of the mouse over the image. Left click activate a double dialog box. User can set label interval in the axes. Optional a slash "/" after the label step allow user to set the "minor thick" of the axis. Es. "10/2" means X labels and major thick spaced 10 meters, minor thick (no label) spaced 2 meters;
- [R(1)]       Colour scale range in logarithmic value. Left click activate a dialog box within the colour scale limits (linear value). User can set the colour scale limits (use semicolon as separator). After this operation TomoLab re-plot the image with the new settings. The number between the brackets refers to the colour scale currently used;
- [Rho]        Show the Log(Rho) at right mouse down;
- [<-]        Show the previous iteration;
- [iter.]       Iteration number currently displayed. Left click activate a dialog box that allow user to set a specific iteration number;
- [->]        Show next iteration;
- [Rho]        Show resistivity in results or pseudosection;
- [m]          Show chargeability in results or pseudosection;
- [nIP]        Show normalized inductively polarization in results or pseudosection;
- [Siem/m]    Show conductivity in results or pseudosection;