X2IPI

Tool box for 2D Electrical Resistivity Tomography and IP measurements

User Manual

Henri ROBAIN [1] and Alexei BOBACHEV [2]

(1) : Henri.Robain@bondy.ird.fr
IRD – R027 GEOVAST
32, avenue Henri Varagnat
93143 BONDY CEDEX
FRANCE

(2) : bobachev@gmail.com
Moscow State University
Geological Faculty, Department of Geophysics
119899, MOSCOW
RUSSIA

Summary

1. General information about *X2IPI* 3
1.1.1. Copyright 3
1.1. System requirements 3
2. Overview of the X2IPI tool box 3
2.1. Input files formats 3
2.1.1. Protocols (sequences) 3
2.1.2. Field data 4
2.1.3. Input file for the inversion software (Res2dinv) 5
2.1.4. Induced polarization decay curve data 5
2.2. Main menu 5
2.2.1. File menu 5
2.2.2. Save menu - SEQ 6
2.2.3. Save menu – DAT 6
2.2.4. Save menu 7
2.2.5. Exchange menu 8
2.2.6. Options menu 9
2.2.7. Contour menu 9
2.2.8. Tool Bar 10
2.3. Main window 10
2.3.1. Status 11
2.3.2. Type of data in Display window 12
2.4. Display window 12
2.5. Tables window 15
2.5.1. Data table 15
2.5.2. Electrodes table 17
2.5.3. Spacing page 18
2.5.4. Soundings page 19
2.5.5. Profiling page 19
2.5.1. INV result pages 19
2.5.1. X correction page 19
2.5.2. Multinode page 20
2.6. Advanced Display window 20
2.6.1. Menu of Advanced Display window 23
2.6.2. The Section Options window 23
2.7. Median window 24
3. Work with X2IPI 27
3.1. Creating [*.seq] files 27
3.2. Sorting the measurement to use modern multi-channel receivers. 28
3.3. Optimization for Schlumberger array 29
3.4. Modifying [*.seq] file 29
3.4.1. Modifying electrodes unit spacing 29
3.4.2. Removing a faulty electrode 29
3.4.3. Shifting electrodes 30
3.4.4. Removing measurement lines 30
3.4.5. Preparing a “Roll along” [*.seq] file 30
3.4.6. Changing Multinodes 31
3.4.7. Transforming AMN to MNB 32
3.5. Working with data files 32
3.5.1. Opening data files 32
3.5.2. Shifting data file 34

3.5.3. Trimming bad measurements 34
3.5.4. Merging data files 34
3.5.5. Generating Schlumberger data from AMN and MNB data 34
3.6. Median Processing 35
3.6.1. Pseudosection decomposition 36
3.6.2. Components smoothing 38
3.7. Exporting to inversion programs 40
4. How to use x2ipi with Terrameter LS (ABEM, Sweden) 40
4.1. Creating protocol files for 4x21 cables set 40
4.2. Read field data of Terrameter LS 44
5. How to use x2ipi with Syscal-Pro (IRIS Instruments, France) 45
5.1. Creating sequence file for Syscal-Pro 45
5.2. Read field data from Syscal-Pro 47
6. How to use x2ipi with Res2dinv format data (Geotomo software, Malaysia) 48
6.1. Remove bad points from data file 48
6.2. Correct X-coordinate 48
6.3. Merge different array and different cable setup in one data set 49
6.4. Input topography 49
6.5. Analysis of inversion result (INV files) 50

1. General information about *X2IPI*

X2IPI - 2D electrical resistivity tomography processing:

- check and correct field data,
- analyze IP data,
- merge or separate data set,
- optimize ERT sequences,
- prepare files for 2D inversion and analyze the result of 2D inversion,
- prepare files for 1D interpretation of VES curves from ERT data.

1.1.1. Copyright

© Alexey A. Bobachev, 1999-2017. All rights reserved. All the trademarks and all the registered trademarks mentioned throughout this manual are the properties of the corresponding owners.

1.1. System requirements

X2IPI may be run on any IBM PC compatible computer with Windows XP - Windows 10 operating system.

2. Overview of the X2IPI tool box

x2ipi is toolbox to process the data of 2D Electrical resistivity tomography. This software helps you

- configure ERT unit protocols (sequences) for optimal measurements procedures,
- test and evaluate the quality of the field data,
- prepare the input files for programs of two-dimensional inversion.

x2ipi works with field data formats of some ERT units:

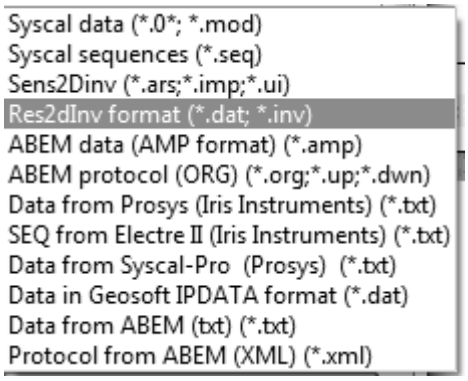
- **IRIS Instruments** (France): ***Syscal-Pro, Syscal-R2***
- **ABEM** (Sweden): ***Terrameter LS, SAS4000/SAS1000***

x2ipi supports ***Res2dinv*** and ***ZondRes2d*** data formats. It is possible to export tomography data and inversion result to ***ipi2win*** software for 1D VES curves interpretation.

2.1. Input files formats

x2ipi software works with different input file types. Three main types are

- protocol (sequence). It describes the order in which measurements are performed;
- field data (output file from the ERT instrument). The data are usually binary and has closed proprietary format. It has to be pre-converted to .txt format;
- input file for the inversion software (Res2dinv). Roughly speaking, it is the result of field data processing;
- input file that contain IP data. This type is designed specifically for the IP decay curve processing.

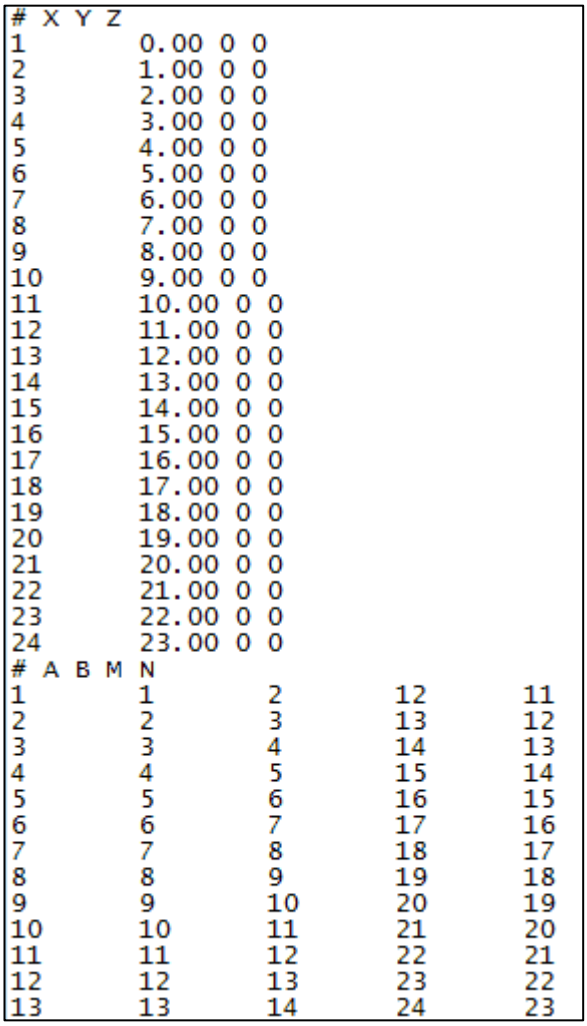


2.1.1. Protocols (sequences)

The primary type of a ERT protocol has .txt format that used by IRIS Instruments in ***Electre II*** software ("*SEQ from Elecell, IRIS Instruments*"). This format is supported by the current version of the program - ***Electre PRO***. The .txt file consists of the two parts. Coordinates of all the electrodes are described in the first part (electrode number, X-, Y-, Z-coordinate). It should

be noted that ***x2ipi*** reads only the electrode number and its X-coordinate. The second part describes electrode numbers for each measurement (number of the present quadripole, A-, B-, M-, N-electrode numbers). For a remote electrode null ("0") must be specified in a corresponding column. This format is compatible with some instruments: Syscal-Pro, Omega-48, SibER-64.

When you export a .txt protocol from the ***Electre PRO*** the third part is added to the result file. It contains information about the changes of the initial file that happed before the export. This part is not supported by ***x2ipi*** yet.



```
# X Y Z
1        0.00 0 0
2        1.00 0 0
3        2.00 0 0
4        3.00 0 0
5        4.00 0 0
6        5.00 0 0
7        6.00 0 0
8        7.00 0 0
9        8.00 0 0
10       9.00 0 0
11       10.00 0 0
12       11.00 0 0
13       12.00 0 0
14       13.00 0 0
15       14.00 0 0
16       15.00 0 0
17       16.00 0 0
18       17.00 0 0
19       18.00 0 0
20       19.00 0 0
21       20.00 0 0
22       21.00 0 0
23       22.00 0 0
24       23.00 0 0
# A B M N
1        1        2        12       11
2        2        3        13       12
3        3        4        14       13
4        4        5        15       14
5        5        6        16       15
6        6        7        17       16
7        7        8        18       17
8        8        9        19       18
9        9        10       20       19
10       10       11       21       20
11       11       12       22       21
12       12       13       23       22
13       13       14       24       23
```

x2ipi supports the old ***Electre*** .seq format also ("*SEQ (Syscal sequences)*").

x2ipi can work with ABEM (Sweden) protocols for ***Terrameter LS*** instrument ("*Protocol from ABEM (XML)*"). Such protocols have XML format. To convert a newly created protocol into actual ABEM format you first has to save it into .org file ("*ABEM protocol (ORG)*"). The .org file extension was used in earlier versions of software for the ABEM instrusments. ***Terrameter LS Toolbox*** software (supplied with the equipment) can convert .org file into .xml. Here, in the .org file, you just need to specify the correct file (spread) that describes the ERT cable. Earlier, this spread-file had an ***.adr*** extension and now it has ***.xml*** too

2.1.2. Field data

The basic field data format is text file from ***Prosys II*** (IRIS Instruments, Франция): *Menu - File - Export and save - Spreadsheet*...
All data are saved in different columns. The order of these columns is arbitrary and some columns may be missing. The type of column is defined by name in the first line.

- **#** - Data point number (corresponding to the memory zone of the resistivity-meter)
- **Spa.1 .. Spa.4** - spacing parameters (corresponding to the electrode array A-B-M-N in meter) (value 99999.99 for remote electrode)
- **Vp**: measured primary voltage (in mV)
- **In**: injected current intensity (in mA)
- **Rho** - resistivity value (in Ohm.m)
- **Dev**: standard deviation (quality factor, in %)
- **M**: global chargeability value (induced polarization parameter (in mV/V – "=0" if only-resistivity data))
- **M1/M20**: partial chargeability values (induced polarization window (in mV/V – "=0" if only-resistivity data))

The field data file can be opened in ***x2ipi*** by two ways:

- *Data from Prosys (Iris Instruments)*
- *Data from Syscal-Pro (Prosys)*

The second way allows to remove non-labeled linking measurements.
The field data from **Terrameter LS** is read by file type *Data from ABEM (.txt)*.

2.1.3. Input file for the inversion software (Res2dinv)

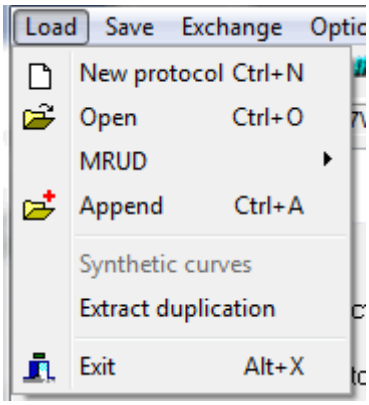
The main goal of ***x2ipi*** is field data processing and the preparation of data file for the 2D inversion software. That is why the result output file has ***Res2dinv*** format. There are two different formats for the ***Res2dinv***: standard format for the basic arrays (e.g. Schlumberger, pole-dipole etc.) and **general** format that allows user to work with any electrode configuration. General format is a very easy way to combine measurements obtained with different electrode arrays into one data file readable by ***Res2dinv***. However, it is inconvenient to use this format when plotting the pseudosection of apparent resistivity (moreover, it is impossible to do in ***Res2dinv***). ***x2ipi*** solves this problem. It analyzes and divides the file into parts by type of the electrode array. Then the program plots apparent resistivity pseudosection for every individual part (array type).
The most of 2D ERT inversion software supports ***Res2dinv*** format. ***x2ipi*** program can also work with data from inversion results file (****.inv***) of ***Res2dinv.***

2.1.4. Induced polarization decay curve data

Standart way to keep IP decay curves is the format of company Geosoft. *Save-Data-GEOSOFT.* Also there is the modification of ***Res2dinv*** data format proposed by Torleif Dahlin. The option *Menu-Save-Save options-Remove IP decay* allows to remove the IP decay curves from data

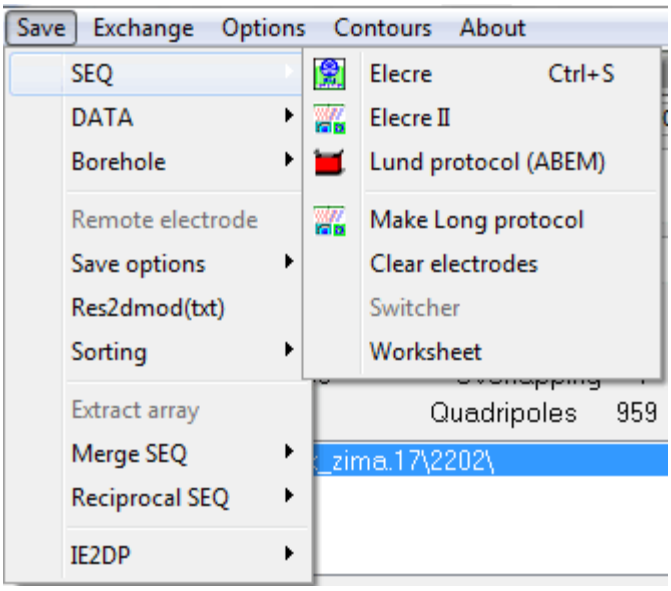
2.2. Main menu

2.2.1. File menu



- *New protocol (Ctrl+N)* : Create a new sequence file.
- *Open (Ctrl+O)* : Open input files.
- *MRUD* : The list of Most Recently Used Directories, open file in another catalog.
- *Append (Ctrl+A)* : Append a protocol, a data file or a [*.dat] RES2DINV file to already opened files of the same type.
- *Synthetic curves* : Replace field data by synthetic data from INV file
- *Extract duplication* : Divide data set with repeated measurements in some data sets. For example, forward and reverse dipole-dipole data into files.
- *Exit (Alt+X)* : Exit ***X2IPI***

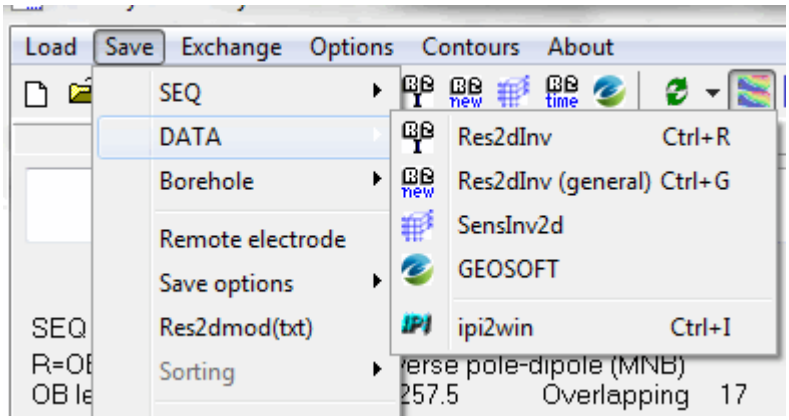
2.2.2. Save menu - SEQ



- *Electre* : Save binary protocol file for old ***Electre*** program (IRIS Instruments)
- *Electre II*: Save text protocol file for ***Electre II*** and ***Electre Pro*** programs (IRIS Instruments)
- *Lund protocol (ABEM)* : Save Lund protocol file **org** (ABEM). Terrameter LS Toolbox software (supplied with the equipment) can convert .**org** file into modern **.xml** format to work with ***Terrameter LS*** and ***Terrameter LS2***.
- *Make Long protocol* : Make protocol with ODD electrode number only - LONG32 type for ABEM 4x21 spreads system.
- *Clear electrodes* : Remove unused electrodes from protocol.
- *Switcher* : prepare protocol for COMx64 switcher box (Nord-West).
- Worksheet : Text protocol file with additional columns.

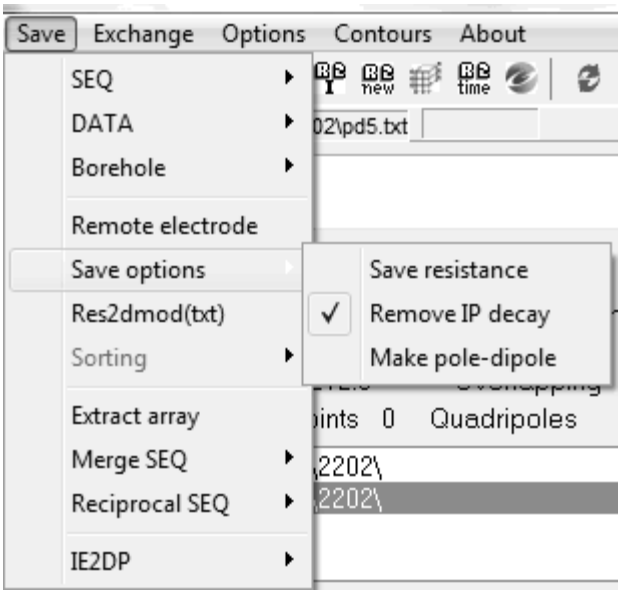
```
68      335.00 0 0
69      340.00 0 0
70      345.00 0 0
71      350.00 0 0
72      355.00 0 0
#       nA      nB      nM      nN      X       AB/2    MN      K
1       1       16      70      55      172.5   135     75      10145
2       1       16      66      51      162.5   125     75      7941
3       1       16      62      47      152.5   115     75      6073
4       1       16      58      43      142.5   105     75      4513
5       1       16      54      39      132.5   95      75      3234
6       1       16      50      35      122.5   85      75      2210
7       2       17      71      56      177.5   135     75      10145
8       2       17      67      52      167.5   125     75      7941
9       2       17      63      48      157.5   115     75      6073
10      2       17      59      44      147.5   105     75      4513
11      2       17      55      40      137.5   95      75      3234
12      2       17      51      36      127.5   85      75      2210
13      3       18      72      57      182.5   135     75      10145
```

2.2.3. Save menu – DAT



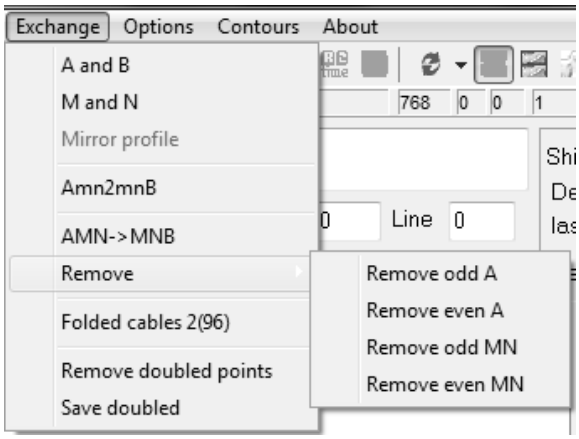
- *Res2dinv (Ctrl+R)* : Export input file for RES2DINV interpretation software with specified electrode configuration format (Schlumberger, pole-pole, pole-dipole…)
- *Res2dinv general (Ctrl+G)* : Export input file for RES2DINV interpretation software with general electrode configuration format. This feature of RES2DINV is to cater for electrode arrangements that do not fall under the usual array types or electrode arrangements, or unusual ways of carrying out the surveys.
- *SensInv2D* : Export input files for SENSINV2D interpretation software
- *GEOSOFT* : Save data in GEOSOFT format, mainly for IP data.
- *ipi2win (Ctrl+I)* : Export input file for 1D interpretation in IPI2WIN software.

2.2.4. Save menu

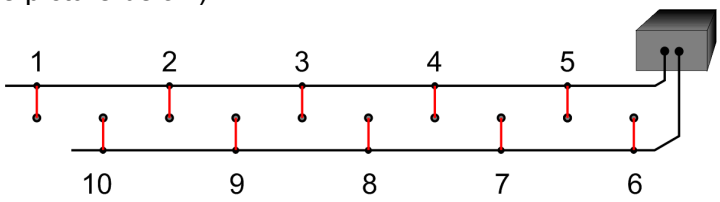


- *Borehole* : Work with boreholes ERT measurements.
- *Remote electrode* : Input remote electrode position for pole-dipole array and apparent resistivity correction for remote electrode position.
- *Save option – Save resistance* : save resistance instead apparent resistivity.
- *Save option – Remove IP data* : remove IP data from data set.
- *Save option – Remove IP decay* : remove IP decay for 2D inversion in Res2din software.
- *Res2dmod(txt)* : TXT format of res2dMod software for work with non-standard array. It allows to calculate 2D sensitivity pseudo-section for arbitrary array.
- *Sorting* : Change the order of measurement in protocol.
- *Extract array* : Save data or protocol for selected array only.
- *Merge SEQ* : Merge protocols files in one protocol file.
- *Reciprocal SEQ* : Save protocol file for reciprocal array.
- *IE2DP* : Convert protocol file into RES2DINV format. Coefficient of array (K) is saved as apparent resistivity.

2.2.5. Exchange menu

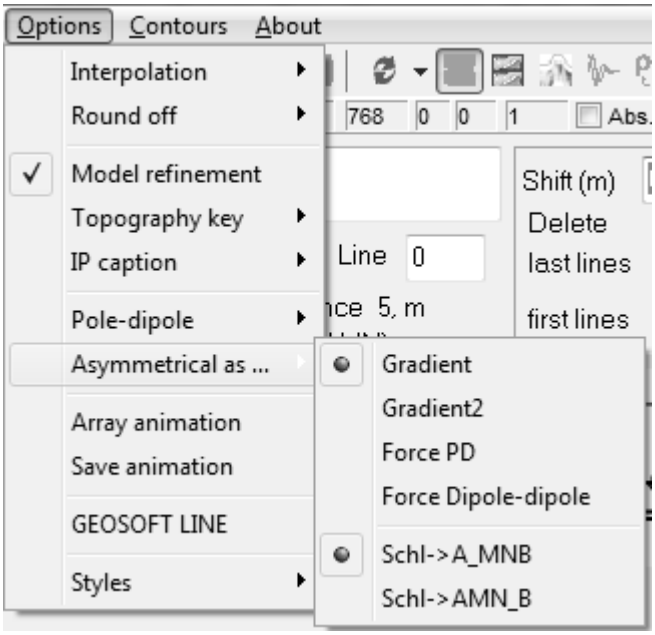


- *A and B* : Exchange A and B electrodes in protocol files.
- *M and N* : Exchange M and N electrodes in protocol files.
- *Mirror Profile* : Reverse the coordinates of electrodes in protocol or data files. For example, if 1st electrode coordinate is 0, 2nd is 1 and last is N, the modified file will have 1st electrode coordinate at N, 2nd at N-1 and last at 0.
- *Amn2mnB* : Transform AMN [*.seq] file (forward pole-dipole) to MNB [*.seq] file (reverse pole-dipole)
- *AMN->MNB* : Transform AMN [*.seq] file (forward pole-dipole) to MNB [*.seq] file (reverse pole-dipole) using electrodes numbers only.
- *Remove* : remove some electrodes for pole-dipole array protocol to decrease time of measurements or for work with nonpolarizing electrodes.
- *Folded cables* : Transform protocol for work with folded cables to decrease inter-electrode spacing twice (see picture below).



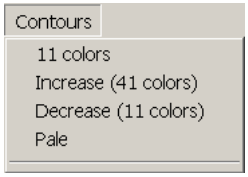
- *Remove doubled points* : remove repeated measurements from two datasets.
- *Save doubled* : extract control readings from two datasets.

2.2.6. Options menu



- *Interpolation* : maximal number of missed points in pseudo-section to interpolate contours. Differently there is blank space on pseudosection.
- *Round off* : round off electrode position to decrease number of spacing.
- *Model refinement* : There are two possible ways to reduce the width of the model cells. The first method is implemented in the **Res2dinv** itself by using the "Use model refinement" option on the "Inversion" menu. The second method is to modify the data file directly using a text editor. The unit electrode spacing, given in the second line of data file, will be twice less inter-electrode spacing.
- *Topography key* : the key of topography for **res2dinv** software. In the case where the actual horizontal and vertical coordinates of topography data points along the survey line are given, enter 1. In most surveys the distances of the points are measured along the ground surface with a tape or using a cable with takeouts at regular intervals. It is not true horizontal distances. In this case, enter a value of 2 for the topography data flag.
- *IP caption* : IP data caption for RES2dinv data file.
- *Pole-dipole* : Reference point for pole-dipole array data. Reload dataset to see changes.
- *Asymmetrical as …* : The variants of asymmetrical (gradient) array data presentation. Reload dataset to see changes.
- *Array animation* : animation of order measurements in protocol file.
- *Save animation* : save a BMP file for each measurements in x2ipi catalog (hundreds of files!!!).
- *Geosoft line* : line number for data file in Geosoft format.
- *Styles* : Change the theme of programs windows.

2.2.7. Contour menu



This menu allows to modify the color scale of the Display window.

- *11 colors :* Display using 11 value levels.
- *Increase(<NUM colors>)* Display using <*NUM*> value levels (<*NUM*> is larger than the currently used number of levels).
- *Decrease (<NUM> colors)* Display using <*NUM*> value levels (<*NUM*> is less than the currently used number of levels).

- *Pale :* Display using less saturated hues.

More option for color scale in Option of pseudo-section window.

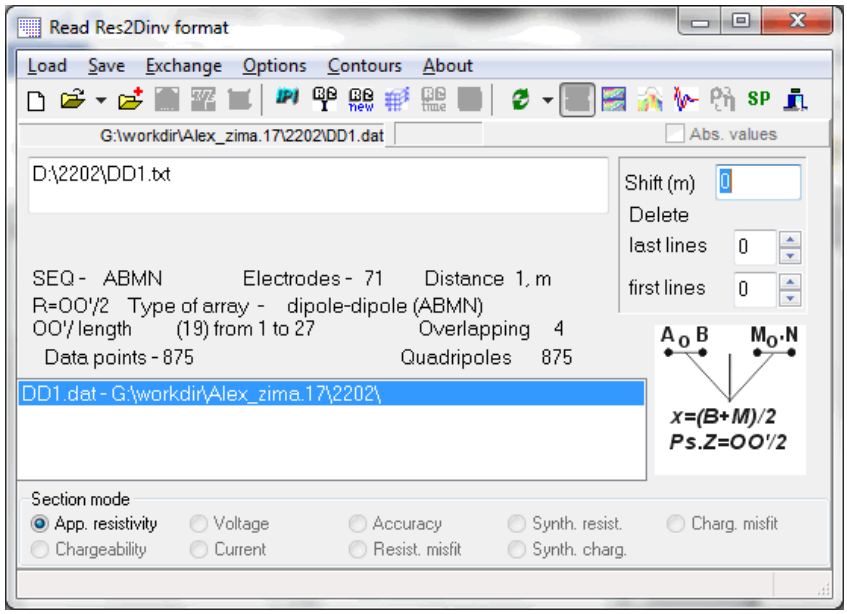
2.2.8. Tool Bar

The following icons are available in the icons bar :

- : Create a new protocol file.
- : Open input file.
- : Append a [*.seq] file, a SYSCAL® data file or [*.dat], [*.inv] RES2DINV file to already opened files of the same type
- *:* Save binary protocol file for old ***Electre*** program (IRIS Insruments)
- : Save text protocol file for ***Electre II*** and ***Electre Pro*** programs (IRIS Insruments)
- : Save Lund protocol file **org** (ABEM). Terrameter LS Toolbox software (supplied with the equipment) can convert .**org** file into modern **.xml** format.
- : Export input file for 1D interpretation in IPI2WIN data format.
- : Export input file for RES2DINV interpretation software with specified electrode configuration format (Schlumberger, pole-pole, pole-dipole…)
- : Export input file for RES2DINV interpretation software with general electrode configuration format.
- : Export input files for SENSINV2D interpretation software
- : Save data in GEOSOFT format, mainly for IP data.
- : Redraw pseudosection in Dispay window.
- : Contours map in Display window ON/OFF
- : Display window ON/OFF
- : Table window ON/OFF
- : Multi section window ON/OFF.
- : Open advanced Display window (only available for data files)
- : Open advanced Display window for dataset with topography.
- : Open Median smoothing window (only available for RES2DINV [*.dat] or [*.inv] files)
- : Show apparent resistivity or IP data in Display window.
- : Show selfpotential window.
- : Exit ***X2IPI***

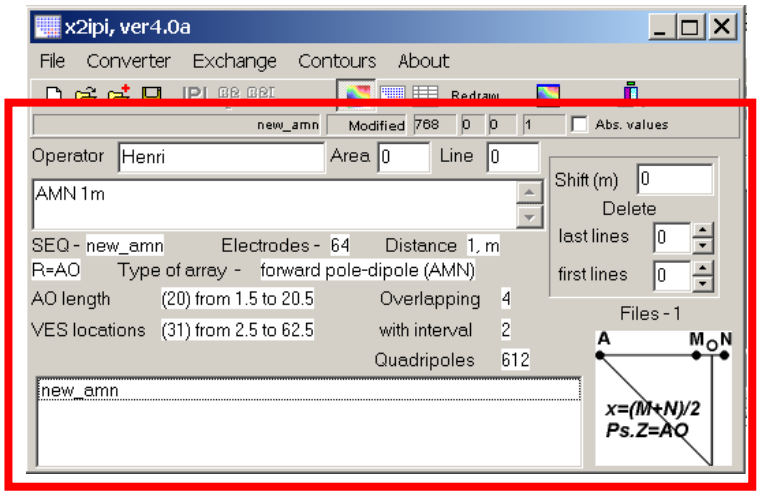
2.3. Main window

The program has some windows. The first three (Main, Display, Table) are default windows.



2.3.1. Status

This part of the main window is general information about the opened files.



The first line shows the name of the last opened file
In this first line, you may check a “Abs values” button (only useful for binary SYSCAL® files)

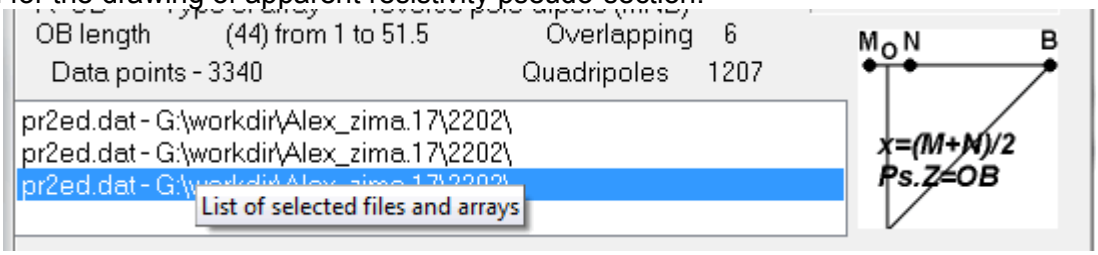
Next are shown the name of the operator, the reference number of the area, the reference number of the line and some commentaries. All those indications may be edited and changed, but they were used only in old binary data format of Syscal. The first line of comments is used in Res2dinv data files.

Next are shown indications concerning the configuration of electrodes: the name of the [*.seq] file used, the number of electrodes, the unit inter-electrode spacing, the type of array, the number of AO lengths, the number of overlapping measurements (for Schlumberger, pole-dipole and dipole-dipole measurements only), the number of vertical sounding locations, the interval between VES and the total number of quadrupoles. None of these indications may be changed.

3 buttons are placed in a dialog box at the right part of the status windows

- A “shift (m)” button which allows to shift by a constant X coordinate of all electrodes
- A “Delete last lines” button which allows to remove a chosen number of lines at the bottom of the pseudo section.
- A “Delete first lines” button which allows to remove a chosen number of lines at the top of the pseudo section.

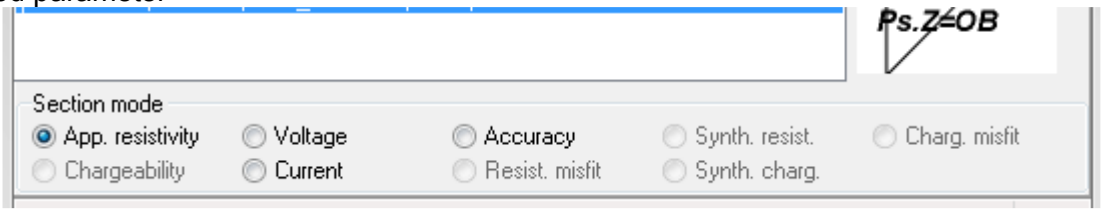
Finally at the right bottom corner, a small plot indicates the default convention of reference point, chosen for the drawing of apparent resistivity pseudo-section.



The list of selected files and arrays allows choose a data, which is visible in Display window.

2.3.2. Type of data in Display window

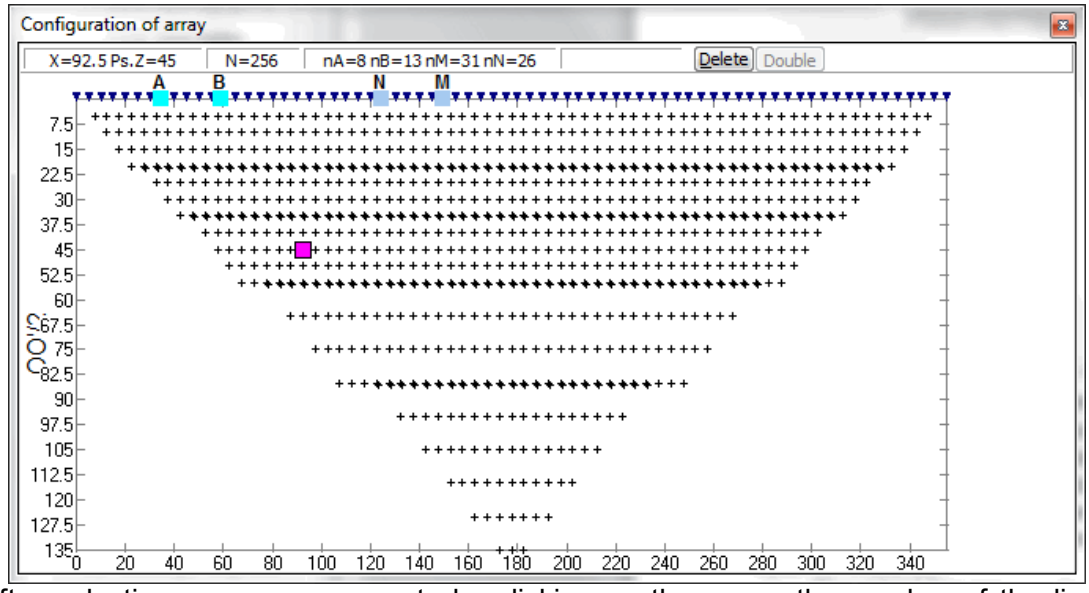
There are two common parameters that characterize obtained ERT data: *apparent resistivity* and *chargeability*. The most common way to visualize such data is plotting **pseudosections**, i.e. map of the parameter in (Distance-Spacing) axes.
There are other parameters that characterize the field data also, such as *Voltage*, *Current* or *Accuracy*. The presentation of these parameters is less common. However, their use allows to analyze the ERT field data also. The user of ***x2ipi*** could view and analyze field data using specified parameter



It is also possible to open *.inv* files (i.e. output files from *Res2dinv* software) in ***x2ipi***. This option allows user to analyze the pseudosection of difference between the field data (inversion input) and the direct problem solution of the final model (inversion output).

2.4. Display window

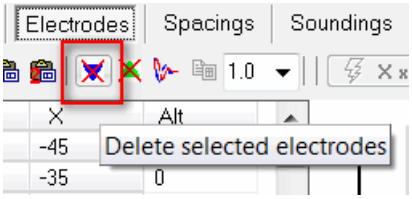
The default display windows gives a plot of data contained in the opened files. Electrode positions are shown by the triangles at the top of the pseudosection
The conventional positions of each measurement is shown by a cross. Bold cross means that two readings have the same position on pseudo-section. By example, two readins of Dipole-Dipole array have the same OO' spacing, but different MN lengths.



After selecting one measurements by clicking on the cross, the number of the line in the protocol file and the reference numbers of A, B, M and N electrodes, are shown in the status bar of

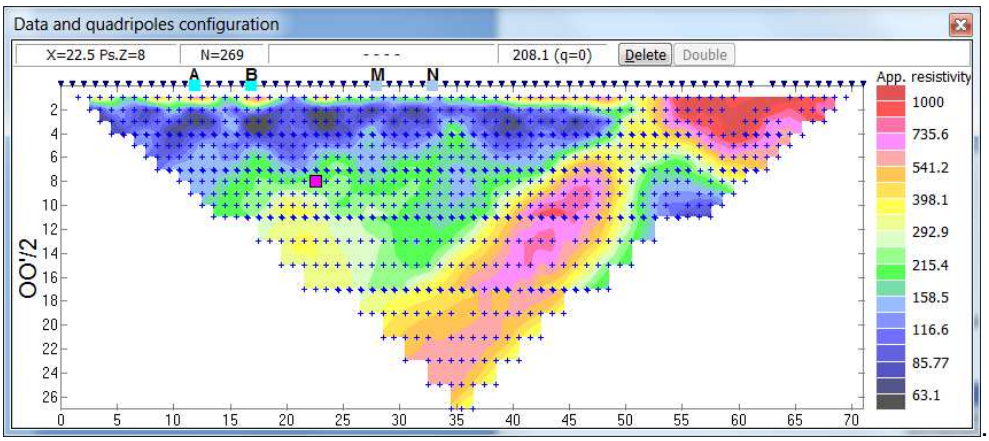
the default display window.The position of A, B, M and N electrodes are also highlighted by squares (blue color for M and N; aqua color for A and B). The selected point may be removed from data file by clicking on the “delete” button in the status bar of the default display window or by double click.

An electrode may also be selected by clicking on the top triangles. All the measurements made using this electrode may then be deleted by clicking on the “delete” button on the Table window.

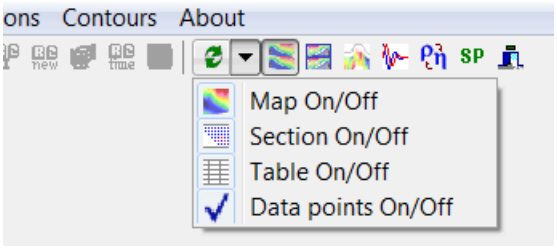


The “double” button is used when two protocol files are opened. The “double” button in the status bar of the default display window removes the repeated measurements from the ***last*** protocol file.

The same possibilities are available to edit data files. But for such files the apparent resistivity pseudo section is also displayed.

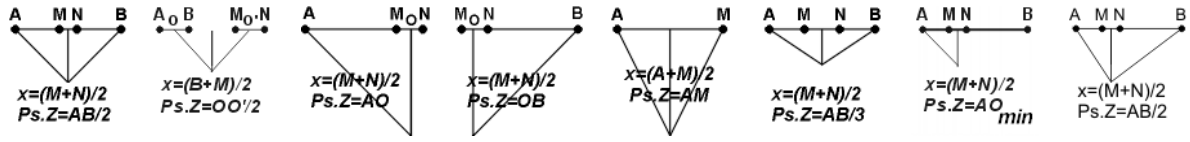


It is possible to remove pseudo section from Display window by “Map ON/OFF” button on the tools bar of the main window. Also you can remove data points from Display window.



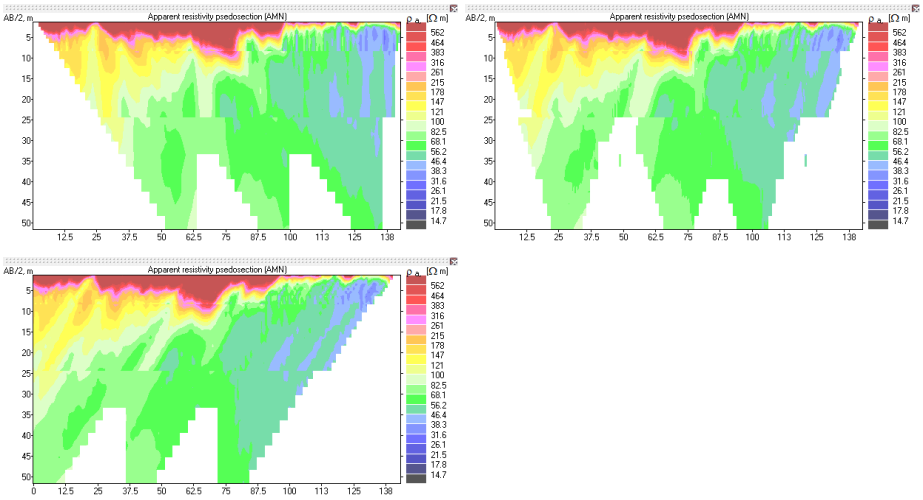
Attention!!! The color scale in Display window is always selected **automatically**. You can increase the range by Menu-Contours-Increase/Decrease (2.2.7).

Spacing (Pseudo Z) and X coordinate of each measurements depend on array and they are shown by picture at the right bottom corner of Main window (2.3.1).

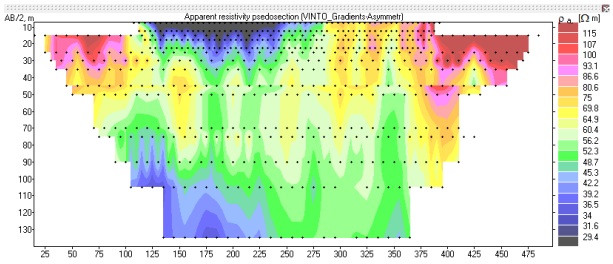
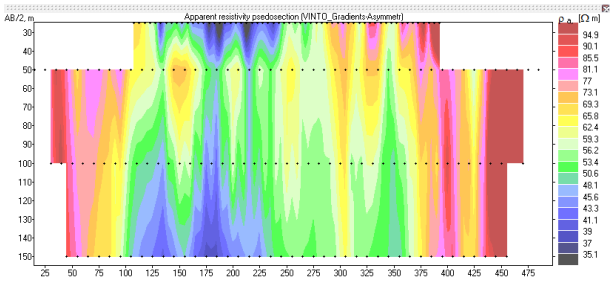
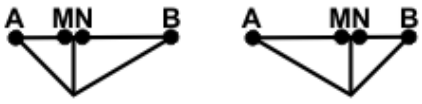
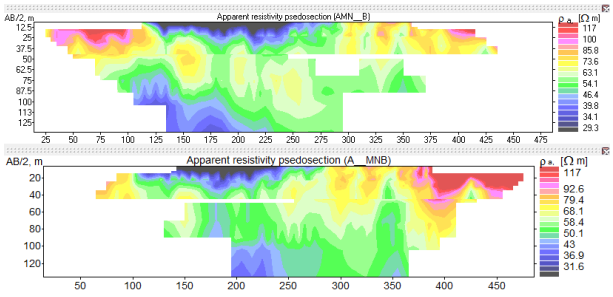


You can change the reference point (X coordinate) for asymmetrical array.

Pole-dipole can be presented using MN center, center of array or position of current electrode depending on **Menu-Options-Pole-dipole** (2.2.6). All these three variants are shown below.



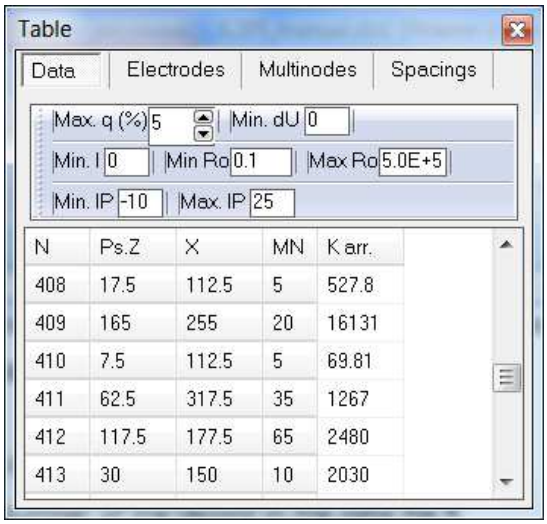
There are some variants for asymmetrical array data presentation - **Menu-Options-Asymmetrical as ...** (2.2.6).

Asymmetrical as - Gradient - classical presentation Multiply gradient array data *x=(M+N)/2* *Ps.Z=AO min*	
Asymmetrical as - Gradient 2 - presentation gradient array data with pseudo depth from AB length x=(M+N)/2 Ps.Z=AB/2	
Asymmetrical as - Force PD - presentation gradient array data like pole-dipole data. It is optimal way to see all data of Multiply Gradient array  *x=(M+N)/2* *Ps.Z=AO* *x=(M+N)/2* *Ps.Z=OB*	
Asymmetrical as - Force Dipole-dipole - presentation for dipole-dipole data with different lengths AB and MN dipoles	

2.5. Tables window

The Table window has some pages : Data, Electrode, Spacing etc.

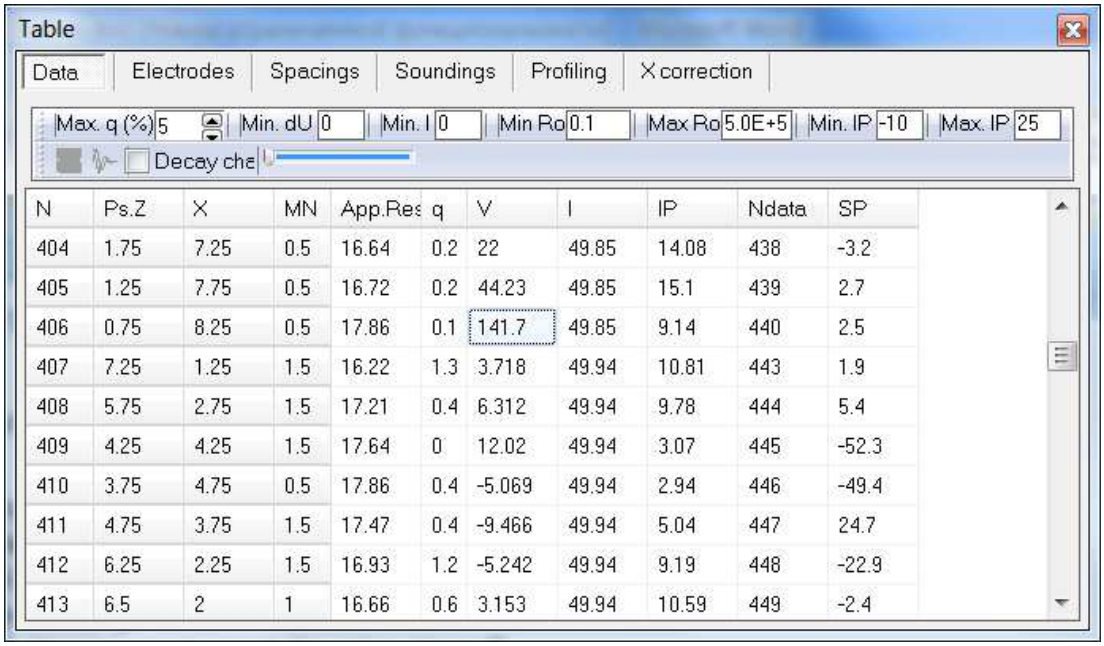
2.5.1. Data table



N	Ps.Z	X	MN	K arr.
408	17.5	112.5	5	527.8
409	165	255	20	16131
410	7.5	112.5	5	69.81
411	62.5	317.5	35	1267
412	117.5	177.5	65	2480
413	30	150	10	2030

The Data table indicates for protocol (sequence) file:

- **N** : the number of the record in the data file,
- **Ps.Z** : the pseudo depth of the apparent resistivity measurement (m),
- **X** : the X coordinate of the apparent resistivity measurement (m),
- **MN** : the MN length (m)
- **K arr.** : the geometrical coefficient of the array (m),



N	Ps.Z	X	MN	App.Res	q	V	I	IP	Ndata	SP
404	1.75	7.25	0.5	16.64	0.2	22	49.85	14.08	438	-3.2
405	1.25	7.75	0.5	16.72	0.2	44.23	49.85	15.1	439	2.7
406	0.75	8.25	0.5	17.86	0.1	141.7	49.85	9.14	440	2.5
407	7.25	1.25	1.5	16.22	1.3	3.718	49.94	10.81	443	1.9
408	5.75	2.75	1.5	17.21	0.4	6.312	49.94	9.78	444	5.4
409	4.25	4.25	1.5	17.64	0	12.02	49.94	3.07	445	-52.3
410	3.75	4.75	0.5	17.86	0.4	-5.069	49.94	2.94	446	-49.4
411	4.75	3.75	1.5	17.47	0.4	-9.466	49.94	5.04	447	24.7
412	6.25	2.25	1.5	16.93	1.2	-5.242	49.94	9.19	448	-22.9
413	6.5	2	1	16.66	0.6	3.153	49.94	10.59	449	-2.4

The Data table indicates the next information for data files:

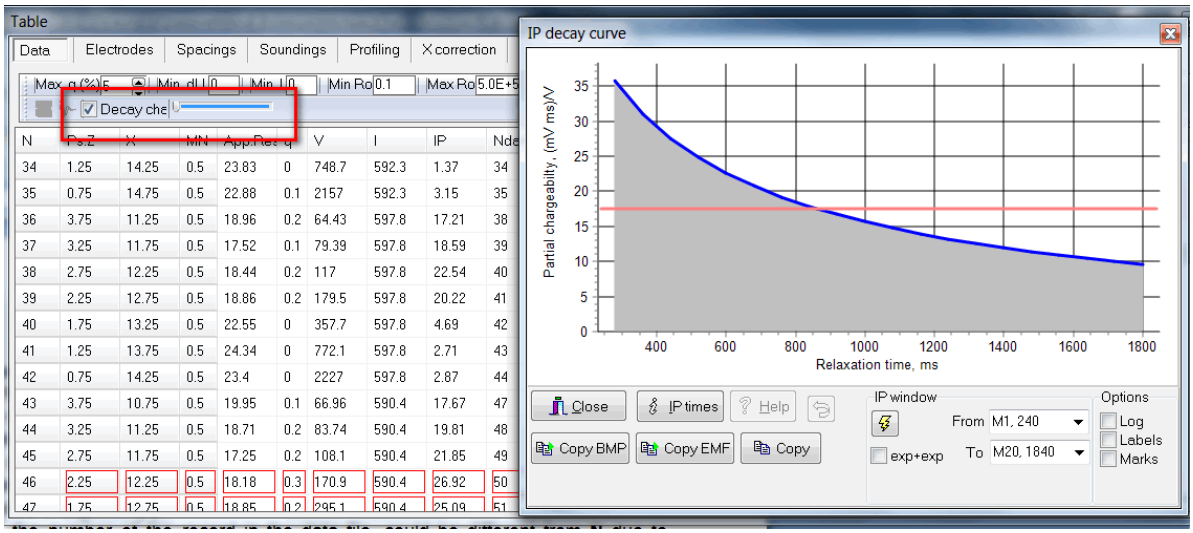
- **N** : the number of the record; it is usual the same as the number of record in the data file,
- **Ps.Z** : the pseudo depth of the apparent resistivity measurement (m),
- **X** : the X coordinate of the apparent resistivity measurement (m),
- **MN** : the MN length (m)
- **App.Res.** : the apparent resistivity value (Ω.m),

- **q** : a “quality” factor given by SYSCAL® equipment (dispersion of stacked measurements : the closer to 0, the most stable are the measurements). This value is put to 0 for RES2DINV data file that only contain apparent resistivity values.
- **V** : the mean potential difference measured between M and N electrodes (mV), not available for RES2DINV data files that only contain apparent resistivity.
- **I** : the mean intensity of current injected between A and B electrodes (mA), not available for RES2DINV data file that only contain apparent resistivity
- **IP** : induced chargeability
- **Ndata** : the number of the record in the data file, could be different from **N** due to sorting data in x2ipi software
- **SP** : self potential data if there is such data in data file. This data could be plotted by SP button.

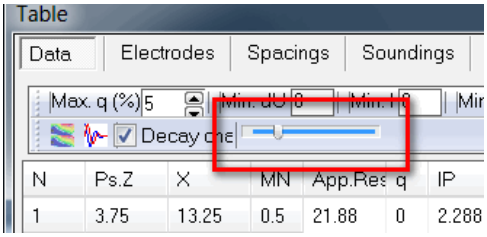
In the case of SYSCAL® data files, the status bar of the data table allows to discard measurements of poor quality following by one of the next criterions :

- **Max. q** : the quality factor. Data points with q higher than the fixed threshold will be discarded.
- **Min. dU** : minimum measured difference of potential (mV) Data points with V lower than the fixed threshold will be discarded.
- **Min. I** : minimum injected current (mA). Data points with the current lower than the fixed threshold will be discarded.
- **Min Ro** and **Max. Ro** : the range of acceptable values of apparent resistivity.
- **Min IP** and **Max IP** : the range of acceptable values of apparent chargeability.

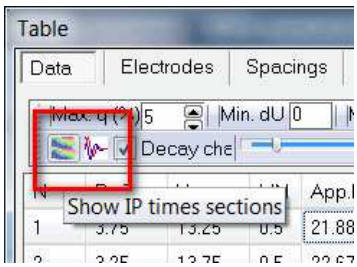
The selected line could be removed from data set or protocol file be Delete button. Repeated press of Delete button will restore this line in data set.



The decay chart check box is available if data set contents the IP decay data. The click in this box will activate IP decay curve window for selected data point.

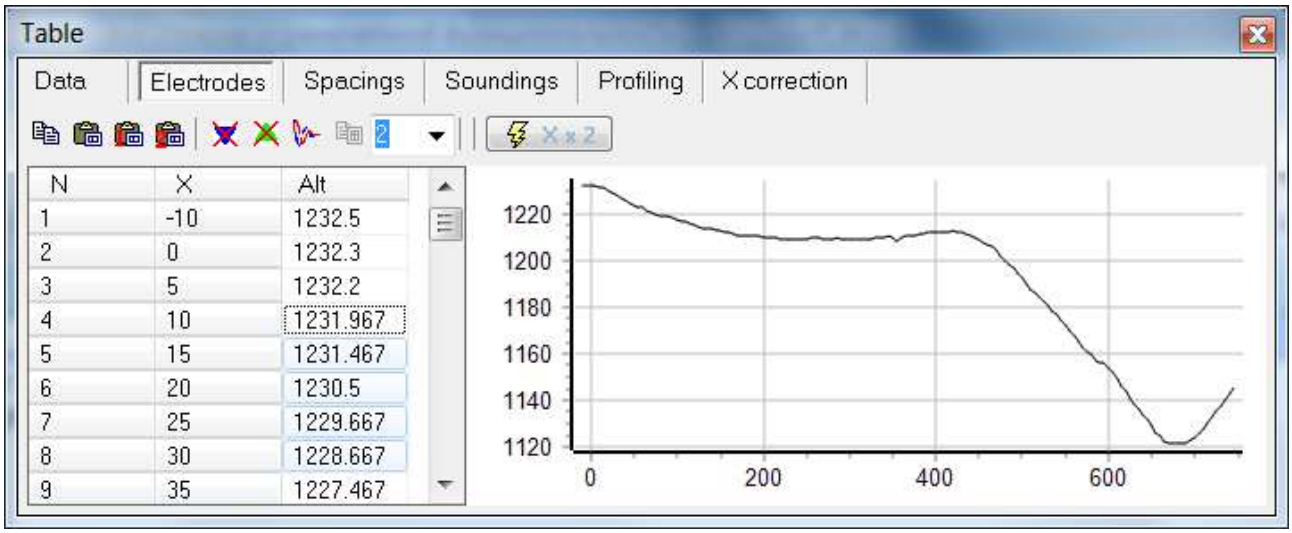


The decay track bar is available if data set contents the IP decay data. It allows to plot pseudo section of partial chargeability in Default Display window.



[Show IP times sections] button will show pseudo section of partial chargeability for all decay times. [Filtering IP time data] button makes the filtration of partial chargeability data for each time separately.

2.5.2. Electrodes table



The Electrodes table indicates :

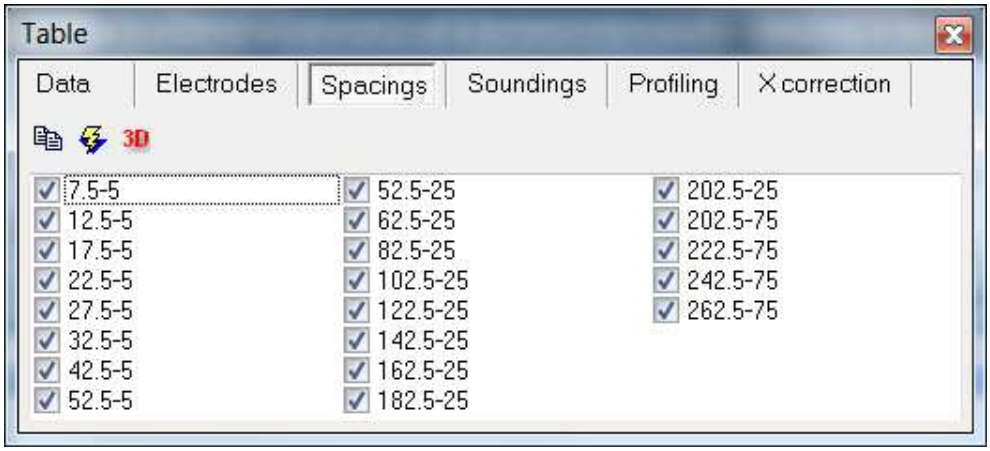
- N : the reference number of the electrodes. In the case of one opened SYSCAL®, the reference numbers fixed by the used MULTINODES® are precised. In the case of several opened SYSCAL® data files, the electrode reference numbers are generally put in the simplest way beginning at 1 and ending at N (N, total number of used electrodes). But if the same MULTINODES® layout is used for all the opened SYSCAL® data files (e.g. time laps monitoring) the reference number will be the same than in the case of only one opened SYSCAL® data file. In the case of one or several opened [*.dat] or [*.inv] RES2DINV file, the reference numbers of electrodes are always put in the simplest way.
- X : the X coordinate of the electrode (m),
- Alt : the elevation of the electrode (m).

The tool bar of the Electrode page allows :

- : to copy all electrode positions (X and Alt) to the clipboard.
- : to paste electrode positions (X and Alt) from the clipboard. Note that the pasted table should have the same number of electrodes.
- to paste topography data (X and Alt) from the clipboard and to find each electrode elevation by linear or square interpolation.
- : to delete measurement made with a selected (faulty) electrode.
- : to delete measurement, when selected electrode is used as potential electrode.

- : to remove a selected electrode and shift the next ones. This is of great use to modify quickly a [*.seq] when one line in a multiconductor cables are broken without possibility of repairing it easily in the field. It works only for protocol files.
- : to multiply by a coefficient the inter-electrode spacing. Apparent resistivity will be recalculated.
- : to copy the vertical electrical sounding closest to one electrode position to the clipboard. The copied data has a header corresponding to the VES location along the profile and then three columns with “AO” length (m), MN length (m) and Apparent resistivity (Ω.m).

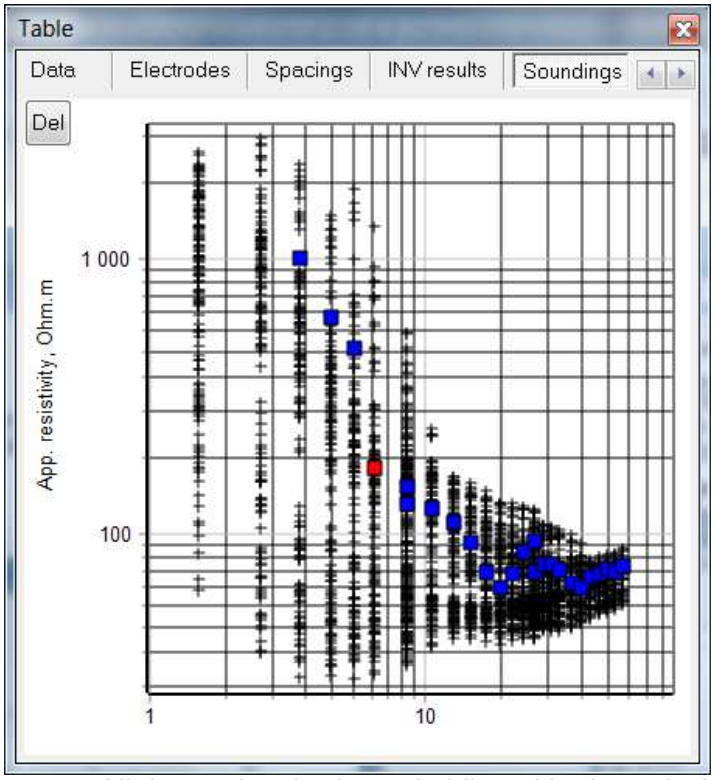
2.5.3. Spacing page



The Spacing page allows to work with different spacing from data file or protocol file. Check boxes allow to remove data from selected spacing. The tool bar of the Spacing page allows :

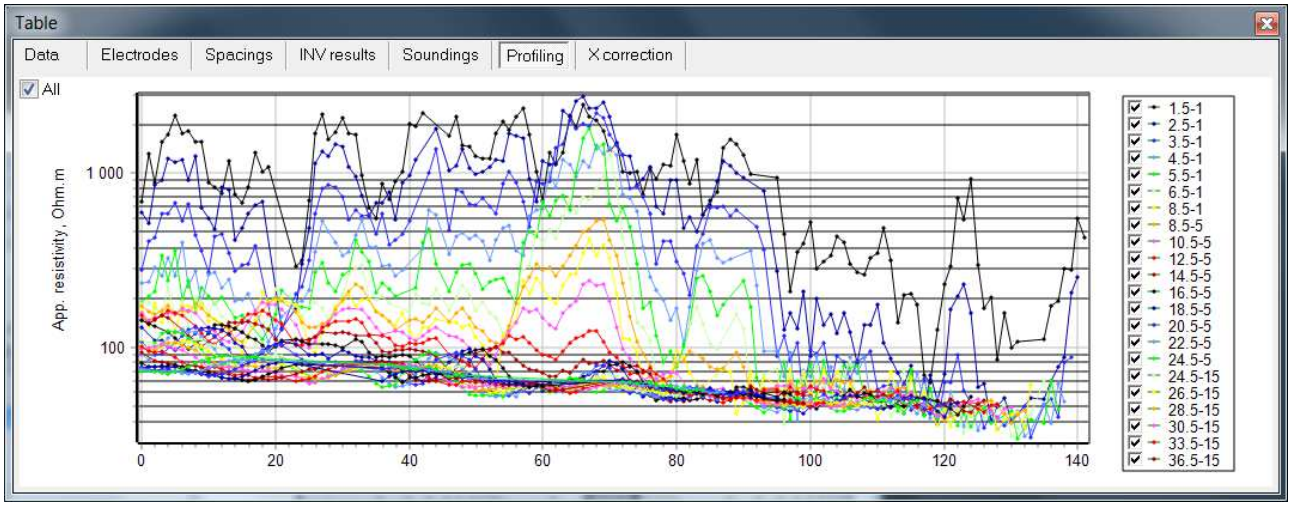
- : to copy data for selected spacing in clipboard,.
- : to copy in clipboard mean VES curve for data set.
- 3D : to create data file for 3D visualization (like Voxler). Input file - *.pln: X of data file, two reserved values, plan coordinate X and Y of data point. Output file has 4 columns: plan coordinate X and Y of data point, minus pseudo depth and logarithm of apparent resistivity.

2.5.4. Soundings page



All data points is shown in bilogarithmic scale. We can selected data point (red) and all data points with the same X coordinate will be plotted by blue squares. Bad data points could be removed by double click.

2.5.5. Profiling page



All data point is shown like profiling graphs. You could remove some spacing. Bad data paints could be removed by double click. If active mode is IP ( ), then IP data will be plotted.

2.5.1. INV result pages

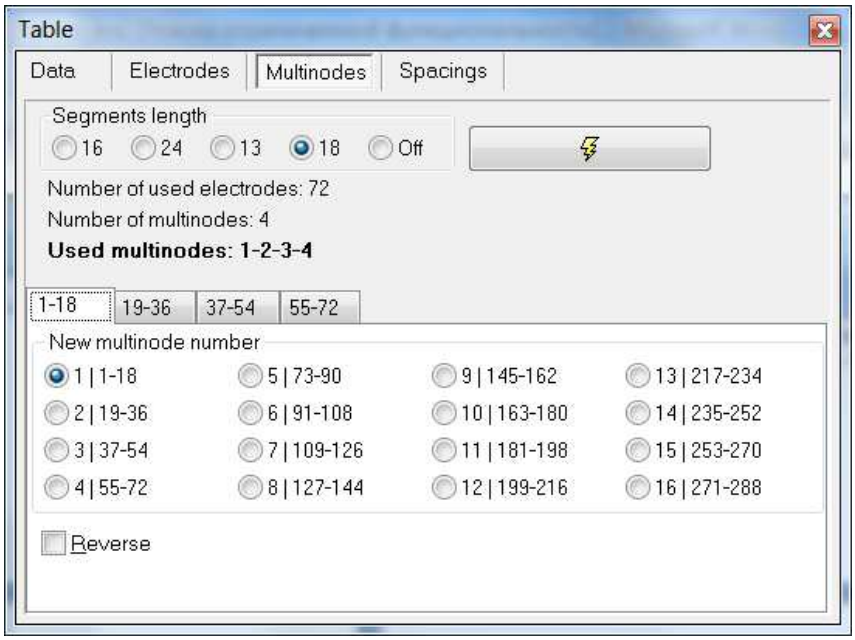
This page allows to work with the model after 2D inversion by Res2din software. You need to read INV file for such processing.

2.5.1. X correction page

This page allows to modify position of electrodes if they differ from protocol file during field measurements. After correction X coordinate all apparent resistivity values will be recalculated. The problem of irregular positions of electrodes is the great number of different spacing.

2.5.2. Multinode page

This page is only available for [*.seq] files. It allows to transform a *seq files prepared for some electrode hard reference numbers to another set of electrode hard reference numbers. For instance a [*.seq] file prepared for MULTINODE® 1, 2, 3 and 4 giving electrode hard reference numbers from 1 to 64 may be transformed to a [*.seq] file using MULTINODE® 5, 6, 7 and 8 giving electrode hard reference numbers from 65 to 128. This is particularly useful if a set of MULTINODE® is split in two parts in order to simultaneously undertake surveys on two different sites.



This page could be useful to indicate cable numbers in Electrodes table.

2.6. Advanced Display window

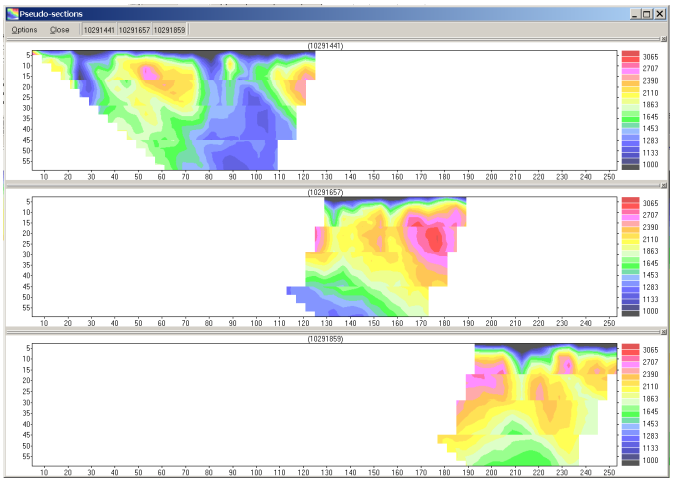
Advanced Display window is used to work with data set including different arrays or with different data files. It allows to plot some pseudosections in equal colors and horizontal scale. Also there are pseudosection's options in this window. There are three forms of Advanced Display window. All of them are controlled by main tool bar.

Advanced Display window is visible under Table window. There is not menu in this window. it helps quick to analyze data and to choose data set in Display window.

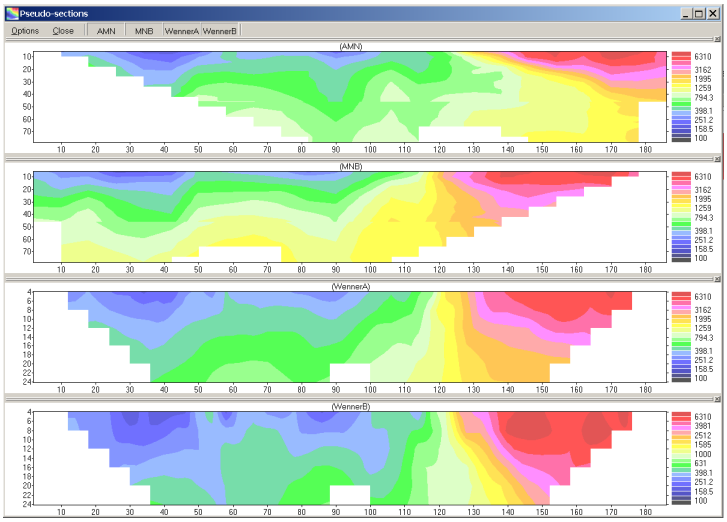
Advanced Display window is shown in new window with menu and options. It is good to prepare report pictures of field data.

Topography Display window is also shown in new window with menu and options. All pseudosection is show with topography.

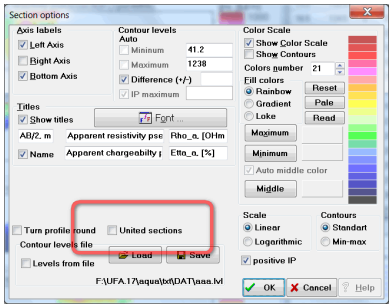
In case of several opened data files using the same electrode configuration (“roll along” survey) the advanced display window allows to display separately each data file.

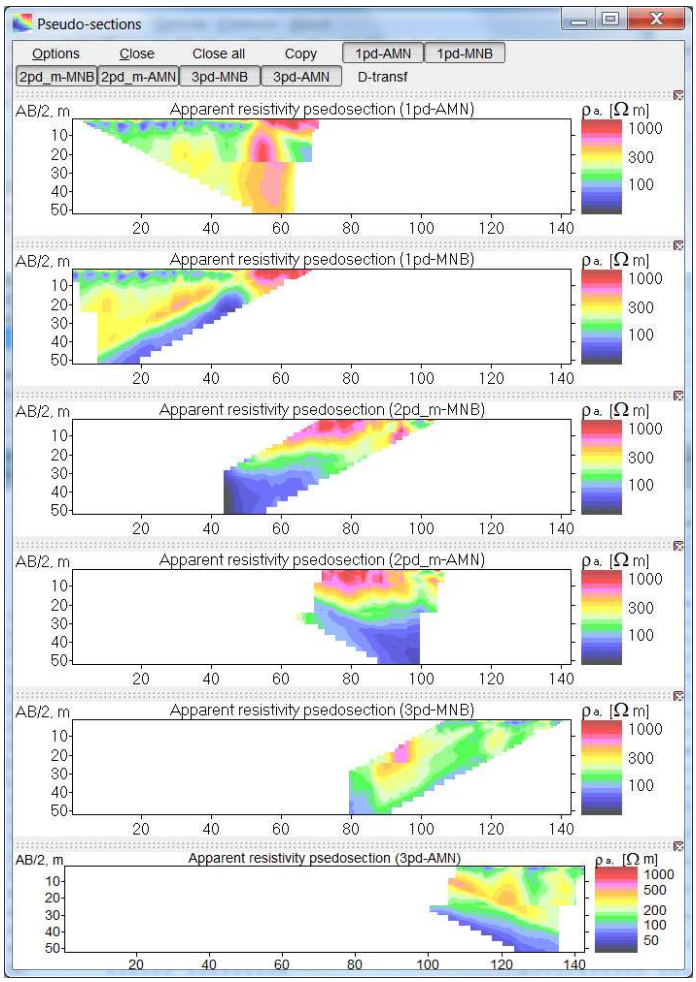


In case of several opened data files using different electrode configurations the advanced display window allows to separate each pseudosection, while the default window only allows to visualize part of the opened data files with the same electrode configuration than the active data file.

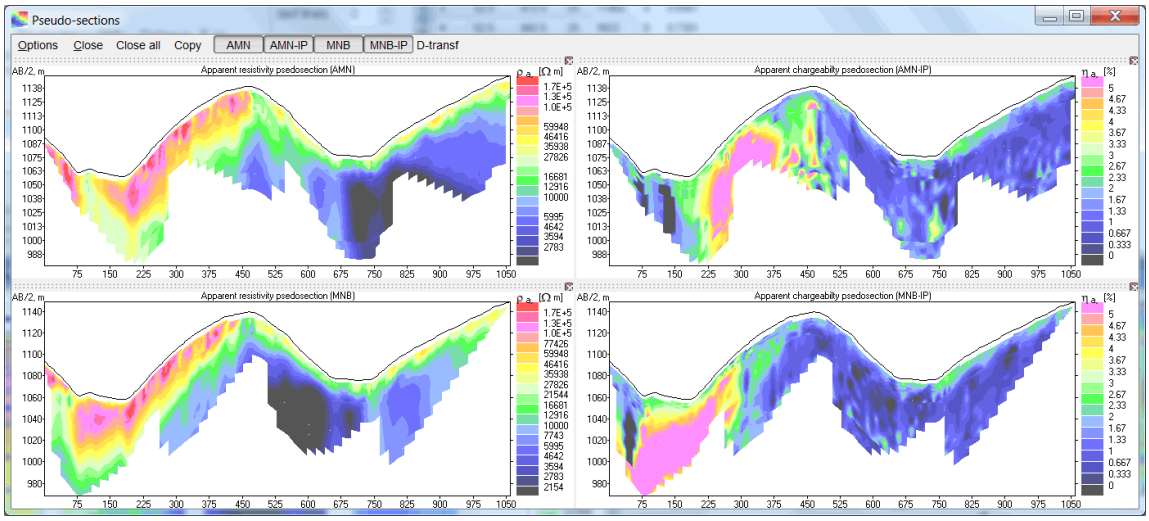


Use ***United section*** options in Section option window (2.6.2) to plot pseudosections for different files with different arrays.





The example of 3 opened files with forward and reverse pole-dipole array in each one for one long profile.



Topography Display window plots field data using effective depth for each measurements.

Array	Effective depth
Schlumberger	AB/2 / **2.63**
Pole-dipole	AO / **2.63**
Dipole-dipole	OO'/2 / **2.05**

Wenner-alpha	a / **1.93** (AB/3 / 1.93)
Wenner-beta	a / **2.404** (AB / 2.404)
Pole-pole	AM / **1.153**

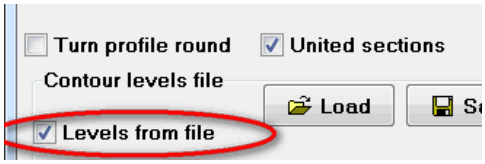
2.6.1. Menu of Advanced Display window

Options - Section options window to control how to plot pseudo sections;
Close - close Pseudo-sections window;
Close all - close all pseudo sections;
Copy - copy window without menu and frame to clipboard;
File-name/array name - switch On/Off some pseudo section to increase the size other ones;
D-transform - plot the differences pseudosection between two data set in percents. It is simplest way to analyze control measurements;
AMNB - calculate Schlumberger array from pole-dipole array;
Mean only - this option adds pole-dipole array data to calculated Schlumberger array.

2.6.2. The Section Options window

The Section Options window allows to fix some options of the advanced display window (Axis labels, Titles, Color scale). The most of items are simple. in some cases you have to close and reopen Advanced Display window to see the result with new options.

x2ipi software can automatically select colors scale range depending on data. But you can choose your own color range. You can type new Minimum and Maximum values or use your LVL file. The LVL file has three lines (empty line, minimum, maximum). Uncheck **Levels from file** box return default values (Reopen Advanced Display window to see the changes).

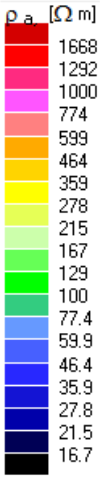


Difference (+/-) - set the range for D-transform pseudosection.

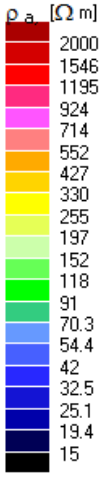
positive IP - if check box is

Contours - Standard - Min-max options. Standard way of contours' selection is using the values like 10, 100 in the range of values. If **Min-max** option is selected, then contours values are exactly between minimal and maximal values. The example of two variants for levels in range from 15 up to 2000:

Standard levels -



Min-max levels -



There are three reserved strings to indicate special symbols:

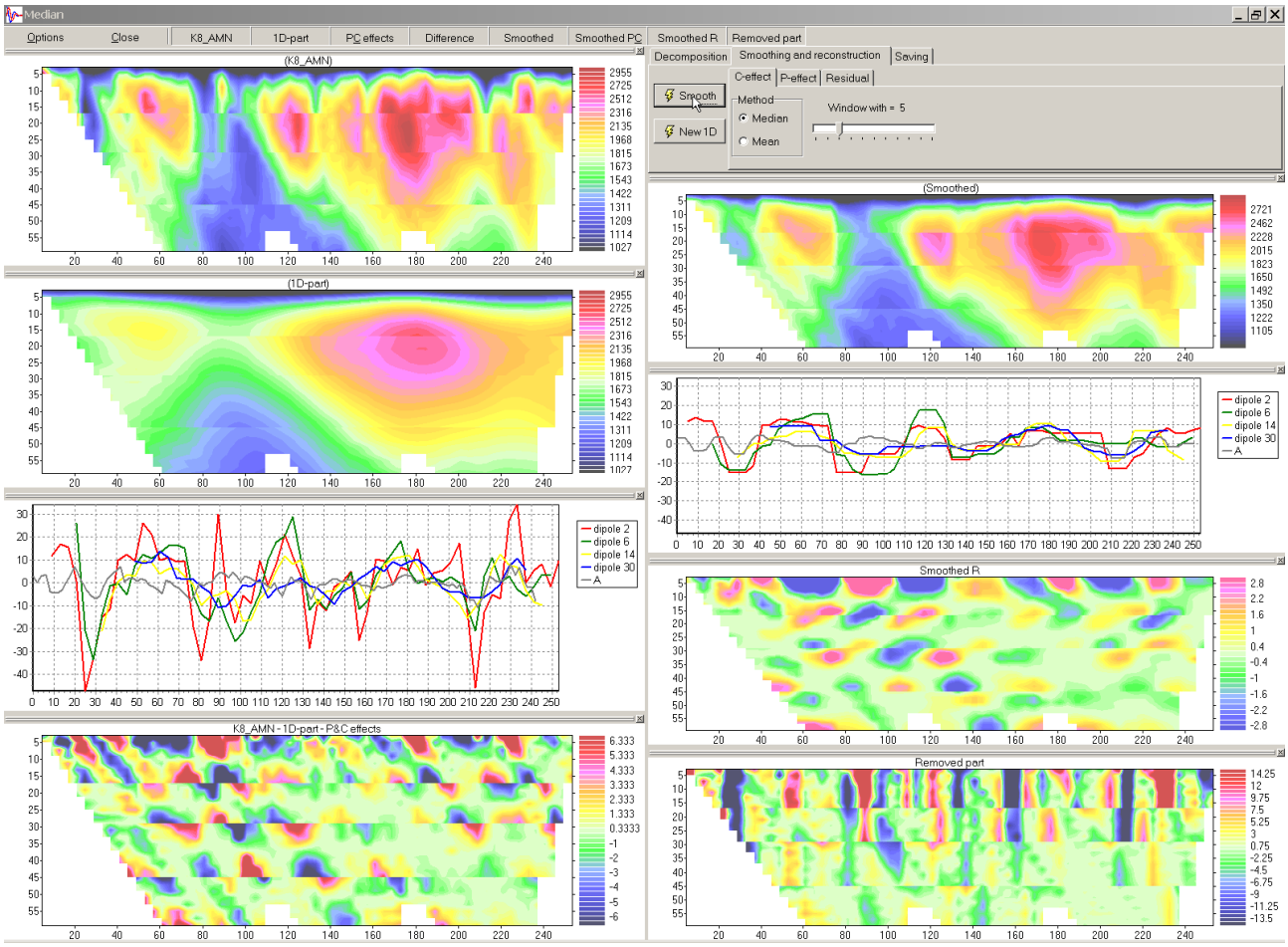
Rho - ρ;
Etta - η;
OHm - Ω.

Also use underline symbol (_) to indicate subscript symbol. For example:
"Rho_a, [OHm m]" will be printed as "ρ_a, Ω m"

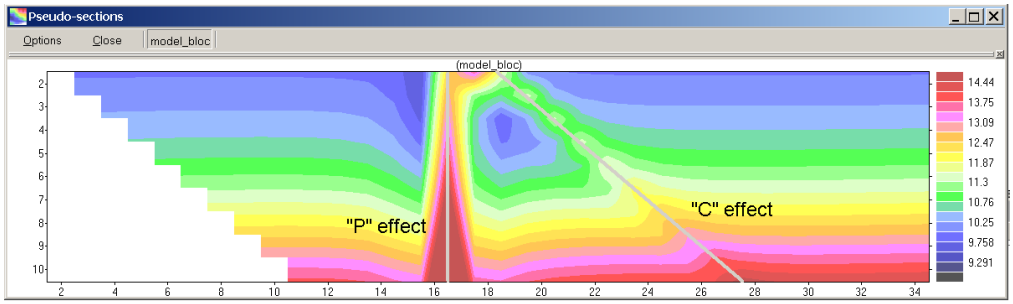
2.7. Median window

There are two kinds of Median window^ for apparent resistivity and for IP data. "The median processing" is available for DAT file in Res2din format.

The median window ( ) allows to remove from the pseudo sections of apparent resistivity the “P” and “C” effects linked to close to surface inhomogeneities.

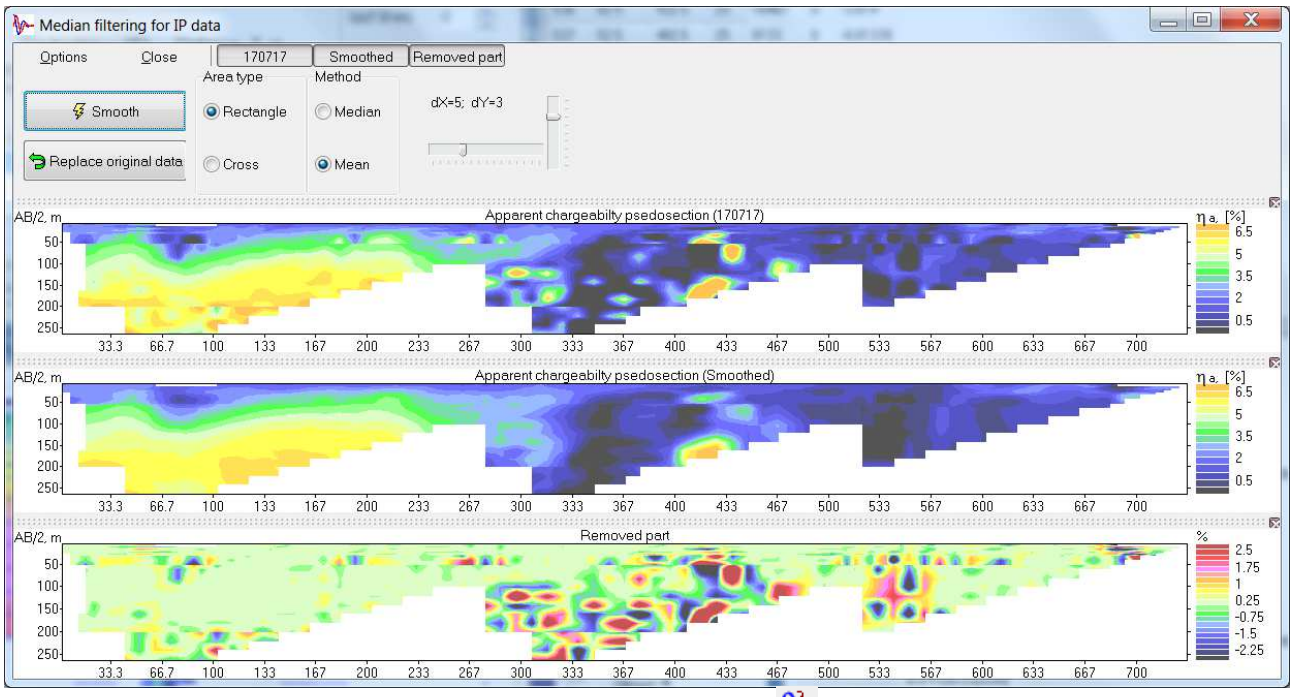


A synthetic examples of these effects is given below. It has been calculated with RES2DMOD program (Geotomo software, M.H. Loke). The chosen model has two layers with ρ_1=10 Ω.m, E_1=8m and ρ_2=500Ω.m. A small bloc with ρ_b= 100 Ω.m L_b=2m and E_b=0.5m is placed at the center of the profile at 0.5m depth. With an AMN array, two strong effects linked to this small inhomogeneity appears : a vertical anomaly, called “P” effect, for the vertical electrical sounding (VES) with MN dipole close to the inhomogeneity and an inclined anomaly, called “C” effect, for all VES with A electrode close to the inhomogeneity.



It is clear that a bunch of these effects linked to close to surface inhomogeneities may hide smoother effects linked to large and deep objects. The median processing allows to reduce a lot the response linked to the close to surface inhomogeneities and consequently to recover clearer 2D responses linked to deep and large inhomogeneities. It will be described step by step in the section 3.6.

Median window allows to smooth data of apparent chargeability:

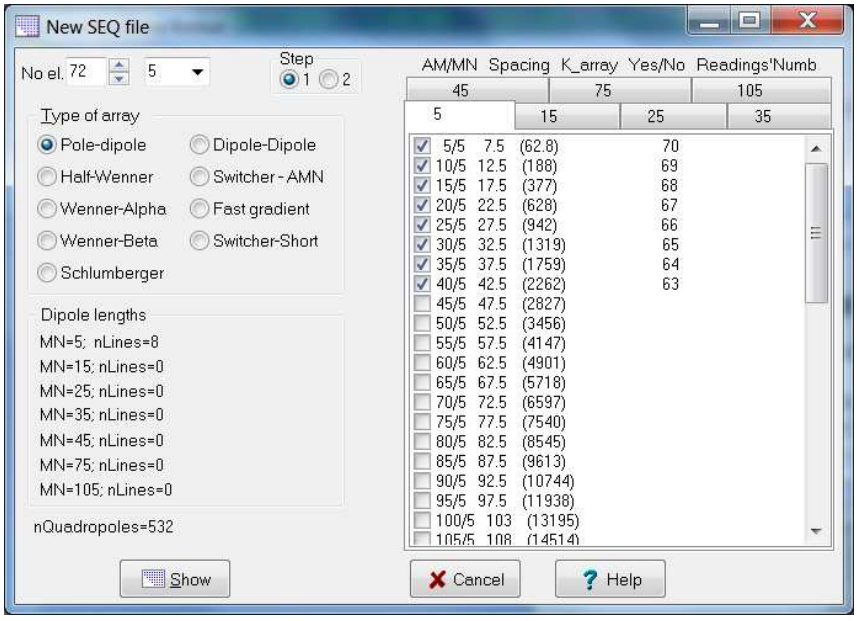


IP data have to be in the Display window for filtration ( ).

3. Work with X2IPI

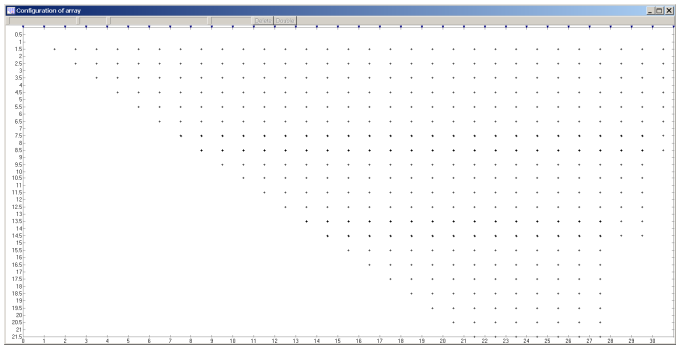
3.1. Creating [*.seq] files

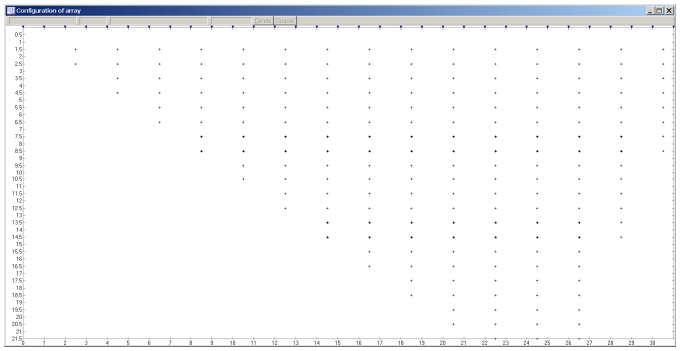
To create a new [*.seq] file (configuration file for multielectrode measurements with SYSCAL equipment), the icon “New sequence” of the icon bar in the main window, or the “Ctrl+N” short cut or the popup menu “File”+”New” may be used. A dialog window is then opened :



The number of electrodes is selected in the **No el.** input field. Close there is inter-electrode spacing.

The “**Step**” group allows to fix the density of vertical electrical soundings (VES) along the profile. Step 1 corresponds to a VES at each inter electrode location. Step 2 corresponds to a VES at each second inter electrode location. An example is given below for pole-dipole array.


AMN with step 1


AMN with step 2

Some types of arrays are available :

- Pole-Dipole
- Half Wenner
- Wenner alpha
- Wenner beta
- Dipole - dipole

The tables in the right part of the dialog window allow to select the different quadripoles that will be used. For Wenner arrays (half, alpha or beta) there is only one table. For other arrays there are several tables with header indicating the length of MN dipole.

The first column with check boxes allows to select the used spacing. The second column indicates the ratio between AM and MN lengths. The third column indicates the spacing. The fourth column indicates the geometric coefficient for selected spacing. When the first column is checked, the last column indicates the number of measurements corresponding to the selected spacing. For some arrays (Pole-dipole, Schlumberger and dipole-dipole) another column also indicates if a measurement using the same spacing is also made with another MN measuring dipole (checked in another table). This allows to easily determine the overlap between the successive segments in the pole-dipole VES. Usually one overlapping points are sufficient to check data quality.

While selecting the desired quadripoles, the dialog box indicates in the left part the total number of measurements and in the case of pole-dipole array the number of AO lengths ("nLines") for each MN length.

The [*.seq] file may then be displayed (or refreshed) in the display window clicking on the "**Show**" button.

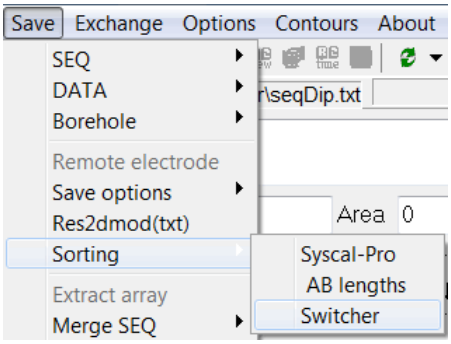
Press **"Cancel"** button to return in Main window to save Protocol file in desired format (see 2.2.2):

- ***seq*** *- Electre* : Save binary protocol file for old ***Electre*** program (IRIS Instruments)
- ***txt*** *- Electre II*: Save text protocol file for ***Electre II*** and ***Electre Pro*** programs (IRIS Instruments)
- ***org*** *Lund protocol (ABEM)* : Save Lund protocol file **org** (ABEM). Terrameter LS Toolbox software (supplied with the equipment) can convert .**org** file into modern **.xml** format.

We recommend to keep all protocols file in TXT format of ***Electre II*** software .

3.2. Sorting the measurement to use modern multi-channel receivers.

The most of modern receivers are multi-channel. We have to optimize our protocol file to use this option. We need the order of measurements, when quadripoles are sorted by injection dipole. Use Sorting menu to change the order of measurements (2.2.4).



There three variants of sorting

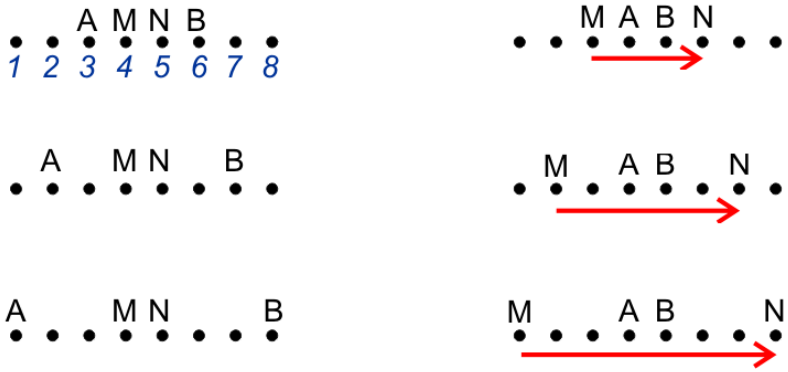
Syscal-Pro mode is sorting by injection dipole or electrode. Sorting for reverse pole-dipole array (MNB) is in reverse order. It allows improve quality of data because we escape the electrode charge-up effects (Dahlin T., 2000. Short note on electrode charge-up effects in DC resistivity data acquisition using multi-electrode arrays. Geophysical prospecting, 48).

AB lengths mode is sorting measurements by current dipole length first and after by currrent dipoles order. We recommended this mode for Dipole-Dipole and reciprocal Schlumberger arrays.

Switcher mode is sorting measurements by injection dipole or electrode. It could results in fastest measurements

3.3. Optimization for Schlumberger array

The Schlumberger array is a classic array and it is used very often. Reciprocal Schlumberger array allows to use multi-channel receiver.

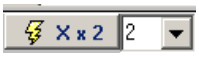


Use menu ***Reciprocal SEQ*** (2.2.4) to convert array in reciprocal one. Reload file with reciprocal array before sorting (3.2).

3.4. Modifying [*.seq] file

Several modifications of [*.seq] files are availables : modifying electrode unit spacing, shifting electrodes, removing a faulty electrode, removing measurement lines, sorting measurements and changing multinodes.

3.4.1. Modifying electrodes unit spacing



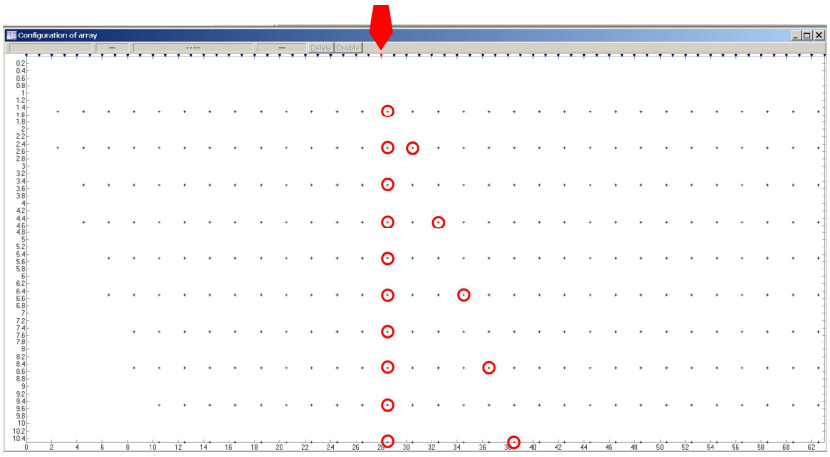
The unit electrode spacing is changed using the “multiply by a coefficient all distances” button in the icon bar of the electrode table. The coefficient is chosen using the scrolling window at right and the multiplication is performed clicking the button at left.

Once the unit electrode spacing has been modified, the [*.seq] file may be saved using the “save” button in the main window.

3.4.2. Removing a faulty electrode

A faulty electrode used in a [*.seq] file may be removed and the ones coming next, shifted of one inter electrode spacing. This is of great use to modify quickly a [*.seq] when one node in a MULTINODE® or one line in a multiconductor cable is broken without possibility of repairing it easily in the field.

The electrode is selected in the electrode table by clicking on the corresponding line or in the display window by clicking on the top triangle. The removal is then performed using the “Broken electrode” button in the icon bar of the electrode table. If there were initialy N electrodes used in the [*.seq] file and if electrode n is removed, the modified [*.seq] file will have N-1 electrodes (with number 1 to n-1 and n+1 to N) but the pseudosection will not have the hole corresponding to a faulty electrode n, showed on the following figure. Of course, such a [*.seq] file skipping a node, has to be coherent with the actual connections of the SYSCAL multi-electrode system.



Alternatively, the selected electrode may be skipped clicking on the “delete selected electrode” button. i.e. only the measurements corresponding to the faulty electrode will be removed from the [*.seq] file. In this case the hole in the pseudo section will remain. The removed electrode as well as the measurements using this electrode are marked in the electrode and in the data tables and in the display window.

Once the faulty electrode has been removed or skipped, the modified [*.seq] file may be saved using the “save” button in the main window.

Note that if the “Broken electrode” button is clicked accidentally, there is no explicit “undo” button. But since the modified [*.seq] file is not saved, a re-opening of the same [*.seq] file will restore the accidentally removed electrode. Furthermore, if the [*.seq] file with removed electrode has been saved, a backup file [*.~eq] with the previous version is kept in the active directory and may be recovered by changing the extension name.

3.4.3. Shifting electrodes

By default the first electrode is located at X=0 in the [*.seq] files generated with ***X2IPI***. All electrodes coordinates may be shifted by entering a value in the “shift (m)” dialog box at the right of the main window. The position of electrodes is automatically updated in the electrode table.

Once electrodes have been shifted, the modified [*.seq] file may be saved using the “save” button in the main window.

Note that this button should preferably be used with just one opened file.

3.4.4. Removing measurement lines

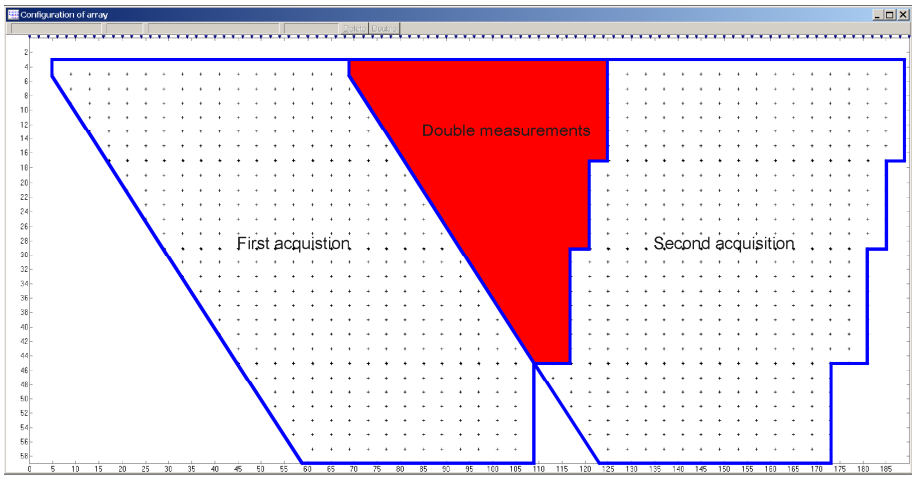
Measurements lines may be removed at the top or at the bottom of the pseudo section respectively using the “Delete first line” or “Delete last line” dialog box at the right of the main window. The deleted lines are marked in the data table and in the display window.

Once the lines electrode has been deleted, the modified [*.seq] file may be saved using the “save” button in the main window.

Note that these buttons should preferably be used with just one opened file.

3.4.5. Preparing a “Roll along” [*.seq] file.

The Roll along technique consists in acquiring progressively a long pseudo section by moving the electrode along a profile. Generally, the multi electrode array is shifted by half of his extent, for example with an even number of electrode 2N, each electrode will be shifted by N+1 positions. When the two pseudosections acquired successively are merged, the total profile includes 3N electrode positions.



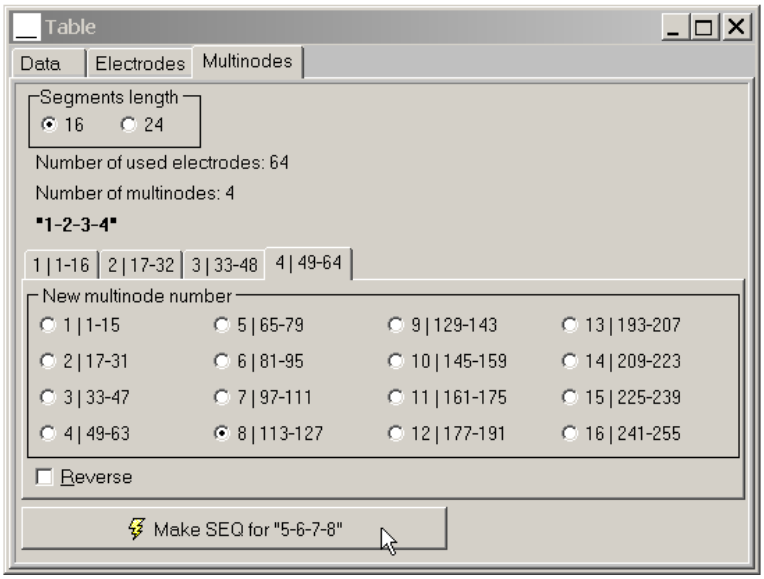
"Roll along" survey

It is not useful to measure twice the apparent resistivities corresponding to the overlapping part of the successive pseudo sections. Hence a second [*.seq] file corresponding to “Roll along” acquisitions which do not includes the measurements already made at the preceding position, may be generated using the following procedure :

- Open a [name1.seq] file (with 2N electrodes and unit electrode spacing a).
- Shift [name1.seq] file by N*a
- Save [name1.seq] as [name2.seq] (the active file is now [name2.seq])
- Open [name1.seq] and append [name2.seq]
- Select [name2.seq] in the main window (the measurements appear in green if they are not in [name1.seq] and in blue if they are doubles)
- Click on the “Double” button in the display window (the double measurements are marked in red color in the display window and in the date table)
- Save the [name2.seq] file

3.4.6. Changing Multinodes

The “Multinodes” table allows to change the numbers of the MULTINODE® used in a [*seq] file, i.e. the hard reference numbers of the electrodes.



The first box allows to select the number of electrode per segment (16 or 24, both available with SYSCAL® equipment).

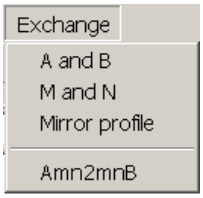
The number of electrodes and MULTINODE® used in the [*.seq] file is given.

A box allows to select which MULTINODE® shall be used for the first 16 electrodes (first table), which shall be used for the 16 next (second table) and so on and so forth. When all the

tables are correct, the button “Make SEQ for …” may be clicked. Note that the modified [*.seq] file has then to be saved using the “save” button of the main window.

The “reverse” button allows to reverse the order of electrode hard reference numbers for each MULTINODE®, e.g. for MULTINODE® 1 giving hard numbers from 1 to 16, it may be useful to have hard reference numbers from 16 to 1, e.g. if the MULTINODE® is placed next to the 16th electrode and not next to the1st one.

3.4.7. Transforming AMN to MNB



The “***Amn2mnB***” option of the *“Exchange”* menu in the main window, allows to transform AMN [*.seq] file (forward pole-dipole) to MNB [*.seq] file (reverse pole-dipole). The procedure is the following :

- Click on the *“Amn2mnB”* button.
- An *“open”* dialog box is displayed where a previously created AMN [*.seq] file may be selected
- A *“save as”* dialog box is then displayed where the name of the new MNB [*.seq] file may be specified
- The new MNB [*.seq] file becomes the active file in the main window.

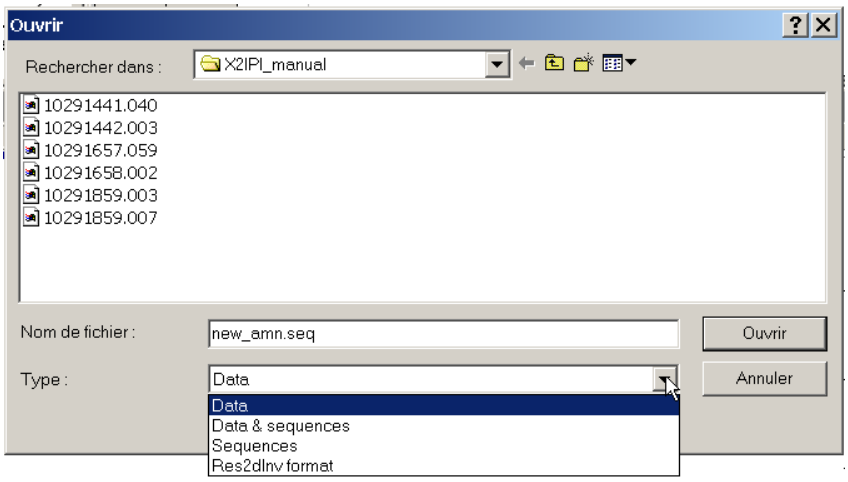
Alternative way is to use the “***AMN -> MNB***” option of the *“Exchange”* menu. The result file in the most of cases is the same.

3.5. Working with data files

3.5.1. Opening data files

3 types of data files are supported by ***X2IPI*** as input files :

- SYSCAL measurements files : [*.0xx], with xx comprises between 00 and 59.
- RES2DINV input data files : [*.dat]. Note that the general electrode configuration format labeled 11 by Loke (see RES2DINV manual) is not supported by ***X2IPI***.
- RES2DINV output data files : [*.inv], in this case the 2D resistivity model is also imported, in order to export it to input files for IPI2WIN software. Note that the imported resistivity model cannot be displayed with ***X2IPI***, but it could be save in RES file for ***ipi2win*** program.



The procedure to open a file is the following :

- Click on the “open” icon .

- Select the directory
- Select the type of file : Data corresponds to SYSCAL [*.0xx] files and Res2dInv to [*.dat] or [*.inv] RES2DINV files.
- Select the file
- A “double click” on the file name in the list or a click on “open” button will load the data file in ***X2IPI***. Note that several files may be selected in the list and then opened in a single step procedure.

The procedure to append a file to already opened files is the following :

- Click on the “append” icon .
- Select the directory
- Select the type of file : Data corresponds to SYSCAL [*.0xx] files and Res2dInv to [*.dat] or [*.inv] RES2DINV files.
- Select the file. Note that several files may be selected and then appended in a single step procedure. Also note that SYSCAL and RES2DINV files may be opened simultaneously.

The opened files are listed in the main window. A click on one file allows to display the data corresponding to the selected file.
Note that by default, all the files corresponding to measurements made with the same electrode array than the last data file in the list, are displayed.

3.5.2. Shifting data file

The electrode positions may be shifted by a constant using the dialog box at the right of the main window. This is particularly important for “roll along” surveys for which the same [*.seq] file with generic electrode positions, is used.

it is **recommended to export the shifted data file instead of altering the original SYSCAL® data files.**

3.5.3. Trimming bad measurements

In the case of SYSCAL® data files, the status bar of the data table allows to discard measurements of poor quality following criterions :

- Max. q : the quality factor. Data points with q higher than the fixed threshold will be discarded.
- Min dU : minimum measured difference of potential (mV) Data points with V lower than the fixed threshold will be discarded.
- Min I : minimum injected current (mA). Data points with I lower than the fixed threshold will be discarded.
- Min Ro and Max Ro : the range off apparent resistivity.
- Min. IP and Max. IP : the range off apparent chargeability.

Once the criterions have been fixed in the dialog boxes, the outlier data are automatically removed. The number of removed data is shown in the main window and in the display window, the discarded measurements are mark in red.

If the outlier measurements correspond to a faulty electrode, all the measurements made using this electrode may be discarded, with the delete button of the electrode table. The faulty electrode is selected in the electrode table or in the display window.

- to delete measurement, when selected electrode is used as potential electrode.

it is **recommended to export the shifted data file instead of altering the original SYSCAL® data files.**

3.5.4. Merging data files

All the opened data files may be merged in a single file. There are two possibilities :

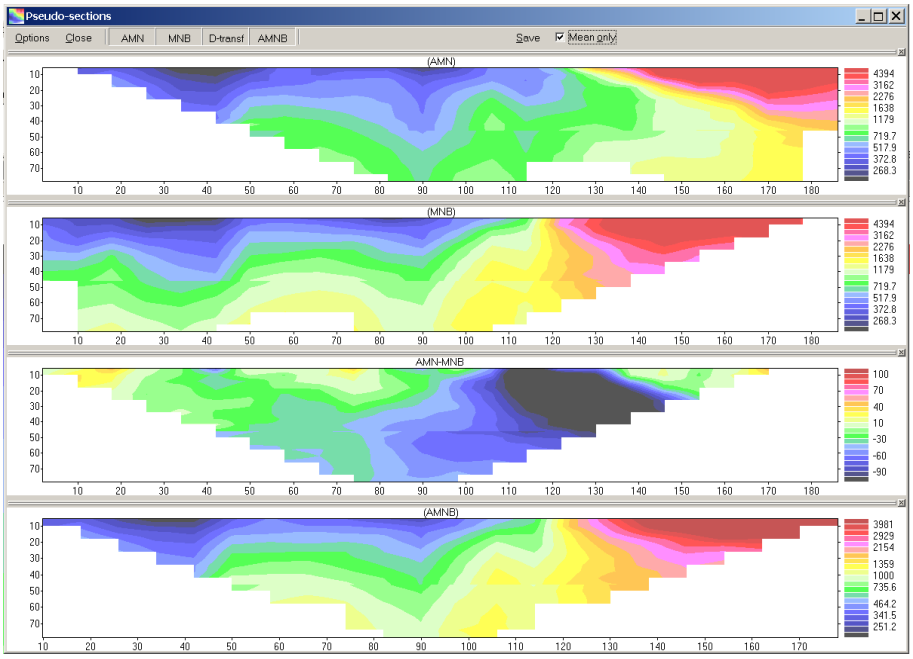
- For measurements using different electrodes but made with the same array (“Roll along”), the merged data set may be exported to any of the formats provided by ***X2IPI*** (RES2DINV or SENSINV2D). In this case double measurements corresponding to eventual overlapping parts in a “roll along” survey, are automatically replaced by their mean.
- For measurements using the same electrodes but made with different arrays, the merged data set may only be exported in “general array” format for RES2DINV.

3.5.5. Generating Schlumberger data from AMN and MNB data

In the particular case of several opened data files using forward or reverse pole-dipole configurations, the advanced display windows also allows to show the difference between the two pseudosections (“D-Transf”). This indicates clearly the “1D” parts of the profile (small difference between AMN and MNB pseudosections) and the “2D” parts (strong differences between AMN and

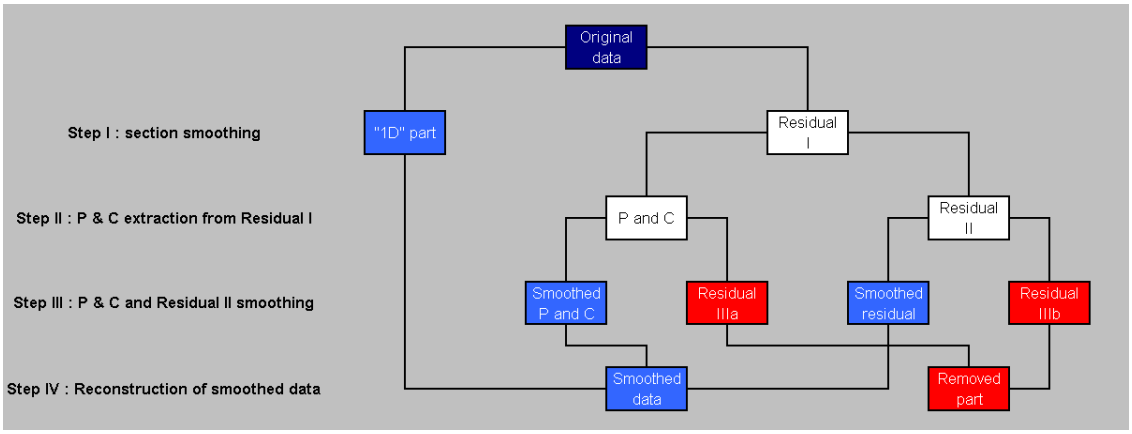
MNB pseudosections). Furthermore, the amplitude of the differences may give some indications about the depth and the size of the objects giving “2D” responses.

The “mean only” button allows to calculate the half sum of AMN and MNB pseudo sections, i.e. the Schlumberger pseudosection. When the “mean only” button is checked only coincident parts of the AMN and MNB pseudosections are used. When the “mean only” button is not checked, the parts where AMN and MNB are not coincident are added to the Schlumberger pseudosection. The button “save” allows to export the Schlumberger pseudosection to RES2DINV [*.dat] file format.



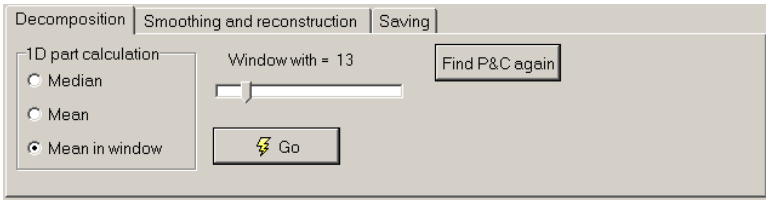
3.6. Median Processing

The median option is only available for RES2DINV data files [*.dat]. The processing flow chart is as following :



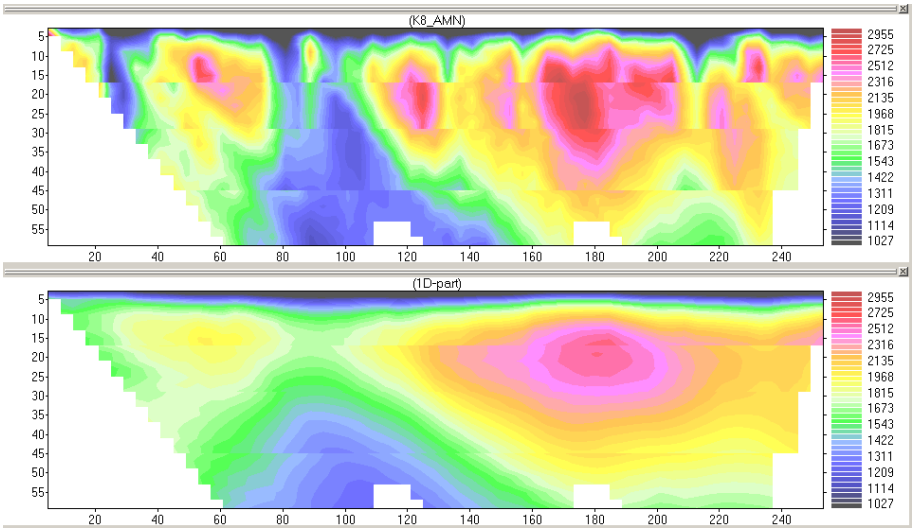
The two first steps correspond to [Original data] decomposition in 3 parts : (1) a [“1D” part] (smoothed pseudosection), (2) [P & C effects] and (3) a [Residual II]. The third step correspond to a smoothing of [P & C effects] and of [Residual II]. The last step corresponds to the reconstruction of [Smoothed data] with (1) the [“1D” part], (2) the [Smoothed P & C effects] and (3) the [Smoothed Residual].

3.6.1. Pseudosection decomposition

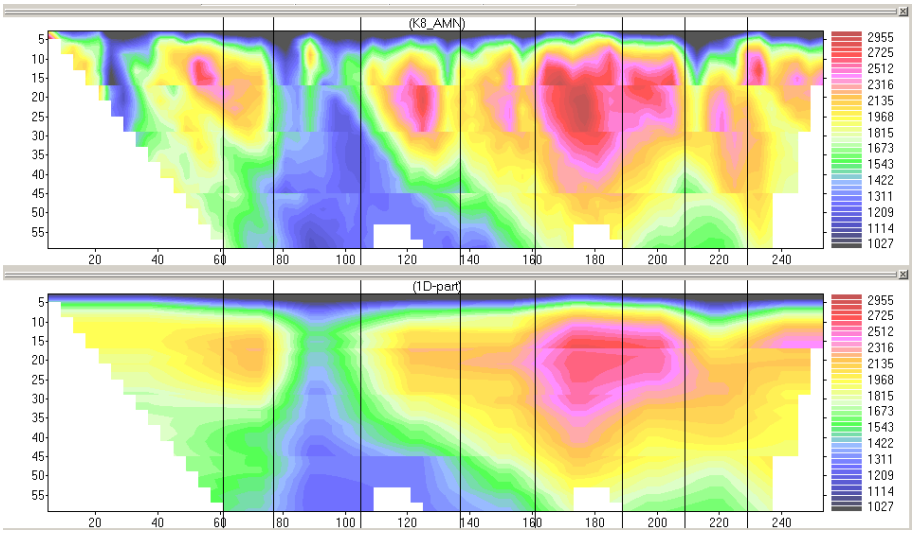


The decomposition window allows to perform Steps I and II at the same time.

The calculation of the [“1D” part], may be performed in a sliding window whose width is defined with the “Window width = …” ruler.

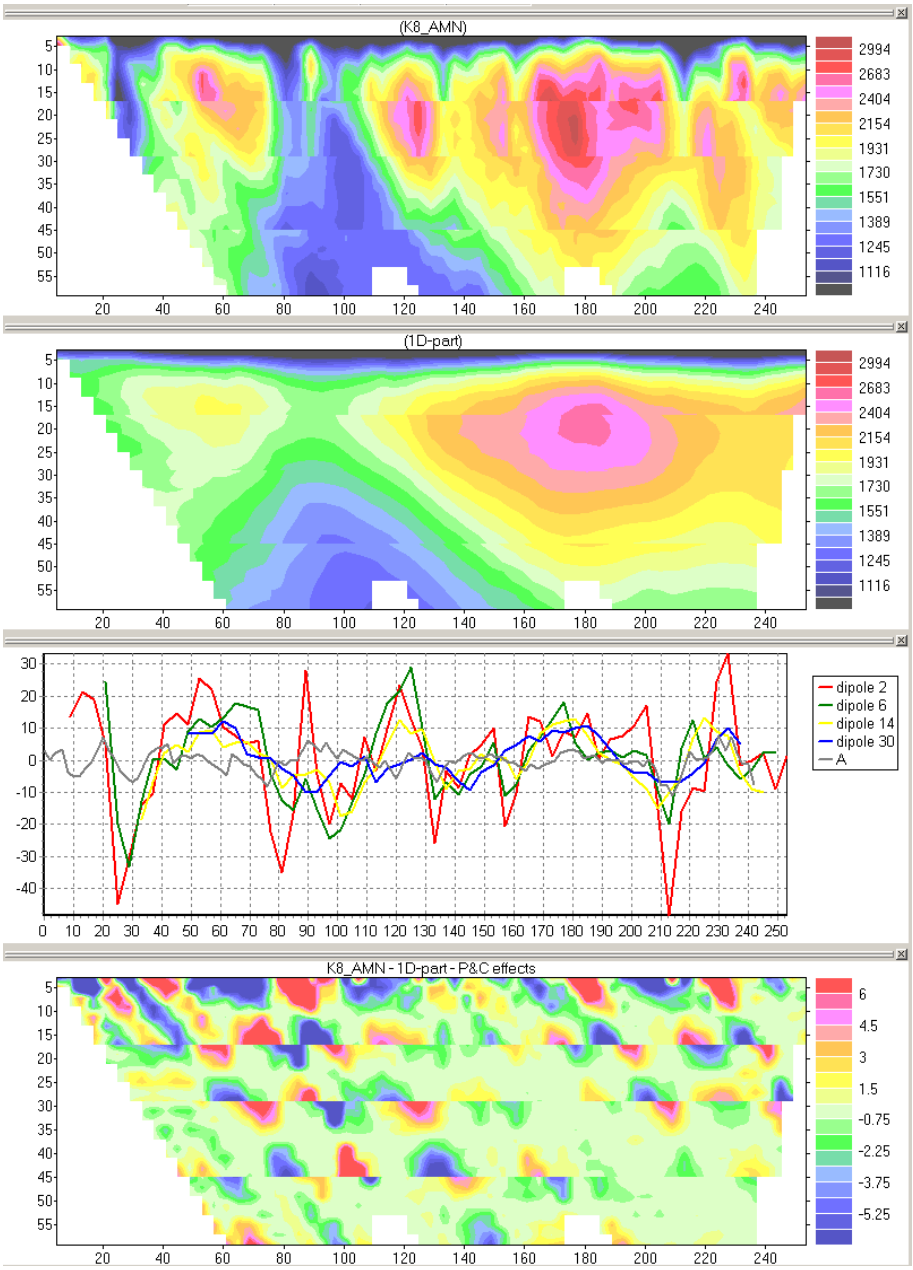


When “Median” or “Mean” buttons are checked, it is also possible to define variable width of smoothing windows by clicking in the “original data” or in the “1D part” plots. The removal of an unsatisfying boundary is obtained by clicking again on the line. The mean or median values are placed at the center of the smoothing windows and an horizontal linear interpolation is calculated to pass from a smoothing window to the next one.



When the configuration of the smoothing scheme is defined, the button “Go” may be pushed and the three components are recalculated. Four plot windows are displayed :

- the [Original data] pseudosection,
- the [“1D” part],
- the [P & C effects],
- the [Residual]. Note that when [P & C effects] plot is not activate in the status bar, the [Residual] plot corresponds to [Residual I], when [P & C effects] plot is activate in the status bar, the [Residual] plot corresponds to [Residual II].



The P and C effects are calculated from the pseudosection
[Residual I] = [Original data] – [“1D” part].

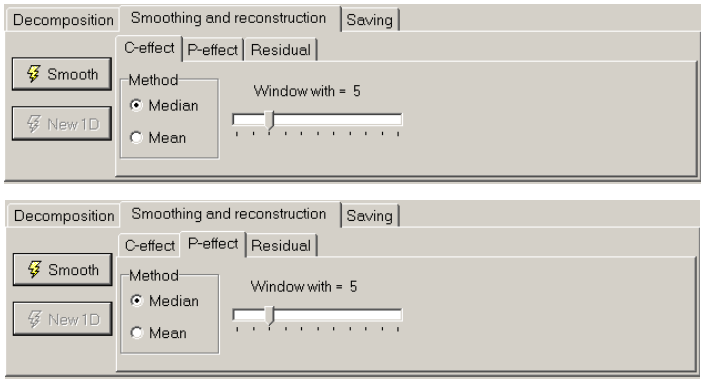
For pole-dipole arrays and Schlumberger array, the different P effects correspond to the different MN dipoles used at each VES. They correspond to the median value calculated for each vertical line in the pseudosection [Residual I].

For of AMN array, the C effect at electrode A, corresponds to the median value calculated for each line with slope -1 in the pseudosection [Residual I]. For MNB array, the C effect at electrode B, corresponds to the median value calculated for each line with slope +1 in the pseudosection [Residual I]. For Schlumberger array, both C effects at electrodes A and B are calculated. They respectively correspond to lines with slope –1 and +1 in the pseudosection [Residual I]. For Wenner alpha array (AMNB), there is no P effect (MN dipole length changes at each pseudo depth) but only C effects at electrodes A, B, M and N. They are respectively calculated for each line with slope –2/3 (A), +2/3 (B), -2 (M) and +2 (N).

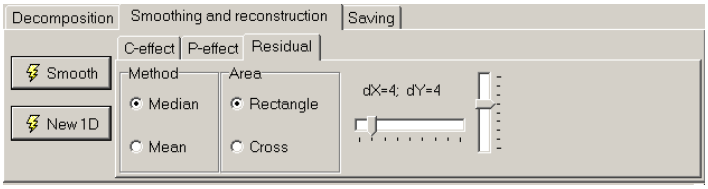
A button, “find P & C again” may be used to refine [P and C effects] calculation as some interferences between P and C effects generally occur.

3.6.2. Components smoothing

Once the three components ([“1D” part], [P & C effects], [Residual II]) are separated, the last two components are smoothed using the “Smoothing and Reconstruction” Window, which allows to perform steps III and IV at the same time.



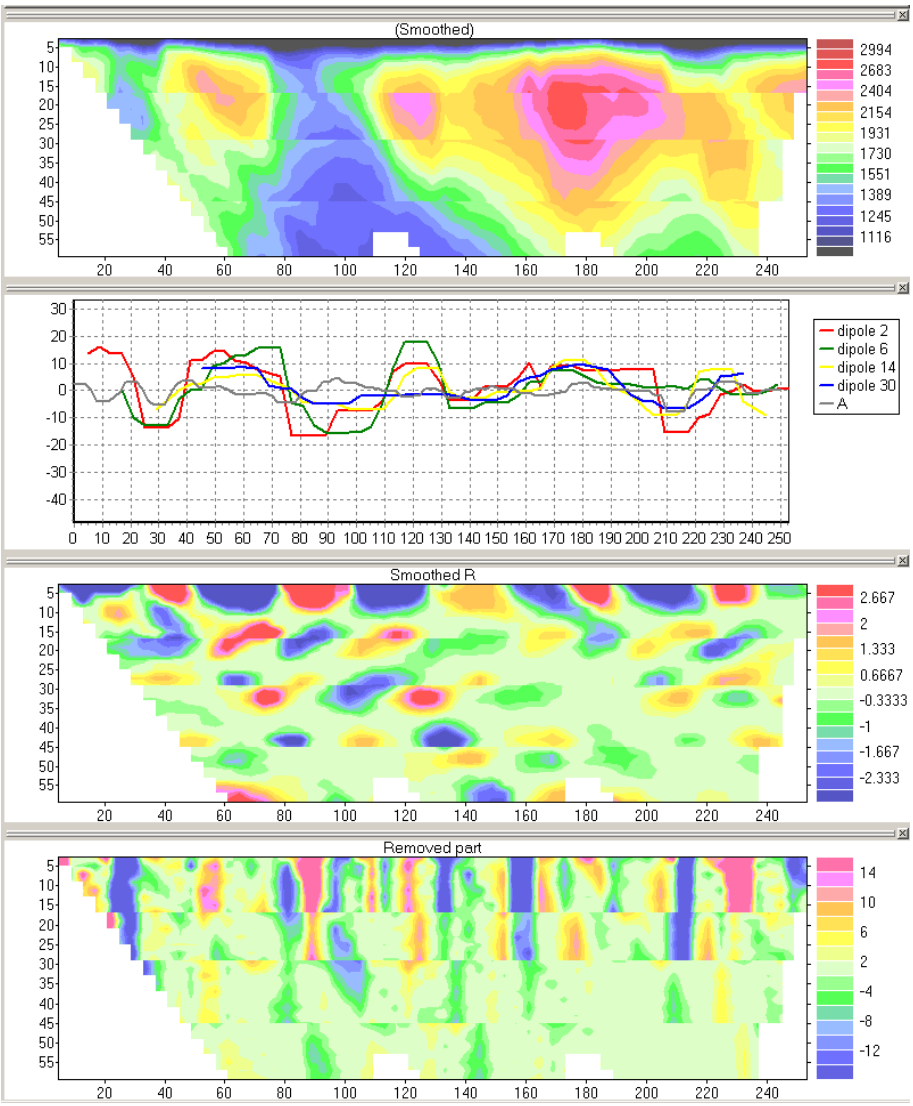
C and P effects may be smoothed using a median or a mean method. The width of the smoothing sliding segment may be adjusted with the ruler “Window width = …”



Residual may also be smoothed using a median or a mean method. The matrix used is a rectangle or a cross (for apparent resistivities with quincunx layout as measurements using Wenner array) The width of the smoothing sliding matrix may be adjusted in X and in Y directions with the two rulers “dX = …” and “dY = …”

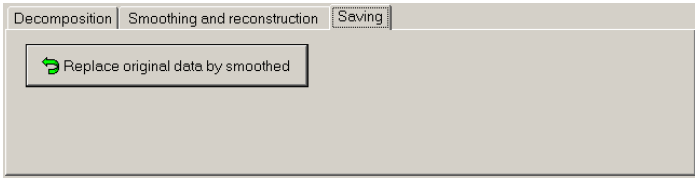
When the configuration of this second smoothing scheme is defined, the button “Smooth” may be pushed. Four new plot windows are displayed :

- the resconstructed [Smoothed data] pseudosection,
- the [Smoothed P & C effects],
- the [Smoothed residual],
- the [Removed part] = [Residual IIIa] + [Residual IIIb].



A new estimation of the [“1D” part] from the reconstructed [Smoothed data] pseudosection may be performed by clicking the “New 1D” button. This allows to refine [P & C effects] calculation. Actually, this corresponds to a feed back step in the flow chart, allowing to recalculate [Residual I] = [Original data] – [“1D” part] and then [P & C effects] from this recalculated residual.

Finally, the [Smoothed data] pseudosection may be saved using the “Replace original data by smoothed” button in the “Saving” window.



The median window may then be closed and the [Smoothed data] pseudosection is exported to the default display window of ***X2IPI***.

Note that at this stage the [Smoothed data] pseudosection is only recorded in RAM. To be saved on a disk, the “Save” icon in the main window icon bar has to be clicked. A “Save” dialog window then pops up to save the [Smoothed data] pseudosection in RES2DINV [*.dat] format.

3.7. Exporting to inversion programs

X2IPI allows to export ASCII files supported by RES2DINV, SENSINV2D and IPI2WIN. Those interpretation softwares are subject to liabilities. Demo versions and user manuals may be downloaded from the following sites :

- RES2DINV : http://www.geoelectrical.com
- SENSINV2D : http://www.geotomographie.de
- IPI2WIN : http://geophys.geol.msu.ru/ipi2win.htm

Hence one may take reference to the user manual of these softwares in order to have informations about the format of the files exported by ***X2IPI***.

4. How to use x2ipi with Terrameter LS (ABEM, Sweden)

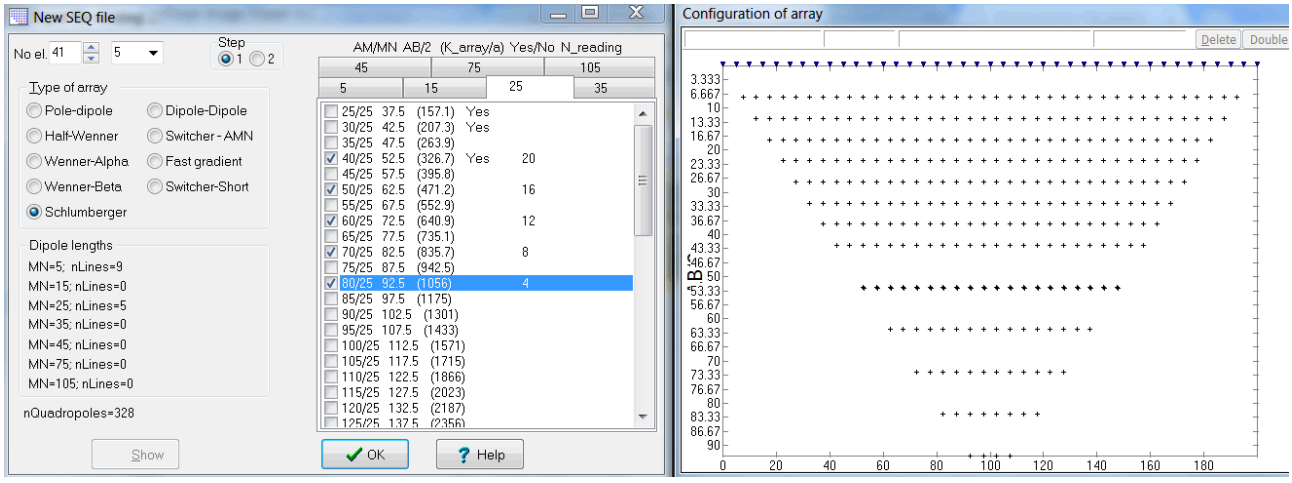
4.1. Creating protocol files for 4x21 cables set

Terrameter LS is 64-electrode instrument with two 32-pole connector for electrode cables (2x32). However the basic recommended set supplied with the equipment is the set of 4 cables with 21 electrodes each (4x21). Since the last and the first electrode take-outs shall overlap at the cable ends, the equipment allows to measure with 81 electrodes for the system layout (4x21 - 3). It provides increase the depth of ERT investigation up to 25%.

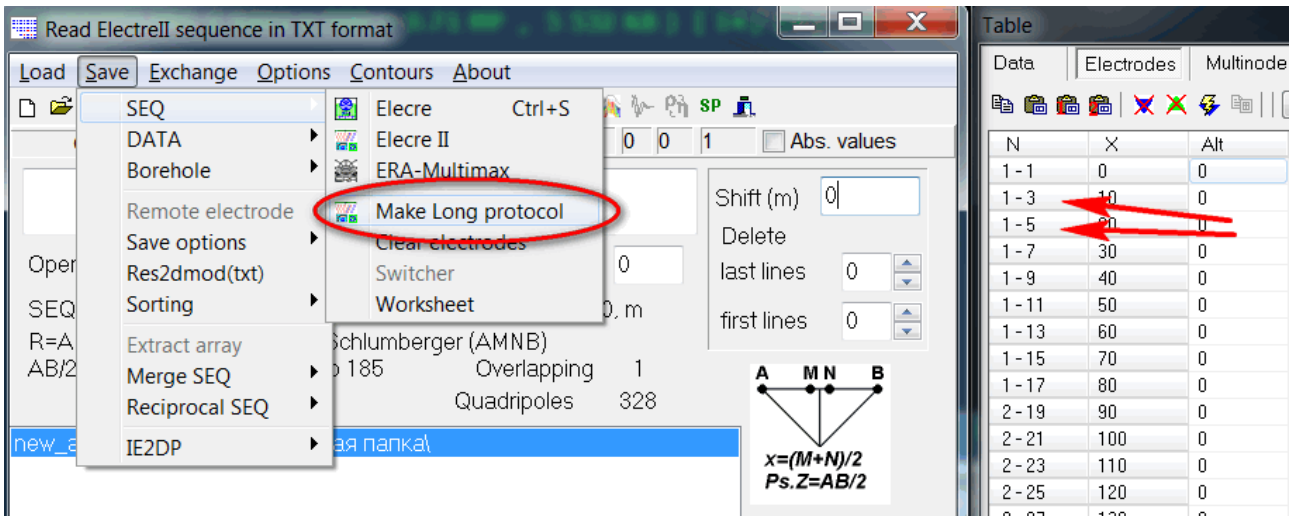
Protocol consists of two types of measurements. The first type - shallow measurements (small electrode spacings). The second type - measurements for deeper parts of the geoelectrical section (large electrode spacings). For example, having cables with 5m spacing between electrode takeouts, LONG32 type (41 electrode with 10m unit electrode spacing) and SHORT32 type (41 electrode with 5m unit electrode spacing) were applied. Two protocols with constant spacing between electrodes each.

x2ipi toolbox provide preparing ABEM protocols for 61-electrode measuring scheme. The example for Schlumberger array. **The first step** is create LONG protocol for long spacing.

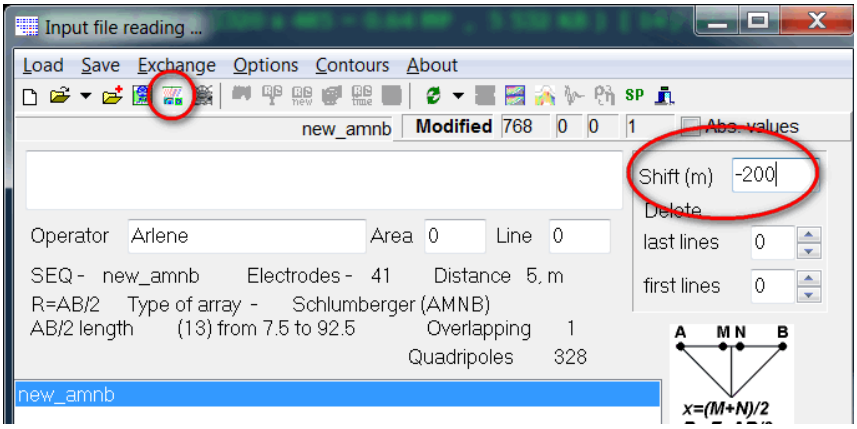
1. create a new protocol file for 41 electrodes with 5 meter spacing [3.1] and save it ***Electrell*** txt format .



2. **Menu-Save-Seq-Make Long protocol**. It creates TXT protocol file with new numbers of electrodes and 10 meter inter-electrode spacing.

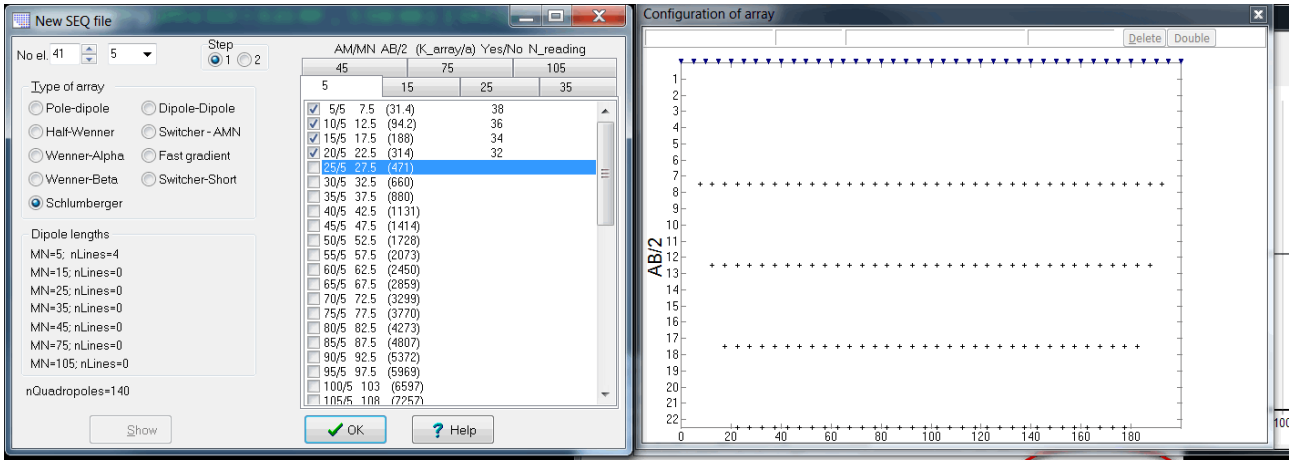


3. Shift X to have 0 coordinate for central electrode. Shift(m) = -200. Save it ***Electrell*** txt format again.



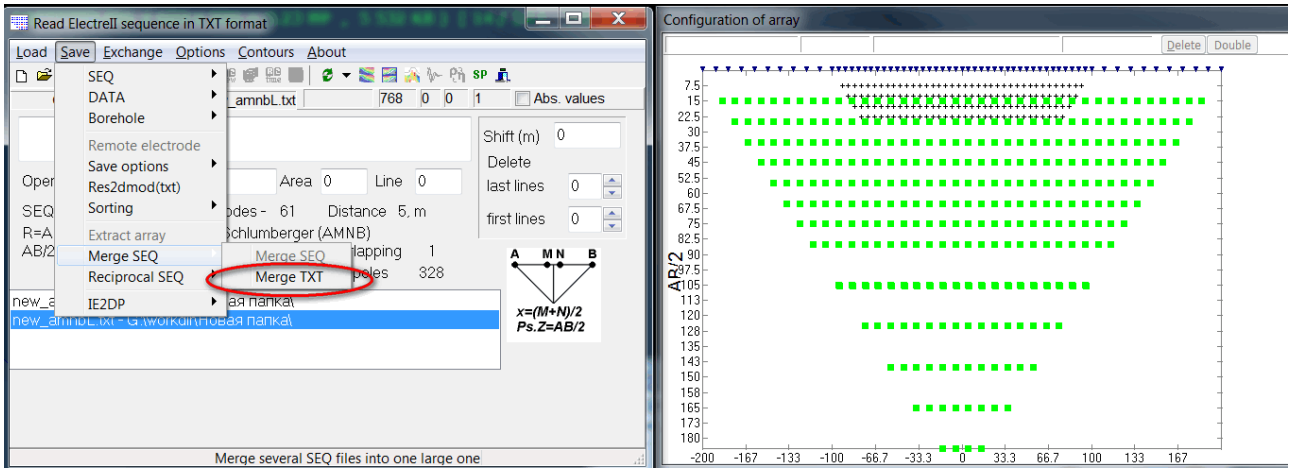
The second step is create Short protocol for central part of profile.

1. create a new protocol file for 41 electrodes with 5 meter spacing and save it in new file in ***Electre II*** txt format . We do not need big number of spacing - just 4 lines could be enough.



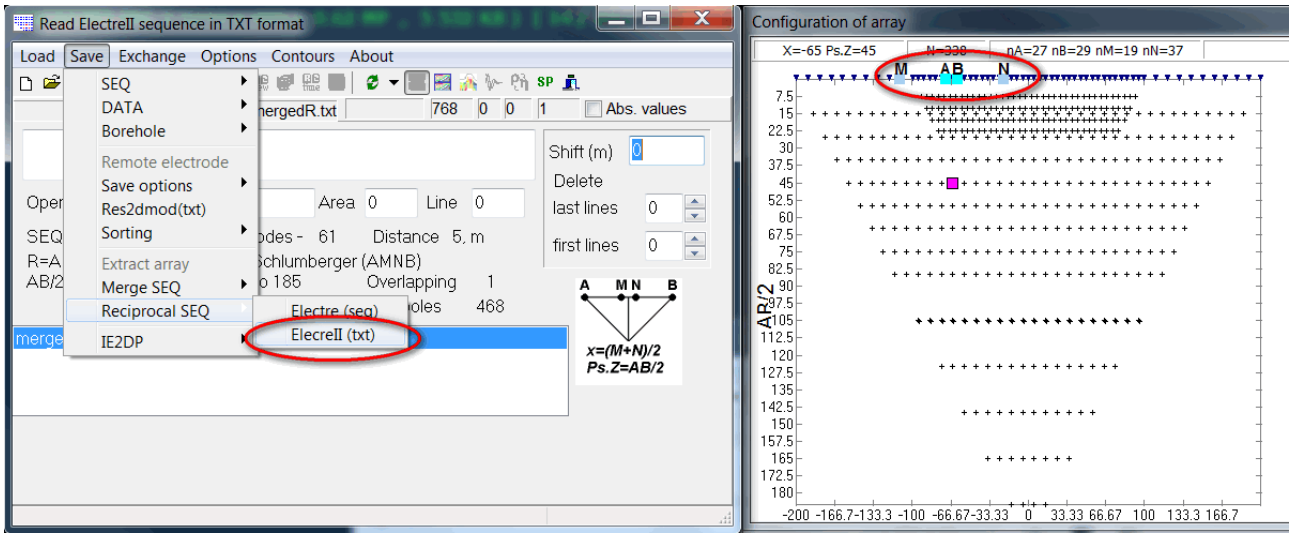
2. Shift X to have 0 coordinate for central electrode. Shift(m) = -100. Save it ***Electrell*** txt format again.

3. Add file with LONG protocol and save two files in one be **Menu-Save-Merge SEQ-Merge TXT**.

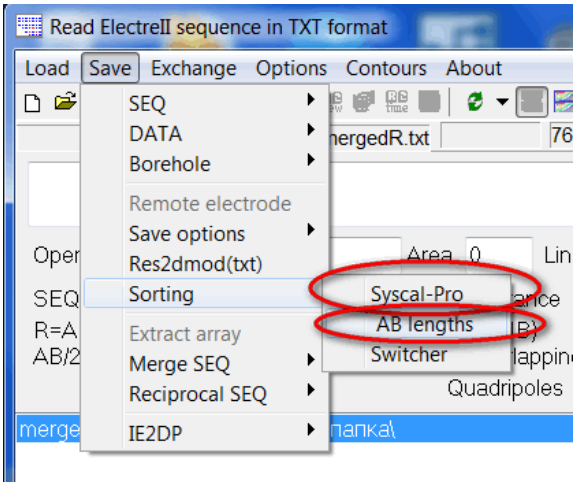


Now we have protocol file for 4x21 cable set. We need to open it and optimize for multichannel receiver. **The third step** is optimization.

1. Make reciprocal Schlumberger array **Menu-Save-Reciprocal SEQ-Electrell (txt)** [3.3]. Open result file.

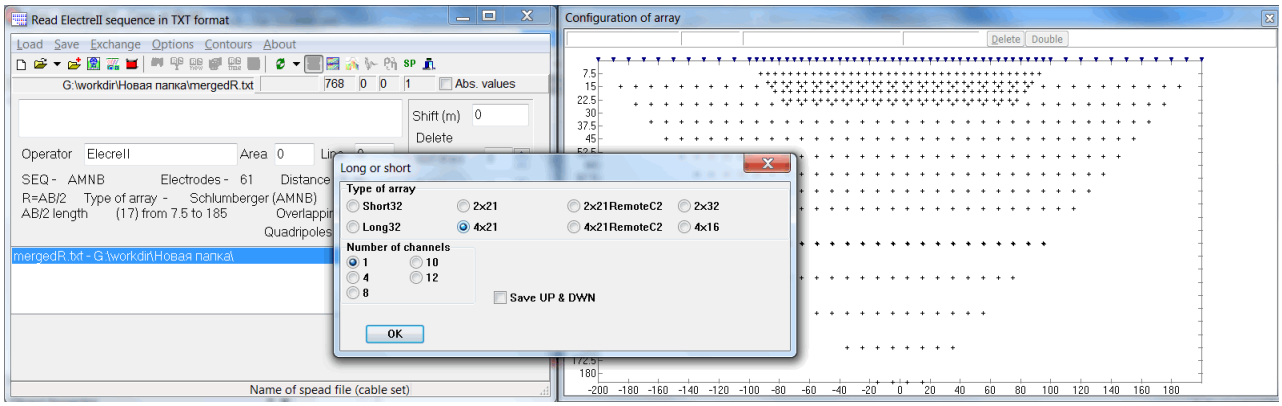


2. Sorting quadripoles. **Menu-Save-Sorting-Syscal-Pro or AB lengths** [3.33.2]



Now we have optimized protocol file for 4x21 cable set. We need to convert it in XML protocol file for Terrameter LS. **The fourth step** is creating XML file.

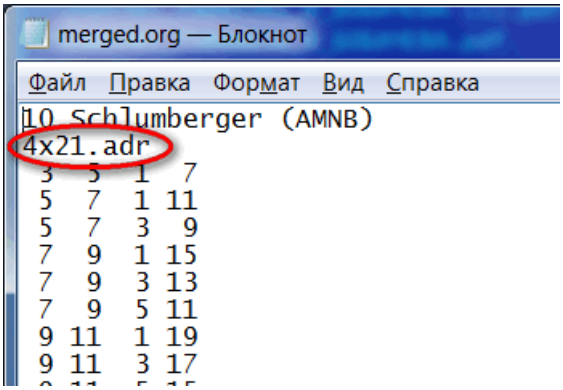
1. We need to open protocol and Save in ORG format of ABEM.



We do not need change number of channels in Long or short Dialog. It was important for SAS4000 ABEM unit. But we have to indicate correct spread file in ORG file.

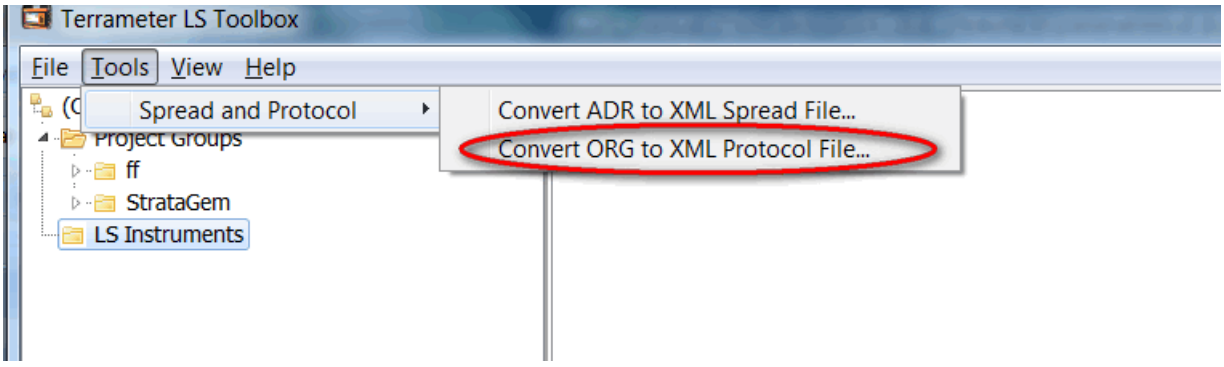
- 4x21.adr - 4 electrodes array for 4x21 cable set
- 4x21RemoteC2.adr - pole-dipole array for 4x21 cable set
- 2x21.adr - 4 electrodes array for 2x21 cable set
- 2x21RemoteC2.adr - pole-dipole array for 2x21 cable set

The correct spread file depends on cable set (2x21, 4x21, 4x16, 2x32 etc) and four or three electrodes array.

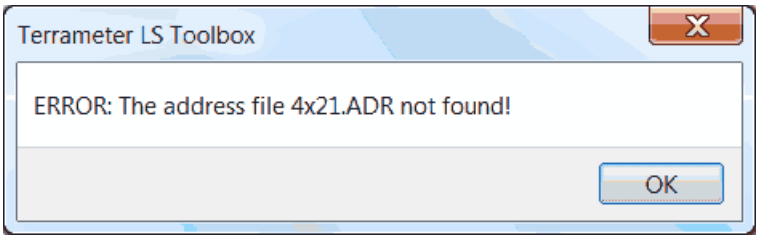


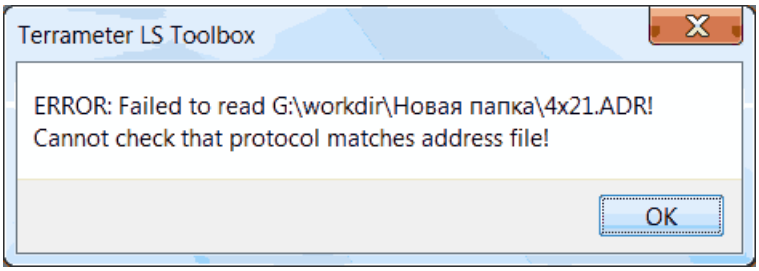
We could also indicate correct spread file in ORG file on the second line of ORG file.

2. Use ***Terrameter LS Toolbox*** software to convert ORG file in XML file.



File 4x21.adr does not exist. It results that error messages will be issued, but it does not mean that there is any error in the protocol file. See "6.2 Conversion of ORG to XML Protocol file" in the manual of ***Terrameter LS Toolbox***.





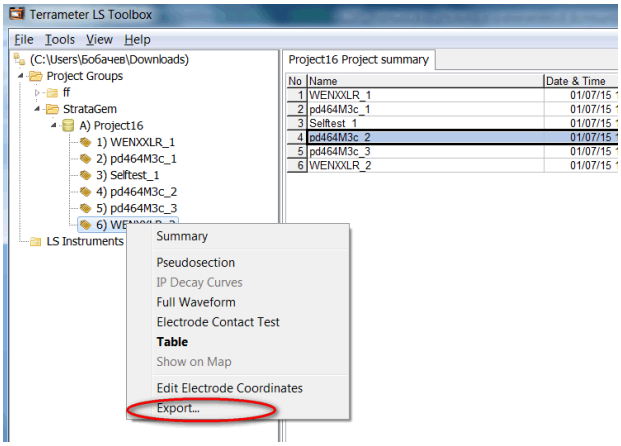
Finally we received protocol XML file with correct spread name, which could be used with **Terrameter LS** and it could be read by ***x2ipi*** software also.

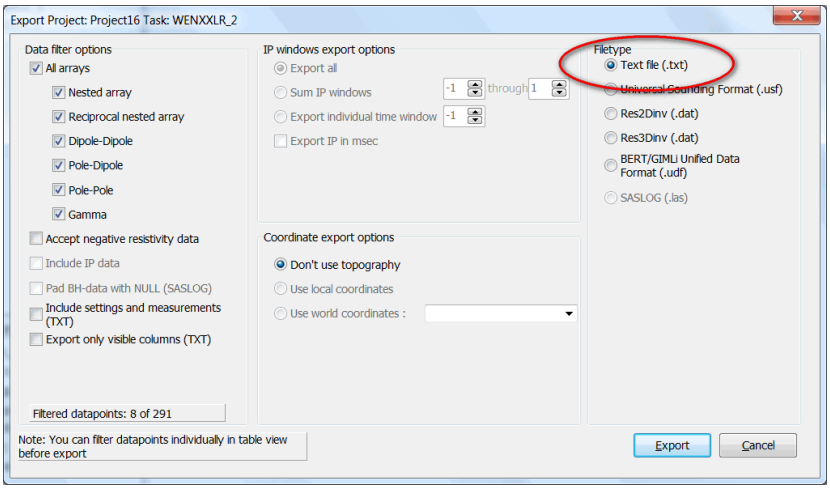
```
<?xml version="1.0" encoding="UTF-8"?>
- <Protocol>
    <Name> merged </Name>
    <Description> A description of the protocol can be written here </Description>
    <Arraycode> 7 </Arraycode>
    <SpreadFile> 4x21.xml </SpreadFile>
  - <Sequence>
    - <Measure>
        <Tx> 3 5 </Tx>
        <Rx> 1 7 </Rx>
      </Measure>
    - <Measure>
        <Tx> 5 7 </Tx>
        <Rx> 1 11 </Rx>
        <Rx> 3 9 </Rx>
      </Measure>
    - <Measure>
        <Tx> 7 9 </Tx>
        <Rx> 1 15 </Rx>
        <Rx> 3 13 </Rx>
        <Rx> 5 11 </Rx>
      </Measure>
```

Note! There is not information about inter-electrode spacing in XML or ORG files.

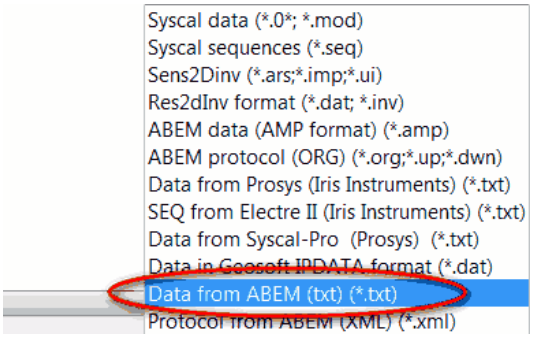
4.2. Read field data of Terrameter LS

Terrameter LS Toolbox software can export field data txt format, which can be read ***by x2ipi*** software





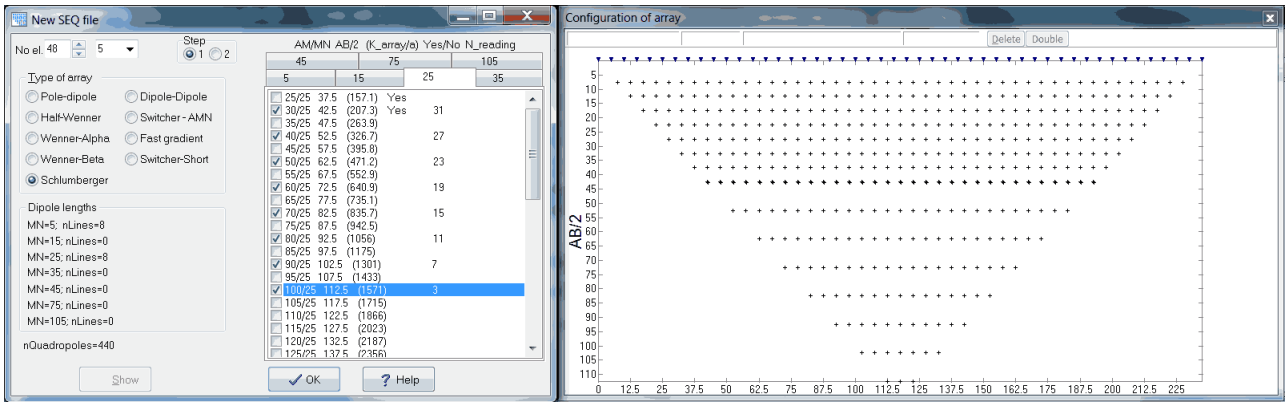
Use **Data from ABEM (txt)** format to read data from ***Terrameter LS Toolbox*** software.



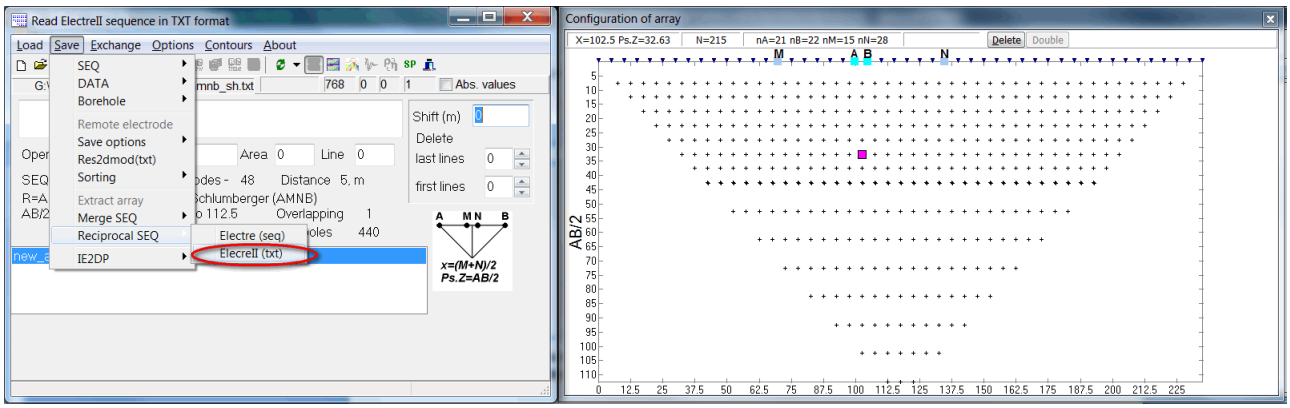
5. How to use x2ipi with Syscal-Pro (IRIS Instruments, France)

5.1. Creating sequence file for Syscal-Pro

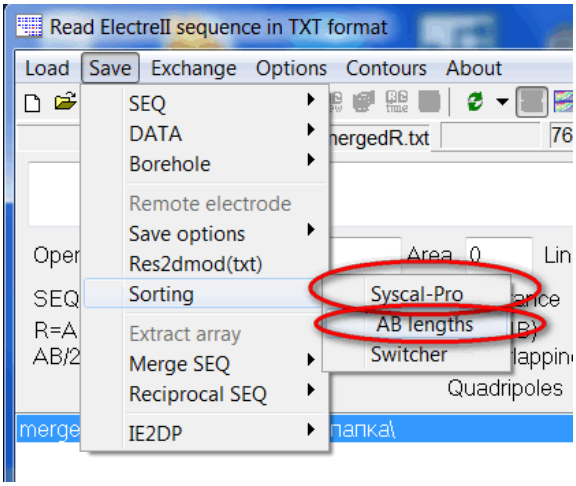
1. create a new sequence file for correct number of electrodes [3.1] and save it ***Electrell*** txt format .



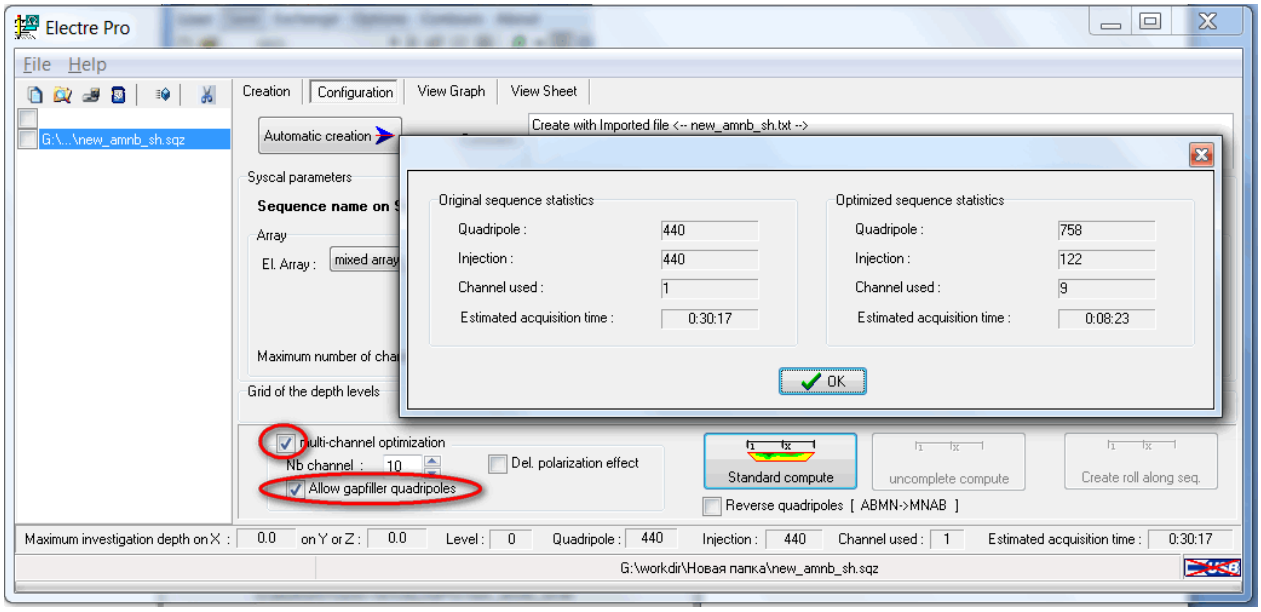
2. Optimize sequence for Syscal-Pro. Make reciprocal Schlumberger array **Menu-Save-Reciprocal SEQ-Electrell (txt)** [3.3]. Open result TXT file.



2. Sorting quadripoles. **Menu-Save-Sorting-Syscal-Pro or AB lengths** [3.33.2]

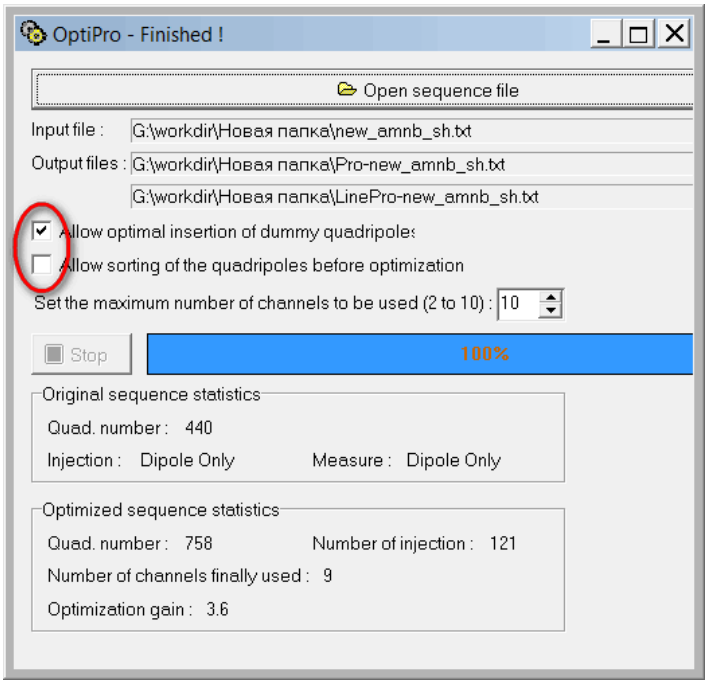


3. Now we need to prepare sequence file for Syscal-Pro and add gapfiller (dummy) quadripoles. We could use ***Electre Pro*** software.



We made optimized sequence file (SQZ), which should be upload in Syscal-Pro for measurements.

Also we could use ***OptiPro*** software from IRIS Instruments. We need uncheck Sorting checkbox, because we already sorted quadripoles. x2ipi uses different algorithm of sorting quadripoles.



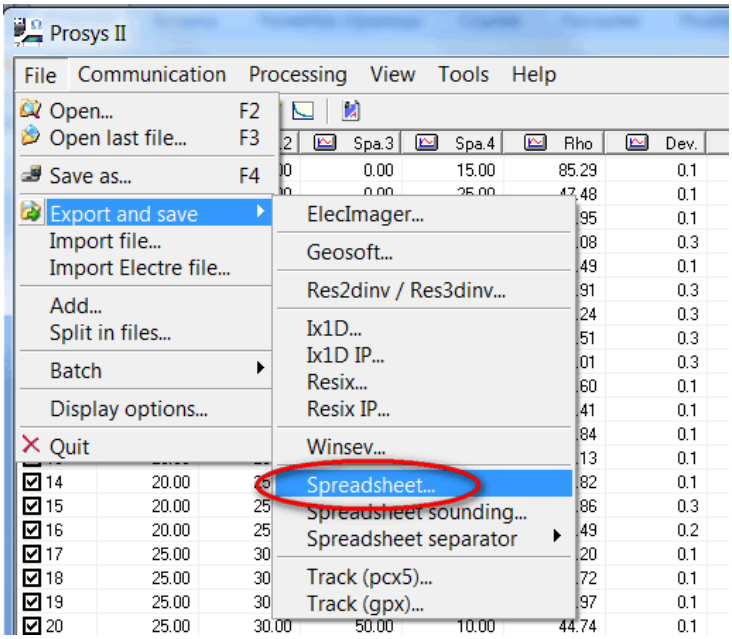
Opti-Pro creates TXT file with long file name. We recommend to rename and to short this file name because Syscal-Pro supports only 10 characters in file name.

Finally we have two sequence file: original TXT file and optimized TXT or SQZ file. We could use original file for Syscal-Pro data processing.

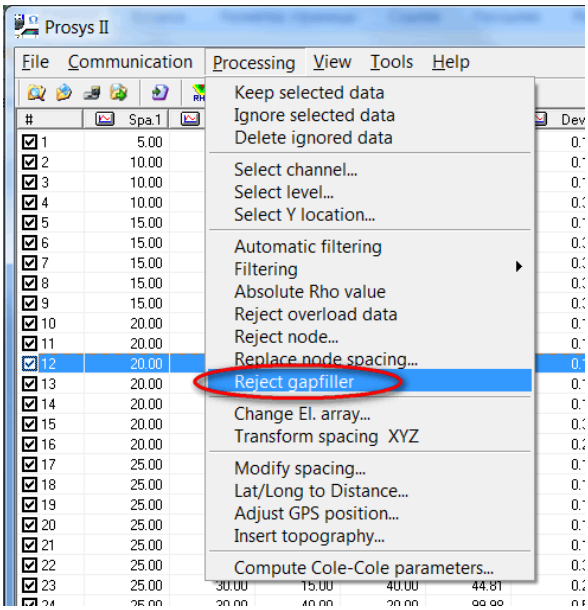
There are many other options to prepare sequence file [3.4].

5.2. Read field data from Syscal-Pro

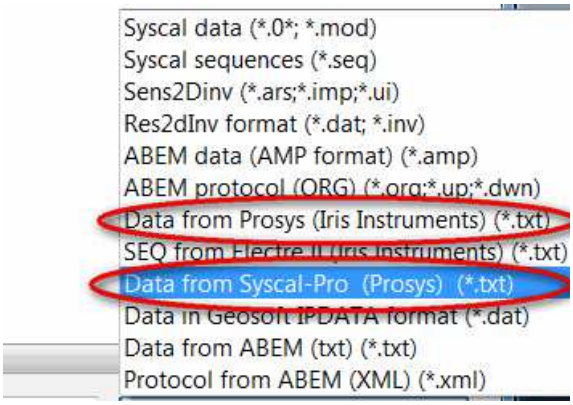
Prosys II software can export field data in TXT format, which can be read ***by x2ipi*** software.



We have to remove gapfiller measurements before data processing. If we made optimization by ***Electre Pro*** software, then we could reject gapfiller by ***Prosys II*** before export spreadsheet.



If we made optimization by ***OptiPro*** software, then we could reject gapfiller by ***x2ipi*** software. There are two options to read data from ***Prosys II*** software. **Data from Syscal-Pro (Prosys)** option allows to reject gapfiller from TXT data file. We read the data file first and the *original* sequence file.



6. How to use x2ipi with Res2dinv format data (Geotomo software, Malaysia)

Res2dinv format is the main format ERT data.

6.1. Remove bad points from data file

There are many options to remove bad point from data file.

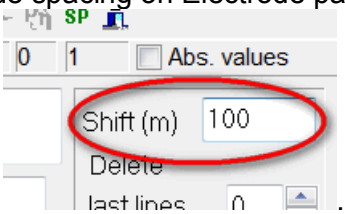
1. Trimming bad measurements signal level, quality factor, apparent resistivity or chargeability range [3.5.3].
2. Remove data from bad electrodes or [2.5.2].
3. Remove bad point on pseudo-section in Display [2.4], on Profiling page [2.5.5] or Soundings page [2.5.4].
4. Remove some spacing on Spacing page [2.5.3]

All removed point could be restored.

6.2. Correct X-coordinate

X-coordinate could be corrected by the next ways:

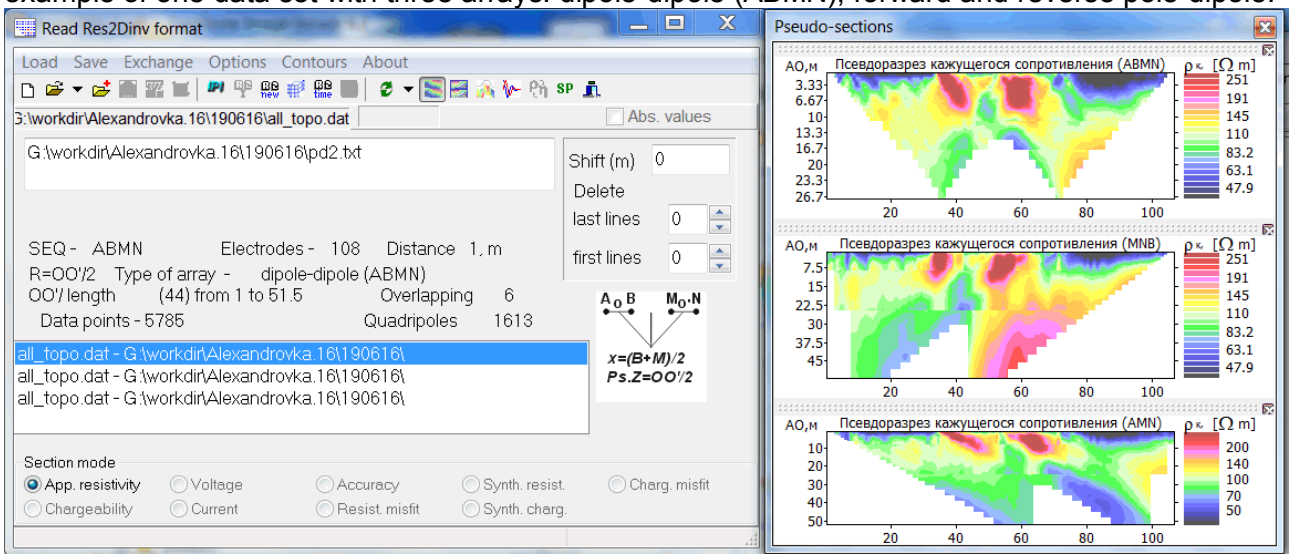
- Change inter-electrode spacing on Electrode page [2.5.2]



- Shift all X-coordinate .
- Mirror profile by Exchange menu [2.2.5].

6.3. Merge different array and different cable setup in one data set

To merge some data set in one file just open all date sets and save them in Res2dinv format . The ***x2ipi*** software could show data for different array on different pseudosections. This is the example of one data set with three arrays: dipole-dipole (ABMN), forward and reverse pole-dipole.

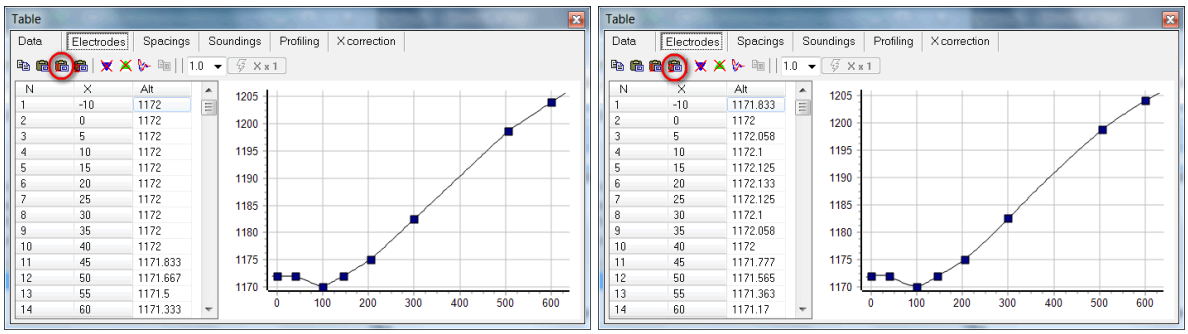


6.4. Input topography

The simplest way is preparing table X and Altitude coordinate table in any spreadsheet application (like Microsoft Excel) and copy it to clipboard.

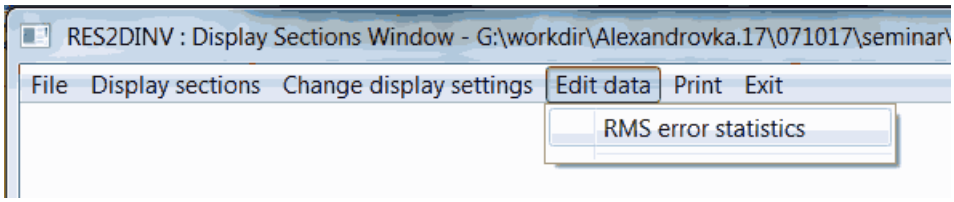
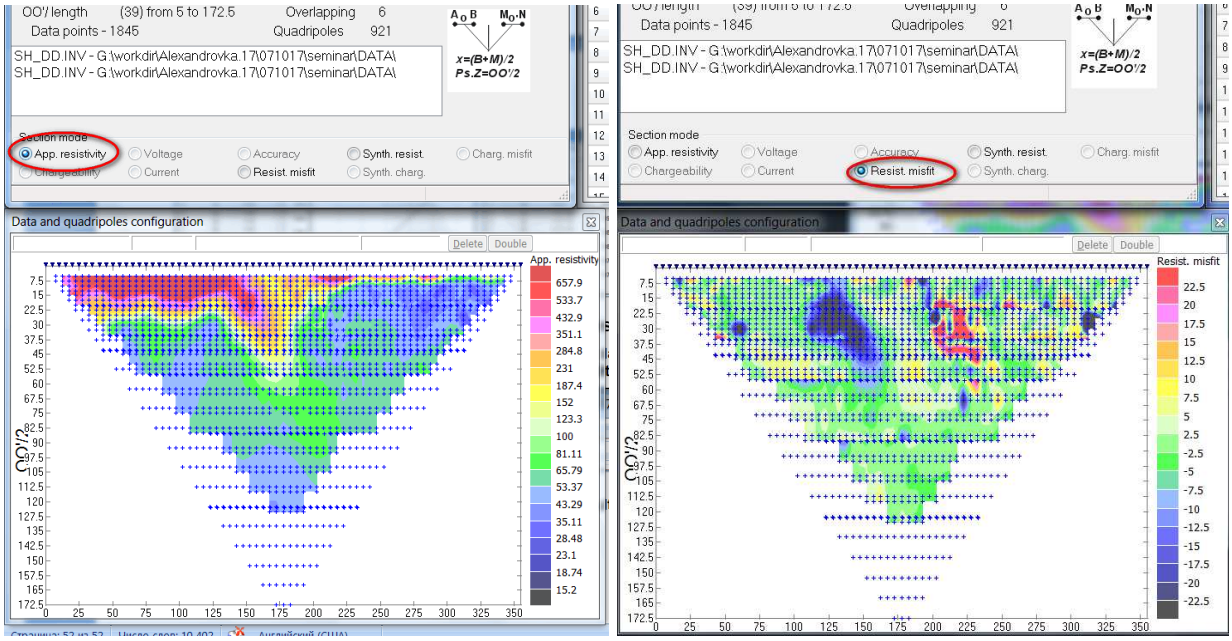
	A	B
1	0	1172
2	40	1172
3	100	1170
4	145	1172
5	205	1175
6	300	1182.5
7	505	1198.7
8	600	1204
9		

Use one of these buttons to paste topography data (X and Alt) from the clipboard and to find each electrode elevation by linear or square interpolation.



6.5. Analysis of inversion result (INV files)

The inversion results could be usually improved, if we remove data point with large misfit. There is an option in ***res2dinv*** software to remove such point - **Menu-Edit data-RMS error statistics**.



x2ipi could plot misfit pseudosection to analyze inversion result and remove data pint with large misfit.