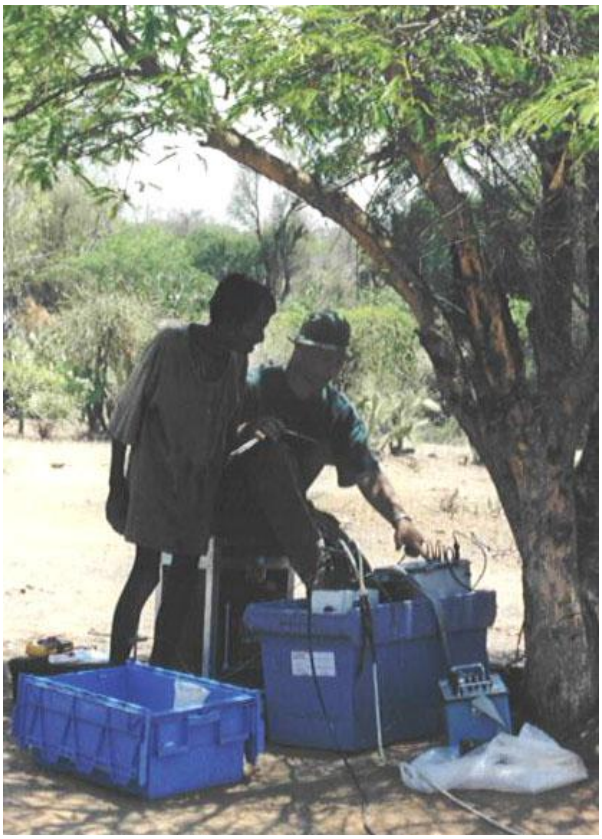
X2IPI

Toolbox for 2D Electrical Resistivity Tomography and IP measurements

User Manual

Henri ROBAIN [(1)] and Alexey BOBACHEV [(2)]



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1. General information about X2IPI

X2IPI — 2D electrical resistivity tomography processing tools that allows you to:

- check and correct field data,
- analyze IP data,
- merge or separate data sets,
- 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. Copyright

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1.2. System requirements

X2IPI is supported by any PC with Windows XP – Windows 11 operating system installed.

2. Overview of the *X2IPI* toolbox

X2IPI is a toolbox designed for data processing of 2D Electrical resistivity tomography. This software helps you to

- 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*
- AGI (USA): SuperSting

X2IPI supports *RES2DINV* (Geotomo Software) and *ZONDRES2D* (Zond Software) data formats. It is possible to export tomography data and inversion results to *IPI2WIN* (Alexey A. Bobachev) 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). Data have usually binary and closed-proprietary format. Before opening it has to be 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

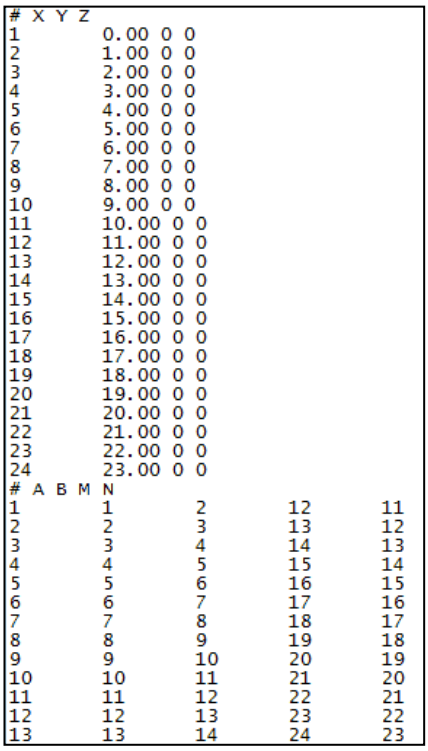
2.1.1. Protocols (sequences)

The primary type of ERT protocols 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*.

A [.txt] file consists of two parts. Coordinates of all electrodes are described in the first part (electrode number, X-, Y-, Z- coordinates).

(*Note!*) ***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 different instruments: *SYSCAL-PRO*, *OMEGA-48*, *SIBER-64*. When you export a [.txt] protocol from *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 (<*Syscal sequences*>).

X2IPI can read ABEM (Sweden) protocols of *TERRAMETER LS* instrument, <*Protocol from ABEM (XML)*> (see ***Ошибка! Источник ссылки не найден. Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***)

2.1.2. Field data

The basic field data file has a [.txt] type and came from *PROSYS II* format (IRIS Instruments, France):

<Menu – File – Export and save – Spreadsheet...>

All data must be 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
- *Spa.1* X-coordinate of electrode A (C1) for a specific measurement line in protocol
- *Spa.2* X-coordinate of electrode B (C2) for a specific measurement line in protocol
- *Spa.3* X-coordinate of electrode M (P1) for a specific measurement line in protocol
- *Spa.4* X-coordinate of electrode N (P2) for a specific measurement line in protocol

  Note! Value 99999.99 is reserved for a 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.

TERRAMETER LS field data should be read by another file type – *<Data from ABEM (txt)>.*

2.1.3. Input file for the inversion software (RES2DINV)

There are two main goals in ***X2IPI*** usage: field data processing and preparation of data file for the 2D inversion software. That is why ***X2IPI*** output file has *RES2DINV* input format [.dat]. The format is supported by the most of 2D ERT inversion software solutions.

There are two different formats for *RES2DINV*: standard format supports basic arrays (e.g. Schlumberger, pole-dipole etc.) and general format 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*. Moreover, it is impossible to do in *RES2DINV* when [.dat] file contains data of more than one electrode array type.

X2IPI solves the problem. It analyzes and divides [.dat] file into parts by the type of electrode array. Then it plots apparent resistivity pseudosection for each array type found in the file.

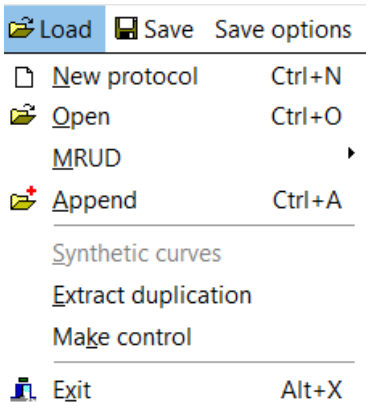
X2IPI can also work with data from inversion results file [.inv] of *RES2DINV*.

2.1.4. Induced polarization decay curve data

Standard way to save IP decay curves is the format of company *GEOSOFT* <*Save – Data – GEOSOFT*>. Also there is a modification of *RES2DINV* data format proposed by Torleif Dahlin. The option <*Menu – Save – Save options – Remove IP decay*> allows to remove IP decay curves from the data.

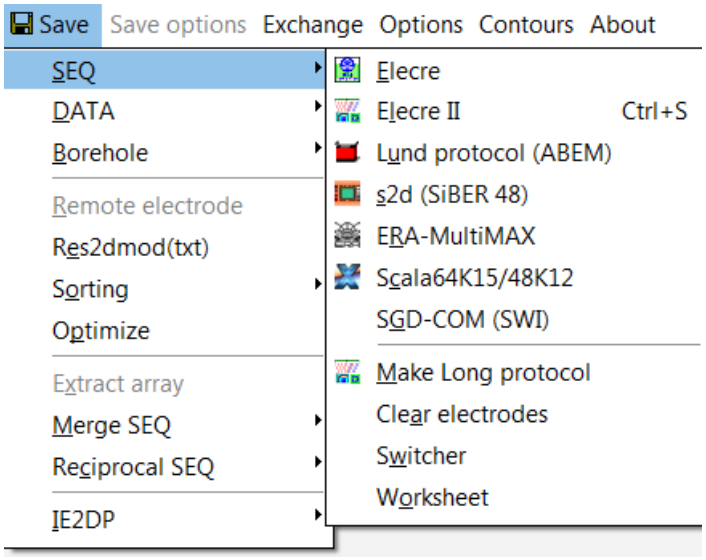
2.2. Main menu

2.2.1. Load 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
- *Make control* — Find repeated readings and svave then in *filename.ctrl.txt* file.
- *Exit (Alt + X)* — Exit ***X2IPI***

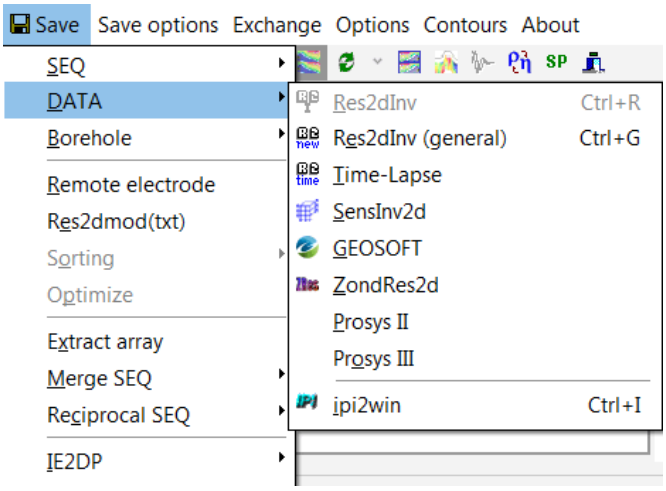
2.2.2. Save menu – SEQ



- *Electre* — Save binary protocol file for old *ELECTRE* program (IRIS Instruments)
- *Electre II* — Save [.txt] protocol file for *ELECTRE II* and *ELECTRE PRO* programs (IRIS Instruments)
- *Lund protocol (ABEM)* — Save Lund [.org] protocol file (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 numbers only – LONG32 type for ABEM 4x21 spreads system
- *Clear electrodes* — Remove unused electrodes from protocol
- *Switcher* — Prepare protocol for *COMx64* switcher box (Nord-West, Russia)
- *Worksheet* — Text protocol file with additional columns (see figure below)

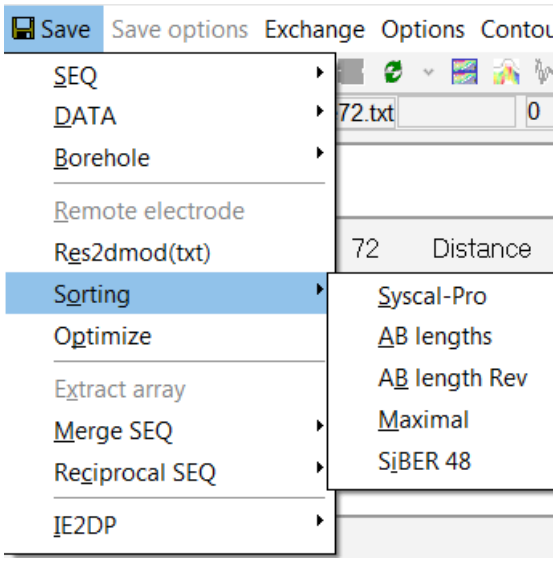
68	335.00	0	0					
69	340.00	0	0					
70	345.00	0	0					
71	350.00	0	0					
72	355.00	0	0					
#	nA	nB	nM	nN	X	AB/2	MN	K
1	1	16	70	55	172.5	135	75	10145
2	1	16	66	51	162.5	125	75	7941
3	1	16	62	47	152.5	115	75	6073
4	1	16	58	43	142.5	105	75	4513
5	1	16	54	39	132.5	95	75	3234
6	1	16	50	35	122.5	85	75	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 data file to *RES2DINV* inversion software with the index based data format
- *Res2dInv general (Ctrl + G)* Export file to *RES2DINV* inversion 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 files to SENSINV2D inversion software*
- *GEOSOFT* Save data in *GEOSOFT* format, mainly for managing IP data
  Note! Available for [.txt] data only
- *ZondRes2d* Export data in *ZondRes2d* format
- *Prosys II / III* Export data in *Prosys* TXT format. It's supported by different software.
- *IPI (Ctrl +I)* Export file to *IPI2WIN* software for 1D interpretation

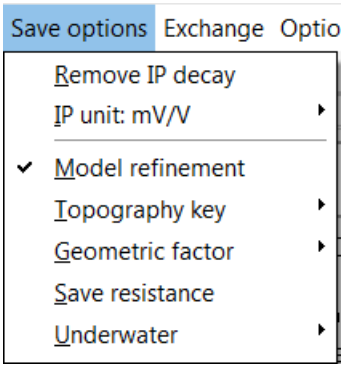
2.2.4. Save menu



- *Borehole* Work with ERT measurements obtained in boreholes
- *Remote electrode* Input coordinates of remote electrode for pole-dipole array. Apparent resistivity will be corrected then according its position

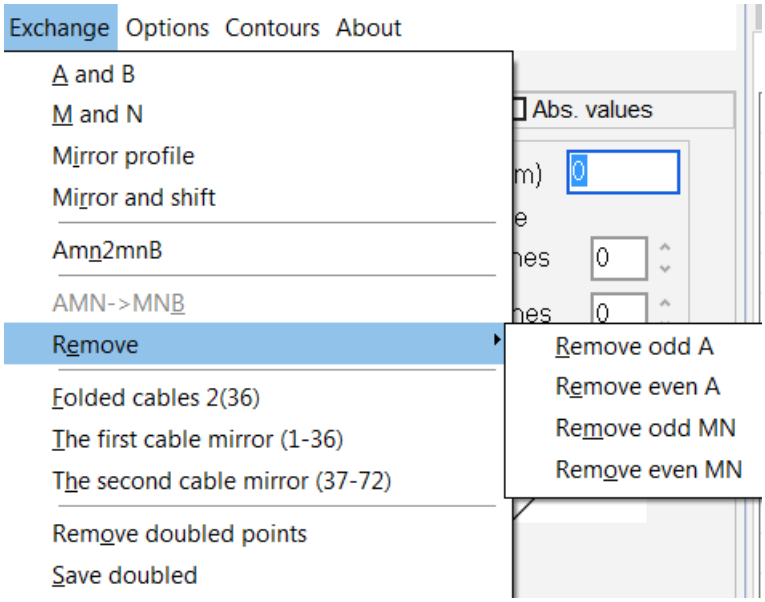
- *Save option – Save resistance* Save resistances instead apparent resistivities
- *Save option – Remove IP data* Remove IP data from data set
- *Save option – Remove IP decay* Remove IP decay for 2D inversion in *RES2DINV* software
- *Res2dmod(txt)* [.dat] format of *RES2DMOD* software. It works with any non-conventional and allows you to calculate 2D sensitivity pseudosection for arbitrary array
- *Sorting* Change the order of measurements in protocol for multichannel equipment
- *Optimize* Optimize the order of measurements in protocol for Syscal Pro
- *Extract array* Save data or protocol for selected array only
- *Merge SEQ* Merge protocols files into one protocol file
- *Reciprocal SEQ* Save protocol file for reciprocal array
- *IE2DP* Convert protocol file into *RES2DINV* format. Geometrical factor (K) is saved as apparent resistivity

2.2.5. Save options menu

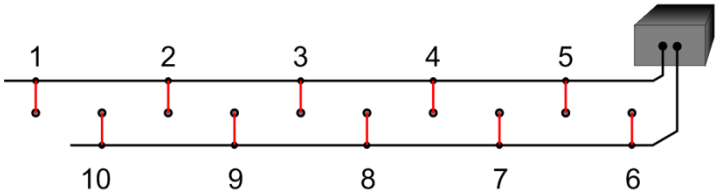


- *Remove IP data* Remove IP data from data set
- *Remove IP decay* Remove IP decay for 2D inversion in *RES2DINV* software
- *IO unit* The label for IP data in Res2dinv data format
- *Model refinement* See "Use model refinement" in Res2dinv Manual
- *Topography key* See Res2dinv Manual s
- Geometric factor See Res2dinv Manual s
- *Save resistance* Save resistances instead apparent resistivities
- *Underwater* Options for underwater ERT survey

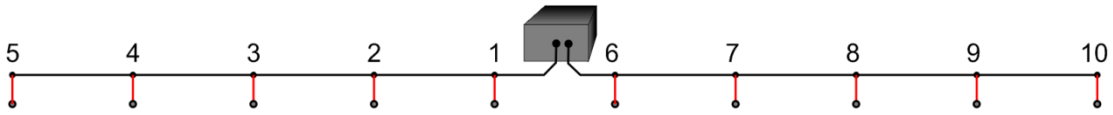
2.2.6. Exchange menu



- *A and B* — Exchange A and B electrodes in protocol file
- *M and N* — Exchange M and N electrodes in protocol file
- *Mirror Profile* — Reverse coordinates of electrodes in protocol or data files. For example, if 1st electrode coordinate is 0, 2nd is 1 and the last one is N, then the modified file will have 1st electrode coordinate at N, 2nd at N-1 and the last one at 0
- *Amn2mnB* — Transform AMN [.seq] file (forward pole-dipole) to MNB [.seq] file (reverse pole-dipole)
- *AMN→MNB* — Transform forward Pole-dipole array to reverse one using electrodes numbers only
- *Remove* — Remove some electrodes for pole-dipole array protocol to decrease time of measurements or work with non-polarizing electrodes
- *Folded cables* — Transform protocol for work with folded cables to decrease inter-electrode spacing twice (see picture below)
  Note! This procedure is available for one electrode array type only (e.g. only forward pole-dipole, only Schlumberger, etc.)

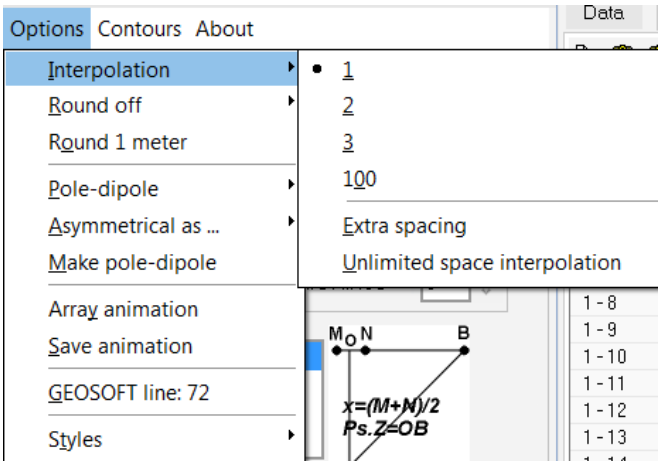


- *The first cable mirror* — Protocol transformation



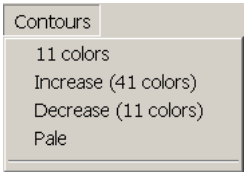
- *Remove doubled points* — Remove repeated measurements from data set
- *Save doubled* — Save repeated measurements into [.dat] file

2.2.7. Options menu



- *Interpolation* — The maximum number of missing points in pseudosection to interpolate contours. If number of missing points in closed area is higher than specified number, the area will be blanked
- *Round off* — Round off electrode position to decrease number of spacing (can be useful in case of irregular unit electrode spacing). This option did not change electrode coordinates in output file
- *Round 1 meter* — Change the position of electodes. Do not change the spacing. It is useful for **Syscal Pro Deep Marine** data (blog)
- *Pole-dipole* — Horizontal position of reference point for pole-dipole array data. Reload data set to see changes
- *Asymmetrical as …* — The variants of asymmetrical (gradient) array data plotting. Reload data set to see changes (blog)
- *Array animation* — animation of measurements order corresponding to the protocol file
- *Save animation* — save a [.bmp] file for each measurements to ***X2IPI*** catalog
  Note! If enabled, hundreds of files will be saved
- *Geosoft line* — line number variable for data file in *GEOSOFT* format
- *Styles* — Choose one of pre-defined window themes

2.2.8. Contour menu



Contour menu allows you to modify the color scale of plotted pseudosections (Display window).

- *11 colors* — 11 value levels will be used to plot pseudosection
- *Increase (<NUM colors>)* — <*NUM*> value levels will be used to plot pseudosection (<*NUM*> is larger than the currently used number of levels)
- *Decrease (<NUM colors>)* — <*NUM*> value levels will be used to plot pseudosection (<*NUM*> is less than the currently used number of levels)
- *Pale* — Less saturated colors will be used to plot pseudosection

Note! More options are available in Advanced Display window

2.2.9. Icon Bar

The following icons are available in the icon bar:

Create a new protocol file

Open file

Append file to already opened file of the same type ([.seq], [.txt], [.dat], [.inv])

Save [.seq] protocol file for old *ELECTRE* program (IRIS Insruments)

Save [.txt] protocol file for *ELECTRE II* and *ELECTRE PRO* programs (IRIS Insruments)

Save [.org] protocol file for ABEM instruments. Use *TERRAMETER LS TOOLBOX* software (supplied with the equipment) to convert [.org] file into modern [.xml] format

Export file to [.dtg] or [.dat] for 1D interpretation in *IPI2WIN*

Export file to [.dat] for *RES2DINV* inversion software with specified electrode configuration format (Schlumberger, pole-pole, pole-dipole, etc.)

Export file to [.dat] for *RES2DINV* inversion software with general electrode configuration format

Export files to [.gem] for *SENSINV2D* inversion software

Save data to [.dat] 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 data set with topography

Open Filtering Field Data window (available for [.dat] or [.inv] files of *RES2DINV* format only)

Show apparent resistivity or IP data in Display window

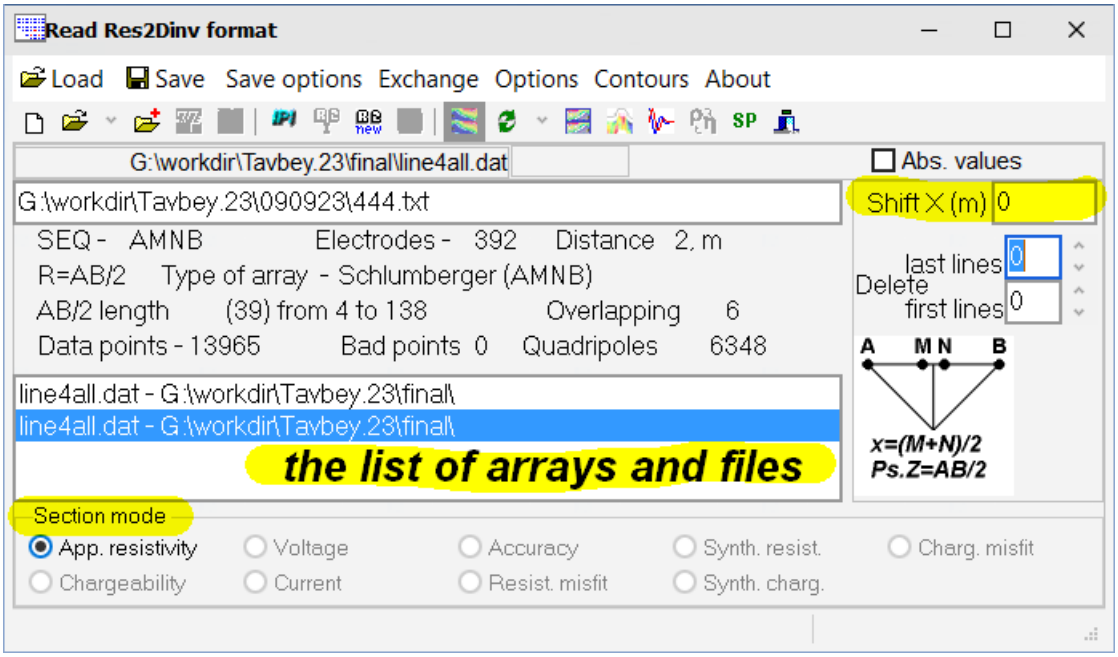
Show self-potential window

Exit ***X2IPI***

2.3. Main window

X2IPI has different windows. The first three (Main, Display, Table) are default windows.

2.3.1. General Information of file



This part of the main window contains general information about opened files. The first line shows the name of the last opened file. In this first line, you may check <*Abs. Values*> button.

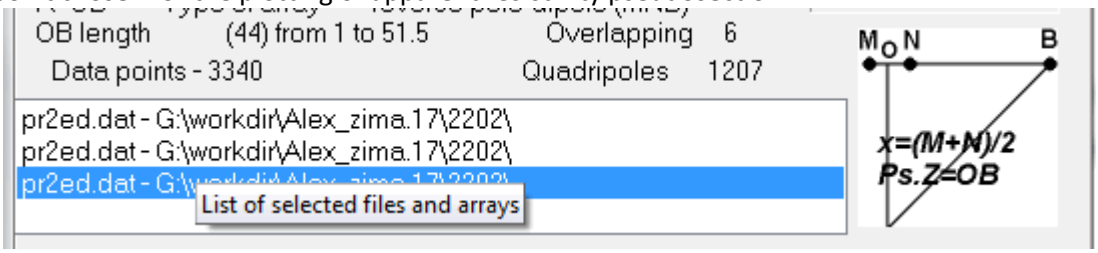
Next goes textbox for comments. It can be edited and saved after to the first line of *RES2DINV* data file. Next few indications are shown concerning the configuration of electrodes: the name of the [.seq] file used, the number of electrodes, the unit electrode spacing, the type of array, the number of AO lengths, the number of overlapping measurements (for Schlumberger, pole-dipole and dipole-dipole measurements only), the total number of quadripoles. None of these indications can be changed.

3 textboxes are placed in a square dialog box at the right part of the window

- *Shift (m)* shift of all electrodes (coordinates) by a constant value
- *Delete – last lines* remove a chosen number of bottom lines of the pseudosection
- *Delete – first lines* remove a chosen number of top lines at the top of the pseudosection

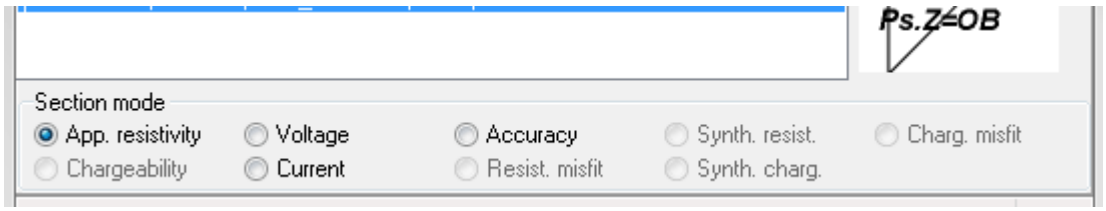
At the bottom you can see the list of selected files and arrays. It allows you to choose data (type of electrode array), which is currently visible in the Display window.

Finally, at the right bottom corner, there is a small picture that indicates the default convention for reference point chosen for the plotting of apparent resistivity pseudosection.



2.3.2. Section mode

There are two common parameters that characterize field data: *apparent resistivity* and *chargeability*. Other field parameters, such as *Voltage*, *Current* or *Accuracy*, can be plotted also. Select parameter you want to plot in *Section mode*

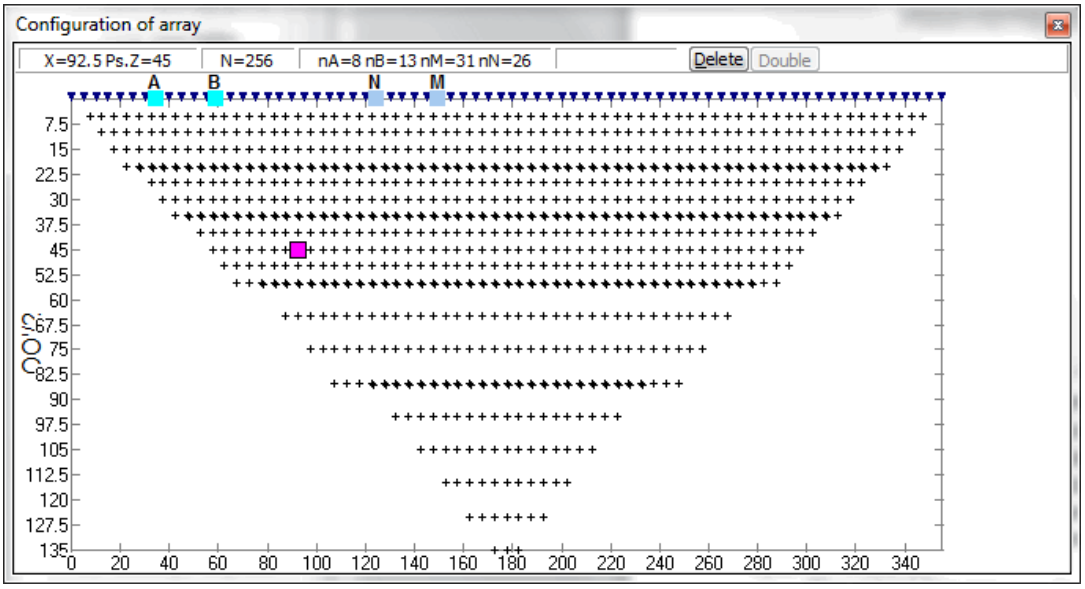


It is also possible to open [.inv] files (i.e. output files from *RES2DINV* software) in ***X2IPI***. It will allow you to analyze the difference (*Resist. misfit*) between field data (inversion input) and the direct problem solution of the final model (inversion output).

2.4. Display window

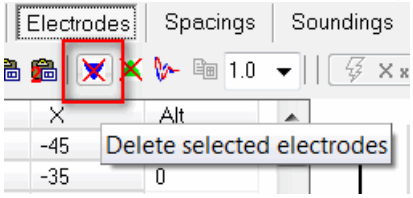
Display Window gives a plot of data contained in opened files. Electrode positions are shown by the triangles at the top of the pseudosection.

The conventional positions (reference points) of each measurement is shown by a cross. Bold cross means that two readings have the same reference point. For example, see next picture where two readings of dipole-dipole array have the same OO' spacing, but different MN lengths (OO'/2 = 20, 35, 55, 85 m).



You can select any particular measurement by clicking on a cross. You will see then information about the measurement at status bar at the top of the Display Window (protocol number of measurement, X- and Ps.Z-coordinates (Pseudo-depth or spacing) of the reference point). Then the measurement number After selecting one measurements by clicking on one 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 (*Note! works for one sequence only*). Positions of A, B, M and N electrodes will be highlighted by squares also (gray color for M and N; blue color for A and B). You can remove the selected point by "*delete*" key, by "*delete*" button at the status bar or by mouse double-clicking.

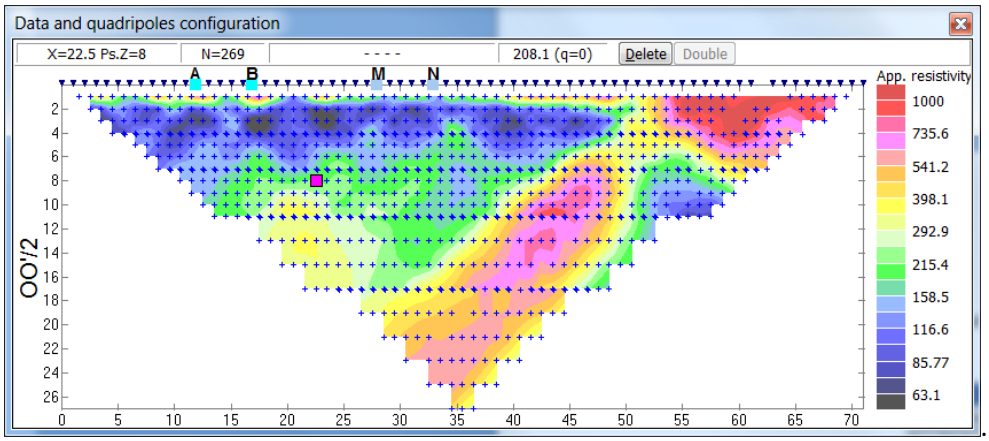
An electrode may be selected by clicking on the top triangles. All measurements made using this electrode may then be deleted by clicking on the "*delete*" button at the Tables window (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).



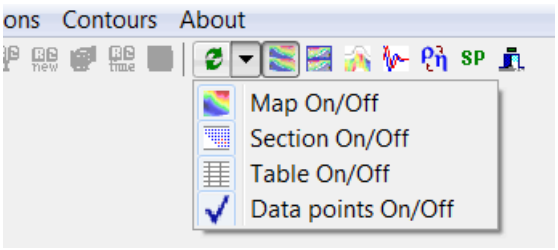
There is a "*double*" button at the status bar of the Display Window. It will be enabled if two protocol files are opened. Clicking it will result in deleting repeated measurements. It is useful for Rolling-along protocol.

Note! This action deletes all repeated measurements from the last opened protocol file!

All mentioned above will be available for data files but the "*double*" button. Additionally, apparent pseudosection behind the crosses will be plotted.

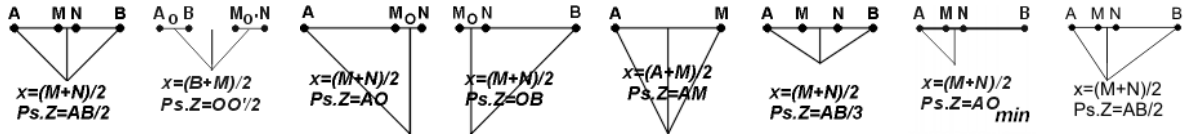


It is possible to remove pseudosection from Display Window by "Map ON/OFF" button on the icon bar of the main window. Also you can remove data points from Display Window (see ***Ошибка! Источник ссылки не найден.****Icon Bar*.***Ошибка! Источник ссылки не найден.***).

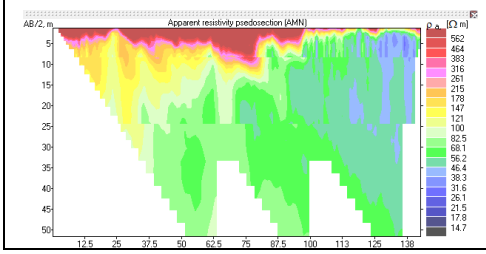


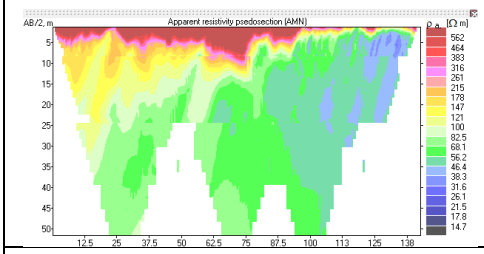
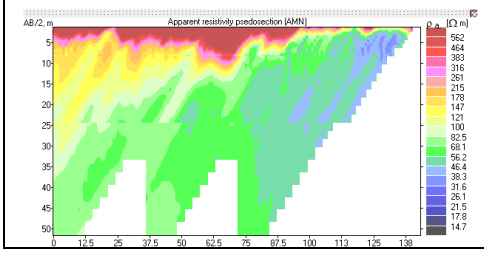
Note! The color scale in Display window is always selected automatically. You can increase the range by <Menu – Contours – Increase or Decrease> (see Contour menu).

X- and Ps.Z-coordinates of every measurement depend on the array type. Different array types and reference points are shown below.

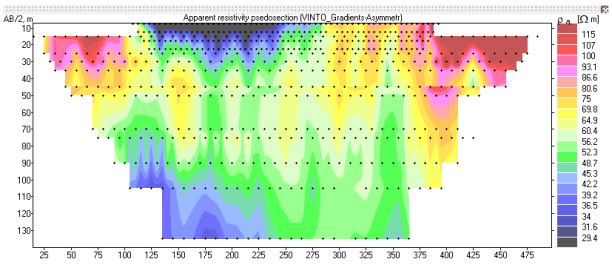
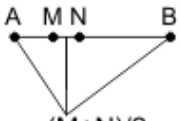
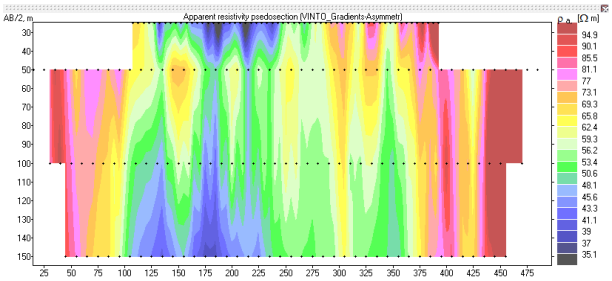
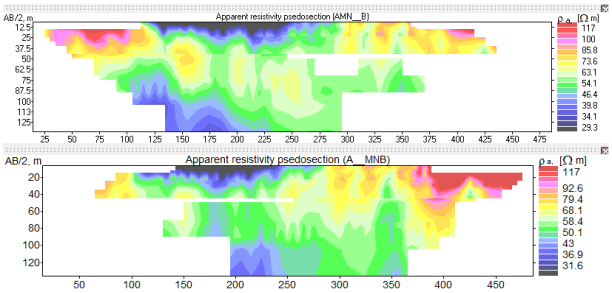


X-coordinate of reference point of pole-dipole array can be set to the center of MN, center of the electrode array, position of the current electrode (<*Menu – Options – Pole-dipole*>) (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***). All these ways for one pole-dipole data set are shown below.

	Center of MN dipole

	Center of array
	Current electrode

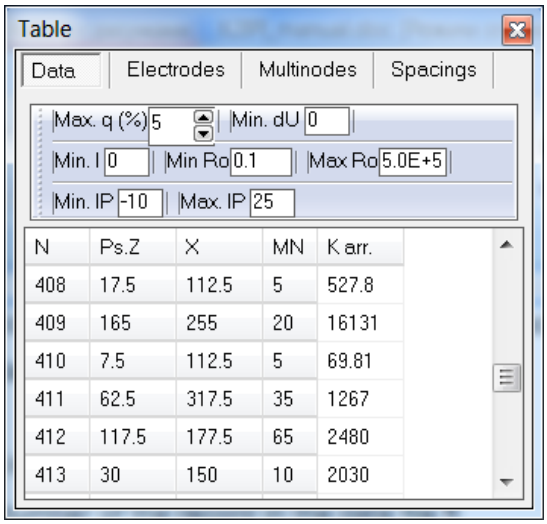
You can change the X-coordinates of reference point for asymmetrical array (<*Options – Asymmetrical as …*>) (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).

<*Asymmetrical as … – Gradient array*> classic presentation of Multiply gradient array data ***x=(M+N)/2*** ***Ps.Z=AO$_{min}$***	
<*Asymmetrical as – Gradient 2*> presentation of gradient array data with pseudo depth depending on AB length  x=(M+N)/2 Ps.Z=AB/2	
<*Asymmetrical as … – Force PD*> presentation of 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 of dipole-dipole data with different lengths AB and MN dipoles	

2.5. Tables window

Tables window has different pages : Data, Electrodes, Spacing, etc.

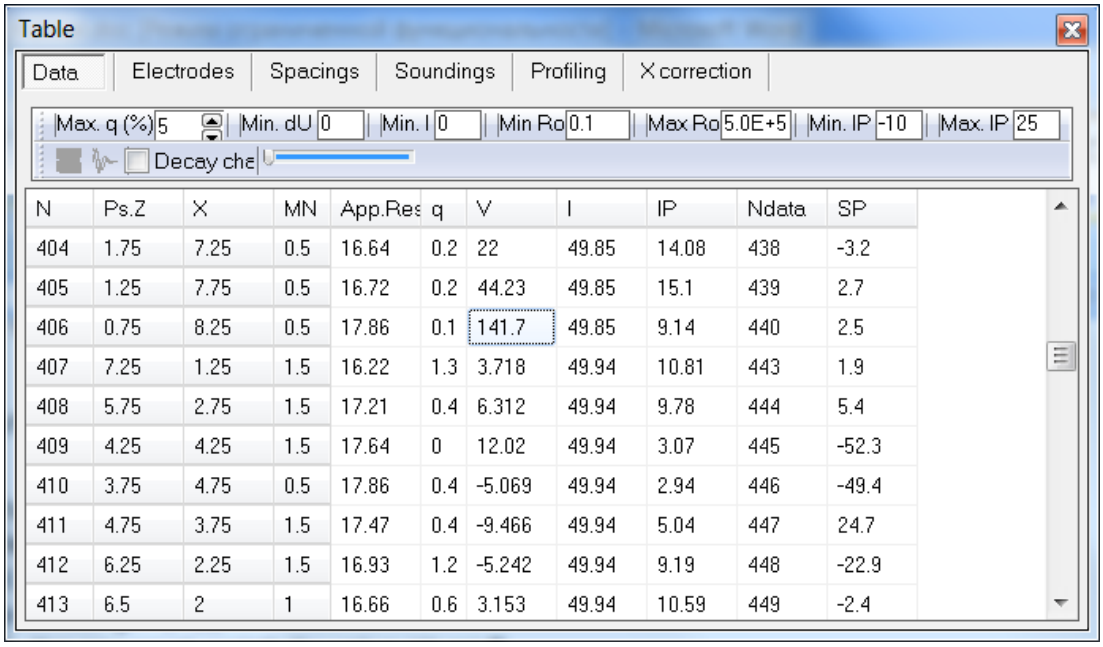
2.5.1. Data table



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

Data page is formed from contents of the file if protocol (sequence) opened ([.seq], [.txt]):

- *N* Measurement number of the specific record in the protocol
- *Ps.Z* Ps.Z-coordinate (Pseudo depth) of the data point (in m)
- *X* X-coordinate of the data point (in m),
- *MN* MN length (in m)
- *K arr.* Geometrical factor of the electrode array (in 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

Data page is formed from contents of the file if data file opened ([.txt]):

- *N* Number of the data point. Usually it equals to measurement number in the protocol
- *Ps.Z* Ps.Z-coordinate (Pseudo depth) of the apparent resistivity data point (in m)
- *X* X-coordinate of the apparent resistivity data point (in m)
- *MN* MN length (in m)
- *App.Res* Apparent resistivity value (in Ohm·m)
- *q* "Quality" factor given by *SYSCAL* instruments (in %). It is a dispersion of stacked

measurements: the closer it to 0, the most stable are the measurements

- *V* Mean potential difference measured between M and N electrodes (in mV)
  Note! Not available for [.dat] files (RES2DINV) ([.dat] files contain only resistivities)
- *I* Mean intensity of current injected between A and B electrodes (in mA)
  Note! Not available for [.dat] files (RES2DINV) ([.dat] files contain only resistivities)
- *IP* induced chargeability (units are determined by the instrument)
- *SP* self-potential data if exists (units are determined the instrument). Can be plotted by SP button (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***)

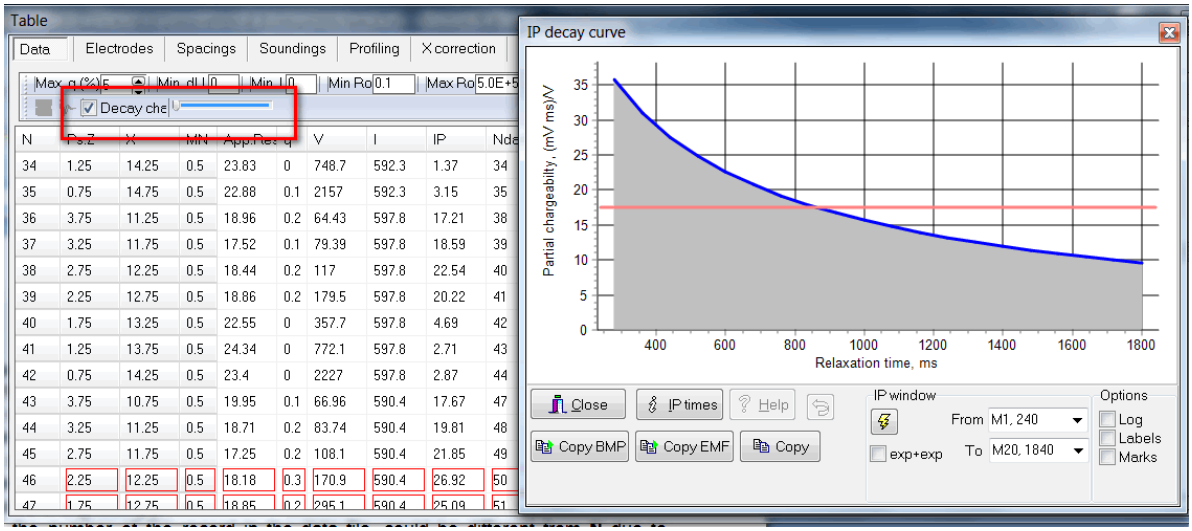
In case of [.txt] *SYSCAL* data files, the upper bar of Data page allows you to delete measurements of poor quality following by one of the next criteria:

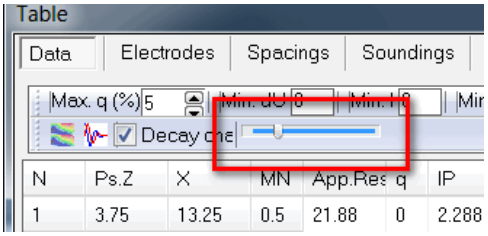
- *Max. q* Quality factor (in %)
- *Min. dU* Minimum measured potential difference (in mV)
- *Min. I* Minimum injected current (in mA)
- *Min Ro* Minimum apparent resistivity (in Ohm·m)
- *Max Ro* Maximum apparent resistivity (in Ohm·m)
- *Min IP* Minimum induced polarization (units are determined by the instrument)
- *Max IP* Maximum induced polarization (units are determined by the instrument)

Note! Data points with values higher or lower than selected threshold will be discarded.

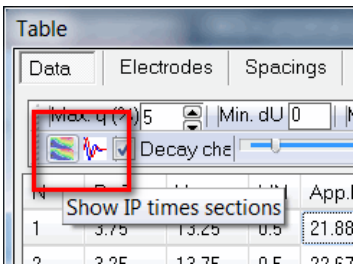
You can remove data point by selecting corresponding line of the table and *"Delete"* key or *"Delete"* button. Repeating this action will undo deleting.

Decay chart checkbox will be available if data set have IP decay data. Clicking on the box will activate IP decay curve window for selected data point.



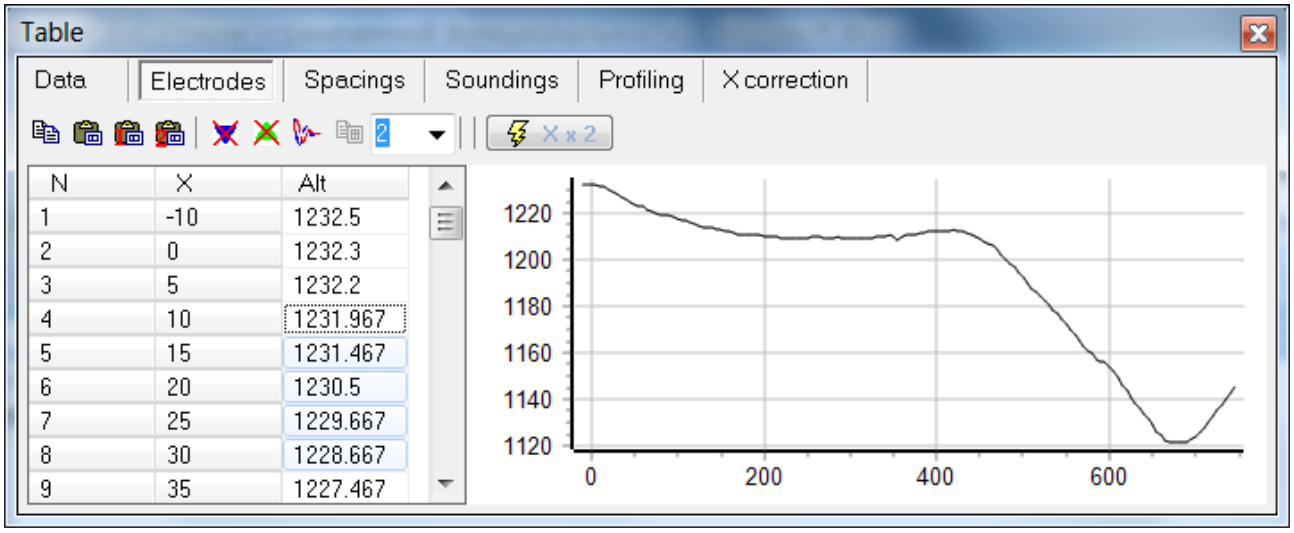


Decay track bar will be available if data set contents IP decay data also. It allows to plot pseudosection of partial chargeability in Display Window.



"Show IP times sections" button will show pseudosection of partial chargeability for all decay time windows. *"Filtering IP time data"* button allows to filter partial chargeability data for each time window separately.

2.5.2. Electrodes page



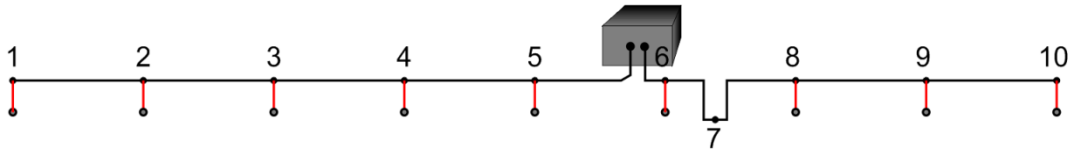
Electrodes page indicates:

- *N* Reference number of the electrode. 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 multinode 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* X-coordinate of the electrode (in m)
- *Alt* Elevation of the electrode (in m)

Tool bar of Electrodes page allows:

- copy all electrode positions (*X* and *Alt*) to the clipboard
- paste electrode positions (*X* and *Alt*) from the clipboard.
  Note! Be sure to past same number of electrodes
- paste topography data (*X* and *Alt*) from the clipboard and calculate electrode elevations by linear or square interpolation
- delete all data points associated with selected (faulty) electrode
- delete all data points associated with selected potential electrode
- remove selected electrode and shift all following ones. This is of great use to modify quickly a [.seq] file when one electrode line in a multiconductor cable is broken without possibility of repairing it easily in the field. It works only for

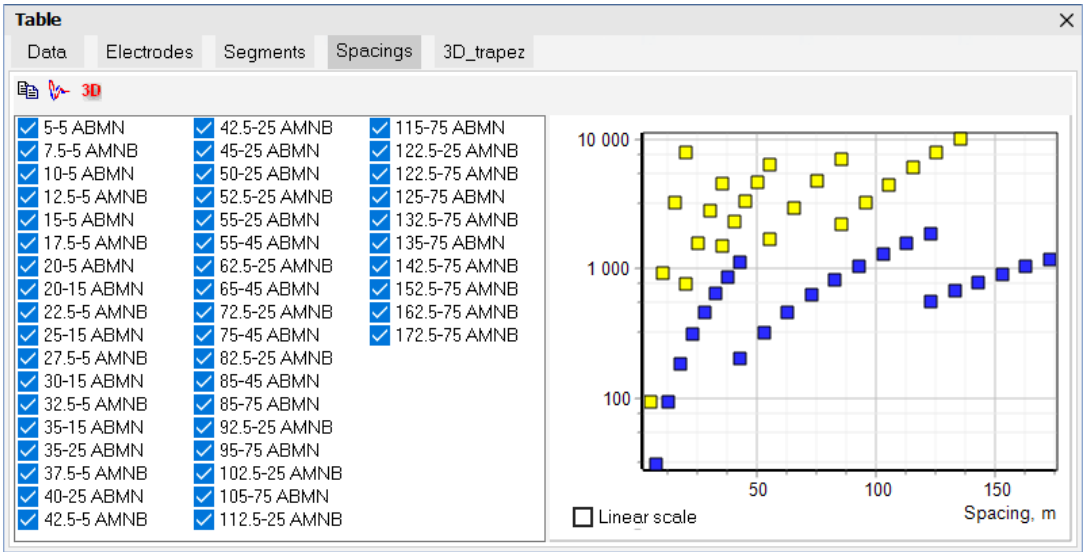
protocol files. See an example with the 7th electrode marked as broken



-

multiply by a coefficient the unit electrode spacing. **Apparent resistivity will be recalculated also**.
-
copy the vertical electrical sounding data closest to selected electrode position to the clipboard. The copied data will have a header corresponding to the VES location along the profile and then three columns with AO length (in m), MN length (in m) and Apparent resistivity (in Ohm·m)

2.5.3. Spacing page



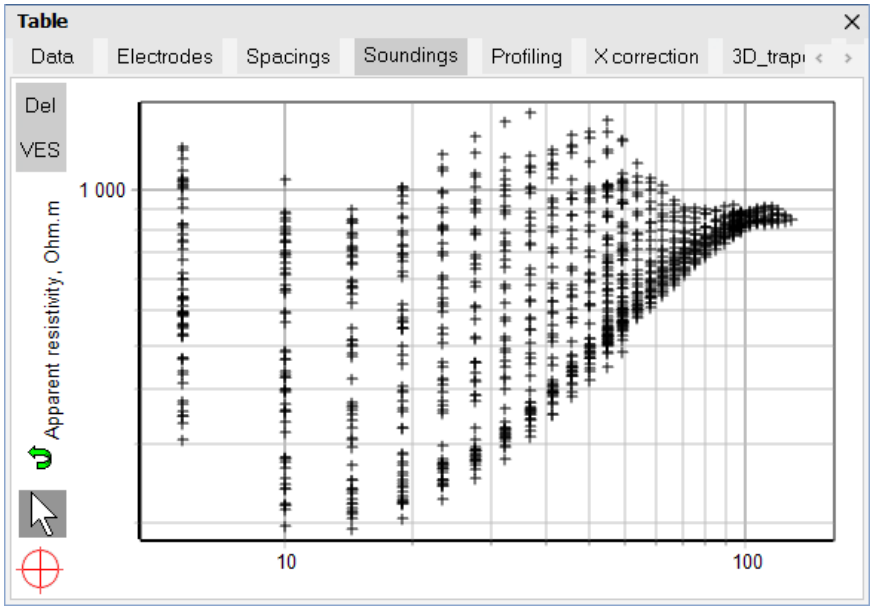
Spacing page shows all spacings and lengths of potential lines available in data set. You can remove data points corresponding to specific spacing by clicking on checkboxes. The icon bar of the page allows you to:

-
copy data for selected spacing to the clipboard
-
copy mean VES curve for the data set to the clipboard
-

Create a [.pln] data file for 3D visualization software (e.g., *GOLDEN SOFTWARE 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 X- and Y-coordinates of data point, minus pseudo depth and logarithm of apparent resistivity.

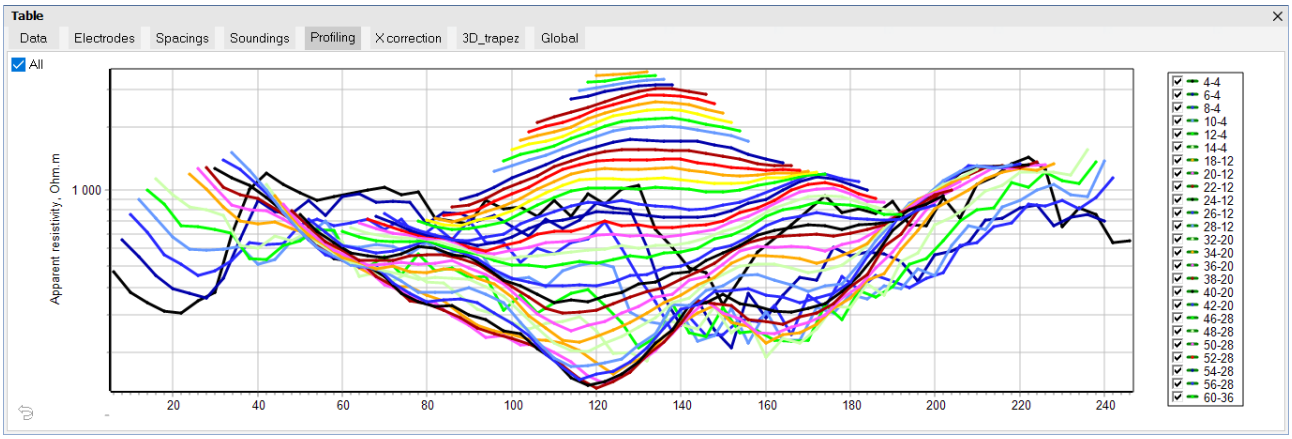
There is a chart which shows geometric factor for each spacing.

2.5.4. Soundings page



All data points are shown in bilogarithmic scale here (vertical axis – apparent resistivity, horizontal axis – spacing). Each data point can be selected by clicking on it (red square). Then, all data points with the same X-coordinate will be marked as well (blue squares). You can delete bad data point by double clicking (white arraow). Also you can delete some points by read cross.

2.5.5. Profiling page



All data point is shown like profiling line plots (vertical axis – apparent resistivity, horizontal axis – X-coordinate, color – spacing). You can delete data points corresponding to specific spacing by clicking on checkboxes (identical to Spacing page). Again, bad data points can be removed by double clicking. If IP mode is active, button, (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***), then IP data will be plotted.

2.5.6. INV results page

The page is available when [.inv] file is opened. Here, you can copy/export resistivity model obtained in *RES2DINV*, average resistivity model, resistivity model corresponding to specific depth interval.

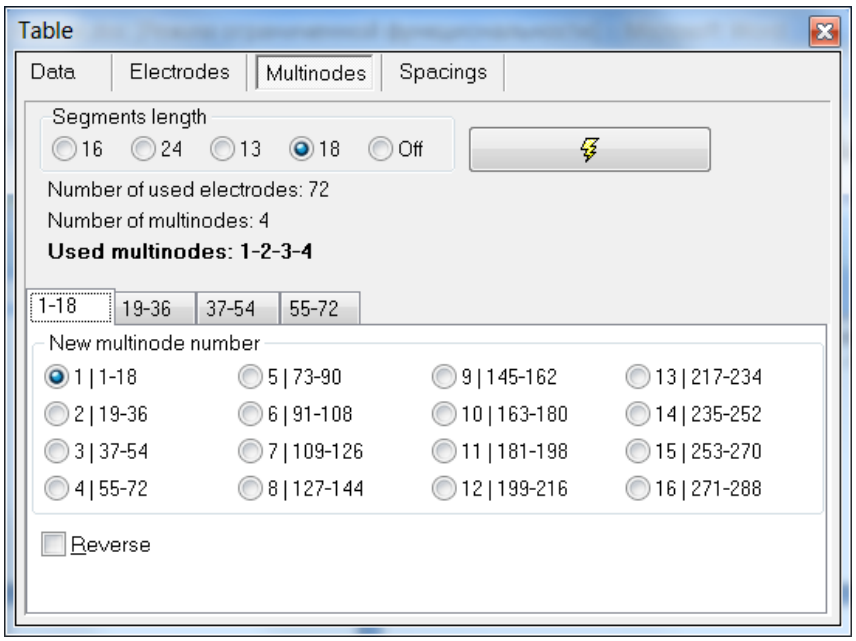
2.5.7. X correction page

X correction page allows you to modify manually position of electrode if its real X-coordinate (by field measurement) differs from its initial value (by protocol). **After the correction procedure all apparent resistivity values will be recalculated.**

Note! Irregular positions of electrodes create a great number of additional spacings.

2.5.8. Multinode page

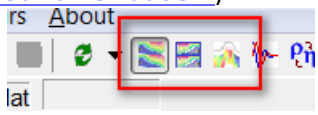
Multinode page is available for protocol ([.seq], [.txt]) files only. It allows to transform file prepared for some electrode reference numbers to another set of electrode reference numbers. For instance, a [.seq] file has been prepared for multinodes 1, 2, 3 and 4 giving electrode reference numbers from 1 to 64. Now it may be transformed to a new [.seq] file using multinodes 5, 6, 7 and 8 giving electrode reference numbers from 65 to 128. This is useful if a set of multinodes are split in two parts in order to simultaneously undertake surveys on two different sites.



This page can be useful to indicate cable numbers in Electrodes page.

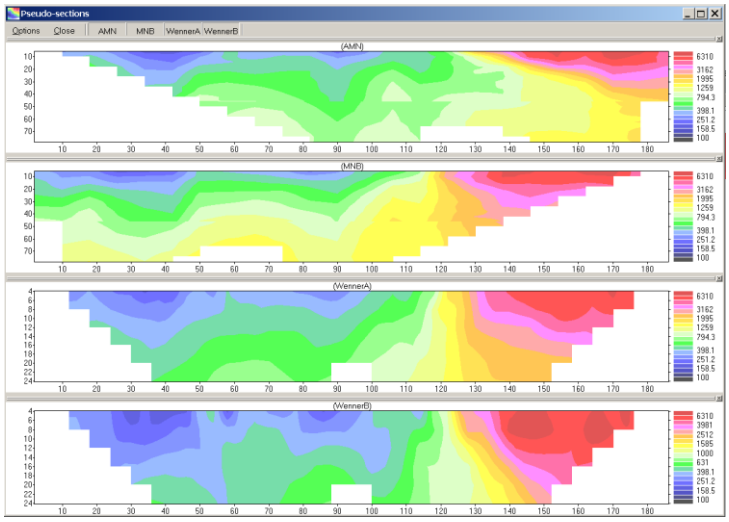
2.6. Advanced Display window

Advanced Display window is used to work with data set including different arrays or with different data files. It allows to plot pseudosections in one color scheme and horizontal scale. Also there are pseudosection options in this window. Advanced Display has three modes (see *Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.*).

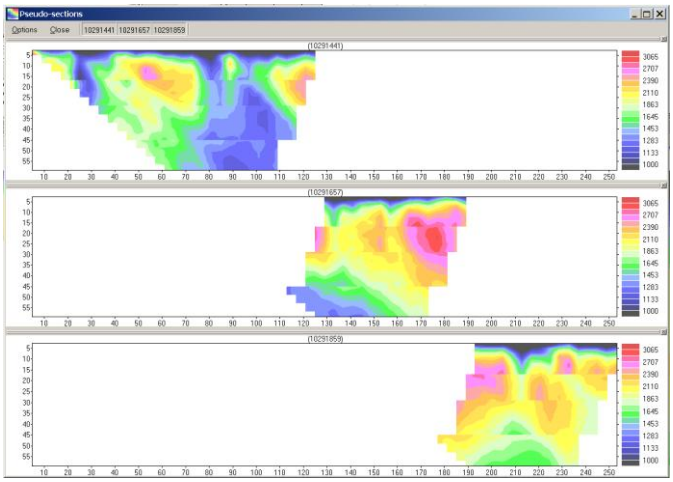


- Advanced Display window is visible under Table window (lower right corner of the screen). There is no menu or special buttons in this window. It only helps to view data and to choose data set to be plotted in Display window
- Advanced Display window is shown separately from the main interface. It has its own menu and options and it is useful for exporting pictures of field data
- Topography Display window is shown separately from the main interface. It has menu and options also. All pseudosections is plotted here with topography

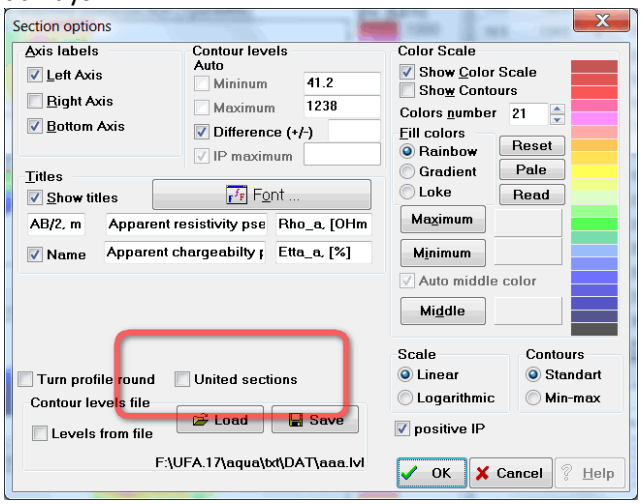
Using Advanced Display window you can plot several pseudosections of different electrode arrays side by side, while Display window allows you to plot only one selected electrode array.



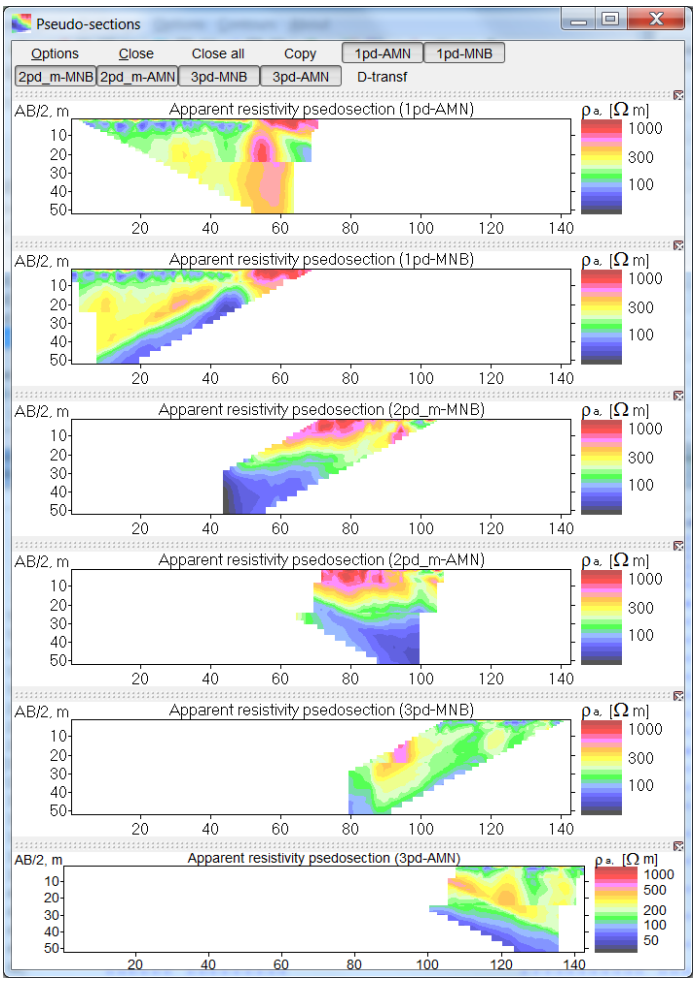
If several opened data files correspond to a roll-along survey (one protocol, but different X-coordinates) Advanced Display window plots pseudosections separately.

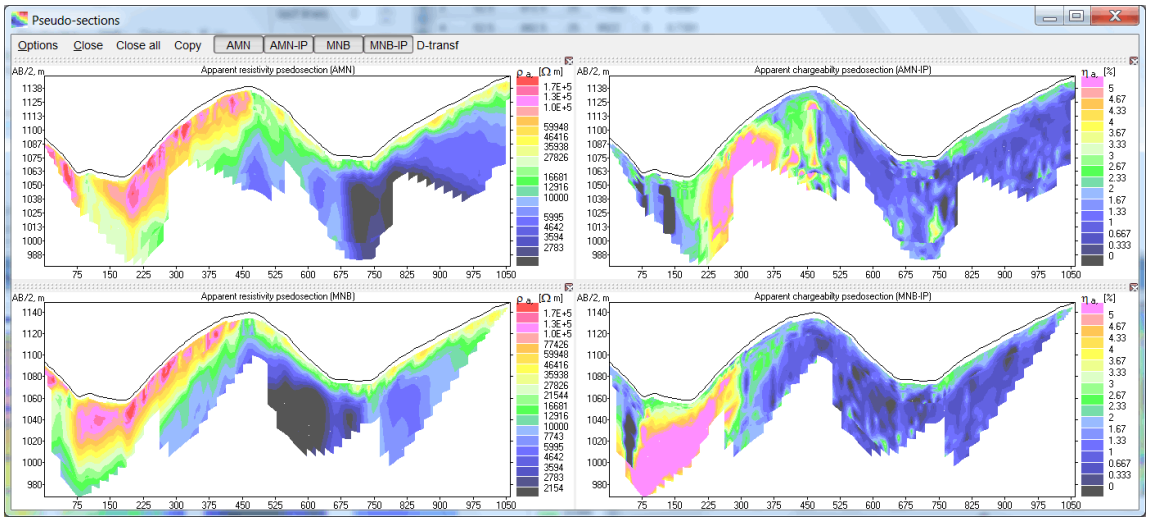


Use *United section* option in *Options* (see Advanced Display window. Options) to plot pseudosections for different files with different arrays.



Next, example of 3 opened files of one roll-along profile is presented below (each data set includes forward and reverse pole-dipole electrode arrays).





Topography Display window plots field data using “effective” depth for each measurements. In the table below you can see effective depths that are used in ***X2IPI*** for typical electrode arrays.

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

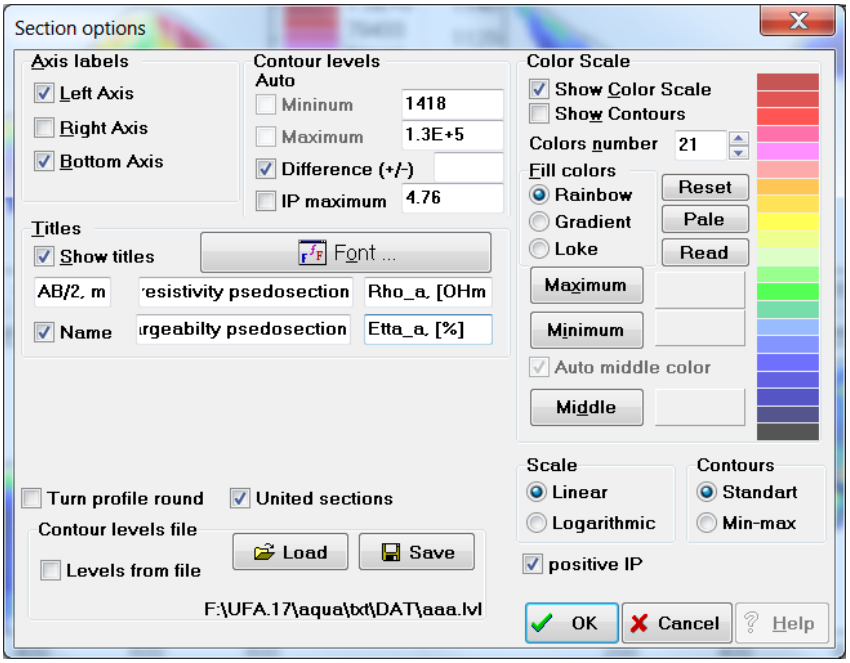
Wenner-alpha	a / **1.93** (AB/3 / 1.93)
Wenner-beta	a / **2.404** (AB / 2.404)
Pole-pole	AM / **1.153**

2.6.1. Advanced Display window. Menu

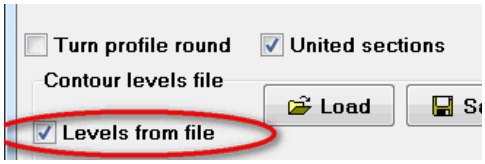
- *Options* — Options of pseudosection plot (axes labels, color scale, titles, etc.)
- *Close* — Close Advanced Display window
- *Close all* — Close all pseudosections
- *Copy* — Copy pseudosections pictures without menu and frame to the clipboard
- *File name / array name* — On/Off switch for specific pseudosection to be drawn
- *D-transform* — Plot the pseudosection of differences between two data sets in percents. It is a simple way to analyze control or time lapse measurements
- *AMNB* — Calculate Schlumberger array from pole-dipole array
- *Mean only* — On/Off switch for including pole-dipole data into calculated Schlumberger array (AMNB)

2.6.2. Advanced Display window. Options

Here you can change default settings for pseudosection plots in Advanced Display window (axes labels, titles, color scale, etc.). Changing one you may need to close and reopen Advanced Display window to changes take effect.

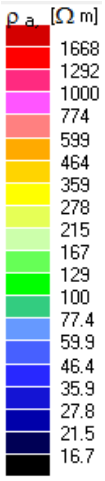


X2IPI automatically select color scale range depending on data by default. But you can choose your own color range. Just type new *Minimum* and *Maximum* values of new color scale or use [.lvl] file. The [.lvl] file has three lines (empty line, minimum, maximum). Uncheck *Levels from file* box to return default values (here, you will need to reopen Advanced Display window).

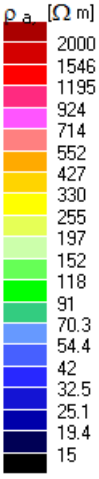


- *Difference (+/-)* — set the range for *D-transform* pseudosection (in %)
- *positive IP* — if checkbox is checked then minimal IP level is zero.
- *Contours — Standard / Min-max* — If <*Contours – Standard*> is selected, then color scale will be based on values of 10^0, 10^1, 10^2, 10^3 etc. If <*Contours – Min-max*> is selected, then contours values will be exactly between *Minimum* and *Maximum* values. Below you can see an examples of color scaling for the range from 15 up to 2000 Ohm·m

Contours — Standard



Contours — Min-max



There are three reserved strings to indicate special symbols:

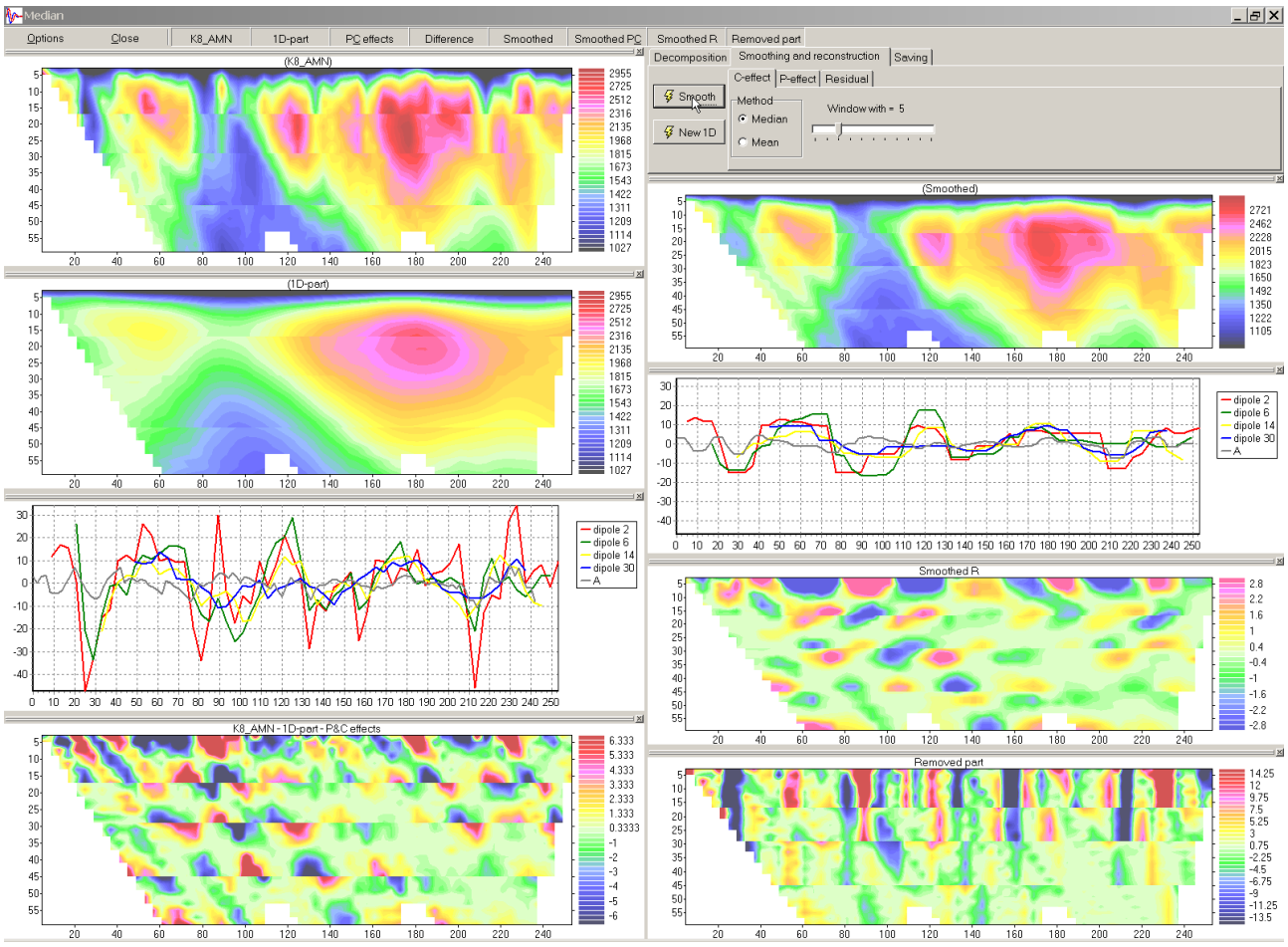
"Rho" = "ρ"
"Etta" — "η"
"OHm" — "Ω"

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

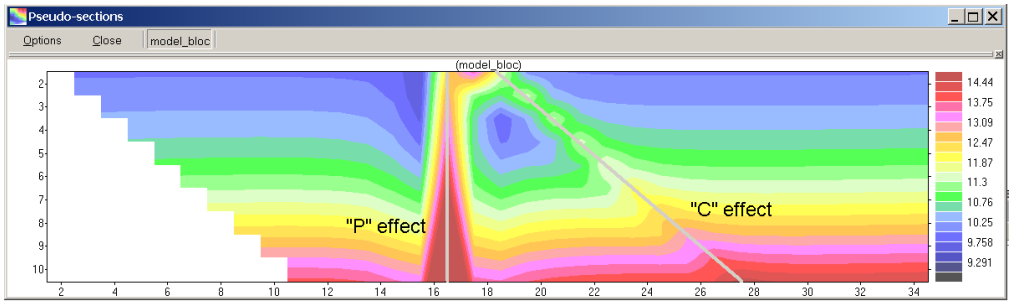
2.7.Filtering field data window (Median window)

Apparent resistivity and induced polarization data can be filtered, smoothed in *Filtering Field Data* window (hereafter, "*Median window*") (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***). Median window allows you to filter out "P" and "C" effects in data caused by inhomogeneities in the upper part of geoelectrical media.

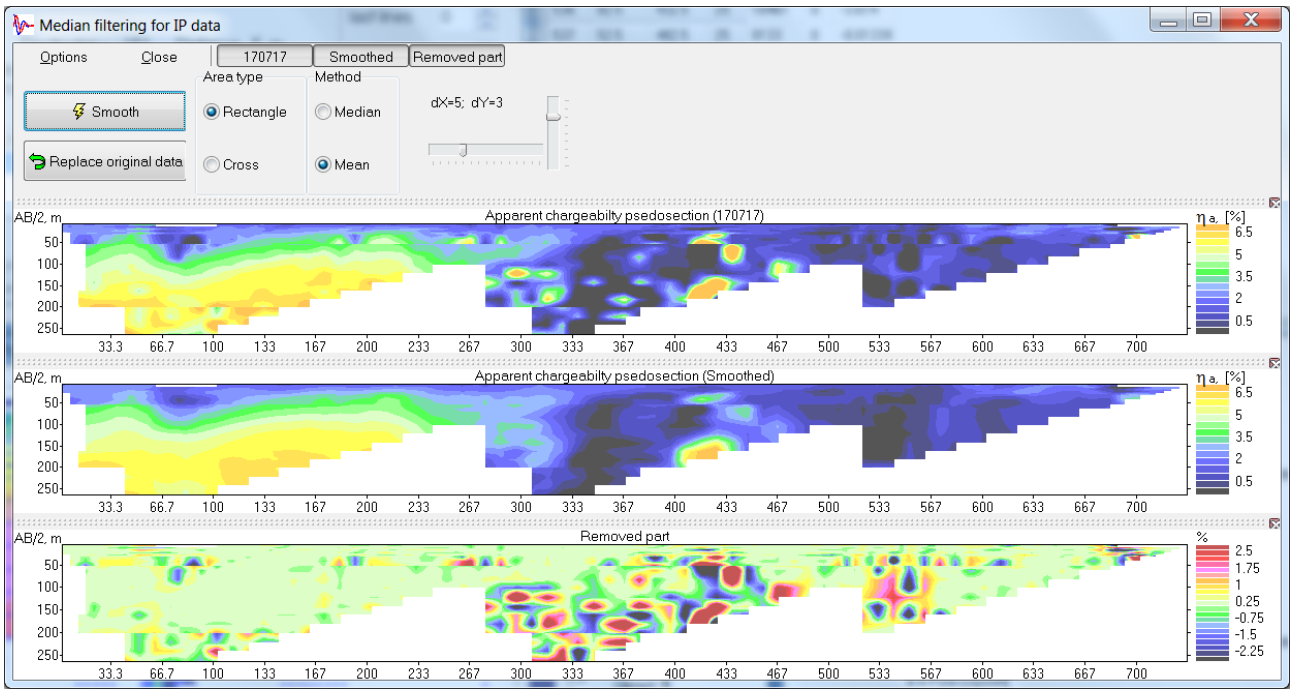
Note! Median window is available for [.dat] and [.inv] files only.



A synthetic examples of these effects is given below. It has been calculated with ***Res2dmod*** forward modeling software (Geotomo software, M.H. Loke). The model has two layers with ρ_1=10 Ωm, h_1=8 m and ρ_2=500 Ωm. A small block with ρ_b= 100 Ωm L_b=2 m and h_b=0.5 m is placed at the center of the profile at 0.5m depth. With an AMN array (1m unit electrode spacing), two strong anomalies caused by the block: a vertical anomaly ("P" effect), related to MN dipole if dipole is close to the block, and an inclined anomaly ("C" effect), related to A pole if pole is close to the block.



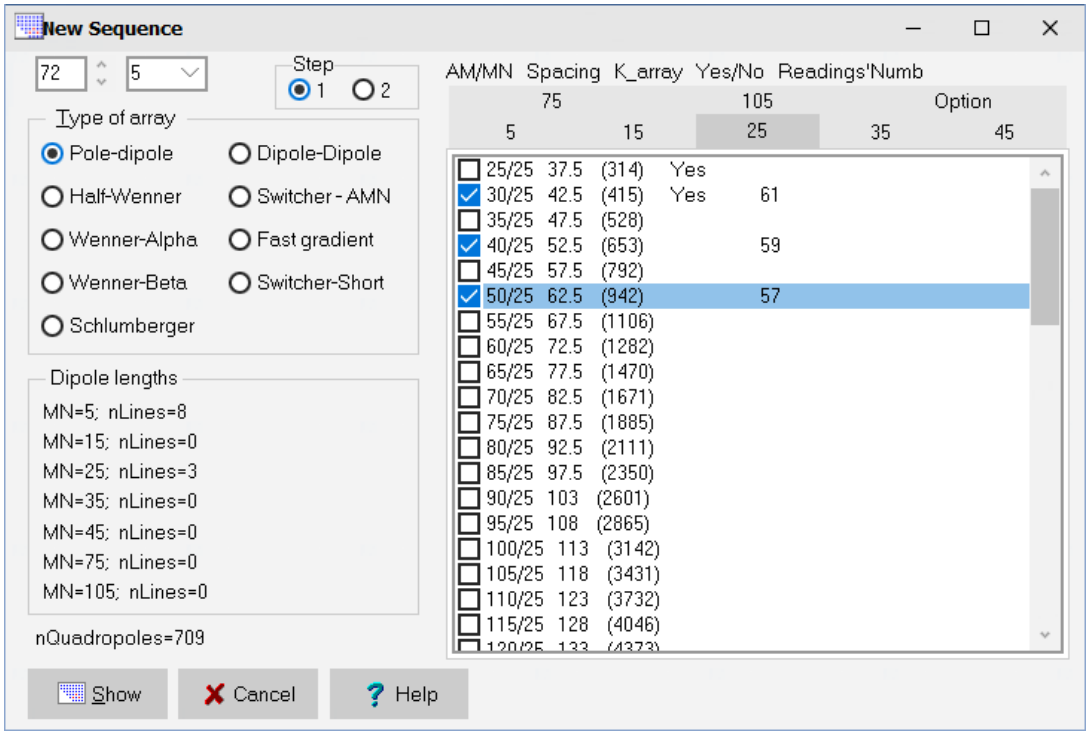
It is clear that a bunch of these effects coupled to subsurface inhomogeneties may hide smoother effects related to large and deep targets. The median processing allows you to reduce this "noise" and, further, to recover clearer 2D apparent resistivity section. It will be described step by step later (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***). To smooth IP data you need to open IP data in Display window ( ) (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).


Median filtering for IP data
Options
Close
170717
Smoothed
Removed part
Area type
Method
Smooth
Rectangle
Median
dX=5; dY=3
Replace original data
Cross
Mean
AB/2, m
Apparent chargeabilty psedosection (170717)
ηa, [%]
Apparent chargeabilty psedosection (Smoothed)
Removed part
%

3. Work with *X2IPI*

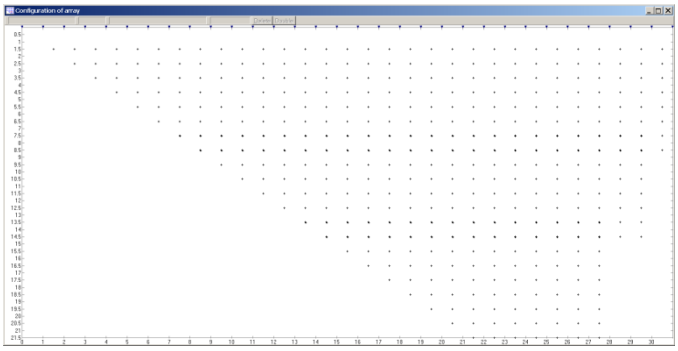
3.1. Creating [.seq] files

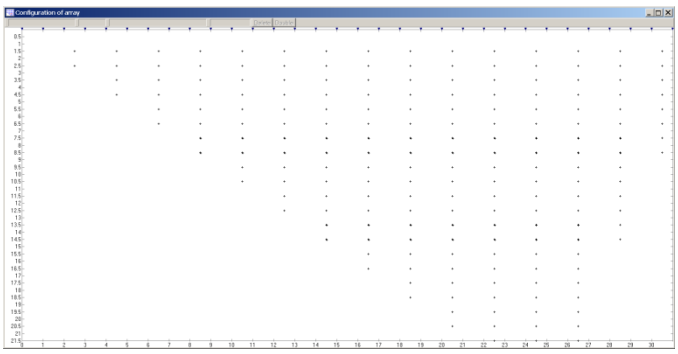
To create a new [.seq] file (electrode configuration file for multielectrode measurements with *SYSCAL* equipment), press icon "*New sequence*" in the main window, or the "*Ctrl + N*" short cut or *<Load – New protocol>*. A dialog window will be opened:



The number of electrodes is selected in ***No el***. Choose the unit electrode spacing there as well.

Step corresponds to the density of data points along the line. *Step* = 1 is for the maximum horizontal density. If *Step* = 2, data points will 2 times sparser along the line. An examples of pole-dipole array with different *Step* values are given below.


AMN with *Step* = 1


AMN with *Step* = 2

You can choose any available electrode array type:

- Pole-Dipole
- Half Wenner
- Wenner-Alpha
- Wenner-Beta
- Schlumberger
- Dipole-Dipole

The table in the right part of the dialog window allow you to specify quadripoles (spacings, potential line lenghts, geometrical factor). You can find several pages in the table with headers indicating the length of MN dipole. For Wenner arrays (half, alpha or beta) there is only one page in the table.

Use the first column of checkboxes in the table to include or exclude particular spacing. The second column indicates the ratio between AM and MN lengths. The third column indicates the spacing. The fourth column indicates the geometric factor for the 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 at the right indicates that selected spacing is checked at different page. It helps to easily understand the overlap between measurements with different MN lengths. This allows to determine easily the overlap between segments of different MN in the pole-dipole VES. Usually one spacing of overlap is sufficient to check data quality.

While checking desired spacings, left part of the dialog box indicates the total number of measurements and the number of spacings ("*nLines*") for each MN length.

Then, all data points can be displayed (or refreshed) in Display window by clicking on the "*Show*" button.

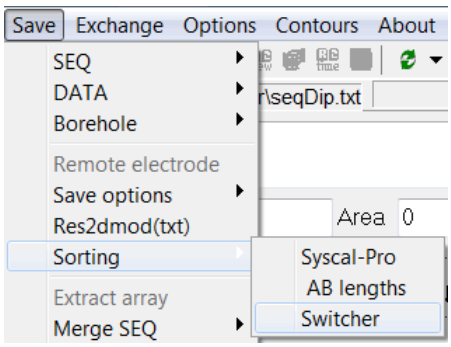
Press "*Ok*" button to return to Main window and save protocol file to desired format (<*Save – Seq*>):

- *Electre* [.seq] save binary protocol file for old *ELECTRE* program (IRIS Instruments)
- *Electre II* [.txt] save text protocol file for *ELECTRE II* and *ELECTRE PRO* programs (IRIS Instruments)
- *Lund protocol (ABEM)* [.org] save Lund protocol (ABEM) file. *TERRAMETER LS TOOLBOX* software (supplied with the equipment) can convert [.org] file into modern [.xml] format.

Note! We recommend to keep all protocols file in [.txt] format of ELECTRE II software .

3.2.Sequence optimization for multi-channel instruments

Today, most of modern ERT systems are multi-channel. We have to optimize protocols to take advantage of this feature. First, quadripoles should be sorted by current dipole. Use <*Sorting*> menu to change the order of measurements (see ***Ошибка! Неверная ссылка закладки..Ошибка! Неверная ссылка закладки.***).



There are three ways of sorting:

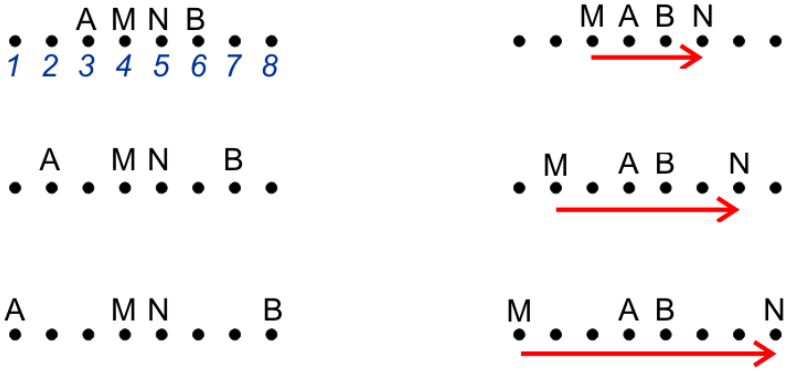
Syscal-Pro mode is for sorting by current dipole or electrode. It's better to sort reverse pole-dipole array (MNB) in reverse order. It results in improving of data quality because electrode charge-up effects will be much lower that way (*Dahlin T., 2000. Short note on electrode charge-up effects in DC resistivity data acquisition using multi-electrode arrays. Geophysical prospecting, 48*).

AB lengths mode starts with sorting by length of current dipole first and only then by current dipole. We recommended this mode for Dipole-Dipole and reciprocal Schlumberger arrays.

Switcher mode is for sorting measurements by current dipole or electrode.

3.3. Optimization for Schlumberger array

The Schlumberger array is a classic array and it is used very often. In order to measure in multi-channel mode you should use reciprocal Schlumberger array.



Use menu <*Reciprocal SEQ*> (see *Ошибка! Неверная ссылка закладки..Ошибка! Неверная ссылка закладки.*) to convert array in reciprocal one. Reload file with reciprocal array before sorting (see *Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.*).

3.4. Modifying [.seq] file

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

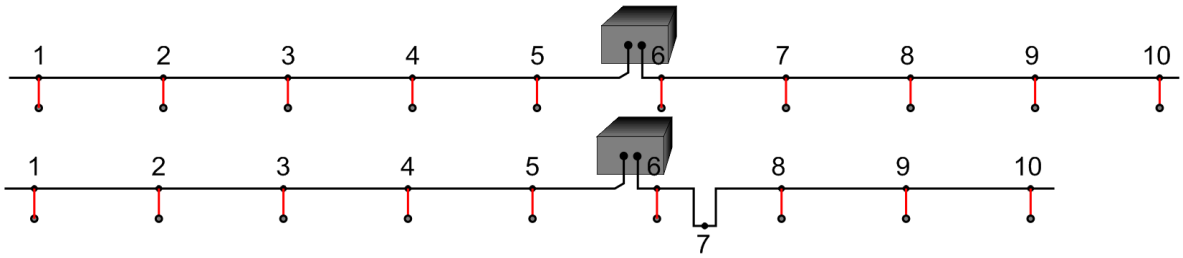
3.4.1. Modifying electrodes unit spacing

The unit electrode spacing can be 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 or tapping the exact number in the coefficient field. Multiplication is performed by clicking the button at left.

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

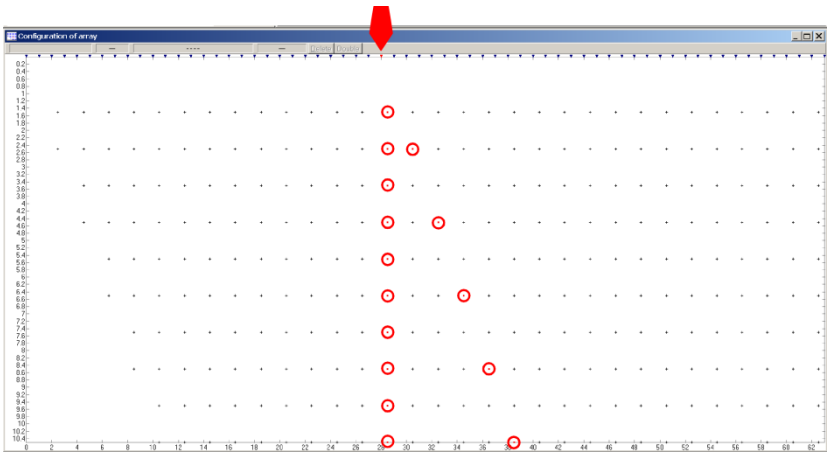
3.4.2. Removing a faulty electrode

Any electrode used in a [.seq] file can be removed and the electrodes coming after it will be shifted. So there will not be any space in place where the deleted electrode was. This is of great use to modify quickly a [.seq] when one node in a multinode or one line of a multiconductor cable is broken without possibility of repairing it easily in the field.



To select electrode in electrode table click on the corresponding line. Another way to do that is to click on top triangle in the Display window. Push <*Broken electrode*> button at the icon bar (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***) to remove selected electrode. Suppose [.seq] file has *N* electrodes and you remove electrode *d.* Then modified [.seq] file will have *N-1* electrodes with numbers from (*1* to *d-1* and from *d+1* to *N*). See the example os setup when 7th electrode is broken.

Note! Pseudosection will not have empty space related to the removed electrode (see 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, bad electrode can be removed by clicking on the <*delete selected electrode*> button. Consequently, all measurements corresponding to the faulty electrode will be removed from the [.seq] file. In this case you can see an empty space in Display window in place where the electrode was. The removed electrode and all related measurements will be highlighted in Data table and in Display window.

Once faulty electrode has been removed or skipped, the modified [.seq] file can be saved using <*save*> button at the main window.

*Note! There is no explicit <undo> button in **X2IPI**. But since the modified [.seq] file is not saved, re-opening of the same [.seq] file will restore the accidentally removed electrode. Furthermore, saving a modified [.seq] file with removed electrode automatically creates a backup file [.~eq] with previous sequence version in the active directory. You can recover the previous version by changing the extension.*

3.4.3. Shifting electrodes

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

Once electrodes have been shifted, the modified [.seq] file can be saved using <*save*> button at the main window.

Note! It is highly recommended to use save button with one opened file only.

3.4.4. Removing measurement lines

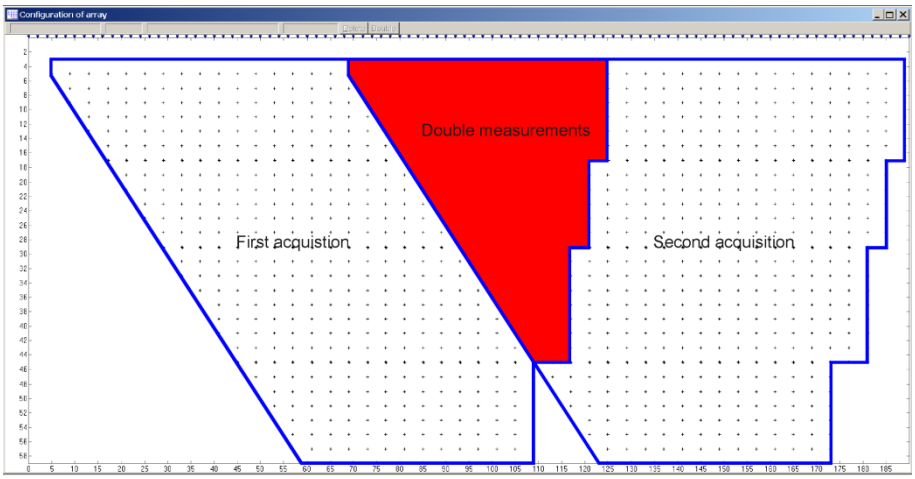
Measurements lines (spacings) can be removed from the top or bottom of the pseudosection using the <*Delete first lines*> or <*Delete last lines*> dialog box placed at the right side of the main window. The deleted lines will be highlighted in the Data table and in the Display window. It is better to use Spacing page.

Once measurement lines have been deleted, the modified [.seq] file can be saved using the <*save*> button in the main window.

Note! It is highly recommended to use save button with one opened file only.

3.4.5. Preparing a "roll-along" [.seq] file.

Roll-along technique consists in acquiring progressively a long pseudo section by moving the electrode along the profile. Generally, a multielectrode array is being shifted by half of its length. So merged data obtained from 2 roll-along cable spreads gives us [1, 2N] electrodes for cable spread 1 and [N+1, 3N] for cable spread 2. Total profile includes 3N electrodes.



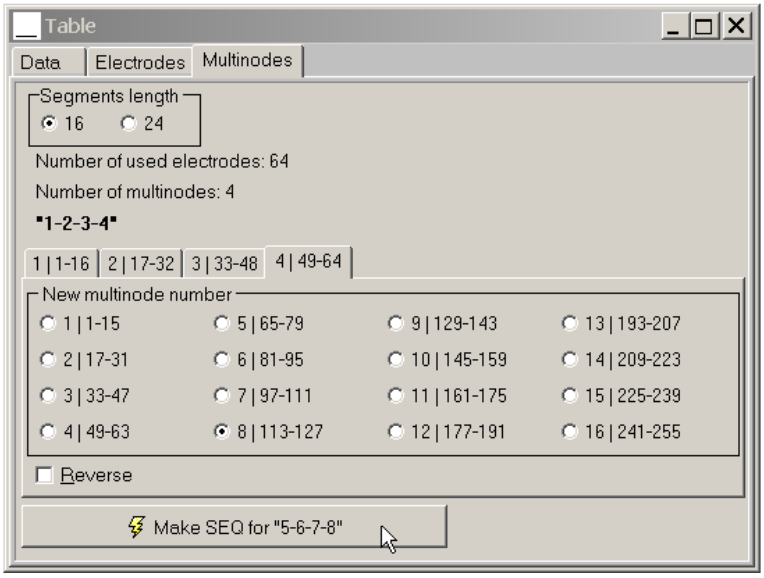
"Roll along" survey

Sometimes it is very time consuming to measure twice resistivities corresponding to the overlapping part of two pseudosections. Hence, a second [.seq] file corresponding to roll-along acquisition which does not include the measurements already made at the preceding station position, can 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] (active file will be [name2.seq])
- Open [name1.seq] and append it to [name2.seq]
- In the main window, select [name2.seq] (measurements will be highlighted green if they are not in [name1.seq] and blue if they are doubles)
- In the display window, click on the "*Double*" button (double measurements will be highlighted red now and in the display window and in the date table)
- Save the [name2.seq] file

3.4.6. Changing multinodes

The "*Multinodes*" table helps you to change numbers of the multinode used in a [seq] file, i.e. hard reference numbers of electrodes.



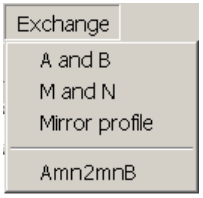
First, you need to choose the number of electrodes per segment (16 or 24, both available with *SYSCAL* equipment). The number of electrodes and multinode used in the [.seq] file is given then.

The bottom box allows you to select which multinode will be used for the first 16 electrodes (first tab), which will be used for the 16 next (second tab), etc. When all tabs are correct, click on the "*Make SEQ for …*" button.

Note! Modified [.seq] file has to be saved using the "save" button at the main window.

The "*reverse*" button allows you to reverse the order of electrode hard reference numbers for each multinode, e.g. for mutinode 1 (hard reference numbers from 1 to 16), it may be useful to have hard reference numbers from 16 to 1. For example, if the multinode is placed next to the electrode 16 and not next to the electrode 1.

3.4.7. Transforming AMN to MNB



To transform AMN [.seq] file (forward pole-dipole) to MNB [.seq] file (reversed pole-dipole) use "*Amn2mnB"* procedure (*<Main window – Exchange – Amn2mnB>).* The procedure is the following:

- Click on the *"Amn2mnB"*
- Select a [.seq] or [.txt] file with AMN array in the "*open...*" dialog box
- Specify name of [.seq] file with MNB array in the *"save as..."* dialog box
- After that, the newly created [.seq] file with MNB array becomes active in the main window

You can also use "*AMN → MNB*" procedure (*<Main window – Exchange – AMN→mnB>*). It is an old version of *Amn2mnB* and in most cases works as good as *Amn2mnB*.

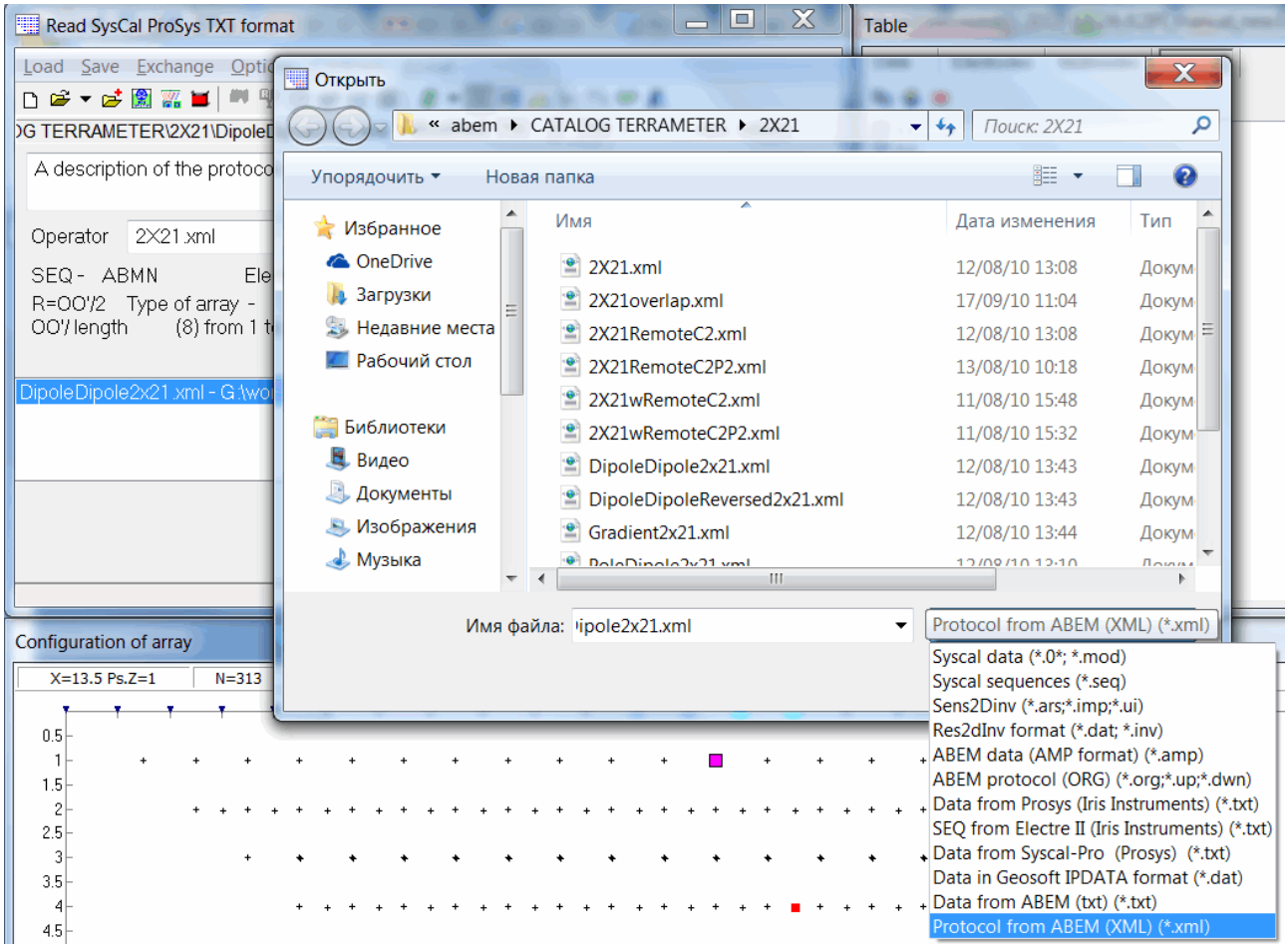
3.5. Working with data files

3.5.1. Opening data files

3 types of data files are supported by ***X2IPI*** as input files (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***):

- *SYSCAL* measurements files: [.0xx], with xx comprises between 00 and 59
- Field data (output file from the ERT instrument) pre-converted to [.txt]
- *RES2DINV* input data files: [.dat]
- *RES2DINV* output data files: [.inv] with calculated resistivities and 2D resistivity model as well.

Note! Resistivity model cannot be displayed but you can save it in [.res] file for IPI2WIN



Please, specify correct data type (*RES2DINV*, *Data from Prosys*, etc.) when choosing file to open.

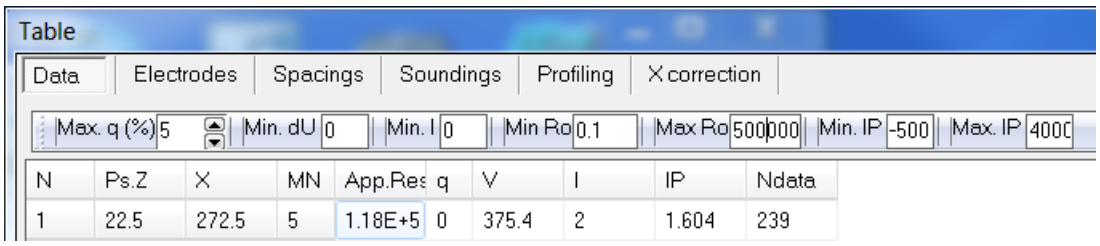
To append a file to already opened one, click on the "*append*" icon (or <*Load – Append*>, or "*Ctrl + A*") and select file you want to append. Data files of different types can be opened simultaneously. You can choose then what data to plot by selecting it in the list of main window.

3.5.2. Shifting data file

The electrode positions can be shifted by a constant using the dialog box at the right of the main window. This is particularly important for roll-along surveys when one [.seq] file used for different station positions.

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

3.5.3. Trimming bad measurements



Any measurement (low quality) can be removed from the data set in the Data table following by next criteria (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***):

- *Max. q* Quality factor (in %)
- *Min. dU* Minimum measured potential difference (in mV)
- *Min. I* Minimum injected current (in mA)
- *Min Ro* Minimum apparent resistivity (in Ohm·m)
- *Max Ro* Maximum apparent resistivity (in Ohm·m)
- *Min IP* Minimum induced polarization (units are determined by the instrument)
- *Max IP* Maximum induced polarization (units are determined by the instrument)

Note! Data points with values higher or lower than selected threshold will be discarded

You can remove data point by selecting corresponding line of the table and "*Delete"* key or *"Delete"* button. Repeating this action will undo deleting.

When criteria fixed, all outliers will be automatically highlighted red and removed from the data set. The total number of removed points will be shown in the main window.

If bad measurements are caused by broken electrode, all the measurements made with this electrode can be deleted. Select faulty electrode in the electrode table or in the display window and press this "*delete*" button.

Use this button in the electrode table to delete all data points associated with selected potential electrode.

3.5.4. Merging data files

All opened data files can be merged into one single file. There are two possibilities:

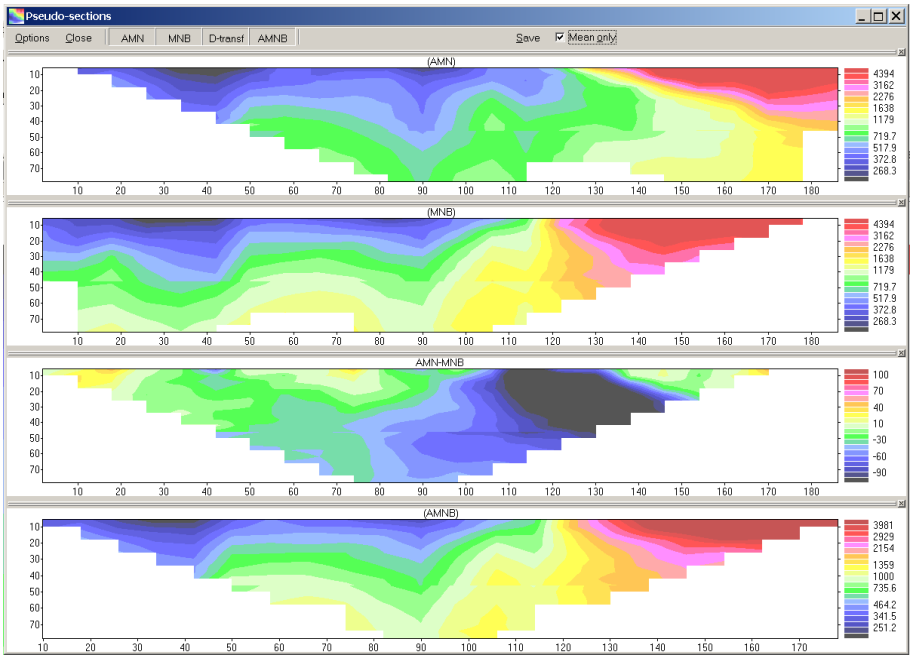
- For a roll-along measurements with one array, complete data set can be exported to any of the formats provided by ***X2IPI*** (*RES2DINV* or *SENSINV2D*). Doubling measurements to overlapping parts in a roll-along survey will be automatically replaced by their mean.
- If measurements was obtained by different electrode arrays, complete data set can be exported to "*general array*" format of *RES2DINV*.

3.5.5. Generating Schlumberger data from AMN and MNB data

For forward and reverse pole-dipole data it is possible to calculate and save Schlumberger data. Open pole-dipole data files and go then to Advanced Display window and click on *"AMNB"* button in right upper corner of the window. If "*mean only*" is checked, only overlapping parts of the AMN and MNB pseudosections will be used. If it is unchecked, parts where AMN and MNB don't coincide will be added to

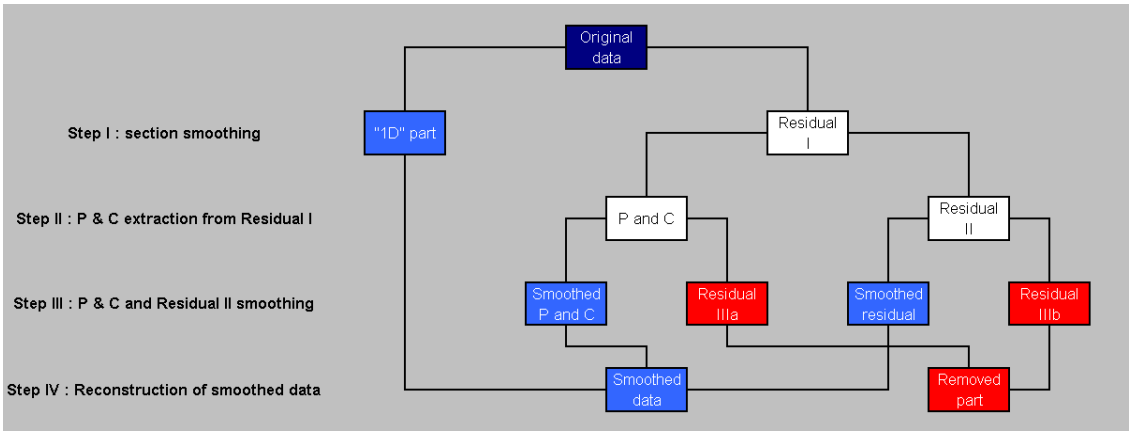
to the Schlumberger pseudosection. Save newly created pseudosection (data) by "*Save*" button in the right upper corner (*RES2DINV* [.dat] format).

Opening pole-dipole data in Advanced Display window allows you see the difference between forward and reversed arrays data ("*D-Transf*"). It indicates "1D" parts of the sections (small values of the D-Transf) and "2D" parts (high values of the D-Transf). Furthermore, values of the D-Transf can give you some information about the depth and the size of the "2D" objects.



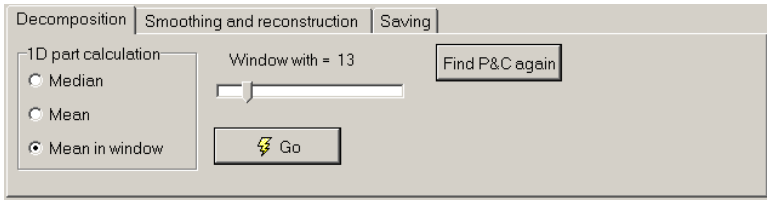
3.6. Filtering field data (Median processing)

"Median" procedure is only available for *RES2DINV* data files [.dat]. The following shows the processing chart of the procedure:

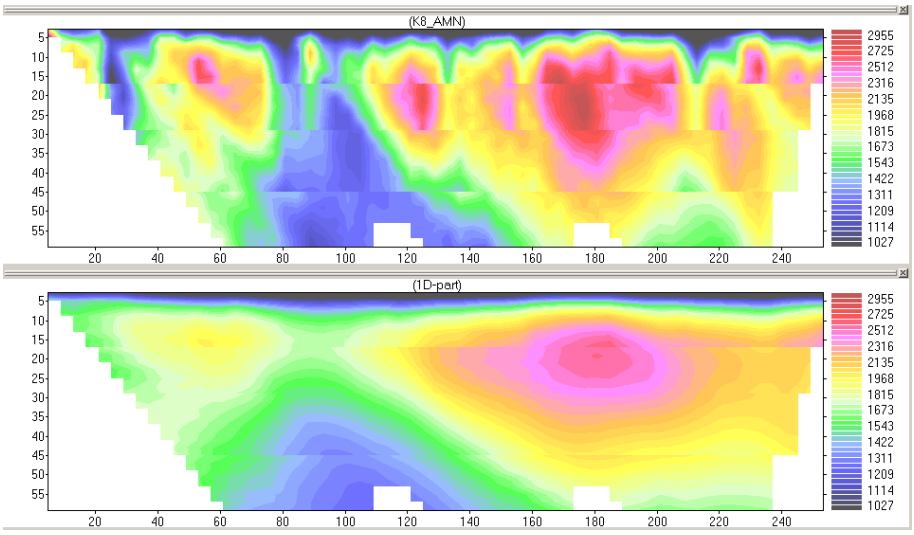


First two steps of the flow correspond to [Original data] decomposition into 3 parts: (1) ["1D" part] (smoothed pseudosection), (2) [P & C effects] and (3) [Residual II]. On third step [P & C effects] and [Residual II] are being smoothed. The last step corresponds to the reconstruction of [Smoothed data] which is composed of (1) ["1D" part], (2) [Smoothed P & C effects] and (3) [Smoothed Residual]. The table in the right upper corner helps you to do all these steps.

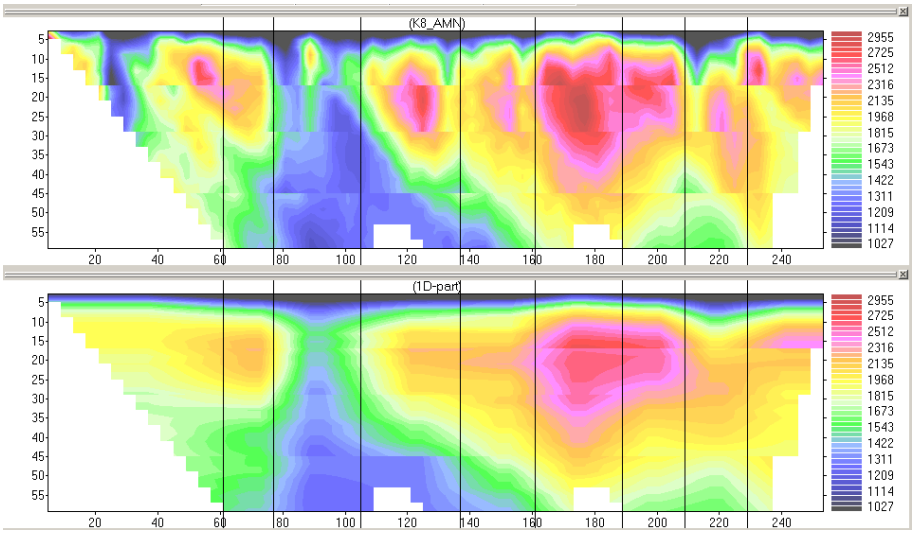
3.6.1. Pseudosection decomposition



First, you need to decompose (Steps I and II) selected pseudosection. Set parameters of the [“1D” part] calculation on the decomposition page. You can calculate it by averaging resistivities in a horizontal window of constant width (“*Mean in window*”).



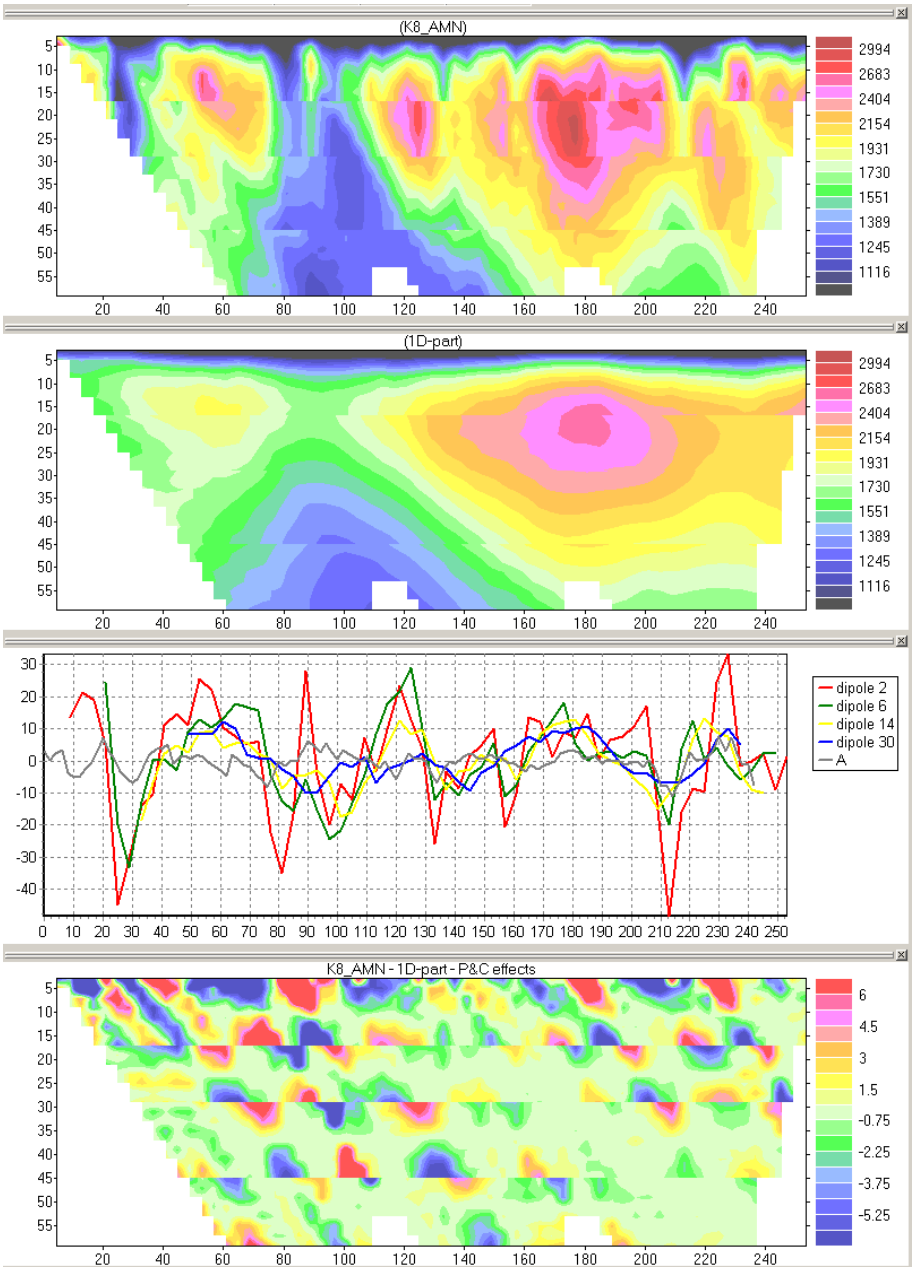
“*Median*” or “*Mean*” options allows you to vary smoothing windows along the line by clicking on pseudosections. If you misclicked and created a window boundary you didn’t want, just click on the boundary again and it will be deleted. Mean (or median) 1D values are placed at the center of the smoothing windows. Data between window-centered values are obtained by linear interpolation between windows.



When the configuration of smoothing is defined, press “Go” button and 3 components will be recalculated and you will see 4 plots:

- [Original data] pseudosection
- [“1D” part]
- [P & C effects]
- [Residual]

Note! when [P & C effects] plot is not active in the status bar, the [Residual] plot corresponds to [Residual I], when [P & C effects] plot is active in the status bar, the [Residual] plot corresponds to [Residual II].



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

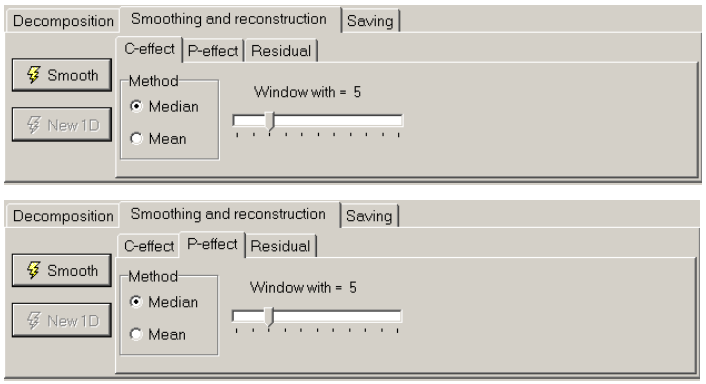
For pole-dipole and Schlumberger arrays, different P effects relate to different MN dipoles used at each VES. They correspond median values calculated for each vertical line in the pseudosection [Residual I].

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

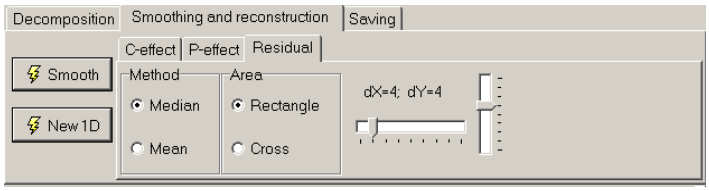
“Find P & C again” can be used to refine [P & C effects] calculation as some interference between P and C effects generally occur.

3.6.2. Components smoothing

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



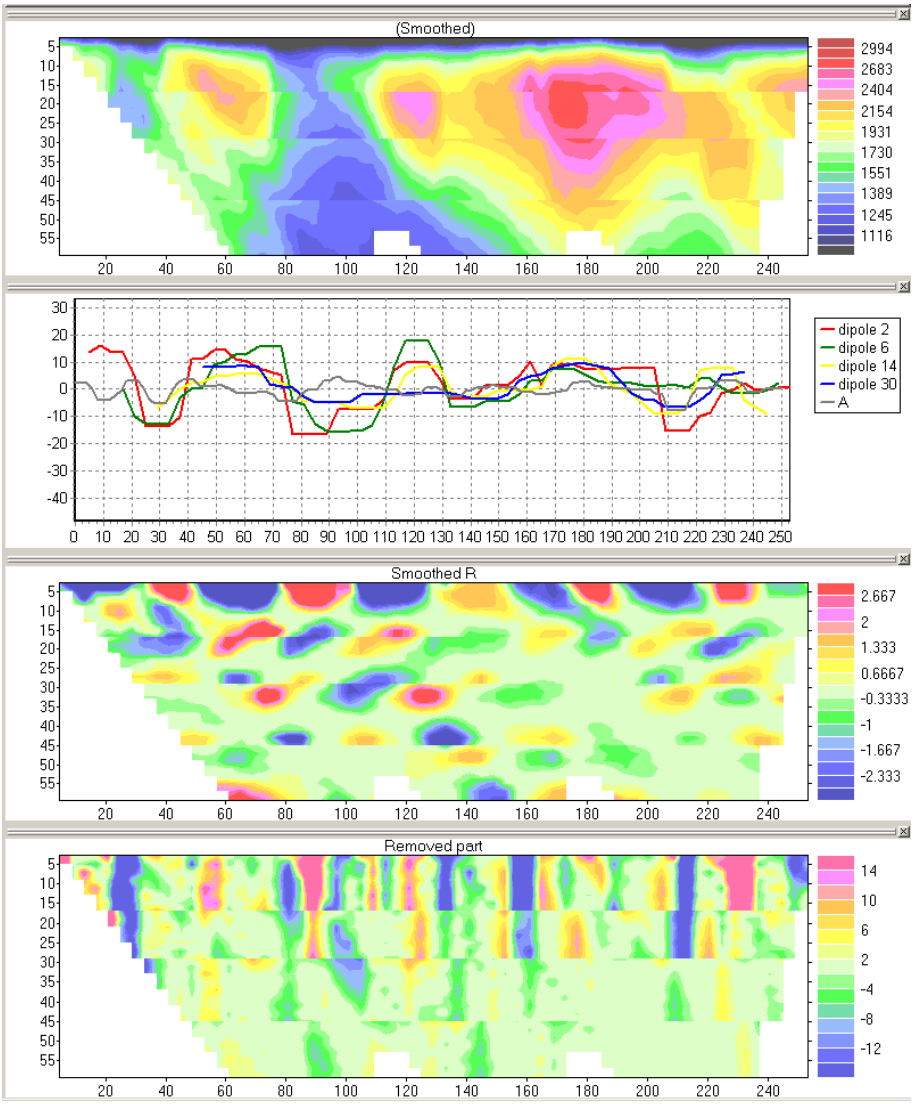
C and P effects can be smoothed using a median or mean method. Choose the width of the smoothing sliding window using the scroll bar “*Window width = …*”



Residual can be smoothed using a median or a mean method also. The applied matrix for that is a rectangle or a cross (for apparent resistivities with chequerwise layout for Wenner array measurements). The width of the smoothing sliding matrix can vary in X and in Y directions by “*dX = …*” and “*dY = …*” scroll bars.

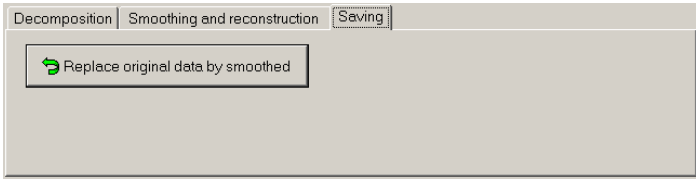
Press “*Smooth*” if the smoothing configuration is set right and new 4 plots will be displayed:

- reconstructed [Smoothed data] pseudosection
- [Smoothed P & C effects]
- [Smoothed residual]
- [Removed part] = [Residual III_a] + [Residual III_b].



A new estimation of [“1D” part] from the reconstructed [Smoothed data] pseudosection may be performed by clicking on “*New 1D*”. It allows you to refine [P & C effects] calculation. Actually, it provides a feedback step in the flow chart shown above, allowing to recalculate [Residual I] = [Original data] – [“1D” part] and then [P & C effects] from recalculated residuals.

Finally, [Smoothed data] pseudosection can be saved using the “*Replace original data by smoothed*” button on the “*Saving*” page.



After “*replacing original data by smoothed*” close the median procedure window. You will find that [Smoothed data] pseudosection has been exported to the default display window.

Note! At this stage the [Smoothed data] pseudosection is only recorded in RAM and needed to be saved.

3.7. Exporting to inversion programs

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

- *RES2DINV* http://www.geotomosoft.com/
- *SENSINV2D* http://www.geotomographie.de/
- *ZondRes2d* *http://zond-geo.com/english/*
- *IPI2WIN* http://geophys.geol.msu.ru/ipi2win.htm

Here, one may take reference to the user manual of these programs in order to have information about the format of the files exported by ***X2IPI***.

HOW TO USE X2IPI WITH...

4. TERRAMETER LS (ABEM, Sweden)

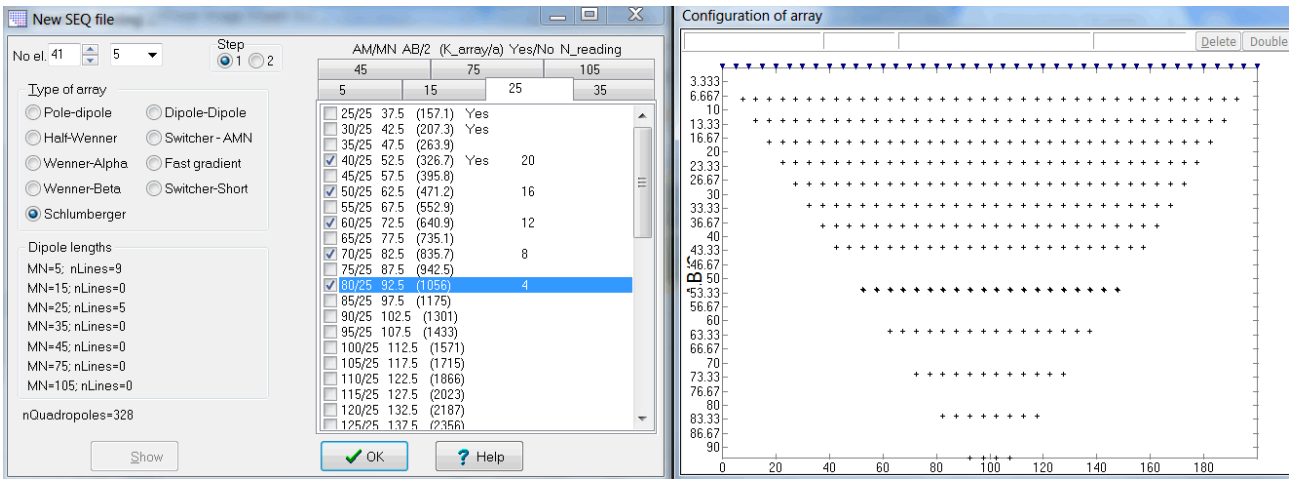
4.1. Creating protocol files for 4x21 cable set

TERRAMETER LS is a 64-electrode instrument with two 32-pole connectors 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 increasing of the depth of ERT investigation up to 25%.

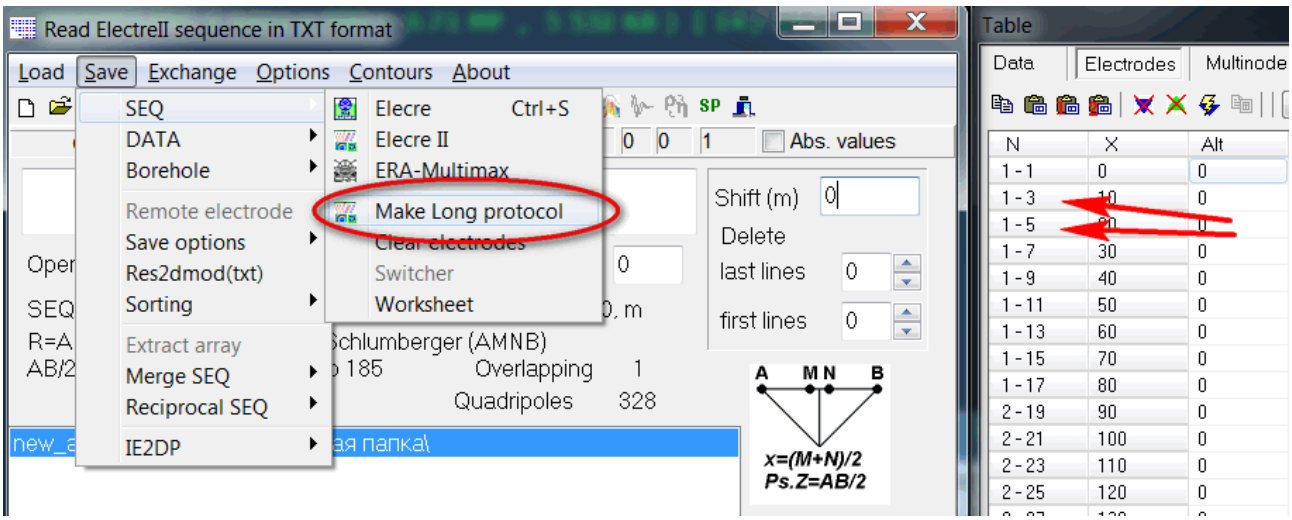
Protocol consists of two types of measurements. The first type – shallow measurements (small electrode spacings). The second type – measurements for deeper parts of geoelectrical section (large electrode spacings). For example, having cables with 5m spacing between electrode takeouts, LONG32 type (41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

X2IPI provides preparing ABEM protocols for 61-electrode measuring scheme. The following is example for Schlumberger array. **The first step** is to create LONG protocol for long spacing.

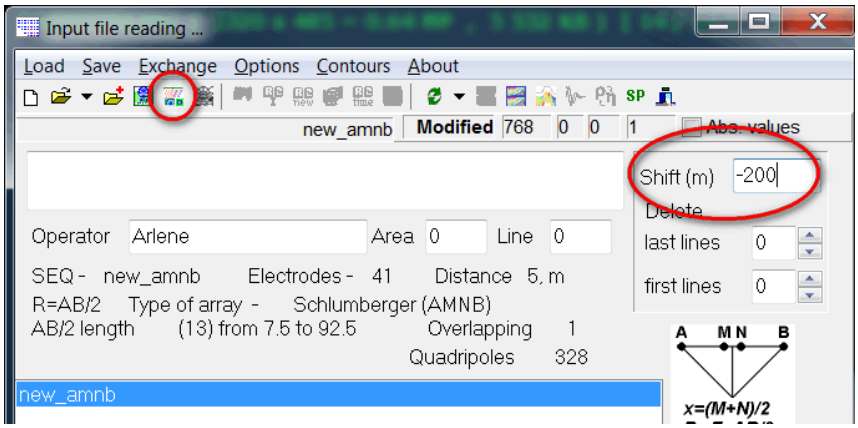
1. create a new protocol file with 41 electrodes and 5-meter unit spacing (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***) and save it to *ELECTRE II* [.txt] format .



2. *<Save - SEQ - Make Long protocol>*. It creates [.txt] protocol file with new numbers of electrodes and 10 meter unit electrode spacing.

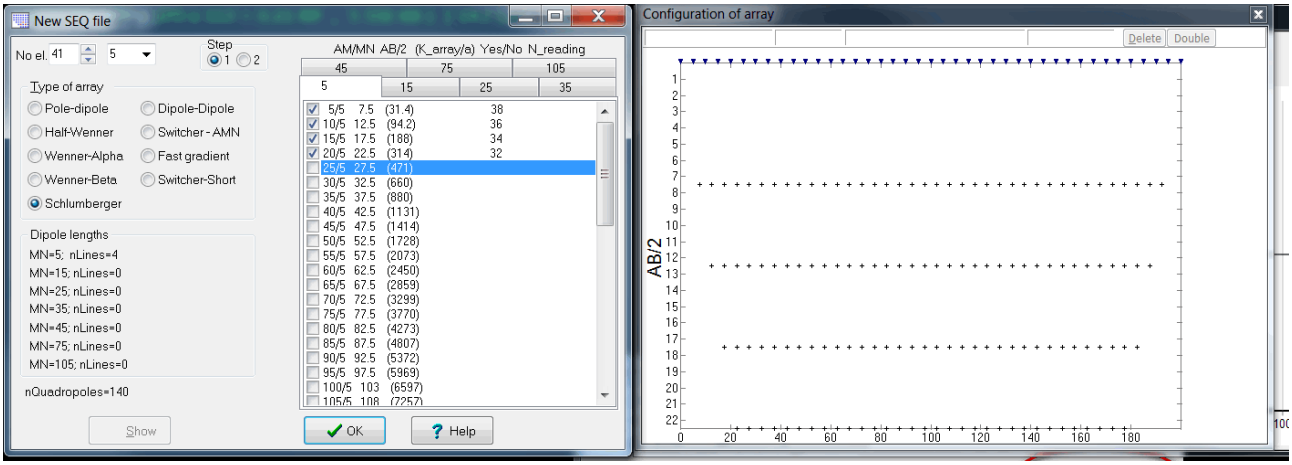


3. Shift X to get 0m coordinate for the central (n=21) electrode (Shift(m) = -200). Save it to *ELECTRE II* [.txt] format again.



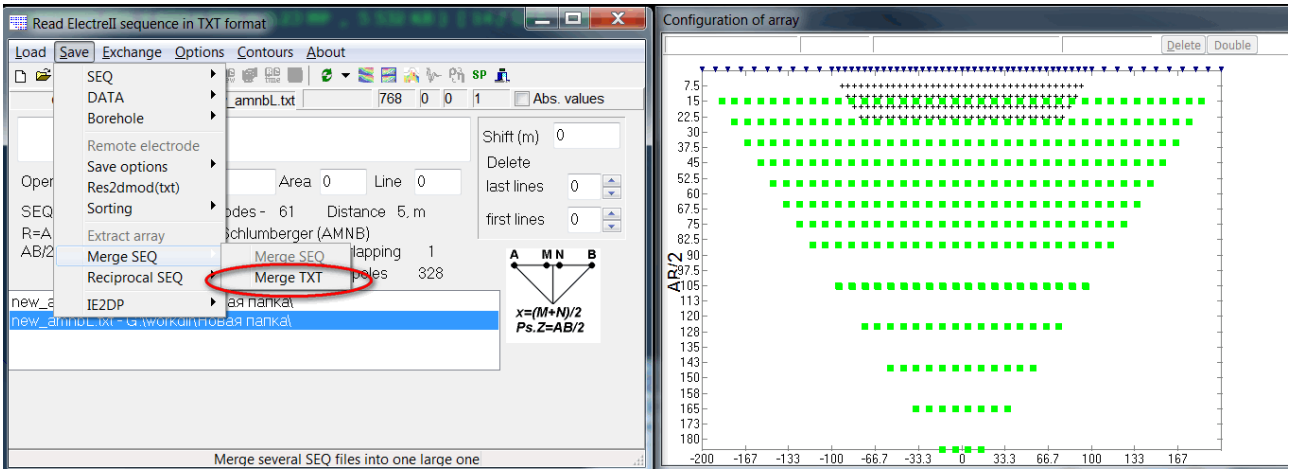
The second step is to create a SHORT protocol for the central part of profile.

1. create a new protocol file with 41 electrodes and 5 meter unit spacing and save it to new file in *ELECTRE II* [.txt] format . There is no need in big number of spacings – 4 lines will be enough.



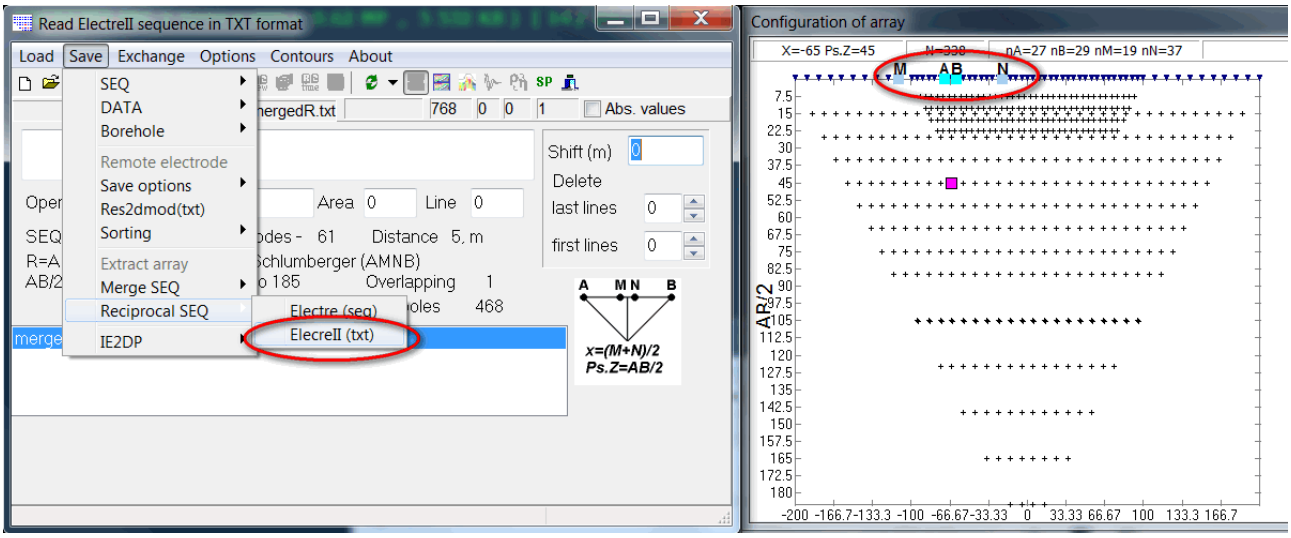
2. Shift X to have 0m coordinate for central (n=21) electrode (Shift(m) = -100). Save it to *ELECTRE II* [.txt] format again.

3. Add file with LONG protocol and save two files into one be <*Save - Merge SEQ - Merge TXT*>.

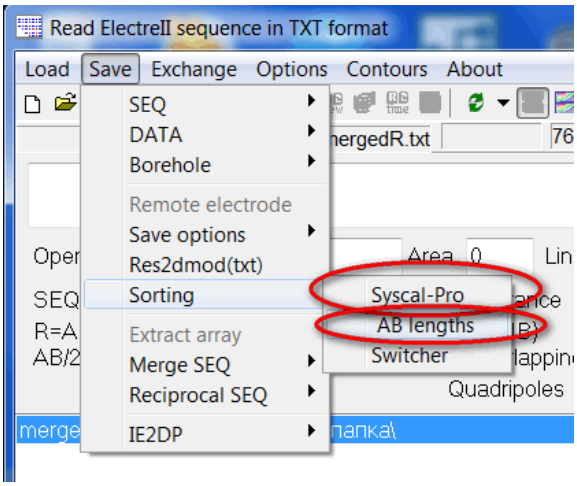


Now we have protocol file for 4x21 cable set. We need to open and optimize it for multichannel receiver. **The third step** is optimization.

1. Make reciprocal Schlumberger array *<Save - Reciprocal SEQ - ElectreII (txt)>* (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***) and open saved file.

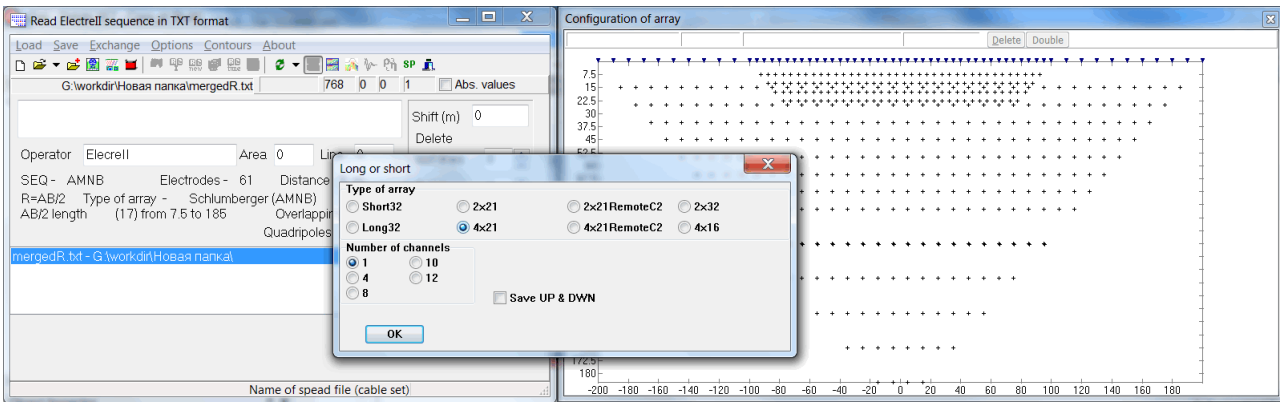


2. Sorting quadripoles. *<Save - Sorting - Syscal-Pro>* or *<Save - Sorting - AB lengths>* (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).



Now we have optimized protocol file for 4x21 cable set. We need to convert it into [.xml] protocol file for *TERRAMETER LS*. **The fourth step** is creating [.xml] file.

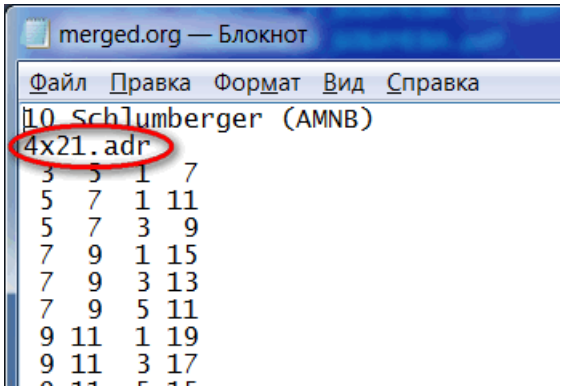
1. We need to open the protocol and save it to [.org] ABEM format.



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 a correct spread file in [.org] file.

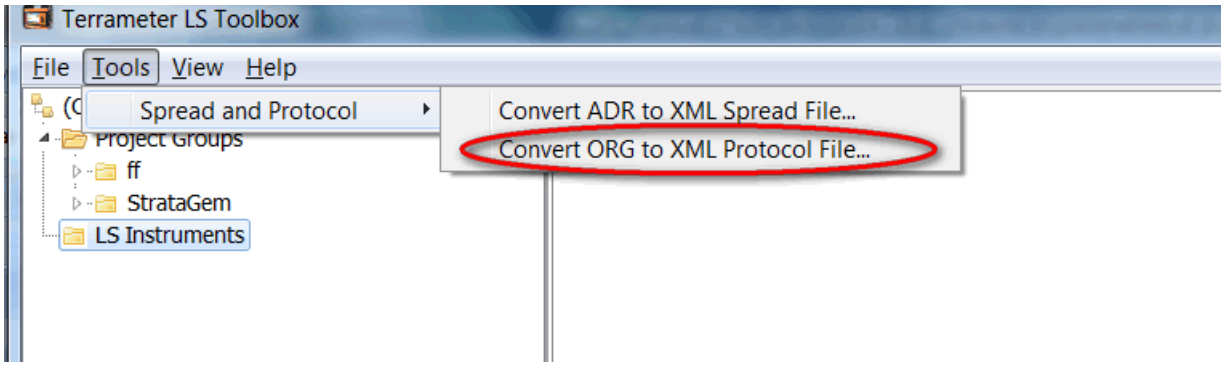
- 4x21.adr – 4-electrodes array for 4x21 cable set
- 4x21RemoteC2.adr – pole-dipole array for 4x21 cable set
- 2x21.adr – 4-electrodes array for 2x21 cable set
- 2x21RemoteC2.adr – pole-dipole array for 2x21 cable set

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

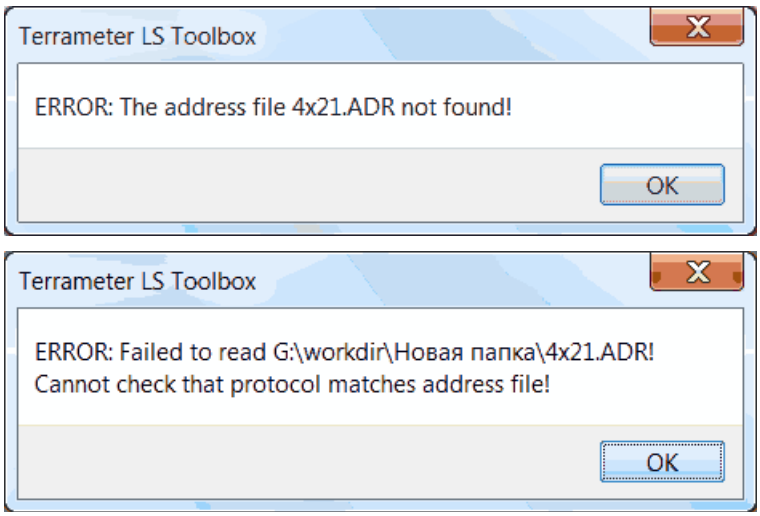


We can also indicate correct spread file in [.org] file on the second line of [.org] file.

2. Use *TERRAMETER LS TOOLBOX* software to convert [.org] file to [.xml] file.



File 4x21.adr does not exist actually. 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 TERRAMETER LS TOOLBOX manual*).



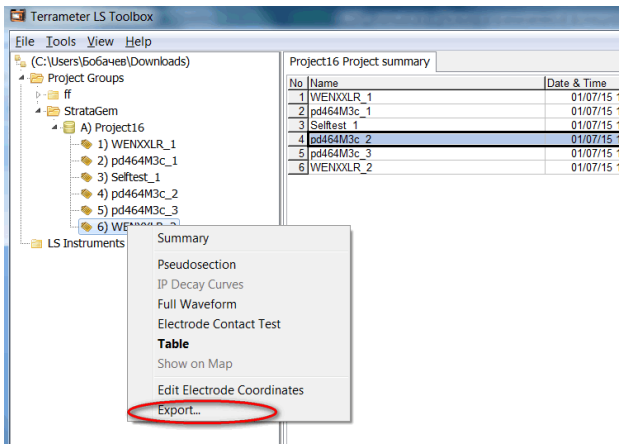
Despite the errors, a new [.xml] protocol file with with correct spread name was created. Now it can be used with *TERRAMETER LS* and it can be read by ***X2IPI*** software also.

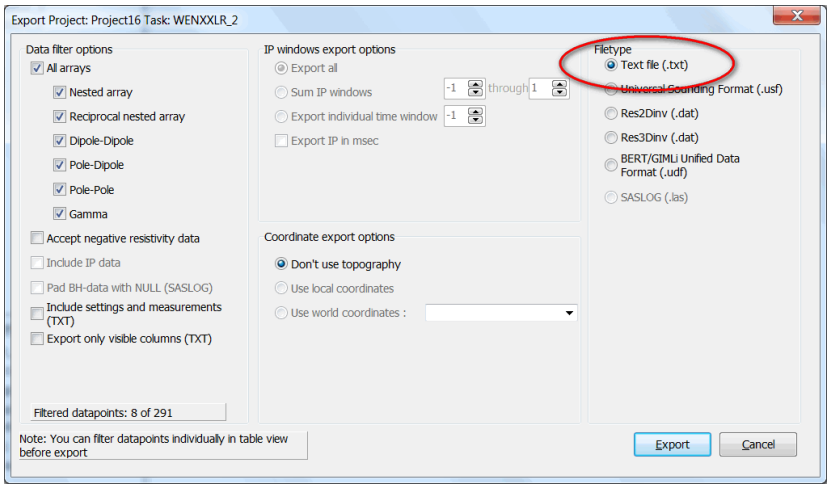
```
<?xml version="1.0" encoding="UTF-8"?>
- <Protocol>
    <Name> merged </Name>
    <Description> A description of the protocol can be written here </Description>
    <Arraycode> 7 </Arraycode>
    <SpreadFile> 4x21.xml </SpreadFile>
  - <Sequence>
    - <Measure>
        <Tx> 3 5 </Tx>
        <Rx> 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 no information about inner-electrode spacing in [.xml] or [.org] files.

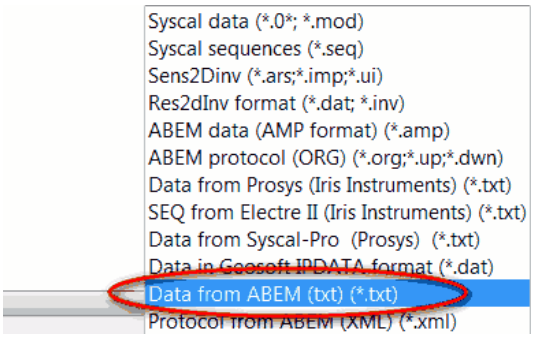
4.2. Read TERRAMETER LS field data

TERRAMETER LS TOOLBOX software can export field data to [.txt] file which is supported by ***X2IPI***.





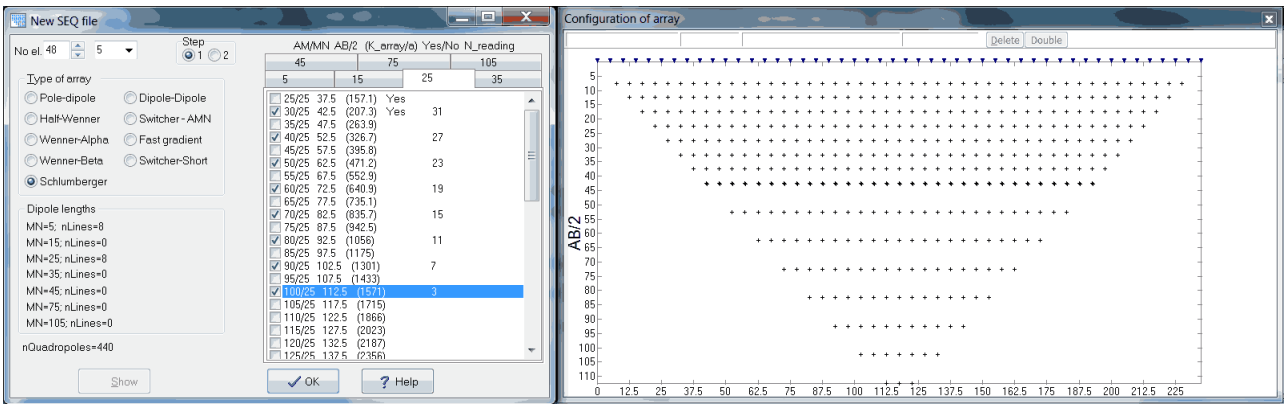
Use <*Data from ABEM (txt)*> format to read data from *TERRAMETER LS TOOLBOX*.



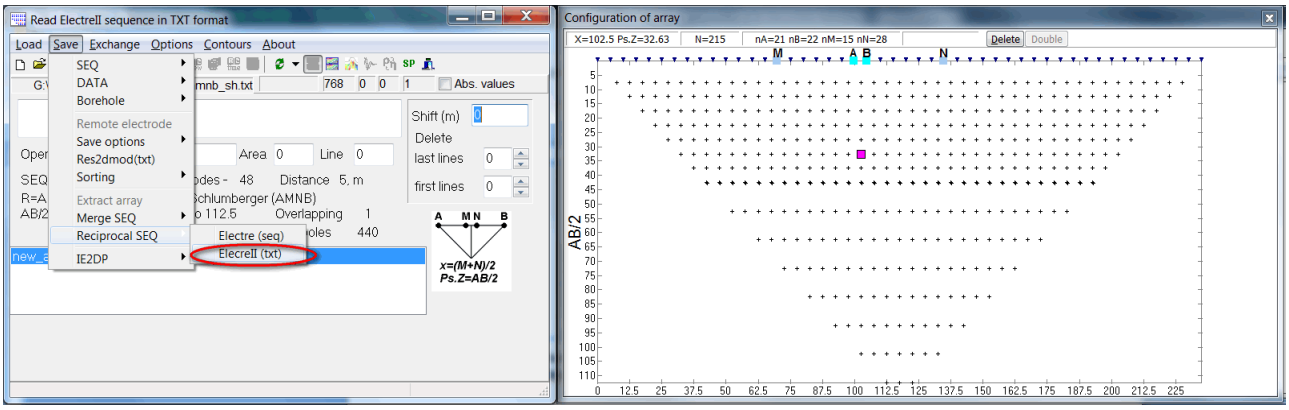
5. SYSCAL-PRO (IRIS Instruments, France)

5.1. Creating sequence file for SYSCAL-PRO

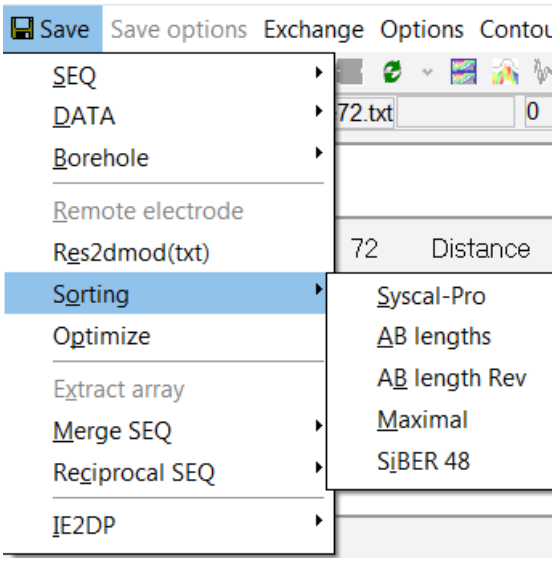
1. create a new sequence file for correct number of electrodes (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***)and save it to *ELECRE II* [.txt] format .



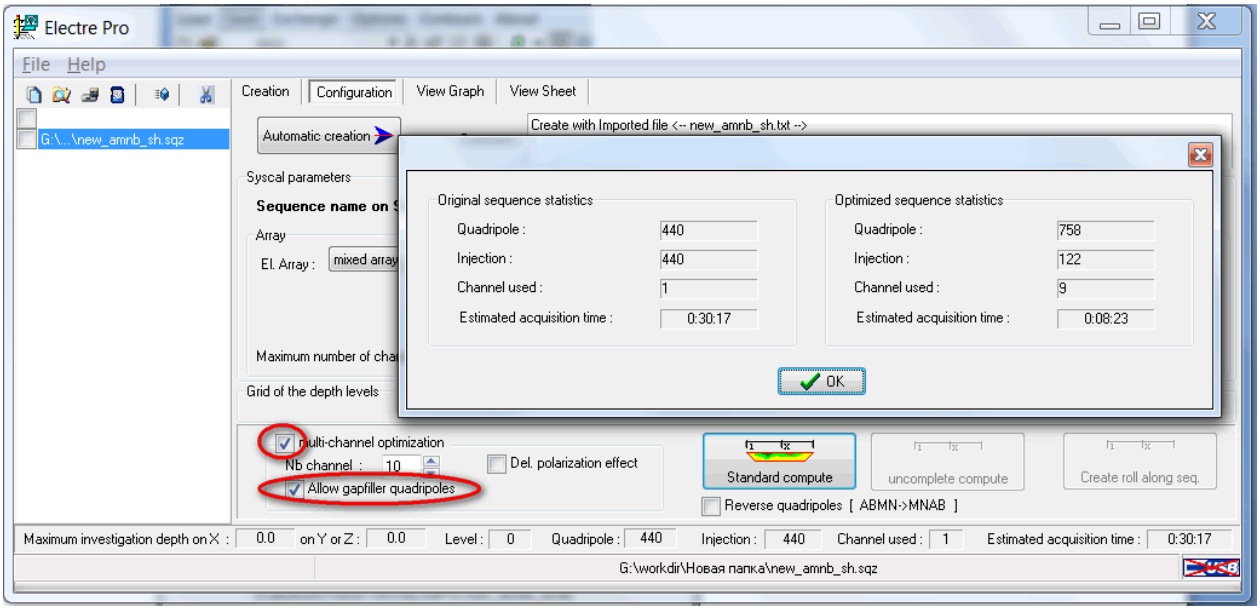
2. Optimize sequence for *SYSCAL-PRO*. Make reciprocal Schlumberger array *<Save - Reciprocal SEQ - ElectreII (txt)>* (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***) and open saved [.txt] file.



2. Sort quadripoles. *<Save - Sorting - Syscal-Pro>* or *<Save - Sorting - AB lengths>* (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***)

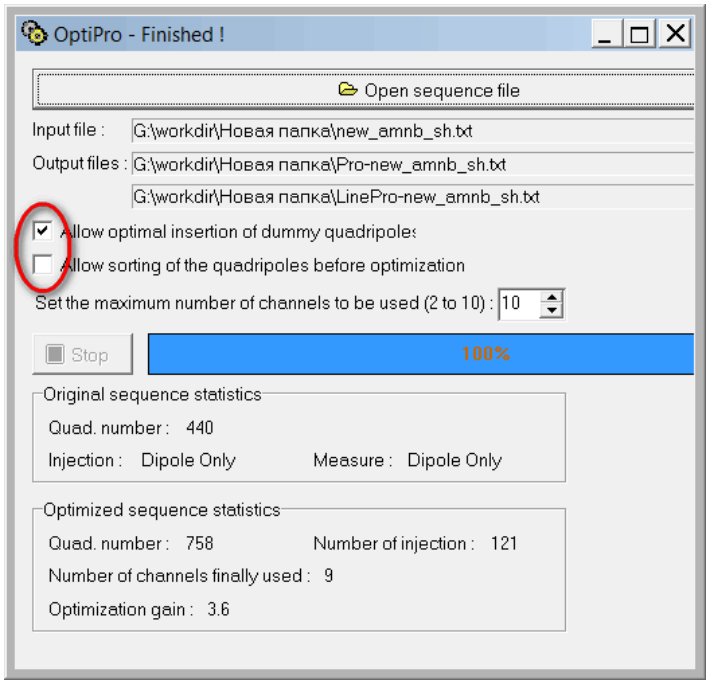


3. Now we want to prepare sequence file for *SYSCAL-PRO* so we need to add gapfiller (dummy) quadripoles. We can use *ELECTRE PRO* (IRIS Instruments) software for that.



Here we made optimized sequence file [.sqz], which should be uploaded to *SYSCAL-PRO* for field measurements.

Also we can use *OPTIPRO* software (IRIS Instruments). We need uncheck sorting checkbox (*"Allow sorting of the quadripoles before optimization"*), because we have already sorted quadripoles. ***X2IPI*** uses different algorithm of sorting quadripoles.



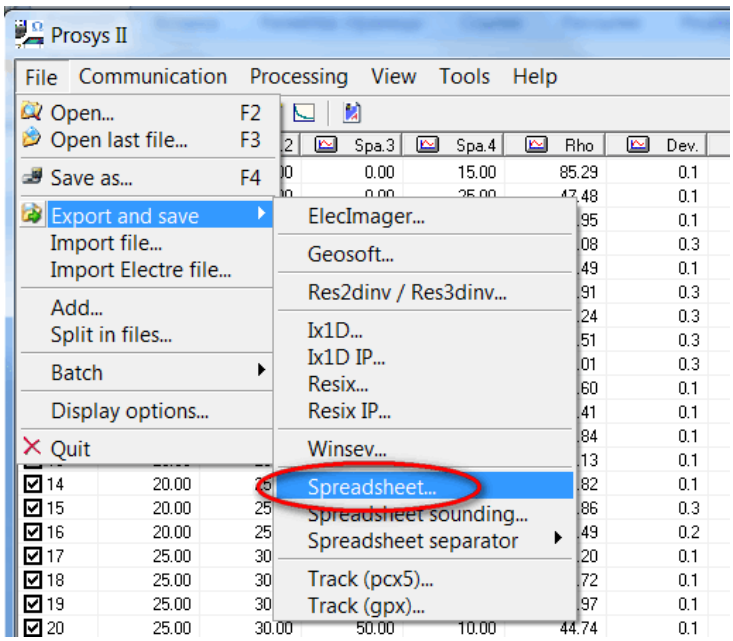
OPTI-PRO creates [.txt] file with long file name. We recommend to rename it short because *SYSCAL-PRO* supports only 10 characters in the file name.

Finally we have two sequence file: original [.txt] file and optimized [.txt] or [.sqz] file. However, we can use original file for *SYSCAL-PRO* data processing.

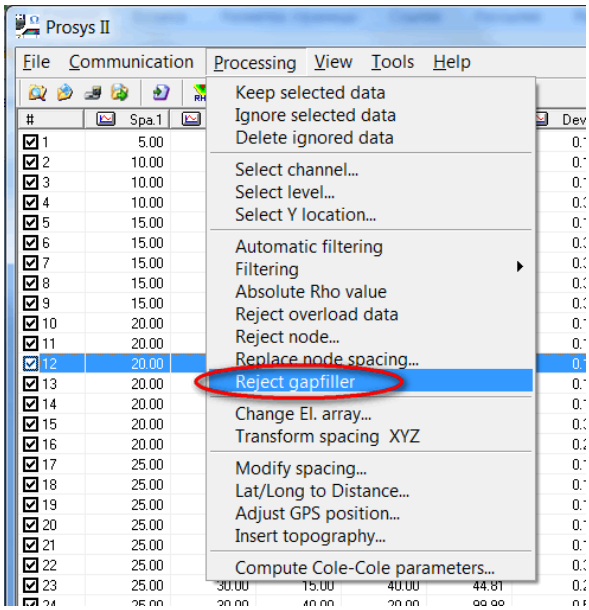
Note! There are many other options to prepare sequence file (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).

5.2. Read field data from SYSCAL-PRO

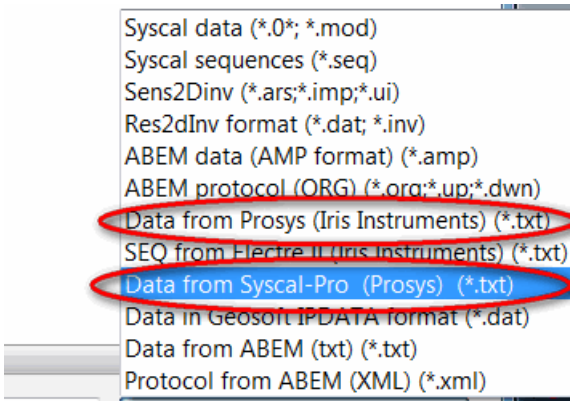
PROSYS II software can export field data to [.txt] format, which can be read *by* ***X2IPI***.



We have to remove gapfiller measurements before data processing. If optimization was made optimization in *ELECTRE PRO*, then we can reject gapfillers by *PROSYS II* before export spreadsheet.



If sequence optimization was made in *OPTIPRO*, then we can reject gapfillers in ***X2IPI***. There are two options to read data from *PROSYS II*. *<Data from Syscal-Pro (Prosys)>* option allows to reject gapfillers from [.txt] data file. We read the data file first and the original sequence file.



6. RES2DINV data format (Geotomo software, Malaysia)

RES2DINV format is the basic for ERT data.

6.1. Remove bad points from data file

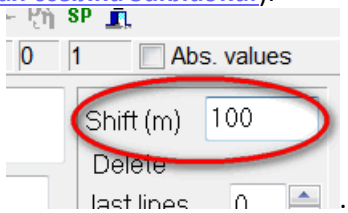
There are many options to remove bad point from data file.

1. Trimming bad measurements signal level, quality factor, apparent resistivity or chargeability range (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).
2. Remove data of bad electrodes or (see ***Ошибка! Неверная ссылка закладки..Ошибка! Неверная ссылка закладки.***).
3. Remove bad points of pseudosection in Display window (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***), on Profiling page (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***) or Soundings page (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).
4. Remove spacing lines on Spacing page (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).

All removed points can be restored.

6.2. Correct X-coordinate

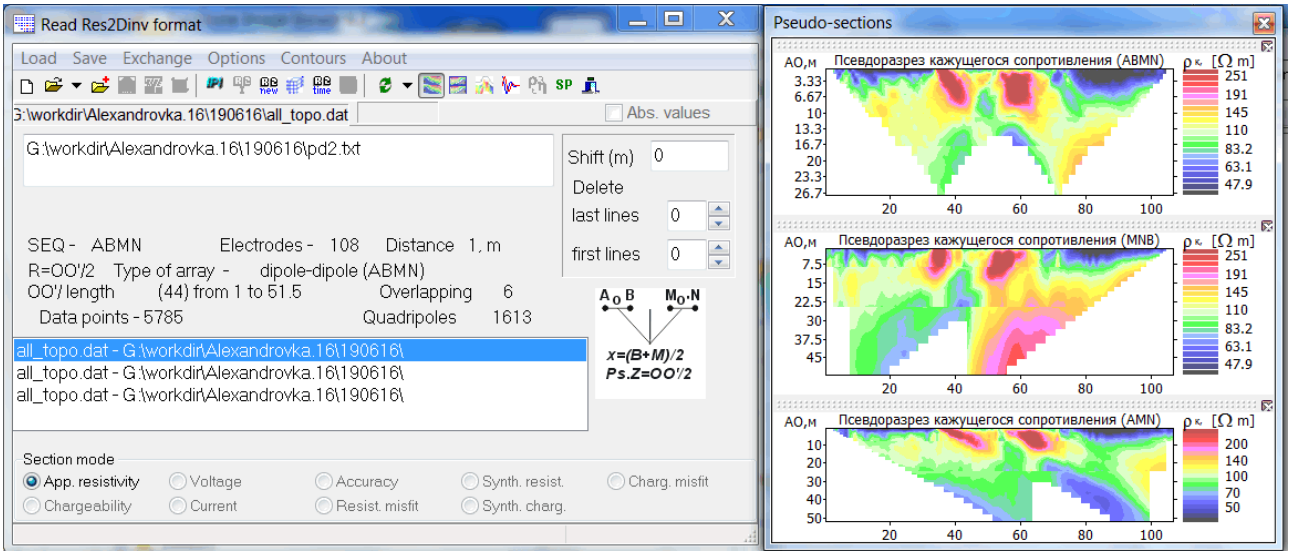
X-coordinate can be corrected by following ways:

- Change inter-electrode spacing on Electrode page (see ***Ошибка! Неверная ссылка закладки..Ошибка! Неверная ссылка закладки.***).
- Shift profile by X-coordinates 

.
- Mirror profile by Exchange menu (see ***Ошибка! Источник ссылки не найден..Ошибка! Источник ссылки не найден.***).

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

To merge different data sets to one file just open all sets and save them to *RES2DINV* format . ***X2IPI*** can show data for different arrays on different pseudosections. This is the example of one data set with three arrays: dipole-dipole, forward and reverse pole-dipole.

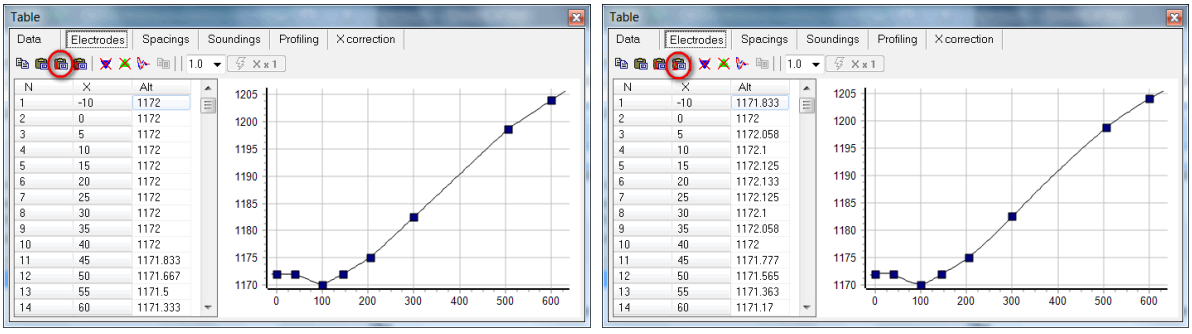


6.4. Input topography

The simplest way to include topography data is to prepare table X- and Altitude- coordinates table in a spreadsheet application (e.g. *MICROSOFT EXCEL*) and copy it to clipboard.

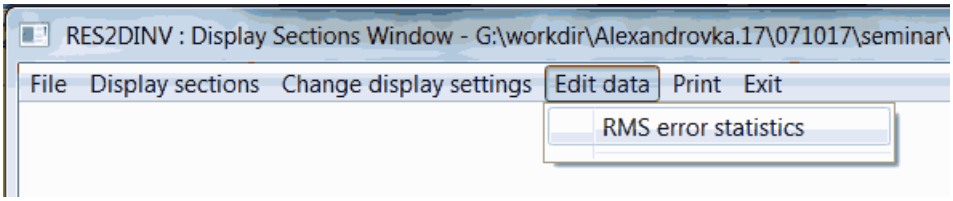
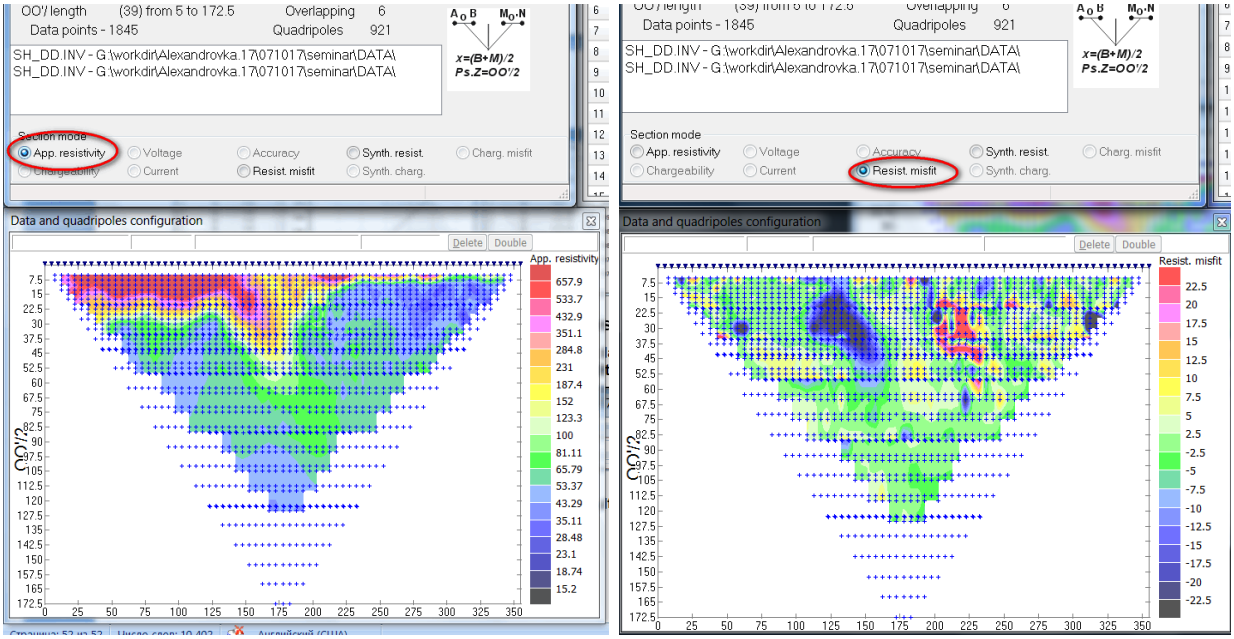
	A	B
1	0	1172
2	40	1172
3	100	1170
4	145	1172
5	205	1175
6	300	1182.5
7	505	1198.7
8	600	1204
9		

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 can be improved usually, if one removes data points with large misfit. There is an option in *RES2DINV* to remove such point – *<Menu – Edit data – RMS error statistics>*.



X2IPI can plot misfit pseudosection to analyze inversion results and remove data points with large misfit.