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BTOMO: THE SOFTWARE PACKAGE USED FOR THE BOLOMETRY ON TCV TOKAMAK

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Contents:

1. Introduction

This manual should be a help for the using of *btomo,* a graphical user interface (GUI) which was created in Matlab 5.2 to analyze the data of the bolometers on the TCV Tokamak in Lausanne (at the CRPP, Centre de Recherche en Physique de Plasma). Principally the use of the GUI should be fairly simple but for the author his program is always simple and so I wrote this manual which gives a deeper understanding of the *btomo* program.
In the first chapter of this manual some general things about bolometry on the TCV Tokamak are repeated. This part was essentially copied from 'Bolometry on the TCV Tokamak' by Mlynar Jan [1].
Then the software package will be presented. It consists of two parts: The *btomo* program and his subroutines *btomodata, btomosetup, btomorun* and *btomographics* are used to calculate the radiation from the measurements data of the bolometers and to give a first simple visualization of the results. The second program *btomoview* is used only to give a complete visualization of results created manually by *btomo* or automatically by *boloti_auto* (A. Refke, not finished yet).

2. Bolometry on the TCV Tokamak

For the evaluation of the plasma energy balance it is important to measure the total radiation emitted from the plasma. The standard diagnostic tool for this measurement are bolometric systems. The system applied on the TCV Tokamak in Lausanne consists of thin golden foil bolometers which absorb the incident energy. The energy flux can then be determined from the bolometers temperature rise which causes a linear increase of the resistance value in the kΩ range. Sixteen arrays of these bolometers, each with four elements, are installed in five pinhole cameras distributed around a poloidal cross-section of the TCV vacuum vessel (see figure 5). It's important to notice that these bolometers are sensitive to both radiation energy loss and energy loss via the flow of neutral particles.
For the reconstruction of the radiation profile a computer tomography (CT) code is used. This allows for example the separation of the energy losses of the confined plasma from the losses which occur outside the plasma volume. So far a rectangular mesh of pixels is used for the CT reconstruction (a concentric mesh determined by the flux surface geometry isn't ready yet). The relation between the lines of view and the radiation of the pixels defined by the mesh is:

$$f_i = \sum_{j=1}^{n} T_{ij} g_j \qquad (1)$$

where f_i = signal level of bolometer i
g_j = emission level of pixel j
n = number of pixels
T_{ij} = contribution factor of pixel j to the signal f_i

With the hypotheses that the plasma is transparent for the radiation and for neutral particles (i.e. for the energy flow) and that the bolometers detect only what is on their line of view the matrix element T_{ij} is proportional to the length of chord number i in pixel number j [2].(This is the 2 dimensional case.) In reality the bolometers detect all that what is inside their cone of view which depends on the geometry of the bolometers. So it's more accurate to use a matrix T which takes into account the etendue of the bolometers (3 dimensional case). Secondly it seems that the plasma is not transparent to the neutral particles flow [1]. Because the most important energy loss is generally located under the plasma (near the X point) the upper bolometers (1-8, see figure 5) are not usable and their signals have to be ignored for the CT reconstruction.
The inversion of the equation (1) including the treatment of the underdetermined and ill-conditioned problem is provided by either a linear or a minimum Fisher regularization algorithm (see [3]).

3. The btomo programs

The software package which performs the data retrieval, the setup of the mesh and the tomographic inversion consists of the main program *btomo,* three independent subroutines called *btomodata, btomosetup* and *btomorun* and the subroutine *btomographics* which visualizes the inversion data of *btomorun.* Of course these programs use a lot of subroutines which I called *btname*. It's absolutely necessary that all these programs are available from the Matlab path. A complete list of all programs is in the appendix A.

3.1 The main program: *btomo*

The main program *btomo* is started with the command 'btomo' in the command window of Matlab 5.2. A GUI appears (see figure 1) with four colored buttons: **Data**, **Setup**, **Run** and **Graphics** which are used to start the subroutines *btomodata, btomosetup, btomorun* and *btomographics*:

1) *btomodata:* This subroutine allows you to choose the shot and the times which you want to analyze. You can eliminate some channels either manually or automatically. You can also treat the data and display them.

2) *btomosetup*: This subroutine is used to specify the grid and the method which are used to calculate the matrix T (see chapter 2: Bolometry on the TCV Tokamak).

3) *btomorun*: This subroutine searches a solution of equation (1) ('inversion' of the matrix T). You can choose the regularization algorithm and some parameters as the error of measurement σ or the smoothing factor λ.

4) *btomographics*: This subroutine visualizes the results, i.e. the poloidal cross-sections of the radiation (A movie of the energy loss is also possible).

At the beginning the **Data** button is green, the **Setup** and **Run** buttons are orange and the **Graphics** button is red. This is a sort of color code to indicate the state of the different subroutines:

1) Green means that the program is ready to continue with this task and that you should press this button. If you are clicking on this button the corresponding subroutine is initialized: All the data which are used by this subroutine are updated, i.e. transferred from the subroutine corresponding to the button on

the left to the subroutine corresponding to the clicked button. (Example: You click on the green **Run** button than the data from *btomosetup* are transferred to *btomorun*.)

2) Orange means that there are no data available from this session and you will be asked to load data from previous sessions.

3) Red means that there are no data available (and you cannot load data!).

4) Yellow means that this task has been executed. As for the green color the corresponding subroutine is initialized by clicking on the button.

Of course the GUI of the subroutines are automatically opened if needed.

In the middle of the *btomo* GUI is a message window which gives you some indications what you have to do or what the program is doing.

In the lower part of the GUI there are also four buttons: **Replace/Hold, View, Save and EXIT**.

1) **Replace/Hold:** With this toggle button you can decide if only the GUI of one subroutine is open at once (the new GUI replaces the old one) or if all opened GUI's stay open until you close them manually.

2) **View**: Clicking on this button opens the program *btomoview* which is a more sophisticated program to visualize the results than *btomographics*. *Btomoview* is a totally independent program. (see chapter 5: A tool for analyzing the results: btomoview).

3) **Save**: With this button you can save the results to the results tree of the bolometry. This button is disabled until you calculated the inversion.

4) **EXIT**: You have to click twice on this button to exit. All subroutines and the main program will be closed. If you don't want to exit after you clicked once you can click any other button to continue the work.

3.2 The choice of data: *btomodata*

The GUI of *btomodata* can be opened by clicking on the button **Data** of the *btomo* GUI. The data GUI is divided into five parts (see figure 2).

3.2.1 Controls of *btomodata:*

1) Head:

The name of the node where the data come from is displayed and you can choose the shot number.

2) Time samples:

In the second part you can choose the time samples in many different ways: You can specify the start and stop point either in seconds or with the number of the time step of the data acquisition system (DAS), you can choose the number of reconstructions or the interval between two reconstructions. A special way to choose the times of reconstruction is given by the **Normal/LIUQE** toggle button: By clicking on it the program is searching automatically the acquisition times of the bolometry which corresponds the best to the LIUQE times. Because there are sometimes a lot of LIUQE times you may be interested to change manually the time interval or the number of reconstructions. This can be done by setting the corresponding edit boxes. The program tries to find a set of LIUQE times which are quite equidistant. The start and stop times are then automatically changed to the nearest LIUQE times. Because the LIUQE times aren't equidistant generally the '<time per frame [s]>' and the '<steps per frame>' boxes display the average. (In the normal case this values are exact.)

3) Deleting unsuitable channels:

The third part allows to delete some channels with bad signals. There are three methods to do this: The method of A. Refke which makes tests on the mean values (**AR autoselect**). The method of Ch. Deschenaux which makes backfiltering tests (**ChD autoselect**). Finally you can delete channels manually on the channel matrix where all the deleted channels are shown (red=deleted). Notice that A. Refke's method is applied automatically when the shot number is set. You can select again the deleted channels by clicking the same buttons as for deleting.

4) Data treatment:

With the **on/off** button in the fourth part you can choose if you want to apply one of two data treatment methods (**BJ/ChD**): One is B. Joye's smoothing and you can choose the number of points which the data are smoothed over. The second is Ch. Deschenaux's backfiltering method and you can set the filter frequency. You can also have a look at the treated data of the channel specified in the edit box by clicking on the **display** button, which opens the GUI *btdsiggui* (see paragraph 3.2.2).

5) GUI functions:

Below the area where the messages of *btomodata* are displayed (in blue), there are five buttons:

APPLY: Packs the complete choice of frames into a matrix. After this the **SHOW** and the **save.mat** buttons are enabled. At the same time the color of the **Setup** button in the main GUI *btomo* changes to green.

SHOW: Calls the program *btddisp* which opens a window where the final data are visualized. You can even create a movie.

save.mat: Opens the save dialog box and saves the data in a *.mat file.

load.mat: Opens the load dialog box to load data from a *.mat file. It's automatically tested if the file chosen by the user contains really data saved by *btomodata.*

dataview: This button opens the program *dataview* which is a good tool to have a look at the data. Since it is totally independent you have to specify the shot number again in this program. (See figure 4.)

EXIT: You can close the GUI by clicking twice on this button. After the first click you will be asked if you really want to quit. If not, you can continue your work by using any other control.

3.2.2 The graphic windows of *btomodata*:

We have seen that there are two graphic windows which are opened by clicking on the **display** respectively on the **SHOW** button.

1) *btdsiggui* (**display** button):

The top window shows the raw, smoothed and treated signals of one channel as a function of time (see figure 3a). You can clear each signal with the **clear** button. You can also zoom in and out by clicking with the left and the right mouse button on the graphic, respectively. The lower window shows the derivative of the smoothed raw signal. You can zoom in and out with the mouse as in the other window.
There are two command buttons, **print** and **exit**, and a pop-up menu to choose the print device. The display window will be closed already by clicking once the **exit** button.

2) *btddisp* (**SHOW** button):

The **SHOW** button opens the btomodata display window with a graphic presentation of the intensity for all channels for a given time (see figure 3b). Here is a list of all controls:

hold off/hold on: 'Hold on' means that a new plot (i.e. the intensity of another time sample) is superposed onto the old one which is not deleted. If the default value 'hold off' is chosen then only one plot is shown and if you change the time then the old plot is deleted.

y fixed/y flows: If y is fixed then the scaling of the y axis stays the same for all time samples. If y flows then the y scaling is adapted corresponding to the maximum value of the intensity. (If you have also set 'hold on' then the scaling doesn't change to smaller values.)

line/points: Determines the plot style (line or points).

<: One time step back.

>: One time step forward.

Edit box 'frame #': You can set the number of the frame (time sample of DAS).

Edit box 'time [s]': You can set the time which you are interested in. The time sample next to the specified time will be plotted and the real time will be displayed in the box.

get movie: Builds the movie matrix used to play the movie (i.e. a copy of the plot of every frame will be saved in the movie matrix). Enables the **play movie** button.

play movie: Plays the movie. The times of playing and the speed are specified by the two following edit boxes.

Edit box 'times': Specifies the number of times the movie will be played. Note that some kind of memory loading (which is fairly slow) will be played first, so that you see always one more movie than specified.

Edit box 'frames per sec': Here you can set the speed of the movie. Of course the maximum speed is determined by the computer.

print: Prints what you see on the axes to the device specified by the following pop-up menu.

Printer pop-up menu: You can choose if you want print to files (m or ps) or to one of the listed printers.

exit: Closes the btomodata display window (by clicking once).

3.3 The setup for the inversion: *btomosetup*

The setup GUI is opened by clicking on the **Setup** button of the *btomo* GUI (figure 1). Note that a default setup is automatically loaded so that you could continue your work with the calculation of the inversion (*btomorun*). The default setup has a grid of 10x28 rectangular pixels and was calculated with the 'Omgrid 3D' algorithm. It can be used in the most cases.
If you want to change the setup you have to click on the **Change** button first (see the following chapter). The setup window is divided into two parts (see figure 5): On the left side there are the control buttons and the message window, on the right side there are two output graphic frames. The list of all the controls is given here. They are divided into buttons which control the GUI and controls (pop-up menu, edit boxes) which are used to set the parameters of the setup.

3.3.1 The GUI control buttons:

Change: Allows to use the setup controls. Actually after having calculated or loaded a T matrix the setup controls are inactive and you have to click the **Change** button to enable them. The setup parameters are not changed.

Load: Loads a saved setup from a *.mat file. It's automatically tested if the file chosen by the user contains really a saved setup. The setup controls are disabled and the **Change** button is enabled.

Apply: Calculates the T matrix depending on the parameters given by the setup controls. Enables the **Save** and the **Change** button and disables the setup controls.

Save: Saves the setup in a *.mat file. This button is disabled by default and is enabled only after the calculation of a T matrix.

EXIT: Closes the setup GUI. By clicking once you are asked if you really want to quit and you have to click a second time to do it. You can continue your work by using any other (enabled) control.

3.3.2 The setup controls:

Type of grid pop-up menu: You can choose a rectangular grid (default) or concentric one ('Flux grid') which is adapted at the magnetic flux surfaces. The setup controls are changed corresponding to your choice (compare figures 5a and 5b):

1) 'Rectangular grid':

Grid size pop-up menu: If you choose 'Part of vessel' then you can change the position of the center and the width of the grid. In the case of 'Whole vessel' (=default) the controls r_0, z_0, w_r and w_z show default values and they are inactive.

n_r: The number of pixels in the radial direction.

n_z: The number of pixels in the vertical direction.

r_0: Radial position of the center of the grid (in centimeters).

z_0: Vertical position of the center of the grid (in centimeters).

w_r: Radial width of the grid (in centimeters).

w_z: Vertical width of the grid (in centimeters).

Calculation method pop-up menu: 'Standard 2D' calculates the T matrix in a fast two dimensional way. 'Omgrid 3D' is very slow but the etendue of the bolometers is taken into account and the T matrix calculated in three dimensions corresponds better to the reality.

2) 'Flux grid' (the flux setup is not ready yet[1]):

Grid size pop-up menu: This menu is disabled for the flux grid and the grid fills always the whole vessel.

n_r: The number of radial grid lines.

n_p: The number of grid lines in the angular direction in the case of a 'grid base function system'.
The maximal order of the poloidal harmonics in the case of a 'harmonic base function system'.

Spacing pop-up menu: Here you can determine if the radial grid lines are 'equally spaced in flux value' or 'equally spaced in averaged radius'.

[1] The program uses the flux setup of the X-ray tomography which is not useful for the bolometry.

Base function system pop-up menu: You can choose between a 'grid base function system' and a 'harmonic base function system' (for more explanation about this two systems see [4]).

Calculation method pop-up menu: 'Single PSI'[2] means that only the magnetic flux surfaces of the first sample are taken into account. This method is useful if the magnetic flux surfaces stay constant, because the calculation of the inversion will be much faster. If you choose 'multiple PSI' the grid is adapted to the magnetic flux surfaces for every time sample.

Notice: The 'flux grid' setup isn't ready yet (August 1999). Actually the program uses the subroutines made for the X-ray tomography which aren't suitable for the bolometry. The setup should be upgraded as soon as the new subroutines are supplied by our Hungarian colleagues.

3.3.3 The graphic windows:

There are two graphic windows: One displays the vessel, the lines of view of the bolometers and the grid or the magnetic flux surfaces, the other shows the distribution of the number of chords per cell (only for the rectangular grid).
You can choose what is displayed in the first window by clicking the right mouse button when the cursor is within the axes but outside the plotted things (as the vessel, the grid, ...): A menu will appear and you can for example delete the vessel. Note that the lines of view of the channels that you deleted in *btomodata* are not visible, but the routine which calculates the T matrix for the rectangular grid ignores this. Actually in this case you can use *btomodata* and *btomosetup* independently one from another (this is not true for the 'flux grid').
The graph with the distribution of the number of chords per cell gives you a clue to choose the number of pixels: If there are a lot of cells unseen by the lines of view then the pixels are probably too small.

[2] PSI=Ψ is the poloidal magnetic flux function.

3.4 The inversion (calculation of the radiation): *btomorun*

The GUI of *btomorun* is opened by clicking the **Run** button of the *btomo* GUI (figure 1). The figure 6 shows the run GUI. At the top there is a message window. In the middle the parameters for the inversion can be set. Finally there are the GUI control buttons.

3.4.1 The GUI control buttons:

Load: Loads a saved inversion from a *.mat file. It's automatically tested if the file chosen by the user contains really a saved inversion.

Apply: Calculates the inversion using the algorithm and the parameters specified with the run controls (see the chapters 3.4.2 and 3.4.3). Enables the **Save** button when finished.

Save: Saves the inversion (and all other useful data) in a *.mat file. This button is disabled by default and is enabled only after the calculation of an inversion.

EXIT: Closes the setup GUI. By clicking once you are asked if you really want to quit and you have to click a second time to do it. You can continue your work by using any other (enabled) control.

3.4.2 The basic functions of *btomorun:*

By default you can choose the algorithm that will be used for the inversion, you can set the errorbars of the signals (sigma) and you can decide if some output is displayed during the calculations.
Note that showing intermediate results will slow down the process. A good value for the sigma is 3 %. If the errorbar is too small then the data may not be consistent which makes it impossible to find a solution for the equation (1) or, at least, leads to undersmoothing (noisy reconstruction); on the other side if the errorbar is too big then information is lost and the solution is oversmoothed. It depends on the type of grid chosen in the setup (*btomosetup*) which algorithms are available: For the rectangular grid you can choose between linear regularizations of order 0, 1 and 2 and the minimum Fisher regularization (see [3] for information about these algorithms). In the case of the flux grid, only the linear regularizations of order 1 and 2 are available, at the moment.
We believe that the most reliable results are obtained with the minimum Fisher algorithm which is the default.

If the button **Rad on** is activated then the radiation in- and outside, above and below the plasma will be calculated and displayed in a graphic window (see figure 8).

3.4.3 The advanced functions of *btomorun:*

If you click on the **Advanced** button a new window will appear where you can change several parameters of the algorithms (figure 7). If you want to understand the function of all these parameters you should read [3] and the Matlab codes of btminfisher_reg.m, btregulo_2d_tcvti.m and btregulo_2d_flux.m too. I will give here only a very short introduction:
All the algorithms try to minimize a functional of the form:

$$\textit{minimize}\ (\phi\,(g) = \tfrac{1}{2}\chi^2 + \lambda R) \qquad (2)$$

where λ is the smoothing parameter, R is the regularizing functional and χ^2 is given by:

$$\chi^2 = \sum_l \left(\frac{\sum_i T_{li} g_i - f_l}{\sigma_l} \right)^2 \qquad (3)$$

where f_l = signal level of bolometer l
g_i = emission level of pixel i
T_{li} = contribution factor of pixel i to the signal f_l
σ_l = error of f_l

The smoothing parameter λ determines the weighting between the goodness-of-fit, represented by χ^2, and the requirements imposed on the solution g by the functional R, e.g. the smoothness of the solution [3]. The problem is to find the 'correct' value for λ. In practice the algorithms begin with an estimated λ, search the solution g of the equation (2) and then calculate χ^2. Then a new value for λ is set and the equation (2) is solved for the new λ. This step is repeated until the desired χ^2 is achieved within the allowed precision ε or the algorithm is gone beyond the maximal number of iterations.
Actually you can set the maximal number of iterations, the targeted χ^2 or the smoothing parameter λ and, of course, the data error σ. In the case of the minimum Fisher algorithm you can also set the number of loops. (The minimum Fisher algorithm changes the regularizing functional R from one loop to the other. See the Matlab code of btminfisher_reg.m.)
The default value of λ (10) is an experimental estimate of a reasonable value of λ. The parameter χ^2 is shown in a normalized form and is multiplied with the number of active bolometers. It's default value is 1 ($\Rightarrow$ 1·# channels). The

reason is given by the equation (3): If the difference of the calculated signal $\sum T_{li} g_i$ to the measured signal f_l is equal to the error σ then χ^2 equals the number of channels. To demand a smaller χ^2 is not reasonable. But sometimes you wish to set a higher χ^2, for example if there are any problems to reach $\chi^2=1$ (or rather $\chi^2=1 \cdot$# channels).
It's important to notice that χ^2 is a function of λ, so either you set the targeted χ^2 or the smoothing parameter λ. By clicking the **Lambda** or the **Chi^2** button you can enable one edit box and disable the other. If you choose a constant λ then the number of iterations box is also disabled (the algorithm doesn't have to try different values for λ). Note that the calculations with a constant λ will be faster (no iterations!). Notice also that if you are calculating the inversion for a given χ^2 you will obtain different λ for the different time samples. If you choose now one time sample and try to recalculate this inversion but this time by fixing the parameter λ to the value calculated before then you will obtain the same inversion and the same χ^2 only in the case of the linear regularizations. Actually the minimum Fisher algorithm changes his regularizing functional R depending on the inversion result of the loop before. But this inversion result depends also on the smoothing parameter λ.

If you click the **OK** button the program *btomorun* will apply the new parameters and close the advanced window. If you click the **Cancel** button the advanced window will close and the parameters are changed back to the default values. (Attention: σ will be set back to 3 % !!!)

3.5 The presentation of the results: *btomographics*

The graphics window is opened by clicking the **Graphics** button in the *btomo* GUI (figure 1). The first five inversion results will be plotted in the new window (see figure 9). Some informations (shot number, method of reconstruction, start and stop time) are displayed on the right side. The functions of the controls are explained in the following lines:

EXIT: As usually you have to click twice to quit the program *btomographics.*

Vessel off/Vessel on: Hides or shows the vessel.

Flux on/Flux off: Shows or hides the magnetic flux surfaces.

<<prev: Shows the previous five emission images.

<: The displayed emission images are shifted one time step back.

>: The displayed emission images are shifted one time step forward.

next>>: Shows the next five emission images.

movie: Shows a movie of the emission as a function of time. (The building of the movie takes some time. Once the movie matrix is constructed the playing of the movie is much faster.)

print: Command to print the displayed emission images to the device specified by the printer pop-up menu. A new window is opened which gives a preview of the printed page. There are also some informations which will be printed with the images.

Printer pop-up menu: Here you can choose the device where you would like to print to.

Plot pop-up menu: You can choose between five different kinds of representations.

Some notices on the plot styles:

It's important to know how the plots are colored: A dark red is attributed to the maximal value (of intensity) and blue to the minimum. The colors of the other

values are interpolated linearly. So the program searches the maximum of all frames and interpolates the colors between this maximal value and zero. In this way the same color in two different plots stands for the same value of intensity.
The lines of the contour plots are made in a similar way: The maximum of all frames is determined then nine levels between this maximum and zero are specified. The contour lines are now plotted for this levels (i.e. the same line in two different plots stay for the same value).
If you choose the labeled contour plot then the values of the different lines are displayed in a normalized form and the normalizing factor nf is displayed in the title.

4. A typical session:

In this chapter a typical session with *btomo* will be described. You will learn how you can change the default values and how much time the different steps take. The text in italic will always refer to the *btomo* main GUI, the other text will refer to the subroutines *btomodata*, *btomosetup*, *btomorun* and *btomographics*.
The times of computation refer to system speed in a typical working hours session in August 1999.

To begin type *btomo* in the command window. The main GUI will open.

The 'Data' button is green, the 'Setup' and the 'Run' button are orange and the 'Graphics' button red. The message area displays: "To begin, click 'data'." Click on the 'Replace' button to change it to 'Hold' so that the GUI's of the subroutines won't be closed automatically. Then click on 'Data'. The message area displays "...busy...".

~20"

The message frame displays: "Analysing of the data !"
The btomo data control window is opened. The default shot number is 15211. Change it to 15539.

~8"

The 'AR autoselect' button was automatically activated so that two channels, 3 and 61, are already out. Click on the 'ChD autoselect' button.

~4"

Now the channels 6, 7 and 8 are out, too. Click on the 'dataview' button to open the dataview program.

~10"

The dataview window is opened. Change the shot number to 15539 in this window, too.

~5"

Now you can have a look at the deleted channels. Click in the upper graph near the channel 61 and you will see in the second graph that the signal of this channel is constant. Repeat this for the channels 3, 6, 7 and 8. You will see that the channel 3 is also constant contrary to the channels which were selected by 'ChD autoselect'. Close the dataview window. (Click on 'EXIT'. A dialog box appears which asks you if you want to save this state as default. Click on 'NO'.)

~1"

Select manually the channels 1, 2, 4 and 5 by clicking on the corresponding buttons of the channel matrix. (Because the plasma isn't really transparent to the radiation and the main source of radiation is near the X point under the plasma, the detectors above the plasma, 1 to 8, don't give consistent signals).
We want to calculate the inversion for some of the LIUQE times, so click on the button 'Normal'.

~4"

The button name changed to LIUQE and a time base corresponding to the LIUQE times was automatically created. Because the number of frames, 255, is too big we change it to 10.
The default values for the data treatment are 'ON', 'BJ' and 'smooth over 15 points'. To have a look at the difference between B. Joyes smoothing and Ch. Deschenaux's backfiltering change the default value 1 in the channel number edit box to 20 and click on 'display'.

~21"

The data treatment window is opened. The raw and the corrected signals of channel 20 are displayed in the upper graph. Zoom in by clicking with the left mouse button on the graph. Notice that the two correcting methods give almost the same results. Only where there is a rapid change of the amplitude (i.e. a big derivative, see second graph) the Ch. Deschenaux's backfiltering method is oscillating and differs from B. Joye's smoothing. Exit the data treatment window by clicking on 'exit'.

~1"

Change the data treatment method to 'ChD'. You could change the default filter frequency of 50 Hz, but let it how it is. Press the 'APPLY' button to finish the data acquisition.

~5"

After the construction of the data matrix 'framedata' a beep sounds which marks the end of the data acquisition. The 'Data' button became yellow (→ finished) and the 'Setup' button became green (→ next task). The message frame displays: "The data window generated new data! To update the setup window, click 'setup'."
The 'SHOW' and the 'save.mat' buttons of the data GUI are activated. Press the 'SHOW' button: The btomodata display window appears. Press the 'get movie' button to construct a movie of the signals.

~5''

Change now the default values of the edit boxes used to specify the number of times and the speed at which the movie will be played: Set for example 2 times and 8 frames per second. Then press the 'play movie' button to see the movie. Notice that the movie is played three times because you see also the memory loading. Quit the window with the help of the 'exit' button.
Save the data matrix (and some other important variables) by clicking on the 'save.mat' button. The save dialog box appears. Choose the directory where you want to save the data and give a name for the file (in the form: 'name' or 'name.mat').
Press the 'Setup' button.

~10''

The setup control window is opened and a default setup is automatically loaded. (Notice that the deleted channels aren't visible.)
So a beep sounds immediately and the 'Setup' button becomes yellow (→ finished) and the 'Run' button becomes green (→ next task). You could continue with the inversion.
If you want to change the setup press the 'Change' button. Notice that the controls are now enabled. With the pop-up menu under the 'Change' button you can choose the type of the grid. Change it to 'flux grid'.

~1'30''

The lines of the magnetic flux surfaces are drawn in blue and the last closed flux surface is drawn in magenta. Because the 'flux grid' isn't functional yet change the grid back to the rectangular one.

~2''

Change the number of the pixels in the radial direction to 12. The number of the pixels in the vertical direction is changed automatically and it's now 34. So there are 408 pixels. If you want to change the other parameters (r_0, z_0, w_r and w_z) you have to choose 'Part of Vessel' of the second pop-up menu which will enable the edit boxes. But don't change the parameters now.
Choose the 'Omgrid 3D' method for the calculation of the matrix (pop-up menu in the third frame). Then press 'Apply'.

~2'53"

Most of the controls are disabled and the message frame displays: "For saving click 'Save' !" Notice that the graph in the lower left corner shows how many cells are seen by a given number of chords. Click on 'Save' to store the setup data in a .mat file.
After the calculation of the T matrix a beep sounded and the 'Setup' button and the 'Run' button changed their colors to yellow and green respectively. You see the message: "The setup window generated a new grid matrix! To update the run window, click 'run'." Follow this order.

~3"

The run control window is opened. Change the algorithm in the first pop-up menu from 'Min. Fisher' to '2th Lin. Reg.'. If you want to see some results during the calculations choose 'Output during iteration' in the second pop-up menu. Change the value of the relative error (sigma) to 4%. Click on the button 'Advanced' to see some more changeable parameters.

~3"

The advanced control window is opened. Notice that the value of sigma is the same (of course!). We want to calculate the inversion with a constant smoothing factor lambda for all time samples. So press 'Lambda'. This enables the 'lambda' edit box and disables the 'chi^2' and the '# of iterations' edit boxes. Set lambda to 30. Notice that if you press 'Cancel' then all the values are set back to the default values (also the sigma in the main run control window!). Press 'OK' instead to change the parameters to the values which you have specified in the advanced run window. The advanced window is automatically closed and the message frame tells you that the changes took place.
(If you don't want that the fractions of radiation in- and outside, above and below the last closed flux surface are calculated after the inversion then press the 'Rad on' button.)
Start the inversion by clicking on 'Apply'.

~ 6'46"

A beep sounds and if you chose 'Rad on' then a window is opened which displays the radiation in- and outside, above and below the plasma. To exit this window click on 'Exit' in the menu bar. The massage frame of *btomorun* displays: "Inversion done. Bad convergence for frames: 2 3 4 5 7 8 9 10". This means that the χ^2 of the reconstruction of these frames are bigger than the specified value (in our case 1) and shows which reconstructions weren't 'successful'. But we set a constant value for λ (i.e. 30) and so the program didn't try to reach the specified value of χ^2.

The main window displays the message: "The run window generated new emission data! To update the graphics window, click 'graphics'." The 'Graphics' button is now green and the other three buttons are yellow.

You can save the results by clicking on 'Save'. The save dialog box appears and asks you where to save the results.

After you have saved the data click on 'Graphics'.

~ 7"

The btomo graphics control window appears. Notice that the shot number, the algorithm, the start and the stop time are indicated on the right side of the window. Par default the plot style is 'pseudocolor', the vessel is on and the flux is off. Click on buttons 'vessel off' and 'flux on' and change the plot style to 'labeled contour plot'.

~ 4"

Notice that the contours are labeled by whole numbers (1, 2, ...,9) and that the normalizing factor nf is displayed in the title of the axes. Click on 'next>>' to see the next five images.

~ 6"

If you click on 'movie' then a movie will be constructed and then played twice.

~ 12"

Return to the graphics by clicking for example the '<<prev' button. Notice that the movie stays stored in a matrix so if you click again the 'movie' button then the movie is played immediately. Only if you change the plot style or if you set the vessel or the flux on or off then the movie matrix will be emptied.

Print now the last five images on paper: Click on 'next>>' and make sure that you see the last frames. Change the print output to 'psc_ppb111_6' (this is a color printer) and click on 'print'.

~ 2"

A new window appears which shows how the graphics will be printed. Notice that there are some informations which are printed with the images.

~ 10"

The print output window disappears and you have only to wait until the printer will have finished his work.

You can save the results also by pressing the 'Save' button in the main window. You will be asked if you want to save the data in the tree or on your disk (same as if you click on the 'Save' button in the btomorun window). Notice that if you try to save to the tree and if there are already some data you will be asked if you want to replace the existing data in the tree.

We are at the end of our session. To quit the whole program click twice on 'EXIT'.

5. A tool for analyzing the results: *btomoview (not finished yet)*

Btomoview is an analyzing tool which is included in the Btomo software package, but it's totally independent from the other programs. The only thing to respect is that *btomoview* can only open the results in the tree and *.mat files which were created in a similar way as by *btomorun* (namely with the same code 'ji99 btrs'[3] and the same names for the variables).
Btomoview allows you to display the emission results with ten different plot styles and about twenty different colormaps. The page setup is automated so that you have only to specify the number of images per page and a optimized distribution of the images on the page is computed. You can also choose which informations appears with the plots on the page (for example the shot number, the method of reconstruction and his parameters, the number of frames, ...). So *btomoview* serves to analyze manually the bolometry results and to print them on paper or in files. But the advantages of this program compared with *btomographics* aren't only cosmetics ones. Actually it can also show the percentage of radiation of different domains of the vessel (in- and outside, above and below the plasma) and you can compute a singular value decomposition SVD (not finished yet). Of course you can also play a movie as with *btomographics* (there are even some more options for the movie).
Btomoview is started either by clicking the **View** button of *btomo* or by entering "btomoview" in the Matlab command window. You will be automatically asked to load a *.mat file with saved data from *btomorun*. After you have done that all frames will be displayed in a window corresponding to a A4 page.

5.1 The structure of the *btomoview* GUI

The *btomoview* GUI is essentially divided into three parts:
1) On the left side there are the parameters which were used by the *btomo* programs *btomodata, btomosetup* and *btomorun*.
2) In the center there is a free place for the graphic window (orientation 'Portrait' or 'Landscape').
3) On the right side you can set the options for the output in the graphic window.

The symmetry of the GUI is disturbed by the message window and the GUI control buttons which are either on the right side or in the top depending on the orientation of the graphic window.

[3] Ji are my initials, 99 is the year, btrs means *btomorun* save routine.

5.1.1 The GUI control buttons:

Load: Opens the load dialog box where you can choose a *.mat file with saved inversion data. Plots automatically all frames on one page and displays the parameters used for the inversion at the left side of the *btomoview* GUI.

Tree: Opens a dialog box which asks you to enter the number of the shot you want to see. If there are some saved results, then they will be presented on the screen (not finished yet).

Apply: Plots the graphs in the style specified by the options on the right side of the GUI. You have to press this button to apply the changes of almost all options.

Print: Prints the graphic window to the device and the number of times specified by the print options.

Exit: After the first click you are asked if you really want to quit and with the second click the *btomoview* windows are closed. (You can continue your work after the first click by using any other control).

5.1.1 The graphic, text and print options:

1) The graphic options:

vessel on/vessel off: Shows or hides the vessel.

flux off/flux on: Hides or shows the magnetic flux surfaces.

Graphics/Movie: Toggles between the graphic controls and the movie controls (both marked with a *).

Plot type pop-up menu: You can choose one of ten plot styles.

Colormap pop-up menu: Here you can choose the colormap matrix used by Matlab to color the graphs.

Paper orientation pop-up menu*: You can choose between 'Portrait' and 'Landscape'. The graphic window will turn to the new position.

# of axes*: Specifies the number of frames shown in the graphic window. The page setup is executed automatically.

frames/s*: Speed of the movie in frames per second.

Width of screen [cm]*: Specifies the size of the movie screen. The bigger the screen is the bigger is the movie matrix and the slower is the building of the movie. (i.e. time of building the movie is a function of the screen size and the number of frames)).

Start at frame*: Specifies the frame at which the movie begins.

Stop at frame*: Specifies the frame at which the movie stops.

Start: Causes the graphic window to show the first page (the first frames).

<<: Causes the graphic window to show the previous page.

<: The displayed emission images are shifted one time step back.

>: The displayed emission images are shifted one time step forward.

>>: Causes the graphic window to show the next page.

End: Causes the graphic window to show the last page.

2) The text options:

On the one hand you can decide if the values of λ and χ^2 are written in the title strings of every axes and on the other hand you can set the size and the weight of the font of the page title string and specify what you want to write to the title. The default choice writes some important data to the title as the date, the shotnumber, the used calculation methods and λ or χ^2 (the one which is constant). If the 'Data', 'Setup' or 'Run' text are chosen then all the parameters of *btomodata*, *btomosetup* or *btomorun* will appear in the title. The user can also write himself in the title edit box or eliminate the title to have more place for the graphs.

3) The print options:

Here you can choose the print device (file or printer) and the number of copies.

5.1.2 Some more options:

If you click with the right mouse button on the graphic window (but outside the axes) then the following menu appears:

'Grid on/off'
'Camera position'
'Shading'
'Brightening'
'Hidden on/off'

Grid on/off: The grid is shown or hidden.

Camera position: A dialog box is opened where the position of the 'camera' can be specified (in XYZ coordinates).

Shading: A dialog box is opened where the type of shading can be chosen. There are three types: 'Flat' fills every pixel with a constant color, 'faceted' is the same except that the grid lines are black and 'interpolated' varies the color across the pixel. To change, type the number of the new shading in the dialog box. (Default is 1, i.e. 'interpolated').

Brightening: A dialog box is opened where you can set a value between -0.99 (dark) and +0.99 (bright) to change the brightening.

Hidden on/off: If hidden is on then the lines in the back of a mesh are hidden by those in front. This is useful only for some plot styles as for example the mesh plot.

6. Conclusion

Btomo is a package of codes which sets a friendly GUI environment with all tools necessary to analyze manually the bolometric data. It allows any newcomer to easily get some results. Nevertheless it allows an expert to change any important parameter. This program should be applied every time when the TCV bolo data or CT reconstruction are supposed to be published.

The following list says what tasks have to be accomplished in the future:

1. Finish the program *btomoview:*
   - movie
   - include SVD (single value decomposition)
   - include a consistency check
   - reading from the tree

2. Supplementary features for *btomo*:
   - searching automatically if there are any data in the tree, loading them and changing all parameters in *btomodata, btomosetup* and *btomorun* according to the parameters stored in the tree.
   - merge new data with the data in the tree.
   - create a new node in the tree to save a matrix with all parameters. (Each parameter will have a defined place in this matrix.)

3. Check if the units of the radiation are right. Check the units of the emission matrix Xinv (i.e. the units in the graphs) and of the radiation in- and outside, above and below the plasma.

7. Bibliographie

1. 'Bolometry on the TCV Tokamak'. J. Mlynar, I. Furno, B. Joye, A. Refke. CRPP Lausanne, 1999. INT 196/99

2. 'X-Ray tomography on the TCV tokamak'. M. Anton, H. Weisen, M.J. Dutch, W. von der Linden, F. Buhlmann, R. Chavan, B. Marletaz, P. Marmillod and P. Paris. Plasma Phys. Control. Fusion 38 (1849-1878), UK, 1996.

3. 'The TCVXTI software package in matlab'. M. Anton, M.J. Dutch, W. von der Linden, J.-M. Moret, Y. Peysson, S. Sagbo. CRPP Lausanne, February 1996.

4. 'Extension of the TCVXTI software package'. S. Kalvin, S. Zoletnik. CAT-SCIENCE Bt., 29 march, 1999.

Appendix A:

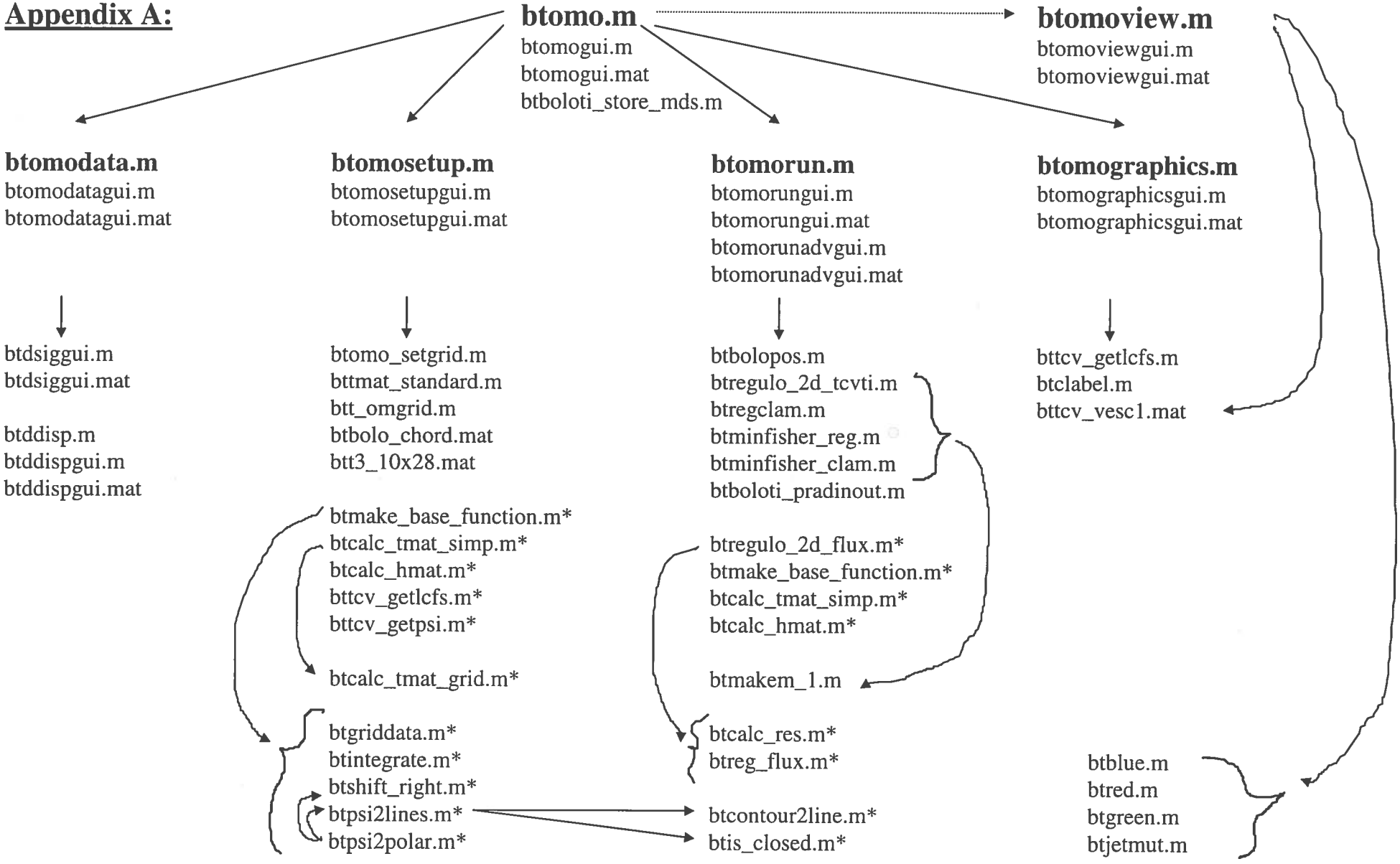

btomo.m
btomogui.m
btomogui.mat
btboloti_store_mds.m
btomoview.m
btomoviewgui.m
btomoviewgui.mat
btomodata.m
btomodatagui.m
btomodatagui.mat
btomosetup.m
btomosetupgui.m
btomosetupgui.mat
btomorun.m
btomorungui.m
btomorungui.mat
btomorunadvgui.m
btomorunadvgui.mat
btomographics.m
btomographicsgui.m
btomographicsgui.mat
btdsiggui.m
btdsiggui.mat
btddisp.m
btddispgui.m
btddispgui.mat
btomo_setgrid.m
bttmat_standard.m
btt_omgrid.m
btbolo_chord.mat
btt3_10x28.mat
btbolopos.m
btregulo_2d_tcvti.m
btregclam.m
btminfisher_reg.m
btminfisher_clam.m
btboloti_pradinout.m
bttcv_getlcfs.m
btclabel.m
bttcv_vesc1.mat
btmake_base_function.m*
btcalc_tmat_simp.m*
btcalc_hmat.m*
bttcv_getlcfs.m*
bttcv_getpsi.m*
btcalc_tmat_grid.m*
btregulo_2d_flux.m*
btmake_base_function.m*
btcalc_tmat_simp.m*
btcalc_hmat.m*
btmakem_1.m
btgriddata.m*
btintegrate.m*
btshift_right.m*
btpsi2lines.m*
btpsi2polar.m*
btcalc_res.m*
btreg_flux.m*
btcontour2line.m*
btis_closed.m*
btblue.m
btred.m
btgreen.m
btjetmut.m

Figure 1: Btomo

Figure 2: btomodata

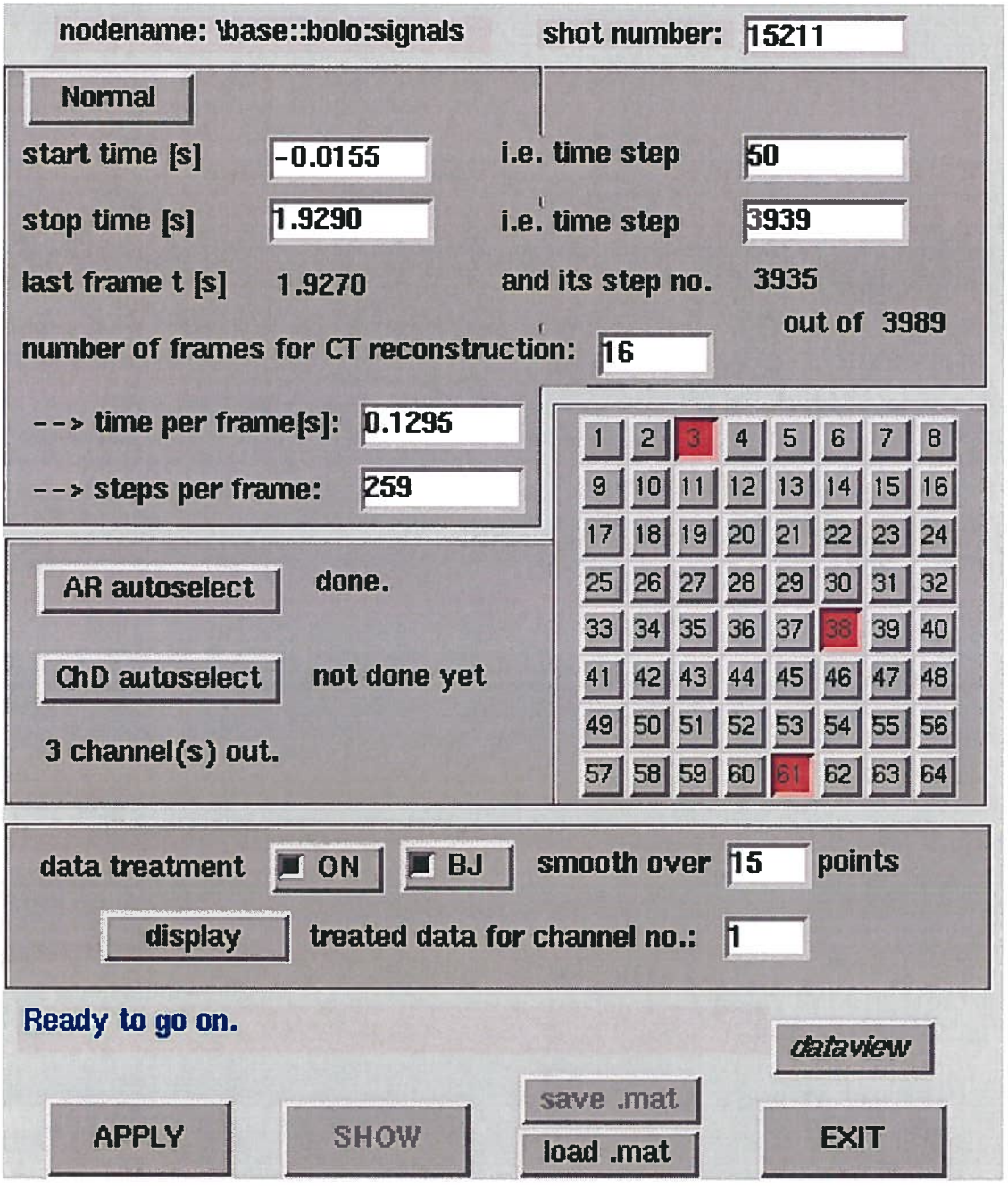


Figure 3a: btomodata "display"

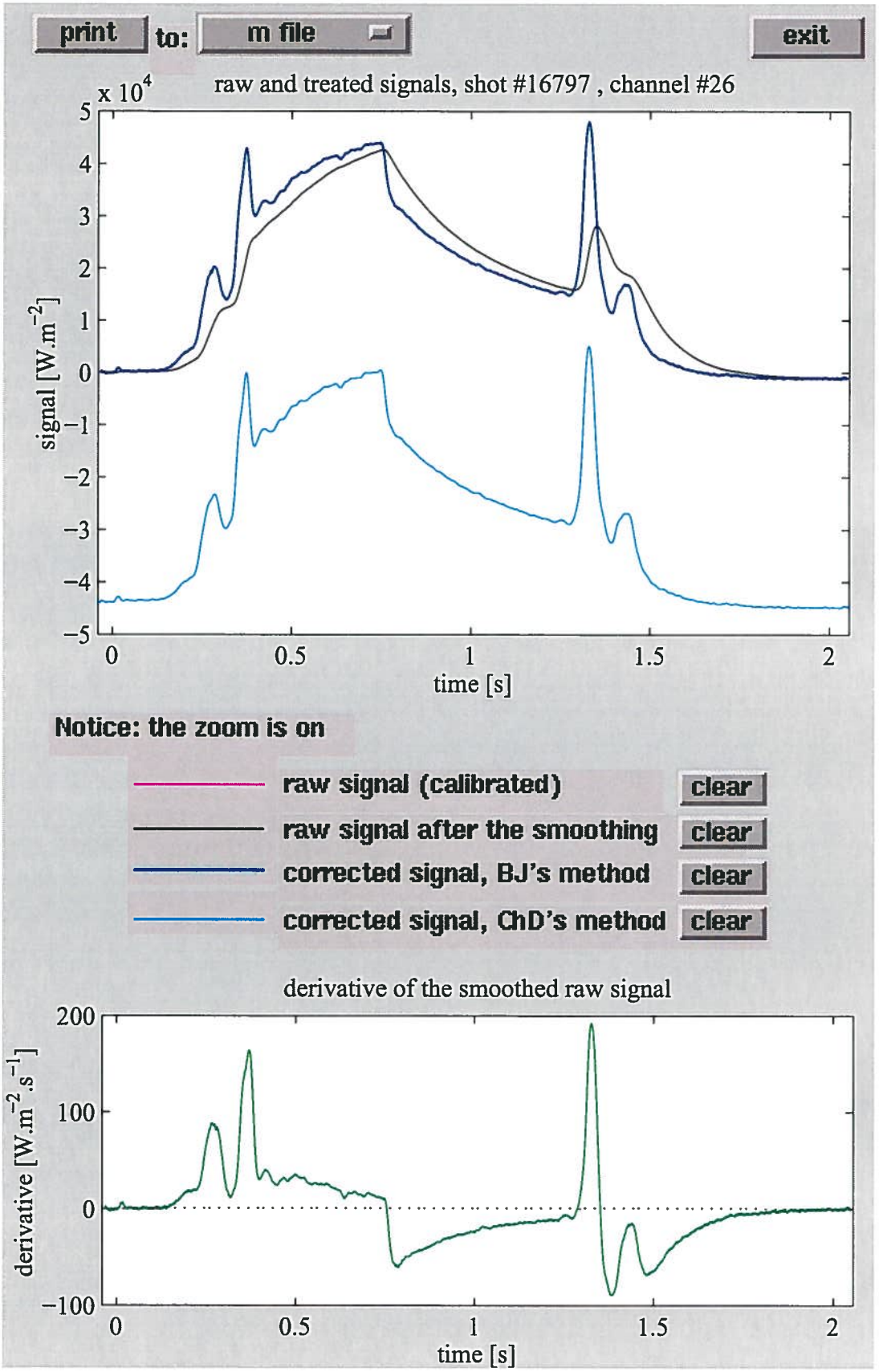


Figure 36: btomodata "show"

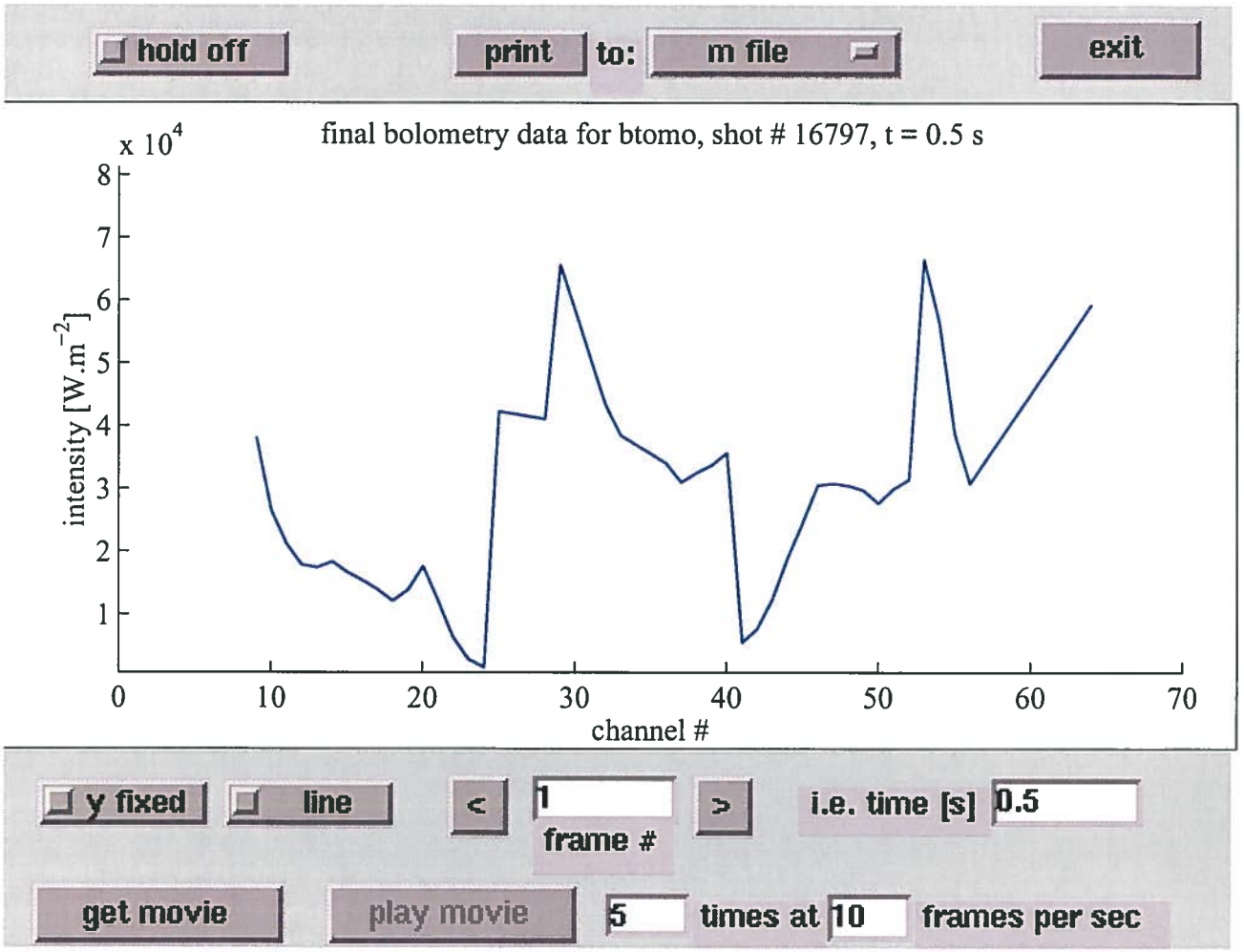
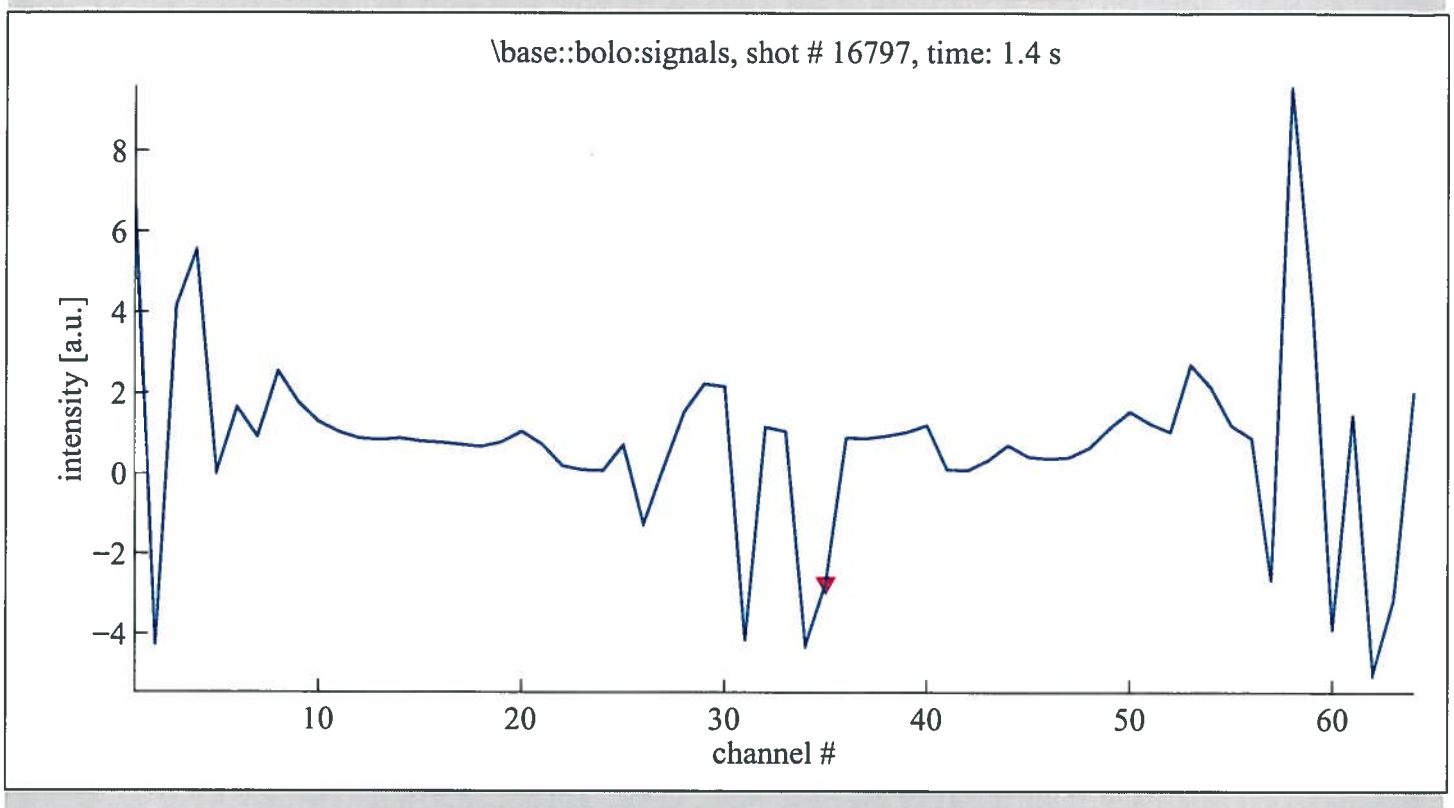


Figure 4: dataview

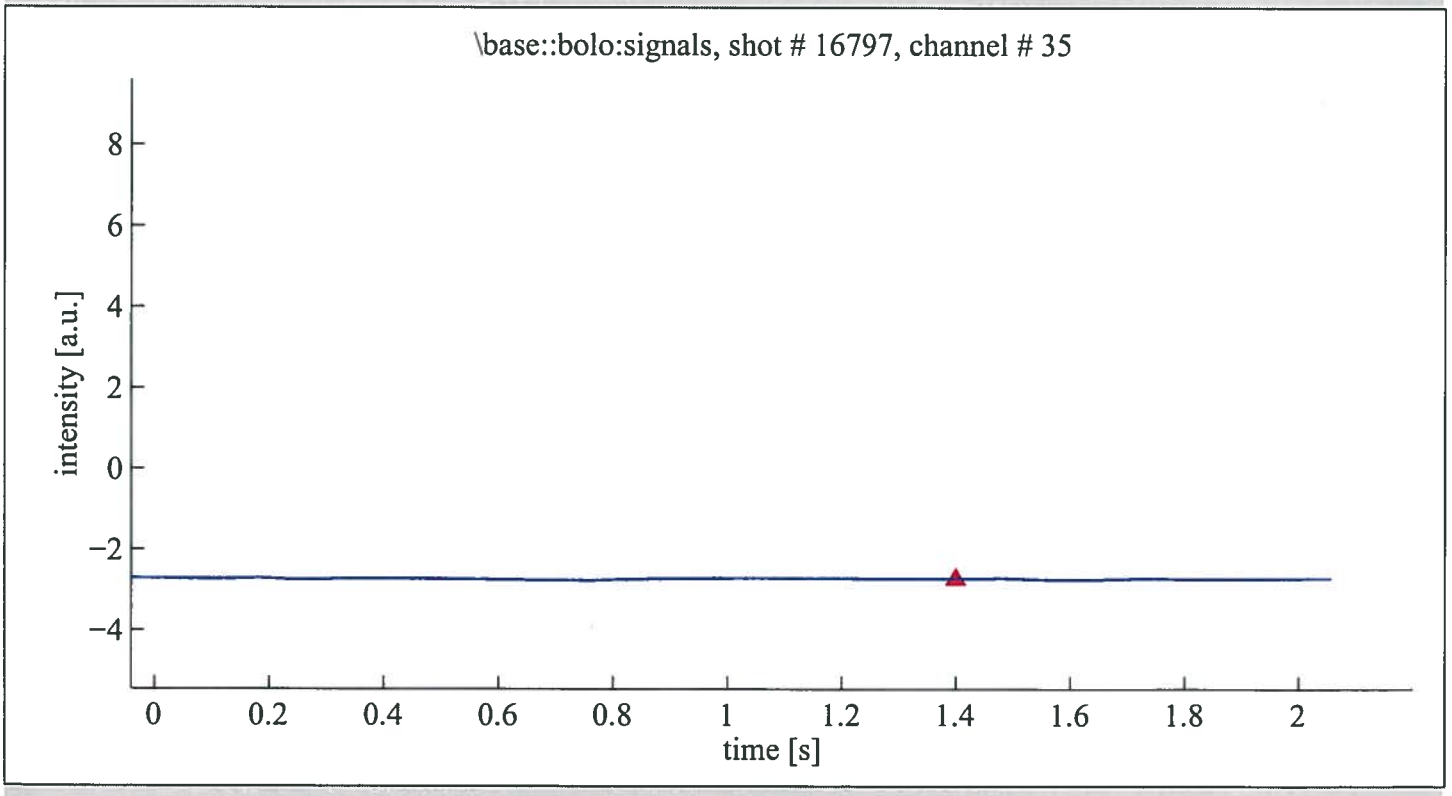


y fixed | line | << | < | 1.4 time [s] | > | >> | i.e. step # 2881 out of 4192 time steps

delete chn | movie

y = -2.72 Ready to go on.

hold off | pointer



y fixed | line | << | < | 35 channel | > | >> | out of 64 channels

save *.mat

load *.mat

PRINT | to: ps file | EXIT

Figure 5a: btomosetup

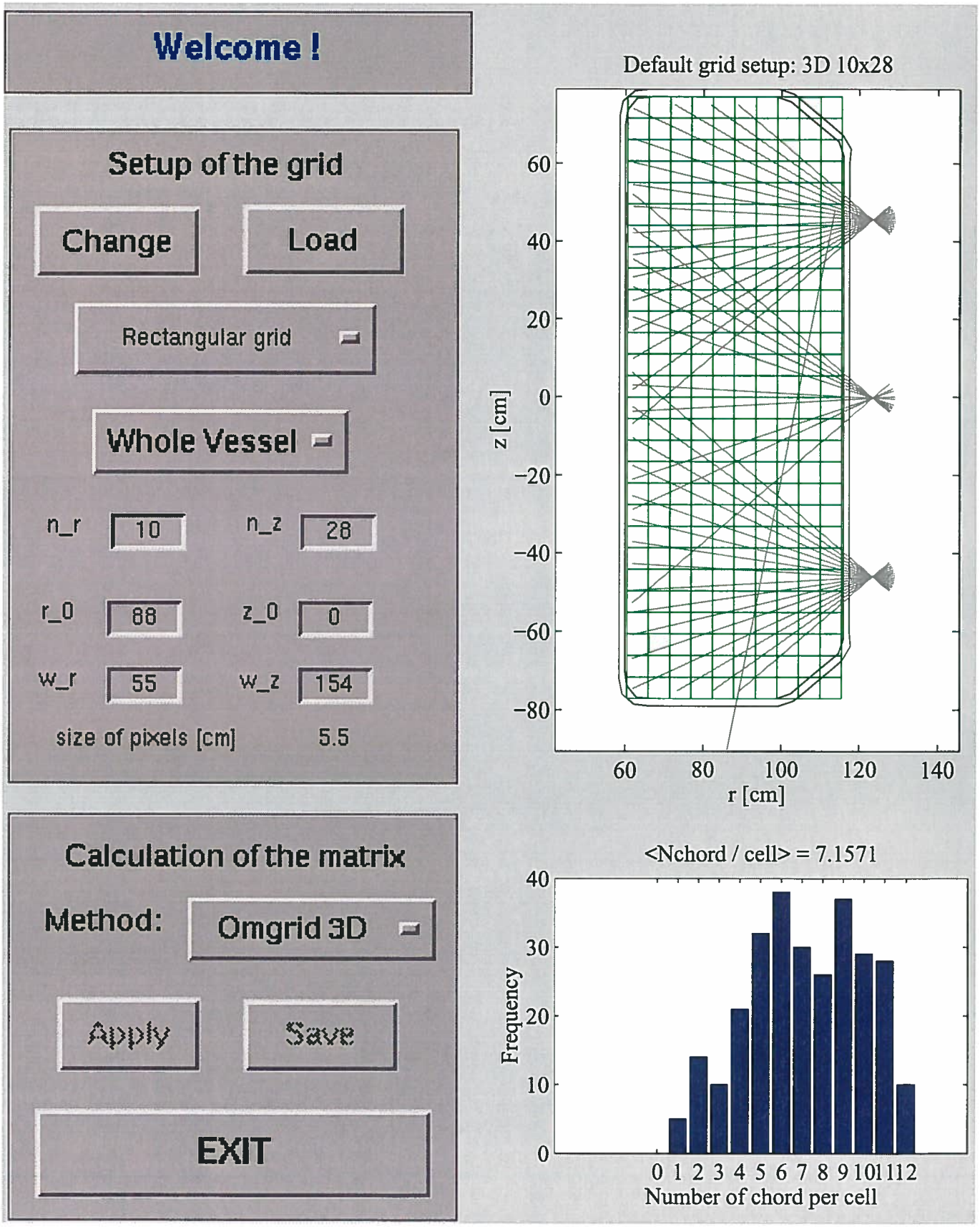


Figure 56: btomoretup

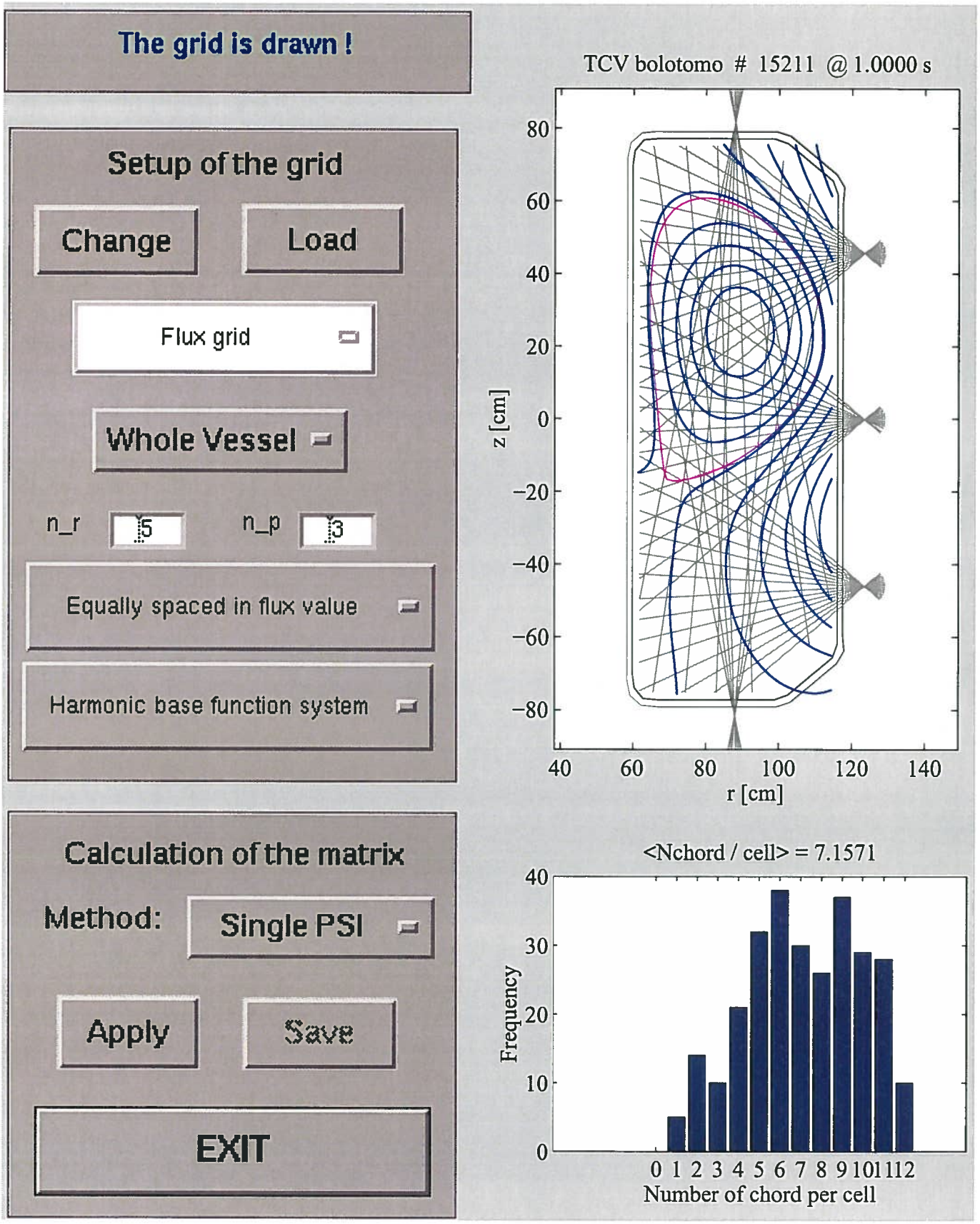


Figure 6: 6tomerun

Figure 7: 6tomorun "advanced"

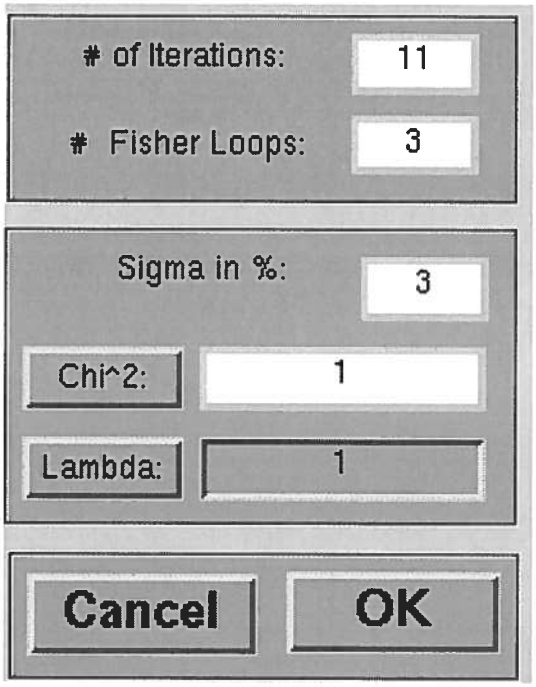


Figure 8: Stemorun "radiation"

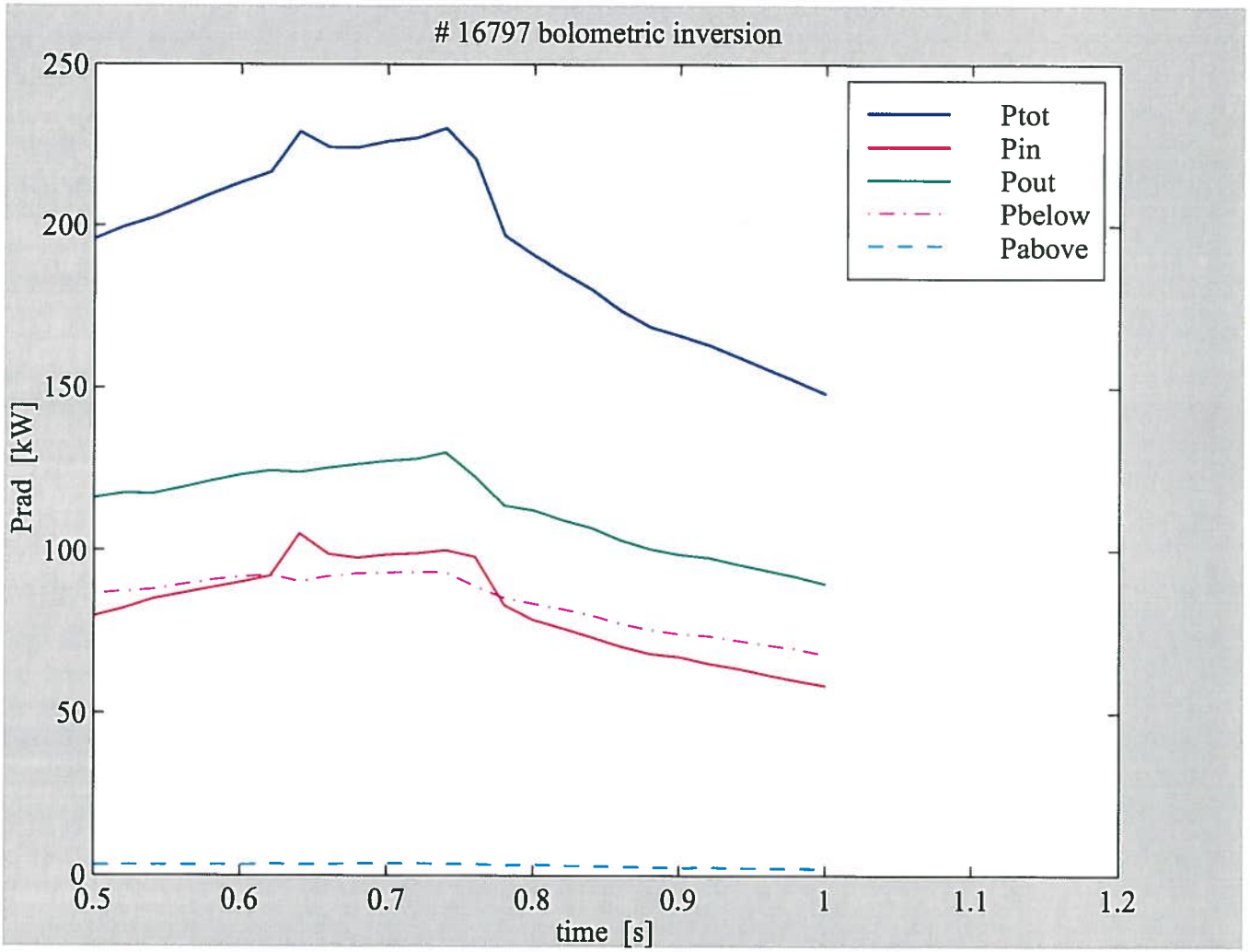


Figure 9: btomographics

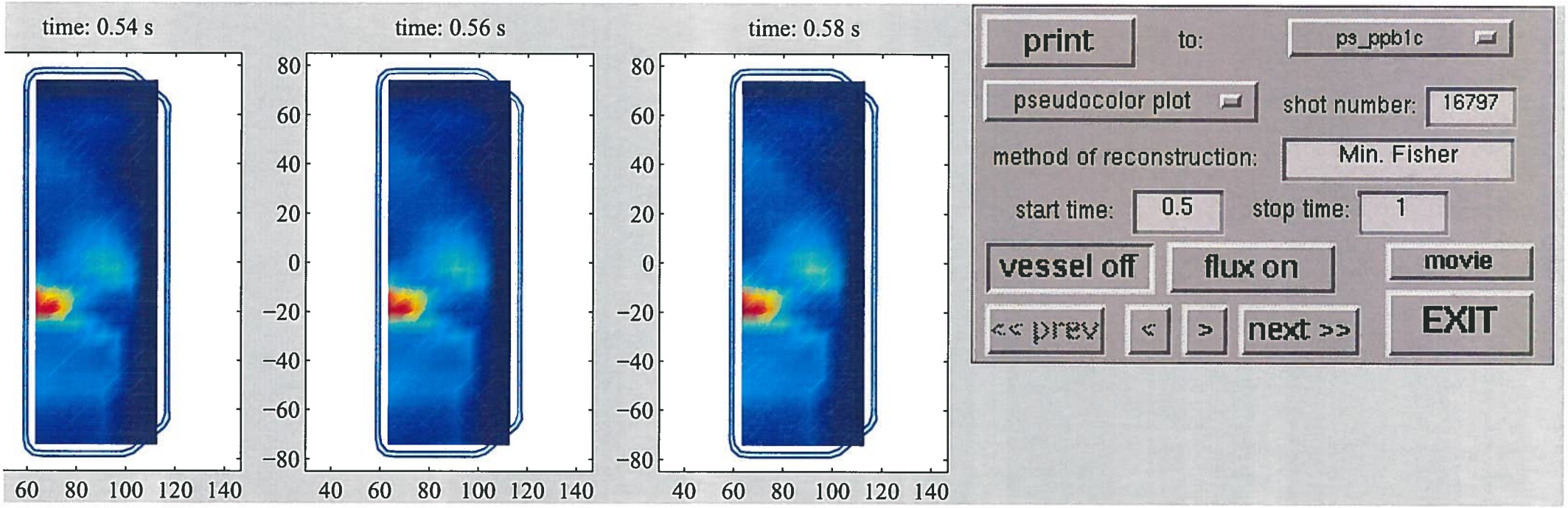
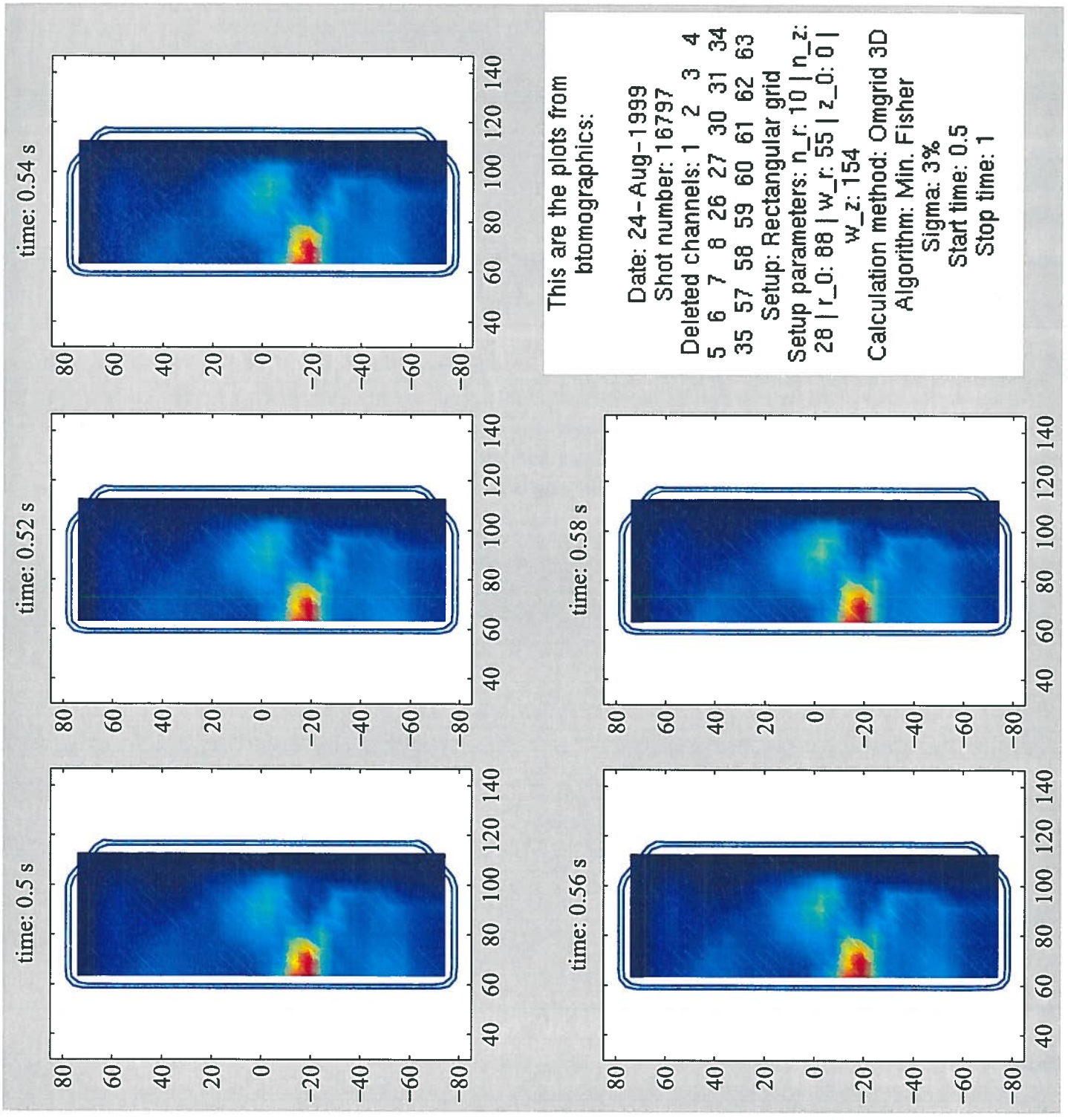
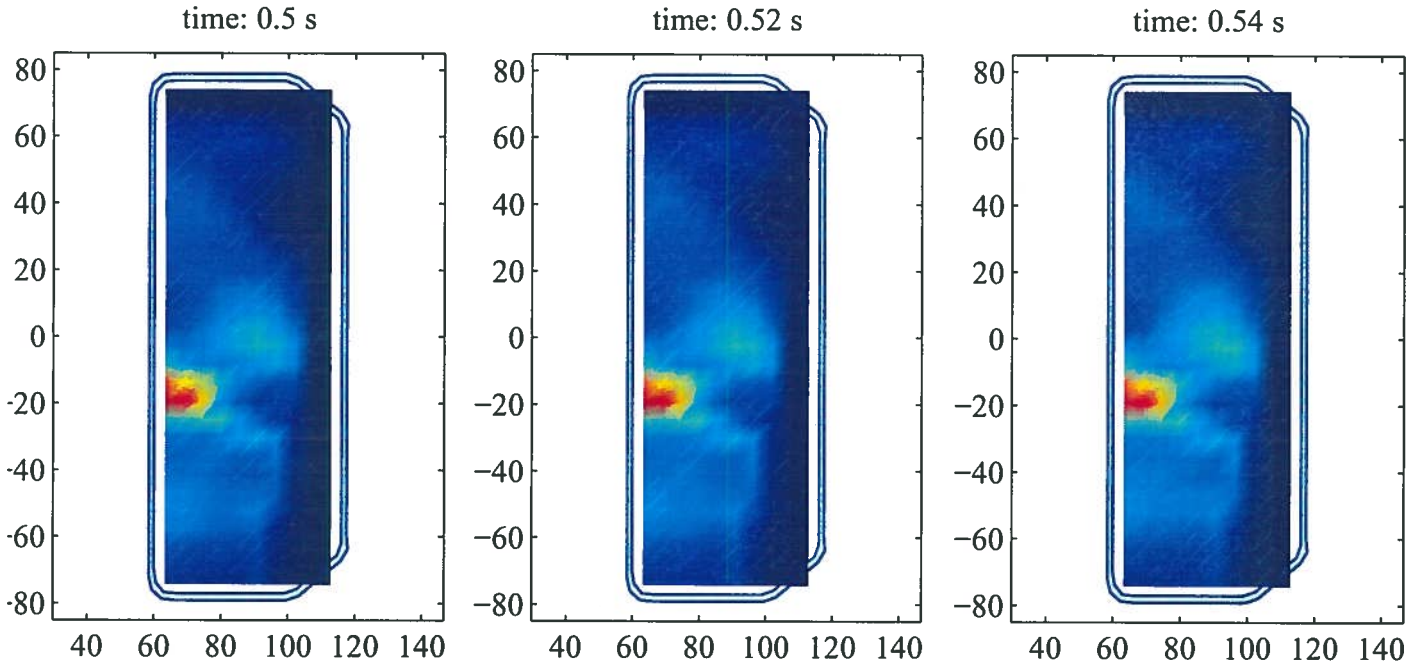
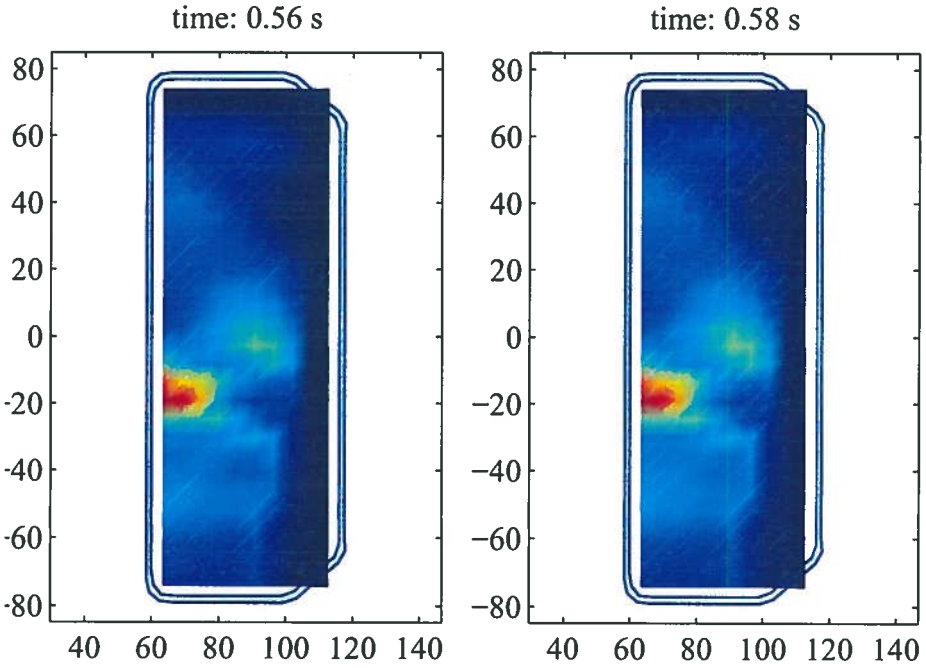


Figure 70: btomographics "print" : page setup







This are the plots from btomographics:

Date: 24-Aug-1999
Shot number: 16797
Deleted channels: 1 2 3 4 5 6 7 8 26 27 30 31 34 35 57 58 59 60 61 62 63
Setup: Rectangular grid
Setup parameters: n_r: 10 | n_z: 28 | r_0: 88 | w_r: 55 | z_0: 0 | w_z: 154
Calculation method: Omgrid 3D
Algorithm: Min. Fisher
Sigma: 3%
Start time: 0.5
Stop time: 1

Figure 77: Btomographic "print"; printed page