PROCESSING THE DATA OBTAINED WITH THE AID OF FFOREST - A HIGH-RESOLUTION FIBER-FEED SPECTROGRAPH

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Tools

To work you will need the **DECH software package (http://www.gazinur.com/setup-xp.zip)** and any file manager, for example,

Total Commander **(https://www.ghisler.com/download.htm)** or

Far Manager **(https://www.farmanager.com/download.php?l=ru).**

Both programs are shareware.

DECH Installation

DECH generally works fine under **Windows emulators** in the Linux and **Mac OS ,** but **Windows** is still preferable.

After unpacking the archive with the installation set of files (**setup-xp.zip**), you need to run **setup.exe**

If you are updating **DECH** , i.e. the package was already installed earlier, you must first uninstall the old version and then run **setup.exe** once again. Follow the program's instructions.

It is necessary to add the name of the directory where the DECH package is installed to **the PATH** environment variable . How to do this (in **Windows**):

Open **Search** and enter **env** . In the new window, select "**Edit environment variables for your account** ":

Select the button " **Environment variables…** ".

In the " **System variables** " section (lower half of the window), find the " **Path** " line in the first column and click " **Edit** ". The " **Edit environment variables** " window will appear.

Add the name of the directory where the **DECH package is installed** , for example **C:\Program Files(x 86)\Dech**

After Windows restart **the DECH** package programs are available for launching from the command line from any directory of the file system.

Data preparation

The obtained spectra should be unpacked so that the spectra obtained during one observing night, in the same spectrograph configuration, are placed in separate catalogs. Below we will consider the processing of spectra of one night.

Creating superbias

First, move all bias images to a separate directory with the command

mv2 dirs OBJECT bias *.fts

Before creating the average, it is recommended to make sure that all images are approximately identical in the signal level. Let's run the following command:

Crosscut *.fts x txt

The **txt** directory will be created **with** text files, each of which is one row (or column, if you specify **y** instead of **x** in the **crosscut** parameters**)** of the corresponding image. Move to the **txt** directory and execute the command

Dech-fits *.txt

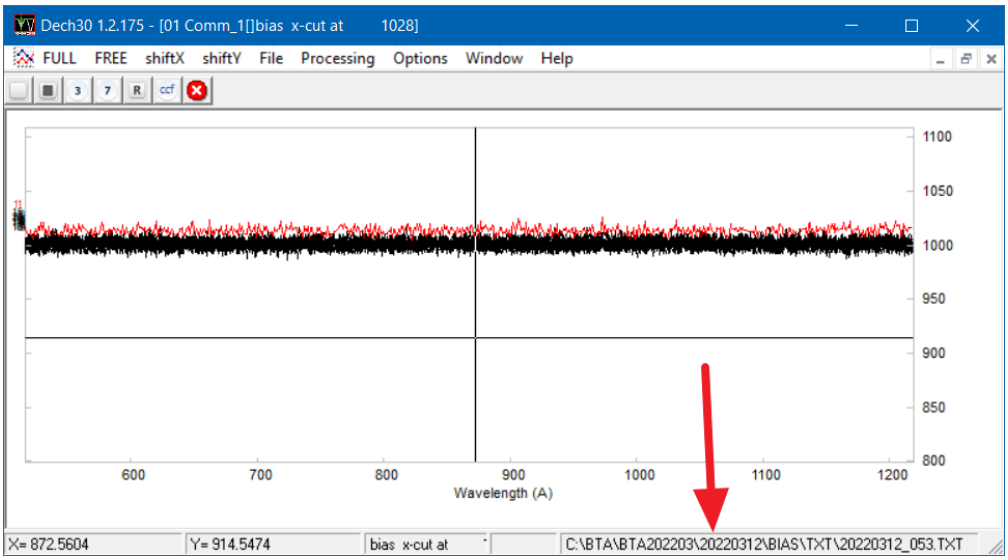


Figure 1Bias image cross-sections

In the white window of the **Dech-fits** program, you can see (Fig. 1) that one of the images (namely 20220312_053) has a slightly different counts comparing to other images. It may be useful to remove this image before averaging with the **Zeroc command.** You can remove the "bad" image from consideration directly from the "white" window of the **dech-fits** program. To do this, activate (with the left mouse button or by selecting, using the "up" and "down" arrow keys) the data-set corresponding to the "bad" image (“active data-set is of red color – Fig. 1)”, then click the right mouse button. In the appeared menu choose the option **“Delete Active Dataset & Mark Image as Bad”**. The **BAD** directory will be created in the **BIAS** directory, into which the images (along with the text files) marked by us as “bad” will be moved. It is recommended to do such pre-selection before any averaging of images. For example, in a stage of creation of a “superflat “.

Now we go back to the BIAS directory and create a cleaned averaged superbias image – the **Zero .fits** file running the command **Zeroc *.fts 3**

So, the **zeroc** command created a superbias file **Zero.fits** . Move this file to one level higher in the directory tree where all other images are stored.

Now we subtract a **superbias** from all other images - the **Sub program** subtracts **Zero.fits** from all ***.fts** images in the current directory:

Sub *.fts

New fits files with the ***sub*** suffix in the name are created. The original files can be deleted along with the **superbias** – there is no need in them anymore:

Del *.fts

Del Zero.fits

Trimming the edges

In the current configuration of the spectrograph (while the main optical camera is assembling, a temporary one with limited capabilities is used), a significant portion of the images is not informative:

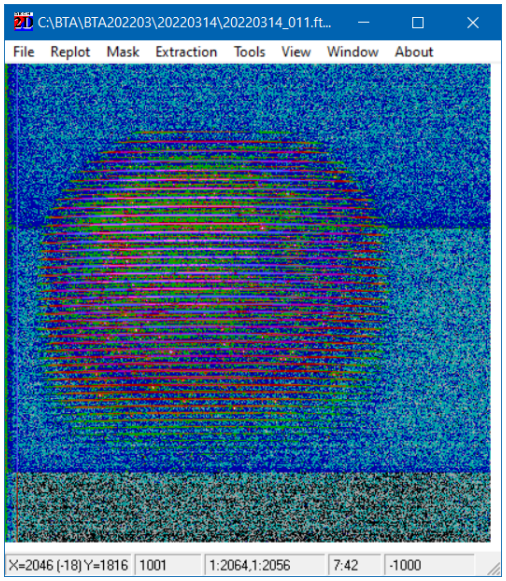


*Figure 2One of the spectral images. Shown in the fivefold compression (**Window/Set Step** for both coordinates is set to 5 (see Figure 7). A large non-informtive space around the spectrum is visible.*

Therefore, we crop the non-informative part of the image:

trim 124 1633 266 1790 *.fits

In the **trim** command the given above coordinates x1 x2 y1 y2 are actual as for May 2022. The original images will be renamed to files with the ***.old** extension. You can delete them (for example, using the **del *.old** command).

Result:

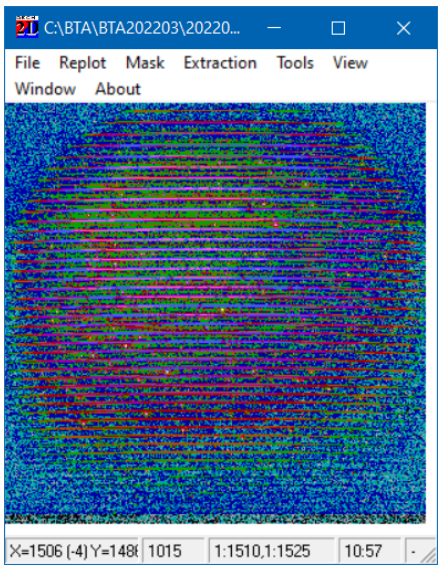


Figure 3Image with uninformative edges cropped.

Creating an averaged flat field (superflat)

We move the flat field images to a separate directory:

Mv2dirs OBJECT flat *.fits

And we go to the **FLAT** directory. We check that all images have a similar level of the counts:

crosscut *.fits y txt

and go to the **TXT** directory. Run the command:

dech-fits * .txt

and we see that the counts level is almost identical in all the flat-field images:

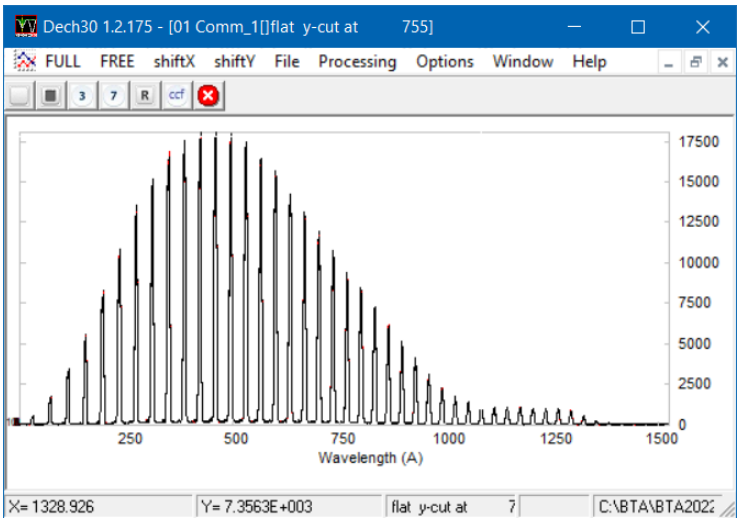


Figure 4Image section across dispersion. Each peak corresponds to one spectral order of the echelle spectrum.

If this is not the case, the "outgoing" images should be removed from consideration as it was shown for the *bias* images. Return to the directory with the **FLAT** images and execute the command:

zeroc *.fits 3 FF.fits

FF.fits file to the main directory with images (i.e. one level higher) and proceed to the stage of extracting spectra (vectors) from images.

EXTRACTION

Creating a mask

A mask is either a table or a set of approximating functions (usually low-order polynomials) that determine the position and curvature of echelle orders in a spectral image. In the BTA fiber-optic spectrograph, each order is split into two sub-orders. Each sub-order can receive a signal from different light sources. For example, the first sub-order records the spectrum of a star, and the second - the spectrum of a wavelength calibration lamp (usually with ThAr lines - hereinafter **ThAr**).

Our task is to determine the position of spectral orders. For this we will use the flat field spectrum **FF.fits**, since only one suborder is visible in it, which simplifies the automation of the process.

We execute the command **Dech95 ff.fits** :

Figure 5Image of a flat field in the black and white mode.

Spectral orders should be oriented horizontally. If not, check the image loading options (File /Load Image). It should be as shown in the picture:

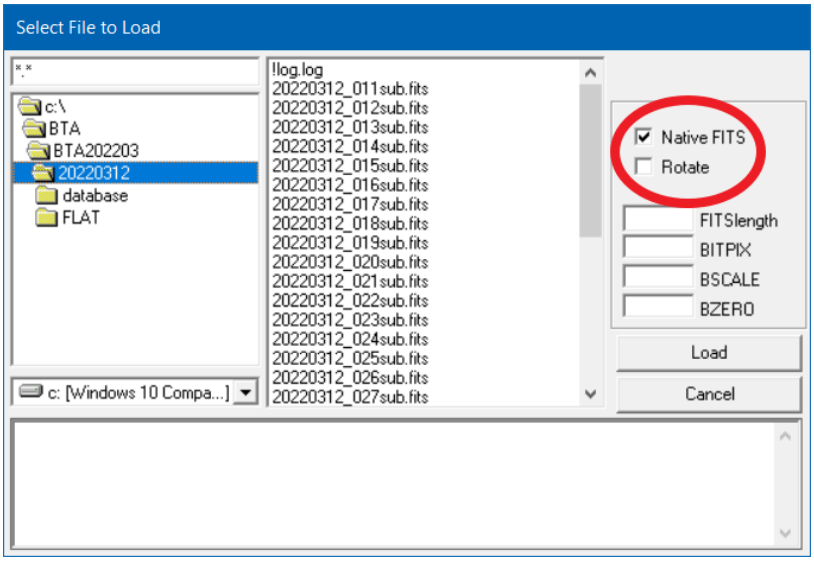


Figure 6Loading parameters for BTA high-resolution fiber optic spectrograph images.

Make sure the **Native FITS** parameter is enabled and the **Rotate** parameter is disabled.

Other useful visualization related parameters :

1. **Window / Set Step** – allows you to zoom-in or zoom-out the loaded image. It is recommended to set the horizontal scale so that the entire order is visible without the need in scrolling the image. The vertical scale can be left as is. For a Full-HD monitor and a CCD spectrograph matrix as of May 2022, the parameters are as follows:

Figure 7Image visualization parameters.

2. The false-color intensity scale can be linear or logarithmic. A black and white linear scale with 256 shades of gray is commonly used

3. :

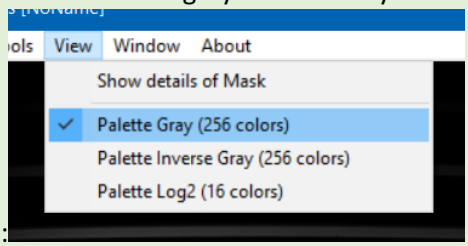


Figure 8Selecting a visualization method (palette).

To get more detail on a particular fragment of the image, select this fragment using the mouse: place the mouse cursor in the upper left corner of the desired fragment, press the left mouse button and, holding it down, move the mouse down and to the right. In this way, construct a rectangle framing the desired fragment and release the mouse button. Click the mouse on the inscription **Replot** .

To initiate the mask creation procedure, select **Mask/Create**. Then appears a small panel with additional parameters for constructing the mask (all parameters in the figure are optimal for the FFOREST spectrograph configuration as of May 2022):

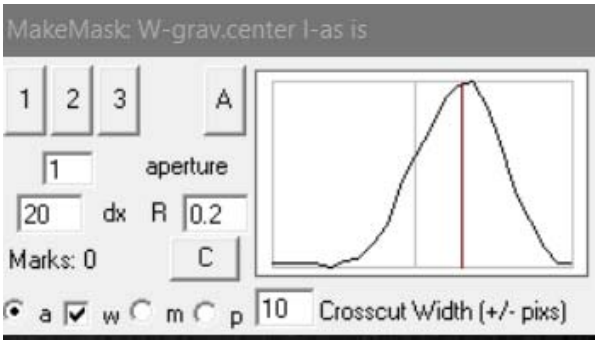


Figure 9Mask construction mode parameters.

Panel parameters. The curve on the right side of the panel is a cross-section of the image in the direction perpendicular to the direction of the main dispersion (i.e. vertically) with the center at the mouse cursor location. The width of the cross-section is determined by the **Crosscut Width** parameter – in the Fig. 9 it is 10 pixels. Thus the length of the entire crosscut is 21 pixels – the central point plus 10 pixels down and up from the cursor position. This parameter is very important for automatic search of the spectral orders. It should be estimated in such a way that, firstly, the width of the crosscut allows us to see any order across its entire width, i.e. the parameter should not be too small. Secondly, the parameter cannot be too large: in any part of the image, including areas, where the spectral orders are located most closely one to

one - no more than one order should be visible. For example, in the figure 10, the **Crosscut Width** parameter is too small, because the order is not fully visible across the width:

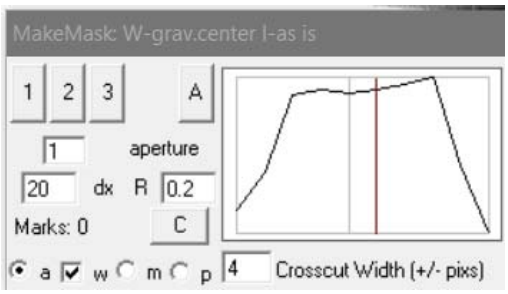


*Figure 10Example of a too short vertical **crosscut Width 4**)*

In the n Figure 11, on the contrary, this parameter is too large – more than one spectral order e is visible in the section:

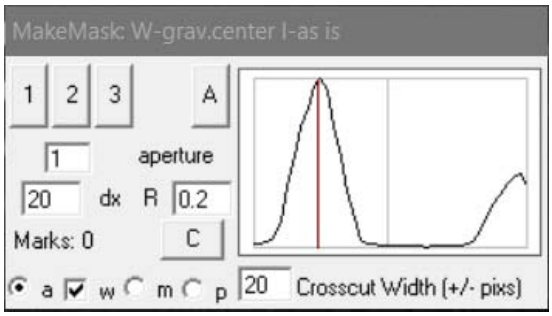


*Figure 11Example of a too long vertical cut (**Crosscut Width 20**)*

At the bottom of the panel there is a zone for choosing the mask construction mode: **a** – semi-automatic (the mask is built manually for the upper 2 orders – then the program will find the rest of orders automatically), **m** – completely manual mask construction, **p** – work with polarymetric spectrum. The parameter **w** in the Figure 11 is "on". This means that in automatic mode the order center is determined not by the maximum signal level, but by the means of the gravitational center of the crosscut. The gravitational center is shown by the red line on the panel. The gray line corresponds to the cursor position.

C button serves to delete existing marks, the number of which is shown by the **Marks** parameter. In the figure 11 it is equal to 0.

dx parameter (in the figure 11 it is equal to 20) determines the distance between adjacent marks for the automatic determination of the orders position.

The parameter **R** from the word *ratio* (in the Figure 11 it is equal to 0.2, i.e. 20%) defines the order boundaries along the dispersion. First, the program finds the order position in the central part of the image, where the signal level is close to the maximum. Taking this level as 100%, the program moves along the order to the left and to the right, placing reference points with a step of **dx** (see the previous point). The program also evaluates the signal level at each mark position. If the signal level is below the **R** criterion (in our case, this is 20% of the maximum), the search for the order terminates.

aperture parameter (in the Figure 11 it is equal to 1) determines the integration boundaries (width) of the order during extraction. It does not matter in the mask construction mode.

Buttons **1, 2, 3** are the degree of the approximating polynomial. Accordingly, linear, parabolic and hyperbolic approximations for available marks. These buttons serves to construct a curve describing the shape (position) of the spectral order in manual and semi-automatic mode.

Button **A.** Automatic determination of the order position. For the FFOREST spectrograph we have to use this button.

So, click on the button **A** :

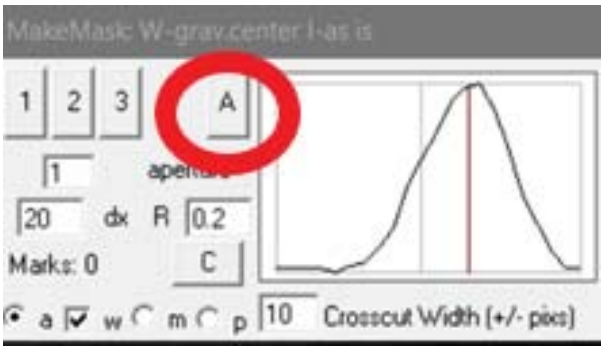


*Figure 12Example of an optimal vertical crosscut (**Crosscut Width =10**). The outlined button **A** serves for run the automatic procedure of the mask creation.*

In the new window that appears, we see a cut of the loaded image. The cut goes exactly over the image center (see the **Ycut parameter**). Below is shown an enlarged fragment of this cut. The size of the shown fragment is 10% of the entire curve (the cut). Click on the **Zoom** parameter to change the size of the fragment. There is a slider in the bottom of the window that serves to view any fragment of the curve (the cut). So, the cut is made exactly in the center of the image (in our case, this is **the 795th** column of the image). However, if necessary, one can make a cut through any other column - just click on the blue **Ycut** title seen in the upper part of the window.

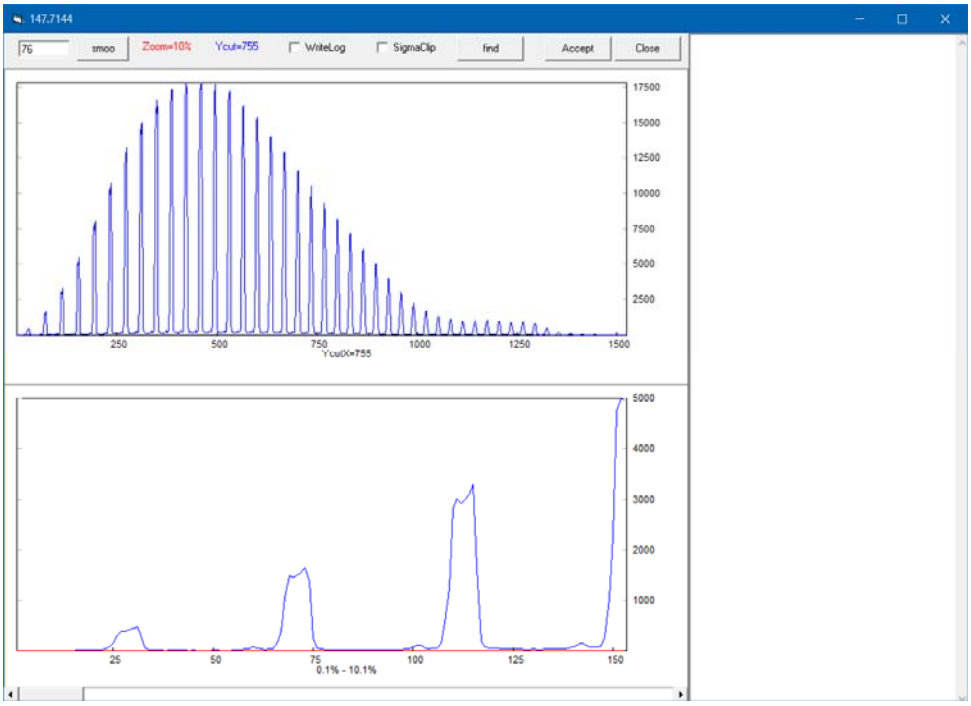


Figure 13Initial window of the automatic mask construction procedure

Now click on the **find** button. The program will search for all isolated peaks with an intensity above the zero. However, if the spectrum is in the negative range of intensities and/or somesing does wrong, one can try the Alternative Method:

Alternative method. Press the **Smoo** button. This is 76-point smoothing (the parameter **76** can be changed directly in the text box). The smoothed curve is shown in red:

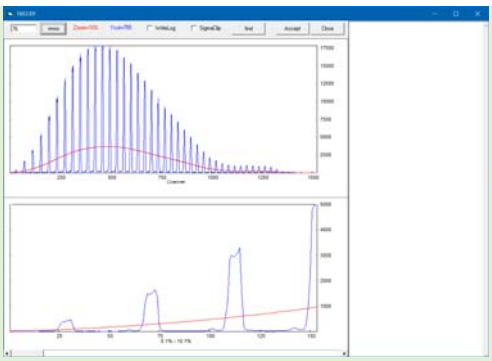


Figure 14Vertical section of the image and its smoothed curve. The search for orders will be based on the part of the blue curve which is above the smoothed (red) line.

The algorithm for finding the spectral orders is as follows: the program finds all the isolated areas of the original spectrum (blue curve) that are above the smoothed (red) one, then program determines *the center of gravity* in each area. The center of gravity is considered as the center of the spectral order.

So, to search for orders, click the mouse on **the find** button. As a result, on the left we will get a table-list of the found orders, where the following information is given: **N** – the order number, **gC** – the coordinate of the order center (the gravity center), **EW** is the order intensity in the arbitrary units, **width** is the order width in pixels, **dx** is the distance between adjacent orders. However, the upper panel in the Fig. 15 shows many vertical red lines in the right part. However, each vertical line denotes the position of a spectral order:

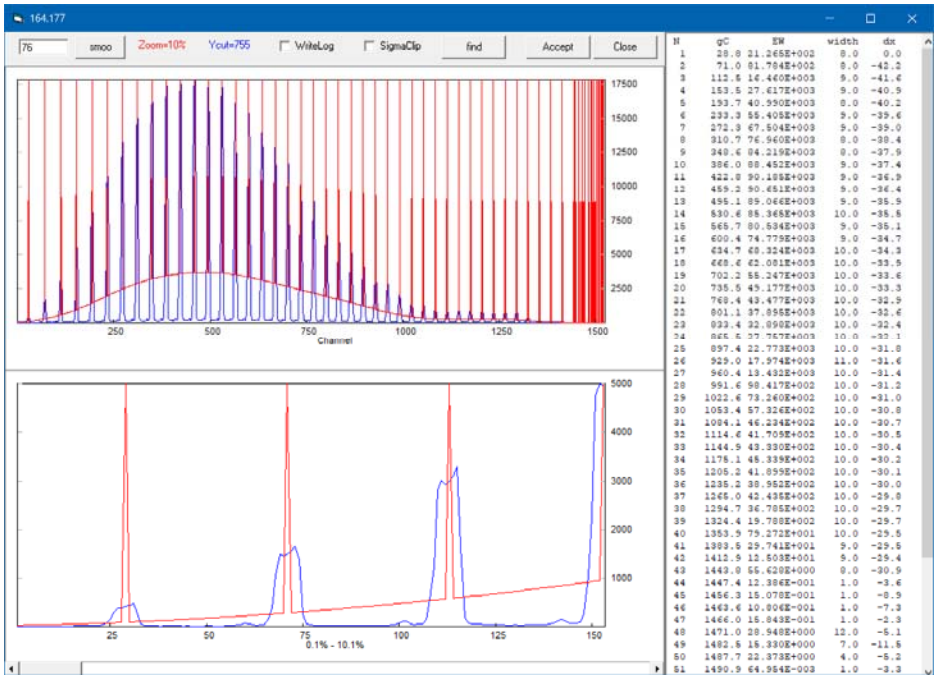


Figure 15Found orders. A lot of "garbage" can be seen on the right.

So, there are many erroneously “discovered” spectral orders in the right part of the cut. The bottom graph in Fig. 16 shows this problematic area of the curve in details:

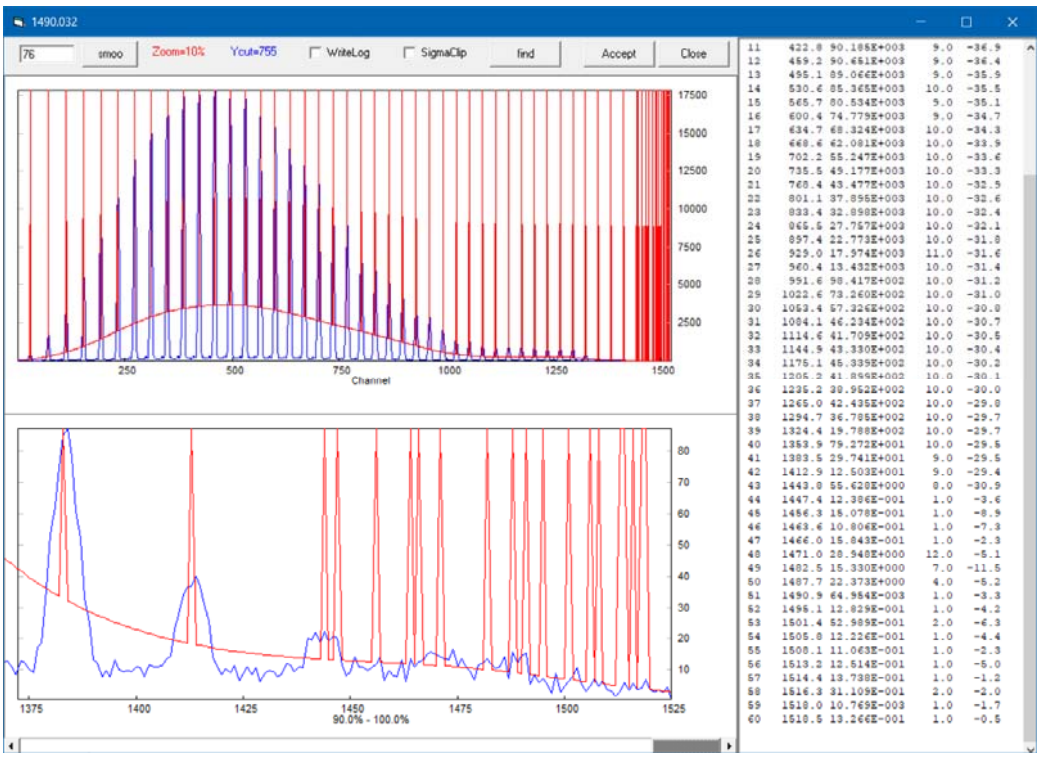


Figure 16Detailed examination of the right part of the spectrum with erroneously found "orders".

A closer look shows that due to the low signal-to-noise ratio in this area of the cut, there are small areas above the "limit". The program mistakenly identifies them as spectral orders. There are two possible solutions: remove the erroneous findings manually by pointing out the cursor close to the "wrong" peak and press **Z** key, and the second, more radical way is to specify the so-called "dead" zones on the left and right edges of the spectrum. In these zones, the search for spectral orders is not performed.

To specify the dead-zone boundary, you need to activate the upper or lower graph of your choice (to do this, simply click on them with the mouse), place the cursor at the location of the intended boundary and press **Y** key. In our case, we will use the lower graph and set the boundary approximately in the region of the 1439th pixel (Fig.17):

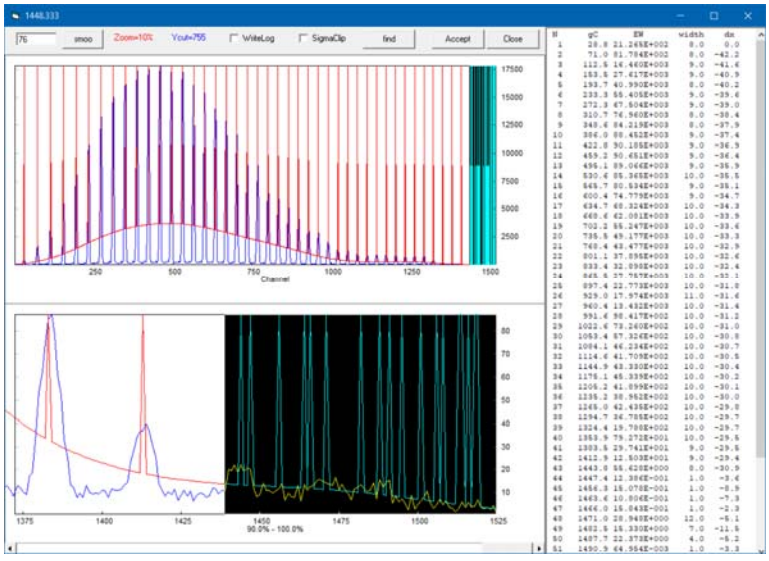


Figure 17The "dead" zone is installed (filled with black).

In the same way, you can set a dead-zone in the left part of the spectrum. However, in our case, it is not necessary. Now we press the button **find** once again:

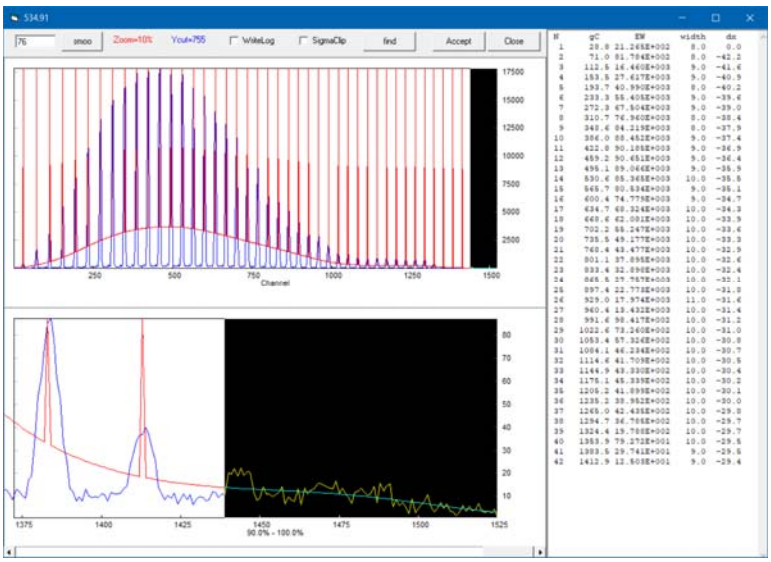


*Figure 18After clicking the **Find button** "garbage" removed. In this vertical section 42 orders were found.*

Now some 42 orders were detected. The graphs and the table on the right (Fig. 18) show that the distance between the orders smoothly decreases from 42 to 29 pixels. The width of the orders varies from 8 to 11 pixels. Click the **Accept** button. The window with the graphs and the table will be closed, the program will return to the window with the image and complete the search for spectral orders.

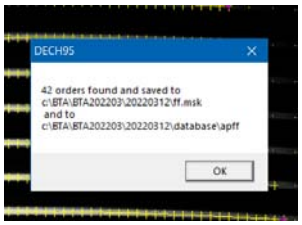


Figure 19Completion of work. 42 orders were found across the entire width of the image.

We close this message and exit the mask construction procedure using **EndProcedure** . The resulting mask is not a final product, since only the position and shape of the orders are defined, but the widths of the orders and the position of the inter-order minima are not defined. It is also necessary to define a method for accounting for scattered light. Next step is the mask edit.

Editing a mask

Enter **the Mask/Edit** procedure. A new window appears with a "vertical" cut through the center of the image. Click on title **CUT X =755** to make a cut through any other column of the image. Btw, the positions of spectral orders are shown in the image window as well. It is recommended to check the correctness of the determination of the position of the spectral orders across the entire image by scrolling over the image.

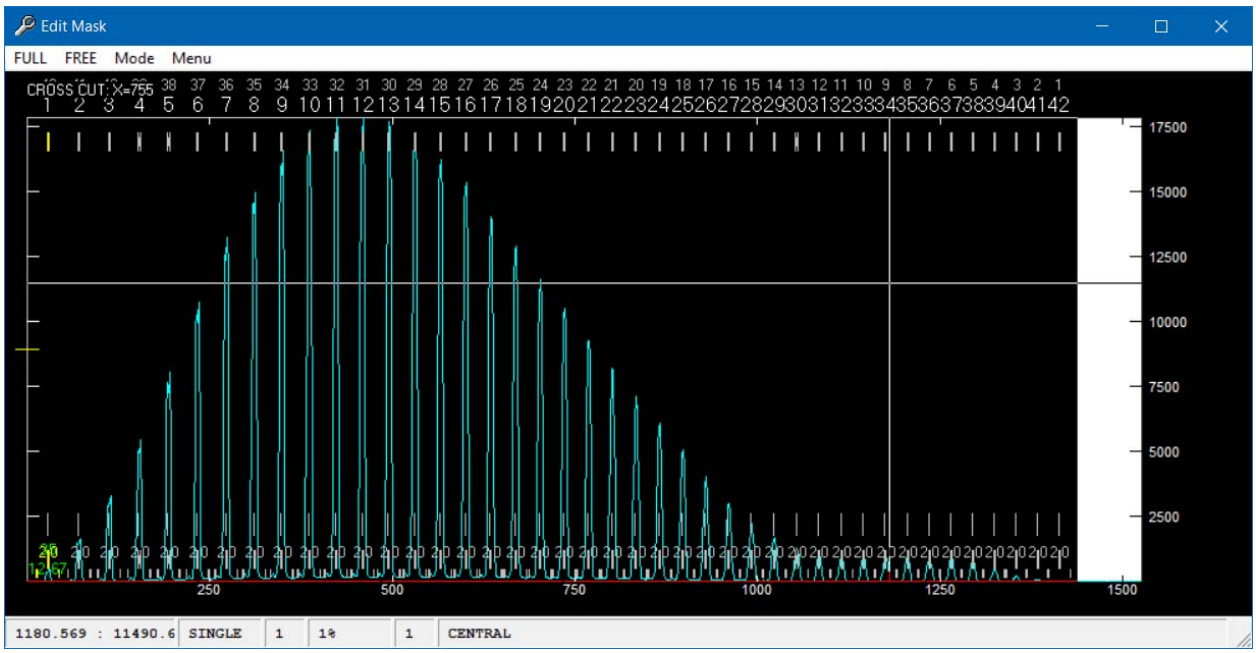


Figure 20Mask editing window. ***FREE*** *serves to examine a spectrum fragment in more detail: click on FREE, then specify the left and right boundaries of the desired fragment by clicking the left mouse button.* ***FULL*** *– show the entire curve(spectrum).*

Let's return to the mask editing window (Fig.20). It is seen 42 spectral orders, numbered in the direct and reverse order (see in the upper part of Fig.20). The first order is "active" and is shown in yellow. To activate any another order, just click on it. Each spectral order has 7 points which can be modified: its center, two zones of inter-order minima to the left and right of the order - each zone has left and right boundaries, and two more adjustable points - the boundaries of the order itself:

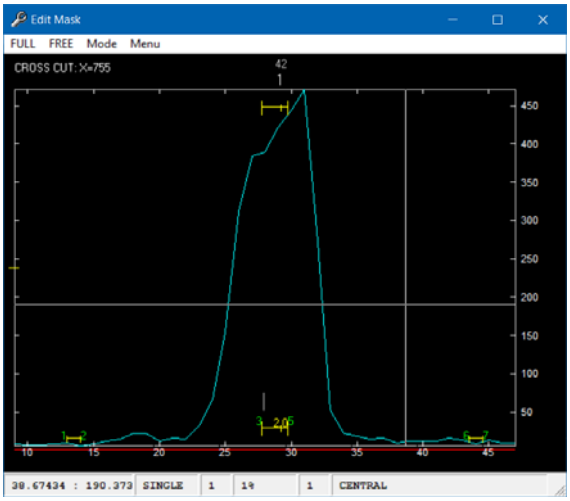


Figure 21Active spectral order (zones are highlighted in yellow).

To change (move) any of the above boundaries and/or the center of the order, move the cursor at the desired position and press keys **1** through **7** (as shown in the figure), where **1** and **2** are the boundaries of the left zone of inter-order minima, **3** and **5** are the left and right boundaries of the spectral order (for example, in Figure 21 the boundaries of the order are set incorrectly - the order is significantly wider than the set boundaries), **6** and **7** are the boundaries of the right zone of minima. Keys **4** or **M** serve to move the entire order together with all zones and borders (they are tied to the center of the order). By default, the ability to move the order is blocked. To unblock it, you need to turn off the corresponding trigger **Mode / Do not move aperture (block "4" and "M" keys):**

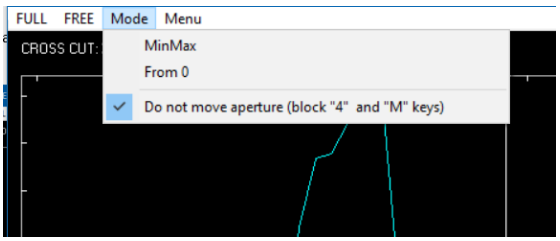


*Figure 22Order Move Lock Trigger – **Do not move …** . **MinMax** – the vertical boundaries of the graph are determined by the maximum and minimum values of the displayed fragment (this mode is set by default), **From 0** – the maximum of the vertical scale is determined by the spectrum, the minimum is set to 0.*

Let's move on the mask edit mode where it is necessary to define the limits of spectral orders, limits of zones of inter-order minima and specify the functions, describing the scattered light. Sequence of action is the following:

1. **Menu/Move Backgr Zones to the middle (Ctrl-M)**. This procedure moves the zones of inter-order minima exactly in the middle between orders. When program asked for the width of the zone, enter 15.

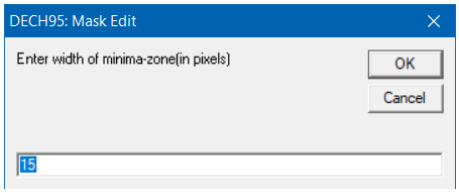


Figure 23Entering the width of the inter-order minima zone (in pixels).

2. **Fit background (Crosscuts) (Ctrl+B)**. This procedure serves for the fit of zones of inter-order minima. In essence, this is the definition of the level of the scattered light. In the parameters panel, one should set the following:

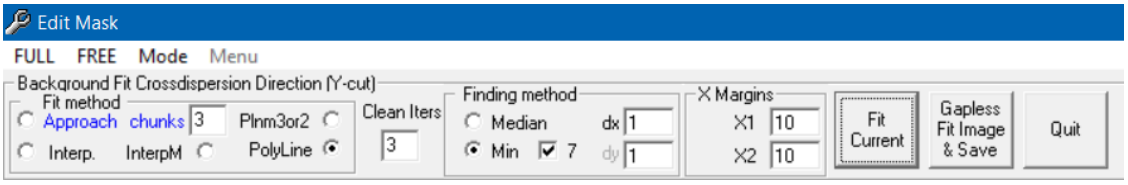


Figure 24Parameters determining the curve of scattered light across dispersion.

And press the button **Fit Current**. The resulting fit can be seen in more detail if you set the intensity limit (vertical scale) closer to the level of inter-order minima:

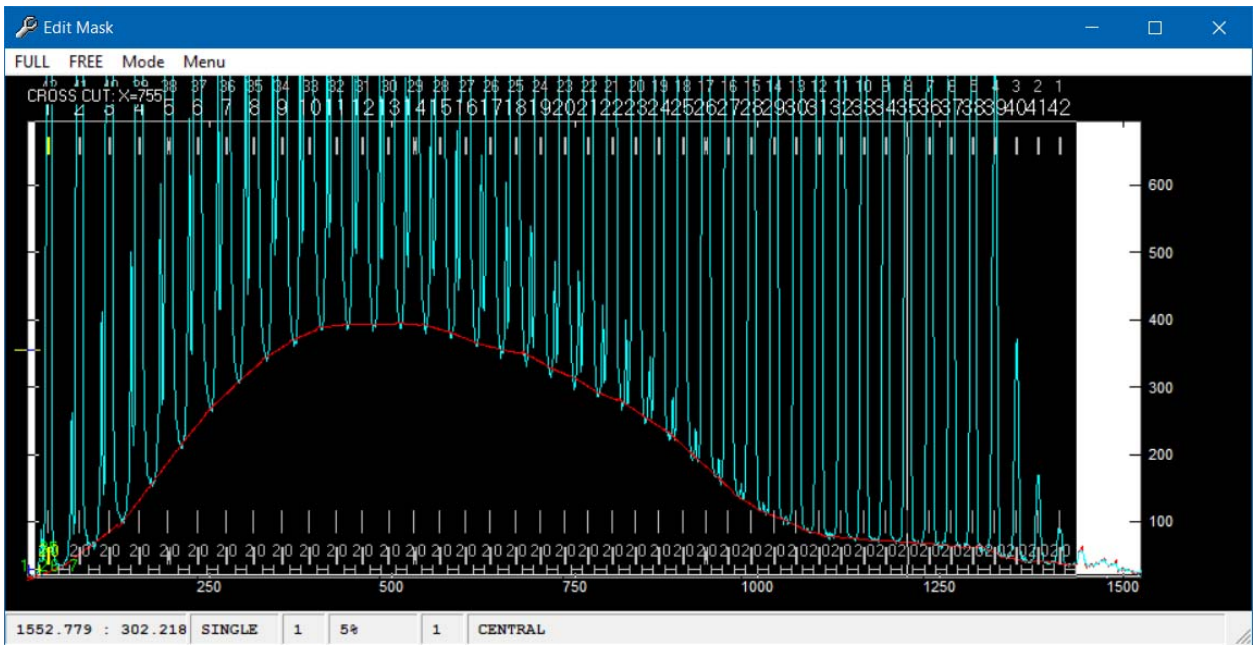


Figure 25Result of approximation of inter-order minima by a broken line.

To set the upper limit of the scale, place the cursor on the desired upper-limit position and press **Shift + T** (i.e., set the *top*). To return to the entire curve, use option **FULL**. Using the keyboard shortcut **Ctrl + B** (i.e. set the *bottom*) one can set the lower boundary of theploty.

For correction of spectral order boundaries (width) use the option **Menu / Resize Apertures (Ctrl + R)**. Enter 0.01 as the parameter. The smaller this number, the wider the order will be:

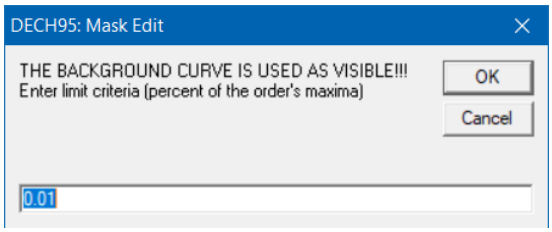


*Figure 26Parameter defining the order width by the **Resize function Apertures** .*

Automatic order width determination may give suboptimal results for orders with low signal-to-noise ratio (i.e. making the width of spectral orders too broad). As it is seen in Fig. Figure 20Mask editing window. **FREE** serves to examine a spectrum fragment in more detail: click on FREE, then specify the left and right boundaries of the desired fragment by clicking the left mouse button. **FULL** – show the entire curve(spectrum)., such kind of problem is seen in the first and last orders. Let's check them in more detail:

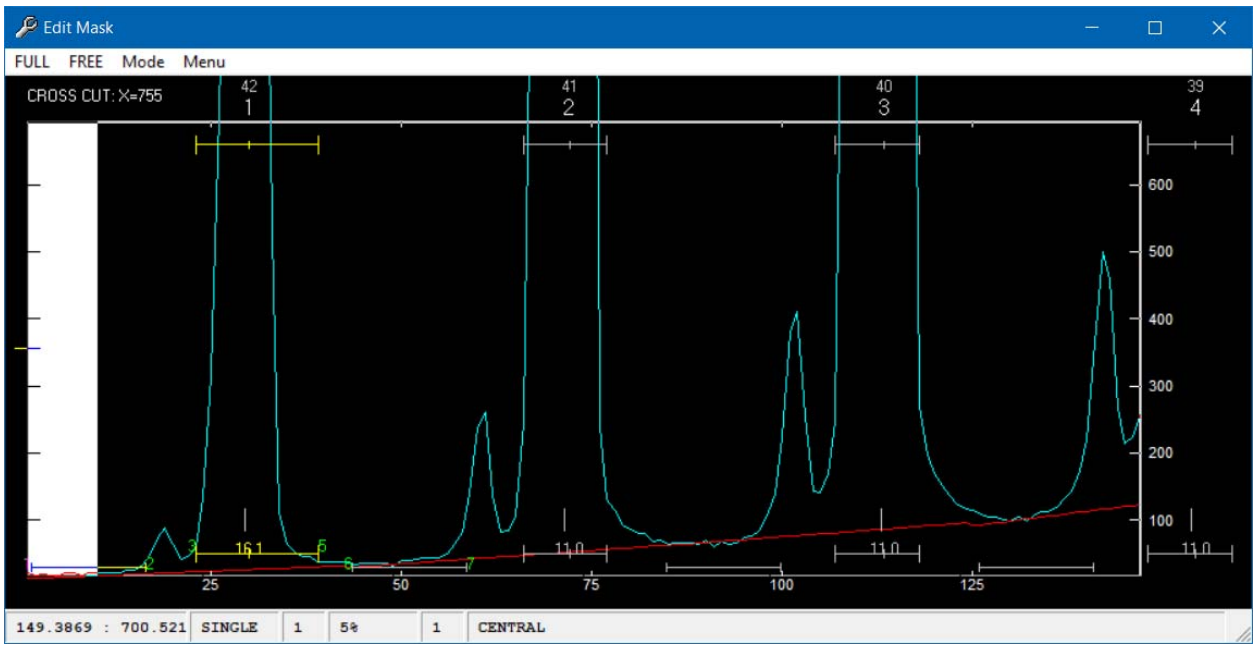


Figure 27The first three orders. It is clear that the first order boundaries are not optimal – they capture areas without useful information.

It is shown In Figure Figure 27 that limits of order #1 (the active one) needs to be edited. At first, click on somewhere close to the center of the order to activate it (the limits of the active order turns to be yellow – see Fig.27) and redefine its position with keys **3** (left border) and **5** (right border). The limits of other orders can be adjusted in the same way (e.g., order 2 in Fig.28):

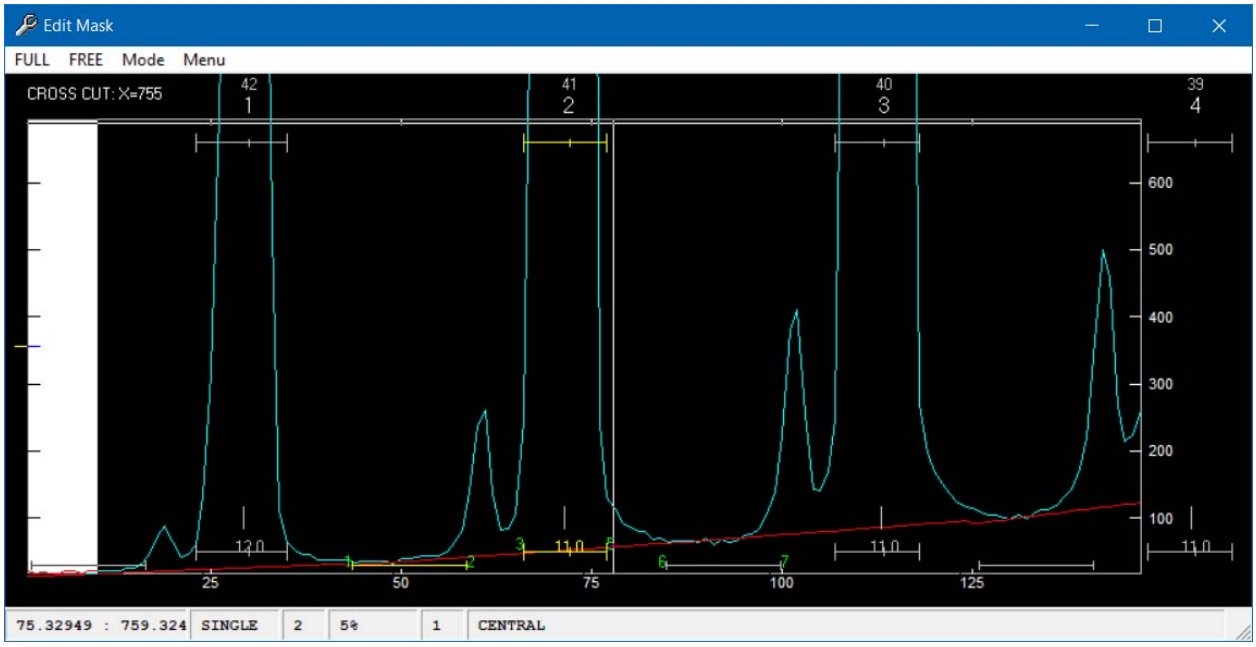


Figure 28Widths of orders 1 and 2 have been adjusted. The second order is active.

Let's check the last orders. In Figure Figure 29it is clear that order 42 has non-optimal limits.

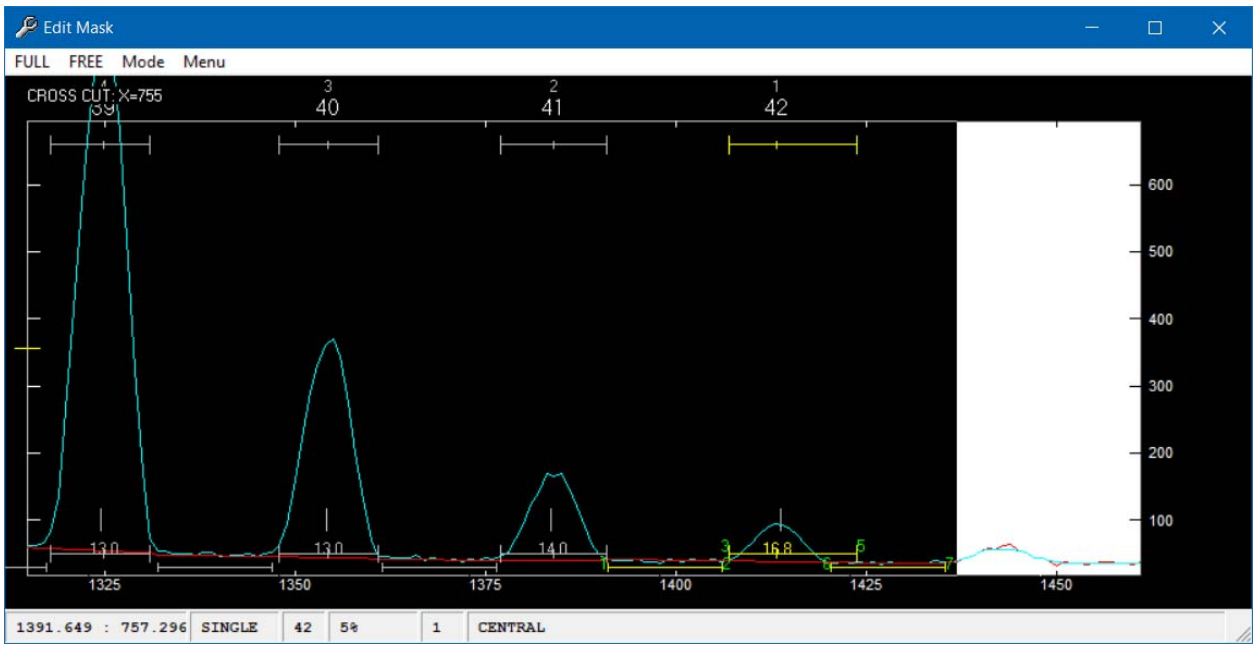


Figure 29Last orders. It is clear that order 42 has a non-optimal width, especially its left border.

Activate order 42 with a mouse click and adjust the borders with keys **3** and **5** :

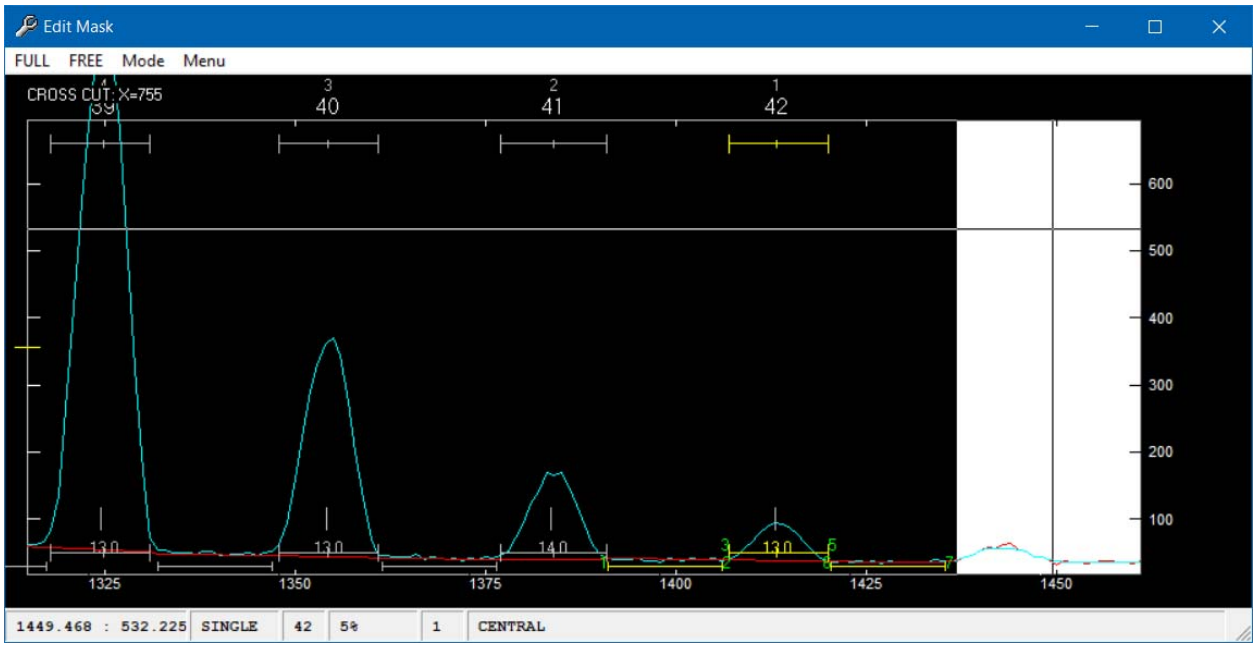


Figure 30Order 42 activated. Boundaries adjusted.

3. *Determination the form of the scattered light curve in the direction along the dispersion*. **Menu/ Fit Background (Over Crosscuts) Ctrl + C** . Set the parameters as it is shown in Fig.31 and click on the **Fit** button**:**

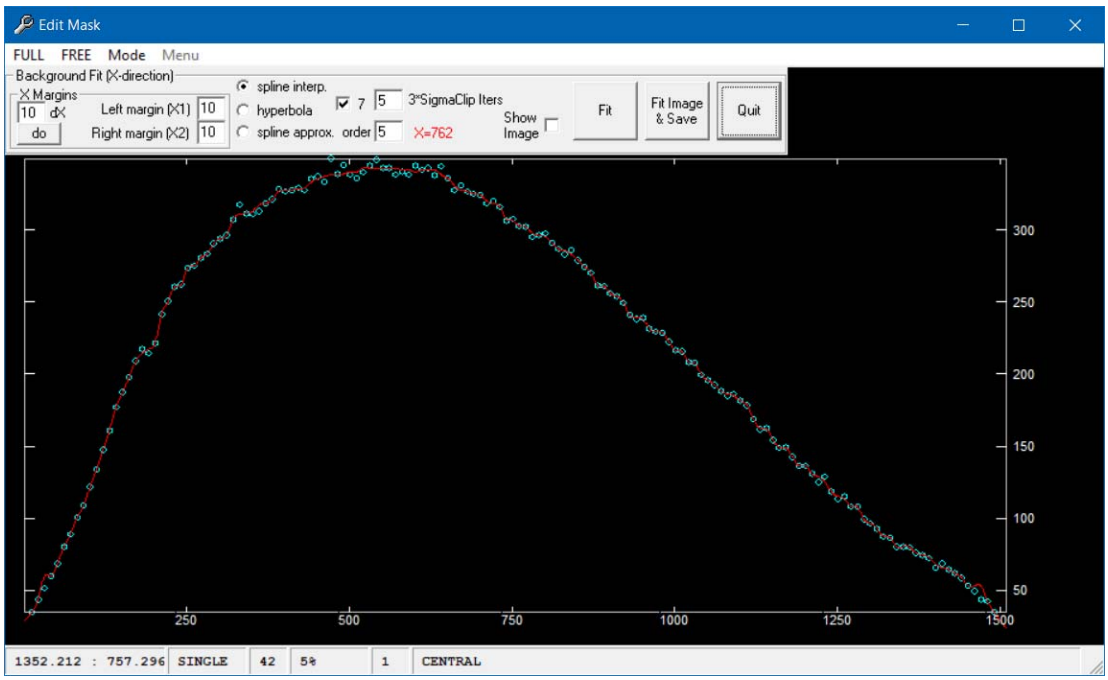


Figure 31Parameters of approximation of the scattered light curve along the dispersion.

Return to the main window using the **Quit** button.

4. Let's save the created mask – use **Menu/Save as IRAF - type mask**. Then set the parameters as indicated in Fig.32 (4 is the degree of the polynomial fit describing the curvature of the orders along the dispersion, 2 is the degree of a polynomial fit for the inter-order minima:

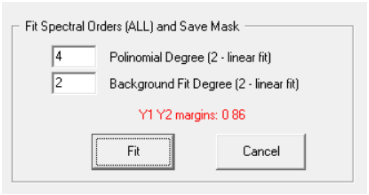


Figure 32Parameters for recording a mask in IRAF format

Click **Fit**, then appears new window (Fig.33):

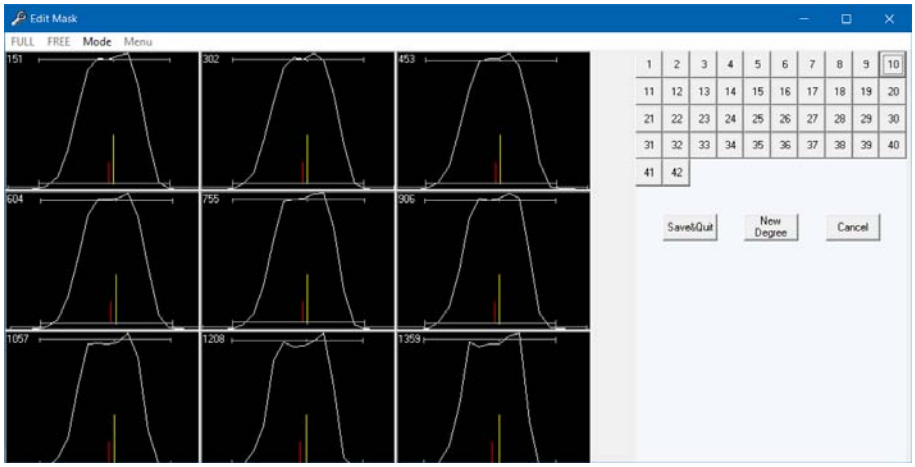


Figure 33Mask quality control window. In the figure we see 9 cross-sections of order number 10 (you can select any order using the corresponding button), made with an equal step along the entire length of the order. The yellow vertical line indicates the central position of the mask (adjusted by key 4 in the editing window, the red line has an auxiliary function and indicates the position of the center of gravity of the order.

In this window, one can check the quality of the created mask (see the caption of Figure 33). For the final save of the mask, use the **Save & Quit** button. Now, the mask is saved as a text file in the **database** directory created by the program in the directory with images. The name of the mask file is based on the name of the original file. It is composed as follows: the base file name is taken (i.e., in our case, without the *.fits extension) and **ap** is added to the beginning of the name , e.g. for the image **FF.fits** the corresponding mask file, stored in the database directory, is **apFF**. This mask can be used in the **IRAF** software package. After saving the mask, we leave the editing window and return to the window with the image - **Menu / Finish**

5. It is necessary to make sure that the **apFF** mask well matches with spectral orders on images of stellar spectra. First, we have to select a well exposed spectrum. Control of the level of the collected signal is also useful for rejecting low-quality spectra (with a very low signal/noise or, conversely, for rejecting the saturated images (overexposed ones)). To do this, we return to the directory with our spectra and execute the command:

Crosscut *.fits y txt

Then, execute the following command in the **txt** directory:

dech-fits *.txt

In the window with "vertical" cuts (Figure 34), the active spectrum is shown in red. In our case, this is a flat-field spectrum. Let me remind you that the flat-field spectrum has only one sub-order, while the stellar spectra have two. The second sub-order of these spectra is a spectrum of ThAr. Therefore, in the spectra of stars, we are interested only in the sub-orders that coincide with the orders of the flat field.

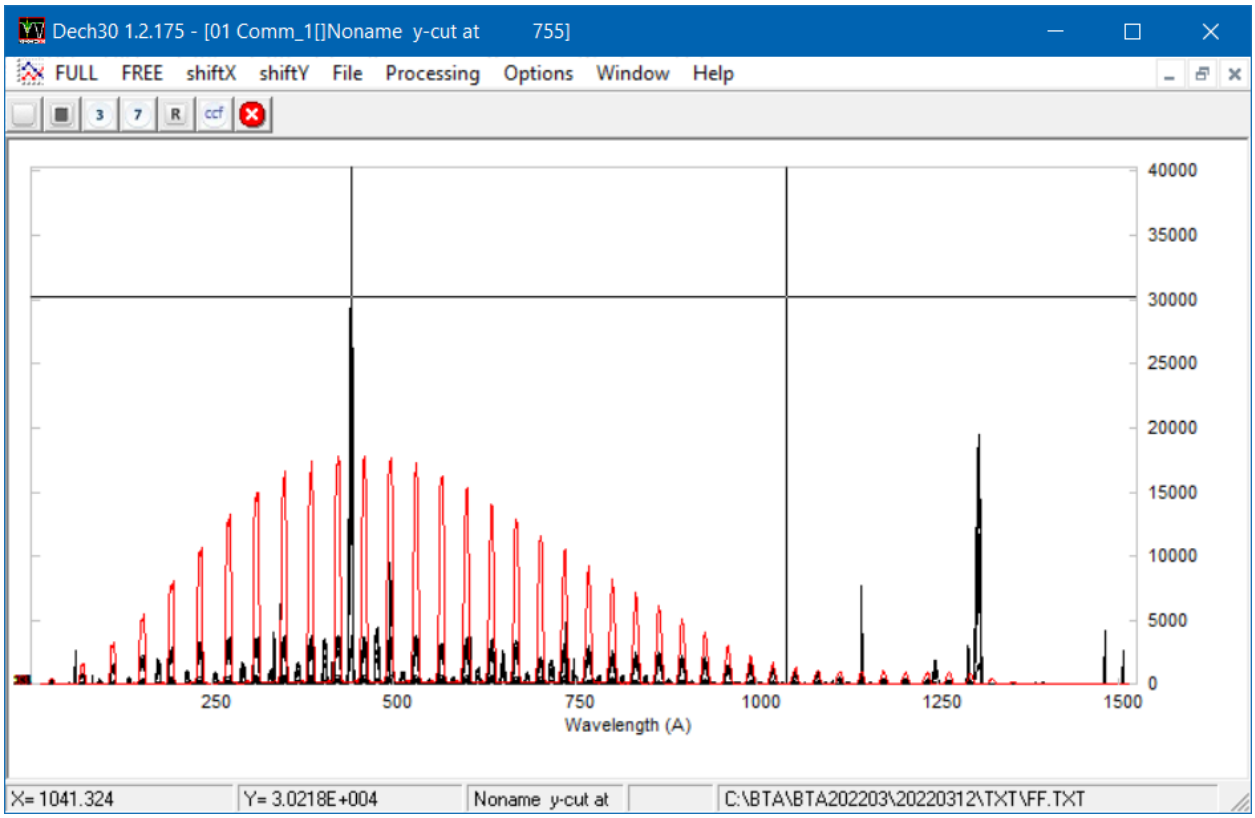


Figure 34A set of "vertical" sections. The "active" spectrum is shown in red. Its name is indicated at the bottom, in the status bar - in this case it is a flat field (FF).

The strong emissions in Figure 34 are sub-orders with ThAr. To find the spectrum of the star with the highest signal, we need to examine the spectra in more detail. To do this, right-click and select **FREE (Box mode)** in the appeared menu:

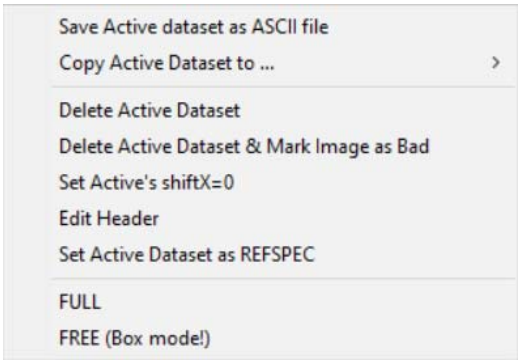


Figure 35Additional menu that can be called by right-clicking.

Using **FREE (Box Mode),** one can specify the upper left and lower right borders of the rectangular fragment to be shown using the left mouse button. As a result, one gets, for example, such a fragment, where the spectra can be seen in more detail:

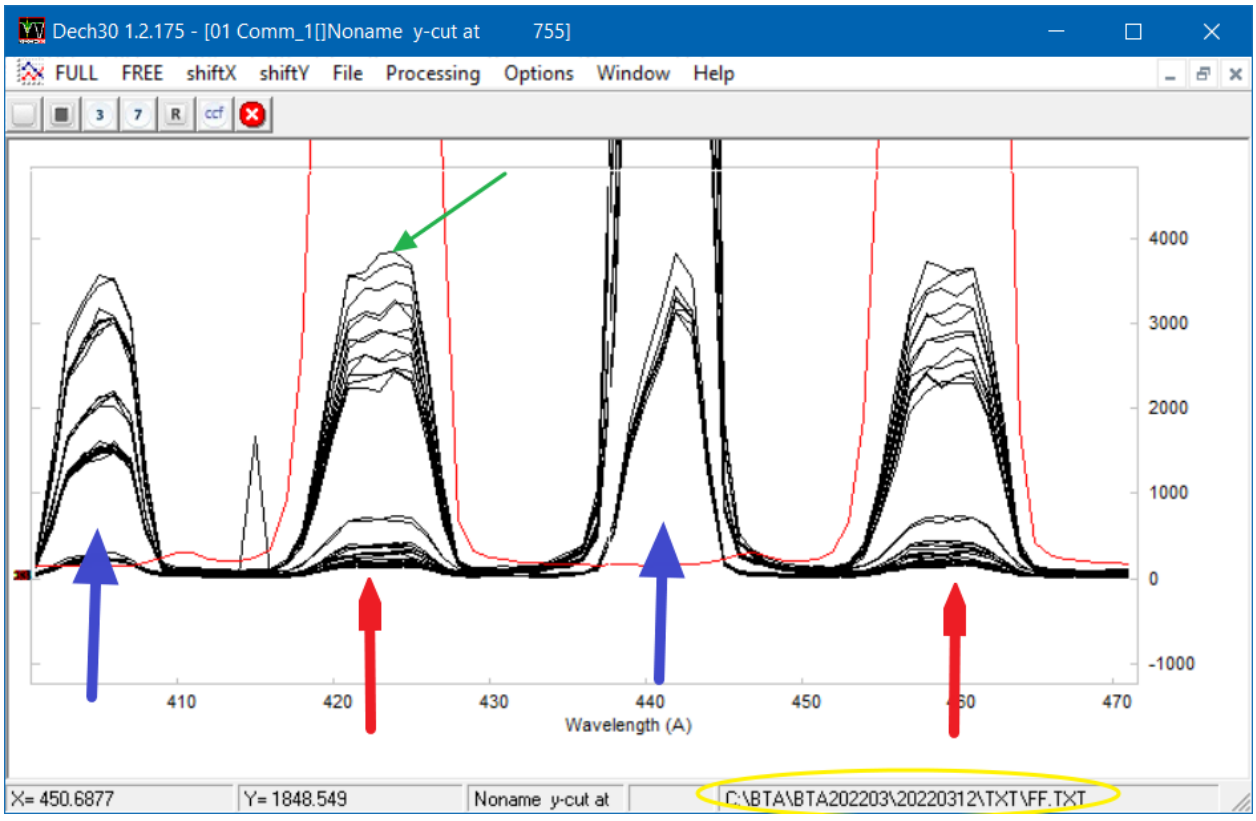


Figure 36Detailed fragment of the set of spectra shown in Figure 34. Red arrows mark sub-orders that coincide with the sub-orders of the flat-field (red curve). Stellar spectra are present in these sub-orders. Blue arrows indicate sub-orders with spectra of ThAr serving for the wavelength calibration and measurement of the positional displacement.

Using the enlarged section of the graph with cross-dispersion cuts, we can find a spectrum with a high level of signal. Figure Figure 36shows that the "active" spectrum is highlighted in red (in this case, it is a flat field). The name of the active spectrum is shown at the bottom, in the status bar (marked by the yellow oval). To find out the name of a well-exposed spectrum (marked with a green arrow), one can click on it with the mouse. The spectrum will become "active" (red), and its name will be shown in the status bar:

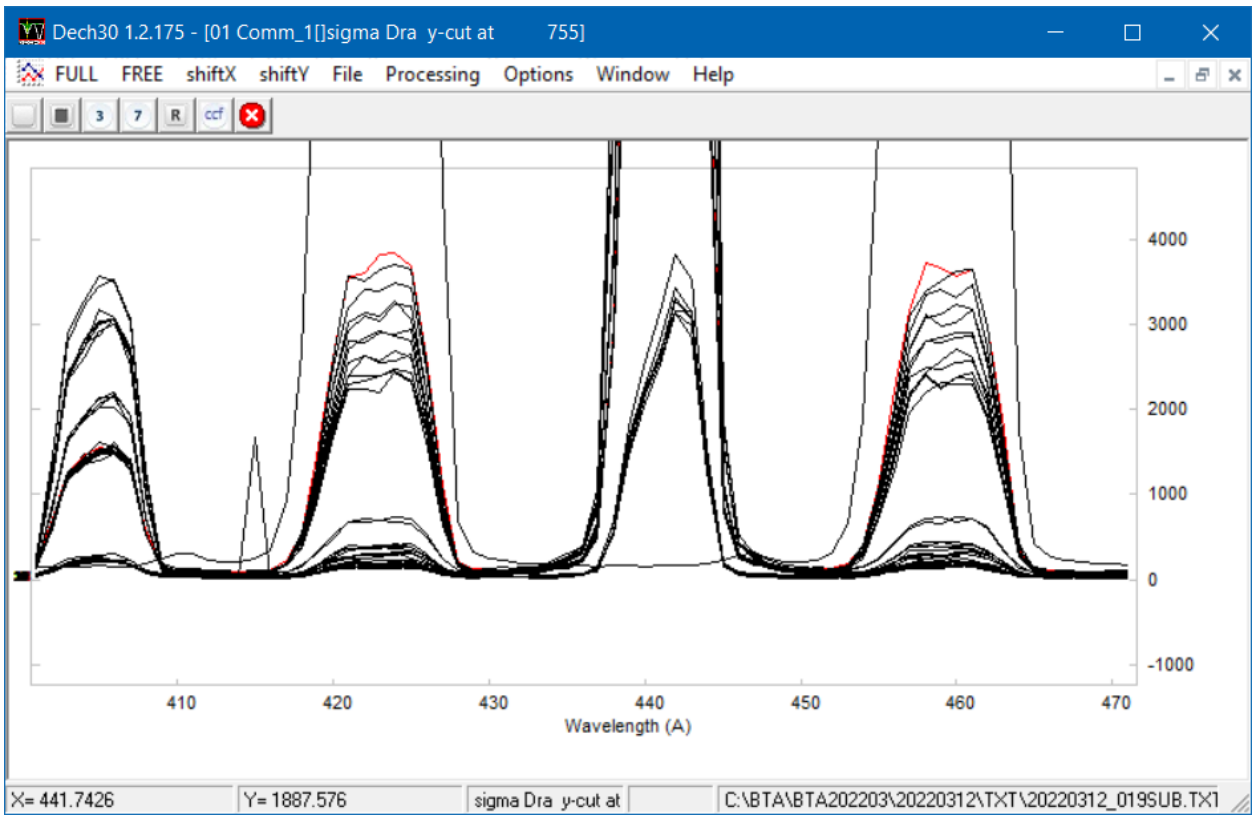


Figure 37A well-exposed spectrum is activated. The name of the file with this spectrum is visible in the status bar.

However, if the spectra are located very closely, sometimes is not possible to activate the desired spectrum by a mouse click. Another way: use the keyboard - up arrow ↑ and/or down arrow ↓ serve to sequentially change the "active" spectrum. In Figure Figure 37, the well-exposed spectrum is activated and its name - 20220312_019 SUB – is shown in the status bar.

6. Then, one has to check how well the mask constructed using the flat-field spectrum fits the stellar spectra. Also, In addition, we will need a second mask to extract sub-orders from ThAr. Let's go back to DECH 95 and load the “well-exposed” image 20220312_019sub .fits.
   Use **File / Load Image** :

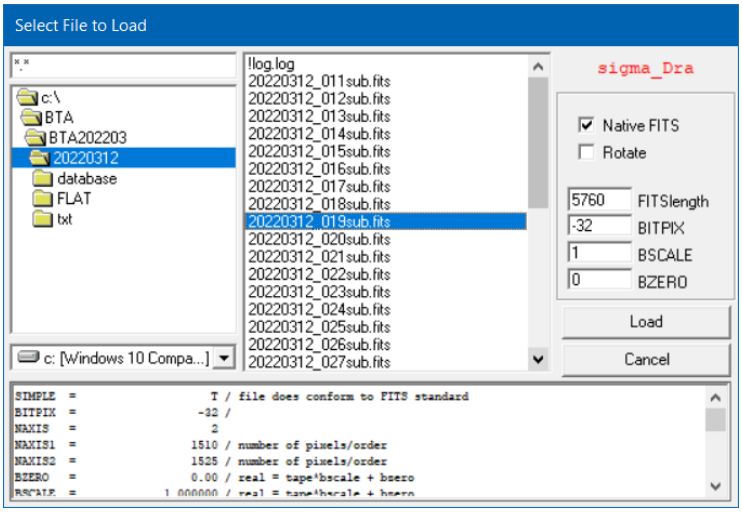


Figure 38Loading a spectral image of a star.

After loading the image, go to the mask editing mode: **Mask / Edit** and load the **apFF** mask:

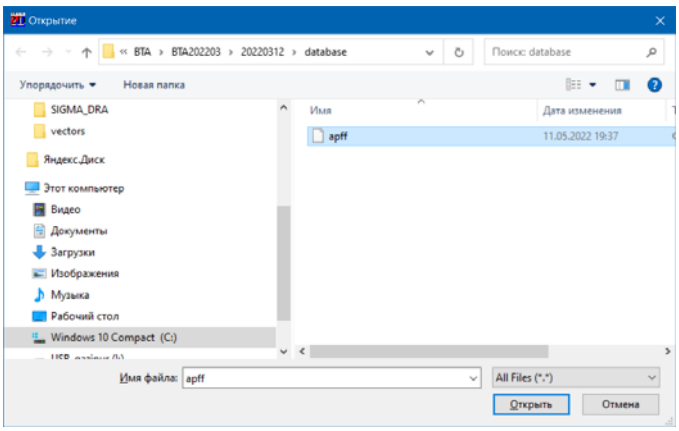


Figure 39Loading the mask.

Fiber optic spectrographs are characterized by high positional stability, so in most of cases the flat field mask is suitable for stellar spectra as well. However, there are two sub-orders in stellar spectral images while in the falt-field image only single sub-order is available. Thus, the inter-order minima zones determined in the flat field spectrum may fall on the ThAr sub-order in stellar spectra. In addition, the collected signal levels may differ greatly, which may affect the order width. Therefore, it is necessary to carefully check the order widths and the positions of the inter-order minima zones. In the mask editor, the sequence of actions is as follows:

- move the zones of inter-order minima to the edges of the orders. We use **"Menu/Move Backgr Zones To Edges (Ctrl+N)."** Width zones minima (*width of minima zones (in pixels))* we leave 15 pixels**.** There is no need to worry if the neighboring sub-order with ThAr falls into the minimum zone. The program will look for the minimum within the boundaries of this zone. Therefore, it is useful to set the zone width with a reserve.

- after entering the mask editing mode, select a small fragment of the spectrum so that the details are visible. If necessary, forcibly cut off the upper border of the graph (using **Shift + T** as shown in Figure 25). It is useful to check the first orders, then at the last ones, where the orders are close to each other. For a detailed view of the entire mask, it is inconvenient to constantly return to the FULL mode and each time select a new fragment using **FREE**. Therefore, there is another way. Select a fragment of the spectrum as, for example, is shown in Fig. Figure 53and "slide" along the spectrum using the left- arrow ← and right- arrow → on the keyboard.

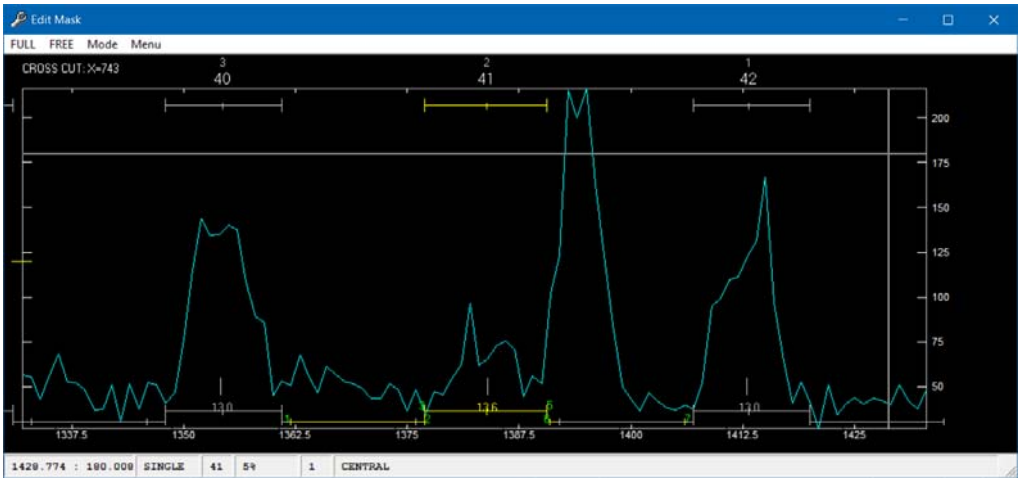


Figure 40Superposition of a flat-field mask on the spectrum of a star. In this fragment, it is evident that the right boundary of order 41 requires correction, and the zones of inter-order minima fall on sub-orders.

As a rule, the flat field mask cannot be used for stellar spectra without correction (see Figure 40). If necessary, we correct the width of the orders. For example, the right boundary of order 41 in Figure 40. To do this, use the **5** key. Using keys **7** and **6,** we move the "right" zone of minima to the outside of sub-orders areas. Using keys **1** and **2,** if necessary, we do the same with the "left" zone of minima. A useful trick: if you move the cursor to the left from the center of the active order and press key **8** , the boundaries of the "left" zone of the active order will coincide with the boundaries of the "right" zone of the previous order. If you do the same on the right side, the boundaries of the "right" zone will be forced to coincide with the boundaries of the "left" of the next order. It is necessary to remember that the ThAr sub-orders are not always visible along the entire length of the order, which can lead to an incorrect set of the zone of minima. For example, in Figure 40, for order 41 it is clearly seen that the right zone of minima falls on the area of ThAr sub-order and should be moved away. In the case of order 42, the right zone of minima should also be corrected in approximately the same way as for order 41. The absence of a visible ThAr sub-order means that the current cut across the dispersion (**CROSS CUT X =755**) does not cross any ThAr emission line in this sub-order. The position of the sub-orders relative to each other smoothly changes from order to order. Therefore, neighboring orders can be used as a sample for adjusting the minimum zones. If necessary, we perform this work across the entire spectrum, each time activating the next order for its correction.

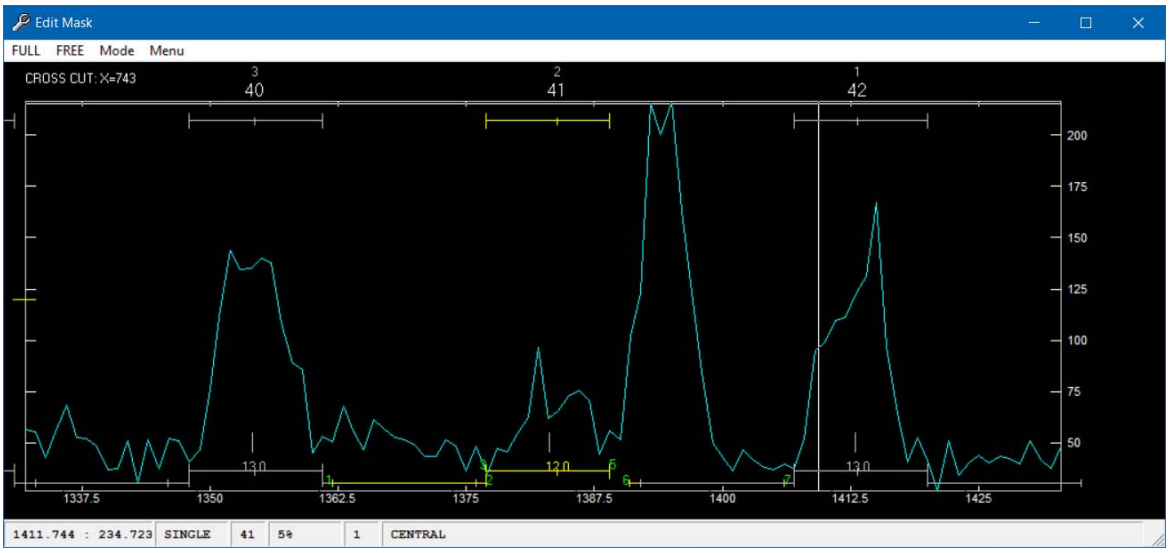


Figure 41Corrected mask. Only the last orders are shown.

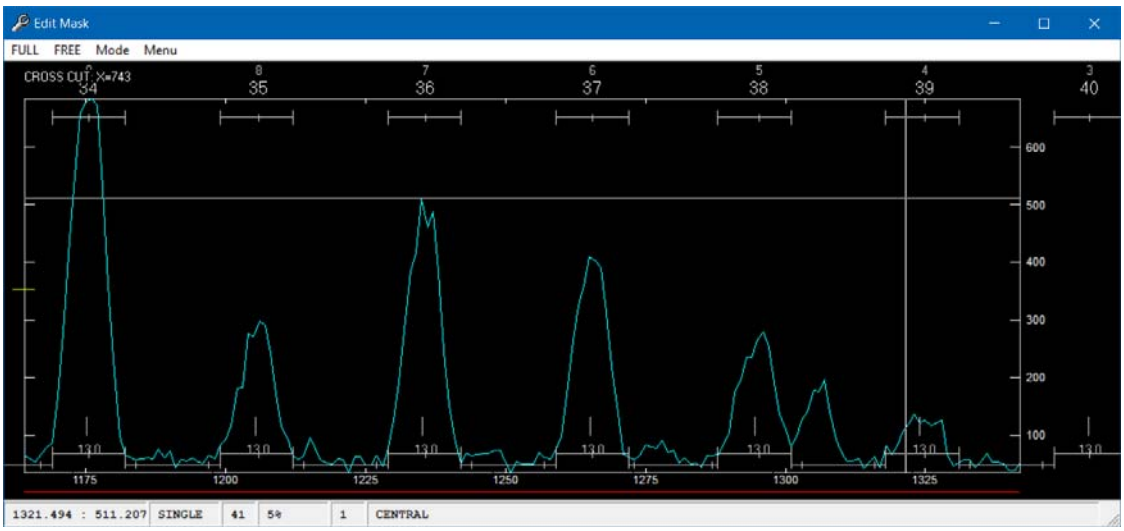


Figure 42Adjusted mask. Continued

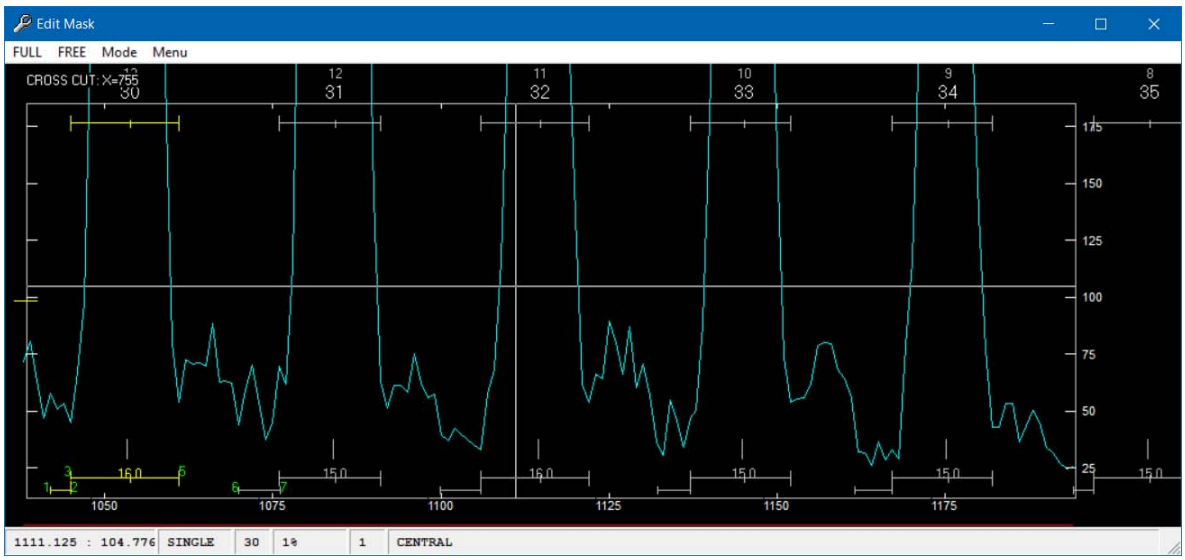


Figure 43Adjusted mask. Continued

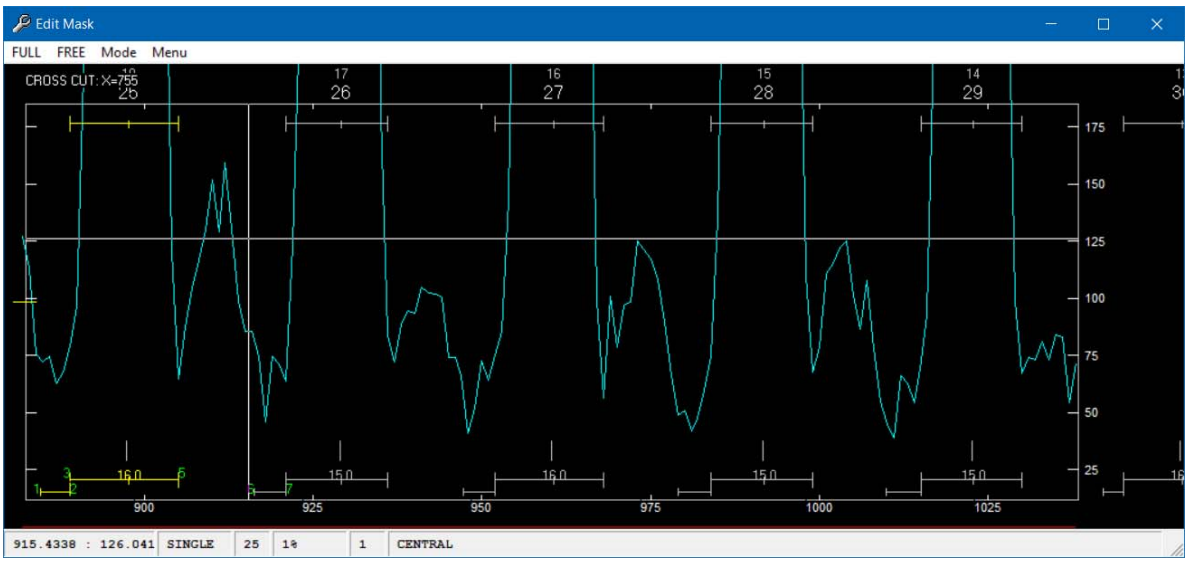


Figure 44Adjusted mask. Continued

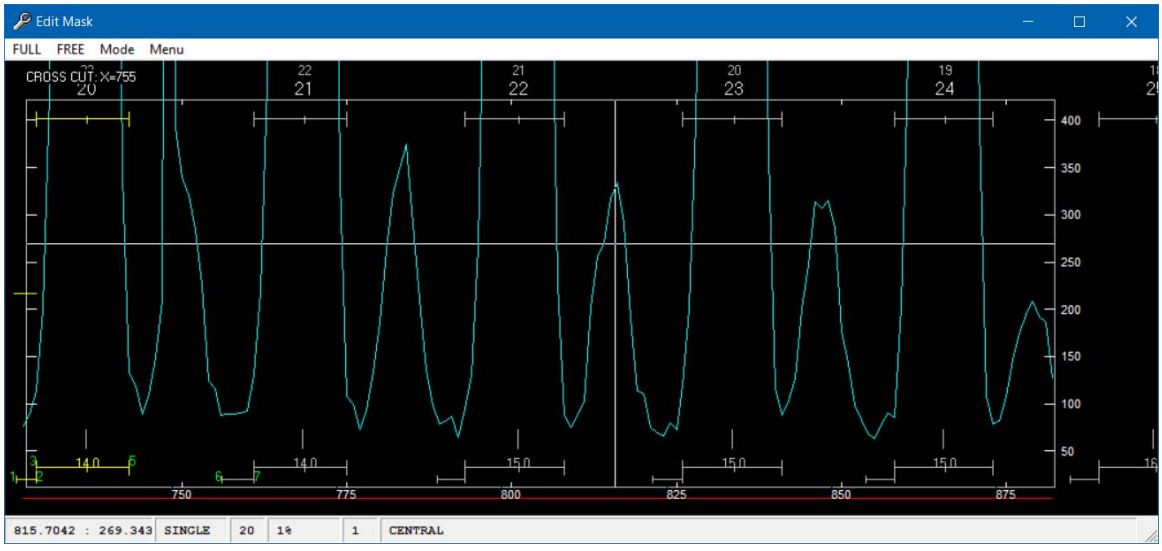


Figure 45Adjusted mask. Continued

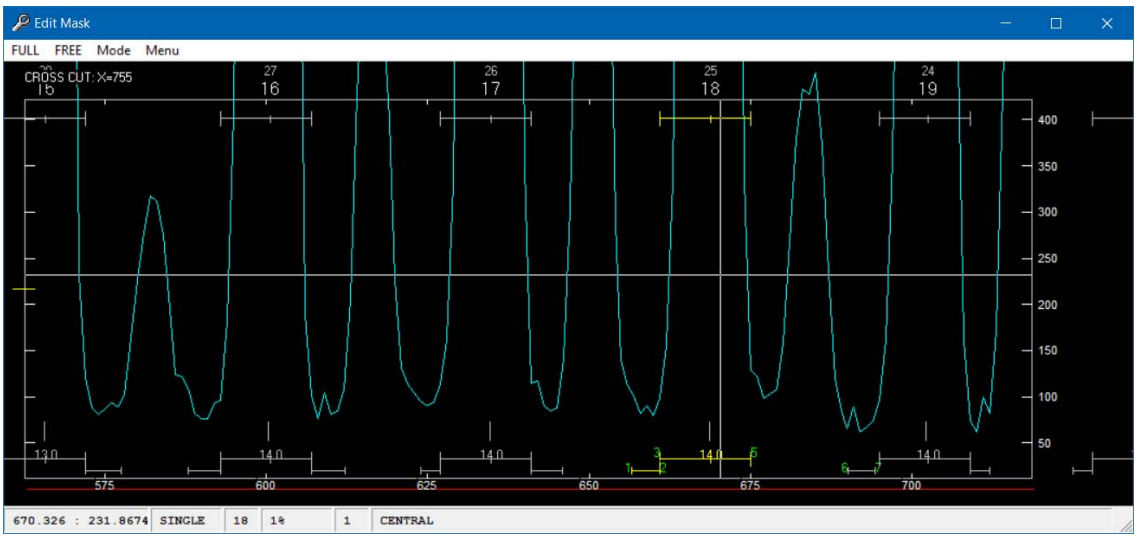


Figure 46Adjusted mask. Continued

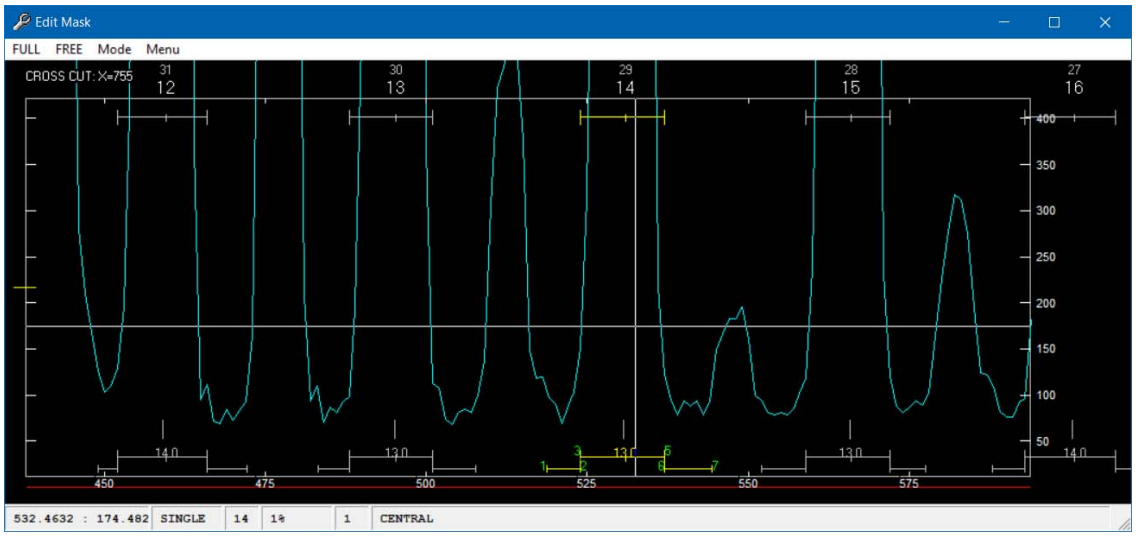


Figure 47Adjusted mask. Continued

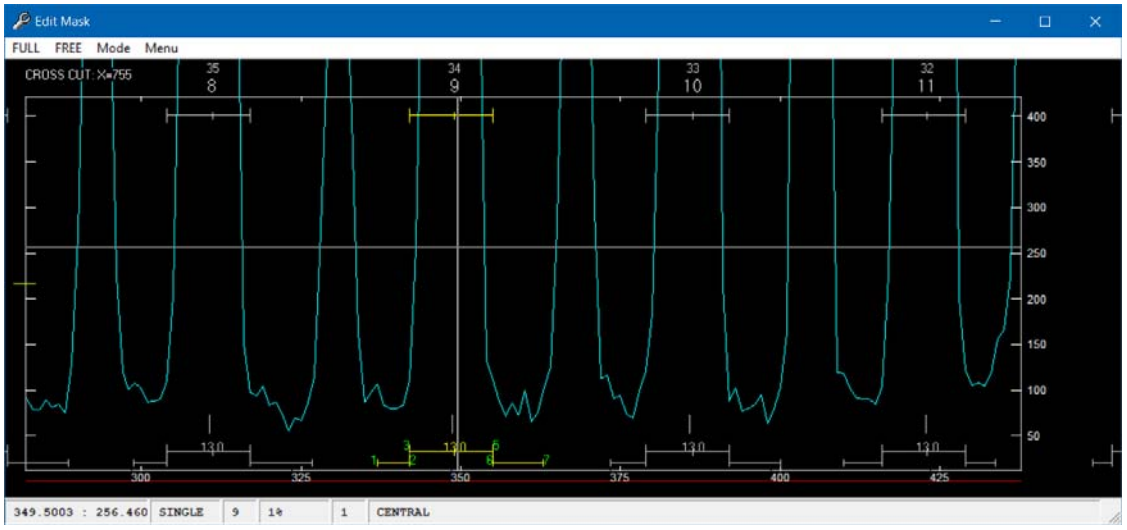


Figure 48Corrected mask. Continued.

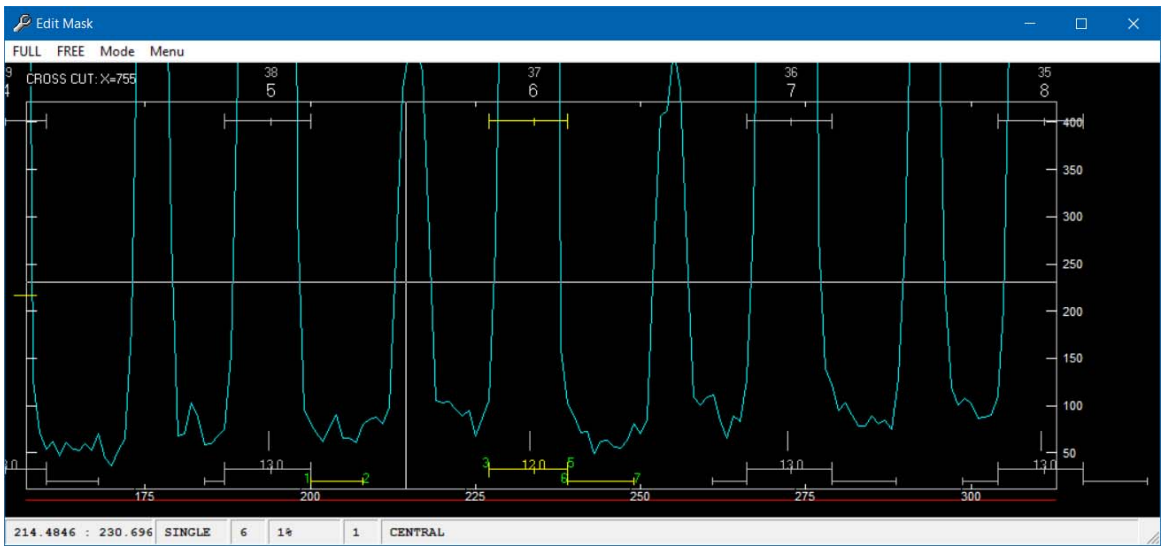


Figure 49Corrected mask. Continued.

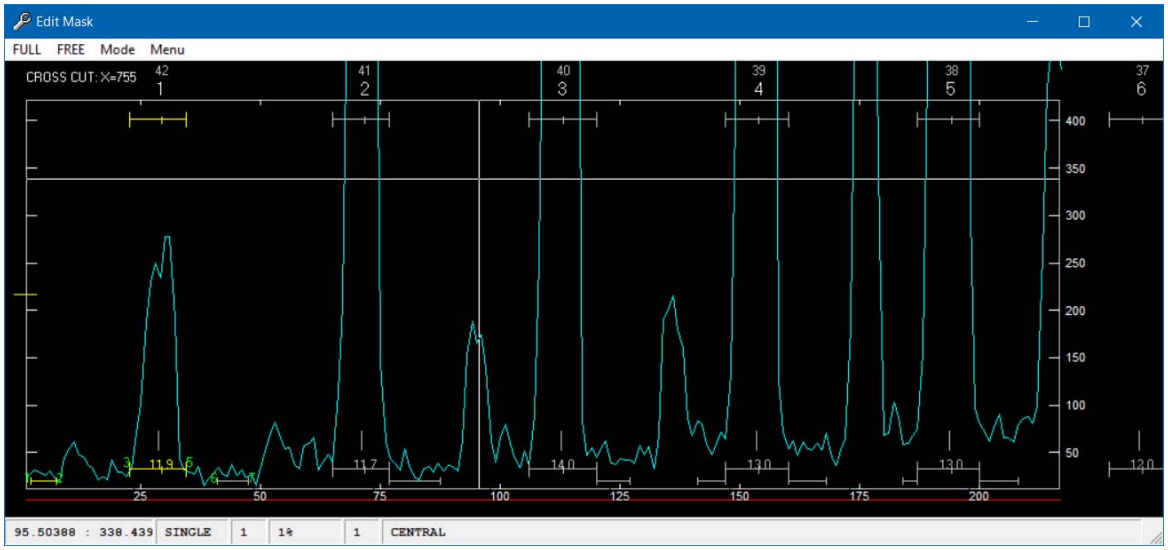


Figure 50Adjusted mask. Continued.

Advice: When one performs the edit of a mask, it is recommended to move from the last order to the first. The edit can be performed in the following way: at first, adjust the right zone of the minima of the last order. Then slightly expand the left zone, edit only its left border with the **1** key. After that, activate the previous order and, placing the cursor in its right part, press **8**. The right zone of minimums will become identical to the left zone of minimums *of the next* order [1]. Thus, we move order by order in descending order. Do not forget to adjust the order boundaries with the **3** and **5** keys, if necessary. Starting from approximately the middle of the entire spectrum (see Fig.Figure 46and following ones) and closer to the beginning of the spectrum (where first orders are located), editing comes down to expanding the minimum zones - use keys **1** and **7.** Upon completion of editing, we perform the fit (approximation) of the minimum zones – use **Ctrl + B** (with the parameters are the same as in Fig. Figure 24).

After approximating the minima, we get something like this:

[1]If you press the **8** key, placing the cursor to the left of the center of the order, the “left” zone of minima will become identical to the “right” zone *of the previous* order.

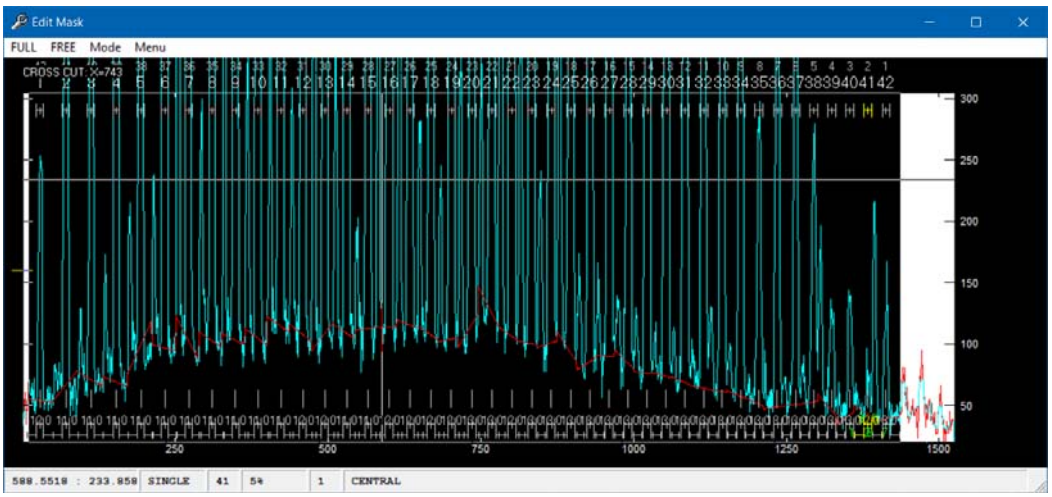


Figure 51Result of approximation of the minima of the star's spectrum.

The quality of the approximation along the dispersion should be checked as well – use **Ctrl+C**. Set the parameters as shown in Fig. Figure 31or Figure 53). The result of the approximation:

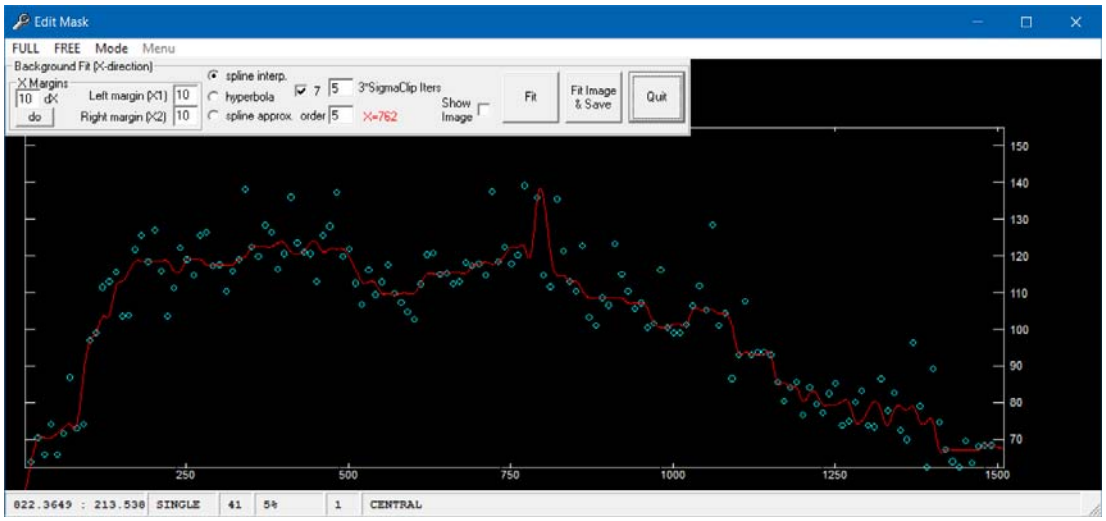


Figure 52Result of approximating the minima along the dispersion.

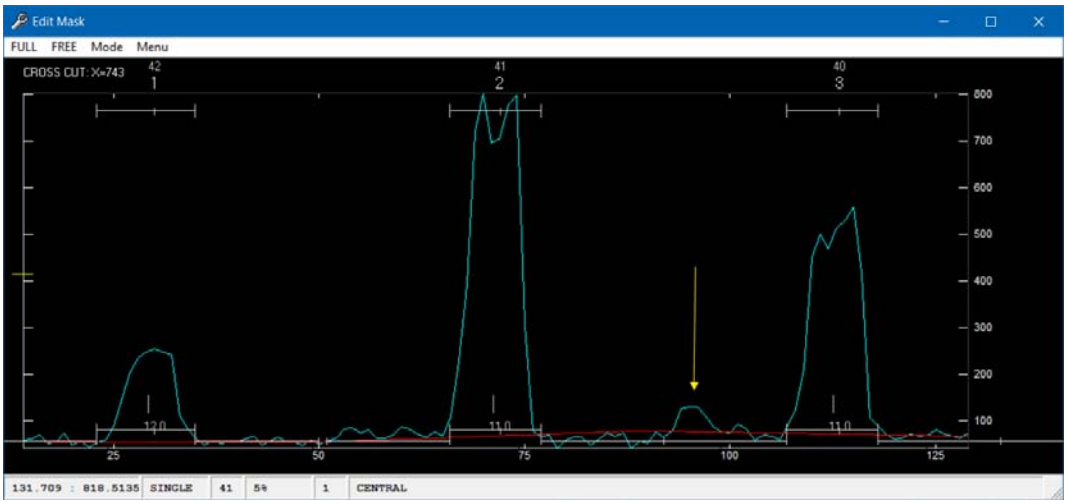


Figure 53Mask after correction. The part of the spectrum that will be subtracted during extraction is shown in red. The yellow arrow marks the sub-order with the 3rd order ThAr spectrum.

Having completed the inspection, we can write the mask using **Menu/Save as IRAF-type mask.** We enter 4 and 2 in the parameters window as it is shown in Figure 33, and press the **Fit** button. In the next window, press the **Save & Quit** button as shown in Figure Figure 33a new mask **ap20220312_019sub** appears in the **database** directory. This mask will be used to extract sub-orders with stellar spectra:

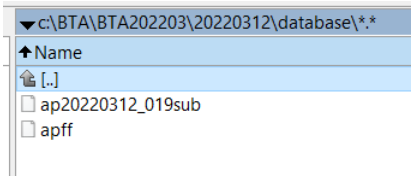


Figure 54List of masks.

However, to extract sub-orders with ThAr spectra we need another mask. One can create it using the existing one. Therefore, we should rename **ap20220312_019sub** to, for example, **ap20220312_019sub-Obj**, i.e. the name tells us that the mask serves to extract stellar spectra (not the ThAr ones).

7. *Creating a second mask – for the ThAr sub-orders*. Let's return to the Mask Edit window. At first, we need to move the entire mask to the left, since the ThAr sub-orders are located to the left of the main (stellar) ones (on the image of spectrum, ThAr suborders are located up to the corresponding stellar sub-orders). However, by default, changing the order(s) position is prohibited. To remove this limitation uncheck the menu item **Mode /Do not move Aperture (block "4" and " M " keys)** – see Fig. Figure 22. There is an additional preliminary operation to be done: by default, all modifications occur only with the active order. I.e., by default the Mask Edit procedure is set to so-called **SINGLE**-mode. To make corrections for **ALL** orders *together* (in unison) it is enough to click the mouse on the SINGLE inscription in the status bar (highlighted with a green circle in Fig. Figure 55) – the Edit-mode changes to the **ALL**. If to click here once again the mode returns to the **SINGLE**.

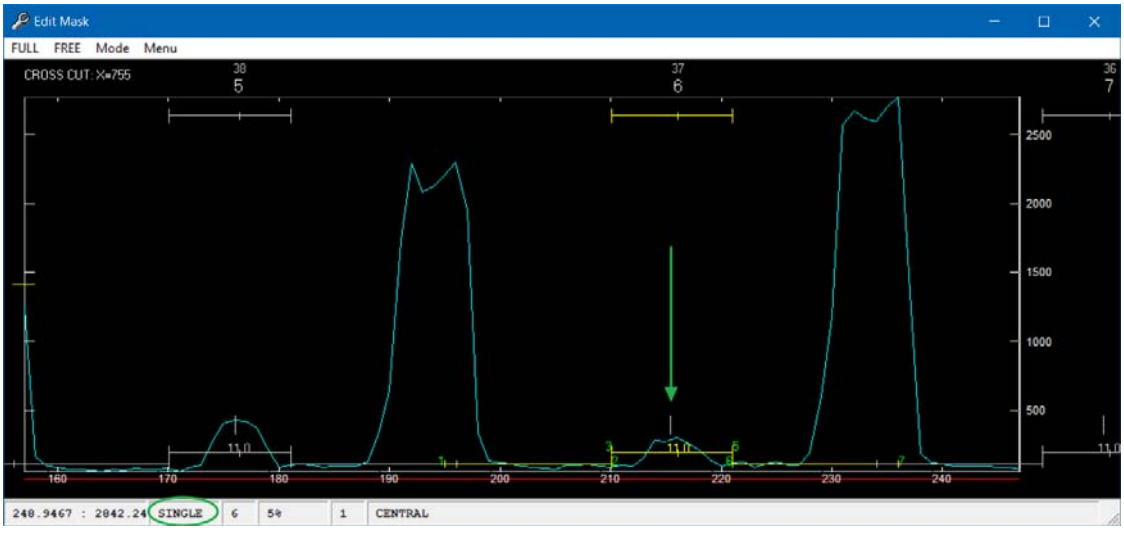


Figure 55Mask before editing the order positions. The green arrow shows the positions of the ThAr- sub-order of the active order and the green oval shows the trigger for switching the correction mode – one order or all orders simultaneously.

After that, activate, for example, the order 3, place the cursor approximately in the middle of the ThAr-sub-order (indicated by the green arrow in Figure Figure 55) and press the key **4**. Position of the

orders (all of them!) will change. You should also adjust the position of the left and right order boundaries using the keys **3** and **5** because ThAr-sub-orders are narrower than the stellar ones.

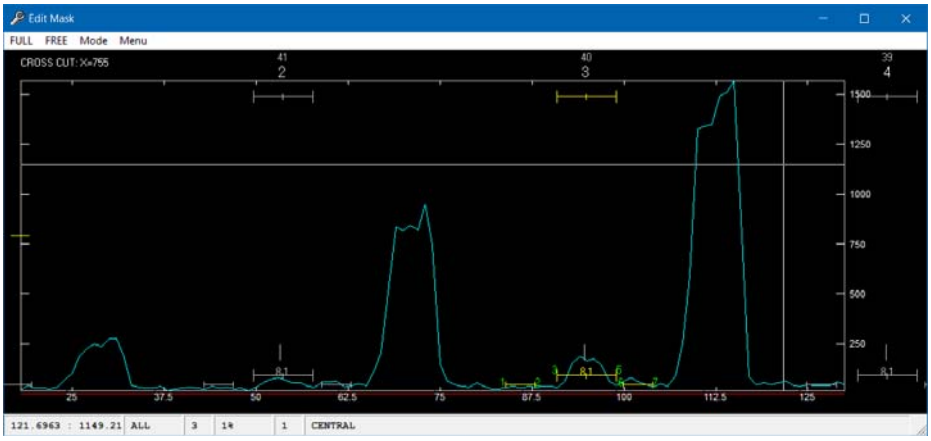


Figure 56Position and width of orders after correction.

Let's move to the last orders:

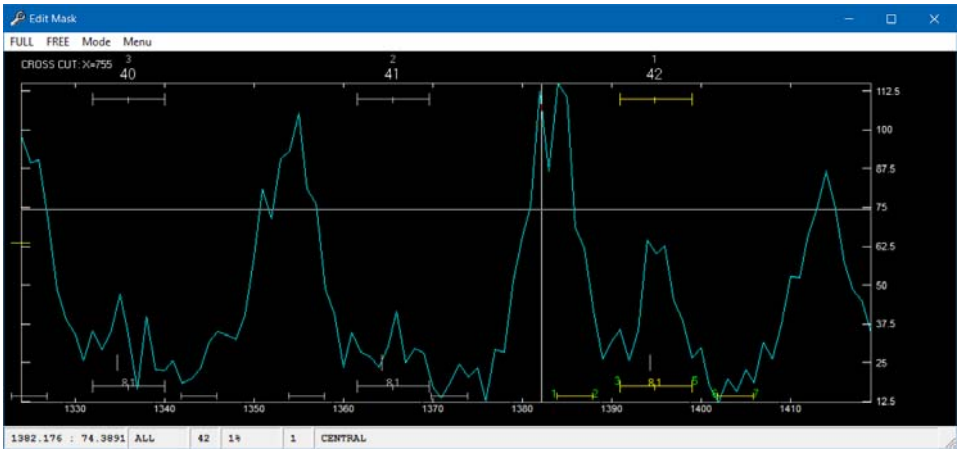


Figure 57ThAr sub-orders, as a rule, have a signal level significantly lower than that in stellar sub-orders. This is due to the emission nature of the ThAr spectrum, where the signal in the continuum is very low.

In Figure Figure 57it is shown that the "left" inter-order minima fall onto the stellar sub-order. Using keys **1** and **2** one can change the position of the zone of "left" inter-order minima. Since the **ALL** mode enabled, this will cause a shift of these zones in all orders! After adjusting the order boundaries, do not forget to move the zones of inter-order minima using the keys combination **Ctrl + N.** As it was before, enter a width equal to **15.**

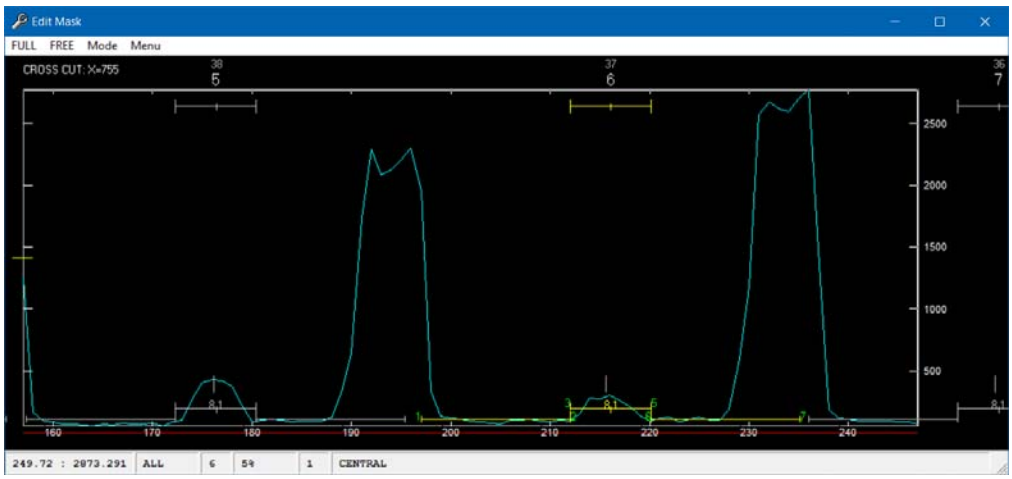


Figure 58Corrected position of the left zone of inter-order minima of order 42.

Switch the **ALL** trigger to **SINGLE** and check the mask of each order individually. Upon completion of the work, check the quality of the fit over minima points using **Ctrl + B**. Save the mask using menu option **Menu / Save as IRAF - type Mask**. Since the newly created mask is for ThAr sub-orders, it is recommended to rename the mask, for example, to **ap20220312_019sub-ThAr.**

Quick mask editing

Mask for sub-orders of the stellar spectrum

A fast way to edit a mask created from a flat field spectrum.

The initial steps are similar to those given in the previous chapter – at first, load a well-exposed stellar spectrum and edit the **apff** mask**.** The next steps are:

- check the width of the orders. If necessary, adjust the position of the boundaries using **3** and **5** keys**.** Be careful with orders blended by neighboring sub-orders (see Fig.Figure 59). In this case, the position of the boundaries may not be obvious, so you can either change the position of the vertical section (click on **CROSSCUT X =…**) and find a column where sub-orders of this order are not blended, or focus on the neighboring free of blending orders and set boundaries basing on the principle of similarity.

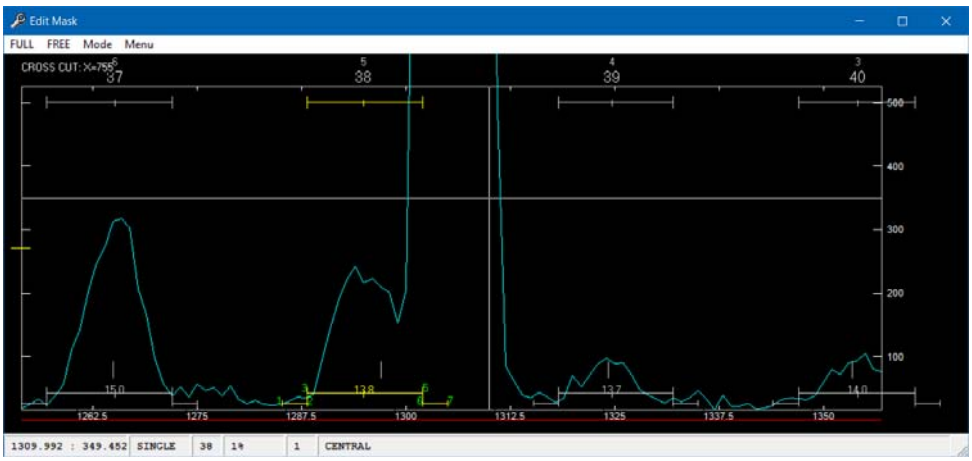


Figure 59Example of order (38) blended with a powerful line from sub-order ThAr

- **Menu/Set Backgr Zones in DECH mode (Ctrl+D**). Set all the space between the orders as inter-order zones.

- **Menu/Fit background (Crosscuts) (Ctrl+B)** . Approximate the minima using the fit parameters shown in the following figure:

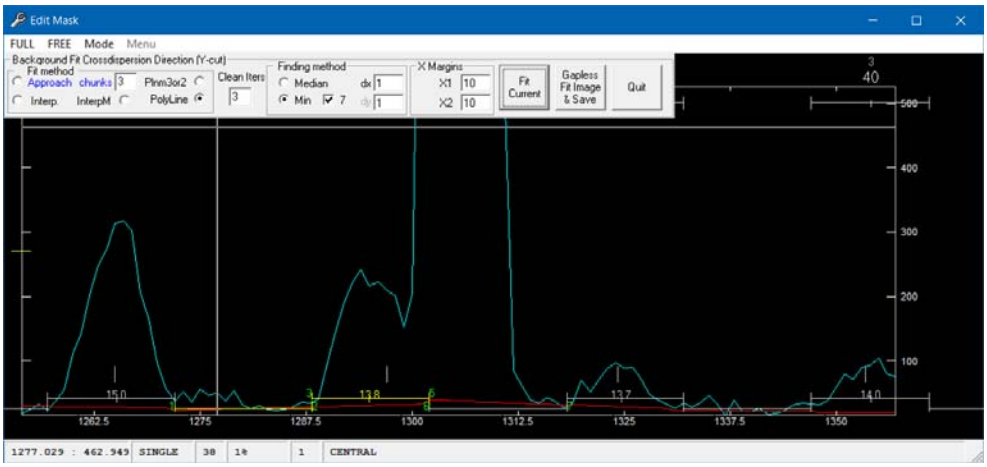


Figure 60Determination of the level of scattered light – fit over the minima.

- **Menu/Fit Background (Over Crosscuts) (Ctrl+C).** Approximate the minima along the dispersion with the parameters indicated in Figure 62.

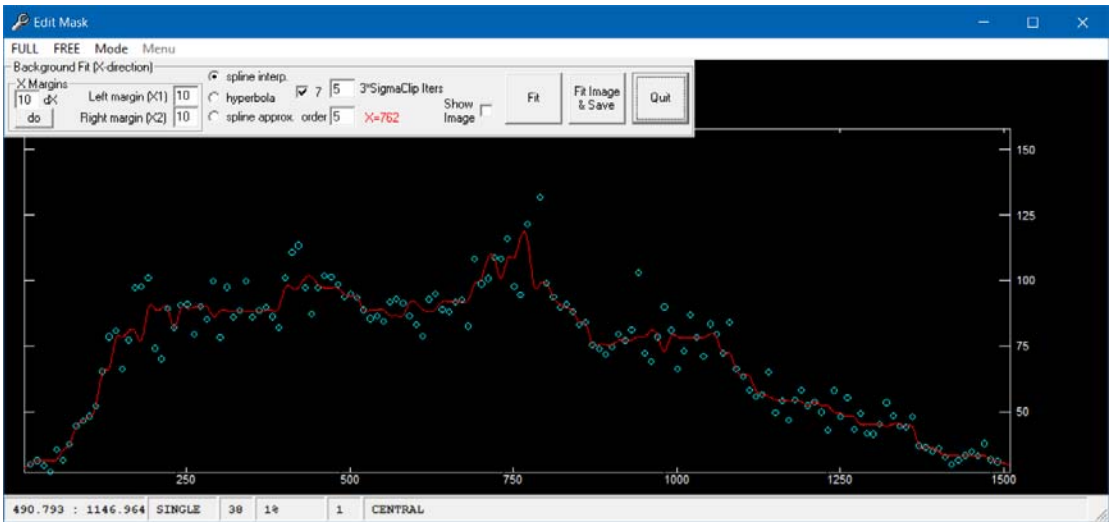


Figure 61Approximation of minima along the dispersion.

- Save the mask using **Menu / Save as IRAF - type mask.** Enter **4** and **2** values in the parameters window as it is shown in Figure 33, then press the **Fit** button. In the next window, press the **Save&Quit button** as it is shown in Figure 34. As a result, a new mask **ap20220312_019sub** appears in the **database** directory. This mask serves for extracting the stellar sub-orders. However, to extract ThAr sub-orders an another mask is necessary. It can be created using the existing one (**ap20220312_019sub**). Therefore, to keep the existing mask we recommend to rename it to, for example, **ap20220312_019sub-Obj,** where "Obj" means that mask serves for stellar sub-orders.

Mask for the ThAr sub-orders

Thus, the **ap20220312_019sub-Obj** is a template for the new mask which serves to extract ThAr sub-orders. Let's turn back to the Mask Edit mode. At first, we move the entire mask to the left, since the ThAr sub-orders are located to the left of the main ones (in the spectrum *image* with horizontal spectral orders, the ThAr sub-orders are higher than the stellar sub-orders). By default, it is impossible to change the position of spectral orders. To remove the block, uncheck the menu item **Mode / Do not move Aperture (block "4" and " M " keys)** – see Fig. Figure 22. There is one more preliminary operation: by default, all

changes occur only with the active order. This is the so-called **SINGLE** mode. To make corrections to be made simultaneously (in unison) for all spectral orders, it is necessary to make a mouse click on the **SINGLE** inscription in the status bar (highlighted with a green oval in Fig. Figure 55), then the **ALL** mode will be turned on.

After that, make activate, for example, the order 3, then place the cursor approximately in the middle of the ThAr sub-order (indicated by the green arrow in Figure Figure 55) and press the **4** key. The position of the orders (all of them!) will be changed together with all minima limits. One should also adjust the position of the left and right order boundaries using the **3** and **5 k**eys because the ThAr **sub-**orders are narrower than stellar sub-orders. It is recommended to check the mask in the area of the last orders – here they are very close one to one which the circumstance can be a source of errors. If necessary, one can adjust the position and boundaries of any spectral order after visual inspection. Remember that any correction made in the **ALL** mode affects all spectral orders.

Menu item **the Menu / Set Backgr Zones in DECH mode (Ctrl + D**) one of the methods to set the limits of inter-order minima. It is recommended as the most flexible way to find the optimal point for subsequent construction of the diffuse light curve.

Switch the **ALL** trigger to **SINGLE** and check the mask of each order individually. Upon completion of the work, check the quality of the fit **(Ctrl + B)**. Then, save the mask (**Menu / Save as IRAF- type Mask**). Since this is a mask for ThAr sub-orders, it is recommended to rename the mask, for example, to **ap20220312_019sub-ThAr**.

Finally, we have made 3 masks: one for the flat field, one for the stellar sub-orders, and one for the ThAr sub-orders). Next step is the spectra extraction.

Spectra extraction

Flat field extraction

1. Load the flat field spectrum FF fits into Dech95.exe.
2. Select **Extraction/Using Mask…**
3. In the appeared window, in the “Mask” panel, turn on the trigger **Fixed Mask for All Images** and indicate **apff** mask stored in the **database** directory. Make sure that “database” is in the same directory as the loaded FF.fits .

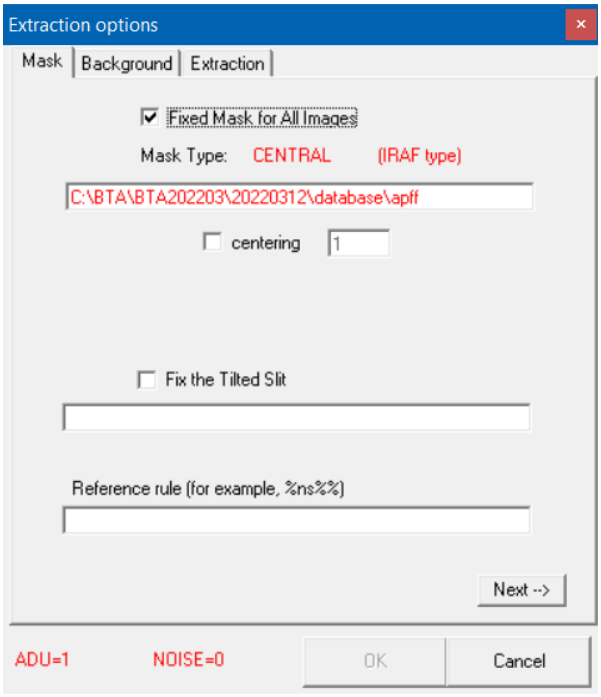


Figure 62The first panel of the extraction parameters settings window. Selecting a mask.

4. go to the **Background** panel and set all parameters as indicated below:

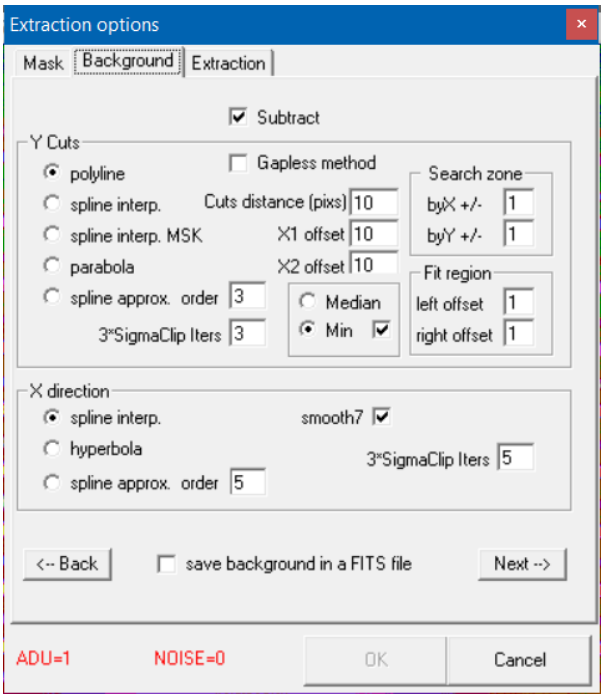


Figure 63The second panel for setting extraction parameters. Settings for taking into account scattered light.

5. go to the **Extraction** panel and set all the parameters as indicated below: the option **Remove Cosmic rays Hits** must be enabled, set **Chunk Options Size** and **nSigma** as indicated in Fig. 65. Then, click the **O**K button. Upon the extraction is complete, exit to the main menu by click on the **EndProcedure.** The extracted flat-field spectrum **FF_v file** appears in the image directory. Extracted spectra are called *vectors,* in contrast to the two-dimensional *images*

Extraction of stellar spectra (sub-order of stellar spectrum)

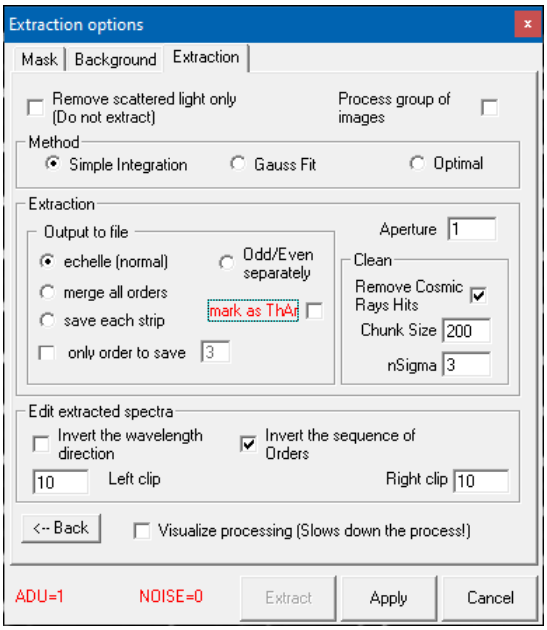


Figure 64The third panel for setting extraction parameters.

6. Return to section 3 above, but specify another mask. Now it is the ap20220312_019sub-Obj serving to extract stellar sub-orders:

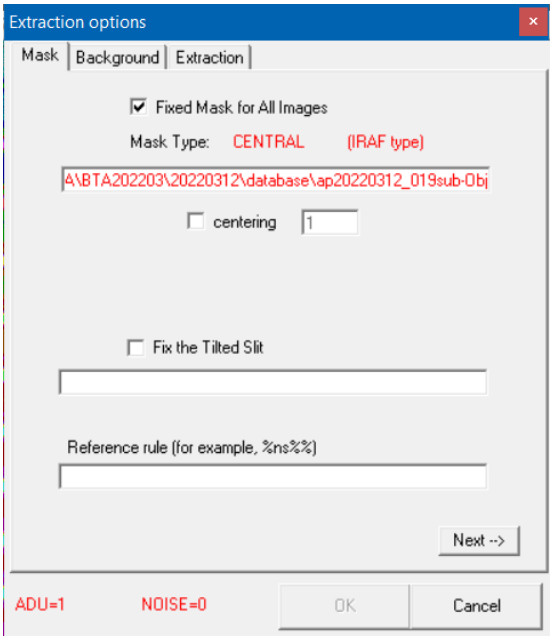


Figure 65A mask is selected for extracting sub-orders of the stellar spectrum.

7. The parameters in the second panel are the same as in Fig. 63
8. Third panel. Turn on the option **Process group of images**

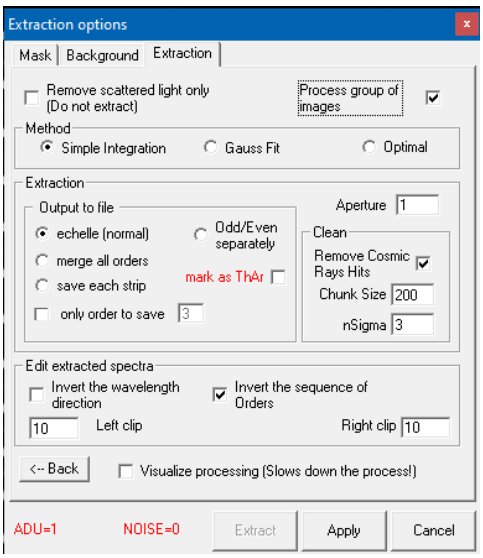
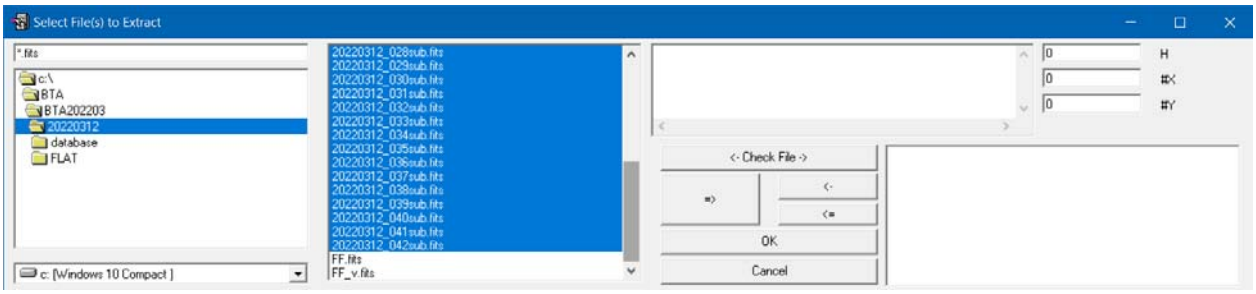


Figure 66Parameters for extracting stellar spectra (multiple files).

9. press the **OK** button. In the window for selecting files to be processed, select all spectra except the FF.fits:



Press the **=>** button, then the **OK.** Wait for the extraction to be completed.

Extraction of ThAr sub-orders in stellar spectra

10. We return to point 3, but specify another mask - **ap20220312_019sub- ThAr** :

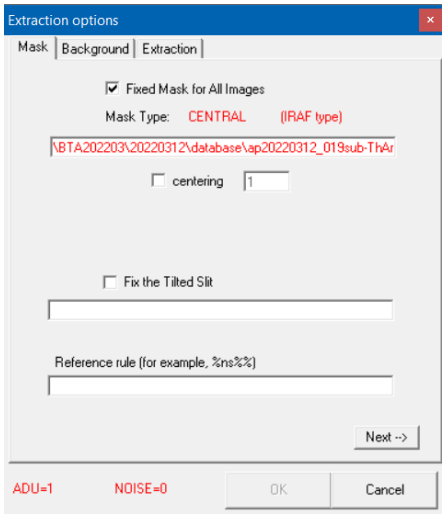


Figure 67Mask selected for sub-order extraction of the ThAr spectrum .

11. The second panel is unchanged (see Fig. 63)
12. The third panel. Turn on the options **Process group of images** and **Mark As ThAr suborders** .

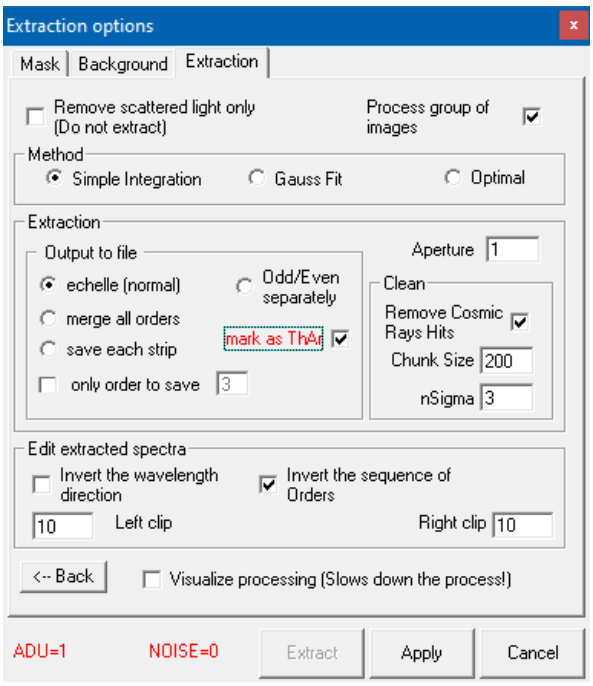


Figure 68ThAr spectra extraction parameters (multiple files).

13. press the **OK** button. In the window for selecting files to be processed, select all spectra except the FF.fits . Do not worry about the selected vectors ***_ v.fits** . After click on the **=>** button, the program automatically excludes vectors from consideration:

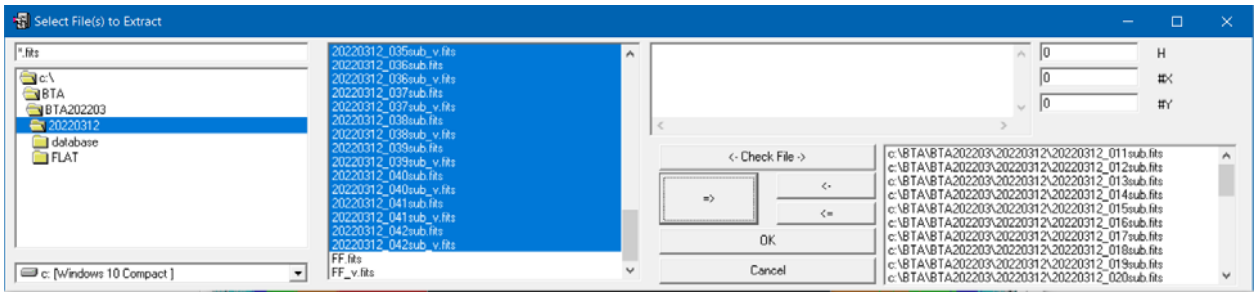


Figure 69Selecting images for spectrum extraction. Vectors are automatically rejected.

Press the **=>** button, then the **OK** button. Wait for the process to be completed. Extraction is done.

The flat field correction for fiber-feed spectrographs is usually performed with the extracted spectra (not with images). For the FFOREST spectra we follow this rule.

1. It is more convenient to transfer the extracted spectra (vectors) to a separate directory, say VECTORS . First, we transfer here only the stellar spectra and the flat field spectrum.
2. Now work with the program **dech-fits.** Use menu item **File / Divide group of FITS files by a FITS file.** Select all files except **FF_v.fits ,** then click on = > button, then click on OK .

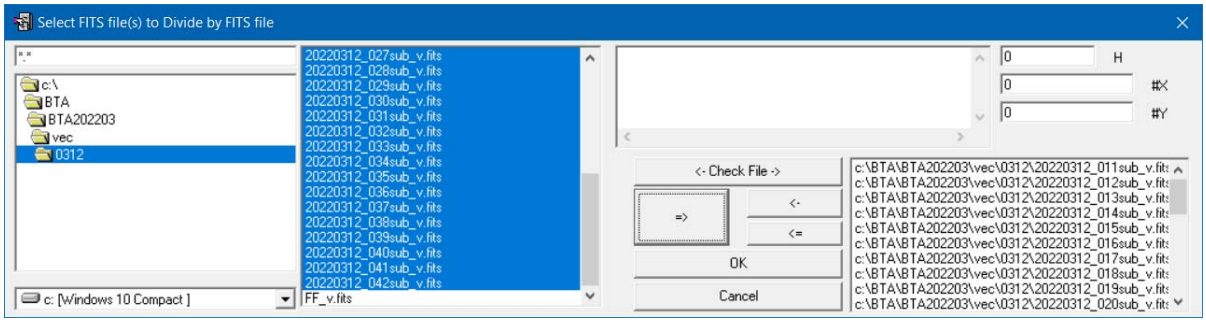


Figure 70Spectra selected for the flat-field correction.

3. In the next window, click on the inscription **Click Here to select Divisor file** and then select **FF_v.fits :**

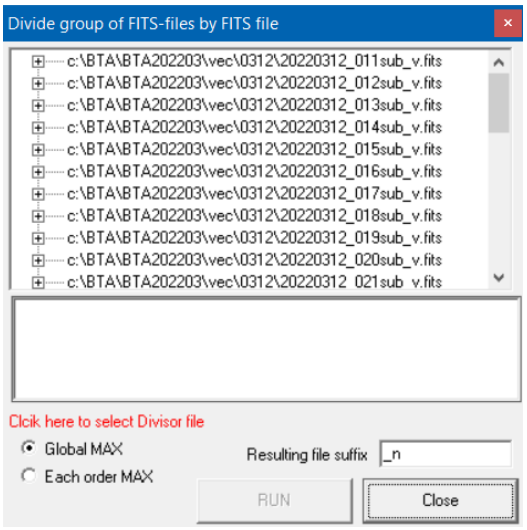


Figure 71Parameters of the window for dividing a group of FITS files by a FITS file.

4. Press the **RUN** button and wait for the process to finish. Then press the **CLOSE** button and exit the program. New files ending with the "**_n.fits"** suffix in their names appear in the **VECTORS** directory. Now original, not corrected for the flat-field files can be deleted:

Del *v.fits

Then we can rename the ***v_n.fits** to ***v.fits** to make the names a bit more short:

Shortname *.fits _n

5. We move the files ***_ThAr.fits** from the directory with images to the **VECTORS** directory.

Cleaning ThAr spectra from traces of cosmic particles (optional)

Launch dech95.exe in the **VECTORS** directory. Use **Tools/Average&clean vectors**. Select all ***_ThAr.fits** files .

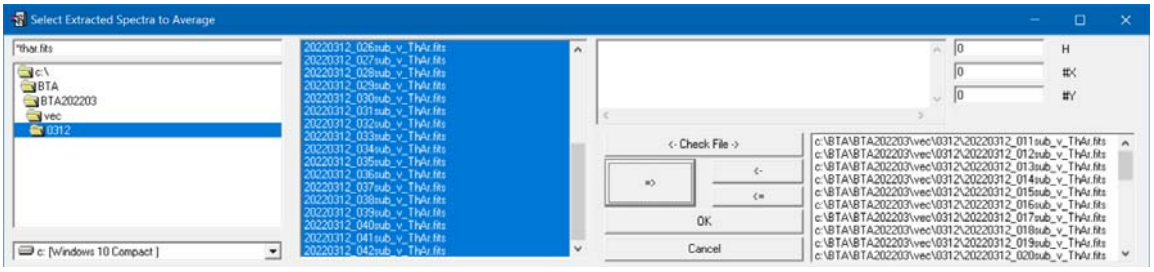


*Figure 72All vectors *_ ThAr . fits selected*

Click on the button **=>**, then **OK**. Set the parameters in the appeared window as it is shown:

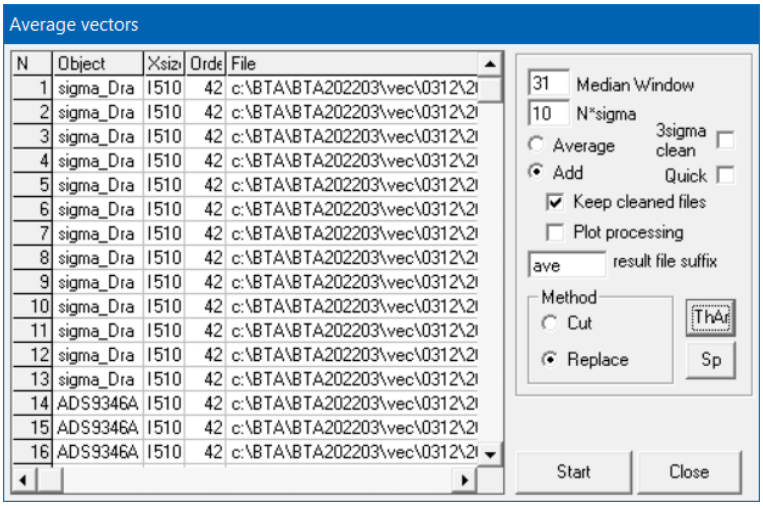


Figure 73ThAr spectra from traces of cosmic particles.

Click on the **Start** button and wait for the process to finish. The created ***_ThAr_cl.fits** and ***ave*** files appear in the **VECTORS** directory. The original ***_ ThAr . fits** can be moved to the newly created **ORIG** directory**.** The ***ave*** files can be deleted:

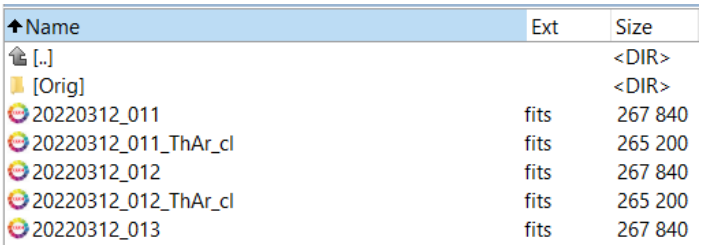
Del *ave*

Identification of the comparison spectrum

For the convenience, we recommend to shorten the names of the files in the **VECTORS** directory:

Shortname *.fits sub_v

This command removes **Sub_v** from the names of all the files in the directory. So, finally we get a paired set of files – each file with a **stellar spectrum** has a corresponding file with a **ThAr comparison spectrum** (**_cl** is added to the file name if the clean was applied as an option of the spectra extraction procedure – see the previous chapter):



Name	Ext	Size
[..]		<DIR>
[Orig]		<DIR>
20220312_011	fits	267 840
20220312_011_ThAr_cl	fits	265 200
20220312_012	fits	267 840
20220312_012_ThAr_cl	fits	265 200
20220312_013	fits	267 840

Figure 74Paired set of files

1. Spectrum revision:

rfits EXPTIME DATE DECH-HJD-OBS *ThAr *.fits > !log.log

It is shown in the **!log.log** that the first spectrum has a short exposure time, i.e. has to be removed from consideration.

EXPTIME DATE	DECH-HJD-OBS	*cl.fits
60.00160	2022-03-12T20:38:30	20220312_011_ThAr_cl.fits
300.00159	2022-03-12T20:44:08	20220312_012_ThAr_cl.fits
300.00159	2022-03-12T20:49:21	20220312_013_ThAr_cl.fits
300.00159	2022-03-12T20:54:34	20220312_014_ThAr_cl.fits
300.00159	2022-03-12T20:59:47	20220312_015_ThAr_cl.fits

Figure 75List of spectra with information about exposure time and observation date.

Both **20220312_011_ThAr_cl.fits** and **20220312_011.fits** files can be removed from the VECTORS directory. The remaining spectra have approximately the same accumulation level, so let's work with the first one:

Dech-fits 20220312_013_ThAr_cl.fits

or

Dech-fits 20220312_013_ ThAr.fits if the cleaning was omitted.

In general, for lines identification in a ThAr spectrum one needs in a ThAr atlas or in the already identified ThAr spectrum. The simplest solution occurs If the latter is an identified ThAr spectrum carried out with the same spectrograph in the same configuration. One can use the list of ThAr lines from the IRAF package. In our case, this file is called **ThAr-iraf.lin**. This file has to be loaded into both spectra: the ThAr spectrum which is already identified (it serves as a ThAr atlas) and another one we are working with. To load a ***.lin** file, use **Help Load Identification (* .LIN file)** procedure in **dech-fits.exe**. In the identified spectrum, many lines will be shown as identified ones, but in a spectrum to be identified nothing is seen because of the absence of the wavelengths scale. Now one needs to find the same parts of the spectrum in both files, as shown in the figure below. For clarity, it is recommended to place the spectra's windows one under the other using the procedure **Window / Tile option Horizontal** in **dech-fits.exe**:

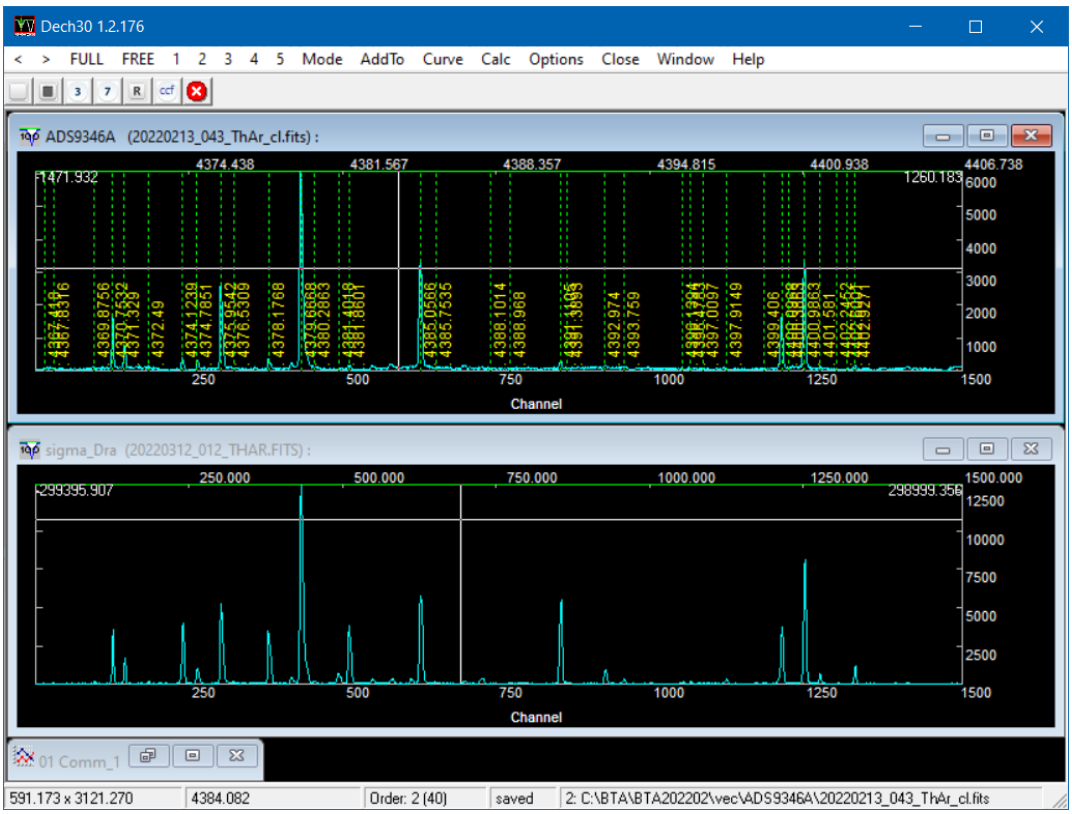


Figure 76Two ThAr spectra with and without wavelength scale.

2. Activate the procedure for creating a wavelength scale **Curve / Dispersion Curve Workshop / Create It(Ctrl+ K)** in the lower (unidentified) spectrum in**.** It is more convenient to work with small sections of the spectrum, to make the wavelength data and line profile details well seen.

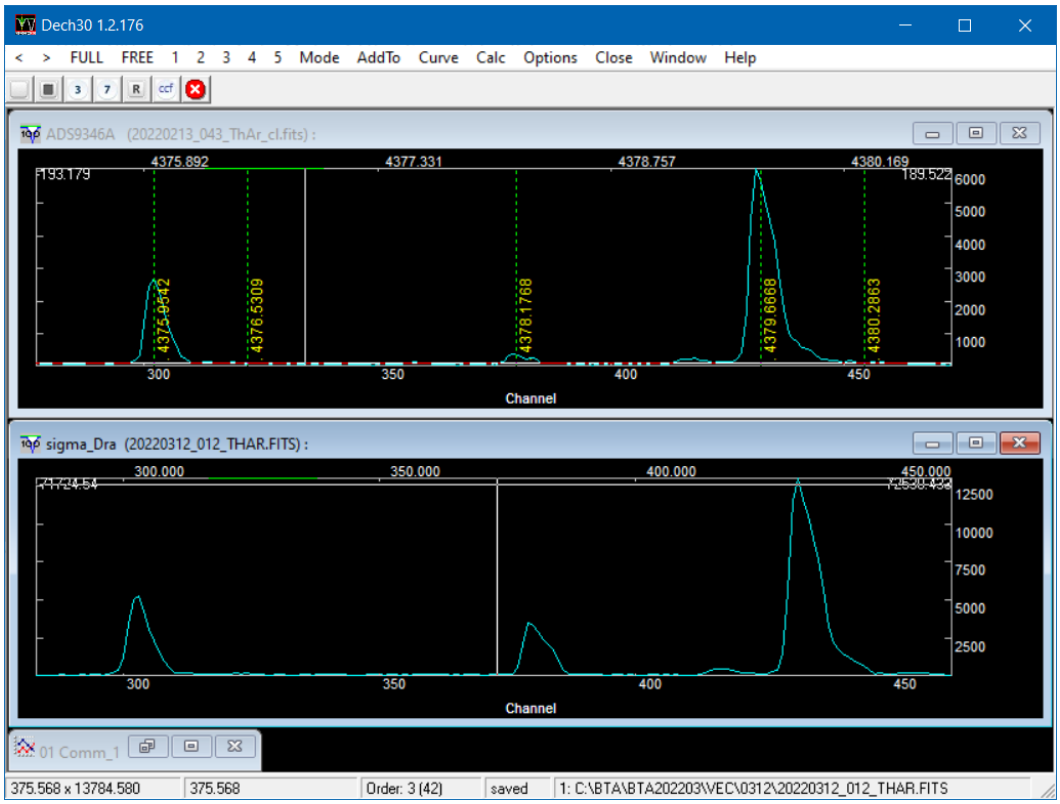


Figure 77A fragment of the spectrum from the previous figure.

To identify a line, move the cursor to approximately the middle of its profile and press the key **F** and enter the wavelength indicated on the above (identified) spectrum. For example, the leftmost line has a wavelength of 4375.9542 Angstroms. The one in the center is 4378.1768, and the one on the right is 4379.6668. Thus, using the key **F** we identify all 3 reference lines.

Note: the key **F** places the reference point at the line's center of gravity. If one use the **I** key instead of **F**, the reference point will be placed exactly where the cursor is locat6ed. To delete the nearest reference point, press **D** (after the word "Delete").

If the position of the reference point needs to be corrected (this may happen if the line is not symmetrical or is blended with nearby lines), move the cursor to the identified line and hit the **B** key. A mirror profile of the line appears. Using the left/right arrows on the keyboard, align the profiles in the position where the center of the line expected to be located. The vertical dashed line serves as a hint – the reference point is placed in its position. To finish the work, press the **Esc** key.

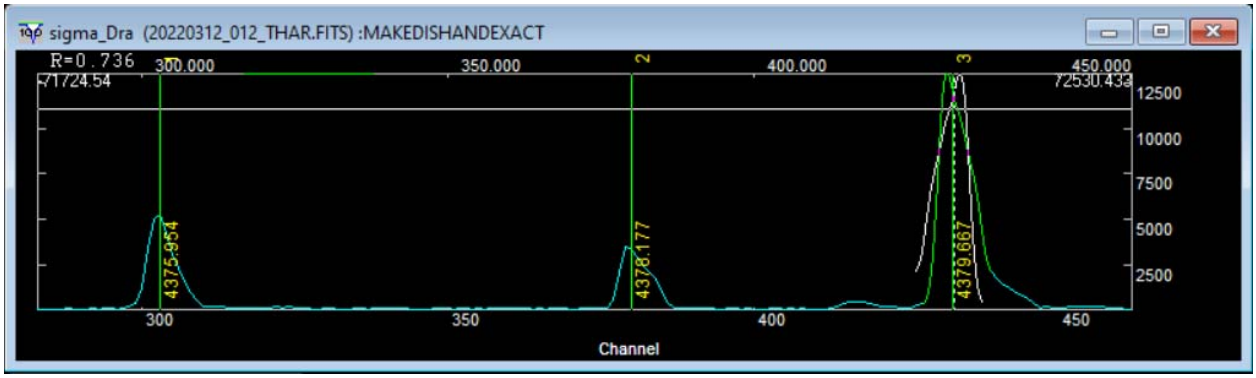


Figure 78The line with its mirror profile is shown on the right.

Now click on **Approach** or hit the **F10** key. Then the click on the buttons **Save Marks** and **Approach**. The program asks for the degree of the polynomial fit. Since only three points were identified, the maximum possible polynomial degree is 2. So, enter 2 and look at the result:

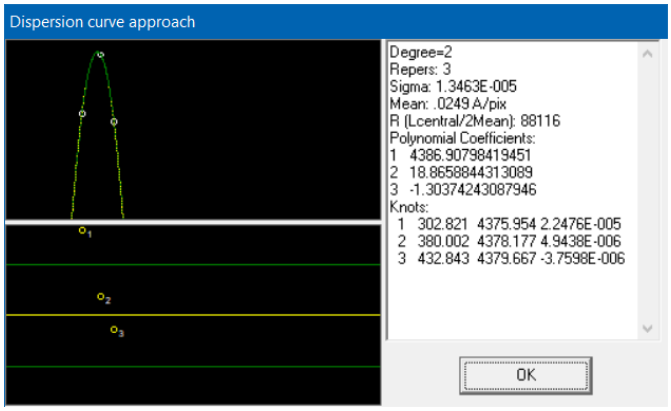


Figure 79Results of approximation of three dispersion curve reference points.

Press the **OK** button and return to the spectrum. Now we need to identify the remaining lines. It is easier to do this now, since we already have a "rough" wavelength scale. It is more convenient to work with spectrum fragments. Spectrum in the window is divided to 5 fragments from left to right – use menu options **1, 2, 3, 4, 5** at the top to select a desired fragment. Since the wavelength scale is available now, one can see how well our spectrum matches the sample. Use **Window/All windows to the same range (Ctrl+A)** . The figure below shows that the identification of the 2 extreme lines need to be corrected.

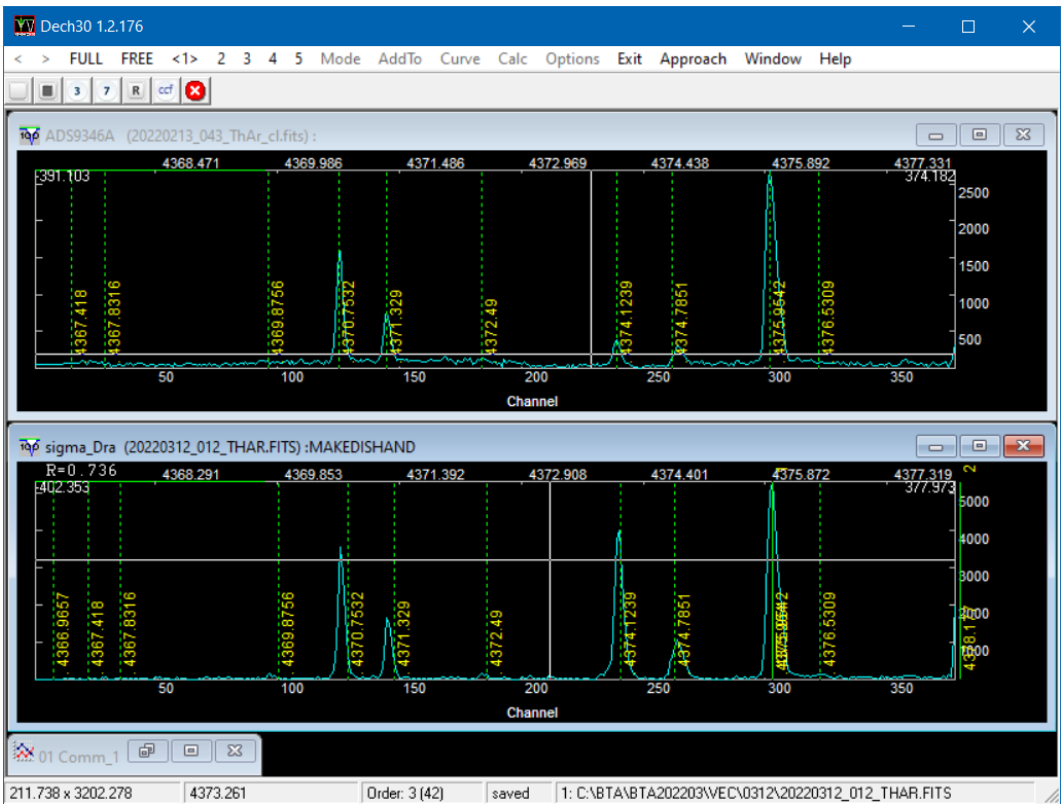


Figure 80Fragment 1 of the processed and sample spectrum after fit over 3 identified spectral lines. It is evident that the wavelength scale has to be corrected.

Move the cursor to the center of the line and hit the **F** key. The program asks to enter the wavelength from the loaded list (**ThAr-iraf.lin** in our case**)**. You can move left and right along the list using the virtual buttons. Finally, you can enter the wavelength manually if the line is not in available in the loaded list. Hit the **OK** button and continue the lines identification over the entire spectral order. Periodically perform a fit over the identified lines to correct the wavelength scale. At this stage, it is not recommended to enter a polynomial degree higher than 3. When the identified lines are placed throughout the entire order, perform a fit with a polynomial degree of 5:

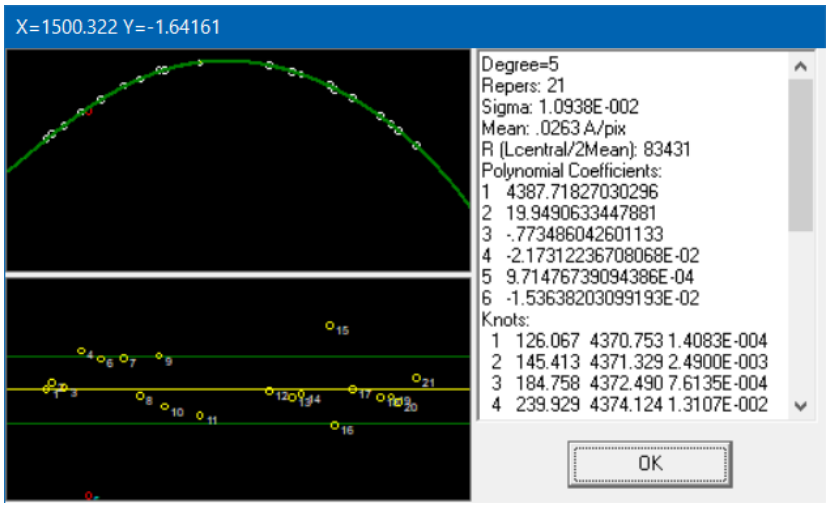


Figure 81Result of approximation by a 5th degree polynomial. It is evident that there is at least one "bad" mark (e.g., the number 3 in the bottom of the lower panel).

Hit **OK** button, delete the "bad" marks if any, then make the fit again until the lack of outliners.

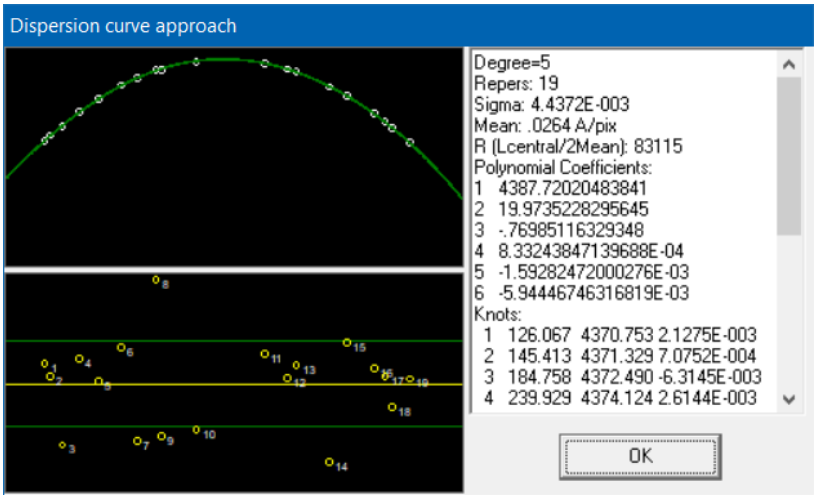


Figure 82An example of a good quality dispersion curve. We observe a "cloud" of points without outliers. The dispersion of the marks 0.004 A is significantly lower than the linear dispersion 0.0264 A/pix.

Press **OK** , then exit the procedure - click on the **Exit** menu item. However, it is necessary to identify at least one more spectral order. It is recommended do not work with the neighboring one. For example, if the identified spectral order is 3, the next order to be identified could be 5.

One can proceed to the creation of a global dispersion curve that links both the pixel number in a spectral order with order's numbers. This solution is called a two-dimensional polynomial which can invoked via **Curve/Dispersion Curve Workshop/Global fit & Create FDS file.** The appeared parameters panel is shown below:

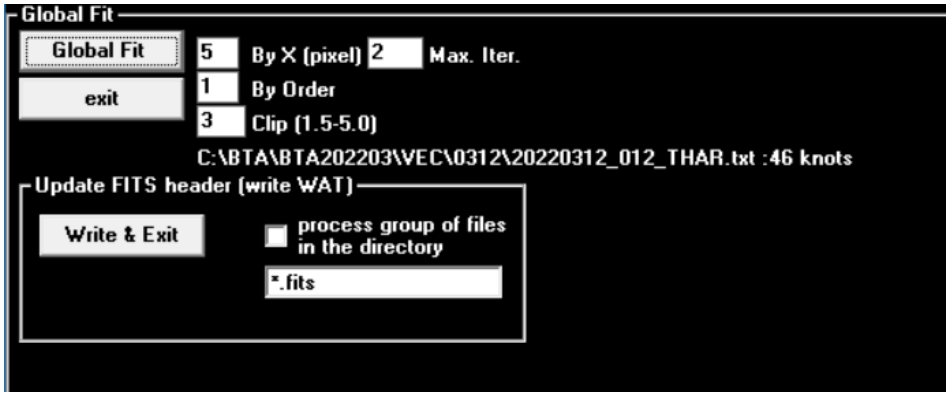


Figure 83Parameters of a fit by a two-dimensional polynomial.

At this point we have only 2 identified orders, so the degree of the polynomial in orders (**By Order**) cannot be greater than 1. The degree of the polynomial within one order (by pixels) remains the same, i.e. 5. We will leave the maximum number of iterations at 2 for now.

Click on the **Global Fit** button. The appeared window shows three graphs and a large number of buttons on the right. The upper graph shows the deviation of the marks from the fitting curve in the pixel scale, the middle one shows the deviation in the order scale and, the lower one shows the deviation in the wavelength scale. The buttons with numbers are used to check the location of the marks in the corresponding spectral order. Click on the **OK** button to return to the previous window (Fig. 84). Then, click the **Write & Exit** button. As a result - all orders have a wavelength scale. Due to the extrapolation, the deviation of the wavelengths of the spectral lines from the correct one can reach significant values. Therefore, it is necessary to identify each order, especially the first and the last one to avoid an extrapolation. Then repeat the global fit with the correct value of the degree of the polynomial **By Order**.

It is recommended to make an approximation after identifying, say, the first, last, and two-three additional in between orders.

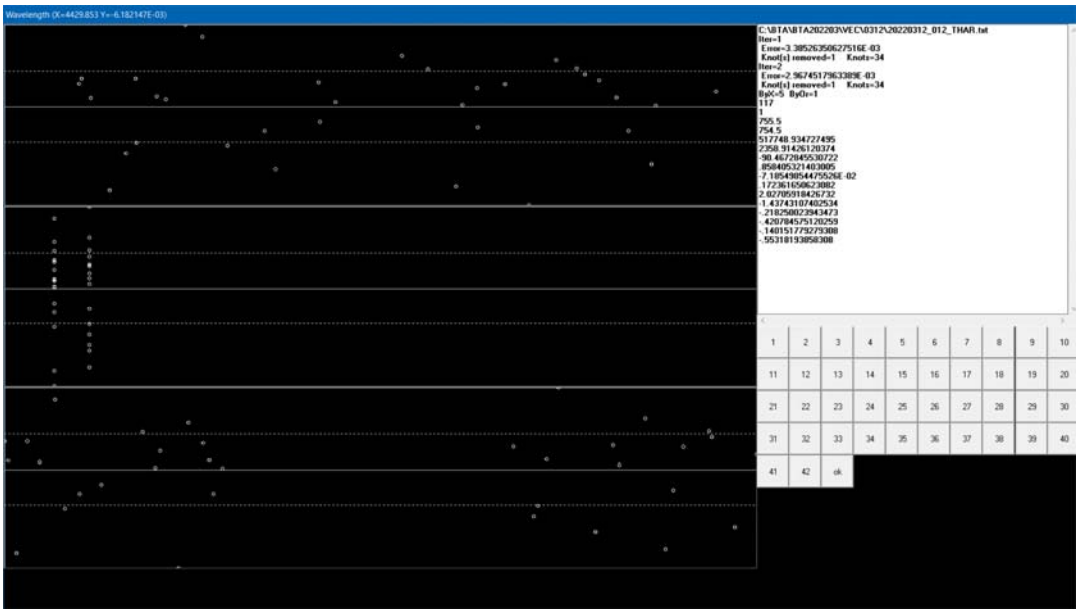


Figure 84Result of approximating 2-order frames with a two-dimensional polynomial.

So, let's identify the lines in the first order:

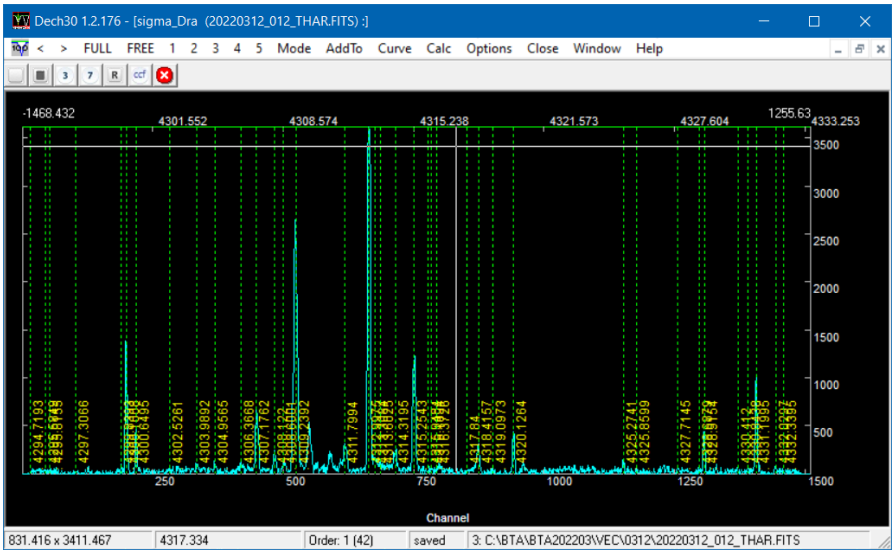


Figure 85First order. It is seen that the identification matches the spectral lines well.

It is clear that the global polynomial has coped well with the extrapolation and the identification matches the position of the lines well. Now let's work once again with the procedure for constructing the dispersion curve **Ctrl + K**. Hit the **L** key. A menu for load the identification marks appears. Set the parameters as it is shown in the figure below:

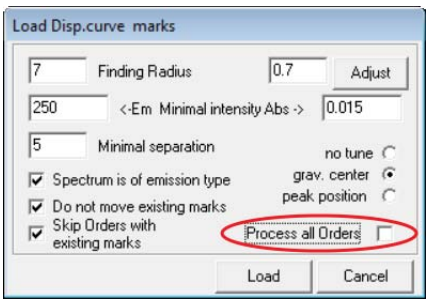


Figure 86Parameters of the identification line loading procedure.

Parameter **250** is used to cut off the weak lines, i.e. **250** is a minimum line's intensity that program will consider to be loaded. We process only the current order. It is indicated that the spectrum is emission. Click on the **Load** button**.**

Now run the polynomial fit via hit the **F10** key or click on the **Approach** menu item using the 5th degree polynomial.

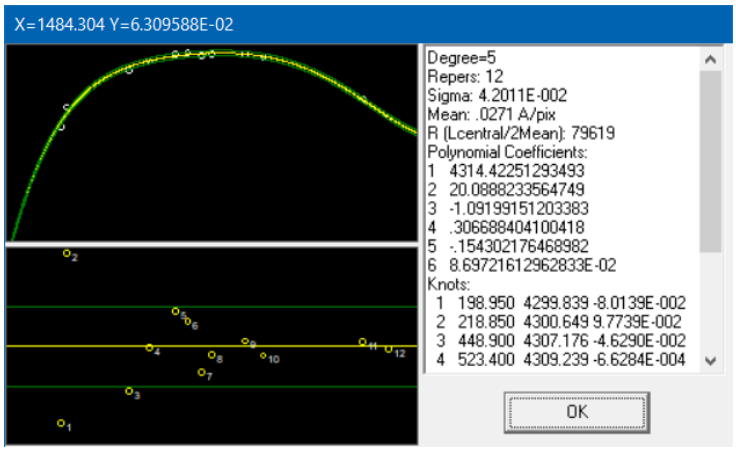


Figure 87First order approximation.

It is clear that the average error is too large. Let's try to remove the first 2 marks and make a fit using the 3rd degree. Now the solution looks better:

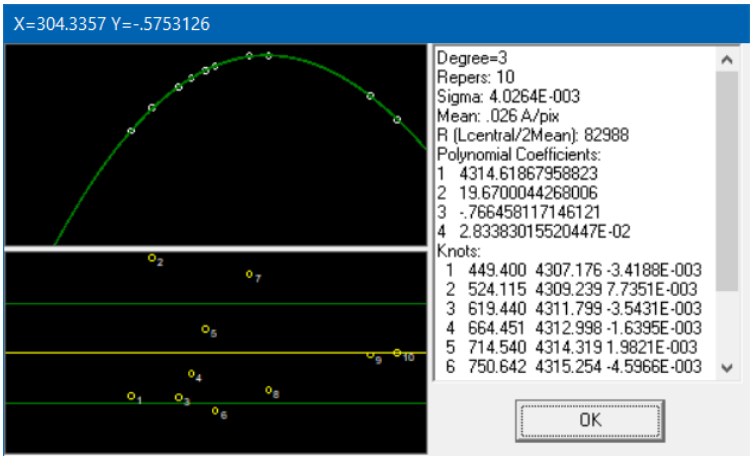


Figure 88First order approximation after removing two frames.

Let's look at the right part of the current spectral order and add some marks using the **F** key.

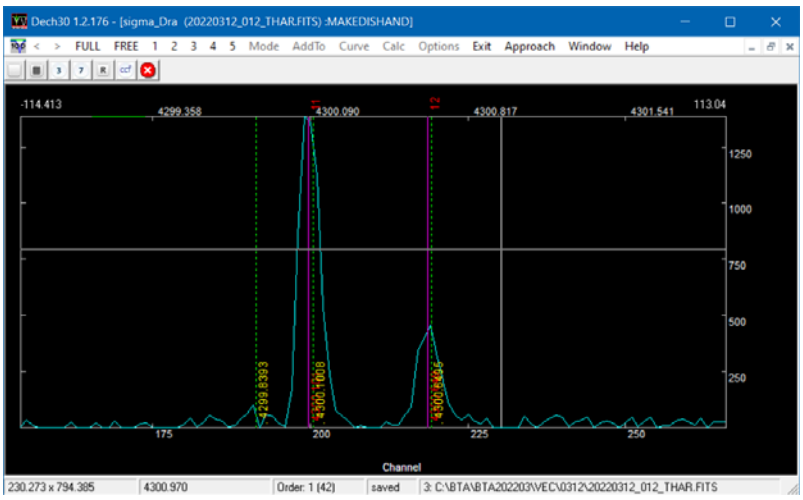


*Figure 89Added 2 anchors using the **F key .***

We again perform the fit with 5th degree polynomial. Now the solution looks better:

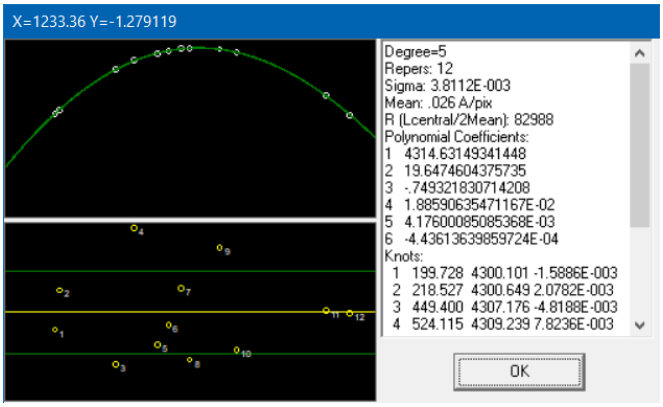


Figure 90Final solution for 1st order.

Let's identify the last, 42nd order. There are few lines here, so we use only the **F** key (no the **L** key to be used). Due to the very distant extrapolation, a discrepancy between the identification and the position of the spectral lines is noticeable. However, the discrepancy is insignificant and does not interfere with the placement of marks:

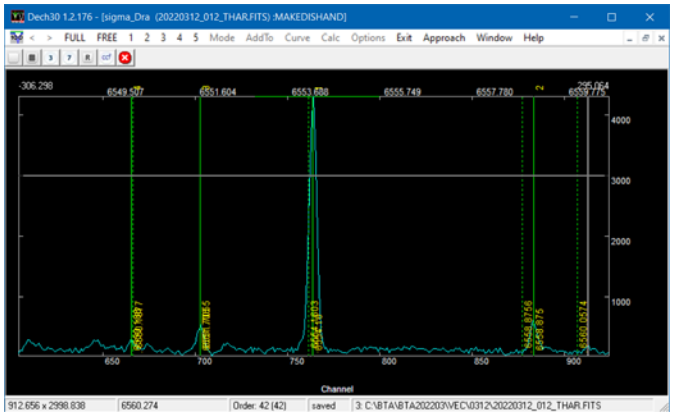


*Figure 91Order 42 **before** approximation. Identification and position of the reference points show some discrepancy.*

There are very few marks in the wavelength range of the 42nd order, so we use a polynomial of the 3rd degree. For reliable fit for the last orders of the spectrum, one should identify a some additional order,

say the 41st one. There are too few marks in the wavelength range of this order too, thus the 3rd degree polynomial fit must be used. Finally, one should to identify an additional spectral order in the central part of the spectrum, say, the 20th one using the 5th degree polynomial fir. After that one can return to the main menu.

Now is time to make a global fit once again: use the menu item **Curve/Dispersion Curve Workshop/Global fit & Create FDS file**. Let's increase the degree **by Order** - set it to 2. Do not forget to save the new wavelength solution by click on the **Write & Exit** button. After that let's go, say, to the order number 2, enter the procedure for creating a dispersion curve **(Ctrl + K)**, press the **L** key and set other parameters - now is time to process all spectral orders:

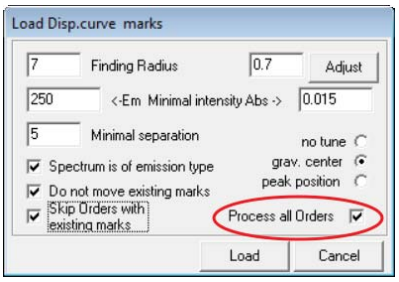


Figure 92Parameters for loading benchmarks across the entire spectrum.

Click on the **Load** button. After finishing the work, return to the main menu. Repeat the global fit once again using the menu item **Curve/Dispersion Curve Workshop/Global fit & Create FDS file** . Let's increase the degree **by Order** – set it to 4. Also, set the maximum possible number of iterations to 20 (instead of 2 shown in the figure below):

Figure 93Parameters of the two-dimensional polynomial for approximation of all orders

Click on **Global Fit** button. A new window appears:

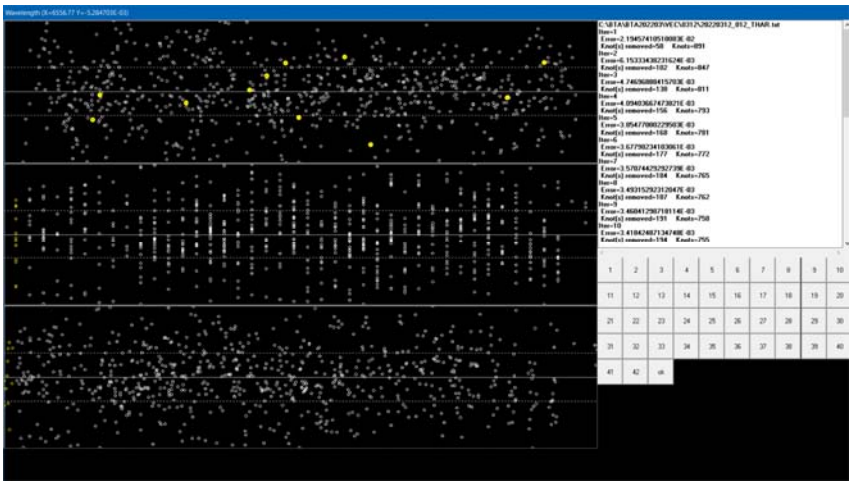


Figure 94Results of approximation of marks of all orders. It is evident that there are no trends, i.e. the degrees of the polynomials are chosen correctly.

Click onthe **OK** button, return to the previous menu. Here we turn on the trigger **Process group of files in the directory**. Select all extracted spectra including both sub-orders of stellar spectra and ThAr spectra. Click on the **Write& Exit** button. Upon completion of the procedure, exit the **dech-fits** program.

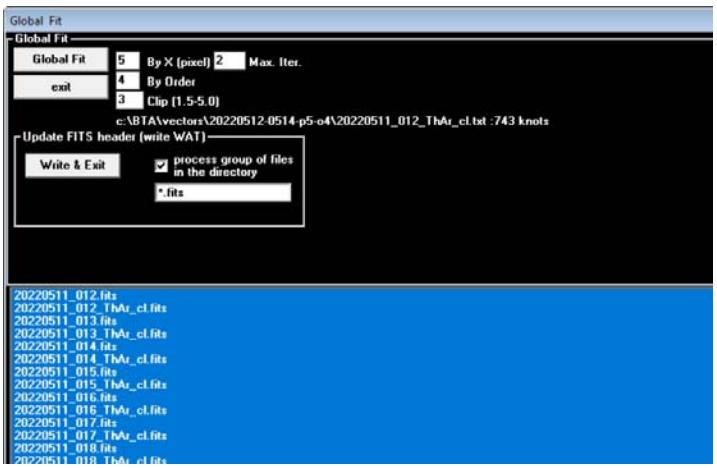


Figure 95Recording the wavelength scale in the IRAF format into the "body" of selected spectra.

Calculation of heliocentric corrections and Julian dates

Move to the directory with extracted spectra. (Now these spectra are "equipped" with a wavelength scale). Let's create a separate directory for the ThAr files, say, the **ThAr** directory and copy to there the spectrum **20220312_012_ THAR . fits** and all related files:

20220312_012_thar	dcm
20220312_012_THAR	fds
20220312_012_ThAr	fits
20220312_012_THAR	glb
20220312_012_THAR	txt

We distribute all the files into separate directories accordingly to the object name stored in the OBJECT keyword in the FITS header of each file:

Mv2dirs OBJECT *.fits

Program creates directories with the names of the objects specified in the OBJECT keyword of each file. The files will be moved to a corresponding directory:

[..]		<DIR>
[ADS9346A]		<DIR>
[ADS9346B]		<DIR>
[lowsn]		<DIR>
[Orig]		<DIR>
[SIGMA_DRA]		<DIR>
[ThAr]		<DIR>
[TOI-1797]		<DIR>
!log	log	1 892

In the SIMBAD database one can find the accurate coordinates for each object. For example:

ICRS coord. *(ep=J2000) :* **14 41 00.8517057456 +57 57 28.073178972 (Optical)**

Go to the **ADS9346A** directory and enter the command:

rvcorr *.fits 2000.0 14 41 00.85 +57 57 28.07 SAO

Instead of entering the star coordinates, you can create the file **RVCORR.DATA** with the coordinates of the program stars and with the location of observations (only SAO is available for now). An example of such a file:

```
SUN       2000.0 0 0 0 0 0 0 SAO
TOI 1568 2000.0 00 35 57.29 +65 01 34.24 SAO
MUCAS 2000.0 01 08 16.30 +54 55 12.56 SAO
TOI 1598 2000.0 01 54 38.50 +37 00 18.45 SAO
TOI1797 2000.0 10 51 06.51 +25 38 28.19 SAO
ADS9346 A 2000.0 14 41 00.85 +57 57 28.07 SAO
ADS9346 B 2000.0 14 41 01.56 +57 57 33.11 SAO
CHIDRA 2000.0 18 21 03.38 +72 43 58.25 SAO
SIGDRA 2000.0 19 32 21.59 +69 39 40.24 SAO
TOI1455 2000.0 20 34 40.78 +66 26 25.06 SAO
TOI1408 2000.0 20 54 02.61 +72 34 49.88 SAO
ADS15571A 2000.0 21 58 12.67 +82 52 10.56 SAO
ADS15571B 2000.0 21 58 19.73 +82 52 15.84 SAO
IOTPEG 2000.0 22 07 00.67 +25 20 42.36 SAO
TOI1516 2000.0 22 40 20.26 +69 30 13.45 SAO
OTAND 2000.0 23 20 01.22 +41 45 17.47 SAO
V413AND 2000.0 23 54 04.04 +39 16 57.04 SAO
```

Then the program can be launched in a short form, for example:

Rvcorr * .fits ADS9346A

The result of the program work is the definition of the heliocentric date, heliocentric corrections and corrections to the Local Standard of Rest stored into the bodies of all the files in the current directory. All these values are entered into the FITS header of the processed files.

In the same way, we make corrections to the spectra of all objects.

Creating a mask for cross-correlation

The displacement of spectra relative to each other is measured using the cross-correlation method. However, spectra may contain sections unsuitable for cross-correlation. Therefore, it is recommended the use of a mask created for each object. The mask is a list of wavelengths limits of fragments (chunks) suitable for cross-correlation. To create a mask, one of the spectra with a good S?N must be selected. Then, in the **DECH-FITS** program, one has to use the procedure **Curve / Masks & etc / Make CCF - chunks mask** (Fig. 96):

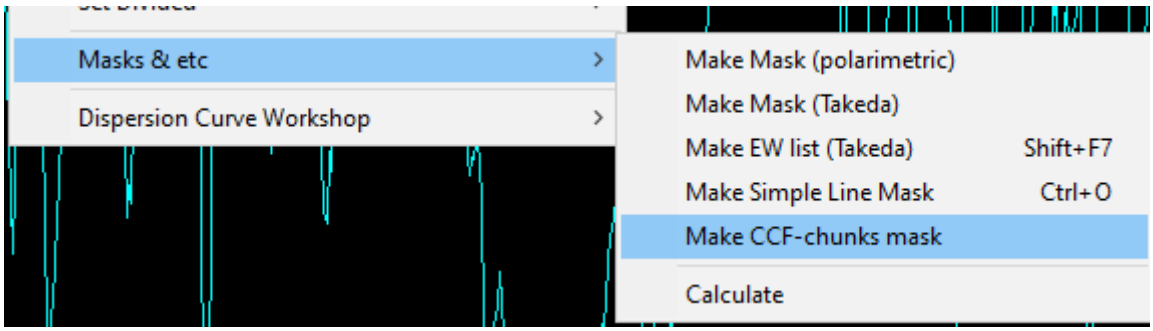


Figure 96.

The sections of a stellar spectrum selected for the analysis should not contain emissions from the nearby ThAr spectrum and other artifacts of the non-stellar origin.

The result of this procedure is a created mask file with the ***.ccfm** extension. An example of a mask fragment:

```
DECH CCF CHUNKS
4372.35 4379.897
4386.217 4396.08
4411.278 4414.703
4419.462 4422.021
4423.501 4435.707
4445.598 4450.299
…continuation
```

Measuring the displacements

First, we create a list of spectra with the information about the exposure time, the date of observations, the heliocentric Julian date, and the heliocentric radial velocity correction:

rfits OBJECT EXPTIME DATE DECH-RA DECH-HJD-OBS VHELIO *.fits > !log.txt

If there are some not well exposed spectra, they have to be removed or moved to a separate directory named, say, LOWSN. These spectra should not be used them for measurements. In addition, the **rfits** command allows one to ensure that both the heliocentric date and the heliocentric radial velocity correction are available in all the files to be analyzed.

It is recommended to begin the work with a radial velocity standard star. It must be observed every night. In our case, this is the star SIGMA DRA. The radial velocity of the objects of the interest have to be corrected taking into account the radial velocity of the standard.

So, we run the **DECH-FITS** command in the directory with spectra, which should contain both the spectra of the objects themselves and the corresponding ThAr spectra :

20210730_007	ccfm	2 850
20210729_007	fits	252 840
20210729_007_ThAr	fits	252 840
20210729_008	fits	252 840
20210729_008_ThAr	fits	252 840
20210729_009	fits	252 840
20210729_009_ThAr	fits	252 840
20210729_010	fits	252 840
20210729_010_ThAr	fits	252 840
20210729_011	fits	252 840
20210729_011_ThAr	fits	252 840
20210729_012	fits	252 840
20210729_012_ThAr	fits	252 840

To enter the measurement procedure, use the **CCF button** of the DECH-FITS program. See Figure 97:

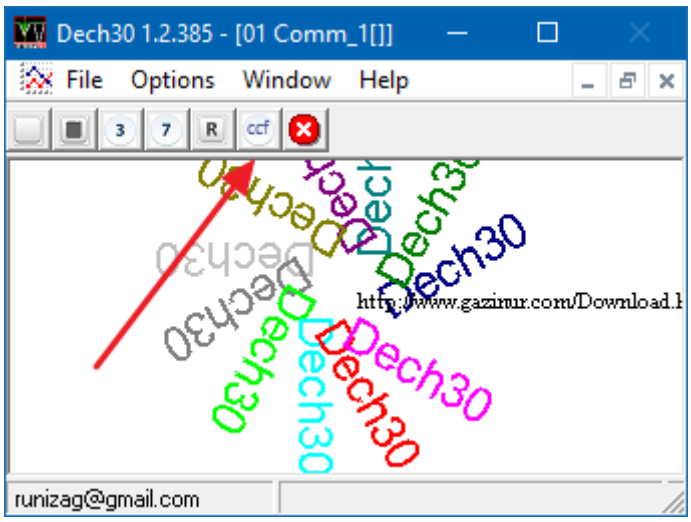


Figure 97

Now we select a group of files for the cross-correlation:

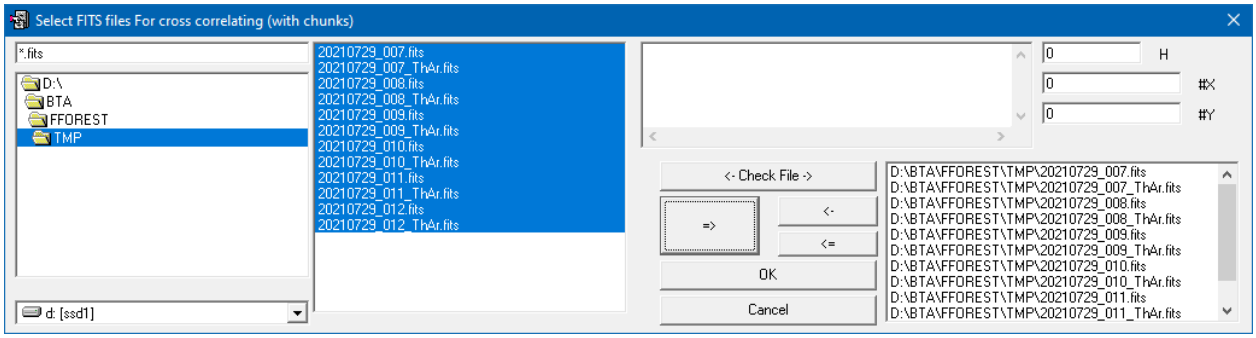


Figure 98

We set the calculation parameters in the new window for calculating the cross-correlation function and offsets:

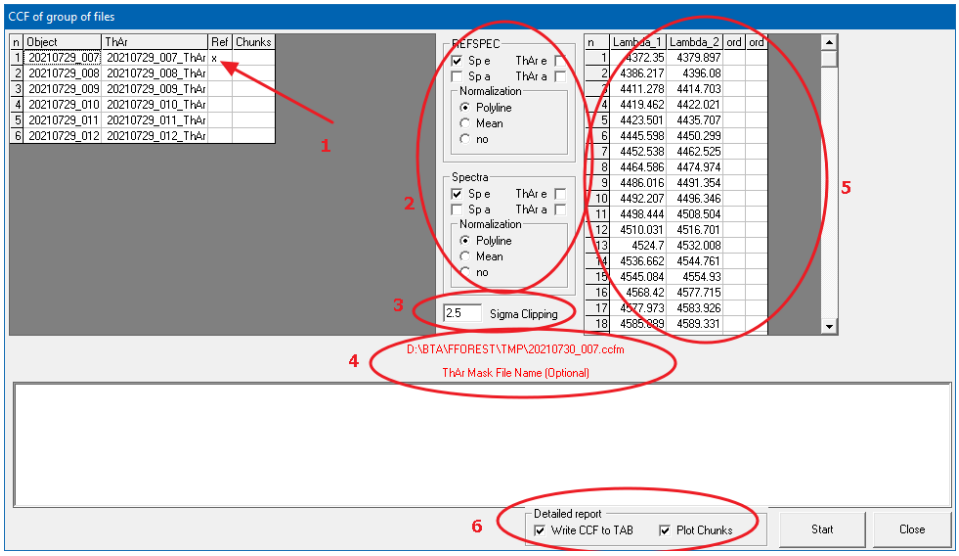


Figure 99

In Figure 99:

1 – the spectrum (a template or REFSPEC) relative to which the displacements will be measured is indicated with a cross in the **Ref** column. In this case, the spectrum **20210729_007** is indicated**,** i.e. the calculation results will be written to the **rez_vs_20210729_007** directory. To select another template, simply click the mouse in the corresponding field of the **Ref** column**, 2** – settings of the cleaning from the artifacts for the template (here marked as REFSPEC) and for the rest of the spectra. The spectra themselves and the corresponding ThAr spectra can be processed in the different way. It is recommended to refuse any cleaning for the ThAr spectra, as it is shown in the picture. One can also select the method of the spectrum normalization (division by pseudo-continuum; division by a constant; no normalization). Division by a pseudo-continuum is preferable. **3** – parameter ***k*.** After all the displacement calculations are completed, the average radial velocity is calculated for all sections of the mask (chunks). In this case, cyclic cleaning from outliers is performed according to the criterion ***k**** Sigma , **4 –** here you can select a mask. If there is only one mask in the working directory, it is specified automatically. To change the mask, click the mouse on the mask file name. For ThAr spectra, it is also possible to specify a mask. If it is not available, the cross-correlation of ThAr spectral orders will be performed for entire of orders, but this reduces the accuracy. Therefore, the presence of a ThAr mask is recommended. Criterion for selecting areas for a mask

in the ThAr spectrum is the following: very strong isolated lines should be avoided. It is optimal if the selected area contains several emission lines of the comparable intensity, **5** – list of the chunks' wavelength in the selected mask, **6** – parameters serves to write the extended information in the resulting output data. For the newly studied hardware or a new type of objects, it may be useful to have the extended output information. The first option in this section creates tables with the cross-correlation function for each chunk in the **rez_vs_20210729_007/CCF** directory. The second option creates graphs for all spectral chunks and the cross-correlation functions of the entire sample in **the rez_vs_20210729_007/Chunks** and **rez_vs_20210729_007/Chunks-ThAr** directories. for object spectra and ThAr spectra separately. Enabling these options slows down the work, creates many files, which requires additional disk space.

To start the calculations, click on the **Start** button. When the calculations are complete, appears something like this (Fig. 100):

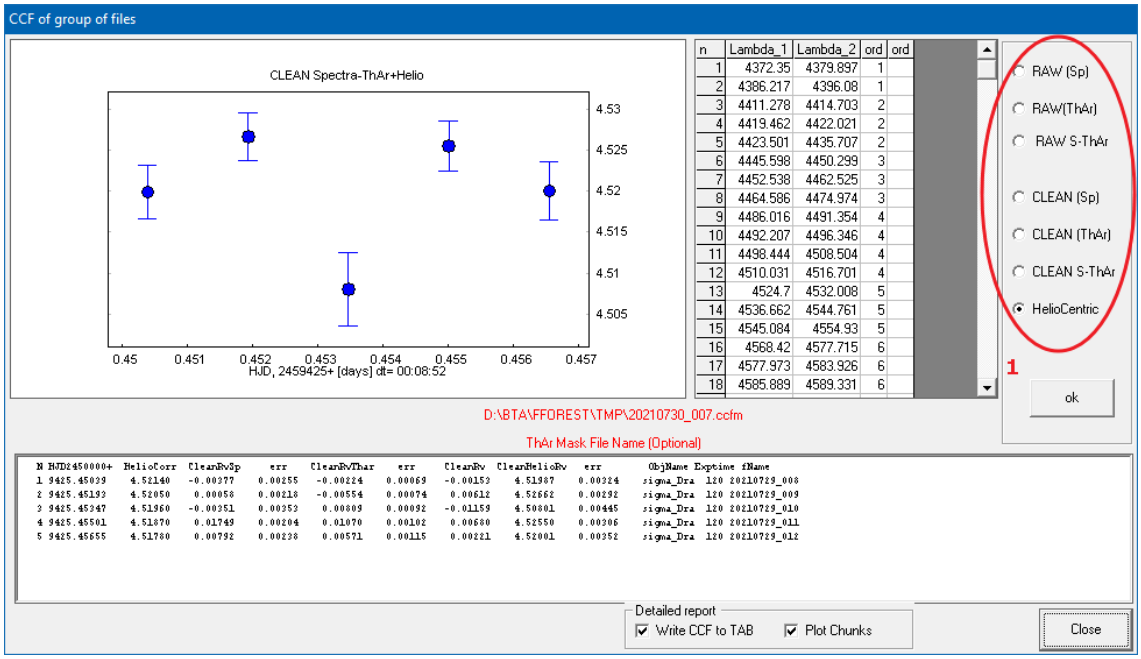


Figure 100

The final result is more accurate when using the mask for ThAr and without some "bad" spectra with large error bars (seen in the middle). When comparing with other spectra, it turned out that the "bad" spectrum has a lower S/N ratio than other spectra in the sample:

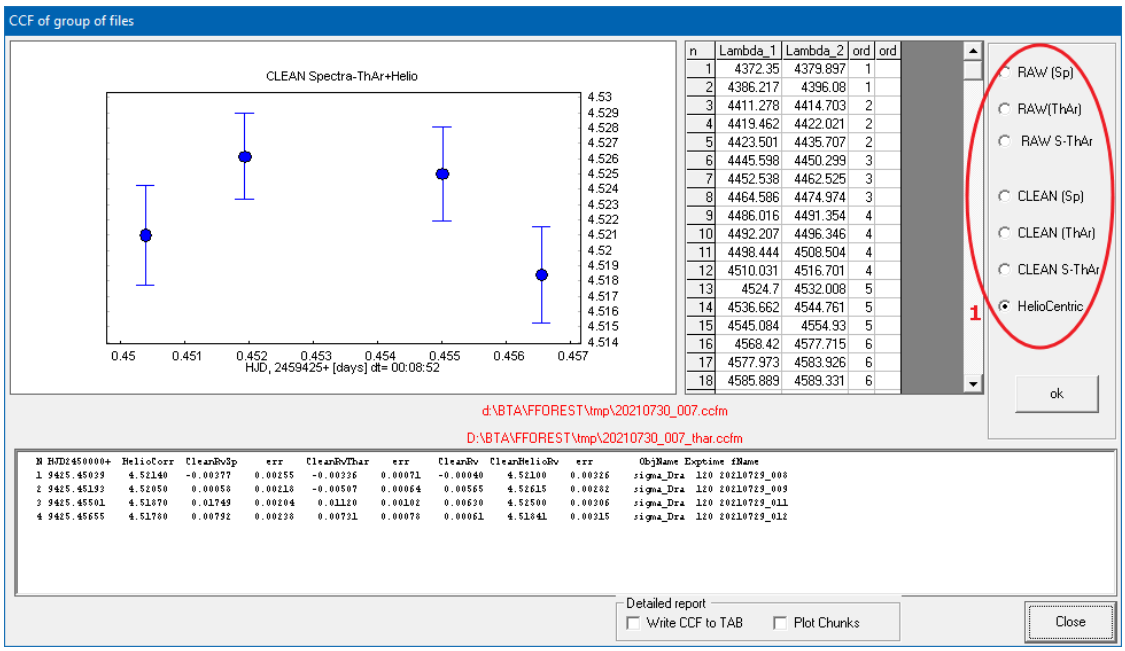


Figure 101

In Figure 101, on the panel on the right (in the oval marked with the number **1**) you can select a graph:

- By default, the so-called **HelioCentric** plot is shown – these are the average radial velocities for each spectrum (relative to the template) after cleaning by the *SigmaSlip* method , taking into account the heliocentric correction and taking into account the instrumental correction for ThAr. The **rez_vs_20210729_007** directory contains the same graph as a *jpg* file **summary-mask=20210730_007_CleanSp-ThAr+Helio.jpg** .
- The plot **CLEAN S-ThAr** – the same, but without heliocentric correction (the corresponding *jpg* file is **summary-mask=20210730_007_CleanSp-ThAr.jpg**).
- The plot **CLEAN (ThAr)** shows the calculations for ThAr spectra cleared of “bad” chunks (the corresponding *jpg* file **summary-mask=20210730_007_ CleanThAr .jpg)** .
- Finally, the plot **CLEAN(Sp)** shows the calculations for the object spectra cleared of “bad” chunks without any corrections (the *jpg* file is **summary mask =20210730_007_ CleanSp .jpg**).

It is also possible to look at the results of averaging without cleaning up the bad chunks and without any corrections: these plots are marked **Raw(Sp), Raw (ThAr), Raw S-ThArr.** The corresponding *jpg* files are:

summary-mask=20210730_007_RawSp.jpg,
summary-mask=20210730_007_RawThAr.jpg
summary-mask=20210730_007_RawSp-ThAr.jpg.

In addition, the **rez_vs_20210729_007** directory contains plots for all chunks for each object’s and ThAr’s spectrum separately. For example, **20210729_008_SpChunks.jpg** and **20210729_008_ThAr.jpg** are plots for the spectrum **20210729_008.fits** and the corresponding ThAr spectrum **20210729_008_ThAr.fits** respectively. Both plots are shown below one by one (Figs. 102 and 103):

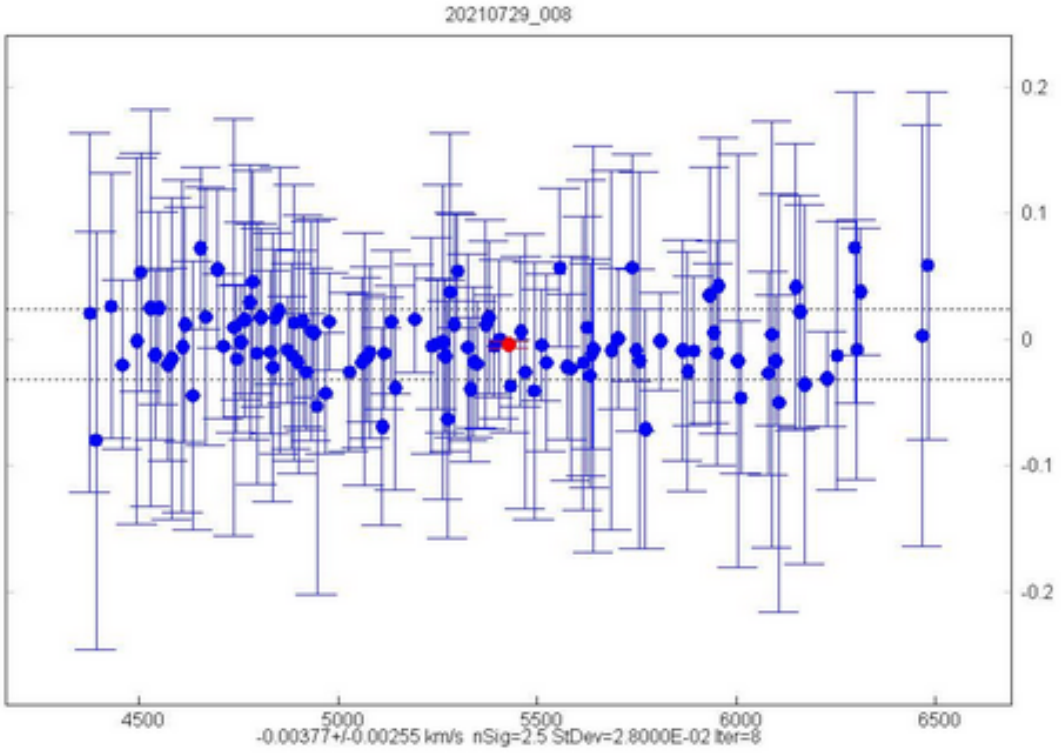


Figure 102

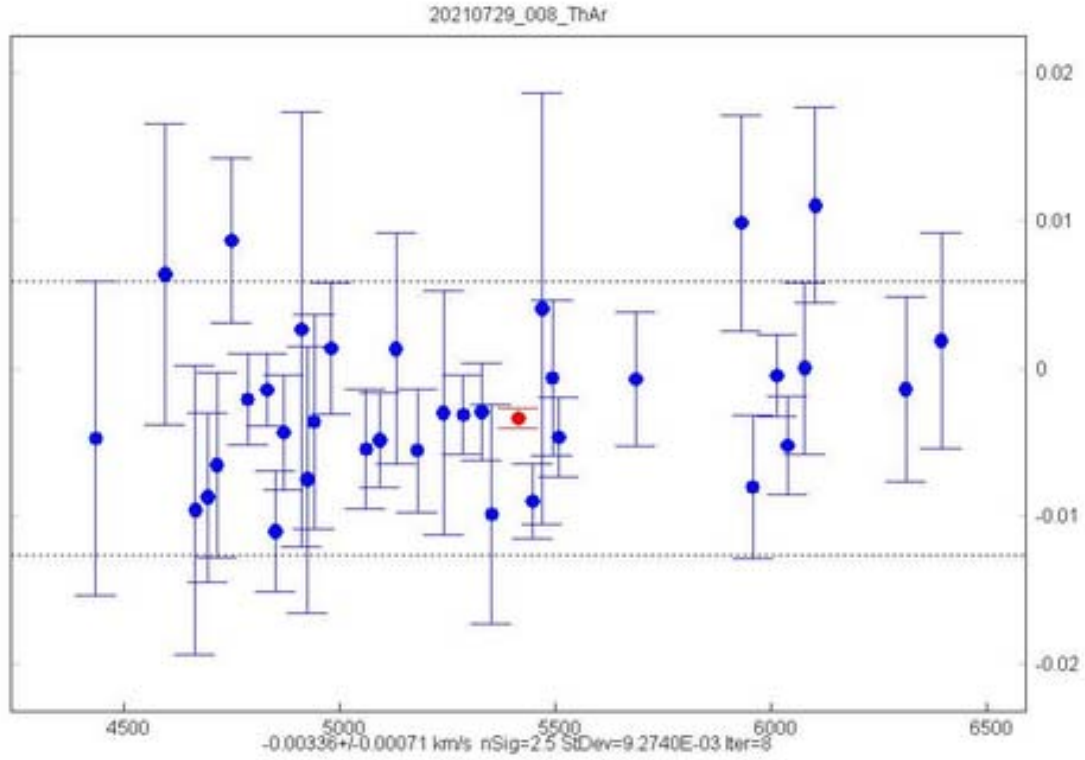


Figure 103

Blue circles with error bars correspond to individual chunks, and the red circle in the center with an error bar is the result of calculating the average value using the *SigmaClip* method. Under each graph, the average value is given as well. The cleaning criterion for the automatic *SigmaClip* algorithm, the standard deviation, and the number of iterations are also indicated. Two dashed lines indicate the boundaries

within which the "good" chunks are located. That is, in this case, it is ***2.5 * StdDev*** up and down from the mean value indicated by the red circle.

The calculation results are also presented in the tables. For example, the spectrum **20210729_008.fits** corresponds to the file **20210729_008.txt**. The first few lines of such a *.txt file look like this:

```
1 0.02092 0. 14234 001 171 431 4376.112
2 -0.07986 0.16535 001 661 1041 4391.149
3 -0.50345 0.51238 002 224 340 4412.978
4 -0.05430 0.23228 002 508 600 4420.742
5 0.02648 0. 10494 002 653 1124 4429.590
6 106.31147 4. 48018 003 101 257 4447.919
7 -0.02010 0.06692 003 334 687 4457.532
8 0.04080 0. 41879 003 762 1166 4469.767
9 0.08586 0. 08467 004 160 337 4488.670
… continuation
```

Here: the first column is a number of a chunk, the second and third columns are the radial velocity (a displacement relative to the template [km/s]) and measurement error for this chunk. It is evident that the 6th chunk shows a large deviation from the average value. Obviously, this chunk will be removed from consideration during the *SigmaClip* cleaning procedure. The 4th column indicates the number of spectral order, the 5th and 6th columns indicate the pixel numbers of the chunk boundaries. Finally, the last, seventh column indicates the wavelength of the chunk center [Angstroms].

The **file summary-20210730_007.txt** provides summary information:

```
Mask=d:\BTA\FFOREST\tmp\20210730_007.ccfm
Mask=D:\BTA\FFOREST\tmp\20210730_007_thar.ccfm
HJD2450000 + HelioCorr CleanRvSp err CleanRvThar err CleanRv CleanHelioRv err ObjName Exptime fName
1 9425.45039 4.52140 -0.00377 0.00255 -0.00336 0.00071 -0.00040 4.52100 0.00326 sigma_Dra 120 20210729_008
2 9425.45193 4.52050 0.00058 0.00218 -0.00507 0.00064 0.00565 4.52615 0.00282 sigma_Dra 120 20210729_009
3 9425.45501 4.51870 0.01749 0.00204 0.01120 0.00102 0.00630 4.52500 0.00306 sigma_Dra 120 20210729_011
4 9425.45655 4.51780 0.00792 0.00238 0.00731 0.00078 0.00061 4.51841 0.00315 sigma_ Dra 120 20210729_012
Mean: 9425.45347 4.52291 0.00180
```

Where the first two lines are the names of the masks for the object spectra and for the ThAr respectively. Then it is is given a table with the calculated values for each of the 4 spectra. Here:

1. Number of a spectrum in order;
2. heliocentric mid-exposure date,
3. heliocentric correction [km/s],
4. "cleaned" radial velocity relative to the template and its error without taking into account the corrections;
5. "cleaned" radial velocity of ThAr relative to the template and its error;
6. "cleaned" radial velocity relative to the template with the instrumental correction;
7. "cleaned" radial velocity relative to the template and its error with both instrumental and heliocentric corrections;
8. The spectrum name

The last line shows the average heliocentric date for all 4 spectra of the sample and the average radial velocity for all these 4 spectra with both the instrumental and heliocentric corrections.

A short version of this table is also provided. The file **summary-20210729_012-HelioRVonly.txt** gives only the "cleaned" radial velocity relative to template and its error with both the instrumental and heliocentric corrections:

```
9425.45039 4.52100 0.00326
9425.45193 4.52615 0.00282
9425.45501 4.52500 0.00306
9425.45655 4.51841 0.00315
```

Finally, the most compact file **summary-20210729_012-mean.txt** contains only the mean value of the radial velocity with both corrections, its error and the quantity of spectra used to calculate these values:

```
Mean_HJD MeanRV MeanRvErr N
9425.45347 4.52291 0.00180 4
```

Taking into account absolute instrumental correction and linking observational sets.

Taking into account the instrumental correction based on ThAr spectra allows us to take into account the displacements of instrumental origin that occur during the observing night. However, instrumental shifts from night to night and of the long time scale cannot be corrected in this way. Possible reasons are: the spectrograph is at the development stage; the continuous nitrogen filling system is not installed, etc. As it was already mentioned above, to take into account such displacements, it is necessary to observe the radial velocity standard for every night. As a result of radial velocity measurements of such a standard, a table is created for different Julian dates when observations were made. From 2021 to the present, the star Sigma Dra (RA 2000 =19 h 32 m 21.59 s DEC 2000 =+69 o 39'40.2”, V =4.68) has been used as such a standard for the FFOREST spectrograph. The results of measurements of this star are saved in the file **sigDra-RV.txt**, which should be stored in the same directory where the **DECH** software package is installed. An example of the file **sigDra-RV.txt**:

```
Mean_HJD MeanRV MeanRvErr N
9425.45347 4.52310 0.00098 4
9426.46364 4.56348 0.01038 8
9427.41249 4.48380 0.00169 6
9428.47909 4.49354 0.00200 3
9429.41474 4.50287 0.00221 5
9478.44291 4.28638 0.00541 8
9484.44658 4.27834 0.00537 12
9486.41812 4.29364 0.00621 12
9508.40333 4.08077 0.00309 15
9509.46081 4.16022 0.00490 16
9510.40542 4.11120 0.00209 14
9511.56899 4.10357 0.00703 9
9532.39449 4.02744 0.00483 10
9536.19269 4.01785 0.00177 11
9537.18538 4.00316 0.00359 11
9538.57710 3.97222 0.00442 9
9540.38661 3.97423 0.00502 11
9624.22170 4.37638 0.00361 12
9625.28754 4.41051 0.00597 12
9626.40484 4.38756 0.00607 12
9632.52312 4.38710 0.00419 18
9651.38205 4.39355 0.00364 10
9653.42544 4.34771 0.00373 11
9659.38719 4.35420 0.00303 10
9660.41936 4.34911 0.00349 12
9661.28440 4.35400 0.00263 10
9662.43184 4.34891 0.00914 12
9711.38521 3.85118 0.00582 12
9712.30653 3.86756 0.00677 11
9713.22916 3.79634 0.00508 14
9714.23832 3.84248 0.00618 12
9745.46681 3.95430 0.00545 12
```

```
9798.25871 4.11460 0.00451 15
9799.35054 4.10256 0.00406 11
9801.23886 4.11501 0.00425 10
9802.22182 4.11983 0.00638 11
9834.18355 4.28531 0.00596 13
9835.19367 4.26189 0.00351 12
9863.42858 4.27322 0.00412 11
9892.16018 4.17115 0.00665 12
9896.12146 4.17238 0.00400 12
9897.13337 4.16785 0.00412 12
9898.47338 4.19801 0.00282 11
9899.12346 4.16888 0.00683 12
9920.32227 4.18142 0.00582 19
9921.12449 4.18136 0.00920 12
9945.14537 4.28405 0.00700 12
9947.16498 4.31101 0.00319 14
9948.16556 4.28977 0.00893 13
```

The file contains the results of Sigma Dra measurements for all indicated dates.

Finally, the correction for the standard star Sigma Drao can be made using a program **SigDra .exe** available in the **DECH** package.

An example of the correction:

1. For example, some spectra were obtained for a certain star over two nights. As a result of processing and analysis, a **summary- SomeObject .txt file** was carried out. The contents of the file are as follows:

```
Mask=C:\BTA\vectors\SomeObject\20220312_031.ccfm
Mask=C:\BTA\vectors\20220321_039_thar.ccfm
HJD2450000 + HelioCorr CleanRvSp err CleanRvThar err CleanRv CleanHelioRv err ObjName Exptime fName
1 9920.50218 12.16660 - 21.07024 0.02192 0.51729 0.01725 -21.58754 -9.42094 0.03917 ADS9346A 300 20221206_088
2 9920.50581 12.16760 - 21.08747 0.02219 0.52048 0.01609 -21.60795 -9.44035 0.03828 ADS9346A 300 20221206_089
3 9920.50943 12.16850 - 21.04960 0.02926 0.51497 0.01757 -21.56456 -9.39606 0.04683 ADS9346A 300 20221206_090
4 9920.51305 12.16930 - 21.07650 0.02269 0.52133 0.01847 -21.59783 -9.42853 0.04116 ADS9346A 300 20221206_091
5 9920.51667 12.17000 - 21.00147 0.02989 0.52275 0.01600 -21.52422 -9.35422 0.04589 ADS9346A 300 20221206_092
6 9921.57292 12.21130 - 21.15881 0.02370 0.53651 0.01801 -21.69532 -9.48402 0.04171 ADS9346A 420 20221207_114
7 9921.57793 12.21000 - 21.13854 0.03124 0.51115 0.02044 -21.64969 -9.43969 0.05168 ADS9346A 420 20221207_115
8 9921.58294 12.20860 - 21.11726 0.02730 0.51681 0.01953 -21.63407 -9.42547 0.04682 ADS9346A 420 20221207_116
9 9921.58795 12.20700 - 21.13627 0.02606 0.55440 0.01609 -21.69067 -9.48367 0.04214 ADS9346A 420 20221207_117
10 9921.59298 12.20520 - 21.15350 0.02519 0.53569 0.01870 -21.68919 -9.48399 0.04388 ADS9346A 420 20221207_118
Mean: 9921.04619 -9.43743 0.01285
```

2. Now run the command **SIGDRA summary-SomeObject.txt**.
3. File **summary-SomeObject.corrected.txt** will be created. The contents of the file are as follows:

```
 HJD RV RVErr orig orig Err SigDraRV SigDraRVErr SigDraHJD Exptime Object FileName
9920.50218 -13.60236 0.04499 -9.42094 0.03917 4.18142 0.00582 9920.32227 300.0 ADS9346A 20221206_088
9920.50581 -13.62177 0.04410 -9.44035 0.03828 4.18142 0.00582 9920.32227 300.0 ADS9346A 20221206_089
9920.50943 -13.57748 0.05265 -9.39606 0.04683 4.18142 0.00582 9920.32227 300.0 ADS9346A 20221206_090
9920.51305 -13.60995 0.04698 -9.42853 0.04116 4.18142 0.00582 9920.32227 300.0 ADS9346A 20221206_091
9920.51667 -13.53564 0.05171 -9.35422 0.04589 4.18142 0.00582 9920.32227 300.0 ADS9346A 20221206_092
9921.57292 -13.66538 0.05091 -9.48402 0.04171 4.18136 0.00920 9921.12449 420.0 ADS9346A 20221207_114
9921.57793 -13.62105 0.06088 -9.43969 0.05168 4.18136 0.00920 9921.12449 420.0 ADS9346A 20221207_115
9921.58294 -13.60683 0.05602 -9.42547 0.04682 4.18136 0.00920 9921.12449 420.0 ADS 9346 A 20221207_116
9921.58795 -13.66503 0.05134 -9.48367 0.04214 4.18136 0.00920 9921.12449 420.0 ADS 9346 A 20221207_117
9921.59298 -13.66535 0.05308 -9.48399 0.04388 4.18136 0.00920 9921.12449 420.0 ADS 9346 A 20221207_118
```

Where in the RV columns and RVerr (second and third) are **the final values of the radial velocity of the studied object for the date specified in the first column**. The last three columns give the closest date of observations of the Sigma Dra standard taken from the **sigDra-RV.txt** table and the radial velocity of the standard along with its error.

Note that mean value (mean date, mean speed and its error), given in the first file as **Mean: 9921.04619 -9.43743 0.01285** do not make much sense, since in this case we are dealing with data for two nights. Therefore, in the **summary-SomeObject.corrected.txt** file, the "mean" is not given. To calculate the mean values for each night separately, we use the **ShowRv.exe** program from the **DECH** package.

An example of working with data from the **summary-SomeObject.corrected.txt** file (see point 2):

- Execute the command: **ShowRv.exe summary-SomeObject.corrected.txt.** The program window (Fig. 104) shows individual measurements of the radial velocity with error bars (in blue) and their average value (in green). Above the graph is information in the digital form.

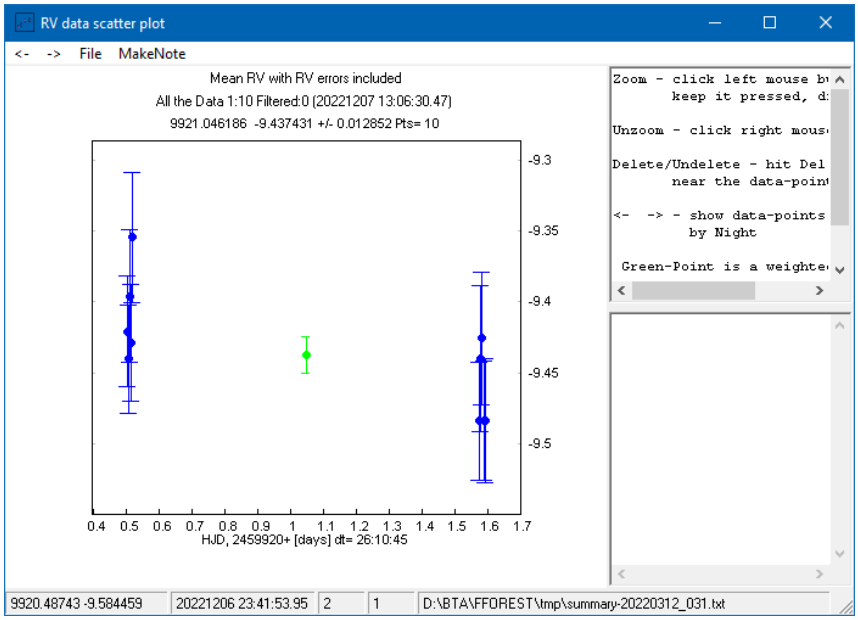


Figure 104

Obviously, the average value for two nights (as it is shown in Fig. 104) is of no interest. To obtain the average value for a selected group of data (e.g. single night separately), two methods are provided (see also the instructions in the upper right panel of the program – Fig. 104):

- select the area with the data of interest using the mouse – press the left mouse button and “draw” a rectangle that includes this group (press the right button to return back) *or*
- use the menu options **<-** or **->** (Fig. 104) to "move" between individual Julian dates

In each case, the average value is recalculated and is shown on the plot as a green circle with the error bars and, is shown in the digital form above the graph. To remove "bad" points from consideration, place the cursor closer to “bad” point and hit **D** key - the point is turned to be red and excluded from consideration. The average value is recalculated as well (Fig. 105). If you press **D** near the "bad" point once again - the point returns to be "good" and, the average value is recalculated again.

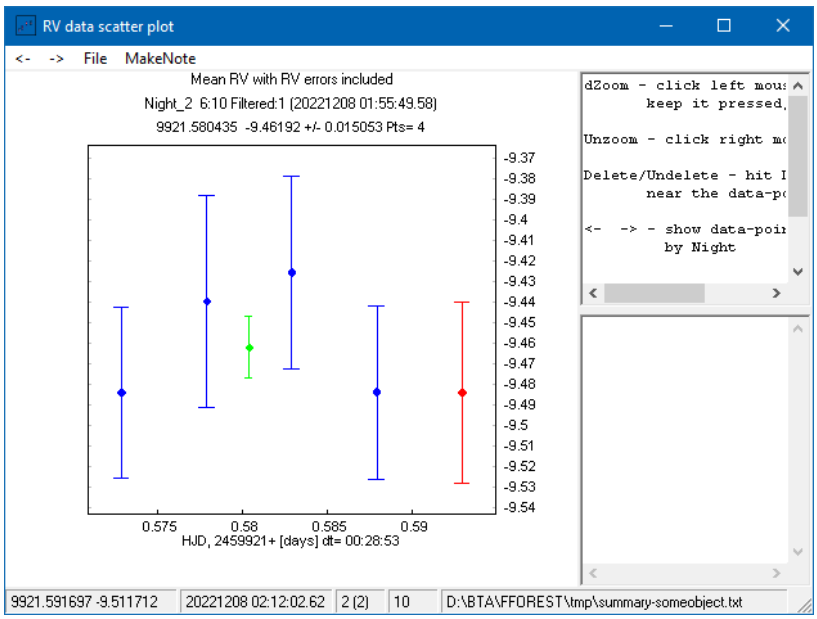

RV data scatter plot
<- -> File MakeNote
Mean RV with RV errors included
Night_2 6:10 Filtered:1 (20221208 01:55:49.58)
9921.580435 -9.46192 +/- 0.015053 Pts= 4
-9.37
-9.38
-9.39
-9.4
-9.41
-9.42
-9.43
-9.44
-9.45
-9.46
-9.47
-9.48
-9.49
-9.5
-9.51
-9.52
-9.53
-9.54
0.575
0.58
0.585
0.59
HJD, 2459921+ [days] dt= 00:28:53
dZoom - click left mous
keep it pressed,
Unzoom - click right m
Delete/Undelete - hit I
near the data-p
<- -> - show data-poi
by Night
9921.591697 -9.511712
20221208 02:12:02.62
2 (2)
10
D:\BTA\FFOREST\tmp\summary-someobject.txt

Figure 105