DMVL manual

Software requirements: Windows 95 or higher.

Installation: In order to install the DMVL software, copy the DMVL folder directly to C:\

1. Preparation of Data with sdiapp software

With **sdiapp** software we can prepare the data of spectra that we want to study with DMVL software. The spectrum should be in ascii format as a **.txt** file. The preparation of data requires:

- a) Red shift correction (in case of galactic spectra)
- b) Normalization of spectrum
- c) Cutting off the spectral range that we will study

Double click on **sdiapp.exe** (C:\DMVL\ANIMALS) in order to open **sdiapp** application. The window of Figure 1.1 opens.

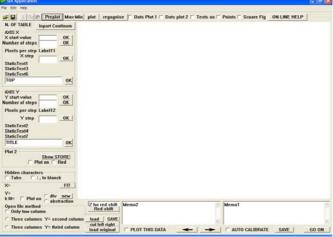


Figure 1.1: sdiapp application

Step 1: Opening the data of the spectrum (Figure 1.2)

On the **File** menu, click **Open** (Figure 1.2a) and select the file you want to open (it should be in ascii format as a **.txt** file). In the place of "**Memo 1**" a two column table with the data of the spectrum appears (Figure 1.2b). The wavelength is given in the first column and the flux in the second.

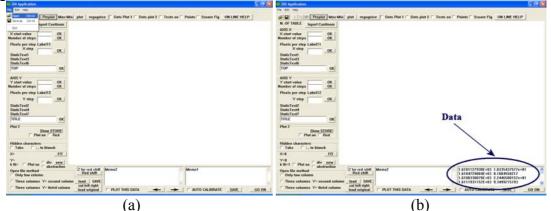
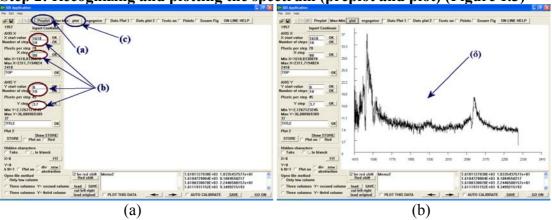


Figure 1.2

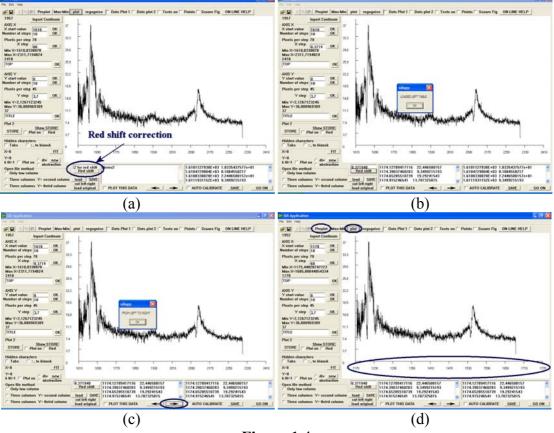


Step 2: Recognizing and plotting the spectrum (preplot and plot) (Figure 1.3)



- (a) Click on the **Preplot** button.
- (b) The fields of Figure 1.3a are filled in.
- (c) Click on the **plot** button.
- (d) The spectrum appears (Figure 1.3b)







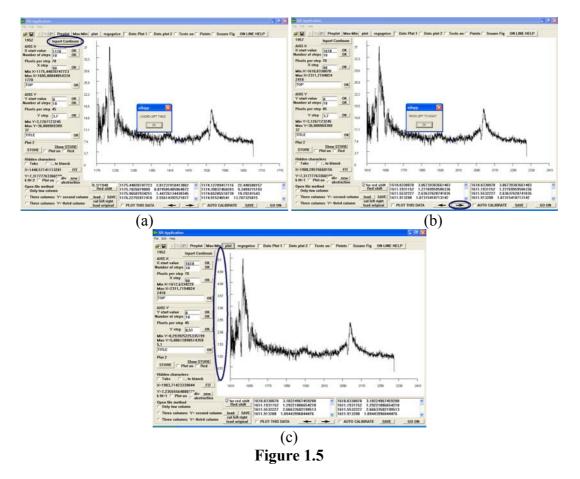
- (a) In the field **Z** for red shift enter the appropriate value of red shift correction. Click on the **Red shift** button (Figure 1.4a).
- (b) In the place of "**Memo 2**" a two column table with the corrected data of the spectrum appears (Figure 1.4b). The wavelength is given in the first

column and the flux in the second. The window "LOADED LEFT TABLE" opens. Click on OK.

- (c) Click on the right arrow \longrightarrow . The data of the left table are transferred in the right table. The window "FROM LEFT TO RIGHT" opens. Click on OK. (Figure 1.4c).
- (d) Click on the **Preplot** button and then the **plot** button. The corrected spectrum is loaded (Figure 1.4d).

Step 4: Continuum definition and normalization of the spectrum (Figure 1.5)

• When the continuum is horizontal



Click on a point of the spectrum, where the continuum should be defined.

- (a) Click on the Inport Continum button. In the place of "Memo 2" a two column table appears (Figure 1.5a). The wavelength is given in the first column and the normalized radiation intensity in the second. The window "LOADED LEFT TABLE" opens. Click on OK.
- (b) Click on the right arrow \longrightarrow . The data of the left table are transferred in the right table. The window "FROM LEFT TO RIGHT" opens. Click on OK (Figure 1.5b).
- (c) Click on the **Preplot** button and then the **plot** button. The normalized spectrum is loaded (Figure 1.5c).

• When the continuum is inclined.

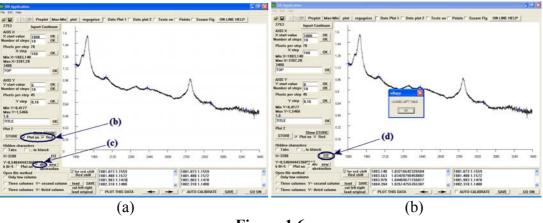


Figure 1.6

- (a) Click on two or more points of the spectrum, where the continuum should be defined. The program will calculate the continuum by these points using the least square method.
- (b) Activate **Plot on** and **Red**, so that the continuum will appear on the spectrum in red color (Figure 1.6a).
- (c) Select **o div** so that normalized spectrum will be calculated by the division of the observed flux by the continuum (Figure 1.6a).
- (d) Click on the **FIT** button. The window "LOADED LEFT TABLE" opens. Click on OK. (Figure 1.6b).

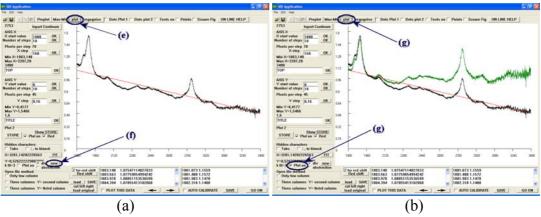
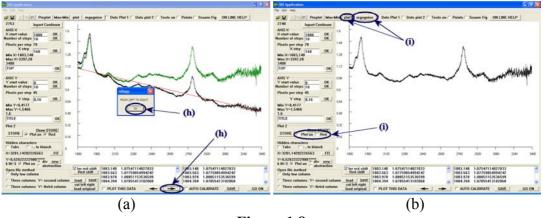


Figure 1.7

- (e) Click on the **pot** button. A red line that corresponds to the continuum appears (Figure 1.7a).
- (f) For a new calculation of the continuum, click on the **new** button (Figure 1.7a) and repeat the steps (a) to (e).
- (g) Activate **Plot on** and click on the **plot** button, so that the normalized and the initial spectra are loaded together (Figure 1.7b).





- (h) In order to load only the normalized spectrum, click on the right arrow
 The data of the left table are transferred in the right table. The window "FROM LEFT TO RIGHT" opens. Click on OK (Figure 1.8a).
- (i) Deactivate **Plot on** and **Red**. Click on the **regognise** button and the **plot** button (Figure 1.8b).



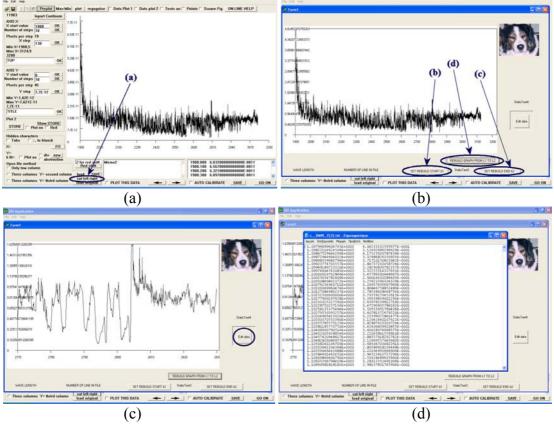


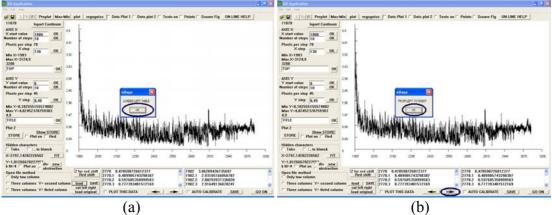
Figure 1.9

(a) Click on the **cut left right** button (Figure 1.9a).

- (b) In the new window click on the point of the horizontal axis that corresponds to the wavelength that should define the beginning of the spectral range. Click on the SET REBUILD START b1 button (Figure 1.9b).
- (c) Click on the point of the horizontal axis that corresponds to the wavelength that should define the end of the spectral range. Click on the SET REBUILD END b2 button (Figure 1.9b).
- (d) Click on the REBUILD GRAPH FROM L1 TO L2 button (Figure 1.9b). The chosen spectral range is loaded. In case we want a smaller spectral range we repeat the steps (b) to (d) (Figure 1.9c).

Edit data

(e) Click on the button (Figure 1.9c). A .txt file with a two column table opens. The wavelength is given in the first column and the radiation intensity in the second. (Figure 1.9d). Close the .txt file and the "Form 1" window.





(f) The window "LOADED LEFT TABLE" opens. Click on OK (Figure 1.10a). Click on the right arrow _____. The data of the left table are transferred in the right table. The window "FROM LEFT TO RIGHT" opens. Click on OK (Figure 1.10b).



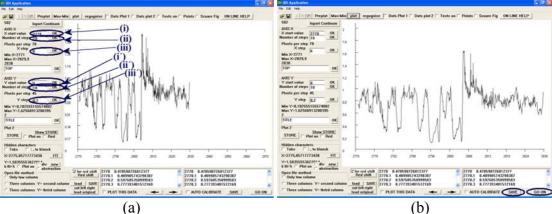


Figure 1.11

- (a) Horizontal axis (Figure 1.11a)
 - (i) Insert the value of the wavelength that should define the beginning of x-axis and click on **OK**.
 - (ii) Insert the number of steps and click on **OK**.
 - (iii) Define the step and click on **OK**.
- (b) Vertical axis (Figure 1.11a)
 - (i') Insert the value of the radiation intensity (or flux) that should define the beginning of y-axis and click on **OK**.
 - (ii') Insert the number of steps and click on **OK**.
 - (iii') Define the step and click on **OK**.
- (c) Click on the **regognise** button and then the **plot** button.
- (d) Click on the **SAVE** button in order to save the final data. (Figure 1.11b).
- (e) The **GO ON** button (Figure 1.11b) leads to DMVL software (Figure 1.12), with which we will analyze the spectrum. On the **File** menu, click **Save As...** and give the extension **.rrks** to the file that will be saved.

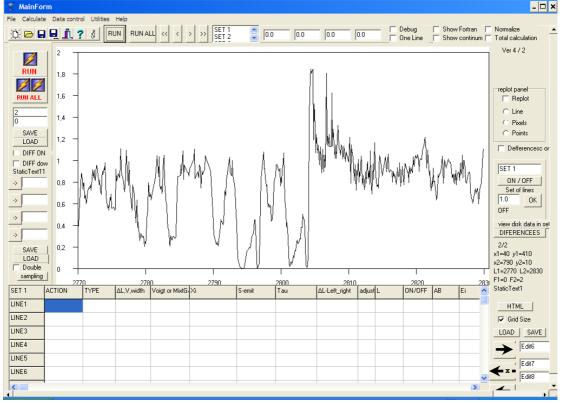


Figure 1.12

2. Reproduction of spectral lines with DMVL software

Open the .rrks file with DMVL software (Figure 2.1)

Double click on **FSC.exe** (C:\DMVL) in order to open **DMVL** application. On the **File** menu, click **Open** and select the .rrks file you want to open. The window of Figure 2.1 opens.

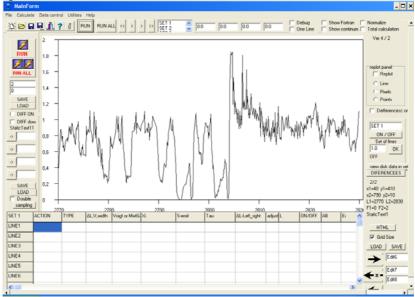
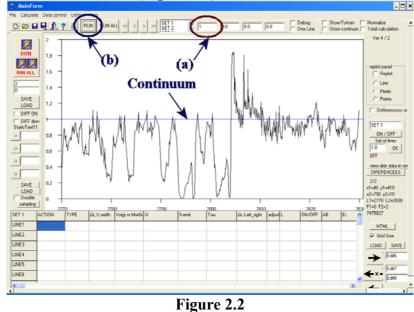


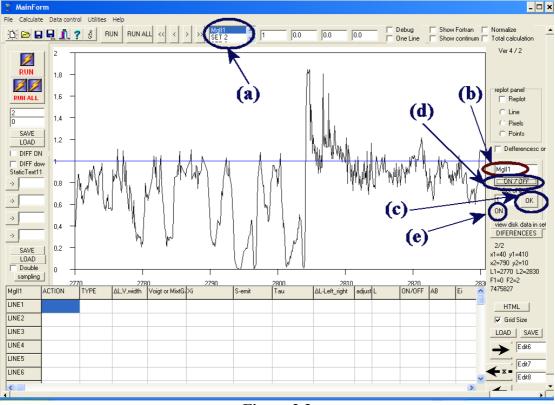
Figure 2.1: DMVL software

Step 1: Continuum definition (Figure 2.2)



(a) Insert the value of the continuum in the field (a) (in the case of normalized spectra, the value is 1).

(b) Click on the **BUN** button, so that the program reads the value and calculates the continuum. A blue line that corresponds to the continuum appears.

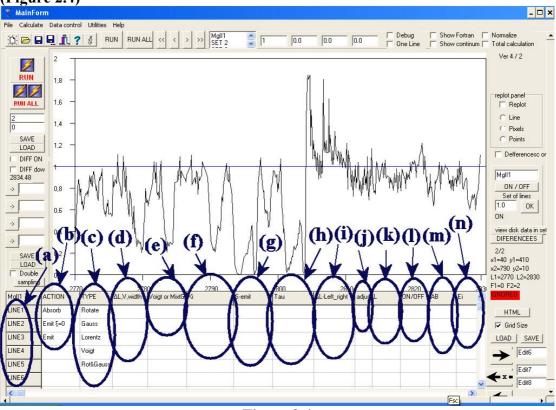


Step 2: Definition of the line under study (Figure 2.3)

Figure 2.3

- (a) Define one by one the spectral lines under study^{*} (by selecting SET1, SET2, ...)
- (b) Give a name for each one of these lines (e.g. MgII 1, MgII 2...).
- (c) Click on the $\Box K$ button to confirm the name o each spectral line.
- (d) Click on the ON/OFF button, in order to activate the selected spectral line.
- (e) The indication "ON" appears and the spectral line is activated.

^{*} The term SET corresponds to a group of satellite components that consist what we call spectral line.



Step 3: Insert values for the parameters, in order to reproduce a spectral line (Figure 2.4)

Figure 2.4

Insert values in the table.

- (a) The lines LINE1, LINE2,, LINE50 correspond to the components in which the spectral line is analyzed. For each one of the components of the spectral line, the respective shells of the table should be filled in. Each one of these components is created in an independent density region.
- (b) In the shells of the column ACTION, define the line as an absorption or emission line. In each shell the parameter changes by a double click and may take the values:

Absorb: Select it in the case of an absorption component.

Emit ξ =0: Select it in the case of emission lines that arise from large and distant shells with small optical depth (very rare case).

Emit: Select it in the case of an emission component.

(c) In the shells of the column type define the distribution function that is appropriate for the reproduction of the specific component. In each shell the parameter changes by a double click and may take the values:

Rotate: Select it when the main reason for the line broadening is the rotation of the density region where the specific component is created.

Gauss: Select it when the main reason for the line broadening is the random motions of the ions in the density region where the spectral line is created.

- **Lorentz**: Select it when the main reason for the line broadening is the collision effects among the ions.
- **Voigt**: Select it when the main reason for the line broadening is the random motions of the ions, as well as the collision effects among the ions, which, in an environment of high pressure and temperature, result to the broadening of the produced spectral lines (synthesis of a Gaussian and a Lorentz distribution).
- **Rot&Gauss**: Select it when the main reason for the line broadening is the rotation of the density region where the specific component is created, as well as the random motions of the ions (synthesis of a Rotation distribution and a Gaussian).
- (d) In the shells of the column $\Delta L.V. width$ give values of:
 - (i) rotational velocity (km/s), if in the shells of the column you selected **Rotate** or **Rot&Gauss**.
 - (ii) typical Gauss deviation, if in the shells of the column **TYPE** you selected **Gauss** or **Voigt**.
 - (iii)factor of Lorentz distribution, if in the shells of the column You selected Lorentz.
- (e) In the shells of the column Voigt or MixtG. give values of:
 - (i) typical Gaussian deviation, if in the shells of the column you selected **Rot&Gauss**.
 - (ii) factor of Lorentz distribution, if in the shells of the column YPE you selected **Voigt**.

(iii)give no value, if in the shells of the column you selected **Rotate, Gauss** or **Lorentz**.

- (f) In the shells of the column xi give values of the optical depth in the center of the line.
- (g) In the shells of the column give values of the source function S (only in the case of emission lines).
- (h) In the shells of the column [au] give values of the product $(S\xi_i)$ of the source function (S) and the optical depth in the center of the line (ξ_i) . The shell of this column is filled in, only in the case when in the respective shell of the column [ACTION] the selected value is **Emit** $\xi=0$. In any other case the shells of this column are empty.
- (i) In the shells of the column $\Delta L-Left_right$ give values for the shift ($\Delta \lambda$) of the center of the spectral line. Give positive values for shifts towards bigger wavelength. Give negative values for shifts towards smaller wavelength.
- (j) In the shells of the column dijust, by double click select between:
 - Adjust: Select it when the specific component of the spectral line has very small width. Sometimes, the variation of the depth of the line does not correspond to the variation of the given values, due to the pixel width. In such a case, we should select this value.

Normal: Select it in any other case.

The default value of the shells of this column is Normal.

- (k) In the shells of the column give the value of the laboratory wavelength of the spectral line under study.
- (1) In the shells of the column \bigcirc by double click select between:

On: It activates the respective component (LINE1, LINE2,, LINE50) so that it will be included in the calculations of the program. In this case by selecting any shell of this component, the sign selection appears, which indicates that the parameter of this specific shell is included in the calculations of the program.

- **Off:** It deactivates the respective component (LINE1, LINE2,, LINE50) so that it will not be included in the calculations of the program. In this case by selecting any shell of this component, the sign **INVEED** appears, which indicates that the parameter of this specific shell is not included in the calculations of the program.
- (m) In the shells of the column AB give the value of the atomic weight of the ion, of the spectral line under study.
- (n) In the shells of the column ^{Ei} give the value of the transition energy of the spectral line under study.



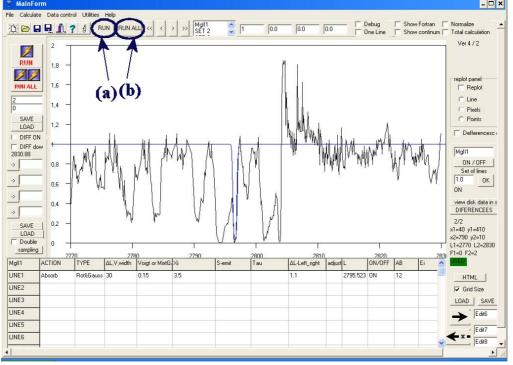


Figure 2.5

(a) When at least one of the lines LINE1, LINE2,, LINE50 of the table is completed, click on the RUN button, so that the program makes the necessary calculations for the reproduction of the spectral line.

(b) In the case of more than one spectral lines (i.e. when more than one sets

from **SET1**, **SET2**, ... are active) click on the ^{RUN ALL}, so that the program makes the necessary calculations for the reproduction of the spectral lines. In the case of more than one spectral lines (more than one active sets) by clicking on the button ^{RUN} the program calculates <u>only</u> the spectral line of the current SET. By clicking on the buttons ^{RUN} and ^{RUN ALL} the theoretical profile (blue line in Figure 2.5) of the spectral line appears. This theoretical profile is the result of the calculations of the program (fit).

Repeat the same procedure for as many components as needed (by filling in the shells of as many of the lines LINE1, LINE2,, LINE50 as needed), in order to accomplish the best fit of the observed profile of the spectral line under study.

Step 5: Save

On the **File** menu, click **Save as...** and give the extension **.rrks** to the file that will be saved. You may save your work any time during the procedure of fitting.

3. Results

a) Figures (fit)

In the folder C:/DMVL there are the figures **xxxx.bmp** and **xxxx2.bmp**. In the file **xxxx.bmp** the observed profile of the spectral line appears. In the file **xxxx2.bmp** both of the observed and the theoretical profiles of the spectral line appear. These files should always be in the folder C:/DMVL You may copy these files in any other folder and treat them as any .bmp file.

b) Values of the parameters (Figure 3.1)

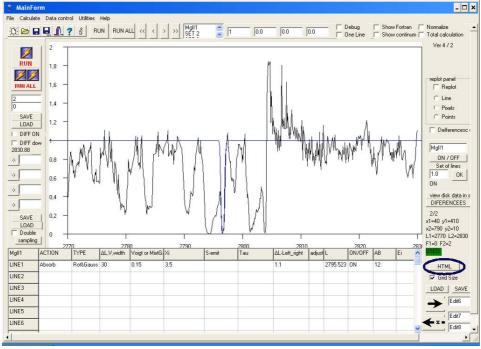


Figure 3.1

Click on the **HTML** button (Figure3.1). In order to save this file, on the **File** menu, click **Save as...** This file exists in the folder C:/DMVL, with the name fsmOut.htm. This file should always be in the folder C:/DMVL. You may copy this file in any other folder. This file includes the final figure with the observed and the theoretical profile of the spectral line, as well as all the calculated values of the parameters.

4. Deciding on the best fit through the F-test

Use the F-Test in order to decide on the best fit.

Step 1: Open the first file with DMVL (file1.rrks).

Step 2: Activate **Vormalize** and **V Total calculation**. Click on the BUN ALL button, so that the program makes the calculations and the theoretic profile of the spectral line appears (Figure 4.1).

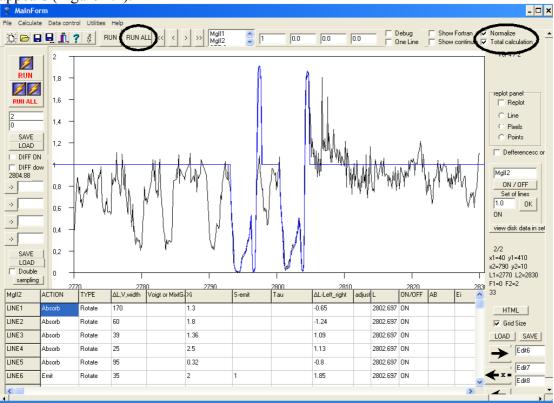
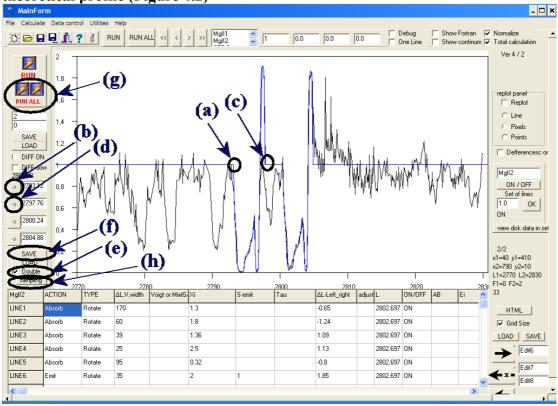


Figure 4.1



Step 3: Definition of spectral range for the first file and calculations for the first theoretical profile (Figure 4.2)

Figure 4.2

- Click on the point on the spectrum, where the theoretical spectral line (a) begins (blue edge).
- Click on the 🕑 button, in order to insert the value of the wavelength of (b) the blue edge in the respective field.
- Click on the point on the spectrum, where the theoretical spectral line (c) ends (red edge).
- Click on the 🕑 button, in order to insert the value of the wavelength of (d) the red edge in the respective field.
- In the case of two spectral lines activate **v Double** and repeat the steps (e) (a) to (d) inserting the values to the respective fields.
- SAVE Click on the button to save these values. (f)



- RUN ALL
- Click on the so that the program makes the appropriate (g) calculations.
- Click on the sampling button. (h)
- The window of Figure 4.3 opens. (i)

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Figure 4.3

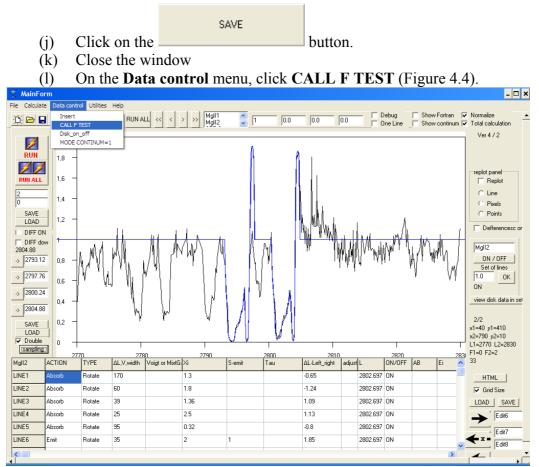


Figure 4.4

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Figure 4.5

(m) In the new window (Figure 4.5) click on the button.

LOAD FORM STAT1

(n) Click on the **SAVE** button.

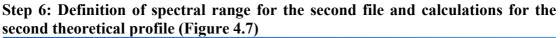
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Figure 4.6

- (o) The window "SAVED" opens. Click on OK (Figure 4.6).
- (p) Close all windows.

Step 4: Open the second file with DMVL (file2.rrks).

Step 5: Activate **Normalize** and **Total calculation** and click on the ^{BUN ALL} button, so that the program makes the calculations and the theoretic profile of the spectral line appears. (Figure 4.1).



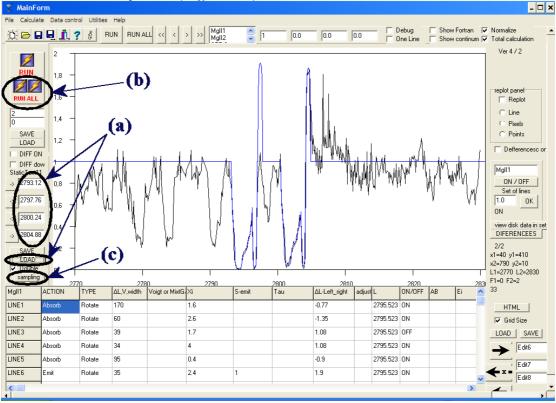


Figure 4.7

- (a) Click on the LOAD button in order to recall the values of the wavelengths that were saved for the first file (file1.rrks).
- (b) Click on the **RUHALL** button, so that the program makes the calculations.
- (c) Click on the sampling button.
- (d) The window of Figure 4.3 opens.

SAVE

- (e) Click on the button.
- (f) Close the window
- (g) On the **Data control** menu, click **CALL F TEST** (Figure 4.4).

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Figure 4.8

- (h) In the new window (Figure 4.8) click on the LOAD button, in order to reload the data of the first theoretical profile of the spectral line.
- (i) Click on the LOAD FORM STAT1 button, in order to load the data of the second theoretical profile of the spectral line (Figure 4.8).

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Figure 4.9

(j) Next to the data of the two theoretical profiles the following symbols appear (Figure 4.9):



: It declares the best theoretical profile.

- : It declares the unacceptable theoretical profile.
- (k) Click on the to call the F-Test (Figure 4.9).

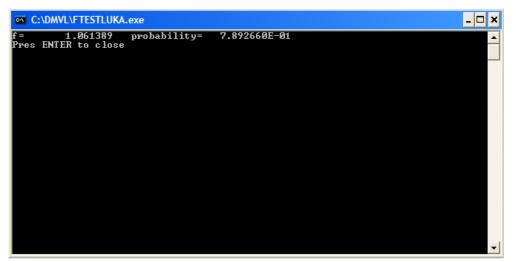


Figure 4.10

(1) A DOS window opens, in which the value of probability appears (Figure 4.10). The confidence of the choice of the most appropriate fitting, according to the F-Test, is given by: confidence=1-probability.