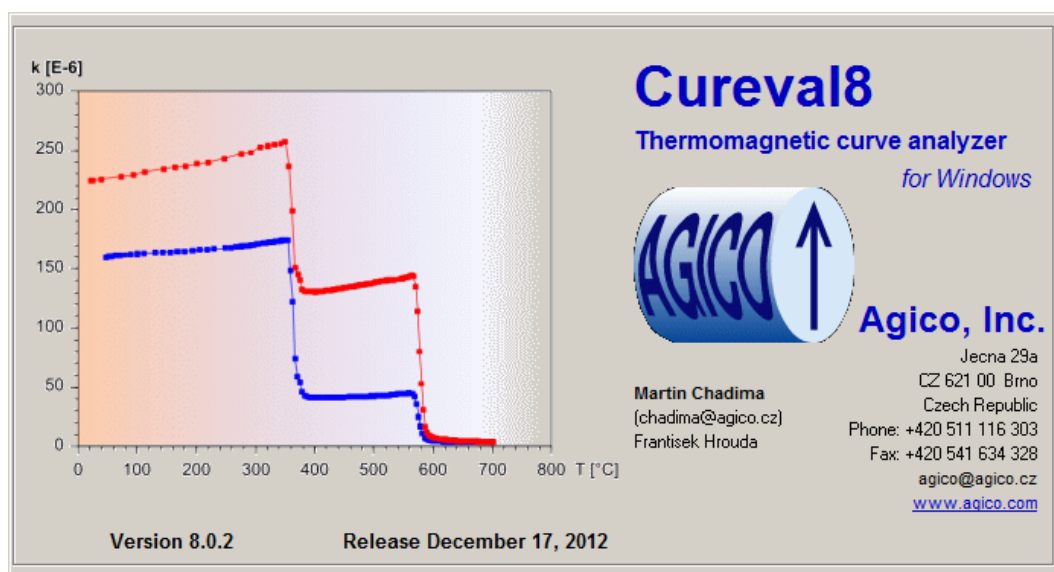



CUREVAL8

THERMOMAGNETIC CURVE ANALYZER



The screenshot displays the Cureval8 software interface. On the left, a plot shows the magnetic susceptibility κ [E-6] on the y-axis (ranging from 0 to 300) versus temperature T [°C] on the x-axis (ranging from 0 to 800). Two curves are shown: a red curve and a blue curve. Both curves show a sharp decrease in susceptibility around 350°C and 550°C, respectively. The red curve starts at approximately 220 at 0°C and drops to about 130 at 350°C, then to 10 at 550°C. The blue curve starts at approximately 160 at 0°C and drops to about 40 at 350°C, then to 10 at 550°C. The background of the plot area is shaded with a color gradient from orange to light blue.

Cureval8
Thermomagnetic curve analyzer
for Windows



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Software Manual

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1 Introduction

Cureval8 is a MS Windows program which serves for the off-line processing and graphical representation of data obtained by measurement of temperature variation of magnetic susceptibility by the means of the CS4 Furnace Apparatus and/or the CS-L Cryostat Apparatus (*.cur and/or *.clw data files, respectively) connected to the KLY5-A/MFK1-FA/MFK1-A Kappabridge, or by means of CS-3 Furnace Apparatus and/or the CS-L Cryostat Apparatus connected to the KLY-4S/KLY-3S Kappabridge. Measurable temperature ranges are from room temperature to 700 °C in case of the CS4 and CS-3, and from -192 °C to room temperature in case of the CS-L. Cureval8 features basic viewing of the thermomagnetic curves – k vs. temperature, 1/k vs. temperature, k vs. time, temperature vs. time – where k represents total, bulk, or mass susceptibility.

Current plots can be directly copied into the clipboard, printed or exported into the Windows Metafile which can be easily opened and edited in a number of vector graphics editors, e.g. CorelDraw, Adobe Illustrator.

In addition, the program features the basic data processing routines, i.e. subtraction of empty furnace/cryostat, calculation of the bulk and/or mass susceptibilities, calculation of the alteration indices [2], resolution of the susceptibility into ferromagnetic and paramagnetic components based on the Curie-Weiss law [1, 3] and manual Curie temperature(s) estimation using the k vs. temperature and 1/k vs. temperature curves [4].

2 Edit data

The **Edit data** interface looks differently according to whether you process the empty cryostat/furnace or the specimen thermomagnetic data. Regardless of your data type, certain features are always applicable:

- **Zoom** – Draw a rectangle around the graph area to be enlarged (**left** mouse button pressed); a mouse click will restore a full view.
- **Select** – Draw a rectangle (**right** mouse button pressed); the enclosed points and corresponding lines in the numeric output will be highlighted. Alternatively, you may select the records directly by clicking on the respective lines in the numeric output. To clear the selection, right-click in the graph area.
- **Delete** – Click on the button to delete the selected records from the file. Note that the records will be deleted permanently so it is always recommended to make a backup file of the original data before you start any editing.

2.1 Empty cryostat/furnace

Empty cryostat/furnace thermomagnetic data are applied to subtract the susceptibility of the empty cryostat/furnace from the specimen thermomagnetic curve. Before the subtraction, the empty cryostat/furnace curves must be got rid of any outlying measurements (spikes or peaks on the curve) and smoothed.

2.1.1 Deleting outlying records

Select individual outlying point(s) on the curve by drawing a rectangle (**right** mouse button pressed) and delete the selected records from the file (see above). Note that you may zoom the graph first.

Alternatively, the outlying measurements may be selected automatically. Set the **Neighboring measurement difference** in the **Mark outlying measurements** frame. Click on the button, the measurements which differ in susceptibility from the preceding measurement more than desired tolerance will be highlighted in green (Fig.1). To clear the auto-selection, click the button. Now you must select the records to be deleted manually (see above, Fig.1). Note that only the pre-selected records will be taken into account (Fig.2). Hit to delete outlying records from the file. The above-described routine may be repeated until all outlying records are deleted.

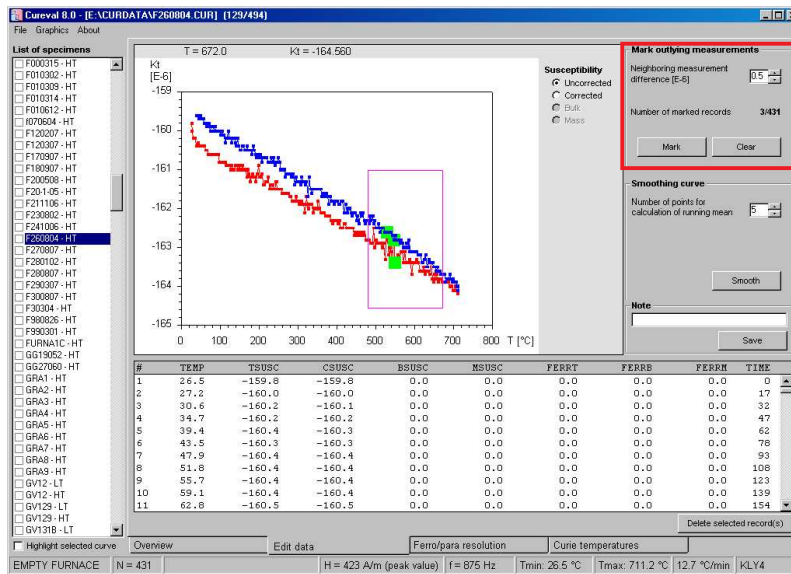


Figure 1: Choosing outlying data and marking for deleting

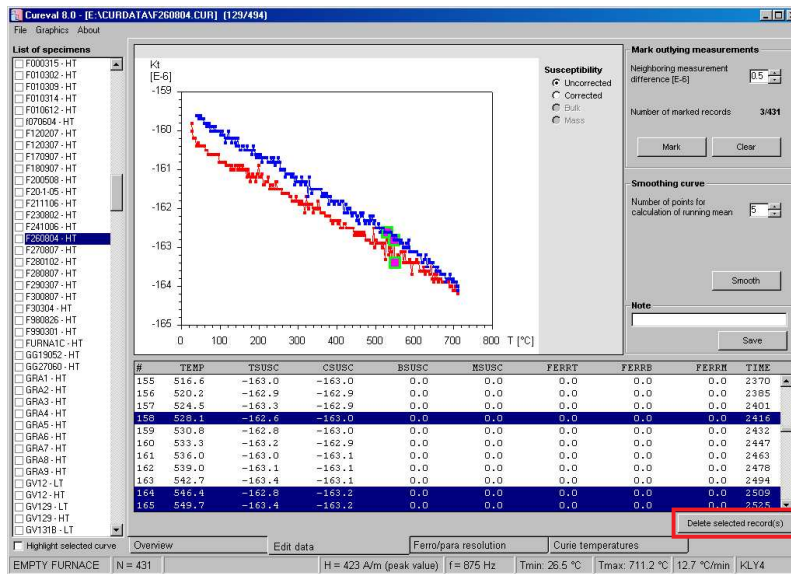


Figure 2: Deleting chosen records

2.1.2 Smoothing the curve

The empty cryostat/furnace thermomagnetic curve must be smoothed before it can be applied to the empty cryostat/furnace subtraction. The smoothing is performed by calculating a running mean of neighboring measurements. You may choose how many neighboring measurements will be included into the running mean calculation (3, 5, 7, 9). Click on the **Smooth** button to perform the smooth-

ing. To view the smoothed curve click on the **Corrected Susceptibility** option in the right-hand side of the graph (Fig.3).

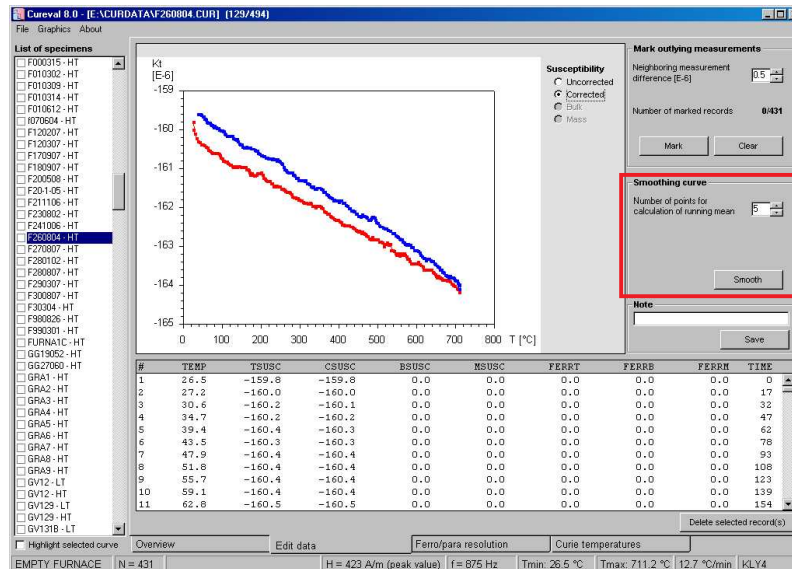


Figure 3: Smoothing of the empty furnace/cryostat curve

2.1.3 Writing a note

To input a user note into the file, write the text in the **Note** frame and hit the **Save** button.

2.2 Specimen

2.2.1 Empty cryostat/furnace subtraction

This routine is the equivalent to the correction for the empty holder. You can either subtract a constant magnetic susceptibility value of the cryostat/furnace (this value represents the cryostat/furnace susceptibility over the entire temperature range) or the empty cryostat/furnace thermomagnetic curve.

- **Constant value** – Enter the empty cryostat/furnace susceptibility and hit the **Subtract** button (Fig. 4).

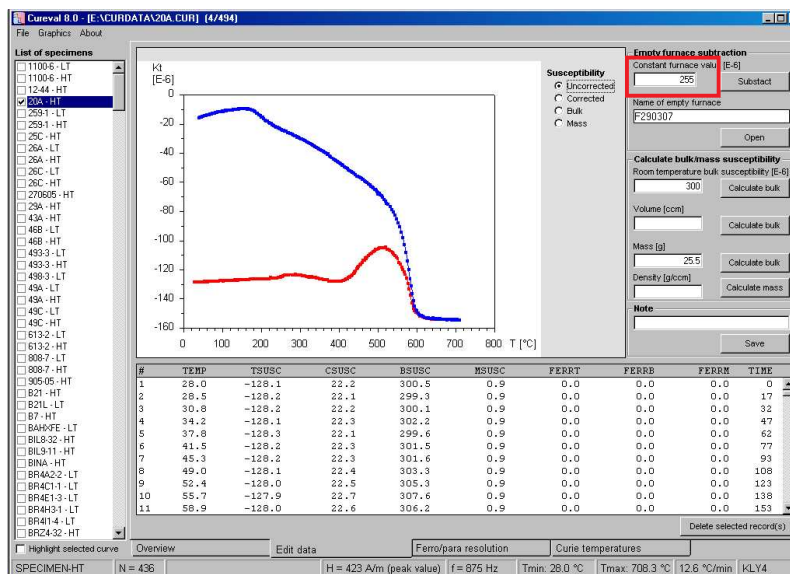


Figure 4: Subtraction of constant value, uncorrected data

- **Empty cryostat/furnace curve** – The file name containing the corresponding cryostat/furnace if displayed (if you had entered its name during data acquisition by Sufyte software). Hit **Open** and select the corresponding file containing empty cryostat or furnace data (Fig. 5). The subtraction is performed automatically after opening the empty furnace or cryostat data file. Note that you may use the same empty cryostat or furnace thermomagnetic curve for many specimens so it is not necessary to measure the empty cryostat/furnace before each specimen. Before the subtraction, the empty cryostat/furnace curves must be got rid of any outlying measurements (spikes or peaks on the curve) and smoothed (see Section 2.1.2).

To view the corrected curve click on the **Corrected Susceptibility** option in the right-hand side of the graph (Fig. 5).

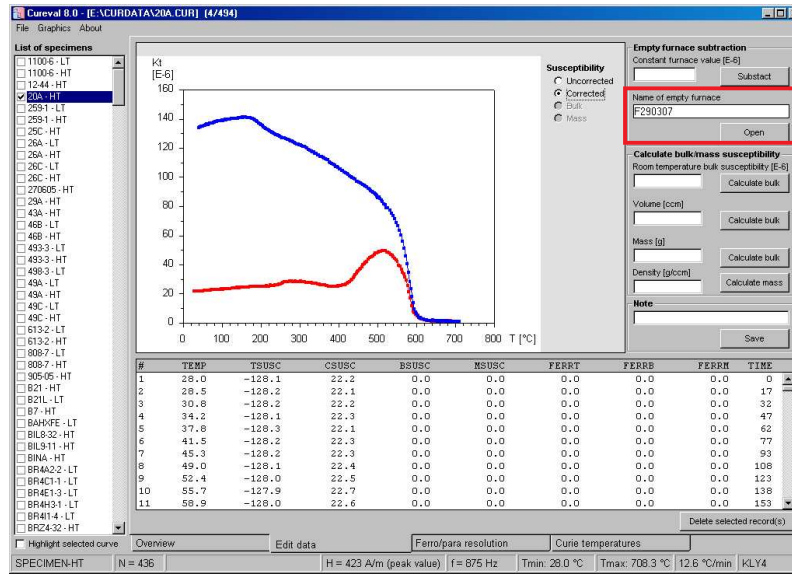


Figure 5: Subtraction of constant value, corrected data

2.2.2 Calculation of bulk/mass susceptibility

The MFK1 Kappabridge primarily measures the total susceptibility, k_T , that is independent of the specimen volume. The total susceptibility is defined as the induced magnetic moment of the specimen divided by the nominal volume of the instrument (being 10 cm^3 for MFK1 Kappabridge). The bulk susceptibility, k_B , is calculated as follows:

$$k_B = \frac{V_0}{V} k_T \quad (1)$$

where V is the actual volume of the specimen and V_0 is the nominal volume. In environmental magnetism studies, the mass susceptibility, χ , is often used. It is related to the bulk susceptibility as follows:

$$\chi = \frac{k_B}{\rho} = \frac{V k_B}{m} \quad (2)$$

where ρ is density, m is specimen mass. The mass susceptibility is then related to the total susceptibility as follows:

$$\chi = \frac{V_0}{V} \frac{V}{m} k_T = \frac{V_0}{m} k_T \quad (3)$$

While the bulk susceptibility is dimensionless, the SI unit of mass susceptibility is m^3/kg . The mass susceptibility in m^3/kg is obtained, if the nominal volume and specimen mass are input in m^3 and kg , respectively.

The bulk susceptibility in the entire curve course can be calculated either from known room temperature susceptibility or known volume of the specimen. Alternatively, the specimen volume can be calculated from the known mass and density. To perform the bulk susceptibility calculation enter the **Room temperature bulk susceptibility** [10^{-6} SI], **Volume** [cm^3], or **Mass** [g] plus **Density** [g/cm^3] and hit the respective **Calculate bulk** button. To view the bulk susceptibility curve click on the Bulk Susceptibility option in the right-hand side of the graph (Fig. 6).

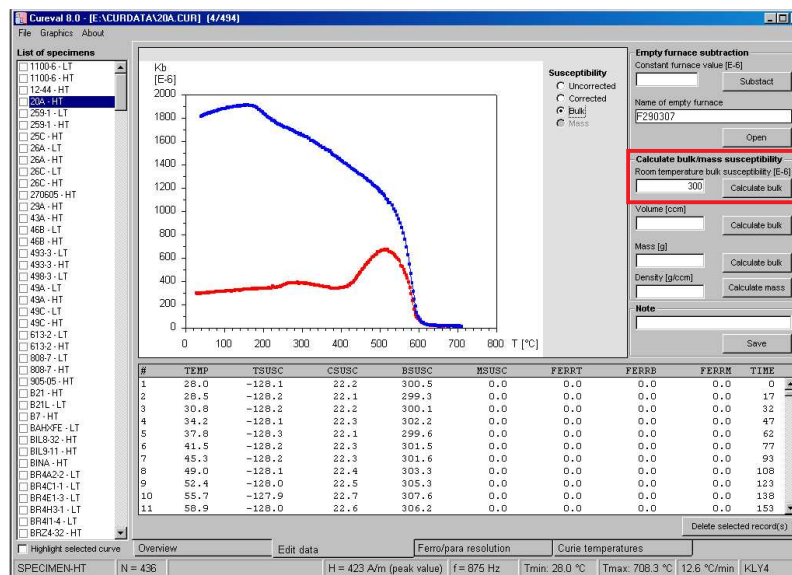


Figure 6: Recalculation from total to bulk susceptibility

The mass susceptibility in the entire curve course can be calculated either from the known mass of the specimen. To perform the calculation, enter **Mass** [g] and hit the respective **Calculate mass** button. To view the mass susceptibility curve click on the **Mass Susceptibility** option in the right-hand side of the graph (Fig. 7).

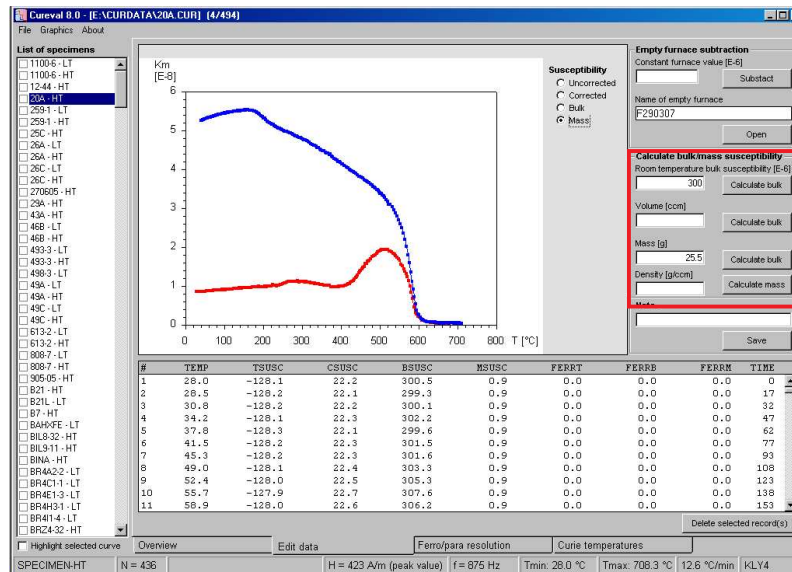


Figure 7: Recalculation from total to mass susceptibility

3 Ferro/para resolution

Ferro/para resolution is based on the hyperbola fitting algorithm to $k(T)$ curves assuming the Curie-Weiss Law [1], [3].

1. Start **Cureval** and Open some files.
2. Select desired file in the **List of specimens**. Note: Since the Empty cryostat/furnace correction is a crucial prerequisite, you are allowed to perform the separation routine only on the corrected data.
3. Switch to the **Ferro/para** resolution tab.
4. Enter the temperature limits in which you want to fit the hyperbola by filling the **text boxes** in lower left or by drawing a **line** in the diagram with the right mouse button pressed.

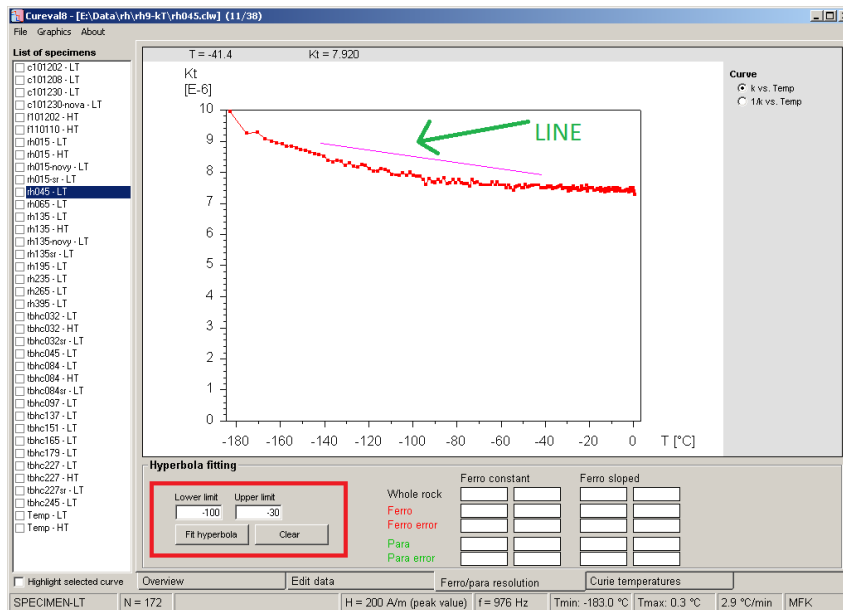


Figure 8: Ferro/para resolution, choosing region for fit

5. The hyperbola fit is performed and the results are shown and stored automatically into the respective file. Please note that the resolution is only semi-quantitative based on the mathematical separation and is strongly dependent on the empty cryostat/furnace correction. Do not treat the results with one-decimal precision.

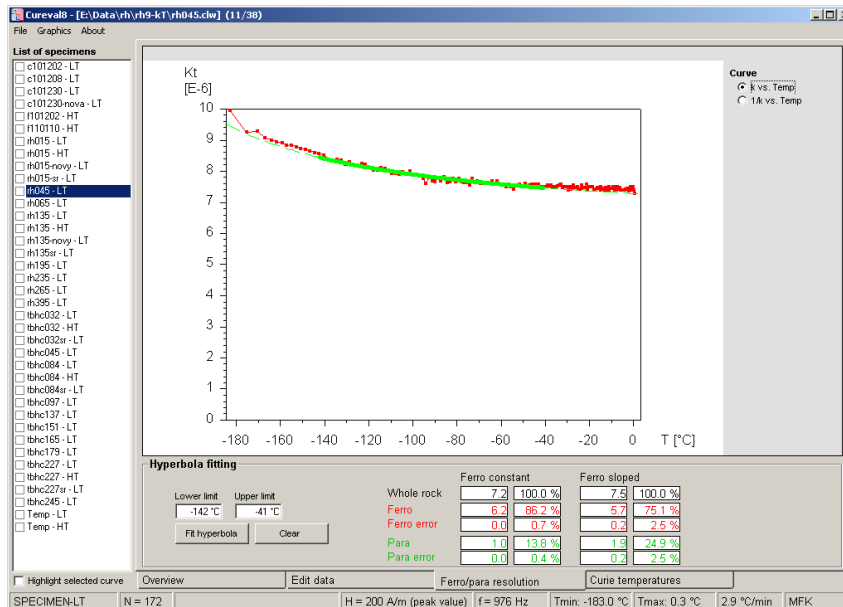


Figure 9: Ferro/para resolution, fitted curve and results of separation

4 Temperature estimates

The Curie (or any characteristic) temperature estimate feature is based solely on the visual analysis of the curves with alternative help of the inverse susceptibility option ($1/k$; above the Curie temperature we deal with paramagnetic hyperbola which is hard to detect visually but transforms into a straight line when inverted [4]).

1. Start **Cureval** and Open some files.
2. Select the desired file in the **List of specimens**. Note: Since the Empty cryostat/furnace correction is a crucial prerequisite, you are allowed to perform the separation routine only on the corrected data.
3. Switch to the **Curie temperatures** tab

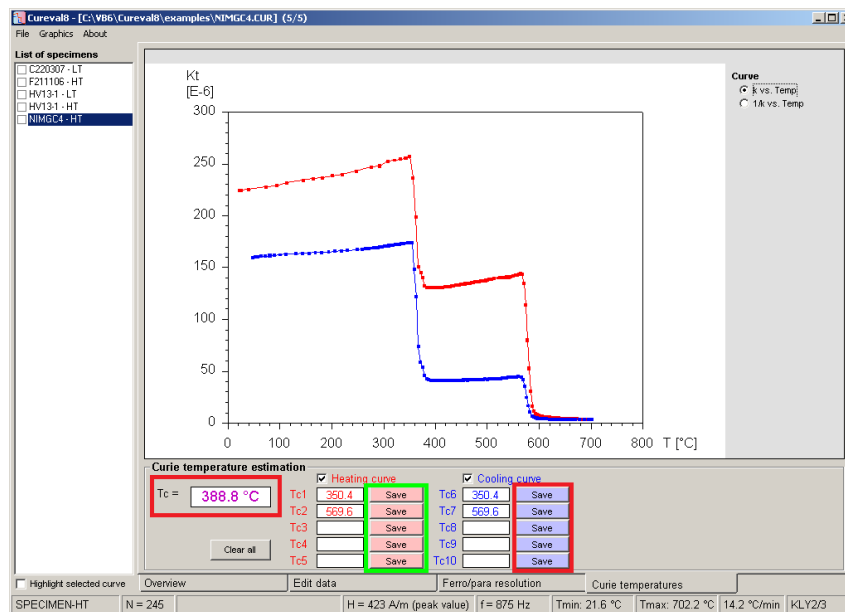


Figure 10: Estimation of curie temperatures

4. Click anywhere in the diagram with the **right** mouse button pressed. The temperature corresponding to the actual cursor position is shown in the lower left **text box**. If you wish you may store this temperature estimate into the file by hitting respective **Save** button; up to five different temperature estimates found on the heating curve and up to five on the cooling curve can be stored.

5 How to delete data points

It is strongly recommended to keep the original data files as the backup and to work with the copies of the original files.

- Click on **respective specimen name**.
- Go to **Edit data** tab.
- Select data points to-be-deleted in the graph by mouse with right button pressed.
- Hit the **Delete selected record(s)** button.

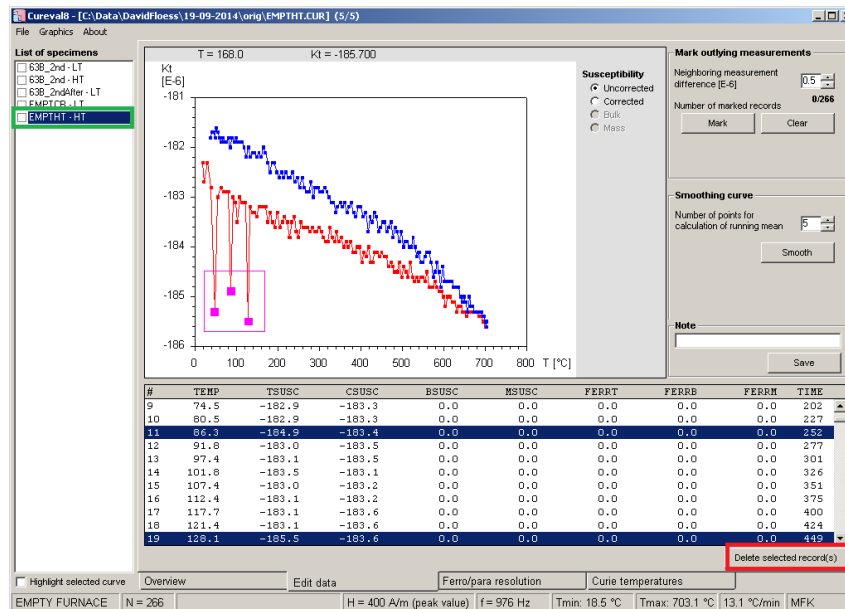


Figure 11: Deleting of the outlying data points

6 Overview window

The tab **Overview** allows user to visualize several curves in one graph, to combine low and high temperature curves and to set the properties of the graph such as colors, line thicknesses and arrange range of the axes. It also visualizes results of the ferro/para separation and estimated Curie temperatures.

6.1 Graphic options

Cureval8 allows to arrange graphs to user's needs. By clicking a little arrow marked by the **green circle** one can switch between graphic options bar and results bar. Colors of the symbols, line thicknesses and styles, symbol shapes, font size and axes can be changed using commands available in the region marked by **red rectangle** on Fig.12. Multiple curves can be displayed by selecting specimens in their **respective check-box**.

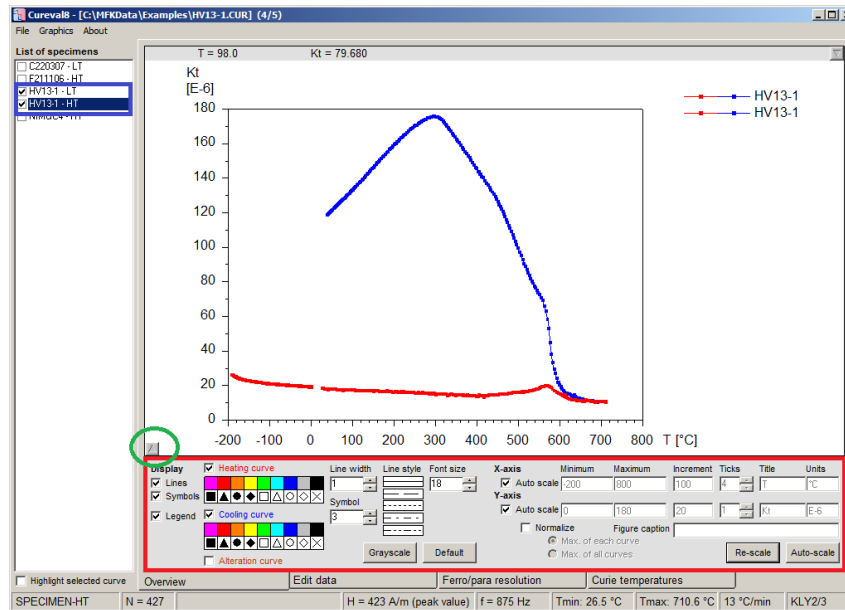


Figure 12: Overview window, graphic options

6.2 Results overview

Complete overview of the results such as Alteration indices, Ferro/para resolution and Curie temperatures are shown in the Overview window bottom bar as seen on Fig. 13. Click on the arrow marked by the green circle shows the dialog for changing of the Curve type.

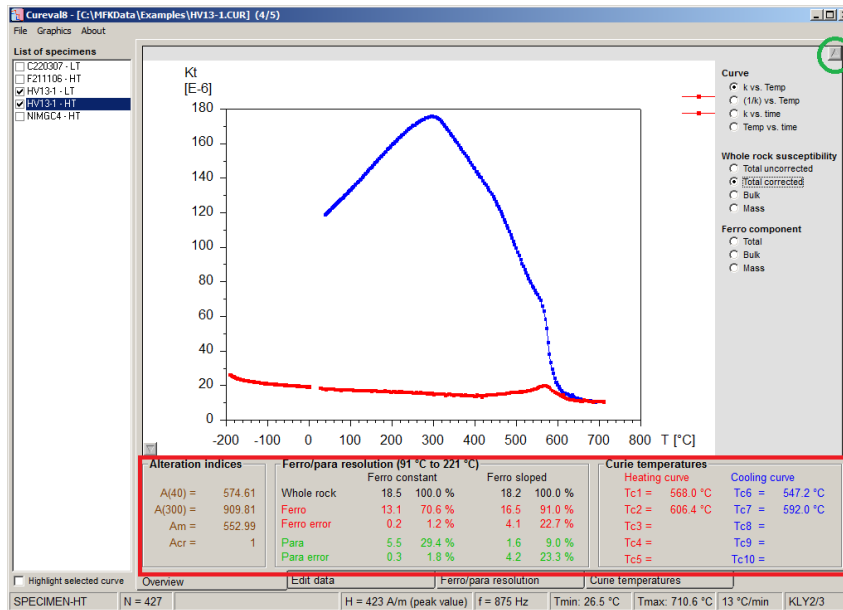


Figure 13: Overview window, results bar

7 References

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