VARIFORC User Manual
Chapter 6:

Central ridge processing

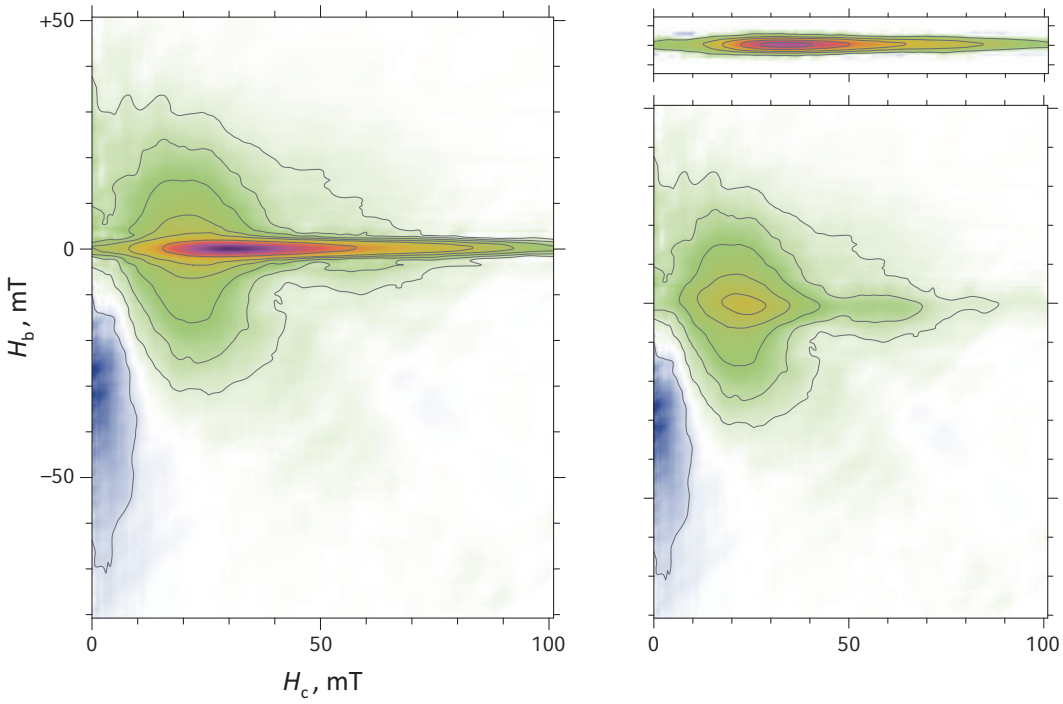


Table of contents

6.1 IsolateCR highlights

`IsolateCR` is a function of the VARIFORC package that is used for isolating the central ridge in FORC diagrams. The central ridge is a quasi-one-dimensional FORC feature occurring near $H_b = 0$ in FORC diagrams of non-interacting single-domain magnetic particles [*Newell*, 2005; *Egli et al.*, 2010; *Ludwig et al.*, 2013], and, to a much lesser extent, of pseudo-single domain particles. It represents the amplitude of first and last magnetization jumps of single magnetic particle hysteresis loops and is an extremely sensitive indicator for the kind of magnetic states encountered during hysteresis measurements. Quantitative analysis of the central ridge is based on its separation from other FORC contributions, and has interesting applications ranging from magnetic unmixing to investigation of magnetization processes in single-domain and pseudo-single-domain particles.

Like other VARIFORC functions, `IsolateCR` is controlled user-defined options stored in a special parameter file that can be used for batch processing. To date, `IsolateCR` is the only available tool for performing central ridge analyses. `IsolateCR` (Fig. 6.1) is based on the following processing steps:

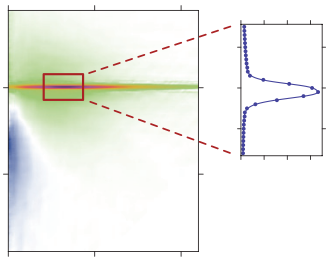
1) Prepare a mean vertical FORC profile on which the central ridge is identifiable.
2) Fit vertical FORC profiles with a linear combination of appropriate models for central ridge and background FORC contributions, based on preliminary results obtained with the mean vertical profile of step 1.
3) Using the profile models obtained with step 2, obtain a FORC diagram for the central ridge contribution and a FORC diagram for the remaining contributions (the so-called background).
4) Use the central ridge FORC diagram for calculating the central ridge coercivity distribution, i.e. the statistical distribution of fields at which first and last magnetization jumps occur on the major hysteresis loop. Plot this coercivity distribution together with the other two coercivity distributions associated with FORC measurements.
5) In case of samples containing exclusively single- domain particles, use the background FORC diagram for calculating the FORC contribution of reversible magnetic moment rotation in the applied field.
6) Calculate total magnetizations related to the central ridge and other FORC magnetization processes.
7) Export FORC diagrams and related coercivity distribution data.

Follow the instructions of this manual to enjoy the full functionality of `IsolateCR`, or refer to the quick VARIFORC guide for using basic options. Refer to the FORC tutorial included in this manual (Chapter 8) for taking full advantage of `IsolateCR` capabilities.

FORC matrix file

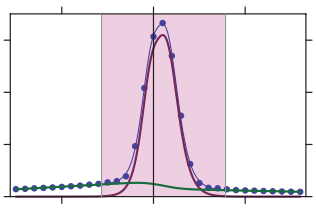
```
VARIFORC v1.0 FORC function -1/2 d2M/(dHr dH).

Field unit magnetization unit and FORC unit
T,mAm2/kg,1e-3 Am2/(T2 kg)

[...]

Data matrix
160.06739183958143,118.37842663606989,115.95472514390212,
0653501062625,6.303779035918211,8.388267301388282,
174646,2.6944584311521567,1.4183993690578518,
```

Import FORC matrix



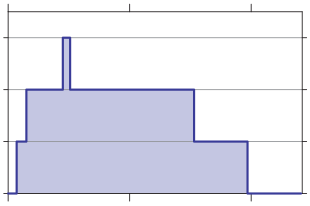
❶ Seed range selection

- Automatic selection over central peak
- Manual selection



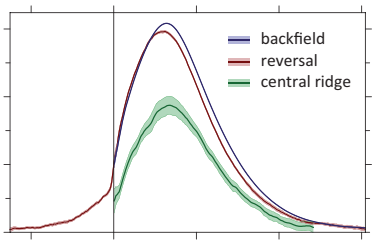
❷ Preliminary central ridge model on seed profile

- Physical model for central ridge profiles
- Physical model for background



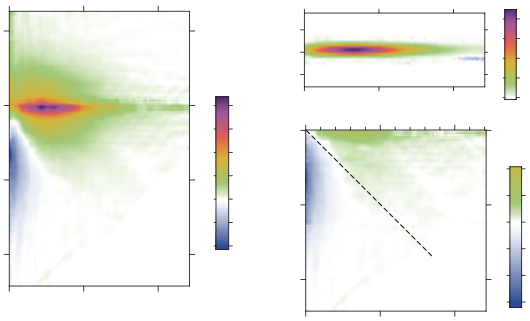
❸ Central ridge processing

- Sequential processing of vertical profiles
- Optimized number of model parameters
- Central ridge separation



❹ Coercivity distributions

- Central ridge coercivity distribution
- Comparison with other FORC coercivity distributions



❺ Separated FORC diagram contributions

- Central ridge FORC diagram
- FORC diagram with subtracted central ride
- FORC diagram for SD reversible contributions

❻ FORC-related magnetizations

```
Total FORC magnetization ..............:  3.917 ± 0.031
Total reversal magnetization ..........:  3.917 ± 0.021
Saturation remanence from backfield .....:  3.872 ± 0.005
Total central ridge magnetization .......:  2.206 ± 0.033
Total magnetization of SD background ....:  0.464 ± 0.073
```

❼ Export FORC and coercivity distribution data

Fig. 6.1: Graphical representation of the `IsolateCR` workflow.

6.2 Using IsolateCR

Like all VARIFORC functions, IsolateCR runs on a Wolfram Mathematica® notebook. A starting copy of this notebook is provided with the VARIFORC installation package under:

```
VARIFORC_Install/Packages/PlotFORC/VARIFORC_IsolateCR.cdf
```

You can copy this file to a different folder for convenience. The Mathematica® notebook stores all processing steps and graphical results for your records. Therefore, you best rename it with reference to the FORC data you want to process.

All IsolateCR notebooks begin with the following command line:

```
Get[FileNameJoin[{$HomeDirectory,"VARIFORC","VARIFORC_IsolateCR_code.txt"}]]
```

for uploading IsolateCR to the computation kernel. This command, as any other command Mathematica® notebooks, is executed by placing the cursor on it and pressing the keys SHIFT and ENTER at the same time. A copyright message will appear below this line, confirming that IsolateCR has been uploaded successfully.

IsolateCR is then called by the command line

```
VARIFORC`IsolateCR
```

to be executed by pressing the keys SHIFT and ENTER at the same time. At this point, IsolateCR starts a system dialog for:

1) uploading a parameter file that contains user-defined processing options,
2) uploading a FORC matrix produced by CalculateFORC, and
3) defining an output file name for exporting results.

The notebook appearance upon performing these steps is shown in Fig. 6.2.

The files required by steps 1) and 2) should be ready before IsolateCR is started. The parameter file is an unformatted text file containing all processing options to be used by IsolateCR. You can find a template of this file with universally valid standard options in the VARIFORC installation package under:

```
VARIFORC/Install/Packages/PlotFORC/Default_VARIFORC_IsolateCR_Parameters.txt
```

You may copy this file to a directory hosting all VARIFORC processing files related to given FORC measurements. Parameters in this file with a text editor according to your processing requirements (see section 6.4 and the VARIFORC quick guide). File upload and output file definition are explained in section 6.3.

❶ Upload source codes

```
In[1]:= Get[FileNameJoin[{$HomeDirectory, "VARIFORC", "VARIFORC_IsolateCR_code.txt"}]]

Function VARIFORC`PlotFORC for plotting FORC measurements.
[VARIFORC package v1.0 for Wolfram Mathematica and Mathematica Player Pro.
 © 2014 by Ramon Egli. All rights reserved.]
```

If used for scientific publications and presentations please cite as follows:
Egli, R. (2013). VARIFORC: An optimized protocol for calculating non-regular first-order reversal curve (FORC) diagrams. *Global and Planetary change 110*, 302-320.
http://dx.doi.org/10.1016/j.gloplacha.2013.08.003

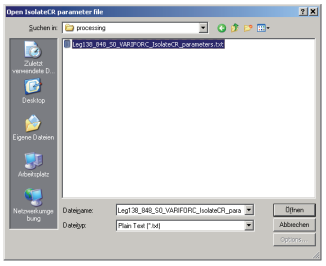
❷ Call IsolateCR

```
In[2]:= VARIFORC`IsolateCR
```

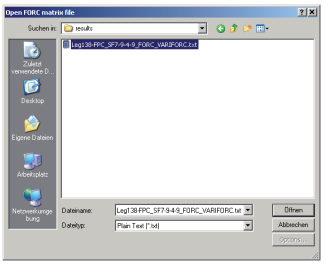
❸ Read auxiliary files

```
Initialization...
```

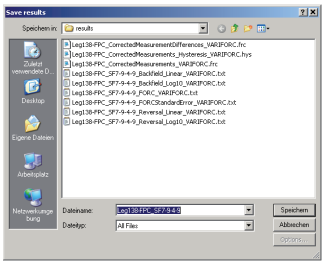
❹ Upload parameter file



❺ Upload FORC matrix file



❻ Define output file names



❼ Begin processing

```
Read parameter file...

Input parameters from C:/.../Example/IsolateCR_Parameters.txt:
INPUT 01. Hc-range of seed vertical profile .....................; narrow
INPUT 02. Hb-range parameters of seed vertical profile ..........; Automatic
INPUT 03. Extra central ridge margin ............................; 0.1
INPUT 04. Weight factor for background model ....................; Automatic
INPUT 05. Maximum freedom degree of central ridge model .........; 3
INPUT 06. Profile selection .....................................; All
INPUT 07. Confidence interval factor for distribution plots.....; 2.
INPUT 08. Scale factor for central ridge coercivity distribution .; 1.9
INPUT 09. Clip negative coercivity distribution values ..........; Yes
INPUT 10. Plotted FORC error parameter ..........................; SNR, 3
INPUT 11. FORC plot ticks specification .........................; Automatic
INPUT 12. Vertical exaggeration of central ridge FORC diagram ....; 3.
INPUT 13. Color scale saturation ................................; 0.9
INPUT 14. Quantile for color scale clipping .....................; 0.01
INPUT 15. Calculate single-domain reversible FORC background .....; Yes
```

Fig. 6.2: Initialization of the `IsolateCR` notebook.

After completing file upload and saving dialogs, IsolateCR proceeds autonomously until the end, without requesting any further action by the user. The processing status is continuously updated by status messages, e.g.

```
Process vertical profiles ...
```

warning messages, e.g.

```
WARNING: Unable to fit vertical profile 57 [code position 13].
```

error messages, e.g.

```
FORC error file not found. Program aborted.
```

summary tables, e.g.

```
Central ridge properties within th seed profile:
Mean vertical position .....................: 0.4133 mT
Mean FWHM ..................................: 1.995 mT
Minimum FWHM due to FORC processing ........: 1.923 mT
Vertical range covered by mean central ridge ..: -2.720 to 3.788 mT
```

and diagnostic plots as well as plots of final results. IsolateCR ends with the following message containing the total computation time:

```
PROGRAM END. Total computation time 1m 7s.
```

You can save the notebook file with all messages and results shown above for your later records and re-use it.

IsolateCR error messages usually produce a program abort. If one of these messages appears, an error was encountered either in the parameter file, e.g.:

```
Maximum CR fitting freedom is not 0, 1, 2, or 3. Program aborted. [INPUT 05]
```

or in the FORC matrix, e.g.:

```
Error encountered in reading FORC matrix file (Data matrix).
   Valid files must be produced by a VARIFORC function! Program aborted.
```

FORC matrix files produced by VARIFORC functions are fully compatible and do not generate reading errors unless accidentally modified. Error messages contain hints about the encountered problem. Errors generated by the parameter file arise from incorrect option specifications (see section 6.5 for acceptable options), or by altered formats. In the latter case, generate a new parameter file from the original copy provided with the installation package.

- Important parts of the `IsolateCR` code are dedicated to error handling in order to avoid unexpected crashes or incorrect results. Although VARIFORC functions have been extensively tested, the occurrence of unexpected errors cannot be completely excluded. Such errors might generate a cascade of other errors and/or a program crash.
- Unexpected errors likely cause Mathematica® notebooks to freeze. In this case, you should forcefully terminate the Mathematica® Kernel as described in Chapter 2.

- All information relative to `PlotFORC` runs is stored in the Mathematica® notebook. You can save the notebook with its content for your records.
- Use only one Wolfram Mathematica at the time.
- In order to avoid excessive memory usage, process a single sample in each notebook.

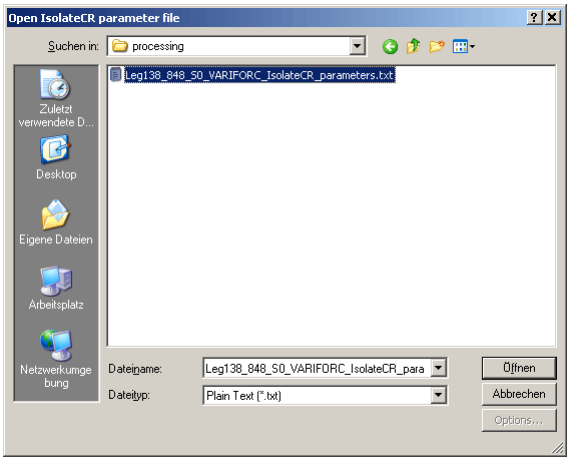
6.3 IsolateCR file management

VARIFORC functions have a modular structure, so that each function performs a specific operation by reading data stored in measurement files or files containing processed data, and export results to one or more files that can be used by other VARIFORC functions. `IsolateCR` is one of the many possible post-processing stages for further calculations based on FORC diagrams. It reads FORC matrix files and associated error matrices produced by `Calculate FORC`.

Results, in form of post-processed FORC diagrams and coercivity distributions, are plotted in the Mathematica® notebook and exported to files with the same user-defined name root. `IsolateCR` calls the file dialog of your operating system in order to let you upload and export files, as described in the following.

6.3.1 Parameter file upload

The parameter file is uploaded with the following dialog window:



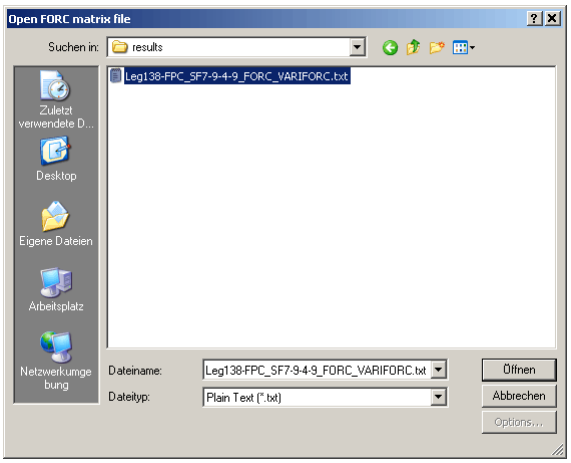
whose detailed appearance depends on your operating system. `IsolateCR` automatically selects file names ending with `VARIFORC_IsolateCR_parameters.txt`, which is the default setting for all `IsolateCR` parameter files. It is strongly recommended to store `IsolateCR` parameter files with this name ending, in order to avoid confusions with parameter files of other VARIFORC functions. The first part of the file name can be related to the sample being processed, e.g.:

```
/.../Sample01_VARIFORC_IsolateCR_parameters.txt
```

If you do not find the parameter file in the expected directory, remove the file name and file type filters: in this case, all files in the chosen directory will be displayed.

6.3.2 FORC matrix upload

The FORC matrix (previously produced by the VARIFORC function `CalculateFORC` as first processing step) is uploaded with the following dialog window:

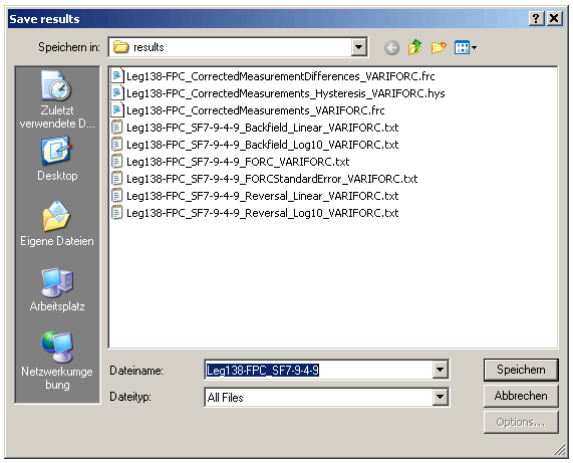


whose detailed appearance depends on your operating system. Be careful to choose a single FORC matrix file in its original format. Only files produced by `CalculateFORC`, whose names end with `_FORC_VARIFORC.txt`, are shown. Related error matrices are uploaded automatically according to their name root, which is the same as that of the corresponding FORC matrix file.

- FORC matrix files (ending with `FORC_VARIFORC.txt`), and corresponding FORC error matrix files (ending with `FORCStandardError_VARIFORC.txt`) should be stored always in the same folder, as when produced by a VARIFORC function.
- VARIFORC functions such as `IsolateCR` automatically look for FORC error matrix files if needed, assuming that these files are stored in the same folder of the corresponding FORC matrix.

6.3.3 Output file naming

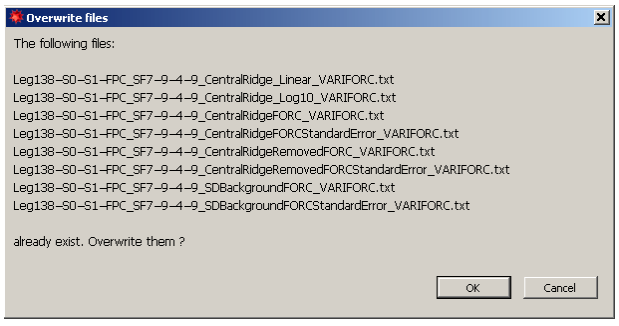
Central ridge processing results are plotted in the Mathematica® notebook and exported as FORC matrices and coercivity distribution files. A root name for all output files created by `IsolateCR` is entered with the following file saving dialog:



whose detailed appearance depends on your operating system. `IsolateCR` chooses by default the same directory of the FORC matrix file and suggests the same root name.

- Default output file names suggested by `IsolateCR` do not contain any reference to the chosen processing parameters (which, however, are stored in output files containing the FORC matrix).
- If you want to store several versions of the same central ridge processing steps, add a hint in the export file names. Otherwise, if chosen file names already exist, `IsolateCR` will open an overwrite file dialog (see below).

If output files with the same name (produced for instance by previous runs) are encountered, `CalculateFORC` opens the following overwrite file dialog:



If you choose to overwrite existing files, IsolateCR will continue processing without further input requests. Otherwise, the program is aborted and you should run it again with different output file names.

If "s1" is the file name root entered with the file saving dialog, the following output files will be generated:

1) /.../s1_CentralRidge_Linear_VARIFORC.txt for the coercivity distribution derived from the central ridge. The coercivity distribution is defined on a linear field scale.
2) /.../s1_CentralRidge_Log10_VARIFORC.txt for the coercivity distribution derived the central ridge. The coercivity distribution is defined on a logarithmic field scale.
3) /.../s1_CentralRidgeFORC_VARIFORC.txt for the FORC matrix of the isolated central ridge.
4) /.../s1_CentralRidgeFORCStandardError_VARIFORC.txt for the standard error matrix associated with 3).
5) /.../s1_CentralRidgeRemovedFORC_VARIFORC.txt for the input FORC matrix after central ridge removal.
6) /.../s1_CentralRidgeRemovedFORCStandardError_VARIFORC.txt for the standard error matrix associated with 5).
7) /.../s1_SDBackgroundFORC_VARIFORC.txt for the FORC matrix of the reconstructed reversible contributions of uniaxial single-domain particles. This file is generated only if the processing option "INPUT 15" has been set to "Yes".
8) /.../s1_SDBackgroundFORC_VARIFORCStandardError.txt for the standard error associated with 7).

6.4 Editing IsolateCR parameters

IsolateCR is controlled by 15 parameters that are uploaded from a parameter file ending with _VARIFORC_IsolateCR_Parameters.txt. This is an editable text file with a template provided with the installation package (see section 6.2). This template contains universal parameters that can be used with practically any type of FORC measurements. You can copy this file to any folder, typically the same folder containing the FORC data and/or the IsolateCR Mathematica notebook, and use it as is. Nevertheless, in order to exploit all IsolateCR capabilities and obtain best results, you should adapt these parameters to your requirements. For this purpose, open the IsolateCR parameter file with a text editor. You will see a table similar to the following example:

```
Input parameters for package VARIFORC_CalculateCR; (version 1.0).

INPUT 01. Hc-range of seed vertical profile .....................; narrow
INPUT 02. Hb-range parameters of seed vertical profile ..........; Automatic
INPUT 03. Extra central ridge margin ............................; 0.1
INPUT 04. Weight factor for background model ....................; Automatic
INPUT 05. Maximum freedom degree of central ridge model .........; 3
INPUT 06. Profile selection .....................................; All
INPUT 07. Confidence interval factor for distribution plots.....; 2.
INPUT 08. Scale factor for central ridge coercivity distribution .; 1.9
INPUT 09. Clip negative coercivity distribution values ..........; Yes
INPUT 10. Plotted FORC error parameter ..........................; SNR, 3
INPUT 11. FORC diagram ticks specification ......................; Automatic
INPUT 12. Vertical exaggeration of central ridge FORC diagram ....; 3.
INPUT 13. Color scale saturation ................................; 0.9
INPUT 14. Quantile for color scale clipping .....................; 0.01
INPUT 15. Calculate single-domain reversible FORC background .....; Yes
```

Each line of this table (except for the first one) consists of a parameter description (e.g. INPUT 01. Hc-range of seed vertical profile) followed by the corresponding parameter value (e.g. narrow). Parameters are separated from their descriptions by a semicolon (;). Multiple parameters in the same row (e.g. a list of numbers) are always separated by a colon (,) and spaces have no meaning. You can change these parameters according to the guidelines given in section 6.5 and save the parameter file with an appropriated name related to its usage context.

Example 1: If you routinely process central ridges in high-resolution FORC diagrams of sediment samples obtained with the same measurement protocol, you can store the parameter file as `Sediment_highres_VARIFORC_IsolateCR_Parameters.txt`, and recall this file every time you plot process a central ridge with `IsolateCR`.

Example 2: Parameters to be used only for a FORC matrix stored in `File_1_FORC_VARIFORC.txt`, can be stored in a parameter file called `File_1_VARIFORC_IsolateCR_Parameters.txt` for later records.

- Always save the processing parameters as an unformatted text file. If you use a text processor such as Microsoft Word, do not forget to save as text (`.txt`) only. Formatted texts are not recognized by `IsolateCR`.
- Do not change the table structure; in particular, do not add new lines. Multiple parameters representing the same input (e.g. `INPUT 10` plotted FORC error parameter) must be entered in the same line, regardless of their length.
- Acceptable parameter formats are explained in detail in section 6.5. Incorrect or unrecognized formats generate error messages referring to the corresponding input line (e.g. `INPUT 01`).

The following suggestions help you with an efficient management of FORC processing parameters:

- Several input parameters can be set to automatic options, letting `IsolateCR` choose optimized values. Use automatic options if possible, unless you have specific processing requirements. For your convenience, the parameter file provided with the installation package is already based on automatic options whenever possible.
- Use consistent FORC protocols for your measurements, so that only few sets of processing parameters are required. For example, all magnetofossil-bearing sediments can be measured with the same protocol and processed with the same parameters.
- If you have generated an invalid parameter file and you do not know how to restore the proper format, create a new file starting from the template provided with the installation package. For this reason, never overwrite templates in the installation package.

6.5 Full references for IsolateCR parameters

All options for defining the import parameters are described in this section. Please refer to the `IsolateCR` quick guide for a brief summary.

Table of contents:

INPUT 01. H_c-range of seed profile

The central ridge is a quasi-1D, high-amplitude FORC feature located in proximity of $H_b = 0$ (Fig. 6.3a). This feature is produced by non-interacting single-domain particles with uniaxial anisotropy [*Newell*, 2005; *Egli et al.*, 2010] and – with much reduced amplitude – by small pseudo-single-domain particles (see Chapter 8). The central ridge is usually overlaid to a regular background, from which it can be isolated in order to obtain additional information about the different magnetization processes. The principle used by `IsolateCR` to perform this operation [*Egli et al.*, 2010, *Egli*, 2013] is based on fitting the FORC region occupied by the central ridge and its immediate surroundings with model vertical profiles of the central ridge itself, and of the continuous background under it (Fig. 6.3c). This procedure is initiated on a "seed" vertical profile of the FORC diagram obtained by averaging profiles located near the central peak of the FORC diagram (red rectangle in Fig. 6.3a), where the adverse effect of measurement noise is minimized.

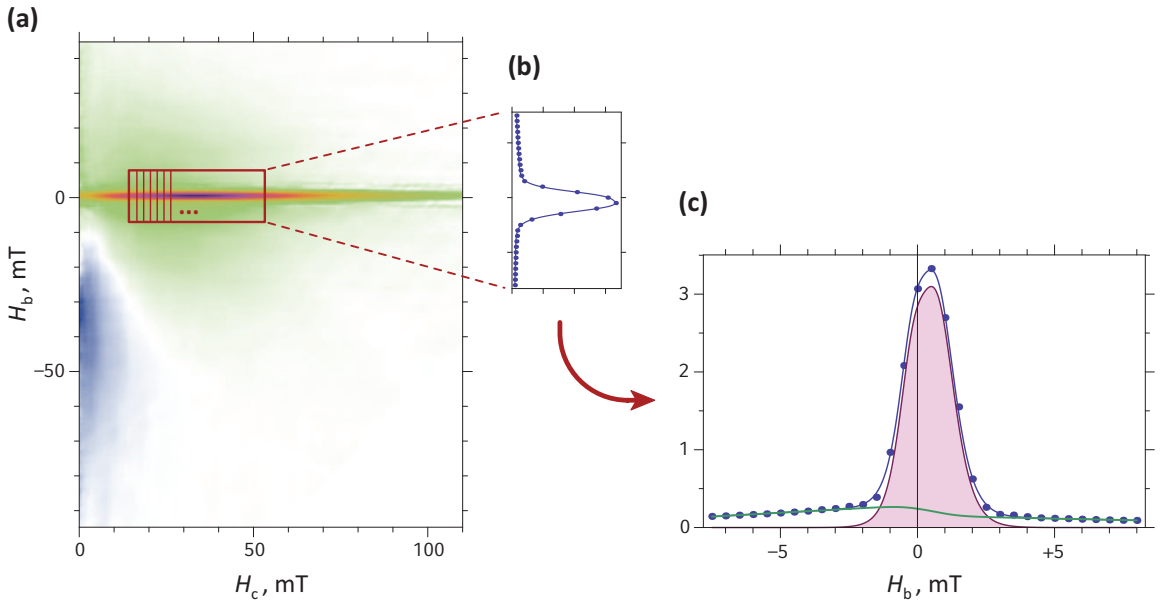


Fig. 6.3: Illustration of how a seed vertical profile is calculated by `IsolateCR`. This profile represents the first step for isolating the central ridge from other FORC contributions. **(a)** FORC diagram of a pelagic carbonate (see the downloadable example "pelagic carbonate"), obtained with advanced smoothing options for optimal resolution of the central ridge. The red rectangle marks the FORC region which encloses FORC profiles (vertical red lines) used to calculate an average "seed" profile shown in (b). In this example, the rectangular FORC region has been selected by setting `INPUT 01` and `INPUT 02` to `Wide` and `Automatic`, respectively. **(b)** Vertical FORC profile calculated by averaging individual profiles enclosed by the rectangular FORC region in (a). This profile is used for obtaining a "seed" model of the central ridge, shown in (c). **(c)** Seed vertical profile of the FORC function (dots) and central ridge model based on the superposition (blue line) of a background (green line) and the central ridge (red line with shaded region indicating the corresponding central ridge magnetization).

The "seed" vertical profile is needed by IsolateCR for obtaining an initial model of the central ridge and the remaining FORC contributions, which is then applied to all vertical profiles in order to obtain a full model. The FORC region used to calculate the seed profile is controlled by parameters chosen with INPUT 01 for its horizontal extension and INPUT 02 for its vertical extension. The main criterion underlying INPUT 01 and INPUT 02 choices is the selection of a FORC region where the central ridge has its maximum amplitude and is better distinguishable from other FORC contributions. In order to facilitate this selection, automatic options are provided in addition to a full manual control eventually needed in special cases.

The automatic options for INPUT 01 are wide and narrow. The option wide, i.e

```
INPUT 01. Hc-range of seed vertical profile ....; wide
```

is used to select a horizontal central ridge range with amplitudes exceeding 70% of the peak amplitude (Fig. 6.4a). This option is suited for the common case where the central ridge is perfectly horizontal. A narrower horizontal range can be chosen with the option narrow, i.e

```
INPUT 01. Hc-range of seed vertical profile ....; narrow
```

In this case, the chosen range is centered on the central ridge peak, and its extension coincides with that of the regression rectangles used for calculating the FORC diagram (Fig. 6.4b). This range corresponds to twice the horizontal resolution of the FORC diagram at the central ridge peak, and contains nearly identical vertical profiles. The narrow option should be chosen in cases where the vertical position and/or vertical width of the central ridge are not constant.

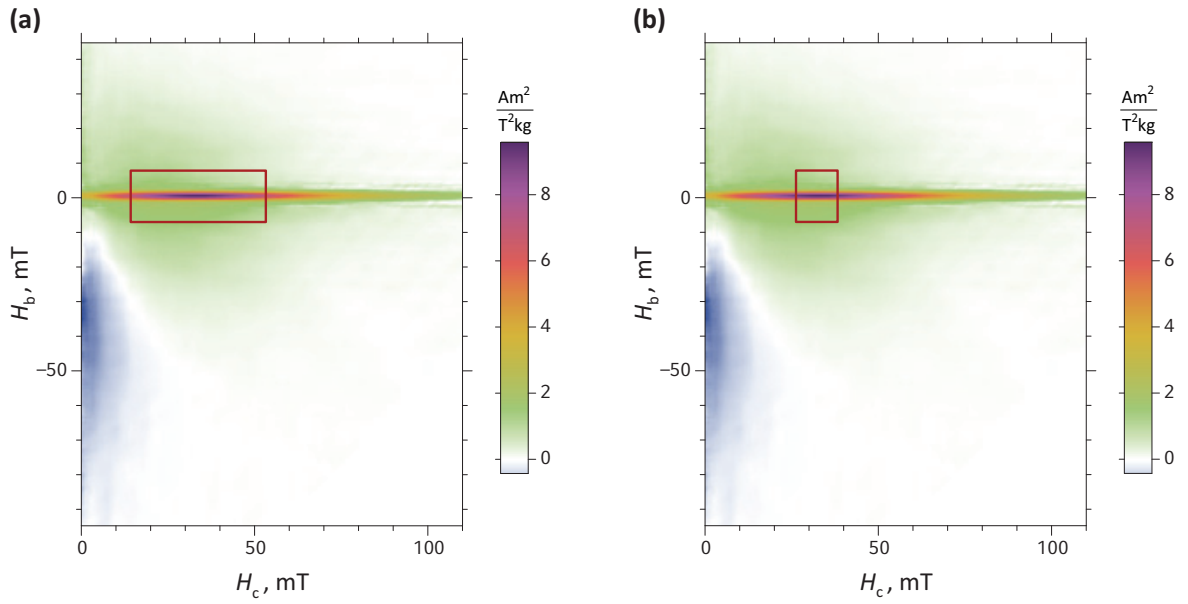


Fig. 6.4: Example seed vertical profile ranges obtained with automatic options from the FORC diagram of a pelagic carbonate (see the downloadable example "pelagic carbonate"). **(a)** INPUT 01 was set to wide. **(a)** INPUT 01 was set to narrow. In both cases, INPUT 01 was Automatic.

The horizontal range can be specified explicitly by entering its left and right limit, e.g.

```
INPUT 01. Hc-range of seed vertical profile ....; 15, 60
```

for selecting all vertical profiles comprised between $H_c = 15$ mT and $H_c = 60$ mT. The range is assumed to be expressed with the same field unit as the imported FORC matrix, as reported in the file header.

The horizontal range used for calculating the seed vertical profile is given in a summary table, e.g.:

```
FORC space considered for calculating the seed vertical profile:
Hc-range: 26.25 to 38.25 mT
Hb-range: -7.01 to 7.84  mT
```

This table can be used as reference for adjusting the choice performed with automatic options, if necessary.

If `INPUT 01` is set to `wide` or `narrow`, `IsolateCR` looks for the horizontal position of the absolute FORC maximum over the range occupied by the central ridge. Inappropriate results might be obtained if this position is not uniquely determined. For example, if the FORC function contains a pronounced vertical ridge (e.g. Fig. 6.5a), the absolute maximum might occur at $H_c = 0$, therefore not coinciding with the central FORC peak. In this case, selected FORC profiles are dominated by the vertical ridge and the central ridge contribution becomes easily subdued (Fig. 6.5b). In order to prevent undesirable vertical ridge contributions, `IsolateCR` excludes all profiles near $H_c = 0$ from the automatic search of a horizontal range for the seed profile (Fig. 6.5c). Nevertheless, a manual range specification might be still needed in special circumstances, e.g. in case of multiple central ridge peaks.

- The automatic selection of the horizontal seed profile range is adequate in most cases. The final results of `IsolateCR` do not depend on the seed profile for a wide range of reasonable choices.
- Explicit horizontal range specifications for the seed profile might be desirable if a group of FORC diagrams need to be processed with exactly the same parameters.

- The automatic horizontal range selection of the seed range can give inappropriate results in case of central ridges affected by excessive noise, or in case of multiple peaks. Explicit range specifications should be entered in these cases.

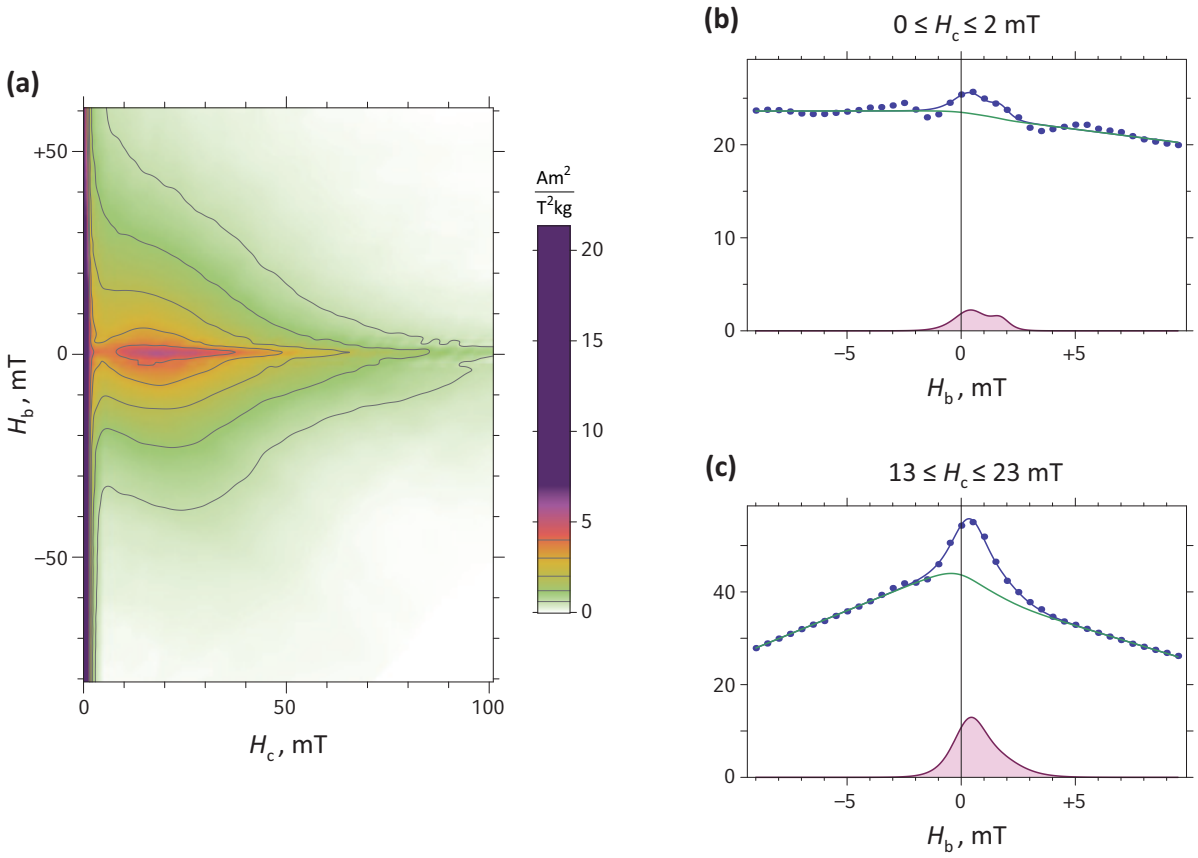


Fig. 6.5: Seed vertical profile examples in case of FORC diagrams with a pronounced vertical ridge. **(a)** FORC diagram of volcanic ash (see the downloadable example "volcanic ash"), obtained with advanced smoothing options. This diagram contains a pronounced vertical ridge and a small central ridge contribution along $H_b = 0$. **(b)** Seed vertical profile (dots) over $0 \le H_c \le 2$ mT (i.e. `INPUT 01` set to `0,2`). The central ridge (red line with shaded area underneath) is heavily masked by the large background (green) produced by the vertical ridge visible in (a). This would be the result of setting `INPUT 01` to `narrow` if the H_c-range occupied by the vertical ridge would not be automatically excluded by `IsolateCR`. **(c)** Same as (b), after setting `INPUT 01` to `narrow`. The seed vertical profile is properly centered over the central peak of the FORC function at $H_c \approx 17$ mT, although this peak does not coincide with the absolute maximum of the FORC function. The central ridge is now clearly identifiable.

INPUT 02. H_b-range parameters of seed profile

A preliminary central ridge model that serves as initialization for further processing is obtained by dividing the seed profile into three sections (Fig. 6.6): a central section that covers the vertical extension of the central ridge, and two immediately adjacent sections with no central ridge contributions that serve as initial reference for quantifying the background under the central ridge. The initial range of the three sections is controlled by options entered with `INPUT 02`. The `Automatic` option, i.e.

```
INPUT 02. Hb-range parameters of seed profile ....; Automatic
```

provides an empirical estimate of the central ridge position and width in the seed profile, as well as the H_b-range of the seed profile itself. This estimate is obtained recursively from the initial assumption of an ideal central ridge centered at $H_b = 0$. The H_b-range of the seed profile is chosen to be twice as large as the estimated vertical extension of the central ridge.

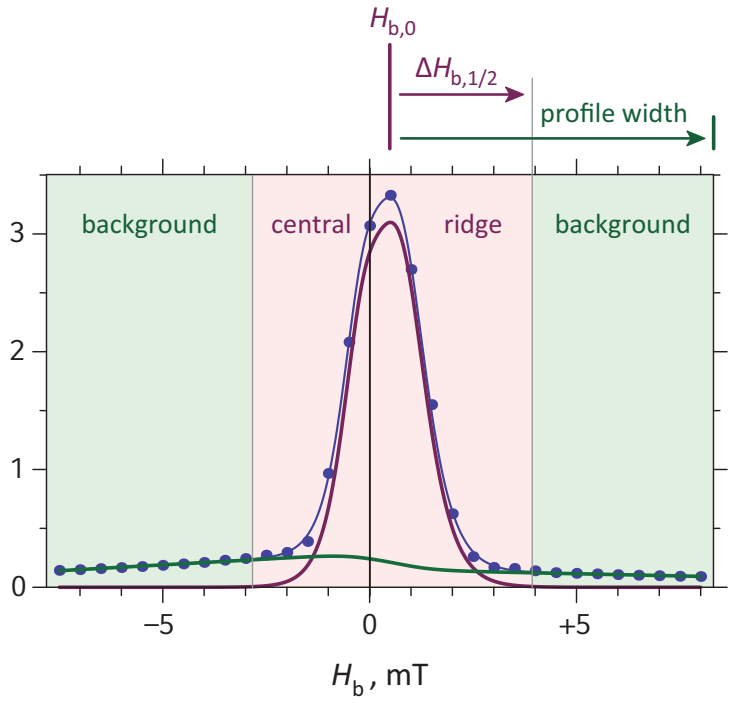


Fig. 6.6: Example of seed profile obtained from the FORC diagram of a pelagic carbonate (see the downloadable example "pelagic carbonate"). Dots represent the calculated profile, and lines are curves obtained from the initial central ridge model (red: central ridge, green: background generated by other FORC contributions, blue: sum of central ridge and background). The three sections of the seed profile used for generating the initial model are highlighted by shaded areas, and represent the H_b-range of the central ridge (pink) and the adjacent regions identified with the background (light green). The three sections are defined by the position $H_{b,0}$ of the central ridge, its half-width $\Delta H_{b,1/2}$, and the half-width of the seed profile. These parameters can be specified explicitly with `INPUT 02`. `IsolateCR` adapts them automatically to the central ridge properties found with the initial model.

Special requirements can be fulfilled by entering the H_b-range parameters explicitly as a sequence of three numbers, e.g.

```
INPUT 02. Hb-range parameters of seed profile ....; 0.4, 2, 6
```

(Fig. 6.6). The first number represents the offset $H_{b,0}$ of the central ridge with respect to $H_b = 0$ in the seed profile. Central ridges produced by non-interacting single-domain particles are characterized by a small (< 1 mT) offset due to thermal activations. Furthermore, positive or negative offsets can originate from small mean interaction fields. The second number represents the vertical half-width of the central ridge, as it appears in the FORC diagram. A finite width is produced by smoothing during FORC processing, even if measurements contains an ideal ridge with zero width. This is the minimum width of any central ridge, and is given by $\Delta H_{b,1/2} \approx s_{b,0}\delta H$, where δH is the field step size of FORC measurements (see Chapter 3), and $s_{b,0}$ is the minimum vertical smoothing factor used to process them with `CalculateFORC` (see Chapter 4). The example of Fig. 6.6 is based on measurements with $\delta H \approx 0.5$ mT and a vertical smoothing factor $s_{b,0} = 4$ over the central ridge, so that $\Delta H_{b,1/2} \approx 2$ mT (i.e. the full vertical width of the central ridge is 4 mT). Real central ridges can be slightly wider, as in Fig. 6.6, due to thermal activation effects and small degrees of magnetostatic interactions [*Egli*, 2006]. The third number represents the half-width of the seed profile, which is taken symmetrically around the mean central ridge position. The seed profile should be 2-3 times wider than the central ridge.

`IsolateCR` uses `INPUT 02` specifications to obtain a first model of the central ridge. The central ridge parameters defined explicitly with `INPUT 02` are updated according to this initial model, and the seed vertical profile is adjusted in order to accommodate the new parameter values. For example, if the central ridge is shifted upwards with respect to the initial parameters defined with `INPUT 02`, the entire profile is shifted upwards. This works also if `INPUT 02` is set to `Automatic`, in which case the initial central ridge parameters are calculated assuming an ideal case with $\Delta H_{b,1/2} \approx s_{b,0}\delta H$. The final parameters used to model the whole central ridge are summarized in a table for the seed profile range, e.g.:

```
FORC space considered for calculating the seed vertical profile:
Hc-range: 26.25 to 38.25 mT
Hb-range: -7.01 to 7.84  mT
```

and a table for the initial central ridge model, e.g.:

```
Central ridge properties within the seed profile:
Mean vertical position             : 0.434 mT
Mean FWHM                          : 1.996 mT
Minimum FWHM due to FORC processing: 1.925 mT
```

These tables can be used as reference for improving initial `INPUT 01` and `INPUT 02` specifications. A seed profile like in Fig. 6.6 is plotted by `IsolateCR` along with the initial central ridge model, so that the suitability of the options entered with `INPUT 01` and `INPUT 02` can be immediately verified.

If INPUT 02 is defined by explicit parameters, the originally chosen proportion between central ridge and seed profile widths will be maintained through all processing steps of IsolateCR. Therefore, explicit INPUT 02 parameters can be used to tune the fraction of the seed profile that is occupied by the central ridge. For example, seed profiles shorter than those defined by automatic options can be chosen with the third INPUT 02 parameter in order to handle a highly non-linear background.

The central ridge model used by IsolateCR is non-linear and has up to 10 degrees of freedom. As with any non-linear model, a unique solution is not always granted, especially if a small-amplitude central ridge is affected by measurement noise, or if the central ridge is overlaid to a very curved background, as for the magnetotactic bacteria example of Fig. 6.7a,b, or to a large background, as for the volcanic ash example of Fig. 6.7c,d. In these cases, the preliminary model obtained from the seed profile depends on the vertical extension of the profile itself. The central ridge amplitude and width is overestimated if an excessively wide seed profile is chosen (e.g. Fig. 6.7b,d), because the central ridge is erroneously used to reproduce the background curvature. Because the background is fitted with a smoothed, piecewise linear function, the seed profile should cover a vertical range where this approximation is valid, (Fig. 6.7a,c). This criterion is mostly fulfilled with the Automatic option of INPUT 02, because the starting model is an ideal central ridge with smallest possible vertical width due to FORC processing. In any case, fulfillment of the piecewise linear background approximation – also for the automatic option – should be checked directly on the seed profile plot shown by IsolateCR. Correctly chosen seed profiles are characterized by a perfectly linear background on each side of the central ridge. If this condition is not fulfilled, smaller seed ranges should be chosen.

- The background under and in proximity of the central ridge is modeled by a smoothed stepwise linear function [*Egli*, 2013]. Accordingly, the two seed profile sections adjacent to the central ridge should be as close to straight lines as possible, compatibly with measurement noise.
- The initial central ridge model depends on the seed profile length, which is the only parameter that, if explicitly entered with INPUT 02 (third parameter), will not be automatically corrected by IsolateCR. This is to maintain a certain manual control over the initial central ridge model, in case ambiguities arise from the superposition of a small central ridge to large background amplitudes (see example discussed below).
- Central ridge processing ambiguities depend strongly on the resolution of the FORC diagram. Therefore, use always the maximum possible measurement resolution for samples containing a central ridge.

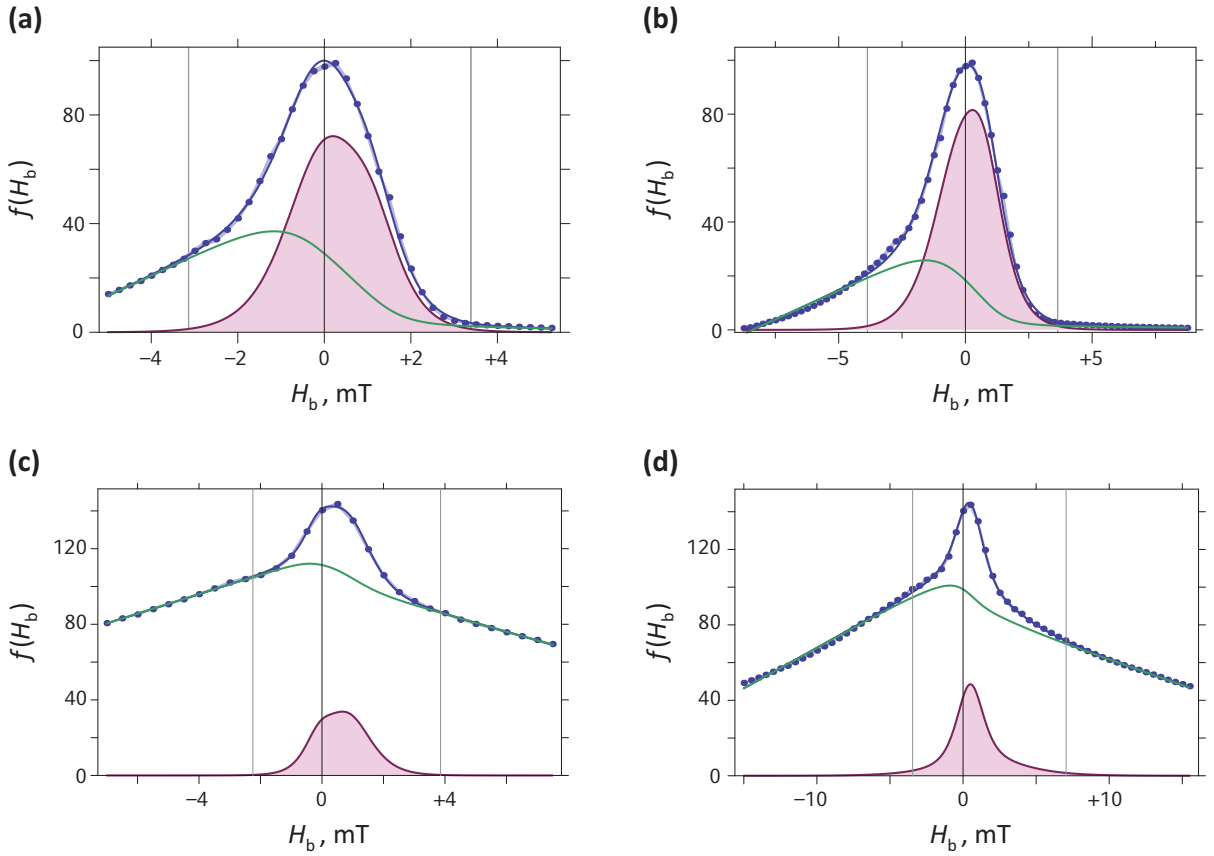


Fig. 6.7: Sensitivity of the initial central ridge model to the seed profile width. **(a-b)** Magnetotactic bacteria (see the downloadable example "Magnetospirillum 1"). **(c-d)** Volcanic ash sample (see the downloadable example "volcanic ash"). FORC data are shown as dots; lines represent initial model profiles for the central ridge (red with shading underneath), background (green), and the sum of the two (blue). Vertical gray lines represent the H_b-range covered by the central ridge. **(a-c)** The vertical range of the seed profile is properly chosen, as seen from the perfect coincidence between background model and data outside the central ridge. **(b-d)** The vertical range of the seed profile is excessively large, because it includes parts of the background that are not correctly approximated by a linear background model, especially over $H_b < 0$. The examples in (b) and (c) have been generated by setting `INPUT 02` to `Automatic`. The automatic option worked properly in (c), but not in (b).

INPUT 03. Extra central ridge margin

An essential stabilization element of the non-linear model used to isolate the central ridge is represented by a two-step fitting procedure where the background alone is modeled at first instance using FORC data immediately adjacent to the central ridge. Once a background profile has been obtained, the central ridge is fitted with a linear combination of the background with a suitable bell-shaped function. The separation of vertical FORC profiles into a central region dominated by the central ridge, and two adjacent ranges with no central ridge contributions (shaded areas in Fig. 6.8) is essential for the correct functioning of the two-step fitting procedure. Because of measurement noise and limitations of the model functions, the boundaries between central ridge and background are affected by an intrinsic uncertainty. Therefore, in order to avoid spurious central ridge contributions to the background during the first fitting stage, an extra margin can be added around the central ridge. The width of this margin is controlled by `INPUT 03`.

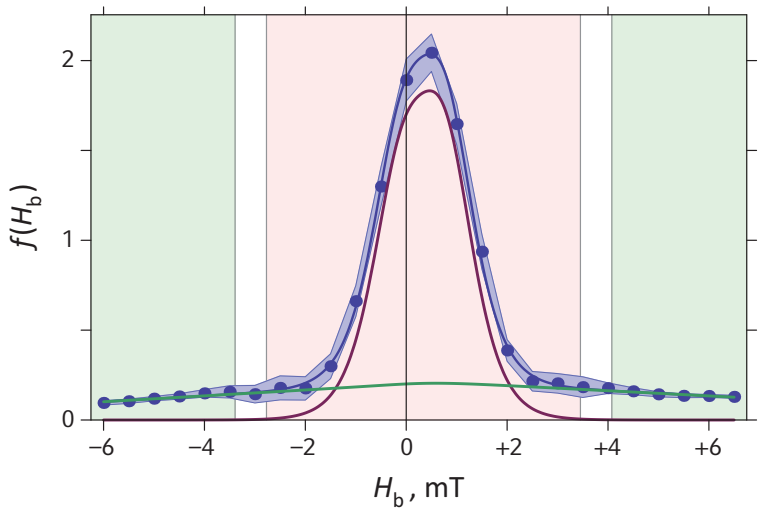


Fig. 6.8: Seed profile obtained from the FORC diagram of a pelagic carbonate (see the downloadable example "pelagic carbonate"). Dots represent the seed profile obtained using a single vertical profile at $H_c = 5$ mT , in order to highlight the uncertainty added by measurement noise to the determination of the central ridge model. Lines are curves obtained from the initial central ridge model (red: central ridge, green: background, blue: sum of central ridge and background). The blue band around points represents the estimated standard error. The three sectors of the seed profile used for calculating the initial model are highlighted by shaded areas, and represent the H_b -range of the central ridge (pink) and the adjacent regions identified with the background (light green). The extra margin around the central ridge, introduced by `INPUT 03` appears as white gaps between sectors of the seed profile dominated by the central ridge (pink) and the background (light green), respectively. The extra margin amounts to 10% of the estimated central ridge width, as set by `INPUT 03` equal to `0.1`. Notice the increase of measurement noise amplitudes over the central ridge, which is due to smaller values of the vertical smoothing factor adopted as part of the variable smoothing protocol used to calculate the FORC diagram (see Chapter 4).

The extra margin to be added around the central ridge is expressed as fraction of the central ridge width. For example

```
INPUT 03. Extra margin around central ridge ....; 0.1
```

means that the extra margin width is 10% of the estimated vertical width of the central ridge. Extra margins are avoided by choosing

```
INPUT 03. Extra margin around central ridge ....; 0
```

The margin entered with `INPUT 03` is a number comprised between 0 and 1. If numbers close to 1 are entered, the number of background points on both sides of the central ridge becomes insufficient for fitting purposes. In this case, `IsolateCR` is automatically aborted with the following error message:

```
FORC background in the seed profile is not defined by at least 3 points
   on each side of the central ridge. Program aborted.
```

The problem is solved by reducing the extra margin around the central ridge, or by increasing the seed profile width specified with `INPUT 03`.

- Reasonable extra margins are comprised between 0 and 10% of the estimated central ridge width. The chosen margin is shown on a plot of the seed profile (e.g. Fig. 6.8).
- Final results of `IsolateCR` are relatively insensitive to the choice of an extra margin, especially if the central ridge is characterized by large signal-to-noise ratios.

INPUT 04. Weight factor for model background

Isolation of the central ridge from other FORC contributions is based on a model for the central ridge itself and another model for the FORC background over the range occupied by the central ridge. Accordingly, there are two possibilities for isolating the central ridge, i.e. (1) the central ridge contribution is identified with the central ridge model, and (2) the central ridge contribution is calculated by subtracting the background from the total FORC function. Similarly, the FORC background can be calculated by (1) using the corresponding model, and (2) subtracting the central ridge model from the total FORC function. Which of the two options is more convenient depends on the central ridge and background amplitudes, respectively. For example, if the FORC background is much smaller than the central ridge, best results are obtained using the background model alone, since even smallest central ridge model misfits might be of the same order of magnitude as the background.

The relative weight given to central ridge and FORC background models is controlled by `INPUT 04`. With the automatic option, i.e.

```
INPUT 04. Weight factor of background model ....; Automatic
```

only the background model is considered for isolating the central ridge from other FORC contributions (Fig. 6.9c). In this case, the central ridge is obtained by subtracting the background model from the total FORC function. This option is recommended in all cases where central ridge amplitudes are much larger than those of other FORC contributions, and with FORC data obtained from variable smoothing procedures (see Chapter 4), because in this case the background model is based on highly smoothed regions of FORC space with effective measurement noise suppression.

The opposite choice with respect to the `Automatic` option is obtained by setting the weight factor of the background model to zero, i.e.

```
INPUT 04. Weight factor of background model ....; 0
```

(Fig. 6.9a). In this case, the background model is completely ignored, and isolation of the central ridge is based entirely on the central ridge model. This option is not recommended, especially with FORC data obtained from variable smoothing procedures, because relatively large errors of the weakly smoothed central ridge are transferred to the FORC background, whose amplitude is usually much smaller than that of the central ridge.

Compromises between the two choices discussed above are based on a weighted linear combination of the background and central ridge models. In this case, the relative weight of the background model is entered with `INPUT 04` as a positive number. In particular,

```
INPUT 04. Weight factor of background model ....; 1
```

(Fig. 6.9b) represents the case where weight factors of the two models are inversely proportional to the square of the corresponding mean amplitudes. If a number <1 or >1 is entered

with INPUT 04, the weight factor of the background model is reduced or increased in a proportional manner. In general, improvements of background reconstructions (i.e. larger numbers entered with INPUT 04) occur at cost of data quality for the central ridge, and vice-versa. In case of central ridges dominating over the background (Fig. 6.9), the data quality of the reconstructed central ridge is relatively insensitive to the choice made with INPUT 04, so that maximum weight should be given to the background model by setting INPUT 04 to Automatic.

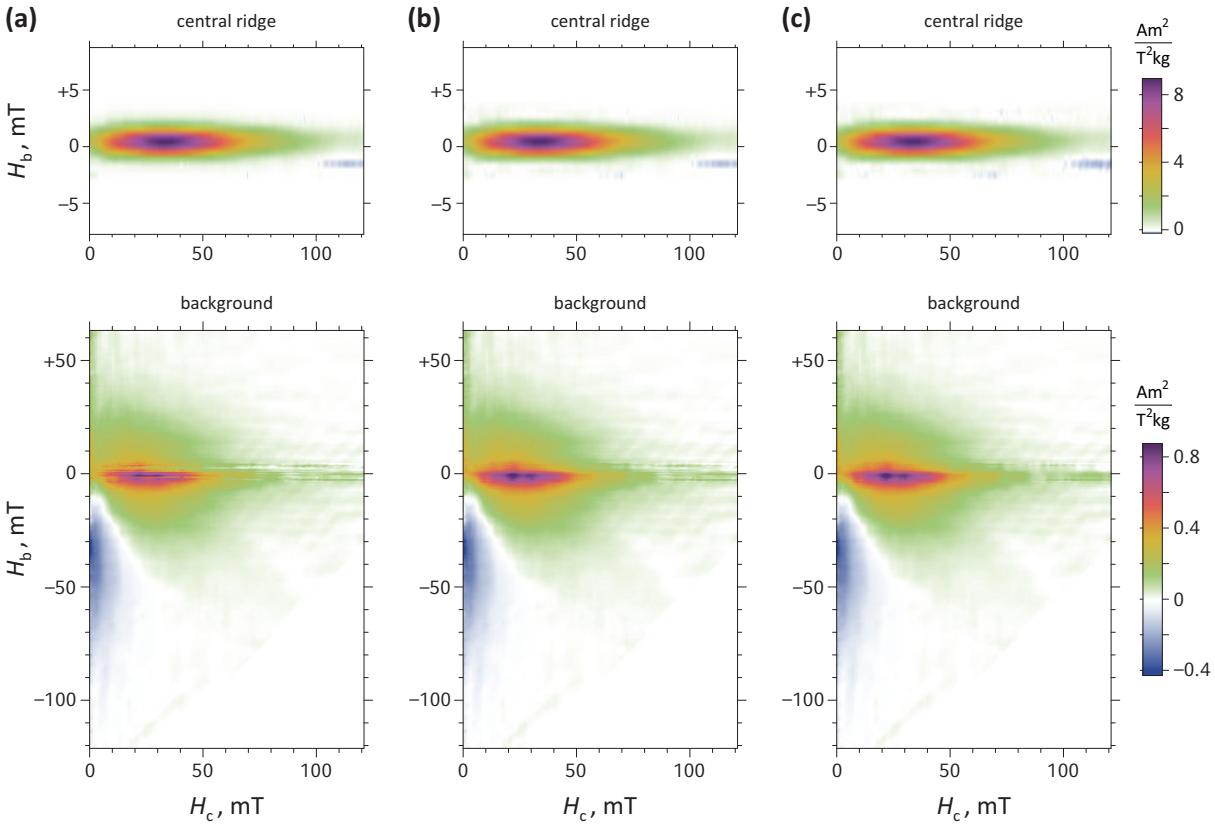


Fig. 6.9: Examples of central ridge separation based on FORC measurements of a pelagic carbonate (see the downloadable example "pelagic carbonate"), obtained with three different INPUT 04 settings. The first and second FORC diagram rows represent the isolated central ridge and the FORC function with removed central ridge (i.e. the background), respectively. Central ridge amplitudes are ~10 times larger than those of the background. Notice that FORC diagrams of isolated central ridges are plotted with a 5× vertical exaggeration. **(a)** Central ridge separation obtained on the basis of the central ridge model alone (i.e. INPUT 04 was set to 0). **(b)** Central ridge separation obtained on the basis of a linear combination of central ridge and background models, weighted by their inverse squared mean amplitudes (i.e. INPUT 04 was set to 1). **(c)** Central ridge separation obtained on the basis of the background model alone (i.e. INPUT 04 was set to Automatic). This choice is equivalent to entering a very large number with INPUT 04. Notice that the choice of INPUT 04 has evident effects on the background, because of its small amplitude, while the same effects are unnoticeable for the reconstructed central ridge.

If central ridge amplitudes are is small compared to the background (Fig. 6.10), the reconstructed ridge becomes more sensitive to INPUT 04 than the FORC background, because of measurement noise.

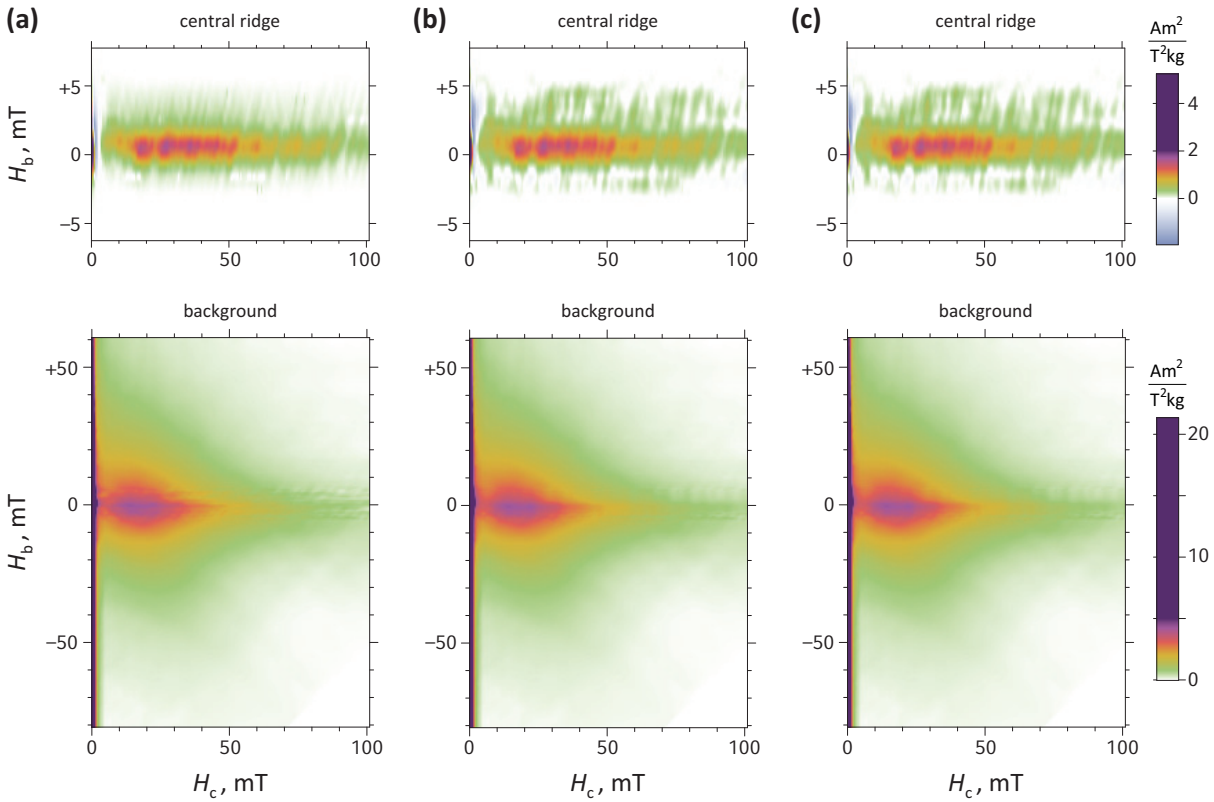


Fig. 6.10: Examples of central ridge separation based on FORC measurements of a volcanic ash sample (see the downloadable example "volcanic ash"), obtained with three different setting of INPUT 04. The first and second FORC diagram rows represent the isolated central ridge and the FORC function with removed central ridge (i.e. the background), respectively. Notice that FORC diagrams of isolated central ridges are plotted with a 5× vertical exaggeration. Almost vertical stripes in this diagram reflect measurement noise along measured FORC trajectories. Contrary to the pelagic carbonate example (Fig. 6.9), the maximum central ridge amplitude is only half of the background peak value (excluding the vertical ridge at $H_c = 0$). **(a)** Central ridge separation obtained on the basis of the central ridge model alone (i.e. INPUT 04 was set to 0). **(b)** Central ridge separation obtained on the basis of a linear combination of central ridge and background models, weighted by their inverse squared mean amplitude (i.e. INPUT 04 was set to 1). **(c)** Central ridge separation obtained on the basis of the background model alone (i.e. INPUT 04 was set to Automatic). This choice is equivalent to entering a very large number with INPUT 04. Notice that the choice of INPUT 04 has evident effects on the central ridge, and, to a lesser extent, on the background.

- Separation of background and central ridge is performed so, that the sum of the two contributions corresponds exactly to the total FORC function. For this reason, central ridge and background processing is coupled and improving performances for one of the two contributions can be obtained only at cost of the other contribution.
- Decoupling of central ridge and background processing is avoided, in order to guarantee that the sum of magnetizations associated to different FORC contributions corresponds exactly to the integral of the FORC function over the measured space.

The recommended `INPUT 04` option is `Automatic` in case of FORC diagrams dominated by a central ridge, and `1` in case of FORC diagrams where the maximum amplitude of the central ridge is comparable with that of other FORC contributions.

Priority to a smooth background is given when `INPUT 04` is set to `Automatic`, while smooth central ridges are obtained with `INPUT 04` set to `0`.

INPUT 05. Maximum freedom degree of central ridge model

Vertical central ridge profiles are modeled with a linear combination of two bell-shaped functions for a total of six model parameters. This model is flexible enough to accommodate real features of central ridge profiles, regardless intrinsic properties and smoothing during FORC processing. Additional four model parameters are used to account for background contributions under the central ridge. `IsolateCR` uses a recursive, hierarchical procedure to fit FORC profiles with a linear combination of model functions for central ridge and background. This procedure is based on successive optimization of an increasing number of model parameters, until a sufficiently good fit is obtained. This minimizes or avoids instabilities that would otherwise be encountered with non-linear models based on up to 10 unknown parameters.

The starting point of the central ridge isolation procedure is represented by background and central ridge models obtained from the seed profile. These initial models are used to fit the first vertical profile, which is located at the midpoint of the range covered by the seed profile. This choice guarantees that the initial model adequately describes this first profile. After parameter optimization, a new model is obtained for the first profile, which is in turn used to fit the next vertical profile to the right, and so on until the high-field limit of FORC space. The same procedure is adopted for proceeding to the left of the first profile, until the last profile at $H_c = 0$ is reached (Fig. 6.11). Therefore, each FORC profile is fitted using the results obtained from an adjacent profile as initial model.

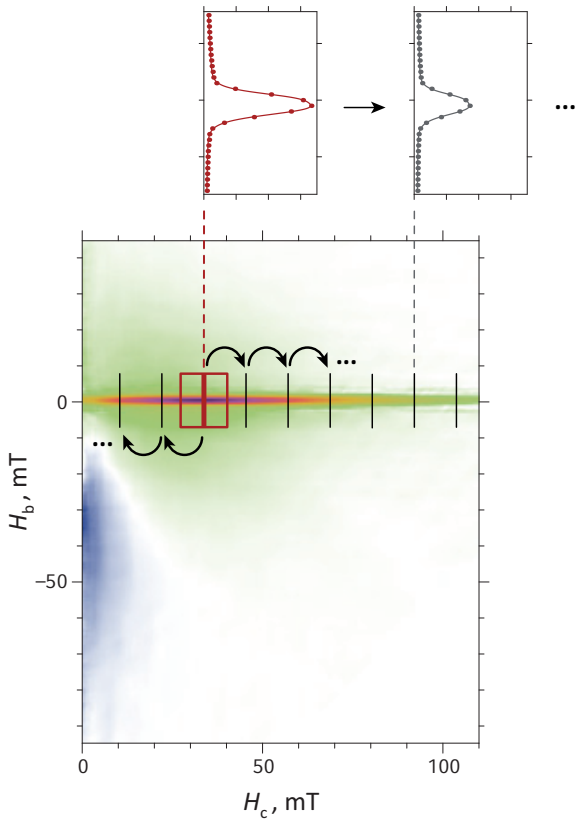


Fig. 6.11: Schematic representation of the recursive fitting procedure used to isolate the central ridge. The FORC range associated with the seed profile (vertical thick red line) is highlighted by a red rectangle. The seed profile (red curve in top graphics), is used as initial model for the recursive modeling of FORC profiles located to the right and to the left of the seed profile (black vertical lines in the FORC diagram, only few are represented for clarity). Each new profile model obtained with this procedure (gray curve in top graphics) is used as initial model for the next profile to the left or to the right (arrows).

The FORC profile fitting procedure is divided into the following four main steps:

1) *Freedom degree 0.* The four background parameters and the *amplitude* of the central ridge model are optimized. Parameters related to the position of the central ridge and to its shape are kept fixed (Fig. 6.12a).

2) *Freedom degree 1.* Model results of the first step are used to perform a new optimization run where the *position* of the central ridge profile is optimized as well. Its width and shape, on the other hand, remains fixed (Fig. 6.12b).

3) *Freedom degree 2.* Model results of the second step are used to perform a new optimization run where *position* and *width* of the central ridge profile is optimized as well. Its shape, on the other hand, remains fixed. The width is optimized by horizontal scaling of the central ridge model (Fig. 6.12c).

4) *Freedom degree 3.* Model results of the third step are used to perform a new optimization run where *all parameters* of the central ridge profile are optimized. This means that the shape of the model profile can change (Fig. 6.12d).

With this procedure, results of the next fitting step are accepted only if the new model provides a significant improvement, i.e. if the fitting residuals have decreased significantly. In this condition is not met, or if the new model simply fails, the fitting procedure is stopped and the model corresponding to the last step that provided a significant improvement is taken as the definitive result for the FORC profile being processed.

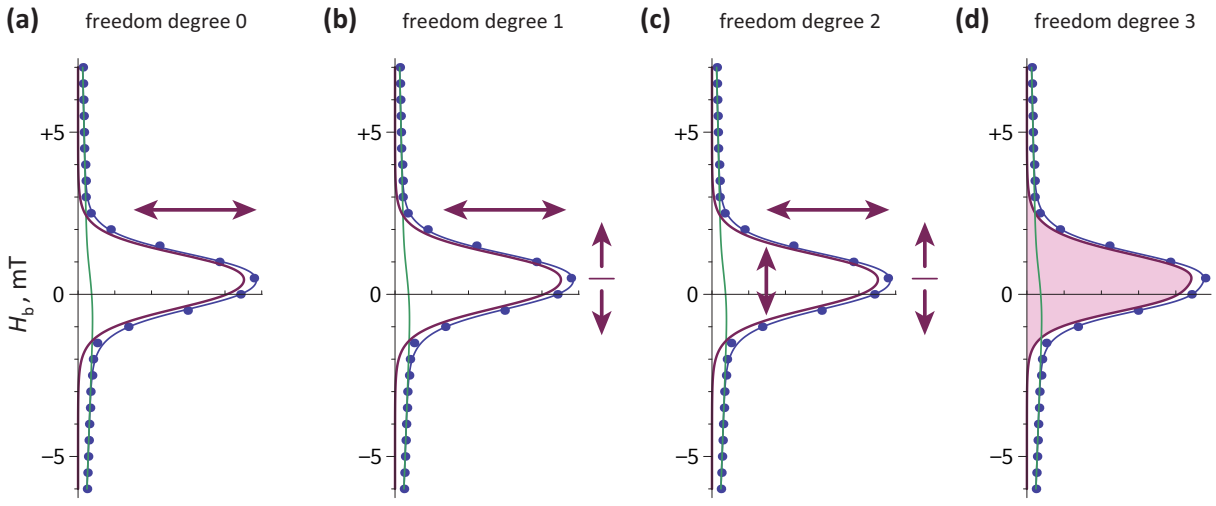


Fig. 6.12: FORC profile models (blue: data, red: central ridge, green: background) characterized by increasing freedom degrees, obtained from an initial model corresponding to the previously processed profile. Because adjacent profiles are very similar, improvements of the new models, from (a) to (d), are small. **(a)** Optimization of the central ridge amplitude. **(b)** Optimization of central ridge amplitude and position. **(c)** Optimization of central ridge amplitude, position, and width. **(d)** Final model where all central ridge model parameter have been optimized.

A key feature of the central ridge isolation procedure illustrated above is that unnecessary degrees of freedom are avoided, preventing model results to be dictated by random features associated to measurement errors. This is particularly important when moving away from the seed profile towards FORC regions where central ridge amplitudes might drop below the significance level. `IsolateCR` produces a plot of the vertical range occupied by significant central ridge contributions in each FORC profile, together with the model freedom degree (Fig. 6.13). In the example of Fig. 6.13, models close to the right FORC space limit have freedom degrees of 0 or 1, because significant central ridge contributions are missing. In this way, the automatic freedom degree limitation imposed by `IsolateCR` avoids unrealistic central ridge models dictated by measurement noise.

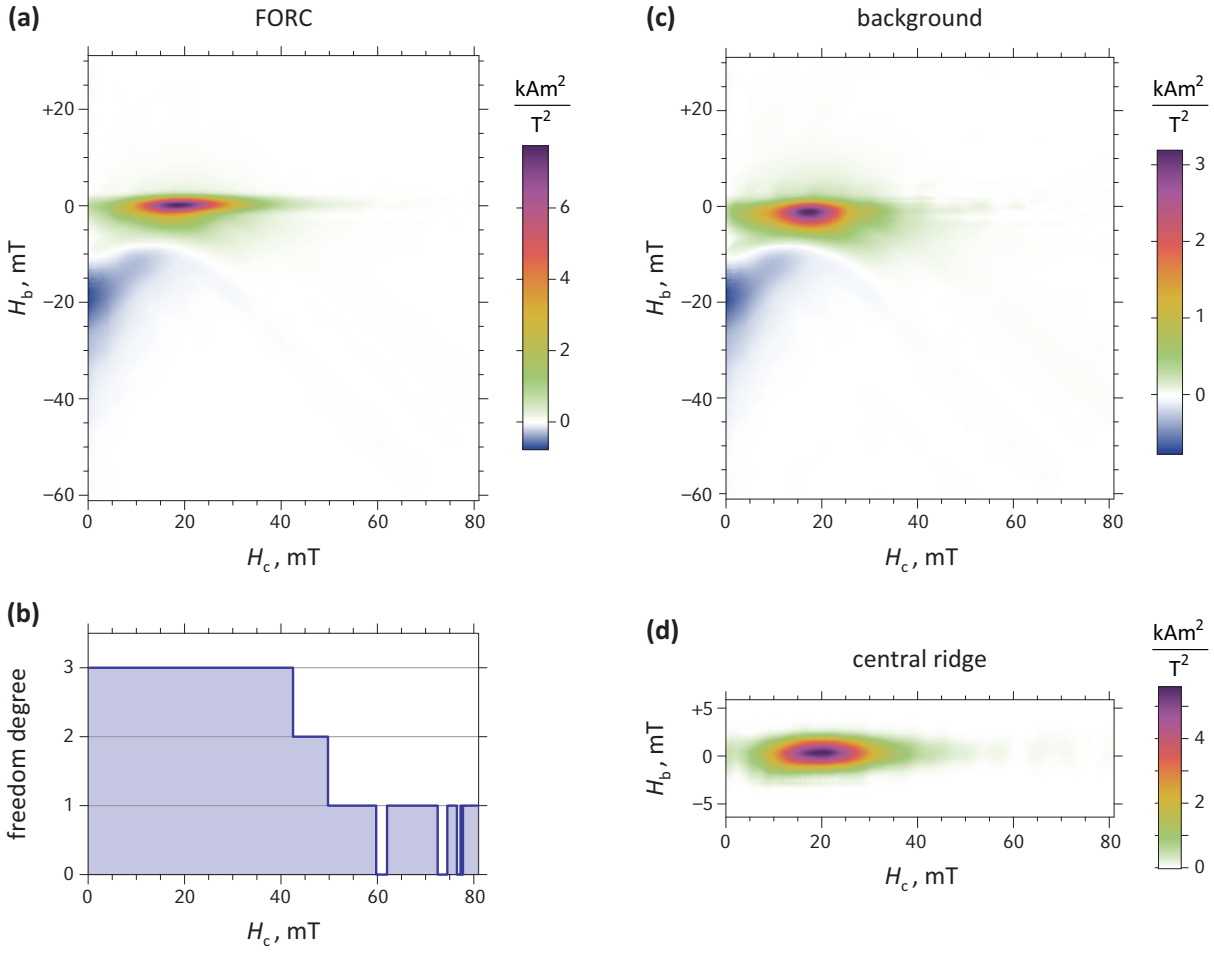


Fig. 6.13: Central ridge processing example based on cultured magnetotactic bacteria (see the downloadable example "Magnetospirillum 1"). **(a)** FORC diagram obtained with advanced smoothing options. **(b)** Freedom degree of the central ridge model as a function of vertical profile position. The freedom degree is maximal over the H_c -range with significant central ridge contributions (i.e up to 40 mT) and declines progressively at higher fields. **(c)** Background FORC diagram obtained from (a) after subtracting the central ridge contribution shown in **(d)** with a 2× vertical exaggeration.

The modeling procedure illustrated above produces stable results with FORC functions dominated by the central ridge (e.g. Fig. 6.13). In some cases, and especially if the central ridge is a minor feature in the FORC diagram, more stringent freedom degree limitations may be required. Such limitations are set with `INPUT 05`, whose possible options `0`, `1`, `2`, and `3`, correspond to the freedom degrees explained above. If

```
INPUT 05. Maximum freedom degree of central ridge model ....; 3
```

is chosen, no additional limitations are applied to the automatic fitting procedure, other than those automatically set by `IsolateCR`. Therefore, all model parameters are optimized if quality criteria are met. On the other hand, choosing

```
INPUT 05. Maximum freedom degree of central ridge model ....; 1
```

implies that the fitting procedure is interrupted at stage 2, after optimization of amplitude and position of the central ridge profile. Width and shape of central ridge profiles, on the other hand, remains always fixed and coincide with those determined on the seed profile. In this case, the maximum number of model parameters is 6: four for the background model, and two for the central ridge model. Maximum fitting stability at cost of model flexibility is obtained with

```
INPUT 05. Maximum freedom degree of central ridge model ....; 0
```

and is recommended in case of central ridges characterized by small signal-to-noise ratios. In this case, the fitting procedure is interrupted at stage 1 after optimizing the central ridge amplitude. An example of results obtained with this limitation is shown in Fig. 6.14, where a maximum freedom degree of 0 (i.e. central ridge models with fixed position, width, and shape) provides a slightly better central ridge stabilization. The marginal quality increment obtained with this limitation for a central ridge that contributes to ~2% of the total FORC magnetization demonstrates how well the automatic freedom degree reduction works even in cases of FORC amplitudes that are only barely above the significance level.

- High-quality FORC diagrams dominated by the central ridge can be processed without any limitation, i.e. by setting `INPUT 05` to 3. If instabilities appear in the FORC diagrams of isolated central ridge and the background, respectively, `INPUT 05` should be set to 2.
- Low-quality FORC diagrams and/or FORC diagrams containing a weak central ridge are best processed starting with `INPUT 05` set to 1. If results are satisfactory, the limit might be increased by one step (i.e. `INPUT 05` set to 2) for a second run.

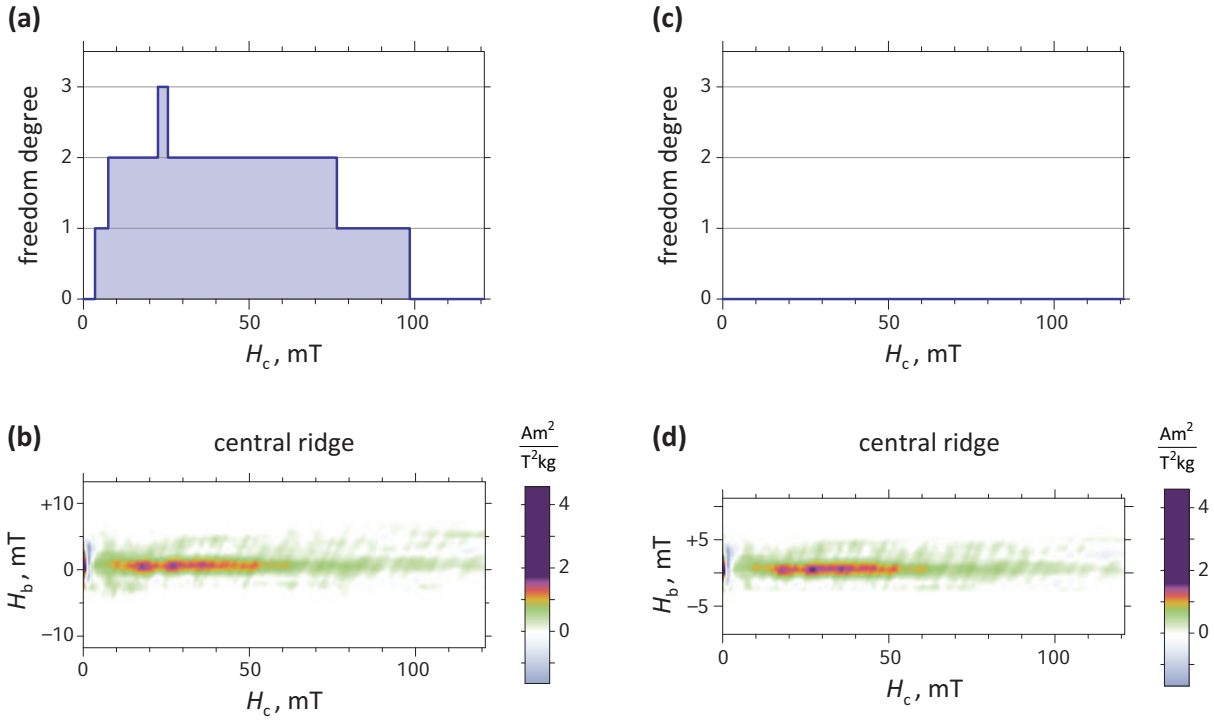


Fig. 6.14: Central ridge processing for a volcanic ash sample (see the downloadable example "volcanic ash") featuring a central ridge that contributes by <2% to the total FORC magnetization [*Ludwig et al.*, 2013]. Top plots show the freedom degree of the central ridge model for each vertical profile, as a function of the profile position H_c. Bottom plots show the isolated central ridge with a 2× vertical exaggeration. The vertical range of the seed profile was chosen automatically by setting `INPUT 02` to `Automatic`. **(a-b)** Results with no freedom degree limitation (i.e. `INPUT 04` was set to 3). **(c-d)** Results with maximum freedom degrees limited to 0 (i.e. `INPUT 04` is `0`). In this case, only the amplitude of a central ridge model with fixed position, width, and shape, was optimized. The resulting FORC diagram of the isolated central ridge is slightly less affected by measurement noise than for the case of no freedom degree limitations (a). The minimal difference between the two results demonstrates the effectiveness of the `IsolateCR` recursive fitting procedure.

INPUT 06. Profile selection

Isolation of the central ridge from other FORC contributions is performed by fitting vertical profiles corresponding to all H_c -values of the FORC matrix with model functions for central ridge and background. As explained with INPUT 05, a recursive strategy is adopted to avoid instabilities related to non-linear fitting procedures. Even so, possible problems with profiles bearing insignificant central ridge contributions cannot be completely excluded. In this case, warning messages such as

```
WARNING: unable to fit vertical profile 125 [code position 16].
```

describe the type of problem encountered at given profile numbers. Warning messages do not stop evaluation, but final results might be unacceptable. Fitting problems are generally avoided by decreasing the maximum number of model parameters through INPUT 05 options. In some cases, it might be useful to visualize intermediate model results for profiles that created error messages such as the one shown above. This option is available through INPUT 06. Regular profile processing and subsequent central ridge isolation is obtained with the default setting

```
INPUT 06. Profile selection ....; All
```

in which case no diagnostic plots relative to individual profiles are shown. The diagnostic mode for a specific profile is selected by entering the corresponding profile number with INPUT 06, e.g.

```
INPUT 06. Profile selection ....; 125
```

for selecting the 125th vertical profile of the FORC matrix. Profile numbers are given in all error messages. If a profile number is entered with INPUT 06, all model fitting steps related to the selected profile are plotted individually. IsolateCR is automatically aborted after the final model for the selected profile has been plotted. A selection of diagnostic plots is shown in Fig. 6.15.

Diagnostic plots are accompanied by a "quality parameter" called misfit-to-error ratio, which is the ratio between the standard deviation of model misfits (i.e. differences between model and data) and the standard error of FORC data. The misfit-to-error ratio is used by IsolateCR for determining the appropriate number of model parameters to be optimized. Misfit-to-error ratios $\gg 1$ indicate that there is a large margin of improvement for the given model. As the number of optimized model parameters increases, the misfit-to-error ratio approaches 1, which means that model residuals are entirely explainable by measurement errors and no further model improvements are possible. Diagnostic plots can be used recognize cases where the stepwise addition freedom degrees produces a runaway of the initial model to a different solution. In this case, the maximum number of freedom degrees should be limited with INPUT 05.

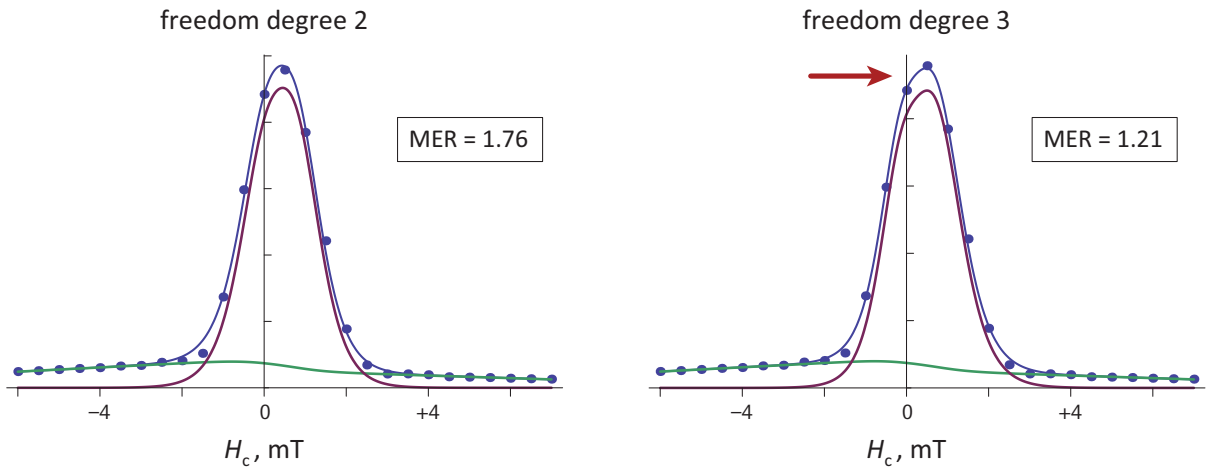


Fig. 6.15: Diagnostic plot examples for vertical profile number 65 (`INPUT 06` set to 65) obtained from the FORC diagram of a pelagic carbonate sample (see the downloadable example "pelagic carbonate"). Data points are represented by dots, and lines refer to the background model (green), the central ridge model (red), and the sum of the two (blue). **(a)** Fitting step with freedom degree 2 (i.e. optimization of central ridge amplitude, position, and width). The misfit-to-error ratio is 1.76, which means that model residuals are significantly larger than the standard error of data points. **(b)** Fitting step with freedom degree 3 (i.e. optimization of all model parameters) obtained using (a) as initial model. A small change in the shape of the central ridge model can be seen near the peak (red arrow). The misfit-to-error ratio has decreased to 1.21: therefore, this model represents a significant improvement with respect to the one shown in (a).

INPUT 07. Confidence interval of coercivity distributions

The central ridge is a quasi-one-dimensional feature whose amplitude depends on the finite FORC diagram resolution, combined with a small intrinsic width due to thermal activations and magnetostatic interactions. On the other hand, the central ridge coercivity distribution curve, which is defined as the integral of the central ridge FORC diagram over H_b, is insensitive to FORC processing parameters and physical processes affecting its vertical width. Therefore, central ridge coercivity distributions, rather than central ridges themselves, provide quantitative information about magnetization processes associated with them.

For this reason, `IsolateCR` calculates the central ridge coercivity distribution and plots it together with the other two coercivity distributions defined by FORC data, with are automatically exported by `CalculateFORC` when calculating FORC diagrams. The three coercivity distributions are represented on a common linear and logarithmic field scale, together with confidence intervals drawn around each curve (Fig. 6.16). The confidence interval is defined as a multiple λ of the estimated standard error. This multiple is a positive number entered with `INPUT 07`, e.g.

```
INPUT 07. Confidence interval factor for distribution plots .....; 2
```

Common choices for `INPUT 07` are λ = 1 for plotting the standard error and λ = 2 as 95% confidence interval in case of Gaussian errors (Fig. 6.16).

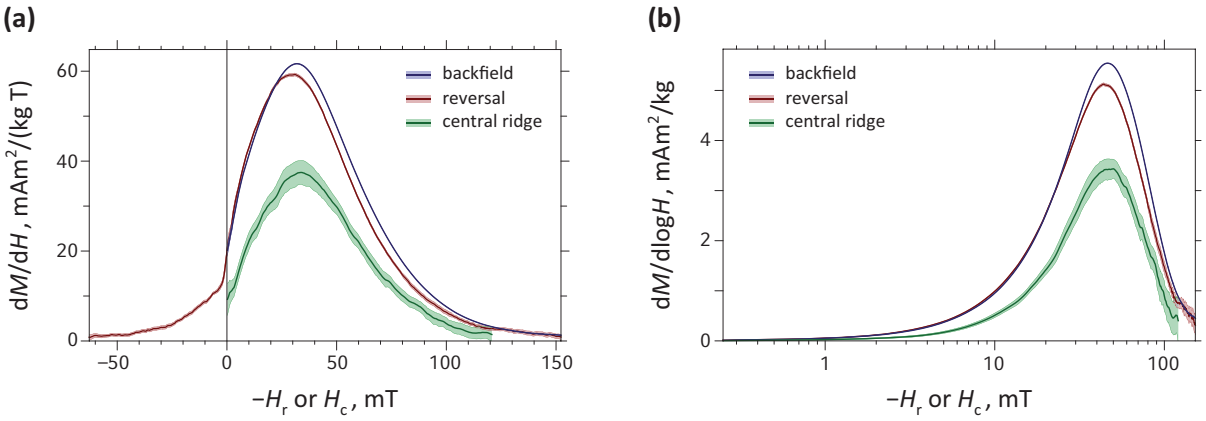


Fig. 6.16: Coercivity distributions derived from FORC measurements of a pelagic carbonate sample (see the downloadable example "pelagic carbonate"), plotted on **(a)** a linear field scale, and **(b)** a $\log_{10}$ field scale. The plotted coercivity distributions are derived from the backfield demagnetization curve $M(H_r,0)$ (blue), irreversible magnetization changes $\Delta M(H_r,H_r)$ at the reversal field H_r (red), and the central ridge $\rho(H_c,H_b)$ (green). Confidence intervals corresponding to twice the standard error (i.e. `INPUT 07` is set to 2) are given as shaded bands around curves. The different horizontal ranges covered by the three distributions reflect their dependence on two different types of fields used during FORC measurements, i.e. the reversal field H_r (backfield and reversal distributions), and the Cartesian FORC coordinate $H_c = (H - H_r)/2$.

INPUT 08. Scale factor for central ridge coercivity distribution

The three coercivity distributions derived from FORC measurements – backfield, reversal, and central ridge – are plotted by `IsolateCR` on common field and magnetization scales. While backfield and reversal distributions cover similar magnetization ranges, being by definition identical at $H_r = 0$, the central ridge distribution is often characterized by much smaller amplitudes (Chapter 8). In order to compare the shape of the central ridge distribution with that of the other two distributions, a scale factor for the central ridge distribution can be entered with `INPUT 08`. The default setting

```
INPUT 08. Scale factor for central ridge coercivity distribution ...; 1
```

plots all coercivity distributions on the same scale (Fig. 6.17a). Very weak central ridges are better represented with scale factors >1, e.g.

```
INPUT 08. Scale factor for central ridge coercivity distribution ...; 10
```

(Fig. 6.17b). Scale factors do not affect the export of central ridge data and are used only for plotting purposes.

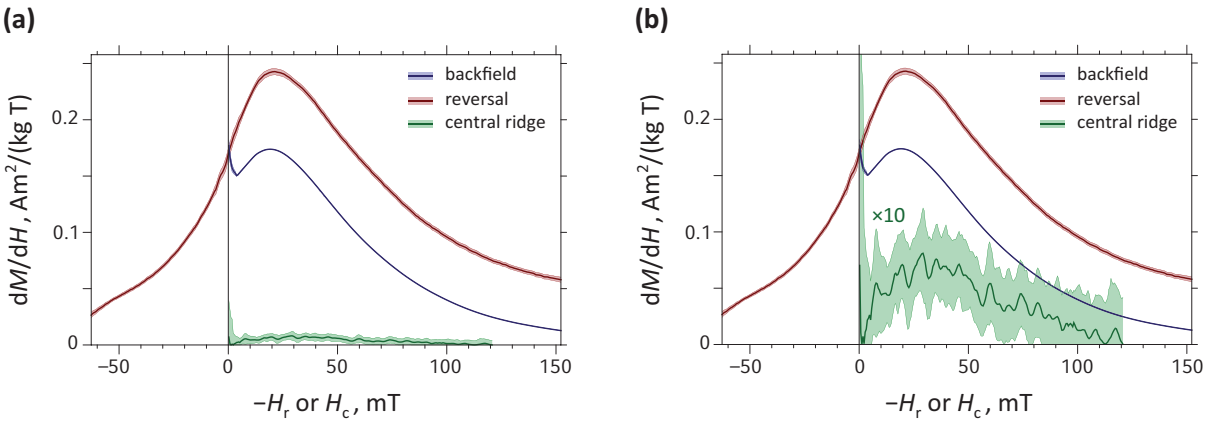


Fig. 6.17: Coercivity distributions derived from FORC measurements of a volcanic ash sample (see the downloadable example "volcanic ash"). The central ridge of this sample is a very weak feature, as seen from its coercivity distribution in **(a)**. For better comparison with other coercivity distributions, the amplitude of the central ridge distribution has been multiplied by a factor of 10 in **(b)** by setting `INPUT 08` to `10`. Notice that the confidence interval is also expanded by the same factor.

The amplitude of the central ridge coercivity distribution is always smaller than that of the other distributions, so that scale factors <1 are not needed.

INPUT 09. Clip negative coercivity distribution values

Coercivity distributions derived from magnetization curves can have negative amplitudes. In most magnetic materials, however, negative elemental contributions are averaged out by convolution with much larger positive values, so that the resulting coercivity distributions are strictly positive functions. In this case, negative amplitudes arise only from measurement noise and do not need to be plotted. `INPUT 09` offers the possibility to clip negative amplitudes in coercivity distribution plots produce by `IsolateCR`, i.e.

```
INPUT 09. Clip negative coercivity distribution values ....; Yes
```

(Fig. 6.17a) while negative amplitudes are preserved with:

```
INPUT 09. Clip negative coercivity distribution values ....; No
```

(Fig. 6.17b). Setting `INPUT 09` to `Yes` avoids unnecessary extensions of the plotting range in case of very noisy data.

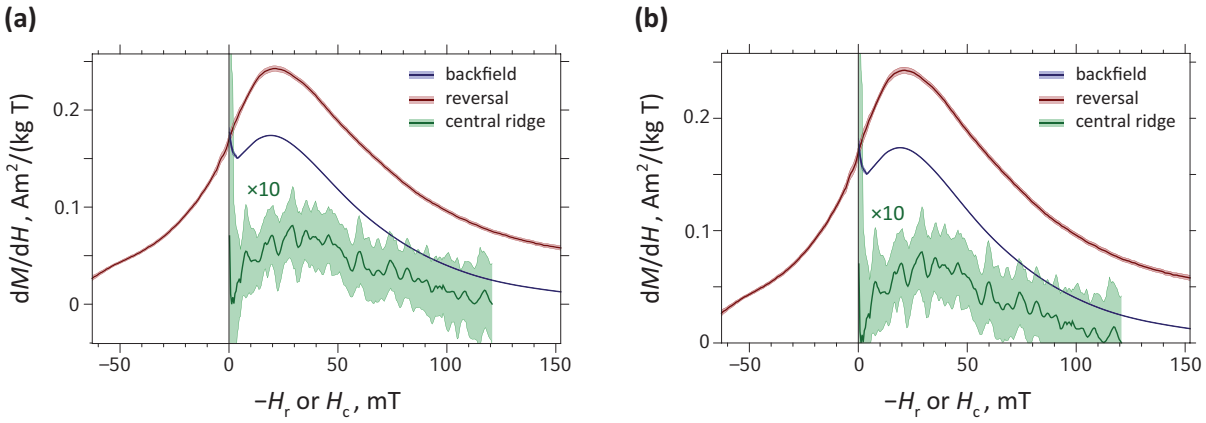


Fig. 6.17: Coercivity distributions obtained from FORC measurements of a volcanic ash sample (see the downloadable example "volcanic ash"). The weak central ridge is multiplied by a factor 10 for better visualization. **(a)** Both positive and negative values are plotted (i.e. `INPUT 09` set to `No`). In this example, negative values are caused by measurement noise. **(b)** Only positive values of the coercivity distribution values are plotted (i.e. `INPUT 09` set to `Yes`).

- `INPUT 09` does not affect the central ridge coercivity distribution exported by `IsolateCR`, which always coincides with unconstrained values.

INPUT 10. Plotted FORC error parameter

FORC matrices and coercivity distributions imported by `IsolateCR` come with standard error estimates based on procedures developed by *Heslop and Roberts* [2012]. Error calculation is extended to central ridge processing, so that all `IsolateCR` results come with a standard error estimate. In analogy to `CalculateFORC`, it is possible to plot FORC error estimates of central ridge and background FORC diagrams as standard errors or as signal-to-noise ratios (SNR). SNR are defined as the ratio between FORC values and their standard error.

`INPUT 10` is an option that controls the type of error parameter that is plotted together with FORC diagrams. Use

```
INPUT 10. Plotted FORC error parameter ....; error
```

for plotting the estimated standard error of the FORC function (Fig. 6.18b,e), and

```
INPUT 10. Plotted FORC error parameter ....; SNR, 3
```

for plotting the estimated SNR (Fig. 6.18c,f), where the significance threshold is set by the numeric parameter (in this case, 3).

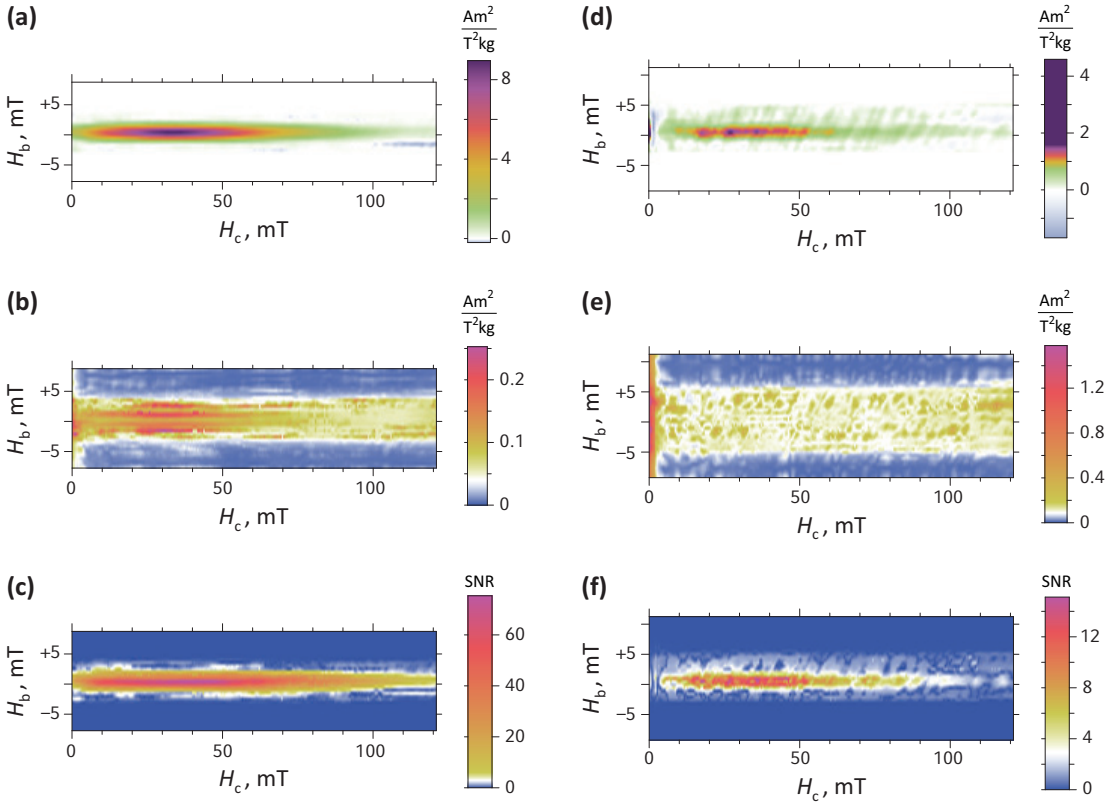


Fig. 6.18: Central ridges isolated from the FORC diagram of **(a)** a pelagic carbonate (see the downloadable example "pelagic carbonate") and **(d)** a volcanic ash sample (see the downloadable example "volcanic ash"). **(b-e)** Standard error diagrams (i.e. `INPUT 10` set to `error`). **(c-f)** Signal-to-noise ratio diagrams with a significance threshold of 3 (i.e. `INPUT 10` set to `SNR,3`).

Both error parameters are plotted with a color scale ranging from zero (blue) to the maximum value (purple), through intermediate values in white, yellow, and red. In plots of the standard error, white coincides with the quadratic mean of the standard error over the measured region of the plotted FORC space. Accordingly, blue pixels represent FORC regions where the standard FORC error is below the average, while yellow, red, and purple pixels are above the average.

In signal-to-noise (SNR) plots, white coincides with the significance threshold set by the numeric parameter. The significance threshold is defined as the SNR value above which the FORC function is ≠ 0 at a given confidence level, usually chosen to be 95% or 99% [*Heslop and Roberts*, 2012]. This threshold depends on the number of measurements considered for polynomial regression. This number is >25 for common choices of the smoothing factors (i.e. $s_c \geq 2$ and $s_b \geq 2$, see Chapter 4), so that significance threshold is always <3 at a 99% confidence level [*Egli*, 2013]. Therefore, FORC values with signal-to-noise ratios ≥3 are significant at a confidence level of at least 99%. Significance thresholds corresponding to standard confidence levels are listed in Tab. 6.1.

In SNR plots, significant FORC values are represented by "warm" colors, i.e. yellow, red, and purple, while blue values are insignificant. This representation enables to immediately spot significant areas of the FORC function as those with a consistent warm color. Therefore, the SNR option of `INPUT 10` is highly recommended. Regardless of the actual option chosen with `INPUT 10`, `IsolateCR` exports the standard error estimates, from which the signal-to-noise ratio can always be calculated.

- Error calculations performed by `IsolateCR` are based primarily on FORC standard errors imported together with the FORC matrix produced by `CalculateFORC`.
- Additional errors are introduced by the procedure used to separate the central ridge from other FORC contributions. These errors are identified with the misfit of central ridge and background models, and are added to the standard FORC errors. Large model misfits will produce large errors and low signal-to-noise ratios.

Often, the background is much weaker than the central ridge or vice-versa. In such cases, the central ridge or the background FORC diagrams might not be significant over certain ranges. Therefore, always check the significance of central ridge and background FORC diagrams with plots of the signal-to-noise ratio.

Tab. 6.1: Significance threshold at given confidence levels $1-\alpha$ for the signal-to-noise ratio of the FORC function calculated with smoothing factors s_c along H_c and s_b along H_b. Significance levels correspond to the $1-\alpha/2$ quantile of the Student *t*-distribution with v degrees of freedom, where $v = 8(s_c - 1)(s_b - 1) + 6(s_c + s_b) - 13$. Signal-to-noise ratios larger than the given significance threshold represent values of the FORC function that are ≠ 0 at a given confidence level.

	$s_c = s_b = 2$	$s_c = 5$, $s_b = 2$	$s_c = s_b = 10$
Degrees of freedom	19	61	755
99% confidence level	2.86	2.66	2.58
95% confidence level	2.09	2.00	1.96
90% confidence level	1.73	1.67	1.65

INPUT 11. FORC diagram ticks specifications

INPUT 11 is used to set the ticks of the H_c - and H_b field scales in the FORC diagram. The default setting is

```
INPUT 11. FORC plot ticks specifications ....; Automatic
```

for placing the field ticks automatically on the FORC diagram. In this case, IsolateCR uses the same tick intervals (e.g. 50 mT for major ticks and 10 mT for minor ticks) for both H_c and H_b, as customary in FORC plots, except for the central ridge representation, where the vertical range is much smaller than the horizontal one and different tick intervals are used (Fig. 6.19a,b). In some cases, you might want to specify the field ticks differently. Explicit tick specifications can be given with INPUT 11 in three ways. The simplest specification consists of a number pair, e.g.:

```
INPUT 11. FORC plot ticks specifications ....; 10, 2
```

where the first number is the field interval used for major ticks, and the second number is an integer >0 that specify the number of minor intervals by which major tick intervals are divided. The major tick interval is assumed to be expressed with the same field unit used in the FORC matrix file. The specification of the above example means that major ticks are drawn every 10 mT, and that the 10 mT intervals are divided by two with 1 minor tick. This specification applies to H_c and H_b. Set the second number to 1 if you want to avoid minor ticks. This type of explicit tick specifications will not apply to the H_b-ticks of central ridge FORC diagrams, which are still chosen automatically in the same manner as with the Automatic option.

Different tick specifications for H_c and H_b, as for instance in case of FORC spaces with very different H_c - and H_b-ranges, can be entered with INPUT 11. In this case, four parameters are needed, e.g.:

```
INPUT 11. FORC plot ticks specifications ....; 50, 5, 20, 4
```

The first two numbers define the H_c-ticks and the third and fourth numbers define the H_b-ticks in the same manner as for the case of a single tick specification. In the above example, major H_c-ticks are drawn every 50 mT (first number), and major H_b-ticks are drawn every 20 mT (third number). Major H_c - and H_b-tick intervals are divided in five and four equal intervals, respectively, by minor ticks (second and fourth number). This type of explicit tick specifications will not apply to the H_b-ticks of central ridge FORC plots, which are still chosen automatically in the same manner as with the Automatic option.

In order to control H_b-ticks of central ridge FORC diagrams, a third pair of number has to be entered for their explicit specification. For example,

```
INPUT 11. FORC plot ticks specifications ....; 50, 5, 50, 5, 5, 1
```

means that major H_b-ticks of all FORC diagrams except those of the central ridge will be drawn every 50 mT, with each major tick interval divided in five equal intervals by minor ticks. Major H_b-ticks of the central ridge FORC diagram, on the other hand, are drawn every 5 mT (fifth number) using no minor ticks (sixth number) (Fig. 6.19c).

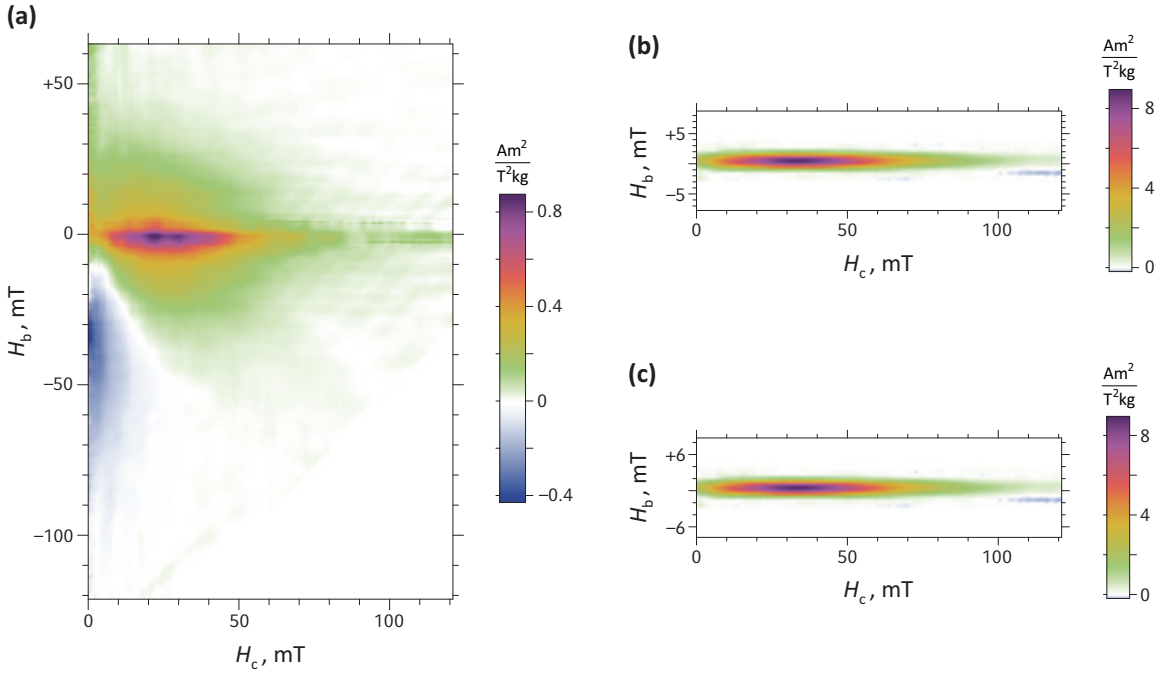


Fig. 6.19: Tick specification examples based on FORC diagrams of a pelagic carbonate (see the downloadable example "pelagic carbonate"). **(a-b)** Automatic ticks generation for background (a) and central ridge FORC diagrams (b), obtained by setting `INPUT 11` to `Automatic`. The same result would be obtained with `INPUT 11` set to `50,5,50,5,5,5`. **(c)** Manual choice of H_b-ticks for the central ridge FORC diagram, obtained by setting `INPUT 11` to `50,5,50,5,6,3`.

- The default tick specification `Automatic` generates satisfactory results in most cases.
- Only few H_b-ticks should be specified for the central ridge FORC diagram, especially if no vertical exaggeration is adopted, because the vertical scale is very limited.

INPUT 12. Vertical exaggeration of central ridge FORC diagram

FORC diagrams are usually plotted with their natural aspect ratio, which means that same horizontal and vertical distances correspond to same H_c - and H_b -differences. Central ridge FORC diagrams, however, have a very small vertical extension, and some magnification is required to enhance two-dimensional details such as small vertical offsets (Fig. 6.20a). Magnification of such details is obtained with a vertical exaggeration factor to be entered with INPUT 12. This factor is defined as a positive number by which the FORC diagram is vertically scaled. Preservation of the natural central ridge aspect ratio is therefore obtained by setting

```
INPUT 12. Vertical exaggeration of central ridge FORC diagram ....; 1
```

(Fig. 6.20a). Vertical exaggerations, on the other hand, are entered as numbers >1, e.g.

```
INPUT 12. Vertical exaggeration of central ridge FORC diagram ....; 3
```

for the example of Fig. 6.20b.

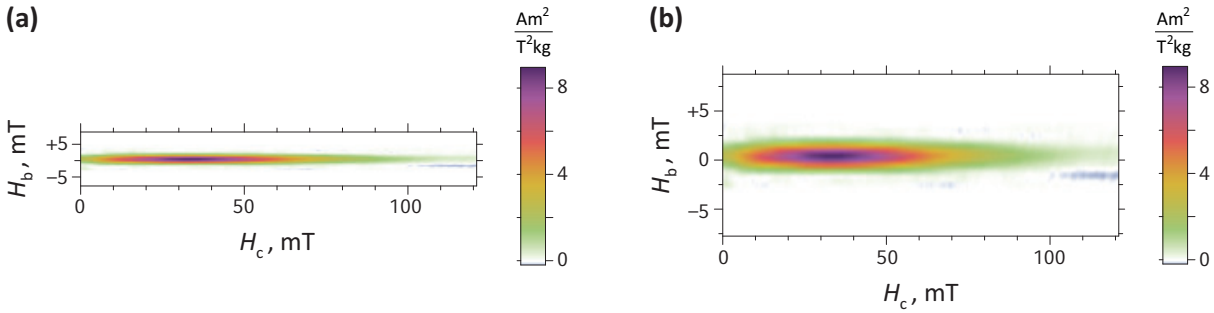


Fig. 6.20: **(a)** Central ridge obtained from the FORC diagram of a pelagic carbonate (see the downloadable example "pelagic carbonate") and plotted with its natural aspect ratio (i.e. INPUT 11 set to 1) **(b)** Same as (a) with a 3× vertical exaggeration (i.e. INPUT 11 set to 1). The slight upward shift of the central ridge is clearly visible in this plot.

Vertically exaggerated FORC diagrams are useful for detecting details usually hidden in the extremely small vertical extension of central ridges. For example, vertical offsets and variable vertical widths reflect thermal activation effects and magnetostatic interactions, respectively.

IsolateCR plots the central ridge mean vertical position and standard deviation as functions of H_c .

INPUT 13. Color scale saturation

IsolateCR uses two standard color scales for plotting FORC diagrams and FORC errors or signal-to-noise ratios, respectively. The color scales are specially designed to give best performances with the special characteristics of FORC functions, as explained in detail in Chapter 5. The color scales are created by blending printable colors for reproducible printing results. Because the gamut of printable colors can vary significantly, it might be necessary to reduce color saturation in order to obtain best results. Color saturation can be controlled with INPUT 13. The default option corresponding to 90% of full saturation is obtained with

```
INPUT 13. Color scale saturation ....; Automatic
```

(Fig. 6.21b). This option is recommended for obtaining best results on monitors as well as with printing. Alternatively, you can specify an explicit color saturation value comprised between 0 and 1, e.g.:

```
INPUT 13. Color scale saturation ....; 0.7
```

for 70% of the full saturation (Fig. 6.21d).

Although color saturation can be set to any value between 1 (maximum saturation) and 0 (pure white), practical saturation values are comprised between 0.8 and 1.

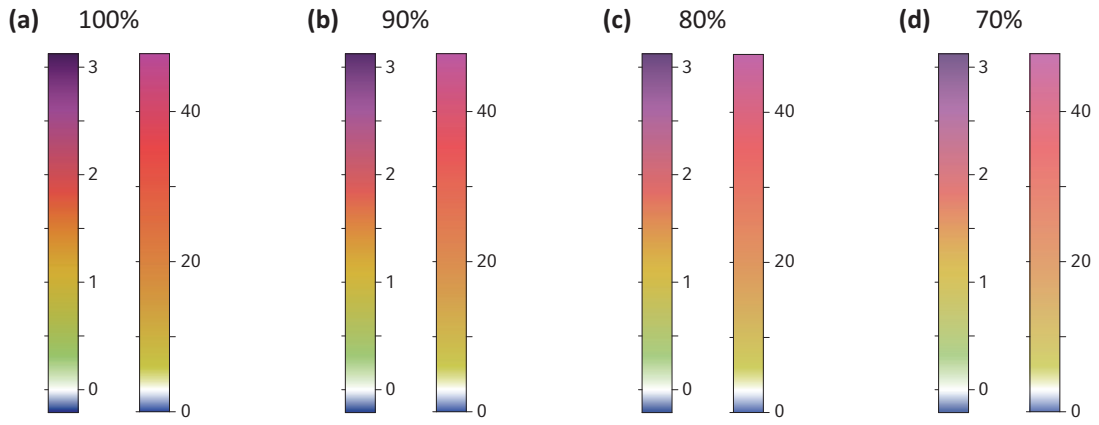


Fig. 6.21: Examples of IsolateCR color scales obtained with different saturation levels specified by INPUT 13, from 100% (a) to 70% (d). The left color scale in each example is used for FORC diagrams, while the right color scale corresponds to plots of FORC errors or signal-to-noise ratios.

- FORC plots produced by `IsolateCR` are mainly intended as first representation of processing results. High-quality plots for presentations and publication purposes are best generated with the VARIFORC function `PlotFORC` using the FORC matrices exported by `IsolateCR`. `PlotFORC` offers extended plotting and contour drawing options (Chapter 5).

Color printing problems usually arise from color conversion between the RGB color space used by `CalculateFORC`, which is best suited to monitors, and the CMYB color scale, which is used for printing and has a much smaller color gamut. Color conversion problems are best solved by reducing color saturation of the original plots, rather than post processing corrections.

INPUT 14. Color scale clipping

The special FORC diagram color scale used by IsolateCR is controlled by the full range of FORC amplitudes and by INPUT 14, which represents the fraction of smallest and larger FORC values lying outside the regular color range. These values are represented with the same colors for minimum (blue), and maximum (purple) values. If you want to extend the color scale to the entire range of FORC amplitudes, use

```
INPUT 14. Quantile for color scale clipping .....; 0
```

(Fig. 6.22a). Otherwise, enter the fraction of minimum and maximum FORC values that should be clipped by the color scale, in form of a number between 0 and 1, e.g.

```
INPUT 14. Quantile for color scale clipping .....; 0.05
```

(Fig. 6.22b). This option is used with noisy FORC diagrams in order to avoid "wasting" part of the color scale with the need of covering minimum and maximum values enhanced by measurement errors. INPUT 14 can also be used to enhance the color contrast of small FORC amplitudes at cost of high-amplitude features. Because the color scale used by IsolateCR is optimized for the representation of typical FORC functions, excellent results already obtained with any value of INPUT 14 comprised between 0 or 0.01.

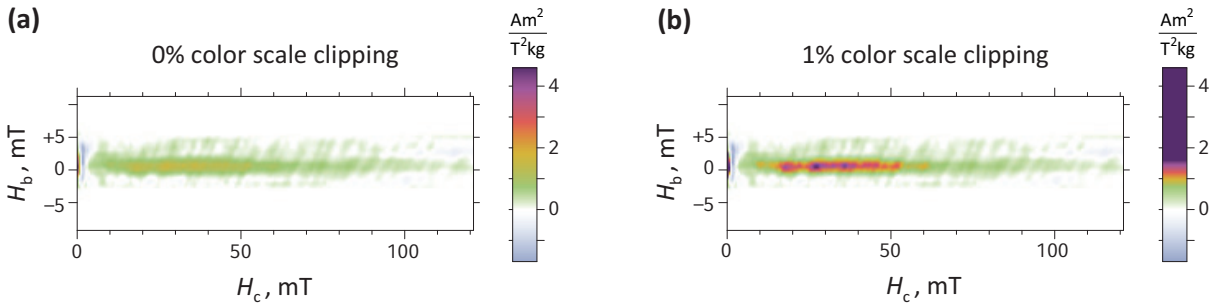


Fig. 6.22: Color range clipping examples generated with the central ridge FORC diagram obtained from a volcanic ash sample (see the downloadable example "volcanic ash"). **(a)** Color scale extends over the entire range of FORC values (i.e. INPUT 14 is set to 0), which is dominated by large positive values near $H_c = 0$. **(b)** Same as (a), with 1% color scale clipping (i.e. INPUT 14 is set to 0.01). High-amplitude FORC values near $H_c = 0$ are now represented with the same end-scale color (purple). Central ridge features with lower amplitudes are now clearly visible.

- Use the VARIFORC function `PlotFORC` for advanced color scale control.
- `INPUT 14` can be set to 0 with good results in most cases.
- Relatively large values of `INPUT 14` (but still <1) can be used to enhance the color contrast over FORC features with very small amplitudes.
- `INPUT 14` has no effects on exported FORC matrices. FORC diagrams with different color scales can always be generated using `PlotFORC`.

INPUT 15. Calculate single-domain reversible FORC background

If the processed FORC diagram reflects exclusively or predominantly the presence of single domain particles with uniaxial anisotropy, further processing is possible to obtain complete information about intrinsic properties of the particles [*Egli et al.*, 2010; *Ludwig et al.*, 2013]. For example, the contribution of reversible magnetic moment rotations [*Newell*, 2000] can be retrieved from the FORC diagram after subtraction of the central ridge. This is done by taking the upper quadrant of the FORC background, which is first reflected about $H_b = 0$ and then subtracted from the lower quadrant of the FORC background (Fig. 6.23). The optional calculation of reversible single-domain contributions is controlled by INPUT 15. Its default setting

```
INPUT 15. Calculate single-domain FORC background ....; No
```

is used to stop further processing after isolation of the central ridge and calculation of the central ridge coercivity distribution. Further processing is meaningless for all samples containing significant magnetic contributions from non-single-domain magnetic particles. On the other hand, the reversible single-domain FORC contribution is calculated with

```
INPUT 15. Calculate single-domain FORC background ....; Yes
```

in which case the corresponding FORC diagram is calculated, plotted, and exported for further use (Fig. 6.23c).

- Reversible rotation of single-domain magnetic moments of non-interacting uniaxial particles produces FORC contributions that are antisymmetric about the remanence diagonal $H_c = -H_b$, with negative (positive) amplitudes below (above) it [*Newell*, 2000]. No FORC contributions are produced by this process over the upper quadrant.
- Together with the total magnetization associated with the central ridge, reversible single-domain contributions provide information about the relative amplitude of magnetization jumps in single-particle hysteresis loops [*Egli et al.*, 2010].

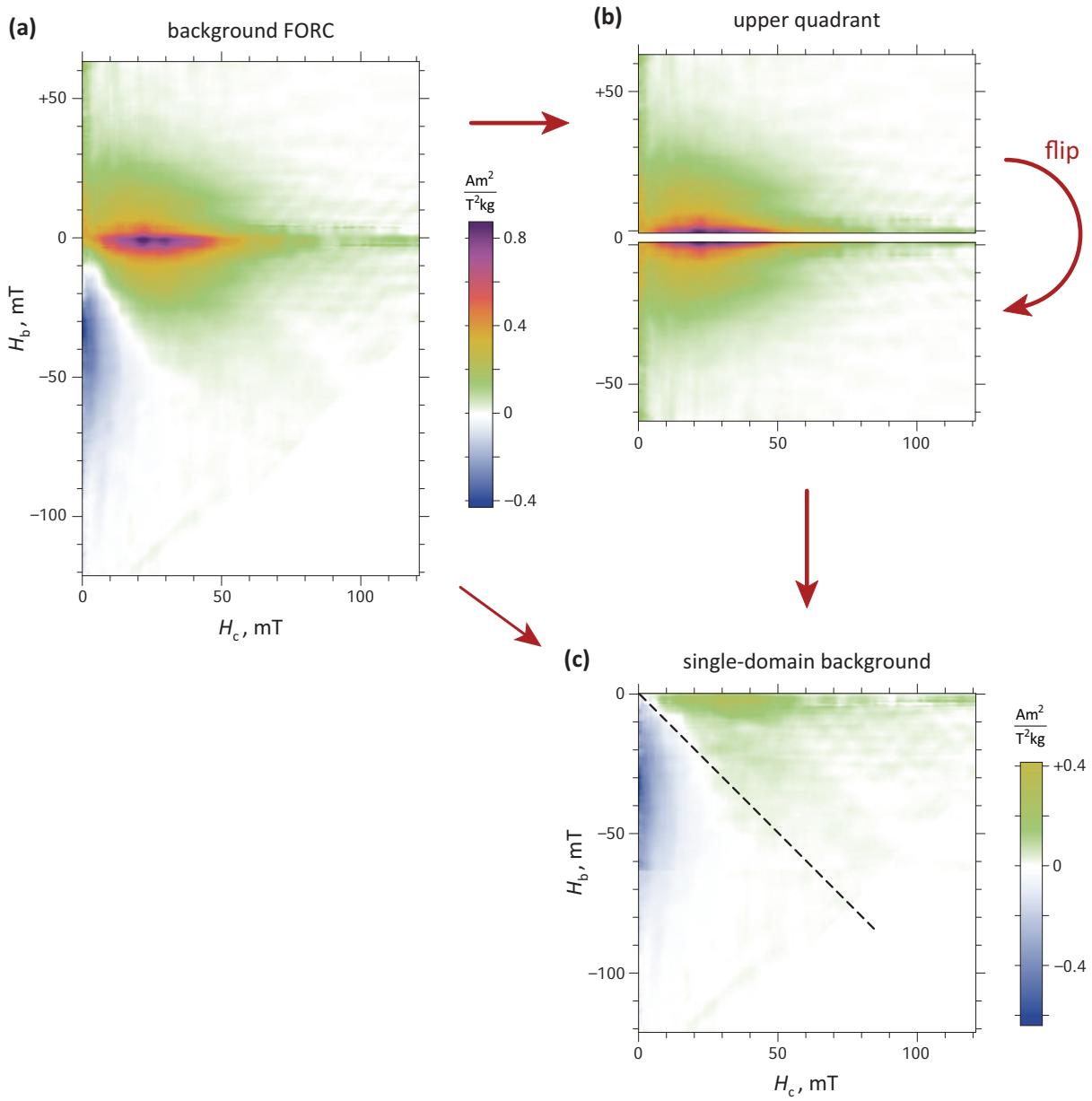


Fig. 6.23: Calculation of single-domain reversible contributions to the FORC diagram of a pelagic carbonate (see the downloadable example "pelagic carbonate"). **(a)** FORC diagram calculated by `IsolateCR` after central ridge subtraction. **(b)** Upper quadrant selection of the FORC diagram in (a), and flipping about $H_b = 0$. (red arrow). **(c)** Single-domain reversible background obtained after subtracting the flipped background in (b) from the FORC diagram in (a). The slight discontinuity visible over negative amplitudes at $H_b = -52$ mT is due to the fact that the FORC space does not extend far enough over the upper quadrant for covering the lower quadrant entirely. The discontinuity is small because FORC amplitudes over $H_b > 50$ mT are almost negligible. The single-domain reversible background is almost perfectly antisymmetric about the remanence diagonal $H_b = -H_c$ (dashed line), as expected for non-interacting uniaxial single-domain particles.

6.6 Data formats exported by IsolateCR

IsolateCR exports processing results to six or eight (if INPUT 15 is set to Yes) files with the following name endings:

1) _CentralRidgeFORC_VARIFORC.txt, for the central ridge FORC matrix,
2) _CentralRidgeFORCStandardError_VARIFORC.txt, for the standard errors of the FORC matrix in 1),
3) _CentralRidgeRemovedFORC_VARIFORC.txt, for the FORC matrix with subtracted central ridge,
4) _CentralRidgeRemovedFORCStandardError_VARIFORC.txt, for the standard errors of the FORC matrix in 3),
5) _CentralRidge_Linear_VARIFORC.txt, for the central ridge coercivity distribution on a linear field scale,
6) _CentralRidge_Log10_VARIFORC.txt, for the central ridge coercivity distribution on a $\log_{10}$ field scale,
7) _SDBackgroundFORC_VARIFORC.txt, for the FORC diagram representing reversible contributions from uniaxial single-domain particles,
8) _SDBackgroundFORCStandardError_VARIFORC.txt, for the standard errors of the FORC matrix in 7).

These files are required by other VARIFORC functions for further processing. They also provide data for other applications, and contain useful summary information. The files are produced with a specific format that is explained in the following.

6.6.1 FORC matrices

All FORC matrices are exported to files with the structure shown in Fig. 6.24. The file header contains summary information about FORC processing options and magnetizations derived from FORC data, followed by a matrix of FORC values corresponding to points of the output grid. The beginning of the data matrix section is univocally located by the title line “Data matrix”, regardless of the actual row number.

Information blocks in the file header begin with a title (e.g. “Field unit, magnetization unit, and FORC unit”), followed by comma-separated parameter lists. Empty lines are used to separate blocks. Line widths are unlimited and might therefore be wrapped by some text editors. The content of most blocks is explained in Chapter 4. Special blocks used only with FORC matrices produced by IsolateCR are explained in the following sections.

```
VARIFORC v1.0 Central ridge FORC function.

Source file
E:\...\Leg138_848_S0_FORC_VARIFORC.frc

Field unit magnetization unit and FORC unit
T,mAm2/kg,1e-3 Am2/(T2 kg)

Hc-range of data points
0.00025,0.12075

Hb-range of data points
-0.007500000000000007,0.0085

[...]

Grid dimensions
242,33

[...]

Smoothing parameters along Hc
7,9,0.08

Smoothing parameters along Hb
4,9,0.08

[...]

Hc-range of seed Hb-distribution
0.02725,0.03925

Hb-range of seed Hb-distribution
0.0004166666666666624,0.0037125,0.007425

Hb-expectation and Hb-FWHM of seed central ridge
0.0004350584558505725,0.0019986489040647515

Hb-range of seed central ridge and extra margin factor used for fitting
-0.0026919782780443053,0.0037557355421728705,0.1

Weight factor for model background and maximum fitting freedom
10000.,3

Mrs from backfield curve and standard error
3.2538852205965836,0.0005484217073363591

Integral of original FORC function and standard error
3.1756091042134997,0.03382798227148518

Total irreversible magnetization at reversal field and standard error
3.148669656568797,0.002317801621604443

Total central ridge magnetization and standard error
2.1194179344933626,0.03655670466674843

Data matrix
0.000017611940876349763,0.0000341987572483049,0.00002832561943932887 5,-0.00002332365063750
82013648e-6,6.914695518389635e-7,-3.326055377783632e-7,-1.871752033366647e-7,1.17027613555
[...]
```

Fig. 6.24: Example of central ridge FORC matrix file produced by IsolateCR. Information blocks begins with a title (highlighted in blue), followed by a list of parameters. FORC data begin after “Data matrix”.

6.6.2 Central ridge FORC matrix

The central ridge FORC matrix files (`_CentralRidgeFORC_VARIFORC.txt` and `_CentralRidgeFORCStandardError_VARIFORC.txt`) contains the following special blocks, some of which are not included in regular FORC matrix files. Blocks are numbered according to their occurrence in the file header:

Block 16: Hc-range of seed Hb-profile

This block contains the horizontal range of the seed profile according to the options entered with `INPUT 01`. Automatic options are replaced by the numerical values used by `IsolateCR`.

Block 17: Hc-range of seed Hb-profile

This block contains the vertical range of the seed profile according to the options entered with `INPUT 02`. Automatic options are replaced by the numerical values used by `IsolateCR`.

Block 18: Hb-expectation and Hb-FWHM of the seed central ridge

This block contains the expectation and full-width to half-maximum (FWHM) of the central ridge profile isolated from the seed profile.

Block 19: Hb-range of seed central ridge and extra margin factor used for fitting

This block contains the H_b-range occupied by the central ridge in the seed profile and the extra margin taken around the central ridge according to `INPUT 03`.

Block 20: Weight factor for background model and maximum fitting freedom

This block contains the weight factor applied to the background model according to `INPUT 04`, and the maximum freedom degree of the central ridge model according to `INPUT 05`. Automatic options are replaced by the numerical values used by `IsolateCR`.

Block 21: Mrs from backfield curve and standard error

This block is taken directly from the imported FORC matrix file and contains the integral

$$M_{\mathrm{bf}} = \int_{H_{\mathrm{min}}}^{H_{\mathrm{max}}} f_{\mathrm{bf}}(H)\,\mathrm{d}H \tag{6.1}$$

of the backfield coercivity distribution f_{bf} and the corresponding standard error estimate (see Chapter 4.6.1). It serves as term of comparison for central ridge-specific parameters.

Block 22: Integral of original FORC function and standard error

This block is taken directly from the imported FORC matrix file and contains the integral

$$I = 2\int_{H_{c,min}}^{H_{c,max}} \int_{H_{b,min}}^{H_{b,max}} \rho(H_c, H_b)\, dH_c\, dH_b \tag{6.2}$$

of the FORC function $\rho(H_c, H_b)$ over the whole FORC space, and the corresponding standard error estimate (see Chapter 4.6.1). It serves as term of comparison for central ridge-specific parameters.

Block 23: Total irreversible magnetization at reversal field and standard error

This block is taken directly from the imported FORC matrix file and contains the integral

$$M_{irs} = \int_{H_{min}}^{H_{max}} f_{irr}(H)\, dH \tag{6.3}$$

of the reversal field coercivity distribution f_{irr} and the corresponding standard error estimate (see Chapter 4.6.1). It serves as term of comparison for central ridge-specific parameters.

Block 24: Total central ridge magnetization and standard error

This block contains the integral

$$M_{cr} = 2\int_{H_{c,min}}^{H_{c,max}} \int_{H_{b,cr,min}}^{H_{b,cr,max}} \rho_{cr}(H_c, H_b)\, dH_c\, dH_b \tag{6.4}$$

of the isolated central ridge $\rho_{cr}(H_c, H_b)$ over its horizontal range $(H_{c,min}, H_{c,max})$ defined by the origin FORC matrix coverage, and the vertical range $(H_{b,cr,min}, H_{b,cr,max})$ of central ridge and background models used by `IsolateCR`.

Block 25: Data matrix

This is the last block and contains the central ridge data matrix with matrix elements

$$\rho_{k,j} = \rho_{cr}(H_{c,j}, H_{b,k}) \tag{6.5}$$

corresponding to central ridge values at the j-th H_c-coordinate and the k-th H_b-coordinate of the output grid. H_c-coordinates are numbered in progressive order from smallest to largest value. H_b-coordinates are numbered in regressive order from largest to smallest value. Each matrix row is a list of comma-separated values and matrix rows are separated by empty lines. The output grid coincides with the FORC space covered by central ridge and background models used by `IsolateCR` for isolating the central ridge.

6.6.3 Background FORC matrix

The background FORC matrix files (`_CentralRidgeSubtractedFORC_VARIFORC.txt` and `_CentralRidgeSubtractedFORCStandardError_VARIFORC.txt`) contains the following special blocks, some of which are not included in regular FORC matrix files. Blocks are numbered according to their occurrence in the file header:

Block 23: Integral of original FORC function with central ridge removed and standard error

This block contains the integral

$$I_0 = 2\int_{H_{c,min}}^{H_{c,max}} \int_{H_{b,min}}^{H_{b,max}} \rho_0(H_c, H_b)\,dH_c\,dH_b \tag{6.6}$$

of the FORC function $\rho_0 = \rho - \rho_{cr}$ with subtracted central ridge over the whole FORC space, and the corresponding standard error estimate.

Block 24: Integral of FORC function with central ridge removed over Hb>0 and standard error

This block contains the integral

$$I_{0,bpos} = 2\int_{H_{c,min}}^{H_{c,max}} \int_{0}^{H_{b,max}} \rho_0(H_c, H_b)\,dH_c\,dH_b \tag{6.7}$$

of the FORC function $\rho_0 = \rho - \rho_{cr}$ with subtracted central ridge over the upper quadrant of FORC space (i.e. $H_b \geq 0$), and the corresponding standard error estimate. $I_{0,bpos} = 0$ for non-interacting single-domain particles with uniaxial anisotropy [*Newell*, 2005].

Block 25: Integral of FORC function with central ridge removed over Hr>0 and standard error

This block contains the integral

$$I_{0,rpos} = 2\int_{H_{c,min}}^{H_{c,max}} \int_{H_c}^{H_{b,max}} \rho_0(H_c, H_b)\,dH_c\,dH_b \tag{6.8}$$

of the FORC function $\rho_0 = \rho - \rho_{cr}$ with subtracted central ridge over the FORC space limited by $H_r \geq 0$ (i.e. $H_b \geq H_c$), and the corresponding standard error estimate.

Block 26: Data matrix

This is the last block and contains the FORC matrix data with subtracted central ridge. The matrix elements

$$\rho_{k,j} = \rho(H_{c,j}, H_{b,k}) - \rho_{cr}(H_{c,j}, H_{b,k}) \tag{6.9}$$

correspond to FORC function values with subtracted central ridge at the j-th H_c-coordinate and the k-th H_b-coordinate of the output grid. H_c-coordinates are numbered in progressive order from smallest to largest value. H_b-coordinates are numbered in regressive order from

largest to smallest value. Each matrix row is a list of comma-separated values and matrix rows are separated by empty lines. The output grid coincides with the grid of the imported FORC matrix.

6.6.4 FORC matrix of reversible single-domain contributions

The FORC matrix of reversible single-domain contributions (`_SDBackgroundFORC_VARIFORC.txt` and `_SDBackgroundFORCStandardError_VARIFORC.txt`) is calculated and exported upon setting `INPUT 15` to `Yes`. The FORC matrix file contains the following special blocks, some of which are not included in regular FORC matrix files. Blocks are numbered according to their occurrence in the file header:

Block 26: Integral of reconstructed reversible uniaxial SD background

This block contains the integral

$$I_{\mathrm{ur}} = 2\int_{H_{\mathrm{c,min}}}^{H_{\mathrm{c,max}}}\int_{H_{\mathrm{b,min}}}^{0} \rho_{\mathrm{ur}}(H_{\mathrm{c}},H_{\mathrm{b}})\,\mathrm{d}H_{\mathrm{c}}\,\mathrm{d}H_{\mathrm{b}} \tag{6.10}$$

of the reconstructed reversible contribution $\rho_{\mathrm{ur}}(H_{\mathrm{c}},H_{\mathrm{b}}) = \rho_0(H_{\mathrm{c}},H_{\mathrm{b}}) - \rho_0(H_{\mathrm{c}},-H_{\mathrm{b}})$ of uniaxial single-domain particles, where $\rho_0 = \rho - \rho_{\mathrm{cr}}$ is the FORC function with subtracted central ridge. Uniaxial non-interacting SD particles yield $I_{\mathrm{ur}} = 0$ [*Newell*, 2005; *Egli et al.*, 2010].

Block 27: Integral of reconstructed reversible uniaxial SD background (1/2 of absolute values)

This block contains the integral

$$I_{\mathrm{ur}}^{+} = \int_{H_{\mathrm{c,min}}}^{H_{\mathrm{c,max}}}\int_{H_{\mathrm{b,min}}}^{0} \left|\rho_{\mathrm{ur}}(H_{\mathrm{c}},H_{\mathrm{b}})\right|\mathrm{d}H_{\mathrm{c}}\,\mathrm{d}H_{\mathrm{b}} \tag{6.11}$$

of the absolute value of the reconstructed reversible contribution ρ_{ur} of uniaxial single-domain particles. Randomly oriented, non-interacting SD particles with uniaxial anisotropy yield $I_{\mathrm{ur}}^{+} = M_{\mathrm{s}}(1-\overline{S})/2$, where M_{s} is the saturation magnetization, and $\overline{S}$ the mean amplitude of magnetization jumps in normalized single-particle hysteresis loops [*Egli et al.*, 2010].

Block 28: Integral of reconstructed reversible uniaxial SD background (negative values)

This block contains the integral

$$I_{\mathrm{ur}}^{-} = -2\int_{H_{\mathrm{c,min}}}^{H_{\mathrm{c,max}}}\int_{H_{\mathrm{b,min}}}^{0} \min\left[0,\rho_{\mathrm{ur}}(H_{\mathrm{c}},H_{\mathrm{b}})\right]\mathrm{d}H_{\mathrm{c}}\,\mathrm{d}H_{\mathrm{b}} \tag{6.12}$$

of negative values of the reconstructed reversible contribution ρ_{ur} of uniaxial single-domain particles Non-interacting single-domain particles with uniaxial anisotropy yield $I_{\mathrm{ur}}^{-} = I_{\mathrm{ur}}^{+}$. Because of this property, I_{ur}^{+} and I_{ur}^{-} provide a consistency check for the hypothesis that the sample contains uniaxial SD particles.

Block 29: Data matrix

This is the last block and contains the FORC matrix data corresponding to the reconstructed contribution of uniaxial single-domain particles. The matrix elements

$$\rho_{k,j} = \rho_0(H_{c,j}, H_{b,k}) - \rho_0(H_{c,j}, -H_{b,k}) \tag{6.13}$$

correspond to function values at the *j*-th H_c-coordinate and the *k*-th H_b-coordinate of the output grid. H_c-coordinates are numbered in progressive order from smallest to largest value. H_b-coordinates are numbered in regressive order from largest to smallest value. Each matrix row is a list of comma-separated values and matrix rows are separated by empty lines. The output grid coincides with the grid of the imported FORC matrix, but is limited to $H_b \leq 0$.

6.6.5 Central ridge coercivity distributions

Central ridge coercivity distributions (`_CentralRidge_Linear_VARIFORC.txt`, `_CentralRidge_Log10_VARIFORC.txt`) are exported to files with the structure shown in Fig. 6.25. The file header contains summary information about FORC processing options and magnetization derived from coercivity distribution data, followed by coercivity distribution values listed in a comma-separated column format with no empty lines. The beginning of the data section is univocally located by the title line “Coercivity distribution on linear field scale”, or “Coercivity distribution on log10 field scale” regardless of the actual row number.

Information blocks in the file header begin with a title (e.g. “Field unit, magnetization unit, and coercivity distribution unit”), followed by comma-separated parameter lists. Empty lines are used to separate blocks. Line widths are unlimited and might therefore be wrapped by some text editors. The content of blocks is explained in Chapter 4. Special blocks used only for central ridge coercivity distributions are explained in the following sections, numbered according to their occurrence in the file header:

Block 19: Total central ridge magnetization and standard error

This block contains the integral

$$M_{cr} = \int_{H_{c,min}}^{H_{c,max}} f_{cr}(H_c)\,dH_c \tag{6.14}$$

of the central ridge coercivity distribution $f_{cr}(H_c, H_b)$ over its coercivity range $(H_{c,min}, H_{c,max})$.

```
VARIFORC v1.0 Coercivity distribution from central ridge data contained in FORC
measurements.

Source file
E:\...\Leg138_848_S0_CorrectedMeasurements_VARIFORC.frc

Field unit magnetization unit and coercivity distribution unit
T,mAm2/kg,1e-3 Am2/(T kg)

Field step of FORC measurements and first point offset
0.0005015553545586107,0.00007597585780746107

Grid mesh size
0.0005

Grid origin
0.00025,0.

[...]

Smoothing parameters along Hc
7,9,0.08

Smoothing parameters along Hb
4,9,0.08

[...]

Hc-range of seed Hb-distribution
0.02725,0.03925

Hb-range of seed Hb-distribution
0.0004166666666666624,0.0037125,0.007425

Hb-expectation and Hb-FWHM of seed central ridge
0.0004350584558505725,0.0019986489040647515

Hb-range of seed central ridge and extra margin factor used for fitting
-0.0026919782780443053,0.0037557355421728705,0.1

Weight factor for model background and maximum fitting freedom
10000.,3

Mrs from backfield curve and standard error
3.2538852205965836,0.0005484217073363591

Total irreversible magnetization at reversal field and standard error
3.148669656568797,0.002317801621604443

Total central ridge magnetization and standard error
2.1194179344933626,0.03655670466674843

Coercivity distribution on linear field scale Hb-mean and Hb-standard deviation
0.00025,9.257522,1.787444,0.000493127,0.0000123134,0.000832156,0.0000211378
0.00075,9.913225,1.534660,0.000471228,0.0000101178,0.000802156,0.0000201778
0.00125,10.749212,1.397910,0.000462781,0.0000152138,0.000792845,0.0000195478
0.00175,10.994184,1.178808,0.000470102,0.0000141276,0.000865478,0.0000164147
0.00225,11.241938,1.087407,0.000481653,0.0000165123,0.000884179,0.0000184143
0.00275,11.626667,1.055365,0.000451127,0.0000131689,0.000812984,0.0000157129
0.00325,11.892767,1.001051,0.000460502,0.0000149854,0.000885413,0.0000174158
[...]
```

Fig. 6.25: Example of central ridge coercivity distribution file produced by `IsolateCR`. Information blocks begins with a title (highlighted in blue), followed by a list of parameters. Coercivity distribution data begin after “Coercivity distribution on linear field scale”.

Block 20: Coercivity distribution

This last block, entitled “Coercivity distribution on a linear field scale Hb-mean and Hb standard deviation”, or “Coercivity distribution on a log10 field scale”, contains central ridge coercivity distribution data in a comma-separated, seven-column or three-column format, without empty lines.

In case of linear field scales, lines are of the form

$$H_k, f_k, \delta f_k, \mathrm{E}(\rho_{\mathrm{cr},k}), \delta\,\mathrm{E}(\rho_{\mathrm{cr},k}), \mathrm{sd}(\rho_{\mathrm{cr},k}), \delta\,\mathrm{sd}(\rho_{\mathrm{cr},k}) \tag{6.15}$$

where

$$f_k = 2\int_{H_{\mathrm{b,cr,min}}}^{H_{\mathrm{b,cr,max}}} \rho_{\mathrm{cr}}(H_k, H_\mathrm{b})\,\mathrm{d}H_\mathrm{b} \tag{6.16}$$

is the value of the central ridge coercivity distribution for the *k*-th field H_k and δf_k is the corresponding standard error,

$$\mathrm{E}(\rho_{\mathrm{cr},k}) = \frac{2}{f_k}\int_{H_{\mathrm{b,cr,min}}}^{H_{\mathrm{b,cr,max}}} \rho_{\mathrm{cr}}(H_k, H_\mathrm{b}) H_\mathrm{b}\,\mathrm{d}H_\mathrm{b} \tag{6.17}$$

is the expectation of the central ridge FORC function profile at $H_\mathrm{c} = H_k$ and $\delta\mathrm{E}(\rho_{\mathrm{cr},k})$ the corresponding standard error,

$$\mathrm{sd}^2(\rho_{\mathrm{cr},k}) = \frac{2}{f_k}\int_{H_{\mathrm{b,cr,min}}}^{H_{\mathrm{b,cr,max}}} \rho_{\mathrm{cr}}(H_k, H_\mathrm{b})\left[H_\mathrm{b} - \mathrm{E}(\rho_{\mathrm{cr},k})\right]^2 \mathrm{d}H_\mathrm{b} \tag{6.18}$$

is the variance of the central ridge FORC function profile at $H_\mathrm{c} = H_k$, and $\delta\,\mathrm{sd}(\rho_{\mathrm{cr},k})$ the standard error of the standard deviation derived from eq. (6.18). $\mathrm{E}(\rho_{\mathrm{cr},k})$ and $\mathrm{sd}(\rho_{\mathrm{cr},k})$ are estimates of the central ridge vertical position and width, respectively.

In case of logarithmic field scales, lines are of the form

$$\log_{10} H_k, f_k^{\log}, \delta f_k^{\log} \tag{6.19}$$

where $f_k^{\log} = f(H_k)\ln 10$ is the value of the logarithmic coercivity distribution for the *k*-th field H_k, and $\delta f_k^{\log}$ is the corresponding standard error.

6.7 Literature

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Heslop, D., and A.P. Roberts (2012). Estimation of significance levels and confidence intervals for first-order reversal curve distributions, *Geochemistry Geophysics Geosystems*, *13*, Q12Z40, doi: 10.1029/2012GC004115.

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