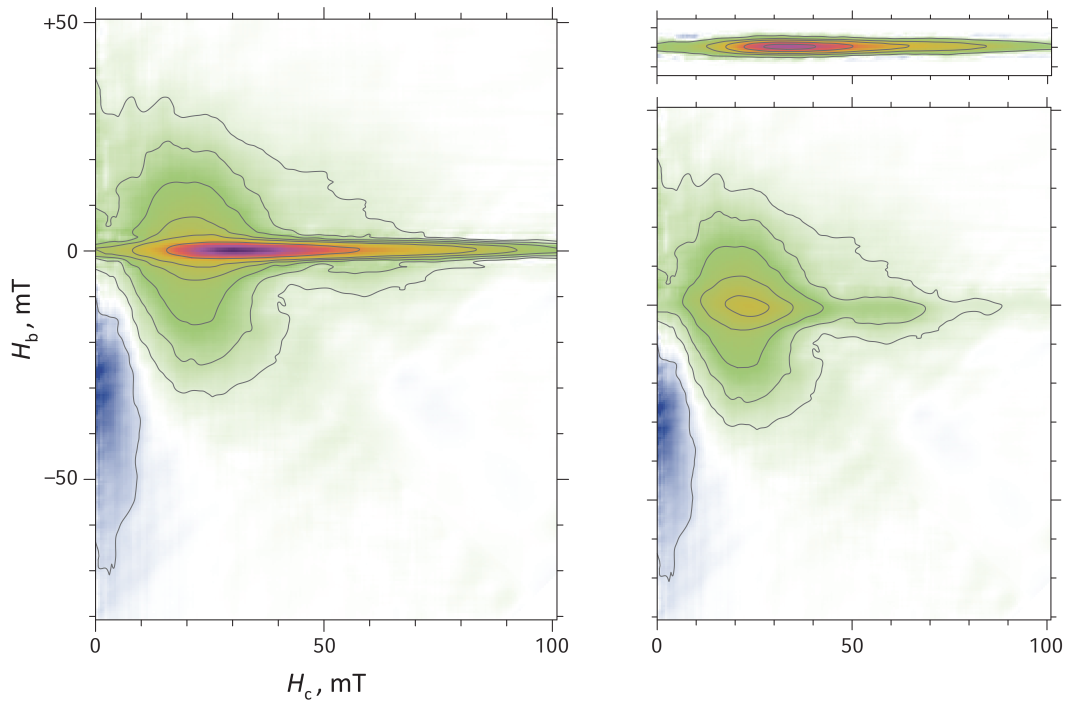
VARIFORC Quick Guide

VARIFORC IsolateCR



4.1 Needed files

Mathematica notebook

(→ User manual p. 6-6)

Files ending with `VARIFORC_IsolateCR.nb`

Location in the installation package:

`VARIFORC_Install/Functions/IsolateCR/Start_IsolateCR.nb`

Parameter file

(→ User manual p. 6-14)

Files ending with `VARIFORC_IsolateCR_parameters.txt`

Location in the installation package:

`VARIFORC_Install/Functions/PlotFORC/Start_IsolateCR_Parameters.txt`

FORC matrix

(→ User manual p. 6-11)

FORC matrix files produced by CalculateFORC (ending with `FORC_VARIFORC.txt`).

4.2 Output files

FORC matrices

(→ User manual p. 6-55)

In all cases:

- Isolated central ridge (`_CentralRidgeFORC_VARIFORC.txt`) and standard error (`_CentralRidgeFORCStandardError_VARIFORC.txt`).
- FORC matrix with subtracted central ridge (`_CentralRidgeRemovedFORC_VARIFORC.txt`) and standard error (`_CentralRidgeRemovedFORCStandardError_VARIFORC.txt`).

Only if INPUT 15 is set to `Yes`:

- Reconstructed reversible contributions from uniaxial SD particles (`_SDBackgroundFORC_VARIFORC.txt`) and corresponding standard error (`_SDBackgroundFORCStandardError_VARIFORC.txt`).

Coercivity distributions

In all cases:

- Central ridge coercivity distribution on linear (`_CentralRidge_Linear_VARIFORC.txt`) and $\log_{10}$ `_CentralRidge_Log10_VARIFORC.txt`) field scale.

4.3 Processing parameters

INPUT 01

(→ User manual p. 6-18)

***H_c*-range of seed profile**

- Option 1 (*wide automatic range*):
  `wide`
  The seed profile is calculated by averaging vertical profiles with peak amplitudes exceeding 70% of the central ridge peak.
- Option 2 (*narrow automatic range*):
  `narrow`
  The seed profile is calculated by averaging vertical profiles within a distance from the central ridge peak that corresponds to the width of local regression rectangles. These profiles can be considered identical up to measurement noise.
- Option 3 (*explicit specification*):
  `Hcmin, Hcmax`
  The seed profile is calculated by averaging vertical profiles with H_c-values comprised between `Hcmin` and `Hcmax` with `Hmin` < `Hmax`.

Option 1 maximizes the signal-to-noise ratio of the seed profile and is best suited to perfectly horizontal central ridges. The seed profile obtained with option 2 is representative for vertical profiles through the central ridge peak. Option 3 is recommended for all cases where the identification of the central ridge peak is ambiguous (e.g. in presence of a vertical ridge).

INPUT 02

(→ User manual p. 6-22)

H_b-range parameters of seed profile

- Option 1 (*automatic*):
  `Automatic`
  The H_b-range of the seed profile is chosen automatically according to the estimated vertical extension of the central ridge. The seed profile is centered at the ridge peak and is twice as wide as the ridge itself.

- Option 2 (*explicit specifications*):
  `Hb0, crw, pw`
  The H_b-range of the seed profile is centered at the peak of a central ridge with vertical offset `Hb0` and vertical half-width `crw` > 0. The half-width of the whole seed profile is `pw` > 0. All parameters are expressed in field units of the imported FORC matrix, as specified in the file header. The central ridge parameters `Hb0` and `crw` are deduced *a posteriori* from central ridge analyses with IsolateCR. About 50-66% of the seed profile should be occupied by the central ridge, so that `pw` ≈ 3 × `crw`. In general, sections of the seed profile that are not occupied by the central ridge should be as straight as possible.

Option 1 performs well in all cases where the central ridge is clearly distinguishable from other contributions. Option 2 should be used for analyzing more difficult cases, once the central ridge properties are known from previous IsolateCR runs with option 1.

The central ridge properties entered with option 2 serve only as initial model, and are updated by a least-squares fit of the seed profile with appropriate central ridge and background models. Only the seed profile width entered with option 2 is not automatically updated.

Examples:

- `0.4, 2, 6` is used for a central ridge with a vertical offset of 0.4 mT and 2 mT half-width, while the half-width of the whole profile is 6 mT. Accordingly, the seed profile ranges from $H_b = 0.4 - 2 = -1.6$ mT to $H_b = 0.4 + 2 = +2.4$ mT.

INPUT 03

(→ User manual p. 6-26)

Extra central ridge margin

- Unique option:
  `d`
  An extra margin $0 \le d < 1$ can be introduced around the central ridge in order to provide a "buffer" between the central ridge itself and the surrounding background. This margin is expressed as fraction of the estimated width of the central ridge profile. Extra margins are avoided with $d = 0$. Recommended values of d are comprised between 0.05 and 0.1.

Extra margins around the central ridge ensures a proper separation between regions dominated by the central ridge and by other contributions, respectively, despite model uncertainties arising from measurement noise.

Examples:

- `0` does not introduce an extra margin around the central ridge.
- `0.1` introduces a 10% extra margin around the central ridge.

INPUT 04

(→ User manual p. 6-28)

Weight factor for model background

- Option 1 (*automatic, recommended*):
  `Automatic`
  With this option, separation of the central ridge is based only on the background model. This means that the central ridge contribution is obtained by subtracting a background model from the FORC matrix.
- Option 2 (*explicit specification*):
  `w`
  With this option, separation of the central ridge is based on a weighted combination of background and central ridge models. The weight factor $w \geq 0$ controls the relative importance of the background model. Central ridge separation is based exclusively on the central ridge model if $w = 0$. On the other hand, option 1 is equivalent to $w \gg 1$. If $w = 1$, weights given to background and central ridge models are inversely proportional to the corresponding mean squared amplitudes.

Option 1 gives best results for background reconstructions, while option 2 with $w = 0$ maximizes the continuity of the isolated central ridge. Option 1 is recommended in case of FORC diagrams dominated by the central ridge, while option 2 with $w = 1$ is recommended for central ridges whose amplitude is comparable with that of other contributions.

INPUT 05

(→ User manual p. 6-32)

Maximum freedom degree of central ridge model

- Unique option:
  F
  The central ridge model can have three freedom degrees (0, 1, 2, and 3) corresponding to an increasing number of parameters available for optimization. Appropriate freedom degrees are automatically chosen for each vertical profile according to data quality, up to a maximum set by $0 \leq F \leq 3$.

High-quality FORC diagrams can be processed with $F = 3$, while $F \leq 1$ avoids modeling instabilities associated with diagrams containing important measurement noise contributions. Model instabilities generate warning message and discontinuous central ridge reconstructions. In this case, IsolateCR should run with a smaller F in order to obtain stable results.

INPUT 06

(→ User manual p. 6-37)

Profile selection

- Option 1 (*for regular runs*):
  `All`
  This option corresponds to a regular run of IsolateCR in which all vertical FORC profiles are analyzed in order to separate the central ridge from other contributions.

- Option 2 (*debugging*):
  n
  With this option, only a single vertical profile indicated by its number $n \geq 1$ is processed, and all intermediate model results are shown. Results for the whole FORC diagram are not produced.

Option 2 corresponds to a debugging run of IsolateCR, typically used in order to verify the source of warning or error messages generated during a regular run for a given profile. Warning/error messages always contain a reference to the profile number for which processing problems have been encountered.

INPUT 07

(→ User manual p. 6-39)

Confidence interval of coercivity distributions

- Unique option:
  λ
  Coercivity distributions derived from FORC data are plotted with a confidence interval defined as a multiple $\lambda > 0$ of the estimated standard error.

Usual choices are $\lambda = 1$ for very noisy distributions, and $\lambda = 2$ for all other cases.

INPUT 08

(→ User manual p. 6-40)

Scale factor for central ridge coercivity distribution

- Unique option:
  c
  The central ridge distribution, multiplied with a scale factor $c \geq 0$, is plotted together with other coercivity distributions derived from FORC data. All coercivity distributions share the same scale if $c = 1$. This option is recommended for samples containing mainly single-domain particles, since all coercivity distributions have similar amplitudes in this case. In other cases, the central ridge contribution might be much smaller, and $c > 1$ is best used for comparison purposes.

INPUT 08 does not affect the exported central ridge distribution and is used only for plotting purposes.

INPUT 09

(→ User manual p. 6-41)

Clip negative coercivity distribution values

- Option 1 (*recommended*):
  Yes
  Coercivity distributions are usually positive functions. Therefore, negative coercivity distribution amplitudes obtained from FORC data can be considered as noise artifacts. With this option, coercivity distribution plots are clipped to positive values.
- Option 2:
  No
  With this option, coercivity distributions obtained from FORC data are plotted over their entire range of positive and negative amplitudes.

INPUT 09 options have no effects on the exported coercivity distributions.

INPUT 10

(→ User manual p. 6-42)

Plotted FORC error parameter

- Option 1 (*standard error*):
  `error`
  This option is used to plot the estimated standard error of FORC diagrams. Errors comprised between 0 and the quadratic mean of all errors are plotted with colors ranging from blue to white, and errors larger than the quadratic mean are coded in yellow, red, and purple.

- Option 2 (*signal-to-noise ratio*):
  `SNR, t`
  This option is used to plot the signal-to-noise ratio (SNR) of FORC diagrams, i.e. the ratio between FORC amplitudes and the estimated standard error. The second parameter, t, is a positive number representing the significance threshold, i.e. the SNR limit below which the FORC function does not differ significantly from 0. Values of t for 90-99% confidence levels are reported in Table 6.1 of the user manual (p. 6.44). Setting t = 3 ensures a confidence level >99%. SNR values ≤t are represented with colors ranging from blue (SNR = 0) to white (SNR = t). Significant regions of the FORC diagram (SNR > t) are coded with colors ranging from yellow to red and purple.

Option 1 is useful for identifying large-scale error patterns, which might reflect excessive smoothing. Option 2 is useful for identifying significant regions of the FORC diagram.

INPUT 11

(→ User manual p. 6-45)

FORC diagram ticks specifications

- Option 1 (*automatic, recommended*):
  `Automatic`
  FORC diagram ticks are chosen automatically. In this case, H_c- and H_b-ranges are divided into ~10 equal intervals by major ticks.
- Option 2 (*same explicit specification for H_c- and H_b*-ticks):
  d, n
  Major ticks are drawn at d-intervals along H_c and H_b, where $d \geq 0$ is expressed in field units of the imported FORC matrix, as reported in the file header. Each interval is divided into n parts by minor ticks. Theses specifications apply in the same manner for H_c- and H_b-ticks of all FORC diagrams
- Option 3 (*different explicit specifications for H_c- and H_b*-ticks):
  d_c, n_c, d_b, n_b
  Same as option 2 for each parameter pair. The first and second pairs control H_c- and H_b-ticks, respectively, for all FORC diagrams.
- Option 4 (*different explicit specifications for the central ridge diagram*):
  d_c, n_c, d_b, n_b, d_{bcr}, n_{bcr}
  Same as option 3 for the first two parameter pairs. The last parameter pair controls the H_b-ticks of the central ridge FORC diagram, which, because of the reduced H_b-range, might require different specifications

Examples:

- `10, 5, 10, 5, 5, 1` places H_c- and H_b- major ticks every 10 mT with minor ticks every 2 mT for all FORC diagrams, except H_b-ticks of the central ridge diagram, which are drawn every 5 mT with minor ticks every 1 mT.

INPUT 12

(→ User manual p. 6-47)

Vertical exaggeration of central ridge FORC diagram

- Unique option:
  `v`
  The natural aspect ratio of the central ridge FORC diagram is multiplied by a positive factor $v > 0$. Use $v = 1$ to keep the natural aspect ratio unmodified. Use $v > 1$ to stretch the central ridge FORC diagram vertically.

Central ridge details, such as vertical offset and width, are better visible if the limited H_b-range of the central ridge diagram is stretched with v = 3-5.

INPUT 13

(→ User manual p. 6-48)

Color scale saturation

- Option 1 (*automatic, recommended*):
  `Automatic`
  The color scale saturation of plotted FORC diagrams is set to 90% of the maximum saturation. This option is best suited for monitors and printing.
- Option 2 (*explicit specification*):
  `S`
  The color scale saturation of plotted FORC diagrams is set to a fraction S of the maximum saturation, with $0 \le S \le 1$. Recommended values of S are comprised between 0.8 and 1.

More plotting options are available with the VARIFORC function PlotFORC.

INPUT 14

(→ User manual p. 6-50)

Color scale clipping

- Unique option:
  `q`
  The color scale extends from the q-quantile to the $1 - q$ quantile of all FORC values. FORC values exceeding this range are represented with the same color for minimum and maximum values, respectively. The color scale extends to the whole range of FORC values with $q = 0$. Otherwise, a fraction q of smallest and largest FORC values is clipped.

This option is used to make the color scale less sensitive to very large FORC amplitudes, so that small amplitudes can be represented with sufficient color contrast. Recommended values for q are comprised between 0 and 0.05. INPUT 21 does not affect the exported FORC matrix and is used only for plotting purposes.

Examples:

- `0.02` means that the 2% smallest and largest FORC values are excluded from the color scale range.

INPUT 15

(→ User manual p. 6-52)

Calculate single-domain reversible FORC background

- Option 1 (*Yes*):
  `Yes`
  The reversible FORC contribution of uniaxial single-domain particles is calculated and exported.
- Option 2 (*No*):
  `No`
  The reversible FORC contribution of uniaxial single-domain particles is not calculated.

Option 1 is used for the analysis of samples whose FORC signature is dominated by single-domain particles.

Notes: