J-difference Editing Toolkit (JET)
About

J-difference Editing Toolkit (JET) is a software package designed for the batch analysis of J-difference editing magnetic resonance spectroscopy (MRS) data, such as MEGA-PRESS MRS spectra.

JET is capable to process Raw data acquired from all major clinical (i.e., Siemens, GE, Philips) and preclinical (i.e., Bruker) MRI scanners.

JET is implemented in Matlab, and is distributed as executables, except for the configuration functions being distributed as source code, allowing necessary users modifications.

JET is fully automated and does not require user intervention to minimize software operator variances in MRS data quantification.

J-difference Editing Toolkit (JET) Team

- **Major Developers**
  Chen "Raphael" Liu, MS; Nanyan "Rosalie" Zhu, MA; Jia Guo, PhD.
- **Contributors**
  Jochen Weber, MS; Kay C. Igwe, MS; Emily Turner Wood, MD, PhD; Wafae Labriji, MS; Vasile Stupar, PhD; Gregory Smith, PhD.
- **Collaborators**
  Scott A. Small, MD; Douglas L Rothman, PhD; Robin de Graaf, PhD; Neil Harris, PhD; Florence Fauvelle, PhD; Yanping Sun, PhD.
- **Inventor and Correspondence**
  Jia Guo, PhD. (Email: jg3400@columbia.edu)

Installation Guide

J-difference Editing Toolkit (JET)

1. Clone from GitHub repository.
   git clone https://github.com/SAIL-GuoLab/JET

2. Organize your data inside "./Data/" folder, in the following hierarchy:
   ./Data/vender/scanner/study/session/

3. Modify and run JET_main_script.m

4. **You can find a more comprehensive tutorial in Installation_Guide.txt.**

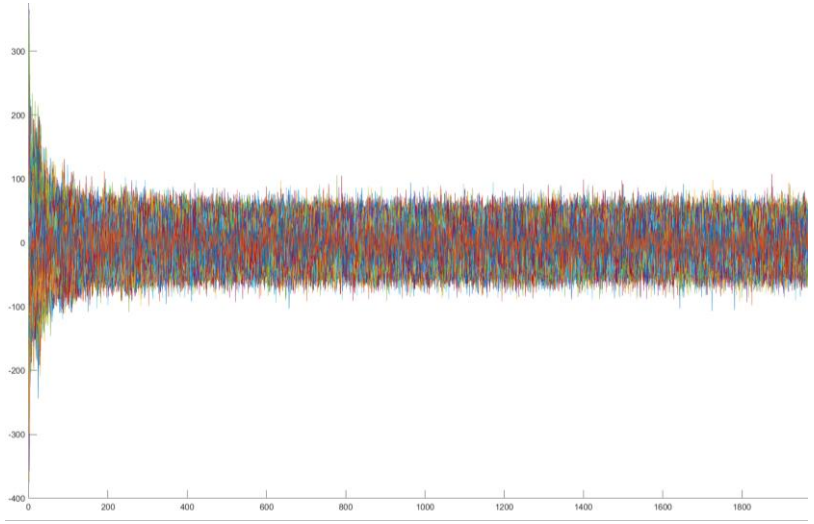
5. For more questions, please contact Dr. Jia Guo at jg3400@columbia.edu.

J-difference Editing Toolkit (JET)

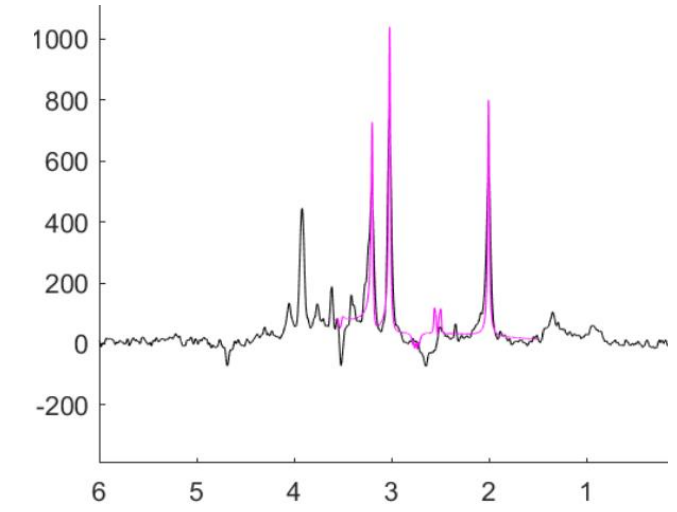
Purpose

To provide a complete toolbox that performs registration and metabolite quantification in MR spectroscopy.

From *this*



To *this*



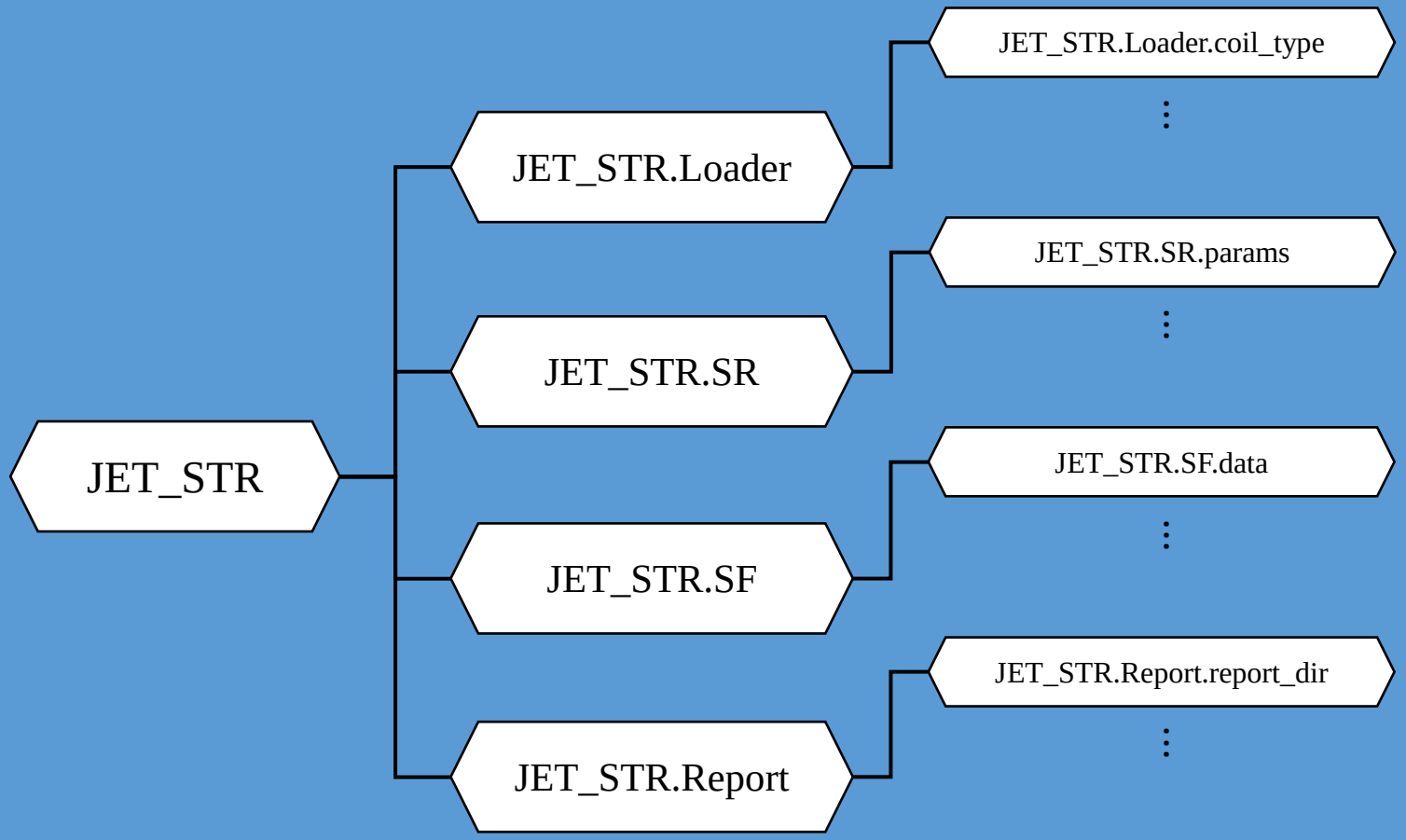
Technical Overview

J-difference Editing Toolkit (JET)

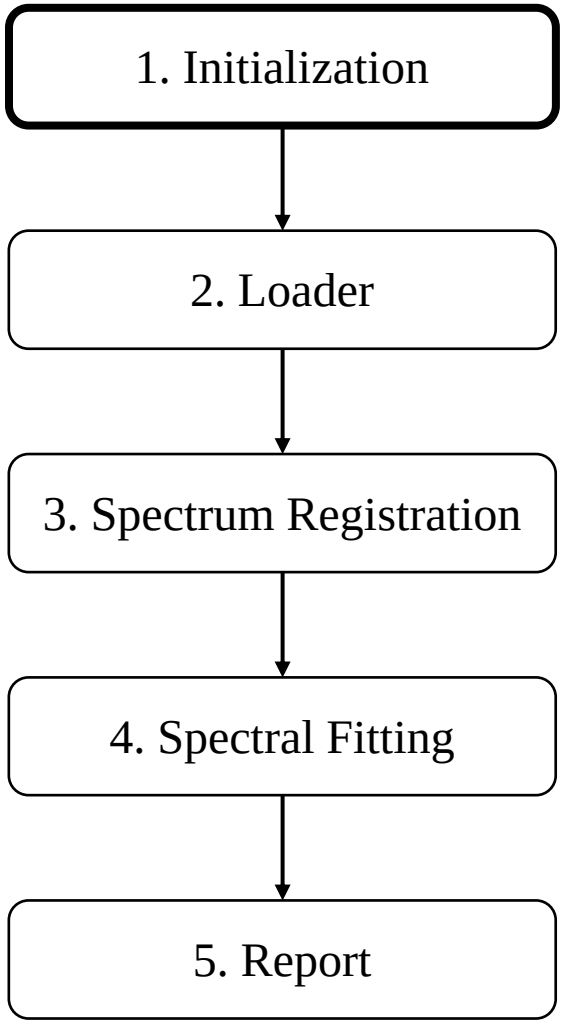
Modules × 5

1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report

Data Structure × 1

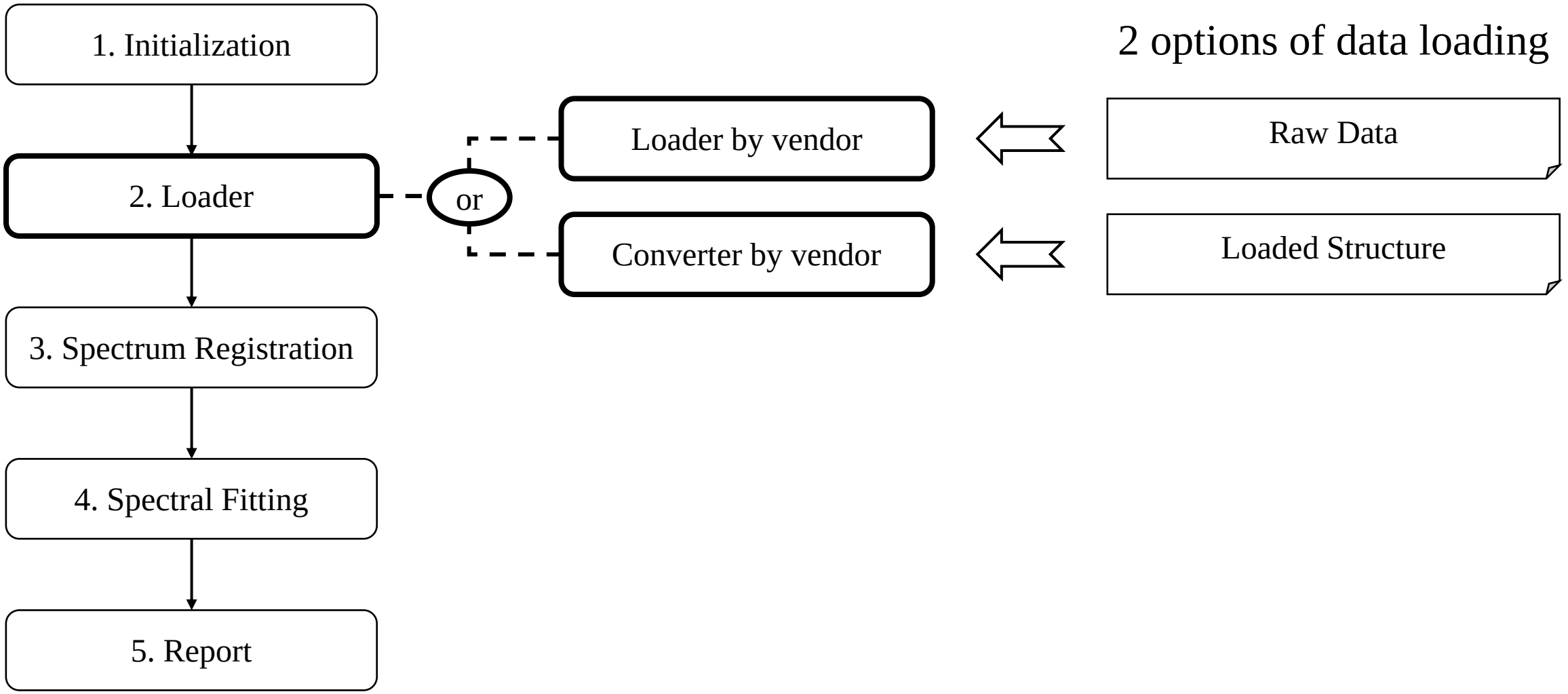


J-difference Editing Toolkit (JET)

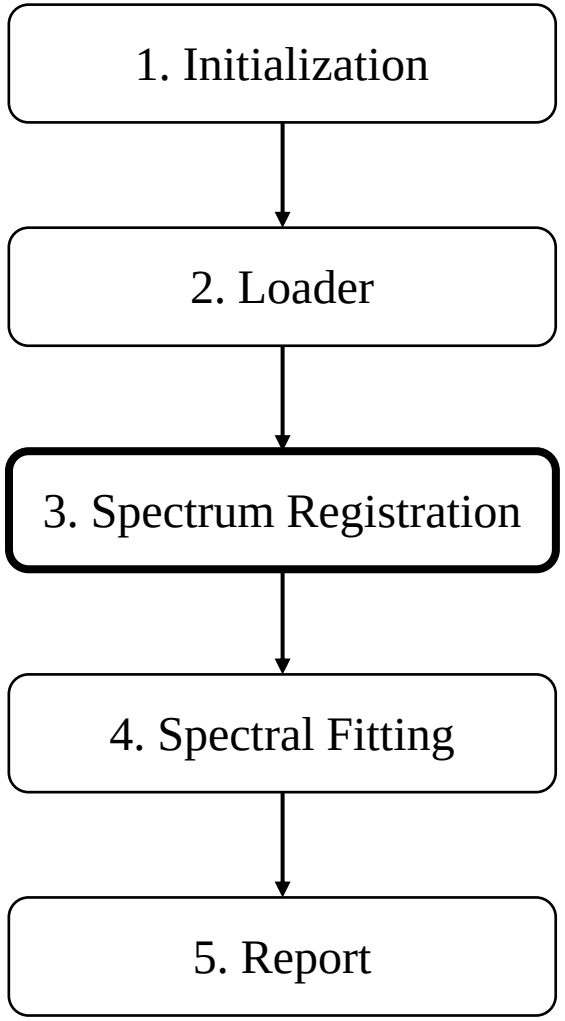


- Define where the raw data are located, where to save the report, where to store the processed data, etc.

J-difference Editing Toolkit (JET)

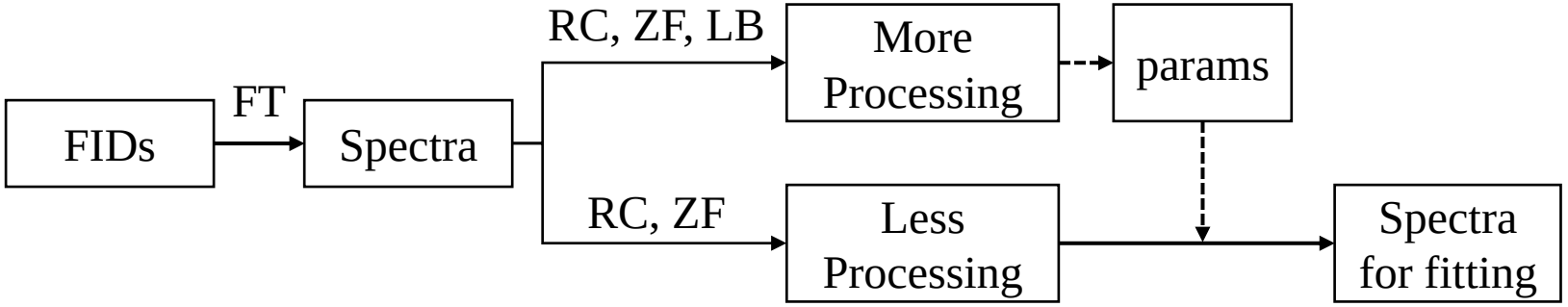


J-difference Editing Toolkit (JET)



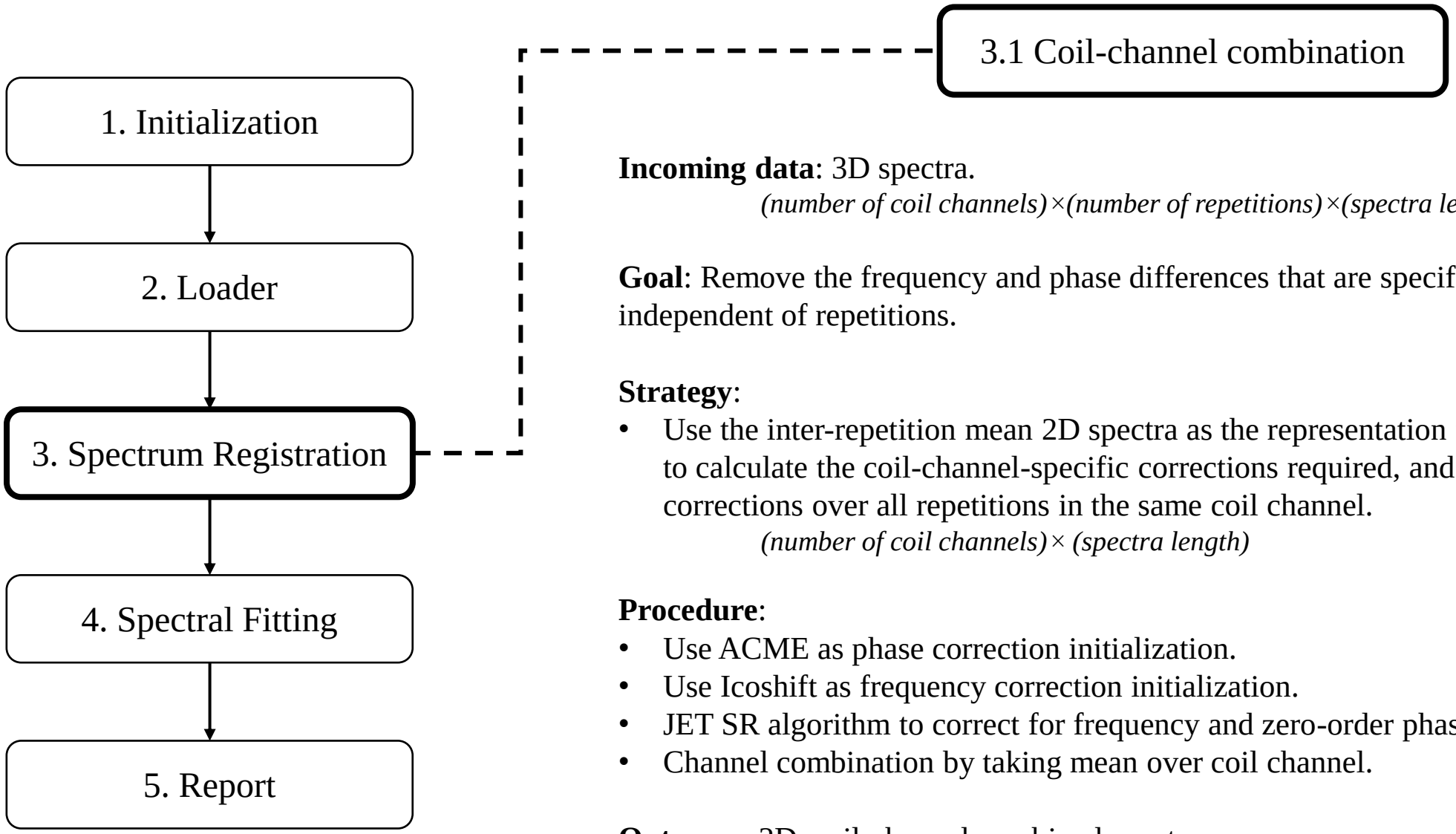
Goal: Combine each individual spectrum from all coil channels and repetitions, after proper removal of frequency and zero-order phase difference, to result in one single ON spectrum and one single OFF spectrum.

Principle: Use a line-broadened version of the spectra (higher SNR, less authentic) as a representation of the version without line-broadening (lower SNR, more authentic) to calculate the necessary frequency and phase shift, and then apply the shift to the more authentic version to prepare it as the input for spectral fitting. Thus we ensure minimal manipulation and great preservation of the signal.



RC: remove compensate points (typically first 68 points in FID)
ZF: zero-filling
LB: line-broadening
params: parameters of frequency and zero-order phase shift

J-difference Editing Toolkit (JET)



Incoming data: 3D spectra.
(number of coil channels)×*(number of repetitions)*×*(spectra length)*

Goal: Remove the frequency and phase differences that are specific to coil-channel but independent of repetitions.

Strategy:
- Use the inter-repetition mean 2D spectra as the representation for each coil channel to calculate the coil-channel-specific corrections required, and apply the same corrections over all repetitions in the same coil channel.
  (number of coil channels)× *(spectra length)*

Procedure:
- Use ACME as phase correction initialization.
- Use Icoshift as frequency correction initialization.
- JET SR algorithm to correct for frequency and zero-order phase.
- Channel combination by taking mean over coil channel.

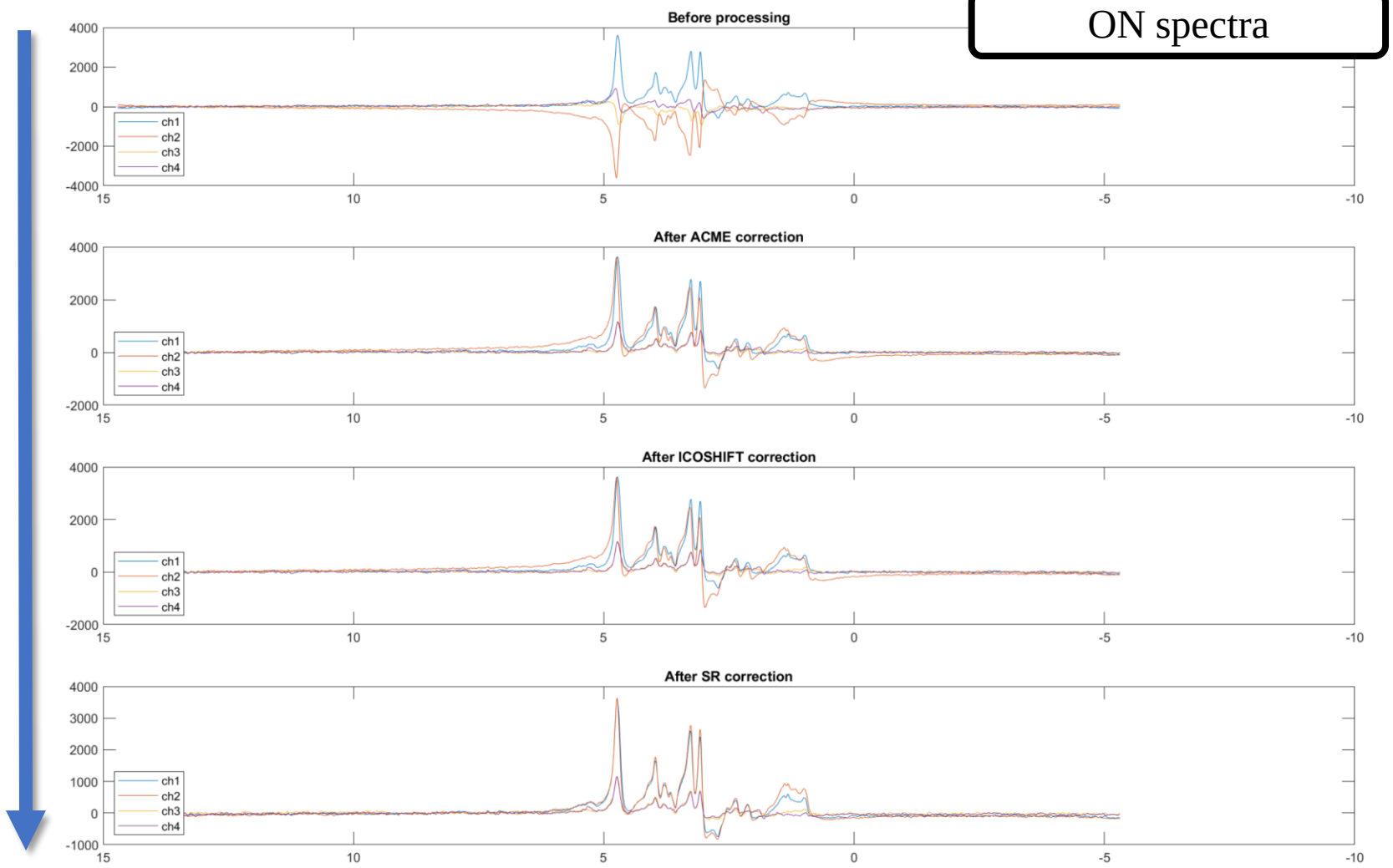
Outcome: 2D, coil-channel combined spectra.
(number of repetitions)×*(spectra length)*

J-difference Editing Toolkit (JET)

1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report

3.1 Coil-channel combination

ON spectra

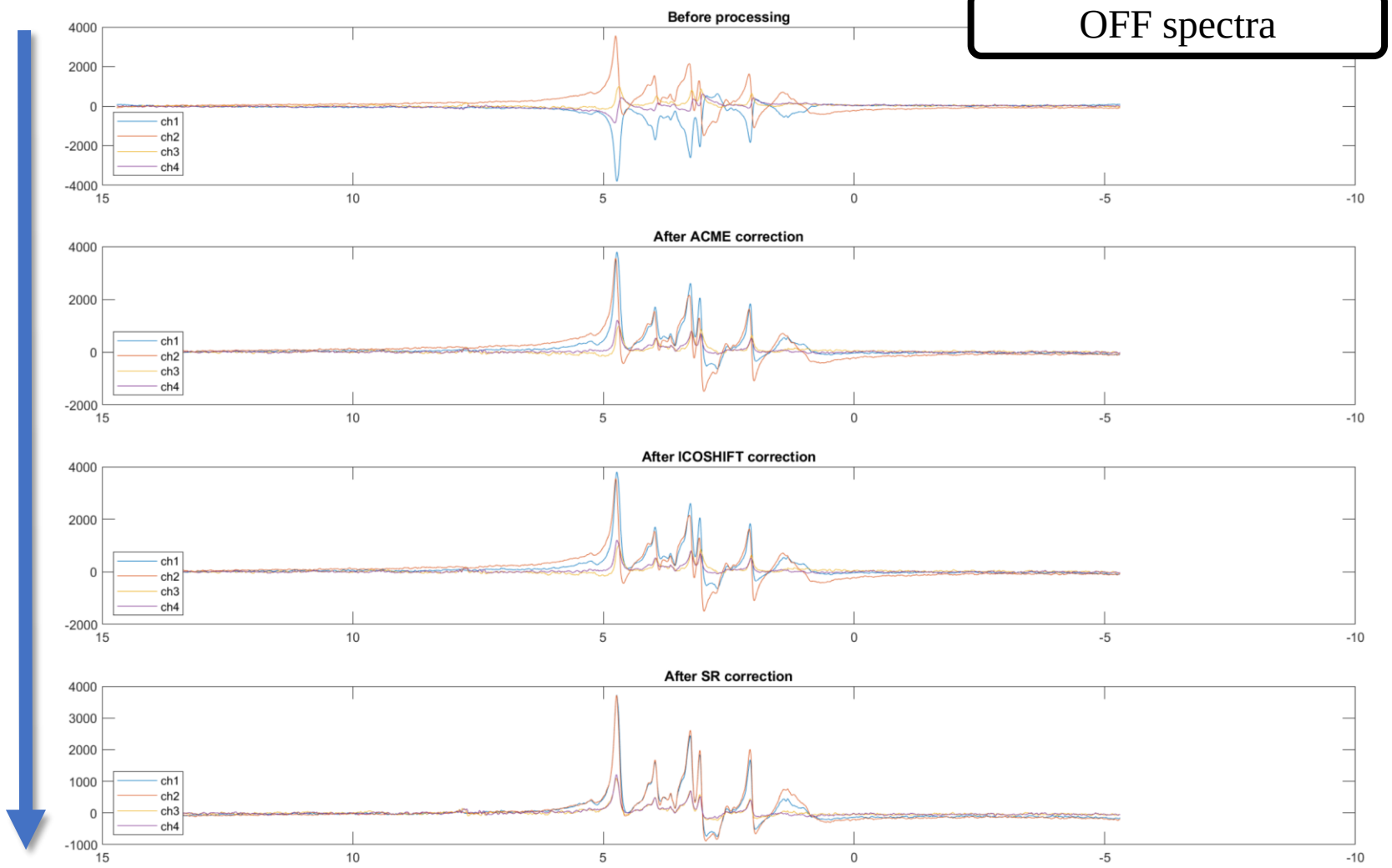


J-difference Editing Toolkit (JET)

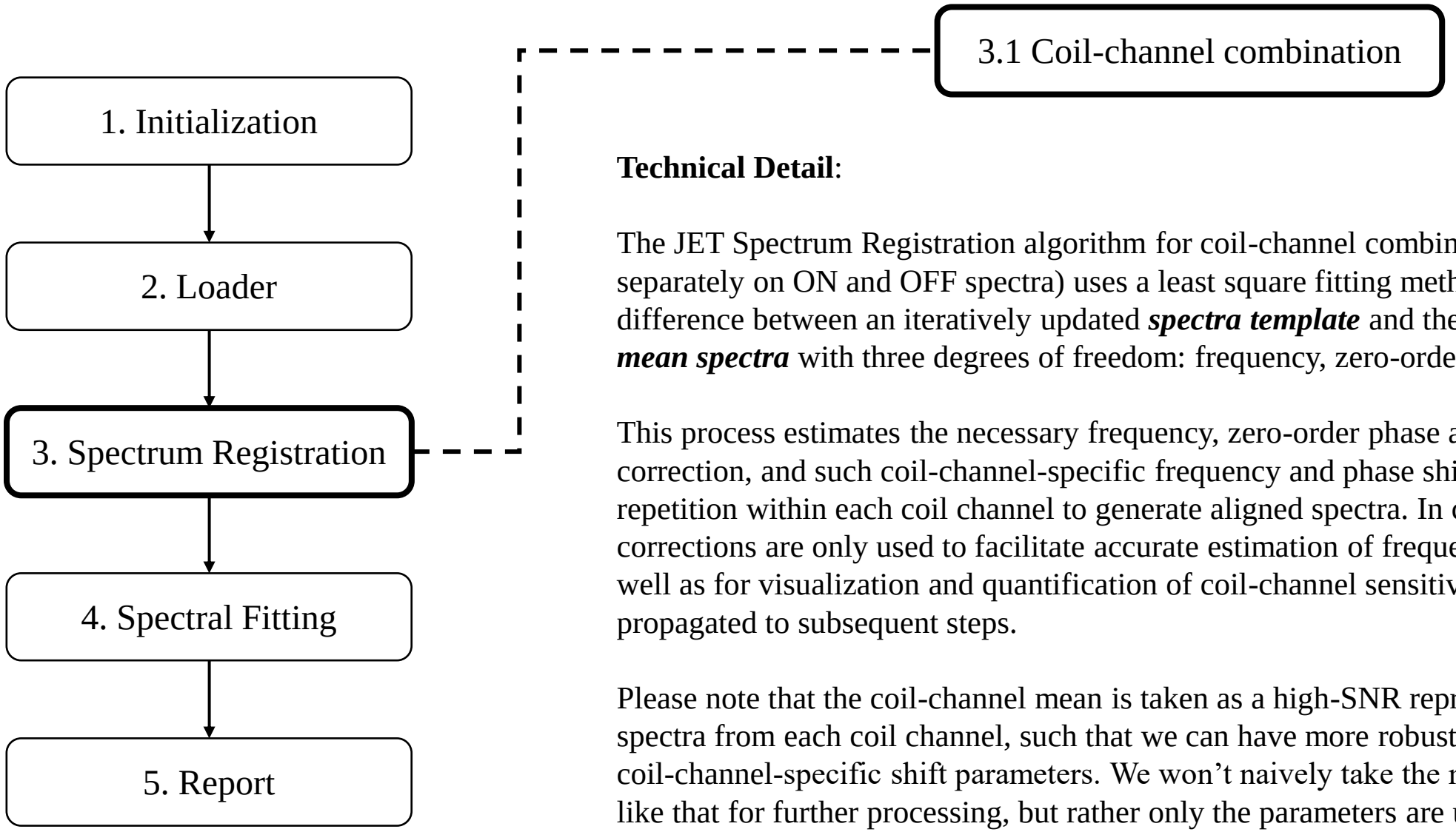
1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report

3.1 Coil-channel combination

OFF spectra



J-difference Editing Toolkit (JET)



Technical Detail:

The JET Spectrum Registration algorithm for coil-channel combination (applied separately on ON and OFF spectra) uses a least square fitting method to minimize the difference between an iteratively updated ***spectra template*** and the ***coil-channel-specific mean spectra*** with three degrees of freedom: frequency, zero-order phase, and amplitude.

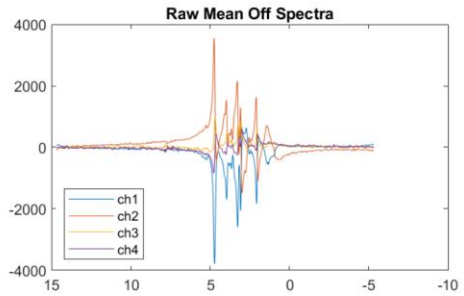
This process estimates the necessary frequency, zero-order phase and amplitude for the correction, and such coil-channel-specific frequency and phase shifts are applied to every repetition within each coil channel to generate aligned spectra. In contrast, the amplitude corrections are only used to facilitate accurate estimation of frequency and phase shift, as well as for visualization and quantification of coil-channel sensitivity, but are not propagated to subsequent steps.

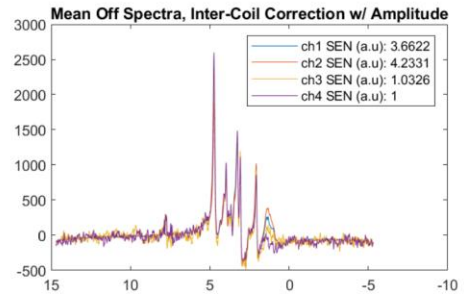
Please note that the coil-channel mean is taken as a high-SNR representation of the spectra from each coil channel, such that we can have more robust estimations of the coil-channel-specific shift parameters. We won’t naively take the mean and leave them like that for further processing, but rather only the parameters are utilized at this step.

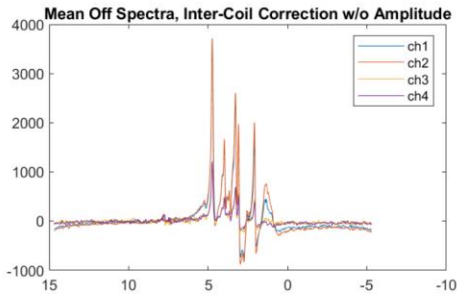
J-difference Editing Toolkit (JET)

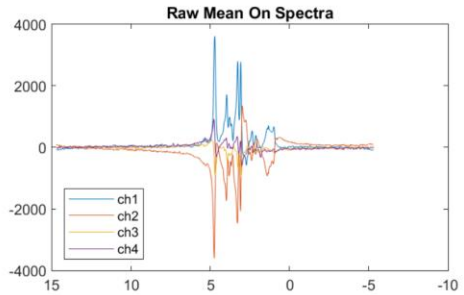
1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report

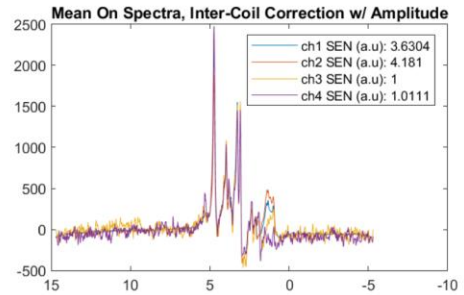
3.1 Coil-channel combination

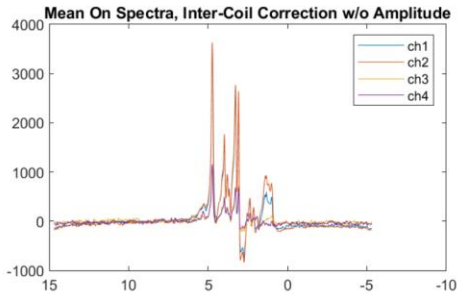


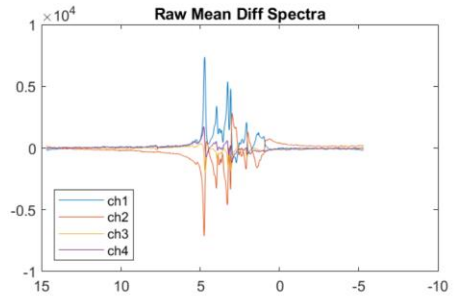


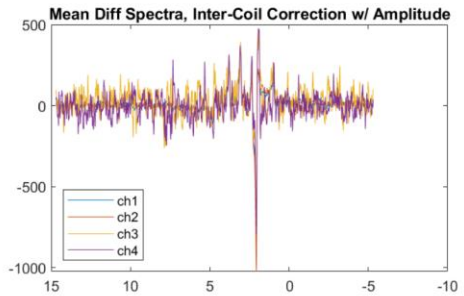


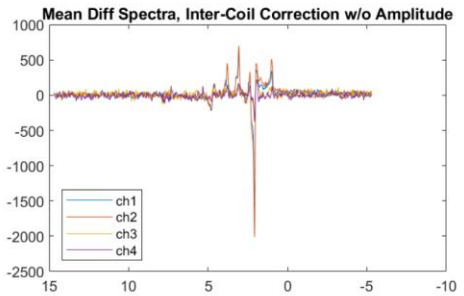




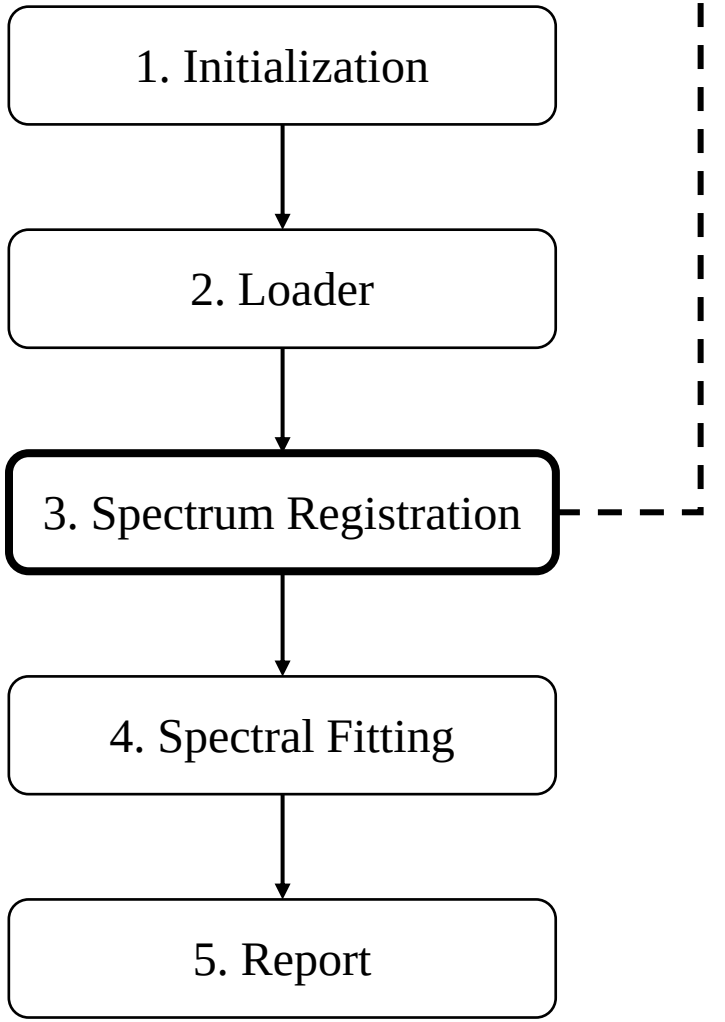








J-difference Editing Toolkit (JET)



3.2 Within-ON/OFF Registration & 3.3 ON-to-OFF Registration

Incoming data: Two 2D spectra (ON spectra and OFF spectra)

Goal: Remove the frequency and phase differences that are specific to each repetition. Also align ON spectra to OFF spectra.

Strategy:

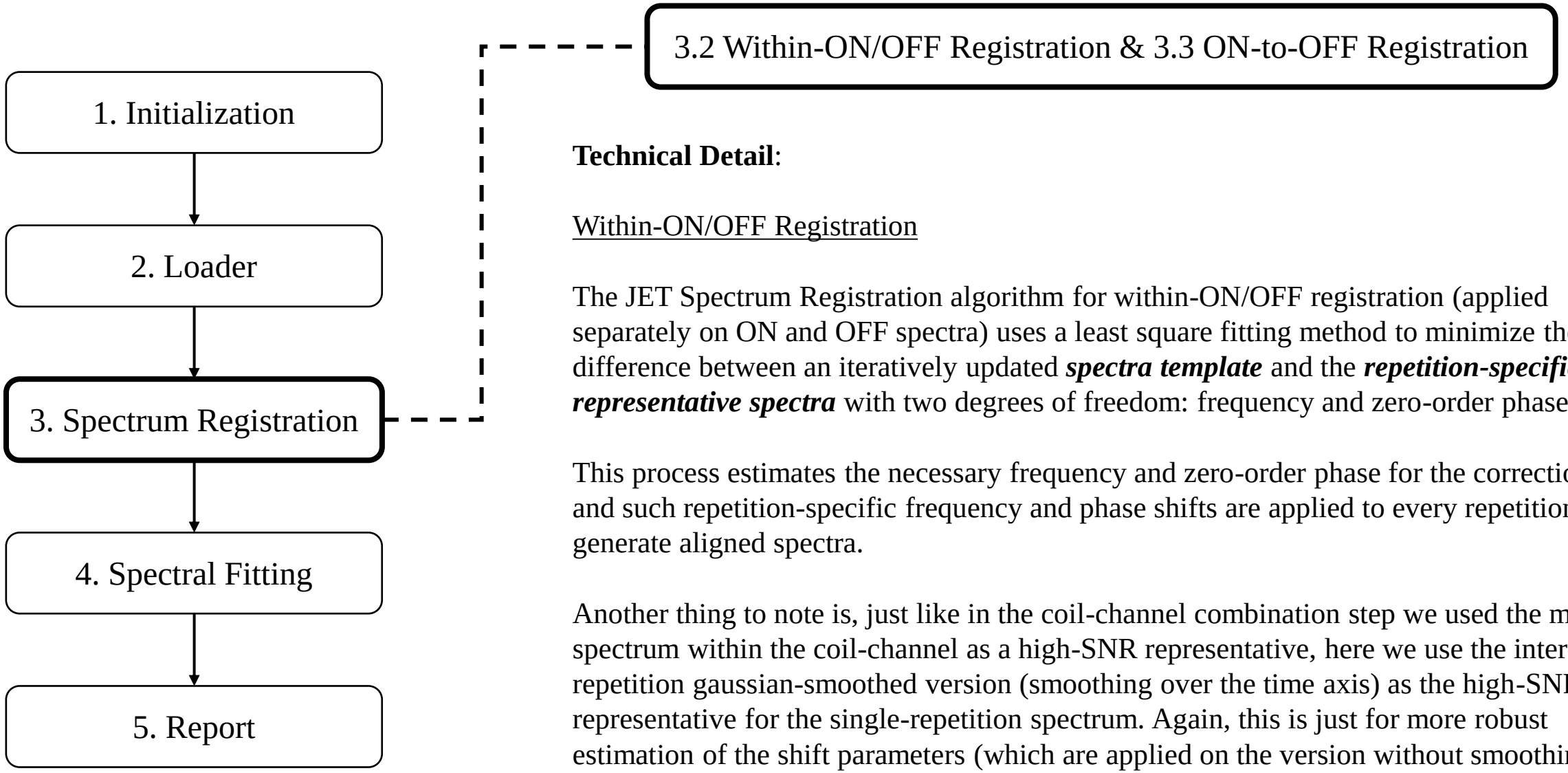
- Use the repetition-wise smoothed 2D spectra as the representation for each repetition to calculate the repetition-specific corrections required, and apply the same corrections over all repetitions in the same coil channel.
- Use the mean of ON spectra and mean of OFF spectra to find the frequency and phase corrections required to match the former to the latter, and apply the correction over all repetitions of the ON spectra.

Procedure:

- Use ACME as phase correction initialization.
- Use Icoshift as frequency correction initialization.
- JET SR algorithm to correct for frequency and zero-order phase.

Outcome: Two 2D spectra (ON spectra and OFF spectra) after corrections.

J-difference Editing Toolkit (JET)



Technical Detail:

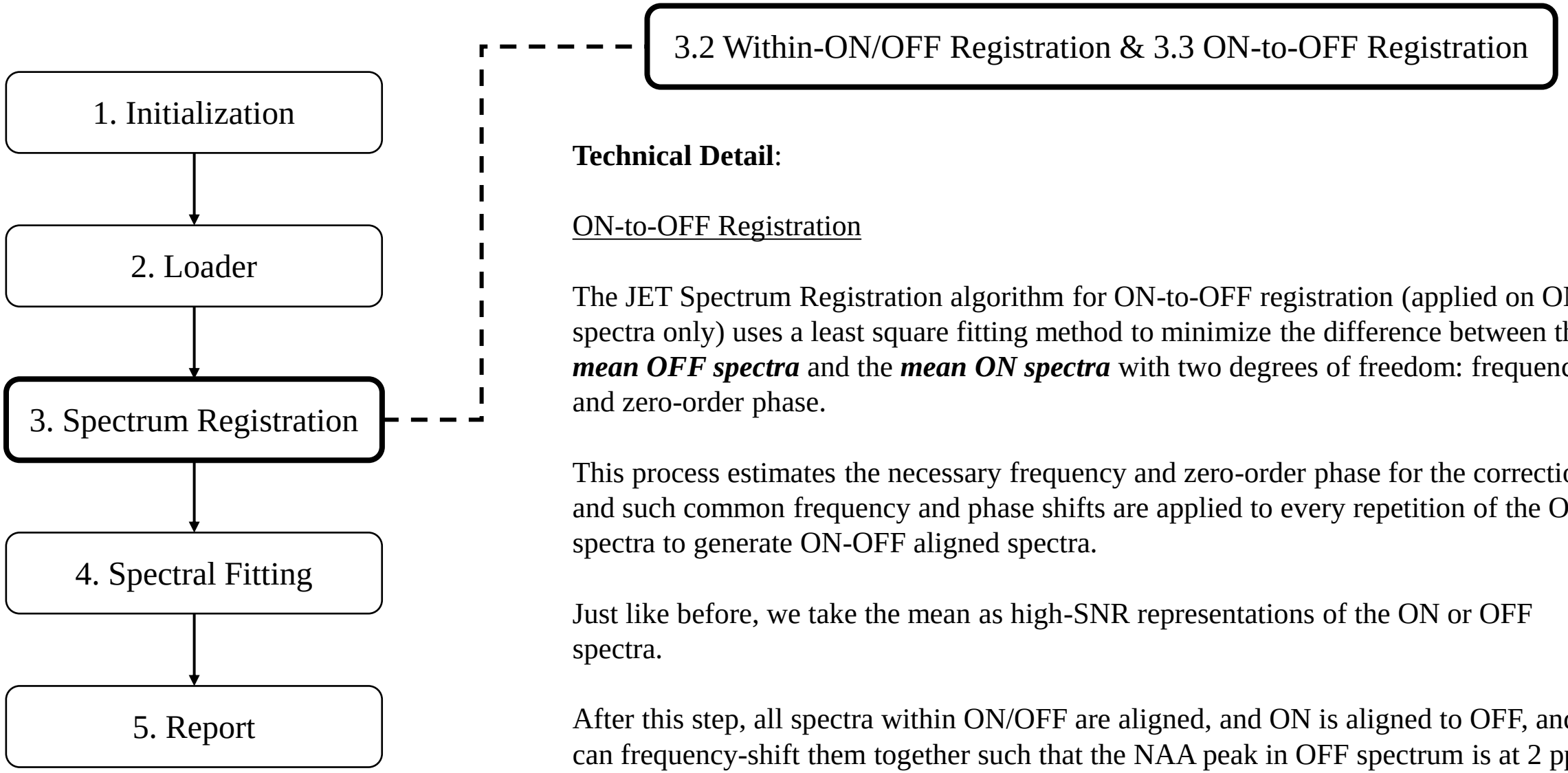
Within-ON/OFF Registration

The JET Spectrum Registration algorithm for within-ON/OFF registration (applied separately on ON and OFF spectra) uses a least square fitting method to minimize the difference between an iteratively updated ***spectra template*** and the ***repetition-specific representative spectra*** with two degrees of freedom: frequency and zero-order phase.

This process estimates the necessary frequency and zero-order phase for the correction, and such repetition-specific frequency and phase shifts are applied to every repetition to generate aligned spectra.

Another thing to note is, just like in the coil-channel combination step we used the mean spectrum within the coil-channel as a high-SNR representative, here we use the inter-repetition gaussian-smoothed version (smoothing over the time axis) as the high-SNR representative for the single-repetition spectrum. Again, this is just for more robust estimation of the shift parameters (which are applied on the version without smoothing), not for any other purpose.

J-difference Editing Toolkit (JET)



Technical Detail:

ON-to-OFF Registration

The JET Spectrum Registration algorithm for ON-to-OFF registration (applied on ON spectra only) uses a least square fitting method to minimize the difference between the ***mean OFF spectra*** and the ***mean ON spectra*** with two degrees of freedom: frequency and zero-order phase.

This process estimates the necessary frequency and zero-order phase for the correction, and such common frequency and phase shifts are applied to every repetition of the ON spectra to generate ON-OFF aligned spectra.

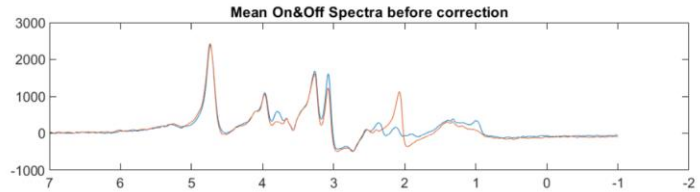
Just like before, we take the mean as high-SNR representations of the ON or OFF spectra.

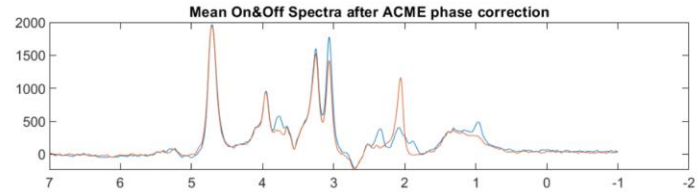
After this step, all spectra within ON/OFF are aligned, and ON is aligned to OFF, and we can frequency-shift them together such that the NAA peak in OFF spectrum is at 2 ppm, and take the mean over repetitions to generate **one single ON spectrum and one single OFF spectrum for spectral fitting**.

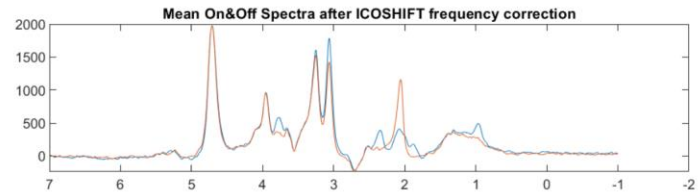
J-difference Editing Toolkit (JET)

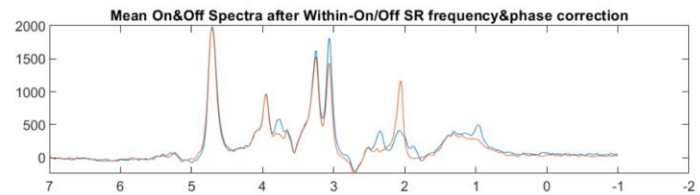
1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report

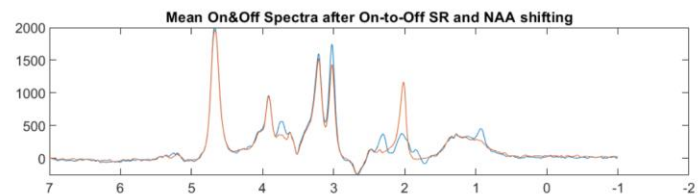
3.2 Within-ON/OFF Registration & 3.3 ON-to-OFF Registration

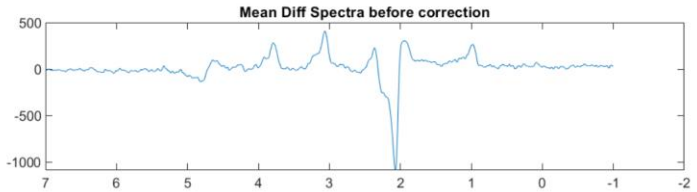


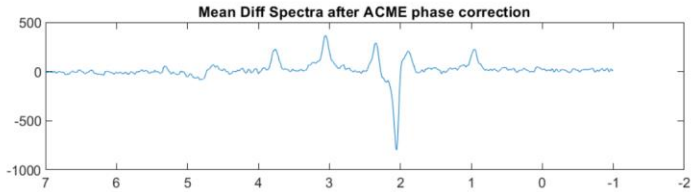


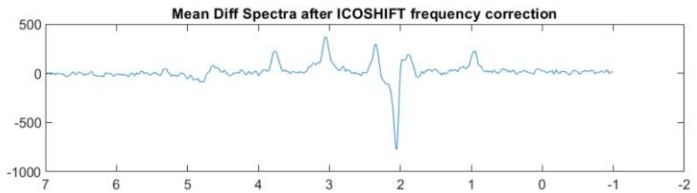


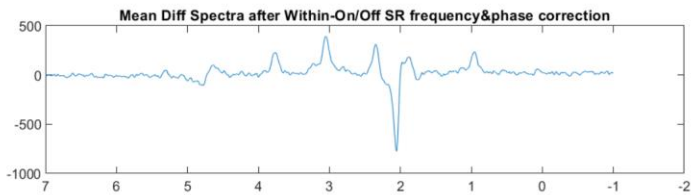


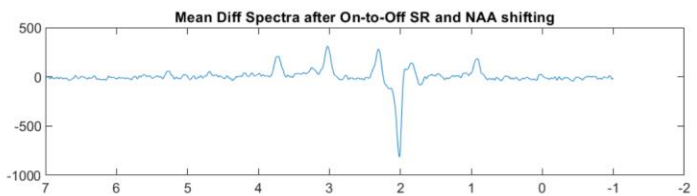




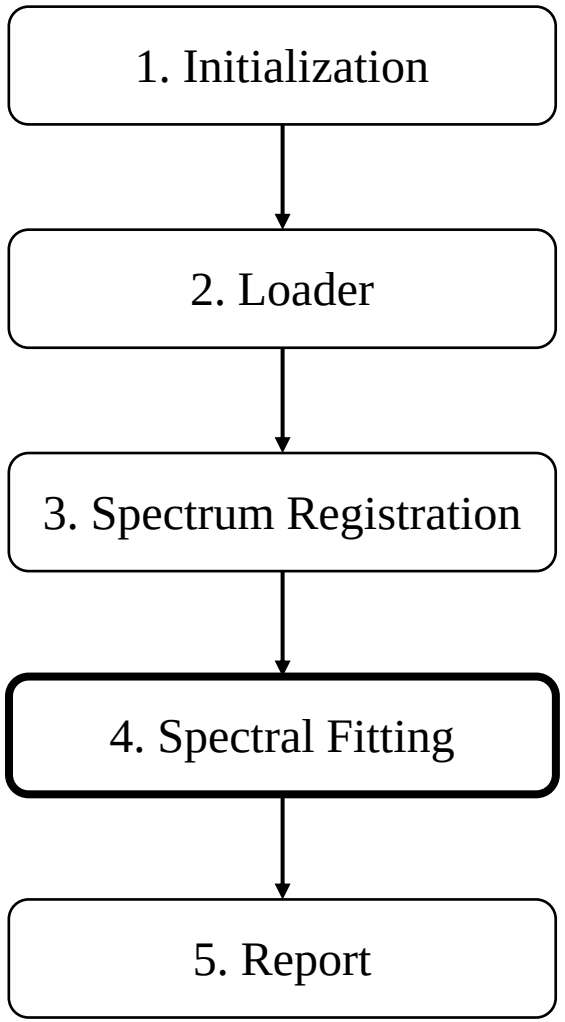








J-difference Editing Toolkit (JET)



Incoming data: Non-edited OFF spectra and the edited DIFF spectra (contains GABA).

Goal: Estimate metabolite levels.

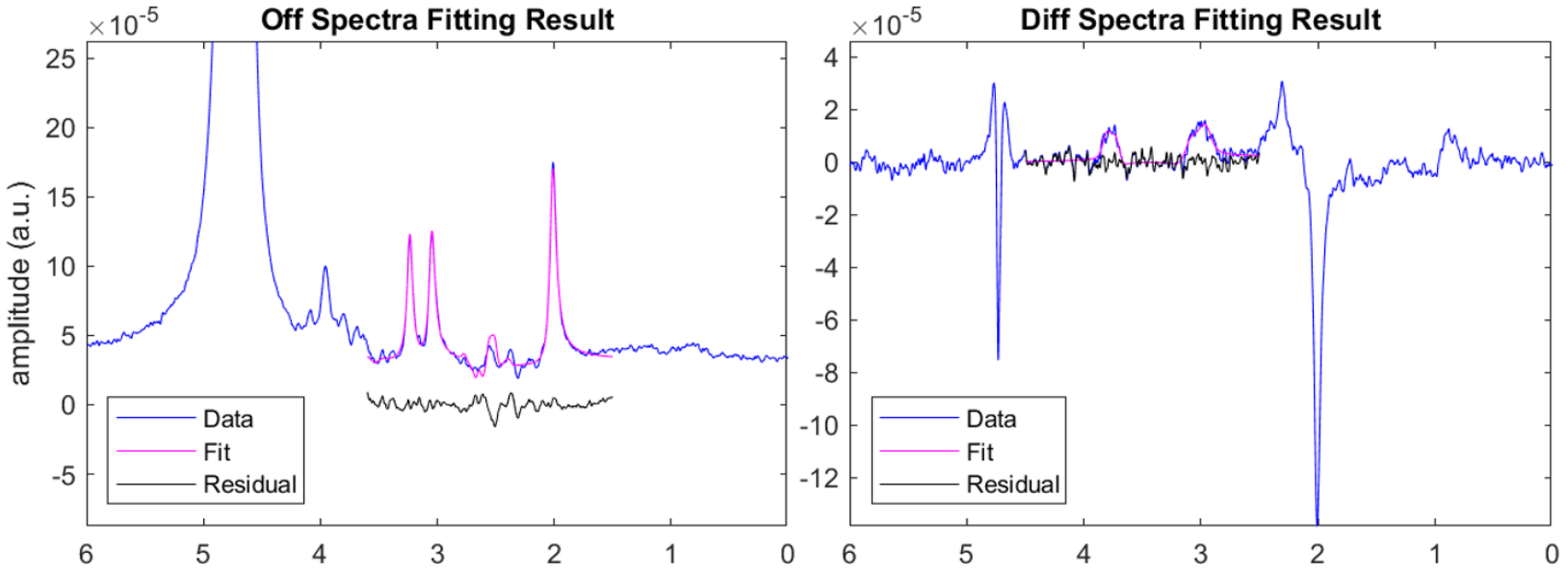
Method:

- Spectral quantification is performed by solving a separable nonlinear least-squares fitting problem with simulated metabolite basis sets (de Graaf, 2011), which was numerically solved using a modified variable-projection procedure (VARPRO) (Poullet, 2007).
- Five metabolites were assigned and quantified: N-acetylaspartate (NAA), Creatine (CR), choline (CHO), Gamma aminobutyric acid (GABA), and GLX (glutamate+glutamine).
- The fitting error, i.e. the standard deviation of the fitting residual, was calculated for each metabolite.
- For GABA, co-edition of macromolecule was not taken into account, so that only GABA+ was obtained.
- JET can further calculated the GABA ratios such as GABA+/GLX and GABA+/CR for cross-subject comparision.

Outcome: Estimated metabolite levels.

J-Editing Toolkit (JET)

1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report



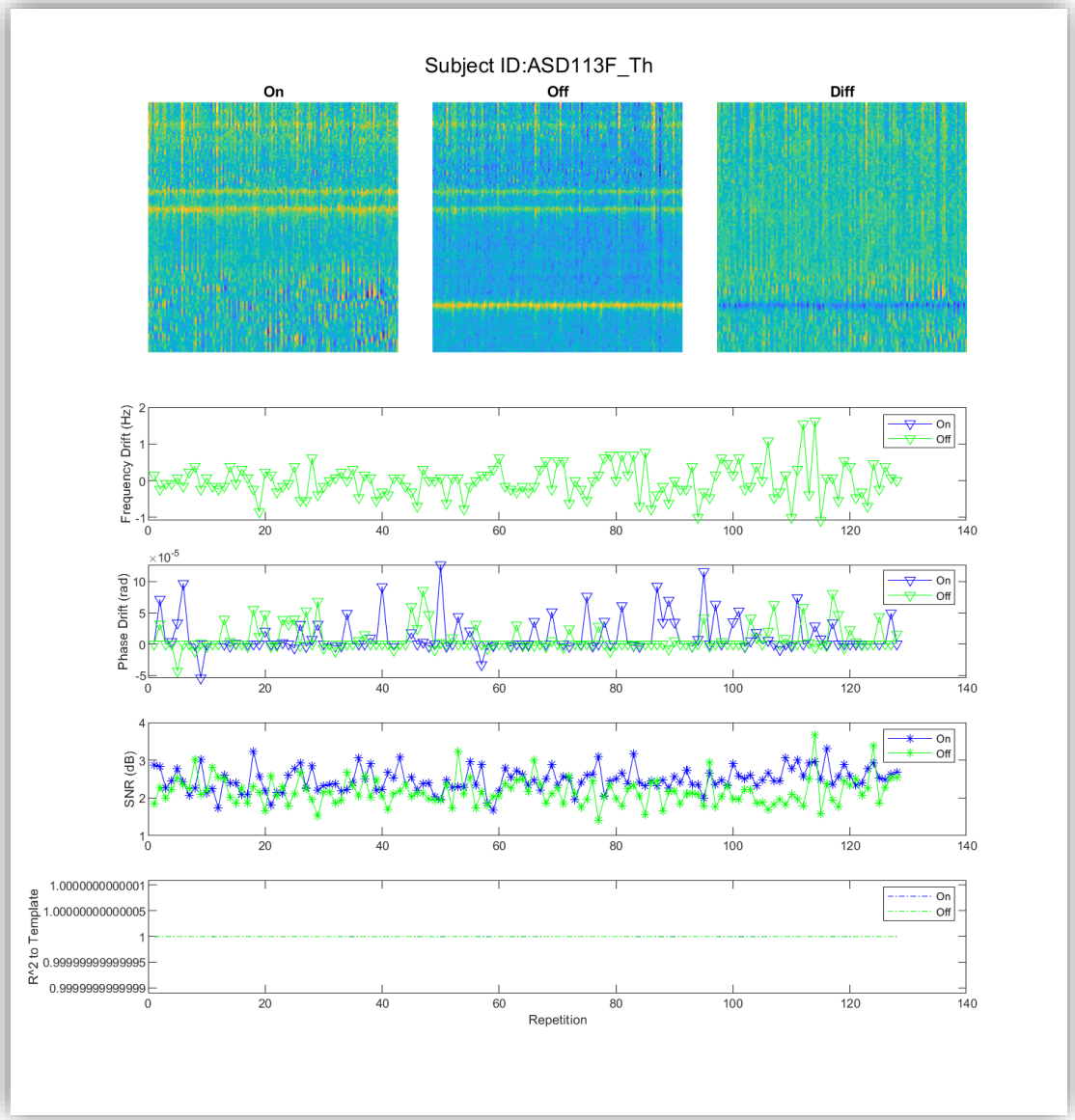
Metabolite	Amplitude	SNR(dB)	SNR(H/std(N))	SNR(A/std(N))	GOF(NMSE)
Cho	9.7359e-07	4.0165	33.6166	11555.9685	99.0973%
Cr	1.5341e-06	4.0165	41.0069	21918.1773	99.1412%
NAA	1.6447e-06	4.2103	61.4459	18442.5166	99.6693%

Metabolite	Amplitude	SNR(dB)	SNR(H/std(N))	SNR(A/std(N))	GOF(NMSE)
Glx	1.6026e-07	0.93403	4.4951	2281.8776	82.3482%
GABA	2.7958e-07	1.5761	5.8121	4125.4703	82.6532%

J-Editing Toolkit (JET)

1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report

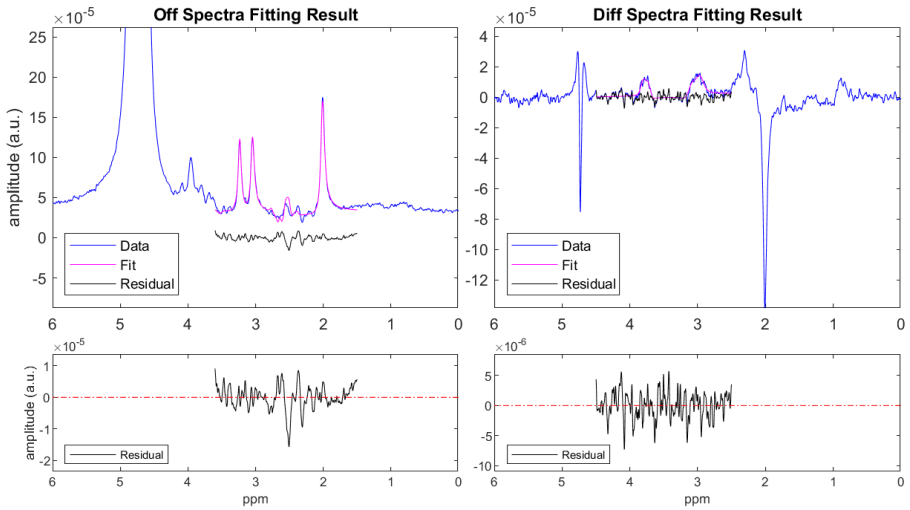
Quality Assurance Summary Report



J-Editing Toolkit (JET)

1. Initialization
2. Loader
3. Spectrum Registration
4. Spectral Fitting
5. Report

Metabolite Quantification Summary Report



Metabolite	Amplitude	SNR(dB)	SNR(H/std(N))	SNR(A/std(N))	GOF(NMSE)
Cho	9.7359e-07	4.0165	33.6166	11555.9685	99.0973%
Cr	1.5341e-06	4.0165	41.0069	21918.1773	99.1412%
NAA	1.6447e-06	4.2103	61.4459	18442.5166	99.6693%

Metabolite	Amplitude	SNR(dB)	SNR(H/std(N))	SNR(A/std(N))	GOF(NMSE)
Glx	1.6026e-07	0.93403	4.4951	2281.8776	82.3482%
GABA	2.7958e-07	1.5761	5.8121	4125.4703	82.6532%

Metabolite	Amplitude Ratio	Metabolite	Amplitude Ratio	Metabolite	Amplitude Ratio
Glx/Cho	0.16461	Glx/Cr	0.10446	Glx/NAA	0.097439
GABA/Cho	0.28717	GABA/Cr	0.18224	GABA/NAA	0.16999