

Indirect Hard Modelling, in Python

*Author:*

Francesco Bruno, Letizia Fiorucci

Version: 1.1.0

Documentation release date:

May 16, 2024



# Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>User guide</b>	<b>2</b>
2.1	Installation . . . . .	2
2.2	Make the deconvolution of the spectra . . . . .	2
2.3	Writing the input file . . . . .	5
2.4	Starting the fit . . . . .	8
2.5	Results . . . . .	9
<b>3</b>	<b>How does PYIHM work</b>	<b>10</b>
3.1	Details about peak simulation . . . . .	10
3.2	Why the fit is in two steps? . . . . .	11
<b>4</b>	<b>List of modules and functions</b>	<b>13</b>
4.1	MODULE input_reading . . . . .	13
4.1.1	input_reading.read_input . . . . .	13
4.1.2	input_reading.read_input_file . . . . .	14
4.1.3	input_reading.select_regions . . . . .	15
4.2	MODULE spectra_reading . . . . .	16
4.2.1	spectra_reading.Multiplet . . . . .	16
4.2.2	spectra_reading.Spectr . . . . .	17
4.2.3	spectra_reading.main . . . . .	19
4.3	MODULE gen_param . . . . .	20
4.3.1	gen_param.as_par . . . . .	20
4.3.2	gen_param.main . . . . .	21
4.3.3	gen_param.multiplet2par . . . . .	22
4.3.4	gen_param.singlet2par . . . . .	23
4.4	MODULE fit_mixture . . . . .	24
4.4.1	fit_mixture.calc_spectra . . . . .	24
4.4.2	fit_mixture.calc_spectra_obj . . . . .	25
4.4.3	fit_mixture.f2min . . . . .	26
4.4.4	fit_mixture.f2min_align . . . . .	27
4.4.5	fit_mixture.main . . . . .	28
4.4.6	fit_mixture.main . . . . .	29
4.4.7	fit_mixture.pre_alignment . . . . .	30
4.4.8	fit_mixture.save_data . . . . .	31
4.4.9	fit_mixture.write_output . . . . .	32
4.5	MODULE plots . . . . .	33
4.5.1	plots.convergence_path . . . . .	33
4.5.2	plots.plot_iguess . . . . .	34
4.5.3	plots.plot_output . . . . .	35

4.6	MODULE GUIs . . . . .	36
4.6.1	GUIs.cal_gui . . . . .	36
4.6.2	GUIs.calc_spectra . . . . .	37
4.6.3	GUIs.select_regions . . . . .	38



# 1. Introduction

pyIHM is a python software designed in order to offer a comprehensive interface to perform quantitative analyses on NMR spectra of mixtures, using the Indirect Hard Modelling<sup>1</sup> approach.

The Indirect Hard Modelling consists into performing a deconvolution of the spectrum of the mixture using the spectra of the individual components as basis set. Conceptually, the algorithm is made of four steps:

1. fit the spectra of the components of the mixture with a hard model (e.g. Voigt);
2. read and process the spectrum of the mixture;
3. make the initial guess using the set of peaks generated at point 1;
4. get the relative concentrations of the components in the mixture.

The routines for reading and processing of the spectra and for the generation of the models rely on the KLASSEZ<sup>2</sup> package.

---

<sup>1</sup>Ernesto Kriesten et al. “Fully automated indirect hard modeling of mixture spectra”. In: *Chemometrics and Intelligent Laboratory Systems* 91.2 (2008), pp. 181–193; Anton Duchowny et al. “Quantification of PVC plasticizer mixtures by compact proton NMR spectroscopy and indirect hard modeling”. In: *Analytica Chimica Acta* 1229 (2022), p. 340384.

<sup>2</sup>KLASSEZ: a package for the management of NMR data. 2023. URL: <https://github.com/MetallerTM/klassez>.

## 2. User guide

### 2.1 Installation

pyIHM can be installed from the associated PyPI repository using `pip` from the command line by typing:

---

```
pip install pyihm
```

---

Alternatively, it is possible to download the `.whl` file, located in the `dist/` folder of the GitHub repository, and install it with `pip`:

---

```
pip install <filename>.whl
```

---

The dependencies of the program are downloaded and installed automatically.

### 2.2 Make the deconvolution of the spectra

A script for the deconvolution of the spectra is provided in table 2.1. It uses the `KLASSEZ` package to read, process and deconvolve the spectrum. The script must be edited in order to adapt the specific user's need. At the end of the run, the `.fvf` file will be saved in the folder of the spectrum. Alternatively, one can set a custom filename, for saving the `.fvf` files in different locations.

If you do not have an experimental spectrum of one (or more) component, you can simulate it with `KLASSEZ`. You have to produce an input file like the one in table 2.2, then use it in the given script. This generates a `.fvf` in the current working directory.

**Table 2.1:** Script for creating a .fvf file, to be used as input for pyIHM.

---

```

#!/usr/bin/env python3

import sys
import klassez as kz

filename = sys.argv[1] # Spectrum
spect = sys.argv[2] # Format
custom_filename = None # Custom filename for the files

# Read the spectrum
S = kz.Spectrum_1D(filename, spect=spect)
# Do FT
S.process()
# Set "if 1" to phase correct
if 0:
    S.adjph()

# Create/read the initial guess for the deconvolution
S.F.iguess(input_file=custom_filename)

# Perform the fit...
S.F.dofit( # ...with the following options:
    u_tol=0.2, # variation on chemical shift /ppm
    f_tol=2, # variation of FWHM /Hz
    vary_phase=False, # Phase correction on the peaks
    vary_xg=True, # Fraction of gaussianity
    filename=custom_filename # Makes <custom_filename>.fvf
)

# Save the figures of the fit, with the residuals
S.F.plot('result', show_res=True, res_offset=0.1, filename=custom_filename)

```

---



**Table 2.2:** Example of input file for `kz.Spectrum_1D`, used to simulate the spectrum of a component. The file consists of two sections. In the first one, one must declare the experimental parameters to set up a virtual experiment, writing them in a `<key> <value>` format. Then, the parameters of the signals follow. They must be declared as a sequence of comma-separated values (`<key> <value 1>, <value 2>, <value 3>, ...`). KLASSEZ is able to simulate multiplets according to their splitting structure, with the given scalar coupling constants. This file should be used in the script provided at the bottom, for the conversion to a `.fvf` file to be used in `pyIHM`.

Input file:

---

```
## PARAMETERS OF THE VIRTUAL SPECTROMETER
BO 16      # Magnetic field /T
nuc 1H     # Observed nucleus
olp 4.7    # Carrier position /ppm
SWp 50     # Spectral window /ppm
TD 2**16   # Number of sampled complex points

## PARAMETERS OF THE SIGNALS
# Chemical shifts /ppm
shifts 4.69, 3.22, 2.79, 8.36, 12.69, 8.43, 4.96, 3.30, 3.15, 1.53
# FWHM /Hz
fwhm 2, 2, 2, 2, 2, 2, 2, 2, 2, 2
# Intensities (area) of the signals, i.e. the number of nuclei the signals integrate for
amplitudes 1, 1, 1, 1, 1, 1, 1, 1, 1, 3
# Fraction of Gaussianity (0 = pure Lorentzian, 1 = pure Gaussian)
x_g 0, 0, 0, 0, 0, 0, 0, 0, 0, 0
# Multiplet structure: s = singlet, d = doublet, t = triplet, q = quartet
mult dqd, dd, dd, s, s, d, ddd, dd, dd, d
# Scalar coupling constants /Hz. They must match the correspondent multiplet (e.g. mult=ddt requires three J constants)
Jconst [11.5, 3.5, 6.3], [17.5, 11.5], [17.5, 3.5], 0, 0, 6.9, [6.9, 7.4, 5.4], [14.2, 5.4], [14.2, 7.4], 6.3
```

---

Script:

---

```
#!/usr/bin/env python3

import sys
import klassez as kz

filename = sys.argv[1] # Path to the input file

# Read the spectrum
S = kz.Spectrum_1D(filename, isexp=False)
# Do FT
S.process()
# Check if the spectrum looks like it should
S.plot()
# Create <filename>.fvf file
S.to_vf()
```

---

## 2.3 Writing the input file

The input file for PYIHM is a plain text file that consists in a series of keywords, that act as separators, followed by their arguments in the next lines. The sections of the file, identified by these keywords, are separated by **ONE** empty line.

A template for the input file is shown in table 2.3. The order does not matter. Not all of them are mandatory!

A detailed explanation of the keyword meanings and the syntax of the related parameters follows. The mandatory keywords are marked with a '\*' sign, whereas the default value for the optional ones is reported after a '&'.

- **BASE\_FILENAME\***  
Root of the name of all files that the program will save. It can also be a relative/absolute path.
- **MIX\_PATH\***  
Path to the input spectrum (raw). The folder/file to be read is the first argument, followed by comma-separated additional parameters. It is very important to specify the spectrometer format to allow proper reading, using the `spect='format'` keyword. The accepted formats are: `bruker` for Bruker, `varian` for Varian/Agilent, `magritek` for SpinSolve benchtop, `oxford` for Oxford Instruments and general `.jdx` files.
- **PROC\_OPTS**  
Processing options for the mixture spectrum.
  - `wf & wf: no`  
Window function options. Syntax: `wf: <mode>, <option>=<value>`. Examples:
    - \* Exponential modulation: `wf: lb, lb=<broadening factor /Hz>`
    - \* Squared sine bell: `wf: qsin, ssb=2`
    - \* Lorentzian to Gaussian: `wf: gb, lb=-<sharpening factor /Hz>, gb=<gaussian modulation /Hz>`
  - `zf & Do not write`  
Zero-filling option. Syntax: `zf: <final shape>`
  - `blp & Do not write`  
Backward linear prediction. Syntax: `blp: pred=<number of points to predict & 1>, order=<number of lp coefficients & 8>, N=<number of points of the FID to use & 2048>`
  - `pkn1 & Do not write`  
Correct the effect of the group delay with a 1st order phase correction. No extra options required.
  - `adjph & Do not write`  
Apply manual phase correction on the spectrum. No extra options required.
- **MIX\_SPECTRUM\_TXT & None**  
Path to a plain text file that contains the intensity values of the real part of the spectrum. This has to be set if the mixture spectrum was processed with an external software: in this way you can use your own. Note that calibration of the chemical shift scale will have no effect. The use of this keyword overwrites all **PROC\_OPTS**.
- **COMP\_PATH\***  
List of the `.fvf` files that contain the parameters of the signals of the components, generated by `KLASSEZ`. See section 2.2 for details. Write one path per row. After the filename, place

a comma and write the number of nuclei that the spectrum integrates, followed by an 'H'.  
Example: `component1.fvf, 10H`

- **FIT\_LIMITS** & Interactive selection with GUI

Limits of the fitting region, in ppm, separated by a comma. Multiple regions can be selected by writing them in multiple lines. If this parameter is not set in the input file, the program starts a GUI to select them interactively.

- **FIT\_BDS\***

Tolerances for the parameters during the fit.

- **utol**: tolerance for the chemical shifts, in ppm. Given the starting chemical shift  $\delta$ , they will vary in the interval  $[\delta - \text{utol}, \delta + \text{utol}]$ . If one of the boundaries happens to fall out the fitting window, the limit of the fitting window is used instead.
- **utol\_sg**: tolerance for the chemical shifts of the signals within the same group, in ppm. Given the starting chemical shift  $\delta$ , they will vary in the interval  $[\delta - \text{utol\_sg}, \delta + \text{utol\_sg}]$ .
- **stol**: tolerance for the linewidths. Given the starting linewidth  $\Gamma$ , in Hz, they will vary in the interval  $[\Gamma - \text{stol}, \Gamma + \text{stol}]$ . If the lower boundary happens to be negative, 0 is used instead.
- **ktol**: tolerance for the relative intensities of the signals in the same spectrum. Given the starting intensity  $k$ , they will vary in the interval  $[k - \text{ktol}, k + \text{ktol}]$ . If the lower boundary happens to be negative, 0 is used instead.

- **FIT\_KWS** & `method='leastsq', max_nfev=10000, tol=1e-5`

Parameters for `lmfit.Minimizer.minimize`.

- **PLT\_OPTS** & `ext='tiff', dpi=300`

Set specific resolution (`dpi`) and format (`ext`) for the figures that will be saved.

**Table 2.3:** Example of the input file, used to run the test located in the `test/` folder of the GitHub repository.

---

```

BASE_FILENAME
mix

MIX_PATH
test_spectrum.fid, spect='varian'

PROC_OPTS
wf: em, lb=1
zf: 2**16
adjph

COMP_PATH
comp/bzac.fvf, 5H
comp/dmso.fvf, 6H
comp/EC.fvf, 4H

FIT_BDS
utol=0.1
utol_sg=0.01
stol=5
ktol=0.01

FIT_KWS
method='leastsq', tol=1e-5, max_nfev=10000

PLT_OPTS
ext=png, dpi=600

FIT_LIMITS
8.032, 7.858
7.676, 7.437
4.548, 4.412
2.553, 2.426

```

---

## 2.4 Starting the fit

The software can be operated from the command line by typing:

---

```
python3 -m pyihm --input <input_file> <options>
```

---

where `<input_file>` is the path to the input file that contains the parameters for the run, and `<options>` are flags for specific functions (see below).

Multiple input files can be given at once, writing their paths in sequence without punctuation signs between them.

---

```
python3 -m pyihm --input <input_file_1> <input_file_2> <input_file_3> <options>
```

---

Here, the possible options for a PYIHM run follow:

- `--debug`: during the fitting routines, a figure that shows how the optimization process is going is saved in the current working directory and updated every 20 iterations.
- `--cal`: before to start the fit, the initial guess can be refined with a dedicated GUI, that allows to shift the spectra to correct for field drifts, and provide a better estimation of the starting intensities.
- `--opt_method`: optimization method for the core fit of pyIHM
  - `tight` (default): two-step optimization, first with Nelder-Mead simplex and then with Levenberg-Marquardt least-squares
  - `fast`: single-step optimization with Levenberg-Marquardt least-squares
  - `custom`: reads the 'FIT\_KWS' section of the input file, and performs the optimization accordingly
- `--help`: displays this message on the terminal.

## 2.5 Results

The following table contains a summary of the files saved by pyIHM at the end of each run.

Directory	Filename	Notes
Current working directory	<filename>.out	Summary of the fit result, which includes the composition of the mixture and the parameters of all the peaks.
<filename>-DATA	<filename>_iguess.csv	Initial guess. The columns contain, respectively: the ppm scale, the mixture spectrum, the total fitting function, and the simulated components.
	<filename>_align.csv	Spectra after the alignment fit. The columns contain, respectively: the ppm scale, the mixture spectrum, the total fitting function, and the simulated components.
	<filename>_result.csv	Spectra after the final fit. The columns contain, respectively: the ppm scale, the mixture spectrum, the total fitting function, and the simulated components.
	<filename>.cnvg	Convergence pathway, i.e. the value of the target function of the main fit as function of the iteration step.
<filename>-FIGURES	<filename>_iguess.<ext>	Initial guess. The spectra relative to different components are drawn in different colors.
	<filename>-align_total.<ext>	Spectra after the alignment fit, only total trace, with residuals.
	<filename>-align_wcomp.<ext>	Spectra after the alignment fit, highlighted with different colors, without residuals.
	<filename>-align_rhist.<ext>	Histogram of the residuals of the alignment fit, compared to a Gaussian curve computed with the mean and standard deviation of the residuals themselves.
	<filename>_total.<ext>	Spectra after the final fit, only total trace, with residuals.
	<filename>_wcomp.<ext>	Spectra after the final fit, highlighted with different colors, without residuals.
	<filename>_rhist.<ext>	Histogram of the residuals of the final fit, compared to a Gaussian curve computed with the mean and standard deviation of the residuals themselves.
	<filename>_cnvg.<ext>	Convergence path, i.e. $\log_{10}$ of the value of the target function as function of the iteration step.

## 3. How does PYIHM work

### 3.1 Details about peak simulation

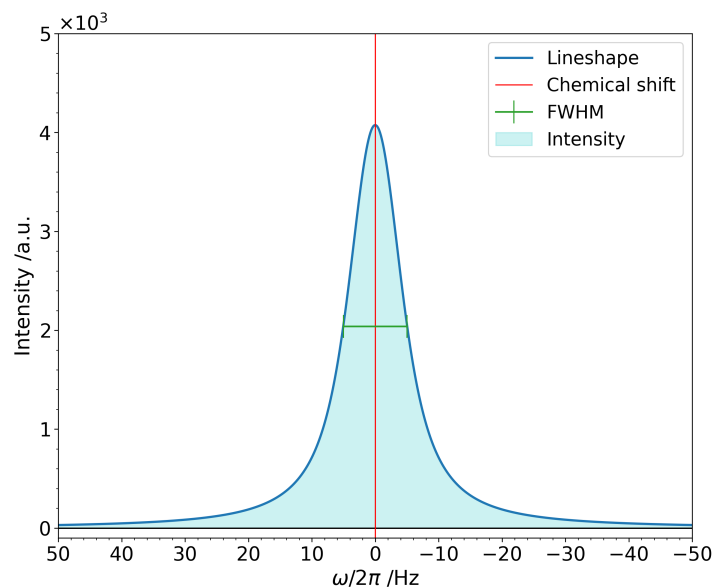
pyIHM represent a spectrum as a collection of `kz.Peak` objects. This means that they are simulated in the time domain with the Voigt model, a mixed Lorentzian-Gaussian lineshape:

$$s^{\text{Voigt}}(t) = I \exp[i\omega t] \exp[-(1 - \beta)\Gamma t/2] \exp[-\beta\sigma^2 t^2/2] \quad \sigma = \frac{\Gamma}{2\sqrt{2\ln 2}}$$

Each peak is described by four parameters:

- the position of the peak,  $\omega$ , which translates in the chemical shift;
- the linewidth, or better, the full-width at half-maximum,  $\Gamma$ ;
- the intensity,  $I$ ;
- the fraction of gaussianity,  $\beta$ , which defines the lineshape.

The fifth parameter, the phase of the peak, is not included in this implementation, as the mixture spectrum is supposed to be phased before to start the fit. Figure 3.1 shows the impact of the aforementioned parameters on the final appearance of the peak, after the Fourier transform.



**Figure 3.1:** Simulated signal with a Voigt model after Fourier transform. The feature of the signal associated with the Voigt parameters are highlighted with different colors.

When we simulate an entire spectrum as sum of peaks, in order to make the model as general as possible, we factorize it as:

$$s^{\text{mixture}}(t) = I^{\text{tot}} \sum_{k=1}^{\# \text{ peaks}} K_k s^{\text{Voigt}}(t | \omega_k, \Gamma_k, \beta_k)$$

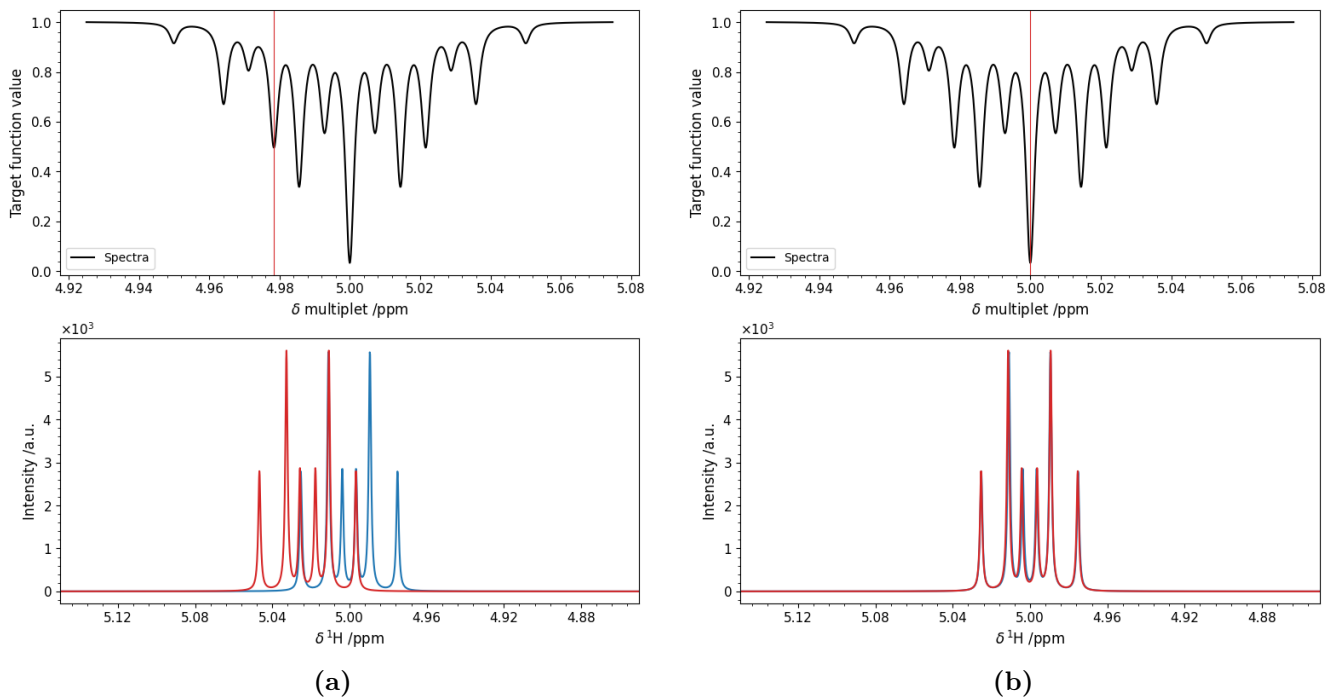
where  $K_k$  is the relative intensity of the  $k$ -th peak, such that  $\sum_{k=1}^{\# \text{ peaks}} K_k = 1$ .

## 3.2 Why the fit is in two steps?

The biggest problem one encounters in a simulation of this kind is the alignment of the chemical shifts.

Let us suppose that we know the structure of the multiplet and the relative intensities of the splitted features. If we try to find the correct 'central' chemical shift that describes the multiplet with a grid-search algorithm, we can draw the error surface associated to this parameter. Figure 3.2 depicts the problem very clearly: a little misalignment between the experimental and calculated signal translates in a local minimum of the error surface, resulting in a sudden arrest of the searching algorithm. Depending on the fine structure of the signal, the actual shape of the error surface may change, but its roughness remains an ubiquitous characteristic.

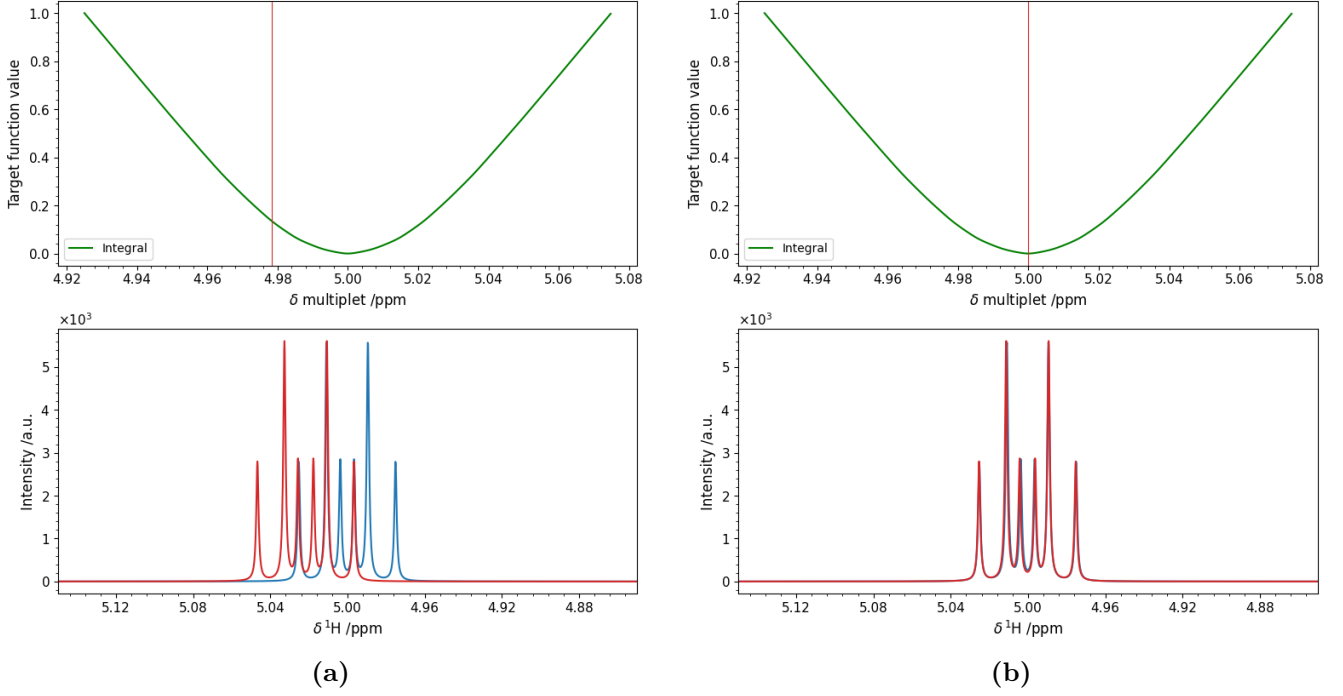
In order to find the correct alignment, it is therefore needed to employ a target function that gives rise to a smoother error surface. Figure 3.3 shows the error surface  $\varphi^{\text{align}}(\delta)$  computed as the difference between the integral (i.e. the cumulative sum) of the experimental and calculated spectrum.



**Figure 3.2:** Simulated multiplet at 700 MHz  $^1\text{H}$  Larmor frequency, centered at 5.00 ppm, with doublet of triplets fine structure ( $J_d = 15$  Hz,  $J_t = 10$  Hz). In the bottom panels, the experimental multiplet is drawn in blue, and the calculated one in red. The target function, calculated as the sum of the squared difference between the red and the blue trace, is sketched in black in the top panels, with a red line that marks the current value of the investigated parameter.

Of note, the alignment fit with this latter target function is insensitive to linewidth overestimates. This means that a model with broader signals than the experimental spectrum will be aligned correctly at the end of the fit. The same cannot be said for sure for a model with narrower signals.





**Figure 3.3:** Simulated multiplet at 700 MHz  $^1\text{H}$  Larmor frequency, centered at 5.00 ppm, with doublet of triplets fine structure ( $J_d = 15$  Hz,  $J_t = 10$  Hz). In the bottom panels, the experimental multiplet is drawn in blue, and the calculated one in red. The target function, calculated as the sum of the squared difference between the integrals of the red and the blue trace, is sketched in green in the top panels, with a red line that marks the current value of the investigated parameter.

Technically speaking, the alignment fit is done by blocking all the parameters except for the chemical shifts. Taken the experimental spectrum  $y$ , the model spectrum computed with only chemical shifts,  $y_c = M(\vec{\omega})$ , and their cumulative sum  $Y$  and  $Y_c$  respectively, the target function is computed as:

$$\varphi(\vec{\omega}) = \sum_{\text{points}} [A(Y - Y_c) + q]^2$$

where  $A$  and  $q$  are the factors that satisfy the least-squares conditions:

$$A = \frac{\langle Y_c Y \rangle - \langle Y_c \rangle \langle Y \rangle}{\langle Y_c^2 \rangle - \langle Y_c \rangle^2} \quad q = \frac{\langle Y_c \rangle^2 \langle Y \rangle - \langle Y_c \rangle \langle Y_c Y \rangle}{\langle Y_c^2 \rangle - \langle Y_c \rangle^2}$$

Once the chemical shifts are aligned, the optimization of the classic target function (i.e.  $\varphi = \sum (y - y_c)^2$ ) is straightforward. The only feature that needs a little bit of explanation is how the chemical shifts of multiplets are treated. We decided not to hard-model a fine structure with the proper splitting given by multiplication of the FID times  $\cos(2\pi J)$ , hence optimizing the  $J$  constants during the fit, because of the possible imperfections that might be present in the experimental dataset, especially at low fields. Therefore, peaks in the same spectrum that have the same 'group' attribute are recognized as part of the same multiplet.

Let us suppose that we have a multiplet composed of  $M$  features. Then, in the dictionary of parameters, the key ' $U$ ' identifies the central chemical shift of the multiplet, whereas the keys  $o_j$  for  $j = 1, \dots, M$  are the *offset* of the  $j$ -th feature of the multiplet with respect to  $U$ . The parameters  $u_j$ , i.e. the actual chemical shifts of the signals, are not optimized, but computed on the fly during the fitting as  $u_j = U + o_j$ .

In this framework, the  $U$  parameters are treated as singlets, and therefore obey the `utol` boundaries. By contrast, the  $o_j$  parameters are more or less fixed with respect to their  $U$ , hence they move according to the `utol_sg`  $\leq$  `utol` boundaries.

## 4. List of modules and functions

### 4.1 MODULE `input_reading`

#### 4.1.1 `input_reading.read_input(filename)`

Reads the input file to get all the information to perform the fit. The values read from the file are double-checked, and the missing entries are replaced with default values, so not to leave space to stupid mistakes.

**Parameters:**

- `filename`: *str*  
Path to the input file

**Returns:**

- `base_filename`: *str*  
Root of the name of all the files that the program will save
  - `mix_path`: *str*  
Path to the mixture spectrum
  - `mix_kws`: *dict of keyworded arguments*  
Additional instructions to be passed to `kz.Spectrum_1D.__init__`
  - `mix_spectrum_txt`: *str or None*  
Path to a .txt file that contains a replacement spectrum for the mixture
  - `comp_path`: *list*  
Path to the .fvf files to be used for building the spectra of the components
  - `fit_lims`: *tuple*  
Limits of the fitting region, in ppm
  - `fit_bds`: *dict*  
Boundaries for the fitting parameters. The keywords are:
    - `utol` = allowed displacement for singlets and whole multiplets, in ppm (absolute)
    - `utol_sg` = allowed displacement for the peaks that are part of the same multiplet relatively to the center, in ppm (absolute)
    - `stol` = allowed variation for the linewidth, in Hz (relative)
    - `ktol` = allowed variation for the relative intensities within the same spectrum (relative)
-

### 4.1.2 `input_reading.read_input_file(filename)`

Runs over the input file, looks for specific keywords, and interpret them accordingly.

#### Parameters:

- filename: *str*  
Path to the input file

#### Returns:

- dic: *dict*  
Read values, organized
-

### 4.1.3 `input_reading.select_regions(ppm_scale, spectrum, full_calc)`

Interactively select the slices that will be used in the fitting routine.

#### Parameters:

- `ppm_scale`: *1darray*  
ppm scale of the spectrum
- `spectrum`: *1darray*  
Spectrum of the mixture

#### Returns:

- `regions`: *list of tuple*  
Limits, in ppm
-

## 4.2 MODULE spectra\_reading

### 4.2.1 spectra\_reading.Multiplet

class

Class that represent a multiplet as a collection of peaks.

#### Attributes:

- `acqu`: *dict*  
Dictionary of acquisition parameters
- `peaks`: *dict*  
Dictionary of `kz.fit.Peak` objects
- `U`: *float*  
Mean chemical shift of the multiplet
- `u_off`: *dict*  
Chemical shift of the components of the multiplet, expressed as offset from `self.U`

#### Methods:

`__init__(self, acqu, *peaks)`

Initialize the class.

#### Parameters:

- `acqu`: *dict*  
Dictionary of acquisition parameters
- `peaks`: *kz.fit.Peak objects*  
Peaks that are part of the multiplet. They must have an attribute `'idx'` which serves as label

`__call__(self)`

Compute the trace correspondant to the multiplet.

#### Returns:

- `trace`: *1darray*  
Sum of the components

`par(self)`

Computes a summary dictionary of all the parameters of the multiplet.

#### Returns:

- `dic`: *dict of dict*  
The keys of the inner dictionary are the parameters of each single peak, the outer keys are the labels of the single components

## 4.2.2 spectra\_reading.Spectr

class

Class that represents a spectrum as a collection of peaks and multiplets.

### Attributes:

- **acqu:** *dict*  
Acquisition parameters
- **peaks:** *dict*  
Dictionary of peaks object, labelled according to the 'idx' attribute of each single peak
- **unique\_groups:** *list*  
Identifier labels for the multiplets, without duplicates
- **p\_collections:** *dict*  
Dictionary of `kz.fit.Peak` and `Multiplet` objects, labelled according to the group they belong to. In particular, `self.p_collections[0]` is a list of `kz.fit.Peak` objects, whereas all the remaining entries consist of a single `Multiplet` object.
- **total:** *1darray*  
Placeholder for the trace of the spectrum, as sum of all the peaks.

### Methods:

**\_\_init\_\_(self, acqu, \*peaks)**

Initialize the class.

#### Parameters:

- **acqu:** *dict*  
Dictionary of acquisition parameters
- **peaks:** *kz.fit.Peak objects*  
Peaks that are part of the multiplet. They must have an attribute 'idx' which serves as label

**\_\_call\_\_(self, I=1)**

Compute the total spectrum, multiplied by I.

#### Parameters:

- **I:** *float*  
Intensity value that multiplies the spectrum

#### Returns:

- **total:** *1darray*  
Computed spectrum

**calc\_total(self)**

Computes the sum of all the peaks to make the spectrum

**Returns:**

- total: *1darray*  
Computed spectrum
-

### 4.2.3 spectra\_reading.main(M, spectra\_dir, Hs, lims=None)

Reads the .fvf files, containing the fitted parameters of the peaks of a series of spectra. Then, computes a list of Spectr objects with those parameters, and returns it. The relative intensities are referred to the total intensity of the whole spectrum, not to the ones of the fitted regions. Employs `kz.fit.read_vf` to read the .fvf files and generate the parameters.

#### Parameters:

- M: *kz.Spectrum\_1D* object  
Mixture spectrum. Used to get the spectral parameters for the `kz.fit.Peak` objects
- spectra\_dir: *list of str*  
Sequence of the locations of the .fvf files to be read
- lims: *tuple*  
Borders of the fitting window, in ppm (left, right)

#### Returns:

- collections: *list of Spectr objects*  
Spectra of pure components, treated as collections of peaks.
-



## 4.3 MODULE `gen_param`

### 4.3.1 `gen_param.as_par(name, value, lims=0, rel=True, minthresh=None)`

Creates a `lmfit.Parameter` object using the given parameters.

#### Parameters:

- `name`: *str*  
Label of the parameter
- `value`: *float or str*  
If it is float, it is the value of the parameter. If it is a str, it is put in the 'expr' attribute of the `lmfit.Parameter` object.
- `lims`: *float or tuple*  
Determines the boundaries. If it is a tuple, the boundaries are `min(lims)` and `max(lims)`. If it is a single float, the boundaries are `(value-lims, value+lims)`. Not read if value is str
- `rel`: *bool*  
Relative boundaries. If it is True and lims is a float, the boundaries are set to `value-lims*value`, `value+lims*value`.
- `minthresh`: *float*  
If given, overwrite the minimum threshold with this value, if the calculated one is lower than it.

#### Returns:

- `p`: *lmfit.Parameter object*  
Object created according to the given parameter
-

### 4.3.2 `gen_param.main(M, components, bds, lims, Hs)`

Create the `lmfit.Parameters` objects needed for the fitting procedure.

#### Parameters:

- `M`: *kz.Spectrum\_1D* object  
Mixture spectrum
- `components`: *list*  
List of Spectra objects
- `bds`: *dict*  
Boundaries for the fitting parameters.
- `lims`: *list of tuple*  
Borders of the fitting windows, in ppm (left, right)
- `Hs`: *list*  
Number of protons each spectrum integrates for

#### Returns:

- `param`: *lmfit.Parameters* object  
Actual parameters for the fit
-

### 4.3.3 `gen_param.multiplet2par(item, spect, group, bds)`

Converts a Multiplet object into a list of `lmfit.Parameter` objects. The keys are of the form ' $S\#_p$ ' where  $\#$  is 'spect' and ' $p$ ' is the index of the peak.

- $p = U$  is the mean chemical shift
- $p = o$  is the offset from  $U$
- $p = u$  is the absolute chemical shift, computed as  $u = U + o$ , set as expression.

#### Parameters:

- item: *fit.Peak object*  
Peak to convert into Parameter. Make sure the `.idx` attribute is set!
- spect: *int*  
Label of the spectrum to which the peak belongs to
- group: *int*  
Label of the multiplet group
- bds: *dict*  
Contains the parameters' boundaries

#### Returns:

- p: *list*  
List of `lmfit.Parameter` objects
-

#### 4.3.4 `gen_param.singlet2par(item, spect, bds)`

Converts a `fit.Peak` object into a list of `lmfit.Parameter` objects: the chemical shift (u), the linewidth (s), and intensity (k). The keys are of the form '`S#_p?`' where '#' is spect and '?' is the index of the peak.

##### Parameters:

- `item`: *kz.fit.Peak object*  
Peak to convert into Parameter. Make sure the `.idx` attribute is set!
- `spect`: *int*  
Label of the spectrum to which the peak belongs to
- `bds`: *dict*  
Contains the parameters' boundaries

##### Returns:

- `p`: *list*  
List of `lmfit.Parameter` objects
-

## 4.4 MODULE `fit_mixture`

### 4.4.1 `fit_mixture.calc_spectra(param, N_spectra, acqu, N)`

Computes the spectra to be used as components for the fitting procedure, in form of lists of 1darrays. Each array is the sum of all the peaks. This function is called at each iteration of the fit.

#### Parameters:

- `param`: *lmfit.Parameters object*  
Actual parameters
- `N_spectra`: *int*  
Number of spectra to be used as components
- `acqu`: *dict*  
Dictionary of acquisition parameters
- `N`: *int*  
Number of points for zero-filling, i.e. final dimension of the arrays

#### Returns:

- `spectra`: *list of 1darray*  
Computed components of the mixture, weighted for their relative intensity
-

#### 4.4.2 `fit_mixture.calc_spectra_obj(param, N_spectra, acqu, N)`

Computes the spectra to be used as components for the fitting procedure, in form of lists of `kz.fit.Peak` objects.

##### Parameters:

- `param`: *lmfit.Parameters* object  
Actual parameters
- `N_spectra`: *int*  
Number of spectra to be used as components
- `acqu`: *dict*  
Dictionary of acquisition parameters
- `N`: *int*  
Number of points for zero-filling, i.e. final dimension of the arrays

##### Returns:

- `spectra`: *list of kz.fit.Peak* objects  
Computed components of the mixture, weighted for their relative intensity
-

### 4.4.3 `fit_mixture.f2min(param, N_spectra, acqu, N, exp, I, plims, cnvg_path, method='leastsq', debug=False)`

Function to compute the quantity to be minimized by the fit.

#### Parameters:

- `param`: *lmfit.Parameters* object  
actual parameters
- `N_spectra`: *int*  
Number of spectra to be used as components
- `acqu`: *dict*  
Dictionary of acquisition parameters
- `N`: *int*  
Number of points for zero-filling, i.e. final dimension of the arrays
- `exp`: *1darray*  
Experimental spectrum
- `I`: *float*  
Intensity correction for the calculated spectrum. Used to maintain the relative intensity small.
- `plims`: *slice*  
Delimiters for the fitting region. The residuals are computed only in this regio. They must be given as point indices
- `cnvg_path`: *str*  
Path for the file where to save the convergence path
- `debug`: *bool*  
If True, saves a figurte of the ongoing fit in the current working directory every 20 iterations

#### Returns:

- `target`: *float or 1darray*  
For Levenberg-Marquardt (`method='leastsq'`), array of the residuals, else  $\sum[(exp/I - calc)^2]$
-

#### 4.4.4 `fit_mixture.f2min_align(param, N_spectra, acqu, N, exp, plims, debug=False)`

Function to compute the quantity to be minimized by the fit.

##### Parameters:

- `param`: *lmfit.Parameters* object  
actual parameters
- `N_spectra`: *int*  
Number of spectra to be used as components
- `acqu`: *dict*  
Dictionary of acquisition parameters
- `N`: *int*  
Number of points for zero-filling, i.e. final dimension of the arrays
- `exp`: *1darray*  
Experimental spectrum
- `plims`: *slice*  
Delimiters for the fitting region. The residuals are computed only in this regio. They must be given as point indices
- `debug`: *bool*  
True for saving a figure of the ongoing fit every 20 iterations

##### Returns:

- `target`: *float*  
 $\sum[(exp - I * calc)^2]$
-



#### 4.4.5 `fit_mixture.main(M, components, bds, lims, Hs)`

Create the `lmfit.Parameters` objects needed for the fitting procedure.

##### Parameters:

- `M`: *kz.Spectrum\_1D* object  
Mixture spectrum
- `components`: *list*  
List of Spectra objects
- `bds`: *dict*  
Boundaries for the fitting parameters.
- `lims`: *list of tuple*  
Borders of the fitting windows, in ppm (left, right)
- `Hs`: *list*  
Number of protons each spectrum integrates for

##### Returns:

- `param`: *lmfit.Parameters* object  
Actual parameters for the fit
-

#### 4.4.6 `fit_mixture.main(M, N_spectra, Hs, param, lims=None, fit_kws={}, filename='fit', CAL_FLAG=False, DEBUG_FLAG=False, ext='tiff', dpi=600)`

Core of the fitting procedure. It computes the initial guess, save the figure, then starts the fit. After the fit, writes the output file and saves the figures of the result. Summary of saved files:

- '`<filename>.out`': fit report
- '`<filename>_iguess.<ext>`': figure of the initial guess
- '`<filename>_total.<ext>`': figure that contains the experimental spectrum, the total fitting function, and the residuals
- '`<filename>_wcomp.<ext>`': figure that contains the experimental spectrum, the total fitting function, and the components in different colors. The residuals are not shown
- '`<filename>_rhist.<ext>`': histogram of the residual, with a gaussian function drawn on top according to its statistical parameters.

#### Parameters:

- `M`: *kz.Spectrum\_1D* object  
Mixture spectrum
  - `N_spectra`: *int*  
Number of spectra to be used as fitting components
  - `Hs`: *list*  
Number of protons each spectrum integrates for
  - `param`: *lmfit.Parameters* object  
Actual parameters
  - `lims`: *list of tuple or None*  
Delimiters of the fitting region, in ppm. If None, the whole spectrum is used.
  - `fit_kws`: *dict of keyworded arguments*  
Additional parameters for the `lmfit.Minimizer.minimize` function
  - `filename`: *str*  
Root of the names for the names of the files that will be saved.
  - `CAL_FLAG`: *bool*  
True for adjusting the initial guess before starting the fit
  - `DEBUG_FLAG`: *bool*  
True for saving a figure of the ongoing fit every 20 iterations
  - `ext`: *str*  
Format of the figures
  - `dpi`: *int*  
Resolution of the figures, in dots per inches
-

#### 4.4.7 `fit_mixture.pre_alignment(exp, acqu, N_spectra, N, plims, param, DEBUG_FLAG=False)`

Makes a fit with all the parameters blocked, except for the chemical shifts, on the target function of the integral. Used to improve the initial guess in case of misplacements of the signals.

##### Parameters:

- `exp`: *1darray*  
Experimental spectrum
- `acqu`: *dict*  
Dictionary of acquisition parameters
- `N_spectra`: *int*  
Number of spectra to be used as components
- `N`: *int*  
Number of points for zero-filling, i.e. final dimension of the arrays
- `plims`: *list of slice*  
Delimiters for the fitting region. The residuals are computed only in these regions. They must be given as point indices
- `param`: *lmfit.Parameters object*  
actual parameters
- `DEBUG_FLAG`: *bool*  
True for saving a figure of the ongoing fit every 20 iterations

##### Returns:

- `popt`: *lmfit.Parameters object*  
Parameters with optimal chemical shifts
-

#### 4.4.8 `fit_mixture.save_data(filename, ppm_scale, exp, *opt_spectra)`

Saves the ppm scale, the experimental spectrum, the total trace and the components in .csv files, to be opened with excel, origin, or whatever.

##### Parameters:

- `filename`: *str*  
Location of the filename to be saved, without the .csv extension.
  - `ppm_scale`: *1darray*  
PPM scale of the experimental spectrum
  - `exp`: *1darray*  
Experimental spectrum, real part
  - `opt_spectra`: *sequence of 1darray*  
Spectra of the components
-

#### 4.4.9 `fit_mixture.write_output(M, I, K, spectra, n_comp, lims, filename='fit.r`

Write a report of the performed fit in a file. The parameters of the single peaks are saved using the `kz.fit.write_vf` function.

##### Parameters:

- `M`: *kz.Spectrum\_1D* object  
Mixture spectrum
  - `I`: *float*  
Absolute intensity for the calculated spectrum
  - `K`: *sequence*  
Relative intensities of the spectra in the mixture
  - `spectra`: *list of kz.fit.Peak objects*  
Computed components of the mixture, weighted for their relative intensity
  - `n_comp`: *list*  
Indices of the components of the mixture
  - `lims`: *tuple*  
Upper and lower boundaries of the fit region
  - `filename`: *str*  
Name of the file where to write the files.
-

## 4.5 MODULE plots

### 4.5.1 `plots.convergence_path(conv_path, filename='conv', ext='tiff', dpi=600)`

Makes the figures of the final fitted spectrum and saves them. Three figures are made: look at the `fitting.main` function documentation for details.

#### Parameters:

- `conv_path`: *str*  
Path to the file of the convergence path
  - `filename`: *str*  
Filename of the final figure
  - `ext`: *str*  
Format of the figure
  - `dpi`: *int*  
Resolution of the figure, in dots per inches
-

#### 4.5.2 `plots.plot_iguess(ppm_scale, exp, total, components, lims=None, X_label='$\delta$ /ppm', filename='fit', ext='tiff', dpi=600)`

Makes the figure of the initial guess and saves it.

##### Parameters:

- `ppm_scale`: *1darray*  
PPM scale of the spectrum
  - `exp`: *1darray*  
Mixture spectrum, real part
  - `total`: *1darray*  
Fitting function
  - `components`: *list of 1darray*  
Spectra used as components, real part
  - `lims`: *tuple or None*  
Delimiters of the fitting region, in ppm. If None, the whole spectrum is used.
  - `X_label`: *str*  
Label for the X\_axis
  - `filename`: *str*  
The name of the figure will be `<filename>_iguess.<ext>`
  - `ext`: *str*  
Format of the figures
  - `dpi`: *int*  
Resolution of the figures, in dots per inches
-

### 4.5.3 `plots.plot_output(ppm_scale, exp, total, components, lims=None, plims=None, X_label='$\delta$ /ppm', filename='fit', ext='tiff', dpi=600)`

Makes the figures of the final fitted spectrum and saves them. Three figures are made: look at the `fitting.main` function documentation for details.

#### Parameters:

- `ppm_scale`: *1darray*  
PPM scale of the spectrum
  - `exp`: *1darray*  
Mixture spectrum, real part
  - `total`: *1darray*  
Fitting function
  - `components`: *list of 1darray*  
Spectra used as components, real part
  - `lims`: *tuple or None*  
Delimiters of the fitting region, in ppm. If None, the whole spectrum is used.
  - `X_label`: *str*  
Label for the X\_axis
  - `filename`: *str*  
Root filename for the figures
  - `ext`: *str*  
Format of the figures
  - `dpi`: *int*  
Resolution of the figures, in dots per inches
-



## 4.6 MODULE GUIs

Module that contains graphical user interfaces.

### 4.6.1 GUIs.cal\_gui(ppm\_scale, exp, param, N\_spectra, acqu, N, I)

Corrects the chemical shifts and the intensities of the spectra to be employed during the fit.

#### Parameters:

- ppm\_scale: *1darray*  
Chemical shift scale of the spectrum
- exp: *1darray*  
Experimental spectrum
- param: *lmfit.Parameters object*  
Parameters of the fit, as generated by gen\_param
- N\_spectra: *int*  
Number of components of the mixture
- acqu: *dict*  
Dictionary of acquisition parameters
- N: *int*  
Number of points that the final calculated spectrum should have
- I: *float*  
Intensity correction for the experimental spectrum

#### Returns:

- param: *lmfit.Parameters object*  
Updated parameters
-

### 4.6.2 GUIs.calc\_spectra(param, N\_spectra, acqu, N)

Computes the spectra to be used as components for the fitting procedure, in form of lists of 1darrays. Each array is the sum of all the peaks. This function is called at each iteration of the fit.

#### Parameters:

- param: *lmfit.Parameters object*  
Actual parameters
- N\_spectra: *int*  
Number of spectra to be used as components
- acqu: *dict*  
Dictionary of acquisition parameters
- N: *int*  
Number of points for zero-filling, i.e. final dimension of the arrays

#### Returns:

- spectra: *list of 1darray*  
Computed components of the mixture, weighted for their relative intensity
-

### 4.6.3 GUIs.select\_regions(ppm\_scale, spectrum, full\_calc)

Interactively select the slices that will be used in the fitting routine.

#### Parameters:

- ppm\_scale: *1darray*  
ppm scale of the spectrum
- spectrum: *1darray*  
Spectrum of the mixture

#### Returns:

- regions: *list of tuple*  
Limits, in ppm
-