Digging Into MUD With Python:
mudpy, bdata, and bfit

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Used to store the results of muon spin rotation ($\mu$SR) measurements at TRIUMF, the Muon Data (MUD) file format serves as a useful and flexible scheme that is both lightweight and self-describing. The application programming interface (API) for these files is written in C and FORTRAN, languages not known for their ease of use. In contrast, Python is a language which emphasizes rapid prototyping and readability. This work describes three Python 3 packages to interface with MUD files and analyze their contents: mudpy, bdata, and bfit. The first enables easy access to the contents of any MUD file. The latter two are implemented specifically for the implanted-ion $\beta$-detected NMR ($\beta$-NMR) experiment at TRIUMF. These tools provide both an API and graphical user interface (GUI) to help users extract and fit $\beta$-NMR data.

I. MOTIVATION

The first muon spin rotation ($\mu$SR) measurements were recorded in 1957, at the Nevis cyclotron in the United States of America.\textsuperscript{1,2} While the field has thrived over its long history, the technique remains restricted to large nationally-supported facilities.\textsuperscript{3} Today, there are only a handful of locations capable of producing the particle beam needed to conduct $\mu$SR, including: TRIUMF, Canada; ISIS, located in the United Kingdom; PSI in Switzerland; and the Japanese facility J-PARC. The Muon Data (MUD) file format is used to store $\mu$SR data taken at TRIUMF.\textsuperscript{4} This is a self-describing binary format (i.e. not ASCII), containing the measurement data, device settings, experimental conditions such as the temperature or the magnetic field, and some metadata.

As with many older science applications, the MUD file application programming interface (API) is written in C and FORTRAN. These statically-typed and compiled languages are known for their computational efficiency, but can be difficult to work with. This is perhaps one of the reasons why scientific computing has, in many communities, shifted to more modern languages such as Python: a dynamically-typed and interpreted language. As a result, Python has amassed a massive library of data analysis tools.\textsuperscript{5-7} The primary advantage of Python is the short development time of programs written in the language. This is particularly important in the context of scientific analysis, which are typically run only a few times by select individuals. As a result, the time taken to write the analysis code is a large part of the program’s effective run time. The aim of this work is to bring this rapid prototyping style of analysis to the $\mu$SR and $\beta$-detected NMR ($\beta$-NMR) communities.

It should be acknowledged that a large body of analysis software exists to support $\mu$SR workers. Examples include WIMDA,\textsuperscript{8} an older Windows application; MANTID,\textsuperscript{9} developed by and for ISIS; and Musrfit,\textsuperscript{10} maintained by the workers at PSI. Data stored in the MUD format are compatible with Musrfit. These programs are quite powerful,\textsuperscript{11} but can be cumbersome outside of their intended scope (e.g. when developing new methods).\textsuperscript{12} The packages introduced here are very lightweight, providing a simple interface to any other Python package, allowing for a great deal of flexibility and sophistication. Like many Python packages, those described in this work are freely distributed through the Python Package Index (PyPI) and GitHub.\textsuperscript{13} This trivializes installation and maintenance by installing missing dependencies, updating packages, and providing a consistent method of version tracking. This is in stark contrast to another popularly used framework, ROOT,\textsuperscript{14} which serves as the basis for Musrfit, and whose set up process can be quite involved.

A closely related technique to $\mu$SR, $\beta$-NMR relies on the same physics principles but uses a radioactive isotope, rather than a muon. At present, the only active and permanent implanted-ion $\beta$-NMR spectrometer is at TRIUMF.\textsuperscript{15-17} Unlike $\mu$SR, $\beta$-NMR does not have an extensive suite of analysis programs well-suited to the specifics of the technique, however it still uses the MUD format as the basis of its data acquisition (DAQ) system. While there have been some recent improvements to this situation,\textsuperscript{18} the analysis required for any non-trivial $\beta$-NMR experiment necessitates the development of new code to meet the individual requirements of each experiment.\textsuperscript{19-22} The packages described in this work immensely expedite this process.

II. SOFTWARE DESCRIPTION

This work describes three Python 3 packages: mudpy, bdata, and bfit. The former is a general-purpose MUD file reader, whereas the latter two are specific to the $\beta$-NMR experiment at TRIUMF.\textsuperscript{15,16} Both mudpy and bdata serve to contribute an object layer between the file and analysis code, whereas bfit implements fitting functionality.

The mudpy package provides a wrapper for each of the
C functions in the mud_friendly API using Cython and a Python class, mdata, which automates file access, saving the contents as object attributes. MUD files store data of five different types: description, histogram, independent variable, scaler, and comment. The description type contains the file metadata and is saved directly as mdata attributes. The remainders are saved as containers organized into specialized dictionaries, as demonstrated in the example section. The histograms contain the primary data: counts from the various detectors needed to measure the nuclear spin polarization. The independent variables may contain experiment settings or measurements such as the temperature. The scalers contain information from secondary readouts of the detectors: total number of counts and the most recent reading. Comments are additional notes from the experimenters.

The bdata object inherits from mdata, providing additional functionality for variable lookup, calculation of the beta-decay asymmetry, and remote fetching of data from the archive. The bdata package also provides the classes bjoined and bmerged for concatenating and merging bdata objects, respectively.

The bfit package provides a suite of analysis tools for β-NMR experiments, accessible through both the Python API and a graphical user interface (GUI). The primary goal of the GUI is to enable inexperienced programmers and external users to do β-NMR, however, it also makes simple analyses very fast and convenient, useful even for experienced users. The GUI supports a number of features, such as: shared parameter fitting, interactive and graphical selection of initial fit parameters, assigning functional constraints to fit parameters (e.g. if a variable is a function of temperature, as is the case for Korrina relaxation), periodic fetching and redrawing of data, and displaying the file contents in a format easily compatible with the MIDAS DAQ system. bfit also supports the dynamic importing of user-defined χ^2 minimizers, allowing for the use of other codes, such as ROOT, in fitting data. The default χ^2 minimizer in bfit is a Levenberg-Marquardt algorithm when no bounds are set, or if the parameter space is bounded, then a Trust Region Reflective algorithm is used. Both are implemented using the scipy.optimize.curve_fit function. The graphical interface for bfit is provided by TkInter, and plotting functionality is implemented using Matplotlib. Numerical calculations employ the use of SciPy, NumPy, and Pandas. These packages run C or FORTRAN code under the hood, providing a huge reduction in computation time.

Given that mudpy exists only to read, write, and store the contents of files, the remainder of this work will focus on the β-NMR-specific implementations. Of critical importance is the calculation of the asymmetry of the average beta-decay direction. This discussion relates the measured asymmetry to the underlying polarization and shows how the fit functions are constructed in the case of pulsed beam measurements. Next, an overview of the global fitting method is presented. Lastly, a few illustrative examples using the three packages will be given.

### III. β-NMR POLARIZATION AND ASYMMETRY

Similar to μSR, implanted-ion β-NMR measures the nuclear spin polarization of an implanted ensemble of radioactive particles through their anisotropic beta decay. A major distinction, however, is that the lifetime (τ) of the isotopes used in β-NMR are much longer than that of the muon. For example, ^7Li, the typical β-NMR probe at TRIUMF, has τ = 1.21 s, as compared to τ = 2.2 µs for the muon. The coarser time resolution of β-NMR results in a very different analysis, despite the similarities in the physical principles.

The probability that an e^- is emitted at angle θ, relative to the spin of the probe nucleus, is

\[ W(θ) = 1 + \frac{v}{c} PA \cos(θ), \]

where \( P \) is the polarization of the nuclear ensemble, \( v \) is the speed of the emitted e^- , c is the speed of light, and \(|A| < 1 \) is an asymmetry parameter. For ^7Li, \( A = \frac{3}{8} \) and the in-flight nuclear spin polarization along the beam axis at TRIUMF is approximately 70%. The ions are implanted at an approximately constant rate, \( R_0 \), which is switched on at \( t = 0 \). Let \( N(t,t')dt' \) be the number of nuclei which arrived in the interval \( (t', t'+dt') \), and survive until time \( t \):

\[ N(t,t')dt' = R_0 \exp(-(t-t')/\tau)dt', \]

where \( \tau \) is the nuclear lifetime. The total number of nuclei in the sample at time \( t > t' \) is then

\[ N(t) = \int_0^{t'} N(t,t')dt' = R_0 \tau \left[ 1 - \exp(-t/\tau) \right]. \]

Let \( p(t,t') \) be the average polarization of an ensemble of probes implanted at \( t' \), at the moment of decay at time \( t > t' \). The simplest case is when \( p(t,t') \) is exponential, \( \exp((t-t')/\tau_1) \), however in general it may be any function of \( t \) and \( t' \). Accounting for all arrival times, the average polarization at time \( t > t' \) is

\[ P(t) = \frac{1}{N(t)} \int_0^{t'} N(t,t')p(t,t')dt' = \frac{\int_0^{t'} \exp(-(t-t')/\tau)p(t,t')dt'}{\tau \left[ 1 - \exp(-t/\tau) \right]} \]

The polarization of the implanted ensemble is measured by counting the emitted betas in the forward (\( F \)) and backward (\( B \)) directions, relative to the beam direction. If \( f(t,t')dt' \) is the number of betas detected in detector \( F \) during the time interval \( (t, t'+dt) \), then

\[ f(t,t')dt' = \frac{1}{2} N(t,t') [1 + ap(t,t')]dt', \]
where \( a \) is a constant of proportionality.\(^{35} \) The average number of betas arriving in detector \( F \) is then:

\[
\mathcal{F}(t) = \int_0^t f(t, t')dt'
= \frac{R_0}{2} [1 - \exp(-t/\tau)](1 + a\mathcal{P}(t)),
\] (6)

and similarly for \( \mathcal{B}(t) \), where \( a \to -a \). In principle, differences in the detectors may lead to unique values of \( R_0 \) and \(|a|\) for each. However, if they are the same, then the asymmetry is proportional to the polarization:

\[
\mathcal{A}(t) = \frac{\mathcal{F}(t) - \mathcal{B}(t)}{\mathcal{F}(t) + \mathcal{B}(t)} = a\mathcal{P}(t).
\] (7)

If the rates, \( R_0 \), are not the same for each detector, then

\[
\mathcal{A}(t) = \frac{\delta + a\mathcal{P}(t)}{1 + \delta a\mathcal{P}(t)},
\] (8)

where \( \alpha \equiv \frac{R_F}{R_B} \) and \( \delta = \frac{a - 1}{a + 1} \).\(^{35} \) The effects produced by the non-ideal case of \( \alpha \neq 1 \) are typically reduced by combining the asymmetry with that of the inverted spin polarization state (denoted by \( \beta \)).\(^{35} \)

\[
\Delta A(t) = \frac{A^+(t) - A^-(t)}{2} = \frac{a\mathcal{P}(t)(1 - \delta^2)}{1 - [\delta a\mathcal{P}(t)]^2}.
\] (9)

Since polarization inversion is equivalent to \( \mathcal{P}_+ = -\mathcal{P}_- \), and in the absence of spectrometer-related distortions \( a_F = -a_B \), then \( \mathcal{F}^\pm = \mathcal{B}^\mp \). Physically, if the spins are pointed at detector \( F \) in the \((+)\) state, then in the \((-)\) state they are pointed at detector \( B \), so the signal is invariant if both polarization and detectors are exchanged. Therefore, one can take the geometric means of these pairings to form a 4-counter asymmetry:\(^{36} \)

\[
\mathcal{A}_4(t) = \frac{\sqrt{\mathcal{F}^+\mathcal{B}^+} - \sqrt{\mathcal{F}^-\mathcal{B}^-}}{\sqrt{\mathcal{F}^+\mathcal{B}^+} + \sqrt{\mathcal{F}^-\mathcal{B}^-}}.
\] (10)

The advantage of this formulation is that the terms \( \sqrt{\mathcal{F}^+\mathcal{B}^\mp} \) share the coefficient \( \sqrt{R_F R_B} \), which cancels and eliminates any dependence on the rate. The 4-counter asymmetry is proportional to the polarization with the same scaling factor as Equation (7), regardless of \( \alpha \).

We now consider the case where the scaling factors of the two detectors also differ: \( \beta \equiv \frac{a_F}{a_B} \neq 1 \). In this case,

\[
\Delta A(t) = \delta_{+}\alpha B\mathcal{P}(t)\frac{1 - \delta_{+}\alpha (\frac{a - 1}{a + 1})}{1 - (\delta_{-}\alpha B\mathcal{P}(t))^2},
\] (11)

where \( \delta_{\pm} \equiv \frac{a^{\pm 1}}{\alpha^{\pm 1}} \). In the limit where \( \alpha \to 0 \) and \( \beta \to 0 \),

\[
\Delta A(t) \approx \frac{1}{2}[\beta + 1 - (\alpha - 1)^2] a_B\mathcal{P}(t) + \frac{1}{2}[\beta - 1 + (\alpha - 1)]^2 (a_B\mathcal{P}(t))^3.
\] (12)

In contrast, if this generalization of \( \beta \neq 1 \) is accounted for in Equation (10), we find that the dependence on \( \alpha \) again is exactly cancelled, however the dependence on \( \beta \) remains. To first order this is

\[
\mathcal{A}_4(t) \approx \left(\frac{\beta + 1}{2}\right) a_B\mathcal{P}(t),
\] (13)

which is the same as the first term of Equation (12) if \( \alpha = 1 \). Differences in rate and scaling are also common sources of systematic error in \( \mu \)SR experiments.\(^{37,38} \)

The implementation of these calculations can be found in both \texttt{bdata} and \texttt{bfit}. In \texttt{bdata}, the asymmetry of each of the individual polarization states is calculated using Equation (7), whereas the combined asymmetry is calculated with Equation (10). The exponential and multi-exponential spin-lattice relaxation (SLR) fitting functions used in \texttt{bfit} are calculable analytically using Equation (4), whereas the stretched exponential relaxation fit function is computed numerically using a double-exponential integration scheme, important for its speed and stability at \( t = 0 \).\(^{39,40} \) Note that in order to measure the SLR, a pulsed beam is used; thus, when the beam is turned off at time \( \Delta \), the integration limit of Equations (3) and (4) is set to \( \Delta \) when \( t > \Delta \).

## IV. GLOBAL FITTING

Global fitting refers to the procedure by which the parameters of best fit are found for a set of data, in the case where one or more of these parameters are shared across the data set. For example: the data set may consist of many Gaussian distributions which are known to be collectively described by a single mean, but have different standard deviations. The global fitting class defined in \texttt{bfit.fitting.global_fitter} takes as input the data, the fitting function, and a list of boolean values specifying which parameters are to be shared. The global \( \chi^2 \), resulting from a simultaneous fit to all the distributions, is then minimized. The global fitting object also allows for the initial parameter values and bounds to be set intelligently, inferring from context whether the input refers to the parameter for a given data set, or should be applied to all data sets.

Continuing with this example, if there are \( N_{\text{dat}} \) points in each distribution, and \( N_{\text{set}} \) distributions in the data set, then the data inputs to the constructor will each be 2D array-like objects with the shape \( N_{\text{set}} \times N_{\text{dat}} \). The input for the function may be a single function handle or a list of handles of length \( N_{\text{set}} \), with the restriction that all functions must take the same inputs in the same order. The length of the list of booleans indicating sharing defines the number of parameters to be minimized. The remaining function inputs should be passed as constant values through the \texttt{metadata} parameter. The constructor may also take a 2D list of booleans indicating which parameters for which distribution are to be fixed to their initial value. These latter two inputs are optional.
Like all the minimization in bfit, the global fitting utilizes the `scipy.optimize.curve_fit` function, which has the basic prototype `curve_fit(f, xdata, ydata)`, f is the fitting function of the type f(x, ...). The strategy is to define f such that it has access to the data through the object attributes, and inflate the 1D array of input parameters from `curve_fit` to match. The call to `curve_fit` is applied to the concatenation of the data arrays. This is described in detail by Algorithms 1 and 2. A similar flattening procedure is applied to the initial parameters and fitting bounds, such that they can be passed to `curve_fit`, and the inverse procedure is applied to inflate the results back to the original input shape.

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**Algorithm 1:** Get a matrix of indices mapping the 1D input to `curve_fit` to a 2D arrangement

**Data:**
Which indices are fixed and which are shared,
The number of data sets, N_{dat},
The number of fit parameters, N_{par}

**Input:** None

**Output:** Matrix L of indices, mapping a 1D arrangement to 2D

1. **Function get_map():**
   2. \( L = N_{dat} \times N_{par} \) matrix
   3. \( u \) = empty vector
   4. for \( i \in \{0, 1, \ldots, N_{dat} - 1\} \) do
      5. for \( j \in \{0, 1, \ldots, N_{par} - 1\} \) do
         6. if parameter \( j \) is shared then
            7. \( L_{ij} = j \)
         8. end
      9. else if parameter \( j \) is fixed then
         10. \( L_{ij} = -1 - j - (i \cdot N_{par}) \)
      11. end
      12. else
         13. \( L_{ij} = j + (i \cdot N_{par}) \)
      14. end
      15. if \( L_{ij} \geq 0 \) and \( L_{ij} \notin u \) then
         16. append \( L_{ij} \) to \( u \)
      17. end
   18. end

/* Remap indices to those from `curve_fit` */

\( L_{ij} = k \) if \( L_{ij} = u_k \) \( \forall \ i, j, k \)

\( L_{ij} = N_{dat} \cdot N_{par} - L_{ij} \) if \( L_{ij} < 0 \) \( \forall \ i, j \)

return \( L \)

---

**Algorithm 2:** Master function for global fitting

**Data:**
- \( X : \) \( N_{dat} \times N_{par} \) matrix, independent variable
- \( M : \) \( N_{dat} \times N_{meta} \) matrix, additional inputs
- \( P : \) \( N_{par} \times N_{par} \) matrix, initial parameters
- \( f(x,p_1,p_2,\ldots,p_{Npar+Nmeta}) \) : fitting function

**Input:** From `curve_fit`, vectors of values for the independent variable \( x \) (unused), and parameters \( p \) (length \( N_{par} \)).

**Output:** An array of values corresponding to the concatenated \( y \) values

1. **Function \( f(x,p) \):**
   2. \( L = \text{get_map}() \)
      3. /* Add initial parameters to input array */
      4. for \( i \in \{Npar - 1, Npar - 2, \ldots, 0\} \) do
         5. for \( j \in \{Npar - 1, Npar - 2, \ldots, 0\} \) do
            6. append \( P_{ij} \) to \( p \)
      7. end
      8. /* Get data for output */
      9. for \( i \in \{0, 1, \ldots, N_{dat} - 1\} \) do
         10. for \( j \in \{0, 1, \ldots, N_{dat} - 1\} \) do
            11. \( Y_{ij} = f(X_{ij}) \)
            12. \( P_{L(i, 0), M(i, 0), M(i, 1), M(i, 0), M(i, N_{meta})} = Y_{ij} \)
      13. end
      14. /* Concatenate the output */
      15. \( y = (Y_{0,0} \ldots Y_{0,N_{dat}} Y_{1,0} \ldots Y_{1,N_{dat}} \ldots Y_{N_{dat},N_{dat}}) \)
      16. return \( y \)

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**V. EXAMPLES**

**A. mudpy**

Our first example uses `mudpy.mdata` to read a MUD file called `041200.msr`, located in the current working directory, and corresponding to an SLR run taken on the \( \beta \)-NMR spectrometer in 2019.

In [1]: import mudpy as mp
In [2]: data = mp.mdata('041200.msr')
In [3]: data
Out[3]:

```python
apparatus: 'BNMR'
area: 'BNMR'
description: 16908289
duration: 622
exp: 1424
experimenter: 'df, ms'
field: '65500.0(0.0)G'
hist: ndict: {'Y': ', 'P+', 'P-', 'P-', ...}
ivar: ndict: {'BNMR:HVBIAS:POS:RDVOL': 'BNMR~
             :HVBIAS:NEG:RDVOL', ...}
lab: 'TRIUMF'
method: 'TD-BNMR'
mode: '20'
orientation: '1'
run: 41200
sample: 'EMIM-AC (LiCl)'
sclr: ndict: {'Back%Segments', 'Front%Segments', ...}
start_date: 'Mon Oct 28 08:34:51 2019'
start_time: 157251691
temperature: '243.9(1.1)K'
title: 'EMIM-AC (LiCl) , B=65500.0(0.0)G, HV~
       ~0 kV, T=200.0(0.7)K (woaming), SLR'
```
As shown, the output is nicely formatted, noting that the full output of the `mdicts` has been truncated to conserve on space in this publication. The object `mdict` belongs to the `mudpy.containers` module and inherits from the standard Python dictionary class. `mdict` allows for dictionary elements to be accessed as attributes. Therefore, `data.ivar.var_name` is equivalent to `data.ivar['var_name']`, subject to restrictions on allowed attribute names (e.g. `data.hist.Fp` is not an allowed syntax; for this special case `data.hist.Fp` can be used, or for the other helicity state: `data.hist.Fn`). `mudpy.containers` also defines the `mcontainer` base class which is the parent for containers specific to the histogram, variable, scaler, and comment data types. `mcontainer` has numerous convenience functions such as nice printing:

```python
In [4]: data.ivar['/Sample/read_A']
Out[4]:

description: 'SampleA temperature'
  high: 250.383
  id_number: 23
  low: 236.001
  mean: 243.9106082123654
  skew: -831.177521713147
  std: 4.067047463404781
  title: '/Sample/read_A'
  units: 'K'
```

as well as redefined mathematical operators that act on the `mean` or `data` attribute, as appropriate:

```python
In [6]: data.ivar['/Sample/read_A'] + 10
Out[5]: 253.9106082123654
```

The other object of interest defined in `mudpy.containers` is `mlist`. This object allows for attribute access to its contents as demonstrated in the following example:

```python
In [1]: from mudpy.containers import mlist
In [2]: class example(object):
   ...:     def __init__(self, x):
   ...:         self.x = x
In [3]: m = mlist([example(i) for i in range(5)])
In [4]: m.x
Out[4]: array([0, 1, 2, 3, 4])
```

If the output is a list of numbers, then it is converted to a `numpy.ndarray`, otherwise it returns another `mlist` object.

### B. bdata

The `bdata` package defines three objects: `bdata`, `bjoined`, and `bmerged`. The first inherits from `mudpy.mdata` with additional formatting and sorting for variables. Additionally, differing variable names are all mapped to a consistent naming scheme. In the following example, we draw the combined asymmetry (calculated with Equation (10)) for the run we fetched with `mdata`. One major difference between the two is that `bdata` requires the full file path to be specified, whereas `bdata` uses the environment variables `BNMR_ARCHIVE` and `BNQR_ARCHIVE` to locate the data on the local machine. If the data is not found, then the data is fetched from the archive.24 If the environment variables are not defined, the default location for the data is `$HOME/.bdata`. The following short example demonstrates how easily one is able to draw the asymmetry of a $\beta$-NMR run:

```python
import bdata as bd
import matplotlib.pyplot as plt

data = bd.bdata(run = 41200, year = 2019)
plt.errorbar(*data.asym('c'))
```

The reader is encouraged to read the docstring of `bdata.bdata.asym` for the many options which vary according to type of data collected.

The `bjoined` and `bmerged` objects both take as input lists of `bdata` objects and combine them. After construction, `bmerged` behaves exactly like a `bdata` object, combining both the data and the other variables, allowing for seamless replacement in code written for `bdata`. This results in a loss of information, namely the individual details of each of the runs. The object `bjoined` solves this issue, taking advantage of `mudpy.containers.mlist` to store the information of each run. In this way data from a set of runs is easily combined, however the operation of `bjoined` is slightly different from `bdata`, returning lists of the data containers rather than single merged containers.

### C. bfit

We now show an example of using the fit functions defined in `bfit` to fit some pulsed beam SLR data:

```python
import bdata as bd
from scipy.optimize import curve_fit
from bfit.fitting.functions import pulsed_strexp

data = bd.bdata(run = 41200, year = 2019)

# define stretched exponential function
# parameters: 1/T1, beta, amplitude
fn = pulsed_strexp(lifetime = bd.life.Li8, pulse_len = data.get_pulse_s())

# calculate combined asymmetry and fit time, asym, error = data.asym('c')
non_zero = error > 0
par, cov = curve_fit(fn, xdata = time[non_zero], ydata = asym[non_zero],
         sigma = error[non_zero], absolute_sigma = True)
```

As a simple, if contrived, example of using the global fitter, consider the following:

```python
import numpy as np
from numpy.random import randint, random
from bfit.fitting.global_fitter import global_fitter

fn = lambda x, a, b : a * x + b

# make some data, irregularly sized
x = [np.arange(randint(low = 3, high = 10)) for i in range(5)]

# have a varying intercept, shared slope of 2
itrct = np.arange(len(x))
y = [fn(xval, 2, 1) for xval, i in zip(x, itrct)]

# random error
dy = [random(len(xval)) for xval in x]

# set up the fitter, sharing the slopes, but different intercepts
gf = global_fitter(x, y, dy, fn, shared = (True, False))

# do the fit (inputs are passed to curve_fit, after flattening)
gf.fit()

# get the results and draw
par, cov, std = gf.get_par()
global_chisq, chi2 = gf.get_chisq()
gf.draw()

VI. SUMMARY

The packages mudpy, bdata, and bfit bring the rapid development style of Python 3 to μSR and β-NMR analysis, complementing established μSR software such as Musrfit. The first package provides an easy interface to MUD files through the mdata class. The second does the same for β-NMR data through the bdata class, but with additional analysis and convenience tools. The third provides both a GUI and an API for β-NMR fitting functions and tools such as the global fitter. All three packages are freely available on PyPI and GitHub.13

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