

# SPIKE Relase Notes

## 0.99.3 - March 2019

- Development of Interactive tools, to be used within Jupyter - *should be extended in further releases* -
  - a tool for displaying multiresolution 2D FT-ICR-MS data-sets
  - simple interface in Jupyter for 1D NMR
  - (that part is not tested in python 2)
- `scale="auto"` in 2D display, choose a level `autoscalethresh` (default is 3) times above the noise floor.
- added `gaussenh` apodisation plugin for one-command gaussian enhancement.
- improved display of FTMS spectra
- improved `findnoiselevel` and `findnoiselevel_2D`
- modified `absmax` in `NPKData` - now a property
- added phase parameters to `NMRAxis`: `.P0` and `.P1`
- removed the old `Visu2D` program - use the jupyter notebook rather !

## 0.99.2 - January 2019

- added number of local peaks in bucketing
- improved Bruker importer and added support for NEO/TopSpin 4.0 files
- improved the `.set_unit()` method
- improved importing DOSY processed with TopSpin
- corrected a bug for min value in bucketing
- changed pylint/QC defaults -> new values (and corrected a bad bug)
- cleaned the code a little

## 0.99.1 - November 2018

- added the sane algorithm
- added the pg-sane algorithm
- added the `NPKData.set_unit(unit)` method for pipelining
- added the `NPKData.load_sampling(axis)` method for pipelining
- improved spinit support
- corrected a few bugs
- `NPKData.save_csv()` now works in python 3
- `NPKData.copy()` is now more robust

## 0.99 - April 2018 - temp release branch

We have been developing a lot this last year, and published quite a few results. The program is now quite stable in most of its features. Additions and improvements were added to the repository in the `devel` branch, however we neglected

updating the more official **default** branch. This release is an effort to bring everything into normal mode, and hopefully, preparing a 1.0 version !

New in 0.99:

- SPIKE is now fully compatible with python 2 AND python 3
- added the SANE noise denoising algorithm and plugin.
  - an improvement to urQRd
  - more faithful to small signal intensity
  - slightly different optimum parameters (optimal rank slightly smaller, less iterations needed)
- added the handling of NUS 2D FTICR acquisition
- added the PALMA DOSY processing algo and plugin (NMR).
- added a Linear Prediction plugin
- added the first trial for a m/z calibration plugin (MS)
- added import from SpinIt (NMR)
- added a primitive set of interactive tools to be used in Jupyter notebooks ( `INTER.py` )
- added the possibility to pass a complete dictionary to matplotlib in the `.display()` method
- added the `.center()` method for NPKData
- added a plugin implementing a subset of Topspin commands: `xf1`, `xf2`, `xfb`. (NMR)
- added an line fitter, still very exploratory, only 1D Lorentzian for the moment
- added more controls on plots (`new_fig` and `mpldic` arguments of `.display()` )
- added a Spinit importer (preliminary) (NMR)
- added a compress mode in Solarix importer (MS)
- added new automatic tests
- improved and extended the Bucketing plugin, with extended features
- improved the baseline correction code
- improved import/export to Topspin/Bruker NMR files
- improved automatic phaser `.apmin()` (NMR)
- improved the plugin mechanism - with added documentation
- corrected the `extract()` method which was broken

- corrected a bug when importing Topspin/Bruker NMR datasets, where \$NC was not used. (NMR)
- corrected a bug and improved 3 parameters FT-ICR calibration (MS)
- corrected the extract function for NPKData
- corrected a bug with contour plots and matplotlib version > 1.5.0
- modified (improved?) plugin loading code, with additional plugin documentation
- modified the way None values are stored into hdf5 files
- modified `.extract()` code to work in current axis unit
- modified `.mean()` to return complex value if axis is complex
- improved python 3 compatibility. It is not finished yet, but most of the program is python 2/python 3 independent, some parts are still missing,
- known bugs
- `NPKData.extract()` method not fully tested
- `NPKData.save_csv()` is buggy in python 3

## 0.9 - 8 sept 2016

*never reached the normal distribution - doc partly redundant with 0.8.3*

- added a baseline correction plugins, already quite developed, with 3 different methods
- added an automatic phasing plugin, `.apmin()` still exploratory (NMR)
- added a wavelet filtering plugin (requires the PyWavelet library)
- added a 3D zoom plugin (requires the Mayavi library)
- added export to Topspin/Bruker files, and added import of processed Topspin files (NMR)
- added the upgrade of files from previous version
- added the `d.axis?.cpxsize`: the size of an axis expressed in spectroscopic points (real or complex) different from `d.axis?.size` which is the size of an axis expressed in data points so
- `d.axis?.cpxsize == d.axis?.size` if axis is real
- `d.axis?.cpxsize == d.axis?.size/2` if axis is complex
- improved the Peak-Picker (mostly the output capabilities)
- improved processing.py for nicer spectra, and possibly faster processing (MS)
- improved visu2D.py, for a greater stability and improved selection syntax
- corrected a bug in `.conv_n_p()` (NMR)
- and many small bugs as well

### 0.8.3 - April 2016

- ALL spectro.
  - added a new `cpxsize` property, associated to axes and dataset, which counts complex and real entries
  - added: `display` and `peak display` now accept a color and markersize arguments
  - improved plugins, plugins with a filename starting with `_` do not load
  - improved: automatic baseline correction algorithms have been improved ( `Algo/BC.py` )
  - `finnoiselevel()` set of functions has been rewritten ( `util/signal_tools.py` )
  - standard test now includes testing for `multiprocessing` - *DOES NOT WORK ON ALL DISTRIBUTION* if it is your case, set `use_multiprocessing = False` in `test.mscf`
- NMR
  - added: BrukerNMR now imports TopSpin processed dataset (1r, 2rr)
  - improved: and corrected Laplace axes - for a new DOSY module to come...
  - corrected: `conv_n_p()` was wrong and has been corrected
  - corrected: `gm_apod()` was wrong and has been corrected
  - corrected: an error in GifaFile access under Windows
- MS
- `processing.py` (2D FTMS) now includes parallel processing in F2 (helping in certain cases)
- and gives sharper lineshape thanks to `kaiser()` apodisation
- files from the previous program version (0.7.x) can now be upgraded and read. just do `python -m spike.File.HDF5File update your_file.msh5`
- improved `.report()` for FTMS datasets

### 0.8.2 - 2 Feb 2016

- corrected a bug in processing when running under MPI parallel
- added warning in `set_col()` and `set_row()` if type do not match.
- starting to work on the documentation

### 0.8.1 - 24 Jan 2016

- corrected a bug for Orbitrap related to `offsetfreq`.

### 0.8.0 - 23 Jan 2016

- first clean version using the new HDF5 file set-up **WARNING**
  - HDF5 files created with this version cannot be read with previous versions

- HDF5 files created with previous versions cannot be read with this version - this should be fixed later - File now contains acquisition parameters files in the attached hdf5 sub-group
- datasets now carry store and retrieve the parameters imported from manufacturers file in d.params
- improved FTMS calibration using 1, 2, and 3 parameters calibration : calibA calibB calibC, retrieve by Import from experimental file
- improved FTMS Hz unit, added the d.axis.offsetfreq parameter
- corrected fine details of F1 demodulation and added the parameter freq\_f1demodu
- unittests extended, in particular in visu2D
- Starting with this version
  - a stable version will be maintained, downloadable as a zip file in the download page <https://bitbucket.org/delsuc/spike/downloads>
  - Two development branches will be used, the **default** for the stable version - improved for bugs, and the **devel** branche, used for developing the new features.

#### 0.7.1 - 5 Jan 2016

- greatly improved internal compression of msh5 files and speed of processing.py
- many small corrections and bug fixes.

#### 0.7.0 - November 2015

- a plugin mechanism has been created which allows to add very simply new features to the program
  - most new features are implemented through this mechanism
- the organisation of the spectral axes has been completely modified, with the introduction of a Unit class
  - each axis holds its own series of possible units (called .units)
  - and the current unit used for display and selection
  - many commands now have a zoom= keyword that works in the current unit
  - additionally, there are itoc and ctoi unit converters
- Thanks to this, NMR data-sets are now correctly handled, DOSY are still in progress and should come soon
  - additionally a plugin for Bruker NMR processing is now implemented
- A complete 1D and 2D peak-picker is now implemented, with many controls and features
- New baseline correction algorithms have been implemented
- the sane algorithm, which is an evolution from urQrd has been separated from urQrd, so both algorithms can now be used independently
- Tests have been reorganized and improved

- Importers have been extended - parameters are now brought back to the user
- many others

#### **0.6.4 - march 2015**

- added Bruker NMR import
- clean-up of the module, still going on
- Tests improved

#### **0.6.3 - march 2015**

- first installable release

#### **0.6.0 - dec 2014**

- Fork to SPIKE
- Large improvements of the display program, renamed visu2D
- Corrected a bug in the hypercomplex modulus, resulting in splitting in 2D-FT-ICR
- many improvements everywhere

#### **0.5.1 - 26 mar 2014**

- processing2.py renamed to processing.py with added features
  - urQRd
- source code reorganized by folders

#### **0.5.0 - 24 mar 2014**

- starting new devl effort
- published ! version of urQRd

#### **0.4.1 - 27 Sep 2012**

- final (?) version of urQRd
- added data arithmetic
- many other optimisation

#### **0.4.0 - 20 apr 2012 -**

new version processing2.py (temporary name) this one

- processing is performed in steps, F2 from infile to interfile (intermediate file) and F1 from interfile to outfile

- steps are optionnal, F2 or F1 can be performed alone - allowing denoising on the interfile
- processing is faster and mpi enabled - speed-up are better for very large files
- has a better way of computing the smaller spectra - done by downsampling - faster and nicer
- vignette is now 1024x1024 - can be changed using SIZEMIN in config file

#### **0.3.11 - 29 mar 2012**

Small tools have been added to modify configuration files and to mix processing.py and ipython visualisation

#### **0.3.10 - 22 jan 2012**

processing is now (hopefully) bug free and RAPID !

#### **0.3.9 - 18 jan 2012**

fticrvisu.py, processing working, getting all parameters correctly from FTICR-Data and Apex

#### **0.3.8 - 13 jan 2012**

fticrvisu.py, processing working, corrected after Marie came

#### **0.3.7 - 12 dec 2011**

correction of Gifa file bug, bug in Apex for narrow band data-sets, changes in msh5 file format

#### **0.3.6**

3 Oct 2011 - added HDF5 file format (.msh5), multiresolution files, configuration files (.mscf), fticrvisu

#### **0.3.5**

5 Sept 2011 - added cadzow in MPI / savitsky-golay / HDF5 still in progress

#### **0.3.4**

26 July 2011 - added autotests / savehdf5 first version

### **0.3.3**

12 July 2011 - first reliable/tagged FTICR version