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List of versions and changes

Squidlab was released publically as version 2.4 (Dec 2019)

Version 2.9.3 (Mar 2024)

- Added new fit functions: `dipoleEquationFixedCentre` and `driftingDipoleEquationFixedCentre`. See Pg 20 of the manual for information on how to use these. The existing `dipoleEquation` and `driftingDipoleEquation` fits had fit parameters for the z position of the dipole centre. These new FixedCentre options instead fix the dipole centre at $z=0$ (make sure to use `CentreX` and/or `ZShift` to get the signal centred around 0 first. The T-dependent offset `TDepShift` postprocessing option also works well with this.
- Improved the MPMS3 importers to handle partially corrupted .raw data files. In rare cases, the MPMS3 can fail to write some lines of data in a 'block' of z position data for a single temperature/field point. In this case, the previous importer would error and 'Import Failed' would be shown, as expected lines of data would not be found in the parsed array. Now SquidLab warns of corrupted data and skips the block, so the rest of the file can still be used.
- Improved logging of warnings (new `Logger.showWarning` method instead of using `warndlg` for those interested) so that warnings will no longer appear hidden behind the window on e.g. Import operations.

Version 2.9.2 (Aug 2023)

- Added T-dependent offsetting of data option in Postprocessing. Uses `circshift` to cycle the data around to preserve z values.

Version 2.9.1 (Oct 2021)

- Bugfixes and optimisations. Checks added for all required toolboxes. More helpful warnings and error handling when installation/setup has an issue.

Version 2.9 (July 2021)

- Added 'Mirror positive field scans to create negative scans' checkbox to the Advanced Input GUI panel. This allows negative-field data to be generated in MvH background scans if one has both -ve and +ve sample data but only +ve field background data. This simply mirrors field and voltage values, doubling the number of scans, and assumes that the background is symmetric in field.
- Scan metadata changed to be Scan, rather than Session-specific. This metadata includes the x axis variable type (T or H), and fit geometry parameters to automatically pre-fill in the fitting panel. The main improvement is that now such details are not lost upon Saving and Loading a Session, as well as better mixing of MvT and MvH scans. As saved Sessions made before v2.9 will not have this information, when an old save is loaded the user will be prompted to enter/confirm metadata, which will be applied to each ScanSet in turn. Saving the Session will upgrade the save to the new version.

- DebugMode property moved to ErrorHandler.m, and tweaks and improvements to error handling and logging. Set this DebugMode property to true if you want to see detailed stack traces of errors rather than nice user-friendly warning boxes (power users).
- Bugfixes - if invalid Matlab variable names were given when renaming or importing ScanSets, errors would be thrown and information could be lost. This is now properly checked and warnings given safely.

Version 2.8 (Apr 2021)

- Added new importers to support use of the MPMS Reciprocating Sample Option (RSO). Basic support of the file handling is implemented, but users may wish to inspect their raw data carefully, as only a simplistic drift-subtraction algorithm has been implemented in the importers. The up-down nature of RSO sweeps means drifts cause multi-valued data points. Users may wish to work on more advanced and robust implementations of the drift subtraction, and as always are encouraged to be in touch.

Version 2.7 (Oct 2020)

- Added new functionality to copy currently displayed data curves to a new Custom Plots tab. This allows quick and easy comparison of eg signal and background traces at 2K (best used with only 1 curve plotted at a time). Particularly useful if there's a z offset the user needs to work out and compensate for by comparing features in the data.
- Added checkbox to Import tab to 'Sort scans by temperature/field'.
- Various improvements under the hood to things like error checking and handling.

Version 2.6 (Apr 2020)

- Added new functionality to Save and Load the currently open 'Session' - all ScanSets and data. This is useful if e.g. you have a large collection of Background scans that will be common to all future measurements - they can be loaded, organised and named, and tidied up/processed then be ready for measurement data to come in. Note that Loading will obviously lose whatever is open at the time!
- New Save Session and Load Session buttons added to the Export tab.
- Minor bugfixes and tweaks.

Version 2.5 (Feb 2020)

- Added importers for Cryogenic S700X magnetometer .dat files, both raw and converted. See the updated manual for details.
- Changed the order of PostProcess steps. TrimX now occurs before CentreX - this otherwise caused very confusing behaviour!
- Added a fix to compensate for the SquidRange=1000 bug that occurs in certain MultiVu versions on MPMS3s. Previous solution was to simply use the ScaleFactor to rescale all data on import - but data files can contain changes of range (especially MvH scans). New CheckBox has been added to the Import tab. Checking it before pressing Import will prompt user to load in the corresponding .dat file to the .rw.dat already selected. Correct values will be lifted from the .dat and applied to the imported scansets. Note that this assumes the Squidrange really is 1000! Don't tick this box unless SquidLab has warned you about your data files with a pop-up message.

- Added checks for empty filepath and invalid filepath/nonexistent file when Import is pressed. Now pops up a warning message and cancels the import.
- Moved the optional Import options to a new 'Advanced' panel to make it clearer they are not required for most use cases.
- Tweaked the visual layout of the GUI for clarity.