cNx suite V27 Release Notes

cNx suite V27 brings a new set of features, mainly focussed on batch operations, finer tuning of autofitting, and much more.

NOTE: *.**CNX and *.XCPD saved with cNx suite V27 are *not compatible* with earlier versions of Chenomx NMR Suite.** However, cNx suite v27 can read older CNX and XCPD files (back compatible)

Profiler module

COMPLETE autofit
A new Autofit Companion Tool to extract, create and edit custom cluster positional restraint. Option added: save only a subset of the best fit solutions.

Batch pH determination
pH optimization based on positions of profiled/selected compounds and peak clusters.

Batch extraction of chemical shifts
Peak Clusters Positional Restraints File can be generated from a series of cnx files, based on their profiled/observed locations. (for use in COMPLETE autofit)

Batch operations
Batch operations based on the chosen region, compounds, or peak clusters. This includes: peak cluster snapping, (un)locking compound concentrations, (un)locking peak positions, clearing peak transforms, etc.

Processor module

Additional NMR file format

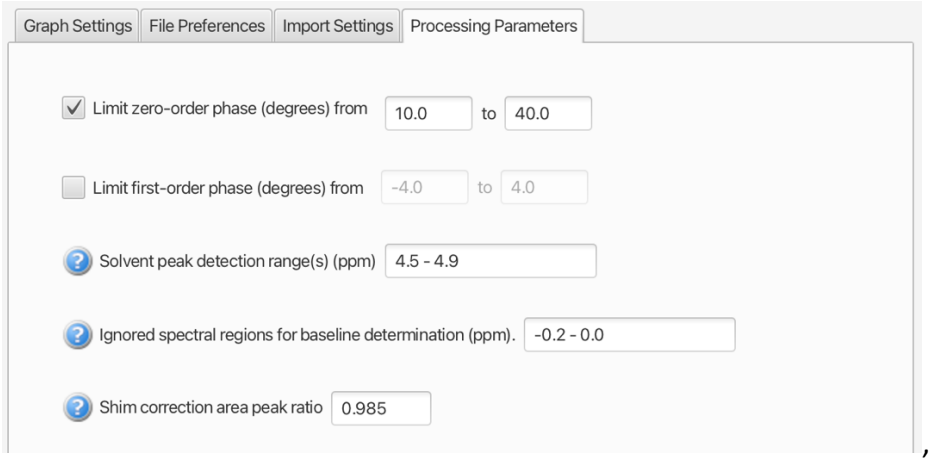
Compatibility with Spectra processed with JEOL JASON NMR software (*.jdh5 and *.jjj)

New line broadening mode

For users wanting to standardize CSI line width in a set of files: Line Broadening can be automatically calculated so that the CSI reaches a target value (also available in batch mode).

Custom control of processing parameters

Custom phasing limits, solvent peaks detection range, ignored regions for baseline determination and automatic range for shim correction have been added to Processor's Preferences:



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