Chenomx is migrating to a new licensing system which uses an online server to manage licenses. License files will no longer be required, and hardware migration will be simplified. Simply download the cNx suite Evaluation Version and send us your Activation Code. We will activate your cNx suite license remotely and send a confirmation email so you can begin your work.

Our license server will be contacted every time cNx Suite launches. Users may work offline for up to 48 hours, then will need to reconnect again to ensure your license remains valid.

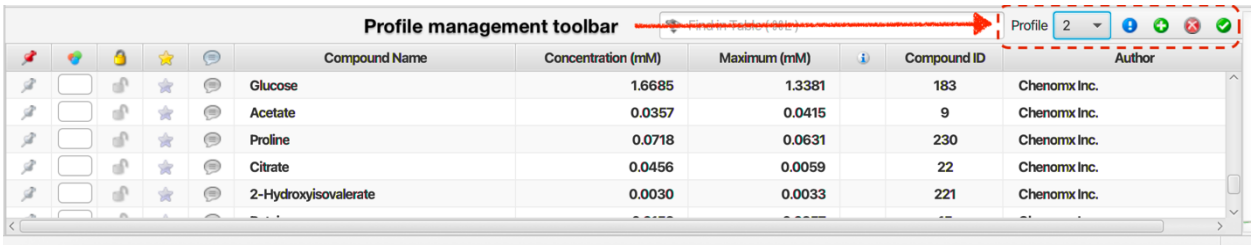
Profiler Updates

Regional weighting

Considerable efforts have been put in automatic fitting over the last versions, with emphasis on allowing users to customize the behaviour of the algorithm. cNx suite Version 26 introduces **regional weighting** when fitting concentrations, where customized weighting can be applied to different parts of your spectra. This feature can be particularly useful to put additional emphasis on regions with less overlap than other part of your spectra.

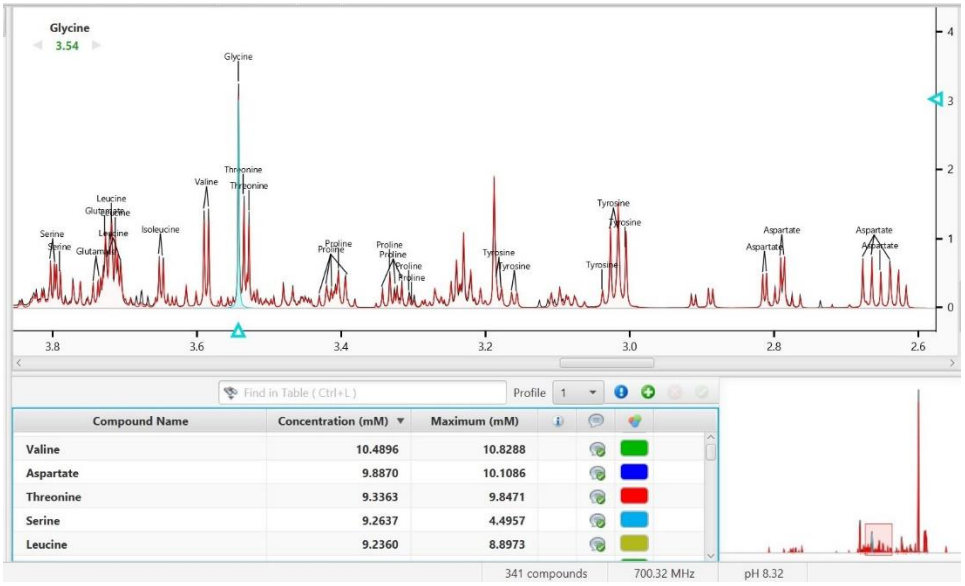
Multi-profiles

Files can now hold more than a single profile. This is particularly meant as a place holder for the different fit solutions output by COMPLETE Autofit. The software offers multi-profile management features, such as the import, addition, deletion, duplication, insertion, etc, of profiles.



Compound Name	Concentration (mM)	Maximum (mM)	Compound ID	Author
Glucose	1.6685	1.3381	183	Chenomx Inc.
Acetate	0.0357	0.0415	9	Chenomx Inc.
Proline	0.0718	0.0631	230	Chenomx Inc.
Citrate	0.0456	0.0059	22	Chenomx Inc.
2-Hydroxyisovalerate	0.0030	0.0033	221	Chenomx Inc.

Smart peak annotations
cNx Profiler can now annotate compounds, updating live as clusters are moved.



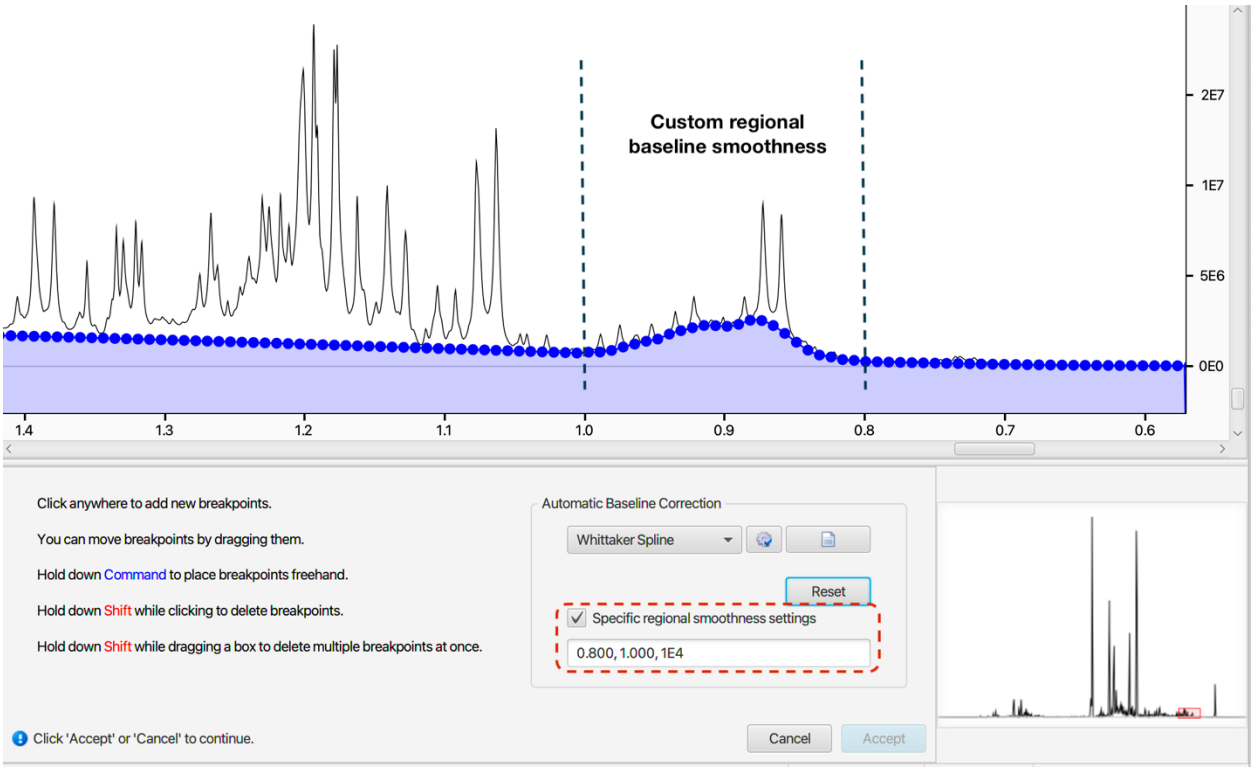
Indirect DSS line width determination
cNx suite uses the experiment line width of DSS to automatically calibrate the compound library on a per spectrum basis. When DSS partially binds to species is in solution, its effective molecular weight increases, and its experimental line width is wider than it should have been. Consequently, the compound signatures also appear wider than they should. This new feature automatically back calculates what the DSS line width should have been, in absence of binding, based on a known and profiled experimental resonance. This feature is available as a batch function, and should be particularly useful for **serum spectra.**

Quantification based on ERETIC signal
Spectra with no internal standards, such as those often acquired in HRMAS, can now be quantified using an ERETIC peak.

Processor Updates

Enhanced baseline correction

Regional degrees of smoothness can now be defined for different spectral regions, allowing for enhanced flexibility and local aggressiveness control in how the baseline is evaluated and corrected.



Library / Library Manager Updates

The 400 MHz reference compound pack has been complemented with simulated compounds from 500 MHz to bring the total number of compounds to 338.

A **natural abundance ^{13}C compound pack** is now available as an independent download. It was developed at the University of Calgary and is provided as is.