FT-ICR MS with In-Hardware Absorption-Mode Capability: Evaluation in High-Resolution and High-Throughput Applications Anton N. Kozhinov, Konstantin O. Nagornov, Yury O. Tsybin Spectroswiss, EPFL Innovation Park, Lausanne, Switzerland

Introduction



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Figure 1. A specialized data acquisition and processing system for FT-ICR instruments. The system is based on the technology detection of ICR transients with in-phase ion signals (generation of mass spectra in absorption mode), that we described in the previous work [1]. Here, we combine the developed electronics and the software-side processing in a single device (system), interface it to numbers of FT-ICR instruments, and benchmark it in highapplications includina petroleomics, and proteomics

Methods



Figure 2. FT , top) vields a mixed-mode spectrum (lef that requires post-processing for it to be represented n absorption mode Right papels. FT of transients with in-



Figure 3. Schematic diagram of the data acquisition electro simultaneously [1-4] and in-line esponding to ions trapped in the ICR cell, with phases The software-side processing integrate vendors' data format exports data into H5, mzML, mzXML, imzML, MGF, TXT files.



(top) and FT spectra Figure 4. Examples of ion phases conventional ICR transients (left) and transie from the external data acquisition-processing system of this work (right). The 2 datasets were acquired in parallel in the analysis of a ubiquitin sample on a commercial FT-ICR MS.

B. Absorption-mode peakshape in FT-ICR MS



Figure 5. Excitation related challenge in absorptionmode FT-ICR MS: unknown signal components in the an ICR transient black) that require shown in red (e.g., post-processing o correct their baseline or pre-processing of transients to correct the missing data points)



with standard (full) apodization and a magnitude-mode FT peakshape without

C. Locked phase function: $\varphi = 0$



to diverse experimental Figure 7. Method excite vs. detect detection freauency and specific experimental conditions (presets) with calibrated phase fine correction parameters, automatic fine tuning algorithm).





Figure 9. Prior to the data analysis, stitched mass spectra were re-calibrated using the non-linear iterative algorithm (Peak-by-Peak). The left panel shows mass error distributions for identified monoisotopic peaks of the N class (DBF) 4 - 41) after the re-calibration. The middle and right panels show C/H plots for the N1 class compounds identified the mass spectra obtained via SIM stitching workflow using spectral (1 run, mFT, RAW) and transient (4 runs, aFT Booster) averaging

Intact protein native analysis, ESI $(12 \text{ T SolariX}^{\text{TM}} \text{ XR FT-ICR MS})$

Robo/Arixtra protein-glycan complex (~23 kDa) on a 12 T SolariX XR FT-ICR MS (Bruker Daltonics) equipped with Paracell. Data were acquired in parallel using (black) original electronics of the instrument and processed in magnitude mode (D folder) and (red) using the external data acquisition-processing system (FTMS Booster X3, Spectroswiss) and processed in absorption mode. Data courtesv of Jon Amster laboratorv at UGA.



Figure 10. Mass spectra of RoboArixtra protein were obtained from averaged (129 scans) transients acquired using (black) built-in electronics of the instrument and (red) the external DAQ. The mass spectra were deconvolved using the high-resolution deconvolution tool (Peak-by-Peak). Deconvolved features were grouped by their charge state. Only proteoforms presented in at least three different charge states are considered and grouped.

Intact mAb native analysis, ESI (15 T SolariXTM FT-ICR MS, Infinity cell)

-ICR MS (SolariX, Bruker acquired in parallel using (black) original electronics of the instrument and processed in and (red) using the external data acquisition-processing system a The results show the implemented aFT acquisition and processing workflow absorption performance of an ICR instrument equipped with the previous generation ICR cell (Infinity). Data courtesy of Joe Loo laboratory at UCLA, Los Angeles.







Figure 12. Averaged mass spectra generated in (black) mFT and (red) aFT mode were deconvolved (low-resolution) using UniDec software. The results show almost twice more number of identified proteoforms for (right) aFT data in comparison with (left) mFT one

Middle-up mAb analysis, MALDI (15 T Solari X^{TM} XR FT-ICR MS)

(Cetuximab) on a 15 T SolariX XR FT-ICR MS equipped with Paracell. MALDI generates low charge state (1+, 2+, etc.) species even for large proteins. Data were acquired in black) original electronics of the instrument and processed in magnitude mode (D folder) and (red) the external data acquisition-processing system and processed in absorption (aFT) mode. Data courtesy of LUMC, the Netherlands (Simone Nicolardi).



Figure 13. Light chain (~25 kDa) of the reduced Cetuximab MALDI FT-ICR MS analysis. The data were acquired with a transient length of 8 seconds. Averaged transients (20 conditionally co-added scans) were processed in (black) mFT and (red) aFT mode. The conditional co-adding allows to eliminate scans with substantial frequency shifts. More proteoforms were identified in deconvolved (Peak-by-Peak) aFT spectra in comparison with mFT one, presented in at least three different charge states (not shown).





DESI imaging (21 T FT-ICR MS)

NanoDESI imaging analysis of a rat brain on a custom 21 T FT-ICR instrument (EMSL, PNNL) equipped with the external data acquisition-processing system (FTMS Booster X3, Spectroswiss). Experimental parameters: transient length of 0.768 s, ~5 hours, spatial resolution: x~25 um and y~180 um. Data courtesy of Gregory Vandergrift at EMSL.



Figure 14. Comparison of data from the (red) external data acquisition-processing system and (black) the original electronics. Absorption (aFT) mode almost doubles the resolution and mass accuracy in comparison with magnitude (mFT) mode. Overall, a high spectral dynamic range in a single scan with more than 3 orders of magnitude was achieved.

Figure 15. The instrument setup allows to construct complementary images only 2.6 mDa at a scan rate of < 1 s from mass spectra processed in aFT mode.

Conclusions

1. A specialized data acquisition-processing system has been developed, that enables to routinely use absorption-mode FT processing in real-life FT-ICR MS applications.

2. The in-hardware absorption-mode method demonstrates its fundamental properties: the method was found to be applicable to various commercial and customized FT-ICR instruments (e.g., 7 T LTQ FT-ICR, 12 T and 15 T SolariXTM XR with ParaCellTM and with InfinityTM cells and the 21 T PNNL system).

3. Absorption mode, detection of full transients, and multiplexing of separate experiments (replicates) translate to expected gains in resolving power, S/N, mass accuracy, and sensitivity.

References

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