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P35 - Quantitative reconstruction of PIXE-Tomography data for thin samples using GUPIX X-ray emission yields

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Characterisation of microscopic specimens using PIXE Tomography (PIXET) has long been restricted by experimental and computational difficulties, mainly: i) the sample must be mounted on a rotation axis to collect data on at least 180°; ii) the long duration of data acquisition; iii) very few reconstruction algorithms available. In recent years, several attempts have been made to design reconstruction algorithms to overcome these difficulties. A major trend is to implement algorithms other than filtered back projection (FBP), in order to use fewer projections. This trend has been recently extended to quantitative reconstruction. A MLEM code, JPIXET, has been designed at the IST/CTN in Lisbon [1]. PIXET data are processed together with Scanning Transmission Ion Microscopy Tomography (STIMT) data. The process is long, which was solved using GPU programming

At CENBG, PIXET was implemented to study biological samples. The major composition of these samples is uniform, whereas the internal structure is complex and not as contrasted as in most inorganic specimens. This led us to develop a specific algorithm, TomoRebuild. We present here a new development of this software package, to perform quantitative PIXET reconstruction. X-ray yields are obtained from the GUPIX code. The GUPIX data base is available for protons up to 5 MeV and also in the 20-100 MeV energy range, deuterons up to 6 MeV, 3He and alphas up to 12 MeV. The main features of the TomoRebuild code were kept: user-friendly design, modular C++ implementation and portability on Windows and Linux operating systems.

In this version, X-ray yields are calculated for thin samples, i.e. without simulating X-ray attenuation. This task is foreseen for the coming months. The distribution of element content (in g/cm³) can be obtained from PIXET data ; only the last step requires STIMT data to get normalised concentrations in µg/g. Images misalignment can be corrected, as well as the difference in beam size between the two experiments. We will give here reconstruction examples on biological specimens of *Caenorhabditis elegans* nematodes, analysed at the microbeam line of the AIFIRA facility of CENBG. The experimental conditions and the different steps of data processing will be discussed. The reconstruction results will be compared between the different codes TomoRebuild, DISRA and JPIXET.

[1] D.G. Beasley, A.C. Marques, L.C. Alves, R.C. da Silva, Nucl. Instr. Meth. B306 (2013) 109-112.

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