

## M-BLANK: A Program for X-ray Fluorescence Data Analysis and Processing

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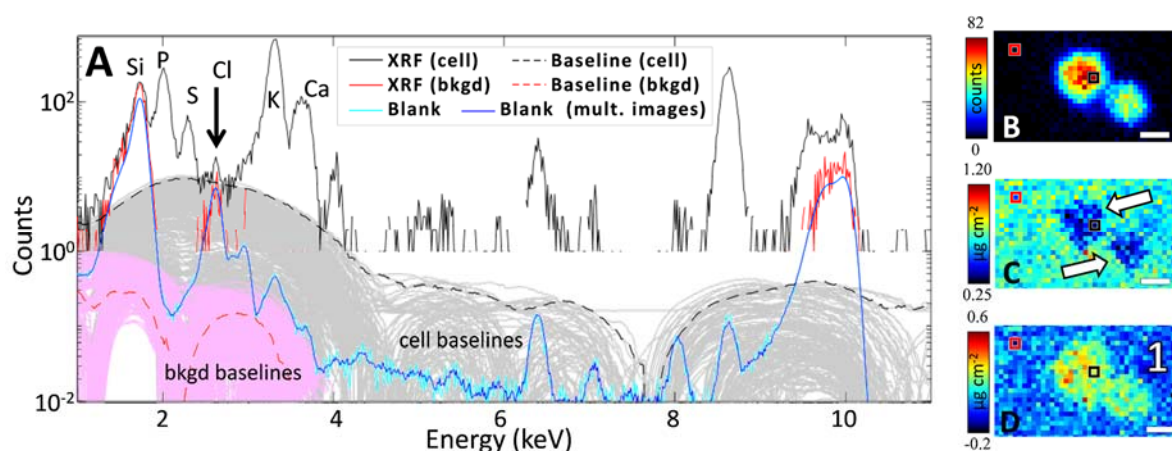
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Due to overlap of x-ray emission lines in energy dispersive x-ray detectors, x-ray fluorescence (XRF) data from x-ray microprobe and nanoprobe measurements must be fitted to obtain reliable elemental maps. To do this, many programs initially remove a per-pixel baseline prior to fitting to account for a background XRF continuum. Using XRF data from yeast and glial cells we show that such per-pixel baseline corrections can incur significant, systematic errors in quantitation and that significantly improved data can be obtained by calculating an average blank spectrum and subtracting this from each pixel.

In doing so, we describe a program, M-BLANK, a MATLAB program that implements a blank correction approach and demonstrate that, when possible, it provides better accuracy, avoiding systematic errors associated with per-pixel baseline subtraction. In some cases, M-BLANK also provides better precision than baseline-fitting programs. In order to compare blank and baseline-analysis procedures, we will discuss the two specific cases mentioned above wherein the XRF data for yeast and glial cells were analyzed by both methods.

By comparison, we demonstrate that per-pixel baseline subtraction can introduce artifacts in the apparent concentration of dilute elements, particularly when there are strong fluorescence peaks nearby, and show that this is important under biologically relevant conditions. In all comparisons we have performed between M-BLANK with other programs that utilize per-pixel baseline correction (e.g., MAPS, PyMCA and PyXRF), we note comparable results. We note specifically that these findings result from the use of per-pixel baseline correction and not any fault with the associated architecture of the software.

M-BLANK, which uses the background-subtraction methodology to be presented, is available on request from the authors. In addition to being both more accurate and more precise, blank subtraction has the additional advantage of permitting linear least-squares fits, as compared with the non-linear fitting that is required by the non-negativity constraints typically used with baseline removal. This allows for much faster fitting and is more easily adapted to real-time analysis.



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