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The first step that is required to extract the correct information from a two-dimensional (2D) diffraction signature is to remove the background accurately. However, direct background subtraction inevitably overcorrects the signal as it does not take into account the attenuation by the sample. Other traditional background removal methods, such as the rolling ball technique, can separate sharp diffraction peaks of crystalline materials from their background. These methods are unsuitable for biological tissue, which is amorphous and does not have sharp diffraction peaks. This technical note proposes a novel method that combines peak fitting and experimental results to estimate the background for 2D XRD signals.

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