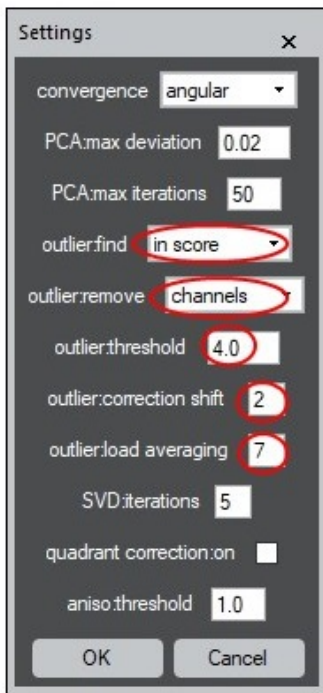


STEM data cubes nowadays consist of a huge number of data points. If some of them are located, for whatever reasons, far away from the main data distribution you have a problem. This is a typical case for EELS data where few sharp peaks due to X-ray spikes are observed. These outliers (sometimes named spikes) might also appear in EDX data.

Even a singular outlier can make your PCA analysis completely wrong. Most cases when people “are disappointed with PCA...” arise exactly from this issue.

The advanced version of **temDM MSA** offers powerful algorithms for removing such outliers *in the course of PCA decomposition*. In contrast to the other methods for removing outliers, **temDM MSA** employs a minimal invasion paradigm. It removes only outliers that directly distort the results of PCA.



The method does not remove outliers in an irreversible manner but rather temporary “seal” them in the course of PCA. This allows to play with the various options for their detection and removal without rewriting the original data. However, if you are sure in your treatment, you can remove all outliers permanently.

A powerful **Check spikes** tool allows to inspect all found outliers and also check the parameters for their “sealing”. The outliers are displayed in two slices - “channel slice” that shows a spectrum, and a “pixel slice” that compares the signal among the neighboring pixels. An easy way to scroll through all detected outliers is provided.

