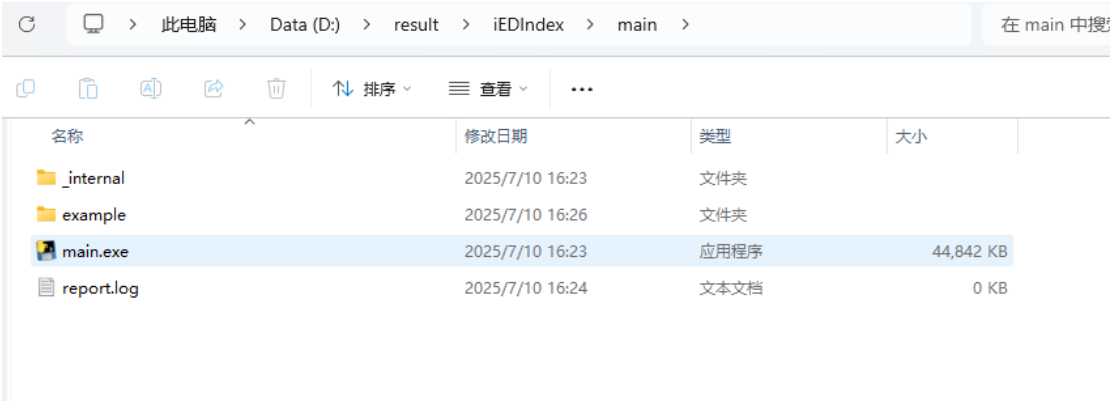
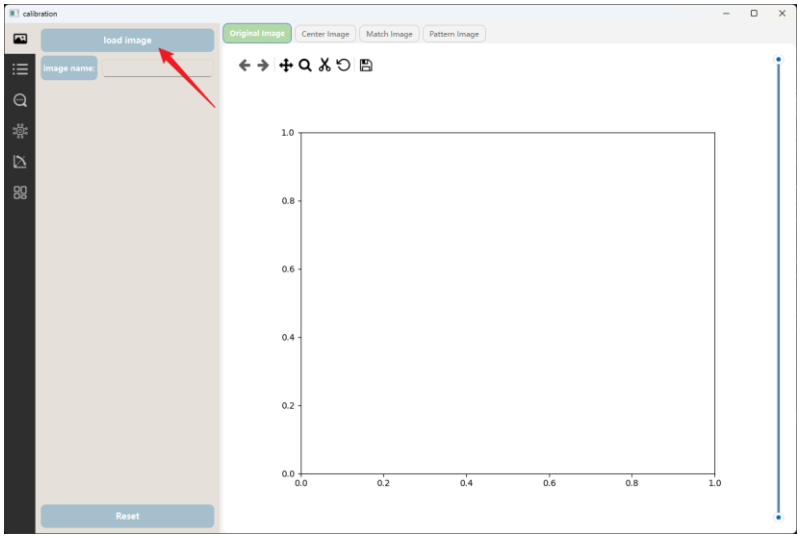
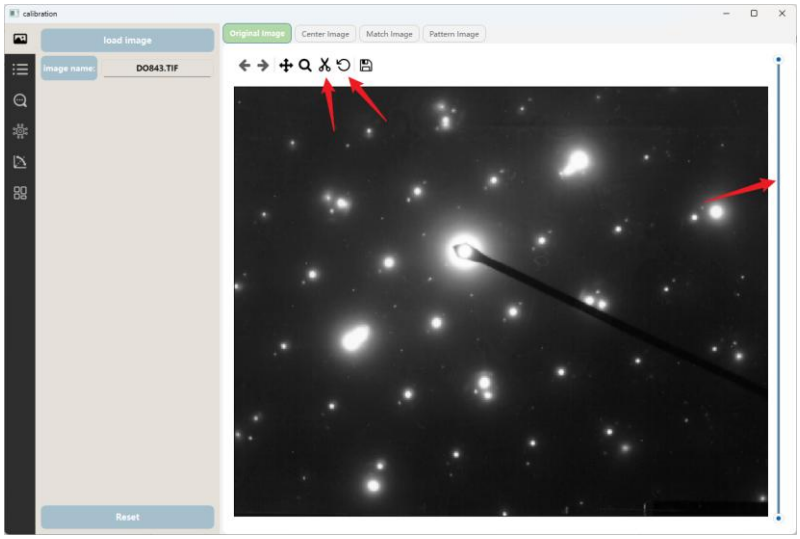
Please download the rar file, extract it to a folder, and then click on main.exe.



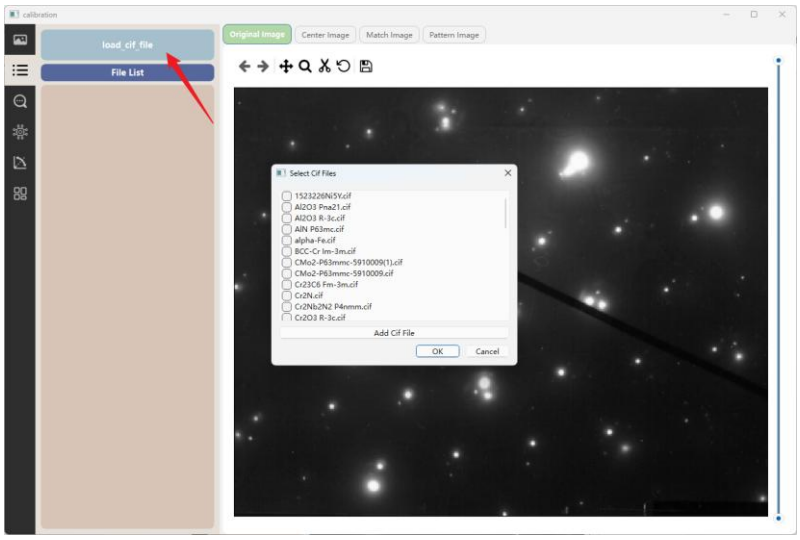
Click the "Load Image" button to select an electron diffraction pattern file from your local file system



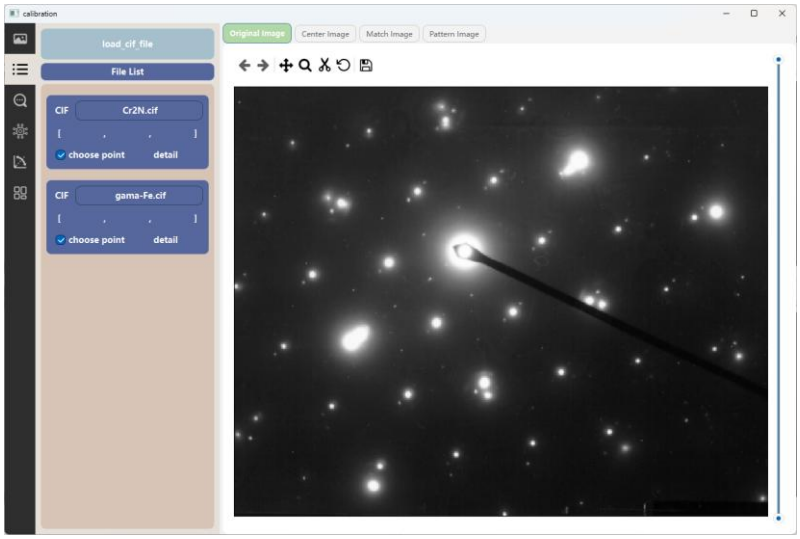
After loading the image, click ✂ then drag the selection box to remove unwanted background areas. If the crop is incorrect, click ↺ to revert to the original image.



Click the "Load CIF File" button to select a CIF from the built-in crystallographic database. If the database lacks the desired structure, click "Add CIF File" to import a local .cif file. The file will be parsed and saved for future access. After selecting a CIF file, click "OK" to proceed.

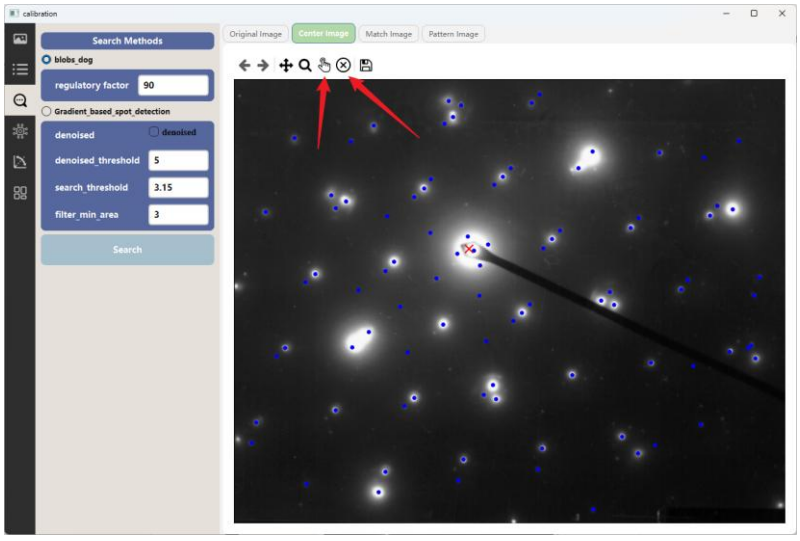


Loaded CIF files are displayed in the "File List" panel in the order of import. Click "Detail" to view complete information of the selected CIF file. The "Choose Point" option is checked by default. Users can uncheck it to hide this CIF file in subsequent results



In the Search Methods section, there are two algorithms available for selection. The blobs_dog algorithm only requires input of the regulatory factor parameter, and clicking the search button will initiate peak detection. The Gradient_based_spot_detection algorithm allows users to optionally perform background denoising by checking the denoised button. After entering the denoised_threshold, search_threshold, and filter_min_area parameters, clicking search will execute the peak finding process.

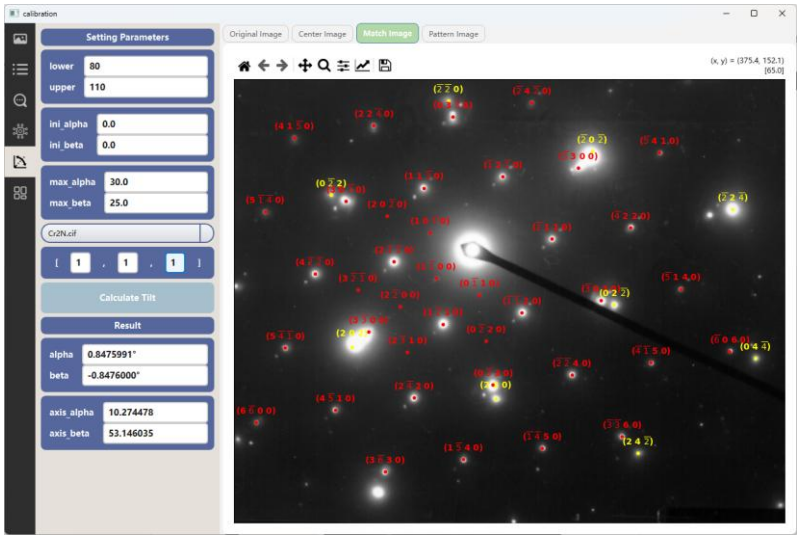
The software can automatically calibrate the center point after peak detection. If the center point is incorrectly calibrated, you can click to adjust it manually. If some erroneous peaks are detected and need to be removed, you can click to eliminate them.



If the correct zone axis is known, it can be directly entered in the CIF file box. If the axis is unknown, check the auto_axis button, and the software will select the correct

axis from its built-in library. max_cal_index is the maximum calculated Miller index value; max_auto_axis_index is the maximum index value for selecting axes from the built-in library; max_show_index is the maximum index value displayed in the results (note that max_show_index cannot exceed max_cal_index); match_threshold is the allowable error value for successful matching between theoretical and experimental diffraction spots. After entering the corresponding parameters, click "Match" to perform the calibration.

The software can calculate the correction angles required for the α-axis and β-axis (denoted as alpha and beta) when the incident beam is misaligned. Users should input the current instrument's starting angle and maximum rotation angle, select the imported CIF file, and specify the target zone axis. The software will then compute the necessary rotation angles (axis_alpha and axis_beta) for the goniometer's α-axis and β-axis to achieve proper crystallographic orientation.



The user can select an imported CIF file and input the target zone axis. Clicking "Draw Pattern" will generate the corresponding theoretical diffraction pattern. When clicking on any diffraction spot, the "click point" field will display its Miller indices (hkl), the "d-spacing" field will show the crystal plane spacing, and the "g-vector" field will present the magnitude of the reciprocal vector. The toolbar above the pattern allows for interactive manipulation of the theoretical diffraction pattern, including zooming, rotating, and translating operations