






POLEVAL: A Python package for HAXPES analysis

Robin Yoël Engel ^{1,2,3} and Patrick Lömker ¹✉

1 Chemical Physics, Department of Physics, Stockholm University, Roslagstullsbacken 21, 114 21 Stockholm, Sweden **2** Wallenberg Initiative Materials Science for Sustainability, Stockholm University, Roslagstullsbacken 21, 114 21 Stockholm, Sweden **3** Centre for X-ray and Nano Science CXNS, Deutsches Elektronen-Synchrotron DESY, Notkestr. 85, 22607 Hamburg, Germany ✉ Corresponding author

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Summary

POLEVAL provides a software toolbox for collaborative, persistent, and reproducible analysis of X-ray Photoelectron Spectroscopy (XPS), and particularly Hard X-ray Photo-Electron Spectroscopy (HAXPES) experiments. It allows to treat, analyze, and visualize the results of an extended experimental campaign in a single Python notebook in a consistent manner. Managing experimental data in adequate objects enables experimentalists to process and analyze measurements in very few lines of code, so as to provide decision aids through online data analysis during e.g. beamtime experiments. The persistent and self-documentary style of the notebook-based analysis allows for easy communication of intermediate results and enables progressive refinements into publishable figures or exporting the results to other programs.

The toolbox facilitates various routines for data treatment (normalization, cropping, etc.) and aggregation of spectra into groups to analyze trends. It also enables quantitative analysis with three major functions:

First, normalization to the photoionization cross-section and probability of emission into the analyzer cone allows for quantitative comparisons between intensities from different core levels. The integrated *haxquantpy* package allows easy retrieval of literature values ([Trzhaskovskaya & Yarzhemsky, 2018](#)) for this purpose.

Second, an extensive fitting functionality is implemented to treat groups of spectra together, rather than spectrum-by-spectrum. This grouping allows reinforcing the fit algorithm with prior knowledge, such as the equivalence of peak widths or positions between spectra, which enables for more consistent, and importantly, more confident fit results for sets of potentially noisy spectra.

Third, a simple formalism to estimate the thickness of adsorbate layers based on the ratio between the substrate's and adsorbate's XPS signal is implemented.

A Publication which made heavy use of the poleval package, even for the final figures, is (Engel et al. (2026)).

Statement of Need

XPS spectra are often analyzed using home-developed tools to perform the analysis. Here, results are reported by specifying spectral shapes and background treatment, but often without a public discussion or publication of the actual procedures, or with the use of commercial software (Casa XPS ([N. Fairley, 2018](#); [Neal Fairley et al., 2021](#)), UniFit ([Hesse et al., 1999](#)), etc.).

We find that common open-source source algorithms, including their publication, discussion, and common development, can be extremely beneficial for both the efficiency and scientific rigor of experimental work.

While some open-source software for XPS is available (i.e. (Nakajima (2024)) or (Stansbury & Lanzara (2020))), published software providing a persistent, notebook-style analysis with capabilities for treating, plotting, and fitting inter-dependent sets of XPS spectra quickly and reproducibly is so far lacking.

Our work is inspired by the special environment of synchrotron-based research, which necessitates a frequent information hand-over and near-online data analysis. This motivates the choice of the Jupyter ecosystem, where a documented form of the proceedings (markdown descriptions, headers and source code together with spectra and analysis results) is inherently generated and can be worked on continually by several shifts of scientists performing an experiment over several days. Complex datasets often probe a certain dimension and vary one parameter over sets of spectra. Consequently, POLEVAL enables quick plotting with many functions being able to get a single line of code to combine a complex data set, while also enabling a smooth transition into non-standard in-depth analysis within the same framework.

The next step after loading and manipulating data is analyzing the spectral contributions. The ability to enforce consistent (or even equal) peak shape parameters over entire measurement series is essential, especially in chemically sensitive applications (Major et al., 2020), yet no software published for XPS so far provides this functionality, to the best of the authors knowledge.

The big strength of XPS is that it is quantitative; a spectrum can be related to the absolute abundance of chemical species in the sample surface-near region. Experiments in the HAXPES regime using grazing incidence X-rays necessitate a modeling of the X-ray penetration length in combination with the electron emission pathway. This feature is implemented in the tool such that, given the incidence angle and an average adsorbate composition, sample surface coverages can be quantified in terms of monolayers.

Implementation

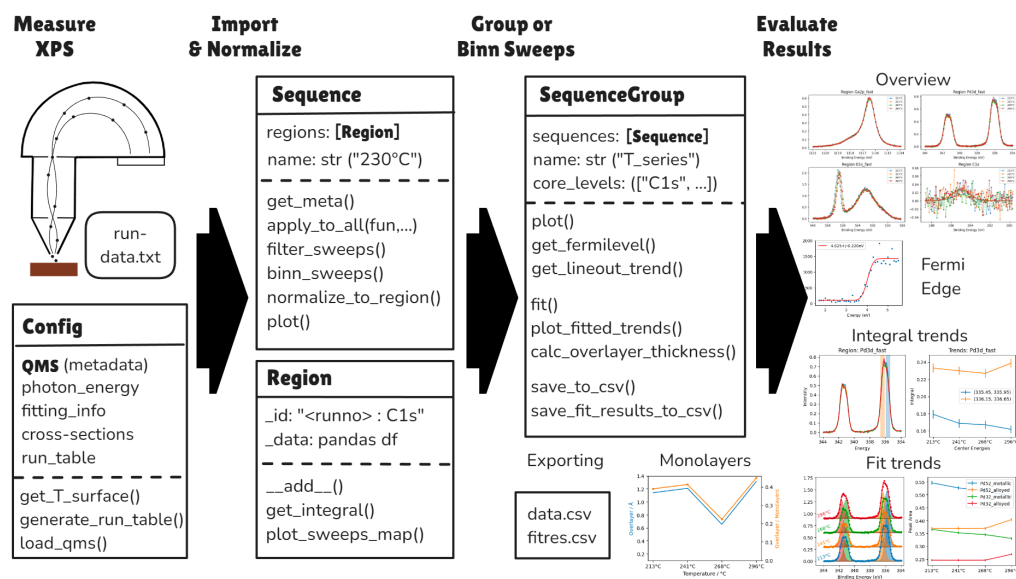


Figure 1: Data pipeline using the poleval package, showing the key classes and their most important properties and methods as well as typical result plots.

The principal functions of POLEVAL are illustrated in **Figure 1**. Spectra and acquisition settings are read from text files generated by the SES software that controls the Scienta XPS analyzer. While XPS data from CSV-, SPECS, and XY-files can be read and other formats could easily be added, the import from Scienta's SES text files is tested most.

Spectra are organized in Region objects that represent electronic core levels. Each Region object represents a single core level spectrum and retains information of the individual sweeps as well as the normalizations applied in the import step.

An experiment typically compares sets of regions, which are recorded together in an interleaved manner; Region objects are thus organized into Sequence objects, which correspond to a loaded file. Key scientific insights often emerge from analyzing trends - be it dependent on time, temperature, gas pressure or other experimental variables. Such comparisons are enabled by the SequenceGroup class.

A SequenceGroup can be generated either from a list of separately imported and treated Sequence objects or, if applicable, by breaking up and binning the sweeps contained in the Regions of a single Sequence. Each of these classes contains rich functionality to facilitate the manipulation and intermediate visualization of data, while also maintaining reproducibility of each data treatment step taken. A Config object is used to store global settings, such as the photon energy, but also fit models for each core level and metadata in form of a QMS object, which can be used for binning or generating a run table as an experiment overview, as well as associating the recorded spectra with simultaneously recorded Quadrupole Mass Spectrometer (QMS) and sample temperature data.

The peak fitting algorithm is based on the `lmfit` package, but operates on all Regions of the same core level within one SequenceGroup, and allows for dependency constraints between fit parameters. Common applications are to enforce a common (yet variable) peak width across multiple peaks and spectra, or to define a fixed ratio or distance between peak parameters in one spectrum. Defining such constraints by imposing prior knowledge helps to restrict the information content that must be extracted from potentially noisy data, and thus reduces the uncertainty of the fit results.

Similarly, the estimation of the adsorbate overlayer thickness requires a set of parameters, such as the lattice and atomic constants of each material involved, to be defined explicitly before an estimate can be computed. The mathematical model is laid out in the README.

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