TexTOM - a software for texture simulations

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January 27, 2025

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1 Introduction

1.1 Texture Tomography

Texture tomography is a way of inverting tomographic X-ray diffraction data into local orientation distribution functions (ODF) of diffracting crystallites. It relies on a priori-knowledge of the crystal structure and from there models diffraction patterns. For parameter optimisation it refines the coefficients of harmonic basis functions constructing the ODF. This approach is particularly suited for polycrystalline materials with relatively wide orientation distributions, such as biomineralized tissue.

For a detailled description of mathematical model and the experimental procedure refer to Frewein, M. P. K., Mason, J., Maier, B., Colfen, H., Medjahed, A., Burghammer, M., Allain, M. & Grünewald, T. A. (2024). IUCrJ, 11, 809-820. https://doi.org/10.1107/S2052252524006547
and references therein.

1.2 Installation

TexTOM was written and tested in Python 3.11 and in principal requires only a python installation (3.9 to 3.12) and a terminal. It is conceived to be used in iPython through a terminal, but can be imported into scripts or jupyter notebooks.

The TexTOM core for reconstructions currently depends on external packages such as Scipy, Numba, H5py, Orix, pyFAI and Mumott.

We recommend creating conda environment and installing the package via pip. Install Anaconda or Miniconda (https://docs.anaconda.com/miniconda/install/)

```
conda create --name textom python=3.11
conda activate textom
```

then

```
pip install textom
```

Two of the packages (pyFAI and Mumott) provide GPU support for their functionalities. These require additional drivers such as Cudatoolkit for Nvidia graphics cards, which can be installed via

```
conda install cudatoolkit
```

Please refer to the documentations of the respective packages and your hardware to find out what drivers are required. In case no drivers are found, the software will fall back to computation via CPU.

To start TexTOM in iPython mode, make sure your environment is activate and type `textom`. All TexTOM core functions (5) will be available in the namespace.

You can also import them into a script or jupyter notebook:

```
from textom.textom import *
```

TexTOM Source code is available on: `https://gitlab.fresnel.fr/textom/textom/`.

2 Configuration

After installing or updating TexTOM, we recommend opening the configuration file primarily to set how many CPUs your machine has for data processing. Type `textom_config` in your terminal and it will open the config file in your standard text editor. A standard config file will look like the following:

```
import numpy as np # don't delete this line
################################################

# Define how many cores you want to use
n_threads = 128

# Choose if you want to use a GPU for integration and alignment (True/False)
use_gpu = True

# Choose your precision
# recommended np.float64 for double or np.float32 for single precision
data_type = np.float32
```

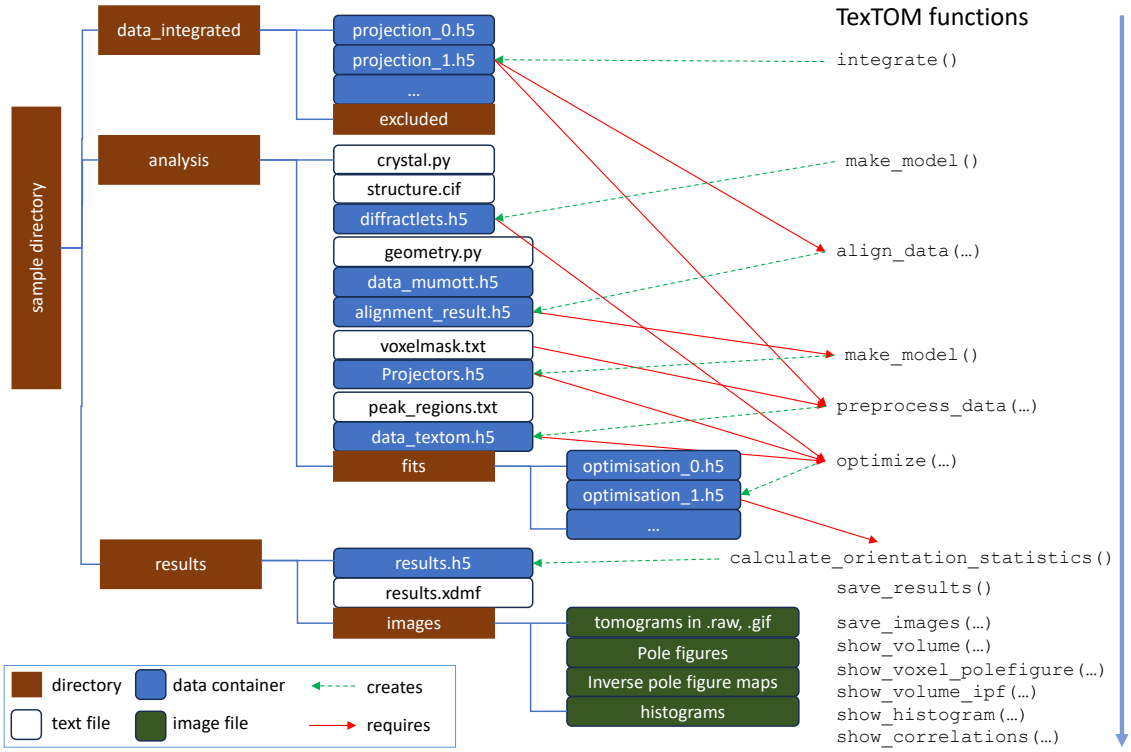
If `n_threads` is larger than the available number, it will fall back to the maximum possible number. After making your changes, you can save the file and close it.

3 Handling of the TexTOM software

TexTOM is conceived as a commandline software in iPython. Its high-level library (section 5) is aimed to be usable without advanced knowledge in python programming. Part of its user-interface consist of files created in the sample directory. In this directory TexTOM organises intermediate results automatically. Any part of the analysis can therefore be revisited and retraced. Upon startup, TexTOM assumes that the sample directory is the one where the program is started, so the recommended way is to type

```
cd /path/to/my/sample/direcory/
```

prior to starting textom via the command line. Alternatively, you can set the sample directory globally via the command `set_path('path')` after starting or importing TexTOM.



The follwing chart shows the structure of the sample directory and its subdirectories (red). It is recommended to start the analysis in an empty directory, the subdirectories will be created automatically.

Blue files are .h5 data containers, created during the workflow. For compatibility it is not recommended to create or modify these other than through the TexTOM pipeline.

White files are human-legible text files, that can be created or modified using a text editor or a custom script. They will be created through user input during the execution of the function in the main line in the graphic. If a .py or .txt file is present in the directory prior to calling the

corresponding function, the present file will be used instead of asking for user input. This is handy for analysing a series of samples that share experimental parameters.

Green files are images for direct usage or export into other software, such as Paraview, Dragonfly or standard image viewers.

The functions on the right are printed in the order of a suggested workflow, as the arrows indicate. There is some freedom in the order of doing the steps, as long as the requirements as shown by the red arrows are respected. The state of the analysis can be checked either by manually inspecting the directory or through the function `check_state()`.

The following table shows functions useful for overall handling of the analysis:

	`set_path('path')`	Set sample directory (or start `textom` there)
	`check_state()`	Shows the progress in analysis of the current sample
	`help('function_name')`	Prints information about TexTOM functions in the terminal

4 Workflow

4.1 Data acquisition

Recording data for texture tomography is a great challenge and can only be done at appropriate synchrotron beamlines. This package contains a few scripts for the experiments but we recommend contacting a beamline scientist experienced in tensor/texture tomography or 3D-XRD in order to create acquisition scripts suitable for the beamline.

4.2 Data integration

The first step in data processing is integration, i.e. azimutal rebinning ("caking") of the 2D-carthesian detector images. Here we rely on the pyFAI package (`https://pyfai.readthedocs.io`). This part already requires good knowledge of your data, as you do not want to miss any peaks when choosing the integration range. We recommend to do a test-integration during the experiment, to set up the correct .poni-file which is needed for the integration. This file defines the geometry of the experiment and can be created using the command pyFAI-calib. Make sure to also collect the correct detector mask and optionally files for flatfield and darkcurrent correction.

To start the integration, in your terminal navigate to a directory which will further contain all textom analysis data (further labelled `sample_dir`).

```
cd /path/to/textom/sample_dir
```

Then start textom by typing textom in your terminal. You can start the integration using the command `integrate()`, upon which a file containing all necessary parameters will open:

```
############ Input ###############
path_in = 'path/to/your/experiment/overview_file.h5'
h5_proj_pattern = 'mysample*.1'
h5_data_path = 'measurement/eiger'
h5_tilt_angle_path = 'instrument/positioners/tilt' # tilt angle
h5_rot_angle_path = 'instrument/positioners/rot' # rotation angle
h5_ty_path = 'measurement/dty' # horizontal position
h5_tz_path = 'measurement/dtz' # vertical position
h5_nfast_path = None # fast axis number of points, None if controt
h5_nslow_path = None # slow axis number of points, None if controt
h5_ion_path = 'measurement/ion' # photon counter if present else None

# Integration mode
mode = 2 # 1: 1D, 2: 2D, 3: both

# parallelisation
n_tasks = 8
cores_per_task = 16

# Parameters for pyFAI azimuthal integration
rad_range = [0.01, 37] # radial range
rad_unit = 'q_nm^-1' # radial parameter and unit ('q_nm^-1', ''2th_deg', etc)
```

```
azi_range = [-180, 180] # azimuthal range in degree
npt_rad = 100 # number of points radial direction
npt_azi = 120 # number of points azimuthal direction
npt_rad_1D = 2000 # number of points radial direction
int_method=('bbox','csr','cython') # pyFAI integration methods
poni_path = 'path/to/your/poni_file.poni'
mask_path = 'path/to/your/mask.edf'
polarisation_factor= 0.95 # polarisation factor, usually 0.95 or 0.99
flatfield_correction = None
solidangle_correction = True
darkcurrent_correction = None
##############################
```

The first part contains information about your data. We assume that these are stored in `.h5` files as common practice at the ESRF. The first line is the overview file that contains links to all datasets. In the second line you can specify which files should be integrated using a pattern with a * serving as a placeholder for other characters. In the following there are the `.h5` internal paths to the necessary metadata for TexTOM, which will be carried into the integrated files. `h5_nfast_path` and `h5_nslow_path` are only relevant if the experiment was performed in scanning mode, upon which all data of one projection will be in the same data array with the horizontal and vertical position not specified. If the experiment was performed in continuous rotation mode, these parameters can be set to None. The last parameter is optional for the measurement of an ionisation chamber or diode, which records the incoming photon flux during the respective measurement.

Then choose the integration mode, 2D is required for TexTOM, 1D can be done additionally e.g. for diffraction tomography.

In the next block declare on how many CPUs you want to work parallely, the `n_tasks` specifies how many files will be integrated at the same time, `cores_per_task` means how many CPUs work on each task.

The last block are parameters for pyFAI, of particular importance are the radial range, which should cover your peaks and the number of points (npt_rad), which should be enough to resolve the individual peaks (although the code will also handle overlapping peaks or peaks which are in a single bin to the cost of some information loss). The required angular resolution depends on the sharpness of the features in the data in azimutal direction, keep in mind that it is recommended to use a similar angular resolution for the construction of orientation distribution functions and diffractlets, where the computation time will scale with the power of 3 of the number of angular sampling points `npt_azi`. Furthermore, point to the files you received from your beamline and specify angular resolution etc. File paths should be compete paths and don't need to be in the sample directory, nor need to be accessible during the following steps.

	`integrate()`	Opens the `integration_parameters.py` file and performs the integration

4.3 Alignment

Data is aligned fully automatically using the function:

```
align_data(
```

```
pattern='.h5', sub_data='data_integrated',
q_index_range=(0,5), q_range = False,
mode='optical_flow', crop_image=False,
regroup_max=16,
redo_import=False, flip_fov=False,
align_horizontal=True, align_vertical=True,
pre_rec_it = 5, pre_max_it = 5,
last_rec_it = 40, last_max_it = 5,
  )
```

The first step of the alignment is the sorting of the data. Go to the `data_integrated` or `data_integrated_1d` directory created by the integration script and make sure that all .h5 files are valid datasets, which you want to use for the reconstruction (other file extensions will be ignored). Move files that you don't want to use to a subfolder (e.g. named excluded). The program uses all data in the `sub_data directory` with pattern in the filename. By default it uses data in `data_integrated/`, you can use others by typing e.g. `align_data(sub_data='data_integrated_1d')`

Next, choose the q-range you want to use for alignment. You can use indices in the to restrain the q-values using the `q_index_range parameter` or give a `q-range` directly in the units specified in the `radial_units` field in the data (this parameter has priority if specified). TexTOM will average over all data in this range and treat them as scalar tomographic data for alignment. We recommend using either the SAXS region of the sample or a bright peak with little azimutal variation.

TexTOM uses the alignment code from the Mumott tensor tomography package, which contains 2 pipelines. By default we use the optical flow alignment, but you can choose phase matching alignment in the parameters. If you want to crop the projections, set the `crop_image` parameter to the desired borders (e.g. ((0,-1),(10,-10)) for the full image in x-direction, while cropping 10 points at the top and bottom) Take note that cropping only works with the phase matching alignment, which will be chosen automatically if crop_image is defined.

The textom alignment pipeline will downsample the data by combining blocks of 2x2 pixels until arriving at the sampling defined by `regroup_max`, by default 16, corresponding to a downsampling to blocks of 16x16 pixels. Then the alignment will start at the lowest sampling, take the found values and proceed to the next highest until it reaches the original sampling. This approach has proven efficient, but can be omitted by setting `regroup_max=1`.

For the remaining parameters see the description further down.

When you start the alignment, it will open a file labelled geometry.py, which contains information about the experimental setup. Most parameters are equivalent to the Mumott notation (`https://mumott.org/tutorials/inspect_data.html#Geometry`), which defines the arrangement of sample, detector, rotation and tilt angles. In addition, you need to define beam diameter, step size and scanning mode.

When you close and save the file, it will be automatically stored in `sample_dir/analysis/geometry.py` and in the following, this file will be used. You can also create a geometry file in sample_dir/analysis/ prior to starting the alignment, then this file will directly be used (e.g. when you have several samples from the same beamtime, copy the geometry file after defining it for the first sample.). The default values are given for the configuration published in Frewein et al. IUCRJ (2024).

After aligning, function will create the file `analysis/alignment_result.h5` in the sample directory, which contains the shifts found in the process. Refer to this file for checking sinograms and tomograms after alignment. You can also use the funciton `check_alignment_consistency()`

to check if there are projections wich deviate from the model. Inspect them and their agreement with the data using `check_alignment_projection(g)`, where g is an integer number corresponding to the projection number. This number is assigned after sorting the data files alphabetically. The x-axis label in the plot shown by `check_alignment_consistency()` uses the same labelling.

If you choose to add, remove or change data or changing the q-range after doing an alignment, redo the alignment with the setting redo_import=True. Else it will not respect the changes you made. If you just want to change the number of interations or the regrouping, this is not necessary.

	`align_data(...)`	Aligns data and provides a tomogram
	`check_alignment_consistency()`	Plots the resiuals per projection
	`check_alignment_projection(g)`	Plots the residuals per pixel for projection g

4.4 Model

Next you have to calculate the model, which consists of 2 parts: Diffractlets and Projectors.

Diffractlets are calculated from the crystal structure given by a `.cif` file, you have to provide. When you start the model calculation using `make_model()`, you will receive another file to edit (`crystal.py`), containing information about the location of your `.cif` file, X-ray energy, q-range and desired angular resolution. Save the file and it will be copied to `sample_dir/analysis/crystal.py`. The function will create the file crystal.h5, containing the diffractlets. As this calculation can be lengthy, it is advised to perform it in advance and reuse `diffractlets.h5` for other samples. If `sample_dir/analysis/` contains already a `diffractlets.h5` file, it will use this without asking.

The projectors contain information on which voxels contribute to which pixel in the data and depend on a finished alignment. Once you finished the alignment you can start calculating the projectors, which requires some more user input for masking the sample. The program will open a histogram of voxels based on the tomogram resulting from alignment. Choose the lower cutoff to mask out voxels with low or zero density of crystallites, upon which you will be shown a 3D outline of the sample. You can remove other parts of the sample using the input in the figure. After processing, this will create a file `analysis/projectors.h5`, which is used in further processing of this specific sample.

	`make_model()`	Creates the model, takes separate input for diffractlet and projector calculations.

4.5 Data Pre-processing

When the model is ready, the data has to pass through a pre-processing step, where it is filtered according to which data is masked, then renormalized and outliers are removed. You will be also asked to choose the q-ranges around the peaks you would like to use for optimization, and to define the detector mask. Text files will be created, these can be re-used for other samples and will be automatically chosen if present in the `analysis/` directory. There is also a simple background subtraction pipeline, which can be turned on using the argument `draw_baselines=order_polynomial`. Note that this feature is still experimental and might not work with every sample.

	preprocess_data()	Imports data and makes them usable for TexTOM

4.6 Optimization

If all previous steps have been performed, you can start an optimization.

	optimize(...)	Performs an optimization of specified order and mode
	optimize_auto(...)	Performs a series of optimizations, stepwise increasing the order
	adjust_data_scaling()	Rescales data for improved azimutal optimization
	list_opt()	Shows stored optimization files
	load_opt(...)	Loads a stored optimization
	check_lossfunction()	Plots the evolution of the loss function through the current optimization
	check_fit_average()	Plots
	check_fit_random(...)	
	check_residuals()	
	check_projection_average()	
	check_projection_residuals()	
	check_projection_orientations()	

4.7 Analysis

	calculate_orientation_statistics()	Calculates mean orientation and standard deviation in each voxel
	calculate_segments(...)	Simple segmentation based on misorientation between voxels
	save_results()	
	list_results()	
	load_results(...)	

4.8 Visualisation

	show_volume(...)	
	show_volume_ipf(...)	
	show_slice_ipf(...)	
	show_voxel_odf(...)	
	show_voxel_polefigure(...)	
	show_histogram(...)	
	show_correlations(...)	
	save_images(...)	

5 Functions

set_path(path)

```
Set the path where integrated data and analysis is stored

Parameters
----------
path : str
    full path to the directory, must contain a folder '/data_integrated'
```

ToC

---

check_state()

```
Prints in terminal which parts of the reconstruction are ready
```

ToC

---

integrate()

```
Integrates raw 2D diffraction data via pyFAI

All necessary input will be handled via the file integration_parameters.py
```

ToC

---

align_data(pattern='.h5', sub_data='data_integrated', q_index_range=(0, 5), q_range=False, crop_image=False, mode='optical_flow', redo_import=False, flip_fov=False, regroup_max=16, align_horizontal=True, align_vertical=True, pre_rec_it=5, pre_max_it=5, last_rec_it=40, last_max_it=5)

```
Align data using the Mumott optical flow alignment

Requires that data has been integrated and that sample_dir contains
a subfolder with data

Parameters
```

```
----------
pattern : str, optional
    substring contained in all files you want to use, by default '.h5'
sub_data : str, optional
    subfolder containing the data, by default 'data_integrated'
q_index_range : tuple, optional
    determines which q-values are used for alignment (sums over them), by
        default (0,5)
q_range : tuple, optional
    give the q-range in nm instead of indices e.g. (15.8,18.1), by default
        False
crop_image : bool or tuple of int, optional
    give the range you want to use in x and y, e.g. ((0,-1),(10,-10)), by
        default False
mode : str, optional
    choose alignment mode, 'optical_flow' or 'phase_matching', by default '
        optical_flow'
redo_import : bool, optional
    set True if you want to recalculate data_mumott.h5, by default False
flip_fov : bool, optional
    only to be used if the fov is in the wrong order in the integrated
    data files, by default False
regroup_max : int, optional
    maximum size of groups when downsampling for faster processing, by
        default 16
align_horizontal : bool, optional
    align your data horizontally, by default True
align_vertical : bool, optional
    align your data vertically, by default True
pre_rec_it : int, optional
    reconstruciton iterations for downsampled data, by default 5
pre_max_it : int, optional
    alignment iterations for downsampled data, by default 5
last_rec_it : int, optional
    reconstruciton iterations for full data, by default 40
last_max_it : int, optional
    alignment iterations for full data, by default 5
```

ToC

---

check_alignment_consistency()

```
Plots the squared residuals between data and the projected tomograms
```

ToC

---

check_alignment_projection(g=0)

```
Plots the data and the projected tomogram of projection g

Parameters
----------
g : int, optional
    projection running index, by default 0
```

ToC

---

make_model()

```
Calculates the TexTOM model for reconstructions

Is automatically performed by the functions that require it
```

ToC

---

preprocess_data(pattern='.h5', flip_fov=False, baselines=1, use_ion=True)

```
Loads integrated data and pre-processes them for TexTOM

Parameters
----------
pattern : str, optional
    substring contained in all files you want to use, by default '.h5'
flip_fov : bool, optional
    only to be used if the fov is in the wrong order in the integrated
    data files, by default False
baselines : bool, optional
    choose if you want to draw polynomial baselines
    set the polynomial order in the argument or False, by default 1
use_ion : bool, optional
    choose if you want to normalize data by the field 'ion' in the
    data files, by default True
```

ToC

---

make_fit(redo=True)

```
Initializes a TexTOM fit object for reconstructions

Is automatically performed by the functions that require it

Parameters
----------
redo : bool, optional
    set True for recalculating, by default True
```

ToC

---

optimize(order=0, mode=0, proj='full', zero_peak=None, redo_fit=False, tol=0.001, minstep=1e-09, itermax=3000, alg='quadratic', save_h5=True)

```
Performs a single TexTOM parameter optimization

Parameters
----------
order : int, optional
    maximum sHSH order to be used, by default 0
mode : int, optional
    set 0 for only optimizing order 0, 1 for highest order, 2 for all,
    by default 0
proj : str, optional
    choose projections to be optimized: 'full', 'half', 'third', 'notilt',
    by default 'full'
zero_peak : int or None
    index of the peak you want to use for 0-order fitting (should be as
    isotropic as possible), if None uses the whole dataset, default None
redo_fit : bool, optional
    recalculate the fit object, by default False
tol : float, optional
    tolerance for precision break criterion, by default 1e-3
minstep : float, optional
    minimum stepsize in line search, by default 1e-9
itermax : int, optional
    maximum number of iterations, by default 3000
alg : str, optional
    choose algorithm between 'backtracking', 'simple', 'quadratic',
    by default 'quadratic'
save_h5 : bool, optional
    choose if you want to save the result to the directory analysis/fits,
    by default True
```

ToC

---

optimize_auto(max_order=8, start_order=None, zero_peak=None, tol_0=1e-07, tol_1=0.001, tol_2=0.0001, minstep_0=1e-09, minstep_1=1e-09, minstep_2=1e-09, projections='full', alg='quadratic', adj_scal=False, redo_fit=False)

```
Automated TexTOM reconstruction workflow

Parameters
----------
max_order : int, optional
    maximum HSH order to be used, by default 8
start_order : int or None, optional
    lowest order to be fitted, if None continues where you are standing,
    by default None
zero_peak : int or None
    index of the peak you want to use for 0-order fitting (should be as
    isotropic as possible), if None uses the whole dataset, default None
redo_fit : bool, optional
    recalculate the fit object, by default False
proj : str, optional
    choose projections to be optimized: 'full', 'half', 'third', 'notilt',
        by default 'full'
alg : str, optional
    choose algorithm between 'backtracking', 'simple', 'quadratic',
    by default 'quadratic'
```

ToC

---

adjust_data_scaling()

```
Reestimates the data based on the assumption that normalization constants
contain noise. To be used after fitting the 0th order
```

ToC

---

list_opt()

```
Shows all stored optimizations
```

ToC

---

load_opt(h5path='last')

```
Loads a previous Textom optimization into memory
seful: load_opt(results['optimization'])

Parameters
----------
h5path : str, optional
    filepath, just filename or full path
    if 'last', uses the youngest file is used in analysis/fits/,
    by default 'last'
```

ToC

---

check_lossfunction()

```
No docstring available.
```

ToC

---

check_fit_average()

```
Plots the reconstructed average intensity for each projection with data

Parameters
----------
```

ToC

---

check_fit_random(N=10, mode='line')

```
Generates TexTOM reconstructions and plots them with data for random points

Parameters
----------
N : int, optional
    Number of images created, by default 10
mode : str, optional
    plotting mode, 'line' or 'color', by default line
```

ToC

---

check_residuals()

```
Plots the squared residuals summed over each projection
```

ToC

---

check_projections_average(G=None)

```
Plots the reconstructed average intensity for chosen projections with data

Parameters
----------
G : int or ndarray or None, optional
    projection indices, if None takes 10 equidistant ones, by default None
```

ToC

---

check_projections_residuals(G=None)

```
Plots the residuals per pix3l for chosen projections with data

Parameters
----------
G : int or ndarray or None, optional
    projection indices, if None takes 10 equidistant ones, by default None
```

ToC

---

check_projections_orientations(G=None)

```
Plots the reconstructed average orientations for chosen projections with
    data

Parameters
----------
G : int or ndarray or None, optional
    projection indices, if None takes 10 equidistant ones, by default None
```

ToC

---

calculate_orientation_statistics()

```
Calculates prefered orientations and stds and saves them to results dict
```

ToC

---

calculate_segments(thresh=10, min_segment_size=30, max_segments_number=31)

```
Segments the sample based on misorientation borders

Parameters
----------
thresh : float, optional
    misorientation angle threshold inside segment in degree, by default 10
min_segment_size : int, optional
    minimum number of voxels in segment, by default 30
max_segments_number : int, optional
    maximum number of segments (ordered by size), by default 32
```

ToC

---

show_volume(data='scaling', plane='z', colormap='inferno', cut=1, save=False, show=True)

```
Visualizes the whole sample by slices, colored by a value of your choice

Parameters
----------
data : str or list, optional
    name of one entry in the results dict or list of entries,
    by default 'scaling'
plane : str, optional
    sliceplane 'x'/'y'/'z', by default 'z'
colormap : str, optional
    identifier of matplotlib colormap, default 'inferno'
    https://matplotlib.org/stable/users/explain/colors/colormaps.html
cut : int, optional
    cut colorscale at upper and lower percentile, by default 0.1
save : bool, optional
    saves tomogram as .gif to results/images/, by default False
show : bool, optional
    open the figure upon calling the function, by default True
```

ToC

---

show_slice_ipf(h, plane='z')

```
Plots an inverse pole figure of a sample slice

Parameters
----------
h : int
    height of the slice
plane : str, optional
    slice direction: x/y/z, by default 'z'
```

ToC

---

show_volume_ipf(plane='z', save=False, show=True)

```
Plots inverse pole figures as a tomogram with a slider to scroll through
    the sample

Parameters
----------
plane : str, optional
    slice direction: x/y/z, by default 'z'
save : bool, optional
    saves tomogram as .gif to results/images/, by default False
show : bool, optional
    open the figure upon calling the function, by default True
```

ToC

---

show_histogram(x, nbins=50, cut=0.1, segments=None, save=False)

```
plots a histogram of a result parameter

Parameters
----------
x : str,
    name of a scalar from results
bins : int, optional
    number of bins, by default 50
cut : int, optional
```

```
    cut upper and lower percentile, by default 0.1
segments : list of int, optional
    list of segments or None for all data, by default None
save : bool/str, optional
    saves image with specified file extension, e.g. 'png', 'pdf'
    if True uses png, by default False
```

ToC

---

show_correlations(x, y, nbins=50, cut=(0.1, 0.1), segments=None, save=False)

```
Plots a 2D histogram between 2 result parameters

Parameters
----------
x : str,
    name of a scalar from results
y : str,
    name of a scalar from results
bins : int, optional
    number of bins, by default 50
cut : tuple, optional
    cut upper and lower percentile of both parameters, by default (0.1,0.1)
segments : list, optional
    list of segments or None for all data, by default None
save : bool/str, optional
    saves image with specified file extension, e.g. 'png', 'pdf'
    if True uses png, by default False
```

ToC

---

show_voxel_odf(x, y, z, num_samples=1000)

```
Show a 3D plot of the ODF in the chosen voxel

Parameters
----------
x : int
    voxel x-coordinate
y : int
    voxel y-coordinate
z : int
    voxel z-coordinate
```

```
num_samples : int/float, optional
    number of samples for plot generation, by default 1000
```

ToC

---

show_voxel_polefigure(x, y, z, hkl=(1, 0, 0), mode='density', alpha=0.1, num_samples=10000.0)

```
Show a polefigure plot for the chosen voxel and hkl

Parameters
----------
x : int
    voxel x-coordinate
y : int
    voxel y-coordinate
z : int
    voxel z-coordinate
hkl : tuple, optional
    Miller indices, by default (1,0,0)
mode : str, optional
    plotting style 'scatter' or 'density', by default 'density'
alpha : float, optional
    opacity of points, only for scatter, by default 0.1
num_samples : int/float, optional
    number of samples for plot generation, by default 1e4
```

ToC

---

save_results()

```
Saves the results dictionary to a h5 file in the results/ directory
```

ToC

---

list_results()

```
Shows all results .h5 files in results directory
```

ToC

---

load_results(h5path='last', make_bg_nan=False)

```
Loads the results from a h5 file do the results dictionary

Parameters
----------
h5path : str, optional
    filepath, just filename or full path
    if 'last', uses the youngest file is used in results/,
    by default 'last'
make_bg_nan : bool, optional
    if true, replaces all excluded voxels by NaN
```

ToC

---

list_results_loaded()

```
Shows all results currently in memory
```

ToC

---

save_images(x, ext='raw')

```
Export results as .raw or .tiff files for dragonfly

Parameters
----------
x : str,
    name of a scalar from results, e.g. 'scaling'
ext : str,
    desired file type by extension, can do 'raw' or 'tiff', default: 'raw'
```

ToC

---

help(method=None, module=None, filter='')

```
Prints information about functions in this library

Parameters
----------
method : str or None, optional
```

```
    get more information about a function or None for overview over all
        functions, by default None
module : str or None, optional
    choose python module or None for the base TexTOM library, by default
        None
filter : str, optional
    filter the displayed functions by a substring, by default ''
```

ToC
