auTomo Documentation

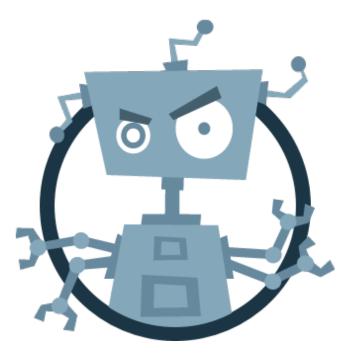
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Contents

1	Features	3
2	Contribute	5
3	Content	7



auTomo provides automation to several tomography data analysis tasks.

CHAPTER 1

Features

- Automatically organizes the directory, creates an individual folder for HDF5 files associated with each sample
- Comes with preset scripts for tomography processing
- Automatically processes single field-of-view and 360-degree samples
- Generates bash commands that calls scripts for mosaic tomography processing (powered by Tomosaic).

CHAPTER 2

Contribute

- Documentation: https://github.com/decarlof/automo/tree/master/doc
- Issue Tracker: https://github.com/decarlof/automo/docs/issues
- Source Code: https://github.com/decarlof/automo/automo

CHAPTER 3

Content

3.1 Install directions

This section covers the basics of how to download and install auTomo.

3.1.1 Installing from source (recommended)

Installing from source can be done easily by running the setup script:

```
git clone https://github.com/decarlof/automo.git automo
cd automo
python setup.py install
```

The script will ask whether you want to add a line in your .bashrc file so that bash will automatically add the macros folder in the Automo source directory to your \$PATH variable. This is necessary if you would like to use the feature of calling Automo script directly from bash command line. If you prefer to have the scripts, the configuration file (automo.ini), and the parameter setting file (automo_params.csv) somewhere else, you need to manually copy them there. For example, to move the files to ~/.automo, follow the above commands by

```
mkdir ~/.automo
cp macros ~/.automo
export PATH=~/.automo:$PATH
```

Subsequently, add the last line export PATH=~/.automo:\$PATH to your ~/.bashrc.

3.1.2 Installing from conda

auTomo has an conda install script that does all the job. Please follow the script:

```
git clone https://github.com/decarlof/automo.git automo
cd automo
conda build .
conda install --use-local automo
```

3.2 Overview

Automo creates and/or executes processing operation commands based on the configuration file (default to be automo_ini) and the parameter setting file (default to be automo_params.csv). You can specify the path to both files when running automo_process_dir and automo_create_commands.

3.2.1 Configuration file

automo.ini contains the settings that define the behavior of Automo as well as the processing processures to be taken for different types of tomography data. Below is the content of a sample file (also available in the macros folder):

```
[settings]
default_h5_fname
                   = data.h5
[robos]
tomo_180
                   = automo_preview, automo_center, automo_search_center, automo_
⇔recon
tomo 360
              = automo_preview_360, automo_center_360, automo_search_center, automo_
⇔recon_360
tomosaic
              = automo_tomosaic_create_meta, automo_tomosaic_reorg, automo_tomosaic_

→preview, automo_tomosaic_center, automo_tomosaic_recon

              = preview, center, recon
std
[robos_move]
tomo_180
                   = new_folder
          = new_fo
= new_folder
tomo_360
tomosaic
             = existing_folder
std
              = new_folder
[robos_rename]
tomo_180
                   = False
tomo_360
               = False
tomosaic
               = False
std
               - True
```

The robos section specifies the workflow that Automo should adopt for each of the three types of tomography data (the *std* entry is for the exception case where Automo fails to recognize the data files as any of the three categories):

- tomo_180: single field-of-view tomography
- tomo_360: off-centered 360-degree tomography
- tomosaic: mosaic tomography using the Tomosaic acquisition scheme

The data type is automatically detected according to the naming pattern of the HDF5 files. It is thus necessary to keep a consistent naming style as listed in the table below:

Data type	Naming pattern
tomo_180	*_180_*.h5 (must contain _180_)
tomo_360	*_360_*.h5 (must contain _360_)
tomosaic	*_y_?_x_?_*.h5 (indices start from 0)

Automo will execute commands (for tomo_180 and tomo_360) or create bash command scripts (for tomosaic) following the order at which operations are listed. The name of the operations, such as automo_preview, or automo_tomosaic_reorg, must match the name of the processing scripts contained in the macros directory.

When running automo_process_dir in the folder containing all HDF5 data files collected in a beamtime, the robos_move section tells Automo whether to move a file into a new directory named exactly after the basename of the file (new_folder) or to move it into an existing folder named after the prefix of the filename (existing folder; useful for tomosaic). It is recommended to keep the default settings as shown in the sample file above.

The robos_rename section specifies whether Automo should rename the moved HDF5 file according to the setting in settings/default_h5_fname. Keep this setting as False for tomosaic unless specifically needed.

3.2.2 Parameter file

automo_params.csv contains the parameter settings for all operations. The parameters of the same operation must stay in the same line with names and values separated by a semicolon (;). The file should follow the format of

operation_name; param_1_name; param_1_value; param_2_name; param_2_value; ...

If an optional parameter is not provided in the csv file, it will use the default value. Please refer to the docstring of an operation script (for example, automo_tomosaic_center --help) to get help on the names and meanings of all its parameters. As in the case of the ini file, operation_name's must match operation scripts contained in the macros folder.

3.3 Demonstration

3.3.1 Starting processing

In the directory containing all collected HDF5 data files, run

```
automo_process_dir
```

You can use the --ini_file and --params_file flags to specify the location and filenames of the configuration and parameter files. Otherwise, Automo will use the files in the macros folder of its source directory. After moving each file to the proper folder, Automo does the following:

- If the file is of type tomo_180 or tomo_360, Automo runs operation scripts according to the sequence and parameters specified in the ini and csv files. After the operations finish, a bash script with executed commands will be created in the folder.
- If the file is of type tomosaic, Automo will not execute the commands, but will create a bash scripts of commands for the user to execute manually in bash.

If the directory has already been organized either by hand or by the beamline control software, the automo_process_dir can be skipped, and you may want to just generate the bash commands used to run processing operations. For this, type

automo_create_commands --type <tomo_180, tomo_360, or tomosaic>

This tells Automo to generate a bash script file at the current folder, with the operations and parameters provided in the specified (or default) configuration file and parameter file.

3.3.2 Tomosaic workflow

This section talks about the workflow of Tomosaic-type data processing using Automo. Tomosaic allows mosaic tomography reconstruction to be performed either after merging all HDF5 files into a single file with stiching and blending in both x- and y-direction (whole-block mode, WBM), or directly by stitching sinograms in the x-direction (single-slice mode, SSM). While image blending and sub-pixel shifting is currently only supported in WBM, SSM provides a light-weight reconstruction option which demands less memory and hard drive space. The major workflow is summarized in Fig. 2 of the Tomosaic paper.

source/img/tomosaic_workflow.png

The general procedure of Tomosaic processing using Automo is described below. Again, you can utilize automo_create_commands to generate the bash commands with a series of operations.

- 1. In the folder containing the data files of all scanned tiles, run automo_tomosaic_creates_meta with position offset in x and y specified using the --x_shift and --y_shift flags. This creates a file called mosaic_meta.py in the current directory.
- 2. Run automo_tomosaic_reorg --ds 1. This creates a folder called data_raw_1x and moves all

HDF5 files in it. If you want downsampled copies of the data files, modify the -ds flag, with different downsampling levels separated by commas (,). For example, $-ds \ 1, 2, 4$. Files downsampled for 2 times will be saved in folder data_raw_2x, and same pattern for the rest.

- 3. Run automo_tomosaic_preview --frame 0 --pano auto to create separate projections and flat fields at 0 degree, as well as stitched panoramas at 0 and 180 degrees.
- 4. (Optional) Run automo_tomosaic_register to realign the tiles. This creates a file called shifts.txt with each line of it following the format of

If this step is skipped (and thus shifts.txt doesn't exist), Automo will use the shift values provided in the mosaic_meta.py for subsequent procesures.

5. Run automo_tomosaic_center --center_st auto --center_end auto --row_st 0 --row_end auto --mode discrete. Automo try to find the rotation centers for specified rows of tiles. If --center_st or --center_end is set to auto, Automo will guess the range for center search using phase correlation. If --method is set to pc, then the phase correlation results will be final. Otherwise, the range for center searching using manual, entropy, or vo will be set to be +/-5 of the phase correlation guess. For manual and entropy, trial reconstructions will be saved as center/<row_number>/ <center_value>.tiff.

If --method is anything other than manual, or if phase correlation is used to provide the initial guess, then Automo will create a file named center_pos.txt at the current directory, with each line indicating the row number and the center position at that row. Otherwise, you need to manually create this file in order to the reconstruction script to read.

Since setting --method to manual or entropy lets Aumoto create reconstructions, it is also a way to generate reconstruction previews.

- 6. (Only needed for WBM) Run automo_tomosaic_merge to fuse the HDF5 files into a single one. The default name and location of the created file is fulldata_flatcorr_1x/fulldata_flatcorr_1x. h5.
- 7. Run automo_tomosaic_recon for final reconstruction. Make sure the --mode flag is set correctly: use merged for WBM, and discrete for SSM. SSM is recommended if there is only one row of tiles.

By using automo_create_commands --type tomosaic, a bash script following the above procedureS (assuming WBM) can be generated:

Correspondingly, automo.ini should contain the following in the robos section:

automo_params.csv should have the following settings:

```
automo_tomosaic_reorg; ds; 1
automo_tomosaic_create_meta; x_shift; 1000; y_shift; 1000
automo_tomosaic_preview; frame; 0; pano; auto
automo_tomosaic_register
automo_tomosaic_merge
automo_tomosaic_center; center_st; auto; center_end; auto; row_st; 0; row_end; 1;_____
mode; discrete
automo_tomosaic_recon; mode; merged; chunk_size; 5
```

3.3.3 Parallelization

Tomosaic and Automo supports parallel computation using Mpi4Py. To enable parallelization, make sure you have Mpi4py installed, and then simply add mpirun $-n < num_threads>$ in front of each command.

3.4 Credits

3.4.1 Citations

We kindly request that you cite the following article [cite:01] if you use auTomo and/or Tomosaic.

3.4.2 References