RO notes on .h5 and .mx files in this folder and its subfolders: /Users/rudolfo/LightFieldMicroscopy/Simulation/Birefringence/2024\_02/

The .h5 and .mx files were created using the Mathematica Notebook BirefrObjectForwardProjFeb2025.nb

Copied from Notes in the above Mathematica Notebook:

Using the light field data in folder SMS\_2024\_0611\_1248\_1, I created the retardance stack SMS\_2024\_0611\_1248\_1\_RetStack.tif that was further processed. The resolution along the Z-axis was increased from 6.75µm to 5µm, making the resolution isotropic. Some black Z-slices were added at top and bottom, bringing the overall dimensions {Z, Y, X} to {43, 128,128}. Furthermore, to reduce the measured retardance values to voxels that represent the spicule but not the tissue surrounding the spicule, the retardance data was thresholded by setting all retardance values below 8nm to zero. Finally, the stack of retardance data was converted to 8 bit and the resultant volume data are stored in SMS1248RetStackRectScaledThresh.tif. Further details can be gleaned from NotesOnImageData.docx residing with the original experimental data in /Users/rudolfo/LightFieldMicroscopy/Experiments/2024\_06\_11\_SUSpicule

Spicule1248Feb12\_RevZ.h5 -> volume arranged for Z-axis imaging and optic axis array with order opt\_axis[[oA, Z, Y, X]] and oA[[Z, Y, X]]. Since the imaging axis is the Z-axis, the Z-component of the optic axis vectors are either zero or positive.

Spicule1248Feb12\_RevZ.mx -> volume arranged for X-axis imaging and optic axis array with order opt\_axis[[Z, Y, X, oA]] and oA[[X, Y, Z]]. Read .mx files into Mathematica Notebook using Get[] or <<.

I think I found the correct arrangement of the spicule data for Z-axis and X-axis imaging.

It also worked for the Bundle1.h5 data, including with negative birefringence values, as in Bundle1N.h5