test

March 7, 2024

Connected to base (Python)

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[]: # This notebook-style script requires a ~500 MB download from https://www.ebi.
     →ac.uk/biostudies/files/S-BIAD1063/PTI-BIA/Anisotropic_target_small.zip
     import numpy as np
     import matplotlib.pyplot as plt
     from numpy.fft import fftshift
     import waveorder as wo
     from waveorder import optics, waveorder_reconstructor, util, visual
     import zarr
[]: n_media = 1.515 # refractive index of the immersed media for objective (oil: 1.
     →512, water: 1.33, air: 1)
     lambda_illu = 0.532 # illumination wavelength (um)
     mag = 63 # magnification of the microscope
     NA_obj = 1.47 # detection NA of the objective
     NA_illu = 1.4 # illumination NA of the condenser
     N_defocus = 96 # number of defocus images
     N channel = 4 # number of Polscope channels
     N pattern = 9 # number of illumination patterns
     z_step = 0.25 # z_step of the stack
     z_defocus = (np.r_[:N_defocus] - 0) * z_step # z positions of the stack
     ps = (
        3.45 * 2 / mag
     ) # effective pixel size at the sample plane (cam pix/mag in um)
     cali = False # correction for S1/S2 Polscope reconstruction (does not affect
     ⇔phase)
     bg_option = "global" \# background correction method for Polscope recon (does_
     \hookrightarrow not affect phase)
     use_gpu = False # option to use gpu or not (required cupy)
     gpu_id = 0 # id of gpu to use
```