

Ad-Hoc Coordinate Change Algorithm For The Split-Aperture Polarization Microscope

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1 Introduction

The split-aperture polarization microscope can measure the azimuth orientation of a single dipole in two rotated views. These notes describe an algorithm for converting noise-corrupted azimuth orientations in two rotated views into the azimuth and inclination orientation. We define the coordinates, outline the algorithm, then show the error in the estimate with noise-free and noise-corrupted measurements. Finally, we test the algorithm on a set of single-molecule data.

2 Coordinates

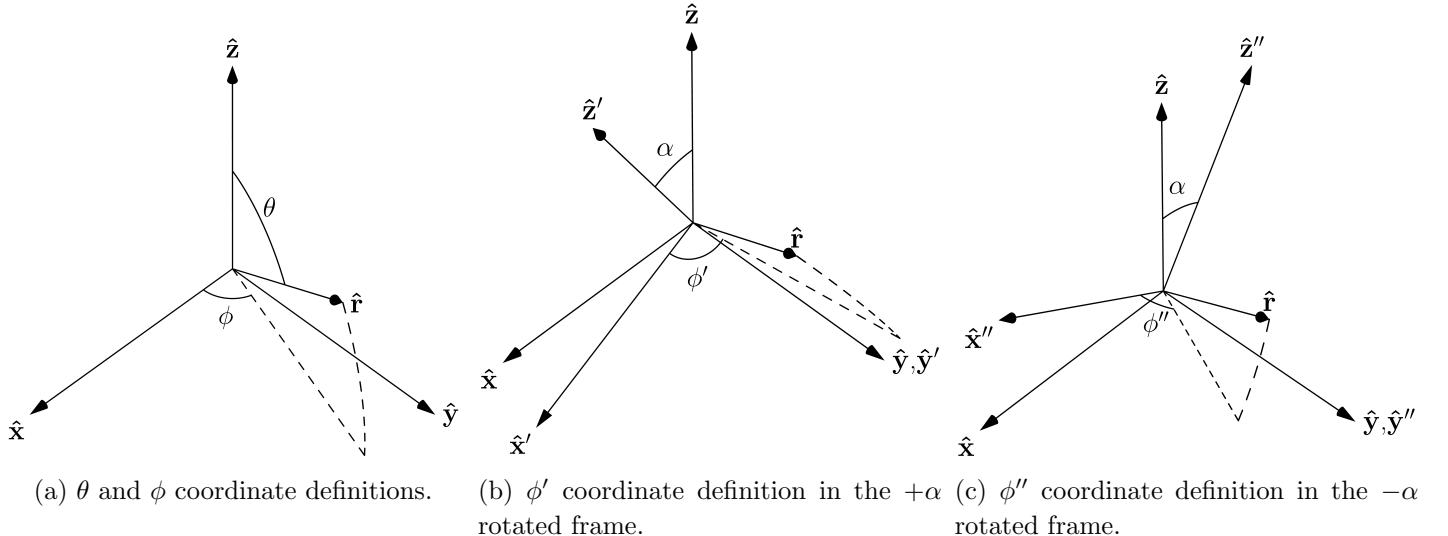


Figure 1: Coordinate definitions.

Figure 1 shows one way of defining the inclination and azimuth angle in the laboratory frame (θ, ϕ) and the azimuth angles in the rotated frames (ϕ', ϕ''). The two rotated frames are given by right-handed rotations about the $+\hat{y}$ axis by an angle α .

In [previous notes](#) I have derived the relationships between the angles in Figure 1. We can reuse those results and write:

$$\phi' = \begin{cases} \arccos\left(\frac{\cos\alpha\cos\phi\sin\theta - \sin\alpha\cos\theta}{\sqrt{1-(\sin\alpha\cos\phi\sin\theta + \cos\alpha\cos\theta)^2}}\right) & 0 \leq \phi < \pi \\ -\arccos\left(\frac{\cos\alpha\cos\phi\sin\theta - \sin\alpha\cos\theta}{\sqrt{1-(\sin\alpha\cos\phi\sin\theta + \cos\alpha\cos\theta)^2}}\right) & -\pi \leq \phi < 0 \end{cases} \quad (1)$$

$$\phi'' = \begin{cases} \arccos\left(\frac{\cos\alpha\cos\phi\sin\theta + \sin\alpha\cos\theta}{\sqrt{1-(\sin\alpha\cos\phi\sin\theta + \cos\alpha\cos\theta)^2}}\right) & 0 \leq \phi < \pi \\ -\arccos\left(\frac{\cos\alpha\cos\phi\sin\theta + \sin\alpha\cos\theta}{\sqrt{1-(\sin\alpha\cos\phi\sin\theta + \cos\alpha\cos\theta)^2}}\right) & -\pi \leq \phi < 0 \end{cases} \quad (2)$$

3 Procedure

Equations 1 and 2 take θ and ϕ as input and give ϕ' and ϕ'' as output. We can rewrite equations 1 and 2 in operator form as

$$\mathbf{g} = \mathcal{H}\mathbf{f} \quad (3)$$

where $\mathbf{g} = [\phi', \phi'']$, $\mathbf{f} = [\theta, \phi]$, and \mathcal{H} denotes the operation in equations 1 and 2. If there is noise introduced in the measurement process then the model becomes

$$\mathbf{g} = \mathcal{H}\mathbf{f} + \mathbf{n} \quad (4)$$

where \mathbf{n} is a noise vector.

Our task is to estimate \mathbf{f} from noise-corrupted measurements \mathbf{g} . To do so, we solve the following problem

$$\tilde{\mathbf{f}} = \operatorname{argmin}_{\mathbf{f}} \|\mathbf{g} - \mathcal{H}\mathbf{f}\|_2 \quad (5)$$

where $\|\cdot\|_2$ denotes the 2-norm. The search space of \mathbf{f} is small enough that a brute-force search is appropriate. First, we evaluate $\mathcal{H}\mathbf{f}$ on a predetermined set of points to construct a lookup table. When we take a measurement \mathbf{g} , we compute $\|\mathbf{g} - \mathcal{H}\mathbf{f}\|_2$ at every point in the lookup table. Finally, we choose the \mathbf{f} that minimizes $\|\mathbf{g} - \mathcal{H}\mathbf{f}\|_2$ and call that our estimate $\tilde{\mathbf{f}}$.

The samples used to construct the lookup table should be equally spaced if we expect the lookup table procedure to introduce an equal amount of error into our estimates. Note that \mathbf{f} is a unit direction ($\mathbf{f} \in \mathbb{S}^2$) so if we equally space the components of \mathbf{f} (θ and ϕ) most of the sample points will be concentrated near the \mathbf{z} axis. Instead of constructing a lookup table with equally spaced θ and ϕ points, I used approximately equally spaced points found using the [Fibonacci sphere algorithm](#).

4 Accuracy Results

I used $\alpha = 30^\circ$ for all tests.

To test the algorithm I chose 2000 equally spaced values of \mathbf{f} , calculated $\mathbf{g} = \mathcal{H}\mathbf{f}$, then used the algorithm with a 500,000 point lookup table to find $\tilde{\mathbf{f}}$. Finally, I found the error $\mathbf{e} = |\tilde{\mathbf{f}} - \mathbf{f}|$ and plotted the individual components of \mathbf{e} in Figure 2.

The 2000 points I tested are not the same points as the lookup table points, so the errors shown in Figure 2 are errors introduced by the lookup table procedure. The error is different for different points because \mathcal{H} is nonlinear and because the points are varying distances from the lookup table points. Each point in Figure 2 took ~ 2 ms to compute. We can trade speed for accuracy in this algorithm by changing the number of points in the lookup table.

I also performed the same test with noise-corrupted data. I chose 2000 equally spaced values of \mathbf{f} , calculated $\mathbf{g} = \mathcal{H}\mathbf{f} + \mathbf{n}$ where \mathbf{n} is a vector of Gaussian noise with $\mu = 0$ and $\sigma = 2^\circ$, then used the algorithm with a 500,000 point lookup table to find $\tilde{\mathbf{f}}$. Again, I found the error $\mathbf{e} = |\tilde{\mathbf{f}} - \mathbf{f}|$ and plotted the individual components of \mathbf{e} in Figure 3.

5 Limitations

Using a precomputed lookup table will always introduce a varying amount of error for different dipole orientations. If we want to have a constant error for all dipole orientations, we could investigate iterative solutions that will stop after a convergence criteria is reached.

This model assumes that

- both views use a narrow detection NA (no D-shaped aperture effects)
- the azimuth angles measured from both views are equally weighted
- the noise on the azimuth angles is normally distributed

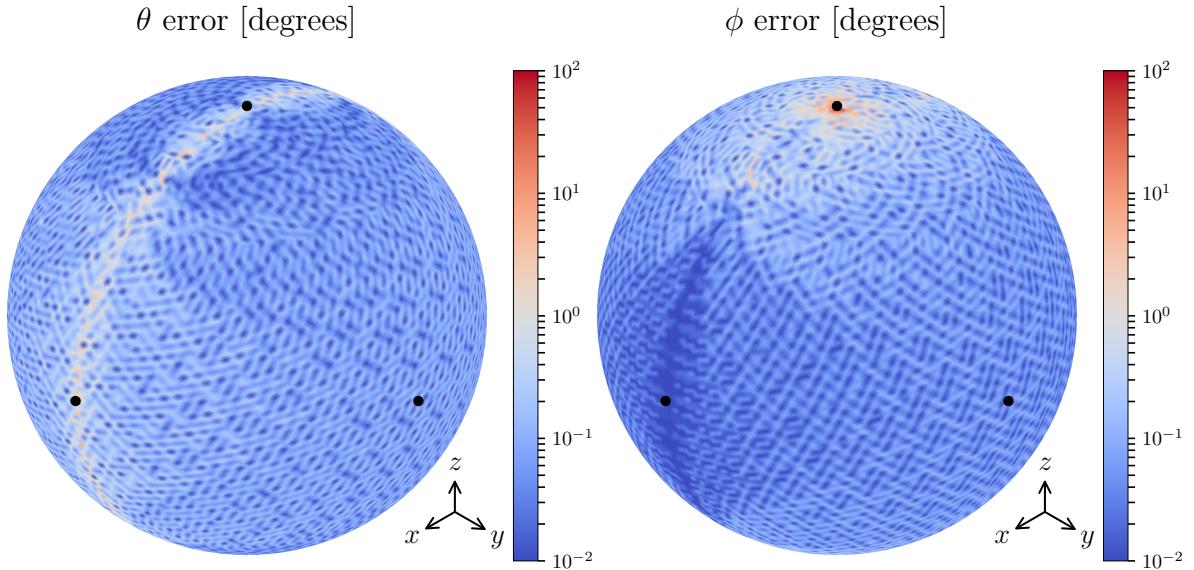


Figure 2: Error introduced by the algorithm with noise-free data.

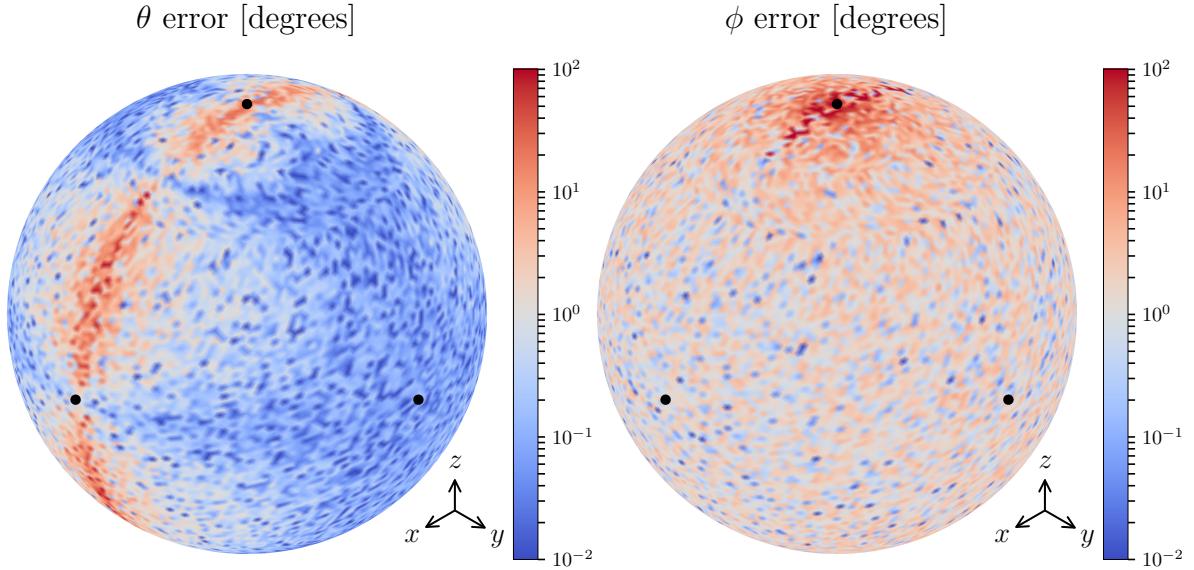


Figure 3: Error in the estimate with noise-corrupted data. I assumed that the two azimuth angle measurements had normally distributed noise with $\mu = 0$ and $\sigma = 2^\circ$.

6 Test Data Results

Tomomi supplied five frames of test data in a .xlsx file. Each frame had ~ 40 single molecules with its x-y position and its azimuthal angle from each view.

I used the algorithm detailed above to calculate the coordinates in the laboratory frame (see Figure 1a)) then plotted the orientations and positions of the molecules in Figures 4-8. The origin is marked by a dot in the top corner. The data was supplied without units, so the scale bar may be in units of μm or pixels.

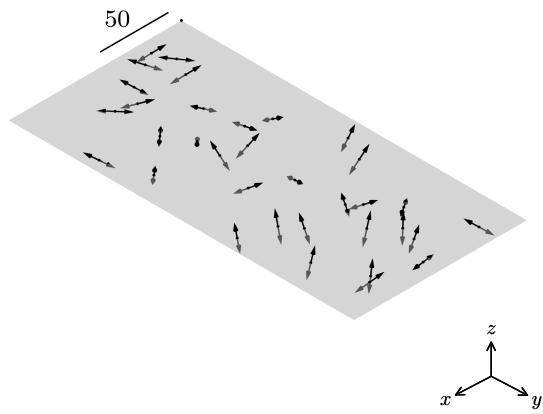


Figure 4: Frame 1.

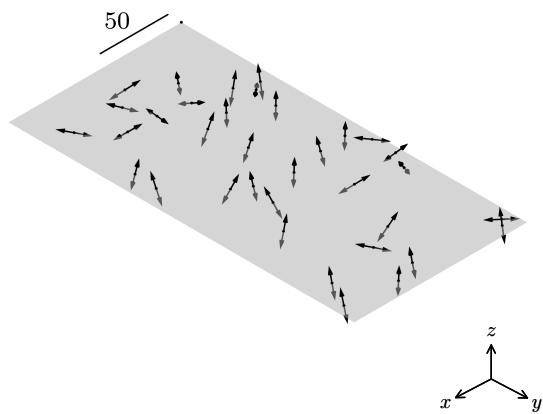


Figure 5: Frame 2.

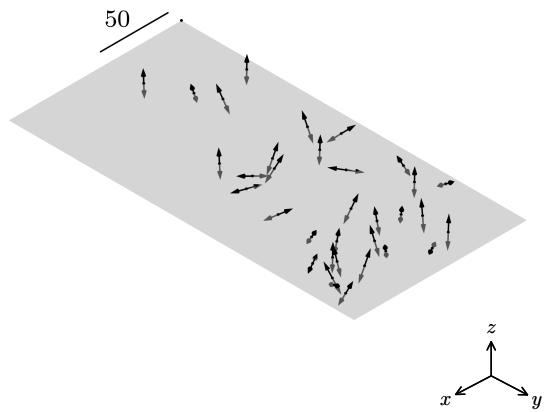


Figure 6: Frame 3.

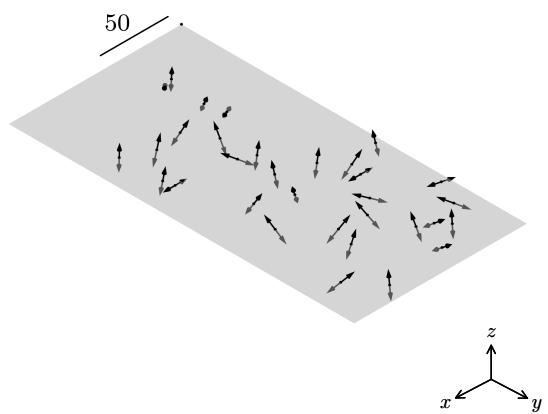


Figure 7: Frame 4.

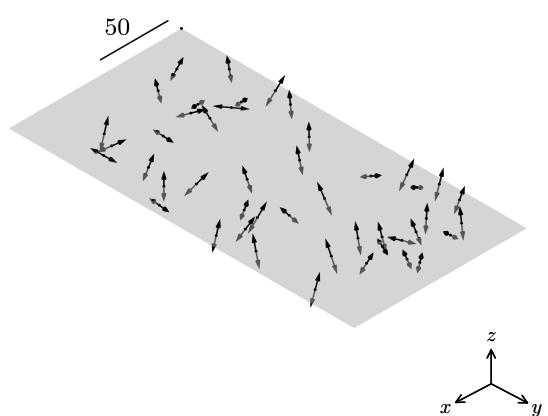


Figure 8: Frame 5.