MaoMi + RANA

Fast tissue optics for microscopy

MaoMi generates microscopy movies from neural anatomy and activity. Its CUDA engine accelerates tissue optics; RANA models the local PSFs, polarization and exposure times that determine the recorded signal.

49.1×

faster optical calculation

NAOMi / MATLAB CPU	**179.644 s**
MaoMi / Standard CUDA	**3.662 s**

Full sampling, closely matching images

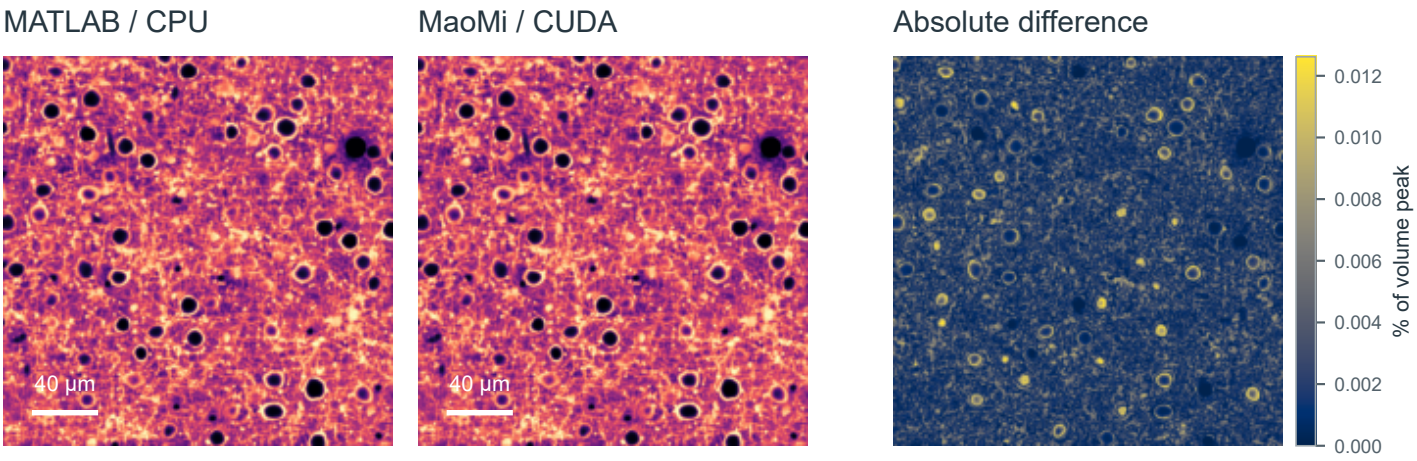


Figure 1. Plane 30 of the 512 × 512 × 60 volume. MATLAB and MaoMi share one linear display range; the difference panel uses the full reference-volume peak. Relative L2 difference over all voxels: **0.00667%**. Scale bars: 40 µm. [1]

WORKLOAD

65 × 65 propagation sites, 0.5 µm voxels, identical saved tissue, scattering input and pupil. Three serial calls per route; medians on Ryzen 9 7950X and RTX 3080, CUDA batch 8.

TIMED OPERATIONS

Phase preparation, propagation, both optical tails and mask assembly. Input generation, static scanning, startup and file I/O are outside the timed stage. [1]

What the optical model changes

RANA combines depth-dependent aberration, vectorial diffraction, finite voxel and scan integration, and pulse/spectral response. This experiment removes those effects one at a time, then all together.

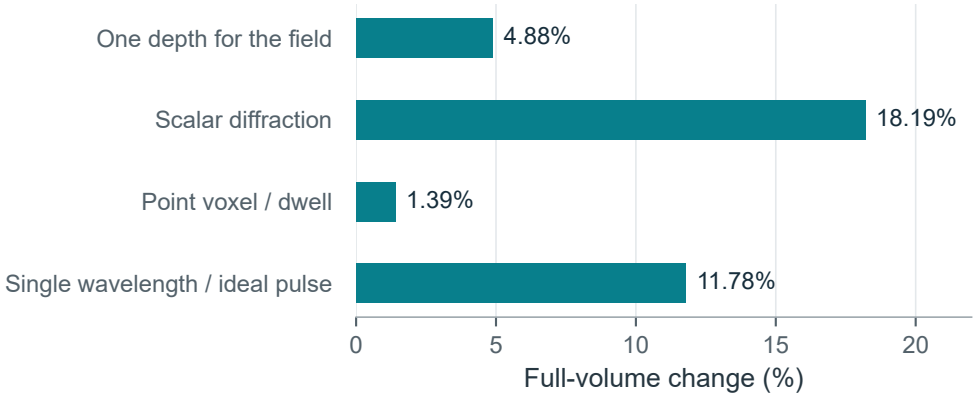


30.31%

Full-volume change from four simplifications. Density and exposure are fixed. The simplified model uses one focal-depth field, scalar diffraction, point sampling and a single wavelength with an ideal pulse. [2]

Figure 2. Plane 9 of the 256 × 256 × 16 volume. The first two panels use one linear scale; the difference is relative to their common plane peak. NA 1.1; specimen/immersion index 1.38/1.33; depth 50–62 µm. Scale bars: 5 µm.

Which effects account for the change?



0.1030%

difference from finer depth, angle, voxel, scan and spectral quadrature.

RENDER COST
0.206 s CPU
0.088 s CUDA
23.42 s CPU PSF build

Figure 3. Full-volume relative L2 change for each separate simplification. This published reference uses MaoMi's standalone global cubic RBF renderer. The shared movie workflow uses compact positive cubic interpolation. [2]

Connect specimens, optics and readout

MaoMi accepts original NAOMi tissue and activity files, editable cell recipes and external PSFs. The RayOptics example produces paired measurements while saving the specimen and individual cell components. [3]

01 Cells Geometry and density > **02 Optics** RayOptics PSF > **03 Signal** Expected electrons > **04 Noise** Poisson + read noise

Separate the specimen from the measurement target

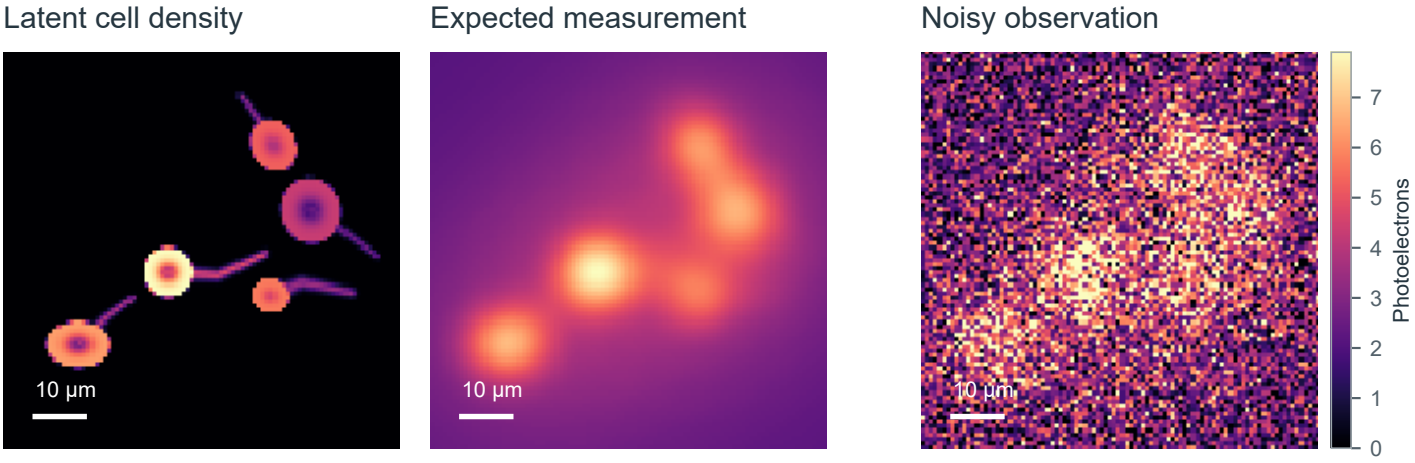


Figure 4. Published RayOptics → MaoMi thin-section example. Five editable cells, a ray-traced lens PSF and 32 detected electrons per density unit; background 2 electrons, read noise 1 electron RMS. The expected and noisy images share a scale. This 96² scene spans 80.88 µm. Scale bars: 10 µm. [3]

Connections beyond the optical path

Cell geometry	Edit position, soma axes, brightness, nuclear depression and branch paths in a cell recipe.
Neural activity	Import cell traces with the tissue; the timed route interpolates activity at exposure times.
Paired datasets	Nine scenes × four doses produce 36 pairs. Keep all dose/noise variants of each scene in one dataset split.

Motion happens during the scan

The RANA movie renderer moves the fluorescent specimen before applying the local PSFs. Each pixel then integrates the changing photon rate over its exposure window; detector noise is applied after integration. [4]

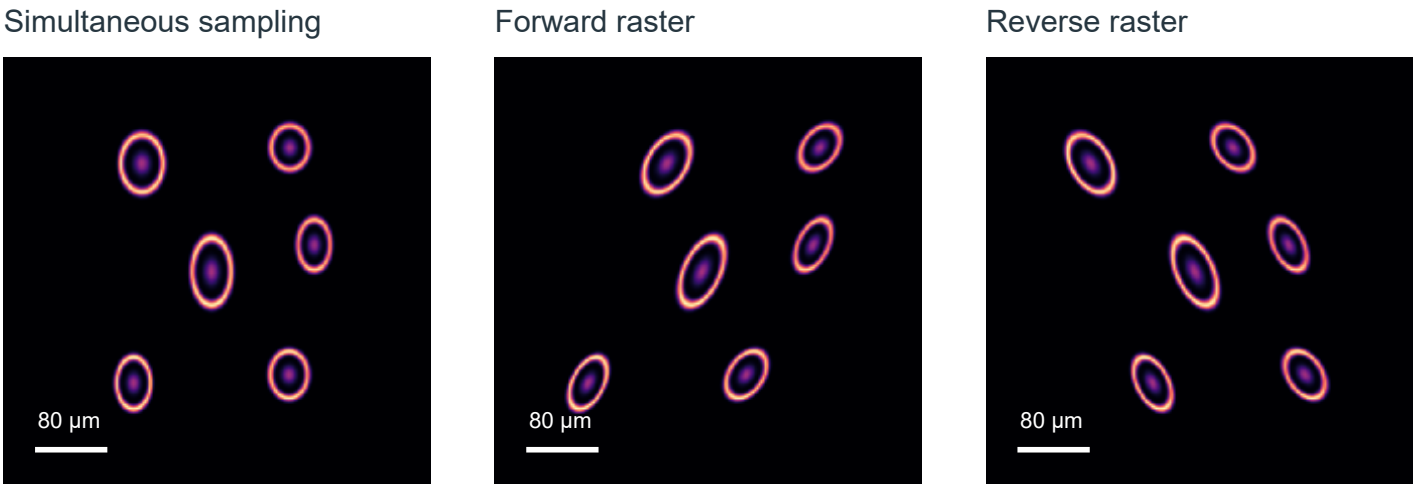
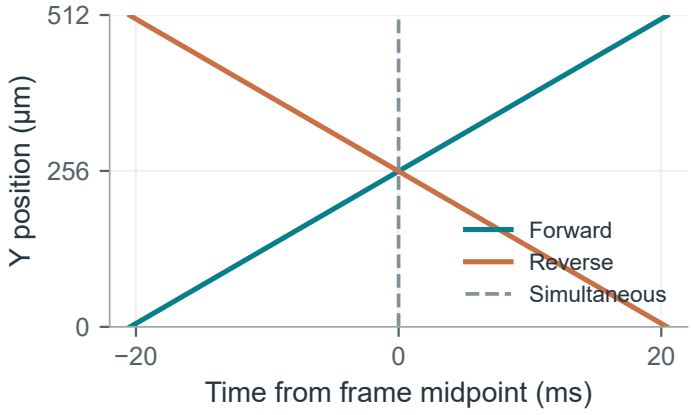


Figure 5. The released 512² moving-cell example, using four spatially varying Gaussian PSFs. Cells move at 4 mm/s along X; the raster scans along Y over 40.93 ms. Dwell is 100 ns and line period is 80 µs. Reversing the row order reverses the shear. All images share the frame midpoint and display scale. Scale bars: 80 µm. [4]



Refine the time sampling

0.1889%

Full-image change from 513 to 1,025 temporal snapshots. This run uses `run_scene` with `RanaAddon` from the released MaoMi package.

Reproduce with MaoMi 0.8.0b1

[1] Song et al., NAOMi, J. Neurosci. Methods 358, 109173 (2021). Matched 4,225-site benchmark: dense_4225/summary.json.
[2] examples/rana_comparison.py · physics, quadrature and costs.
[3] examples/rayoptics_custom_psf.py · cell recipes and paired data.
[4] examples/timed_acquisition.py · clock, units and movie integration.
New figures 4–5 were executed on 27 October 2026; figures 1–3 reuse the recorded MaoMi benchmarks.