The apparent position of single molecules changes depending on the degree of rotational confinement, parameterized by a cone half-angle $\alpha$, even though the molecule isn’t truly moving in $x$ or $y$.

These localization errors can be as large as $\sim 170$ nm, compared to $\sim 10-20$ nm localization precision for single molecule-based super-resolution microscopy. Mislocalization errors be bounded to $\leq 10$ nm only for cone angles $\alpha > 60^\circ$.

Simulations demonstrate how low or high rotational mobility can cause resolution degradation or distortion in super-resolution reconstructions.