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The Molecular Atlas Project JESSE SILVERBERG, PENG YIN, Wyss Institute for Biologically Inspired Engineering, Harvard University — The promise of super-resolution microscopy is a technology to discover new biological mechanisms that occur at smaller length scales then previously observable. However, with higher-resolution, we generally lose the larger spatial context of the image itself. The *Molecular Atlas Project* (MAP) directly asks how these competing interests between super-resolution imaging and broader spatially contextualized information can be reconciled. MAP enables us to acquire, visualize, explore, and annotate proteomic image data representing 7 orders of magnitude in length ranging from molecular (nm) to tissue (cm) scales. This multi-scale understanding is made possible by combining multiplexed DNA-PAINT, a DNA nanotechnology approach to super-resolution imaging, with "big-data" strategies for information management and image visualization. With these innovations combined, MAP enables us to explore cell-specific heterogeneity in ductal carcinoma for *every cell* in a cm-sized tissue section, analyze organoid growth for advances in high-throughput tissue-on-a-chip technology, and examine individual synapses for connectome mapping over extremely wide areas. Ultimately, MAP is a fundamentally new way to interact with multiscale biophysical data.

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