# High Throughput Connectomics

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─── **Abstract** ───

Connectomics is an emerging field of neurobiology that uses cutting edge machine learning and image processing to extract brain connectivity graphs from electron microscopy images. It has long been assumed that the processing of connectomics data will require mass storage and farms of CPUs and GPUs and will take months if not years. This talk will discuss the feasibility of designing a high-throughput connectomics-on-demand system that runs on a multicore machine with less than 100 cores and extracts connectomes at the terabyte per hour pace of modern electron microscopes. Building this system required solving algorithmic and performance engineering issues related to scaling machine learning on multicore architectures, and may have important lessons for other problem spaces in the natural sciences, where until now large distributed server or GPU farms seemed to be the only way to go.