In recent decades, stereology-based studies have played a significant role in understanding brain aging and developing novel drug discovery strategies for treatment of neurological disease and mental illness. A significant obstacle to further progress in a wide range of neuroscience sub-disciplines remains the lack of high-throughput technology for stereology analyses. Though founded on methodologically unbiased principles, commercially available stereology systems still rely on well-trained humans to manually count hundreds of cells within each region of interest (ROI). Even for a simple study with 10 controls and 10 treated animals, cell counts typically require over a month of tedious labor and high costs. Furthermore, these studies are prone to errors and poor reproducibility due to human factors such as subjectivity, variable training, recognition bias, and fatigue. This presentation highlights some of the previous deep learning approaches for detection and segmentation of nuclei in histopathology images and application of unbiased stereology. Additionally, a deep learning approach will be presented for automating cell count in unbiased stereology. Moreover, an iterative deep learning with a human-in-the-loop approach is shown to enhance unbiased stereology counting performance of a model.