# **Nucleus Counting Challenge**

The conference will run a nucleus counting challenge to evaluate the-state-of-the-art nucleus multi-channel segmentation algorithms from fluorescent images of brain tissue. The choice of brain tissue is motivated by the complexity and variability of nuclei morphology and staining patterns and intensity in the brain, which requires multiple stains and multi-channel segmentation analyses.

**Challenge:** Participants of the nucleus counting challenge will be able to download three sets of 2-channel fluorescence images of the brain tissue from the NIST web site (URL link). The images are 2048 x 2048 pixels or 666 micrometers x 666 micrometers, 16 bits per pixel, in Tiff file format. Two nuclear labels for each image dataset are provided: DAPI, which is a ubiquitous stain of all nuclear DNA and NeuN nuclear protein, which is specifically expressed only in neurons. The tasks for the participants is to count the total number of cells and neurons visually and then use/design/customize any algorithm that will report a segmentation mask and the number of segmented nuclei in both DAPI and NeuN channels. As some of the neuronal nuclei stain well for NeuN but not with DAPI, an algorithm providing the associative nuclear masking using both DAPI and NeuN channels is required to obtain high-fidelity nucleus counts. The mask and the visual and algorithmic estimates of total and neuronal nucleus counts should be emailed to the challenge chair. The masks should be in a Tiff file format. The submission and notification deadlines follow the conference paper deadlines.

**Evaluation:** The challenge committee will determine visually the nucleus mask and the counts of total number of nuclei and nuclei specific to the neuronal population for each image dataset. The accuracy of the nucleus counting results will be determined by comparing two measures: (1) visual estimates of nucleus counts and (2) nucleus masks. All participants of the challenge would meet at the conference to reach the consensus of visual counts and to identify the best algorithm.

**Nucleus Counting** **Chair:** Dr. Dragan Maric, NIH

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