



# St. Jude BioHackathon

## **Title**

Automated quantification and classification pipeline for tissue sections and specific morphologies

## **Category**

Image Analysis

## **Challenge**

Develop an automated quantification and classification pipeline for immunohistochemical (IHC) or immunofluorescent (IF) images stained for proteins like Iba1, a cytoplasmic microglial marker. Image analysis of this kind usually involves using paid software, which can be prohibitive to some groups, require lots of hands-on interaction, do not perfectly capture all of the real signals within an image, and usually cannot perform more advanced morphological classification. Plugins for open-source image software like ImageJ/Fiji have been developed, and while these work well for images with isolated cells, they tend to struggle with tissue sections with densely packed cells.

## **Benefit**

Many groups at St. Jude rely on IHC or IF to identify, quantify, and classify different cell types in diverse tissue types. Identification of different cell states (i.e. activated vs inactivated microglia, which are both positive for Iba1 but differ in morphology) is a key step to understanding underlying biological processes.

## **Helpful Tools, Packages, or Software**

Possibly ImageJ/Fiji and associated plugins (i.e. adapting something like AutoNeuriteJ), Python, Cell Pose (<https://www.cellpose.org>), or other imaging software.

## **Test Data**

TIFF images from adult mouse brains with various tumor types that have been stained for Iba1 (a cytoplasmic marker), Olig2 (a mutually exclusive nuclear marker), and DAPI (a nuclear stain), which we would be happy to share (n>4).