

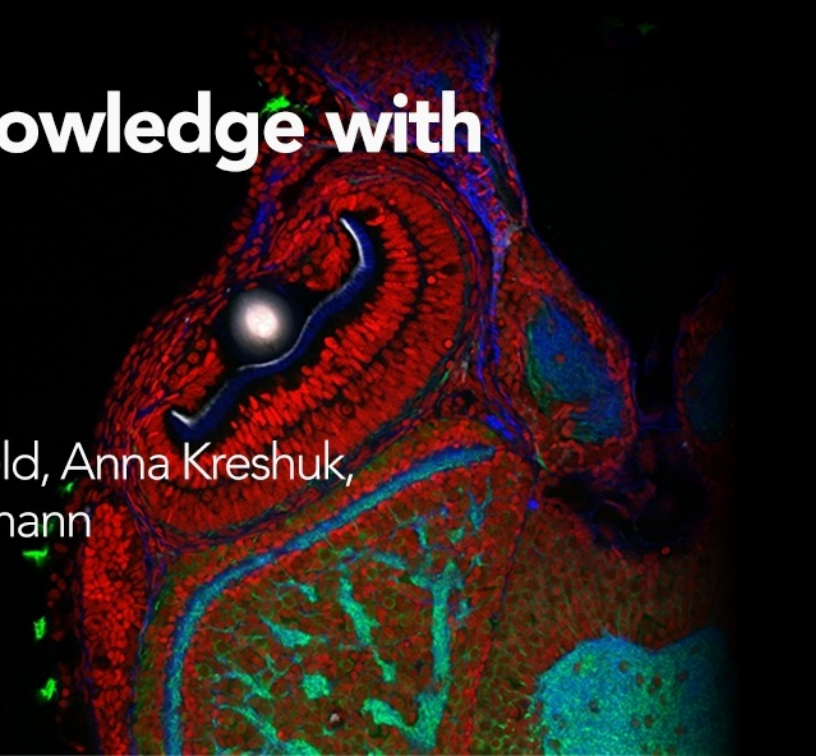
# From Images to Knowledge with ImageJ & Friends

virtual conference

**Nov 30 - Dec 2, 2020**

Stephan Preibisch, Stephan Saalfeld, Anna Kreshuk,  
Pavel Tomancak and Virginie Uhlmann

hhmi | janelia  
Conferences



## Cellpose and Suite2p: functional and anatomical algorithms for cellular segmentation

**Tutors:** Carsen Stringer ([stringerc@janelia.hhmi.org](mailto:stringerc@janelia.hhmi.org))

**Session 1:** 2020-11-30 15:00 UTC – 2020-11-30 19:00 UTC

**Session 2:** 2020-11-30 21:00 UTC – 2020-12-01 01:00 UTC

## Cellpose and Suite2p: functional and anatomical algorithms for cellular segmentation

Many biological applications require the segmentation of cell bodies, membranes and nuclei from microscopy images. We therefore developed a generalist, deep learning-based segmentation algorithm called Cellpose, which can very precisely segment a wide range of image types out-of-the-box and does not require model retraining or parameter adjustments. Additionally, many scientists acquire functional imaging data of neural activity. We developed Suite2p, a functional segmentation algorithm, that performs well on a variety of functional imaging data. In this tutorial we will run cellpose using a variety of images. We will also run suite2p on a short segment of calcium imaging data. We will cover how to assess the performance of the algorithms' results using the graphical user interfaces provided by each software tool.

### Tutorial:

At the beginning of the tutorial, participants will need to create an anaconda environment using a text file that I will provide (that will contain all the dependencies of both software packages). The participants will therefore need to have Anaconda for Python 3 installed on their laptops. The computing resources required for both packages are low so a standard laptop will work. We will next run sample images in cellpose and look at the output. We will discuss how to train models on new image labels if performance is poor. If students bring their own data we can discuss the results too and potential solutions to issues with the segmentation. Next we will run suite2p on a short segment of data and discuss the output of the pipeline. Just like with cellpose, if participants have their own data and certain aspects of the processing fail, we can discuss how the software can be improved to fit their data.