

Tutorial on how to generate xml files for ggPlantmap

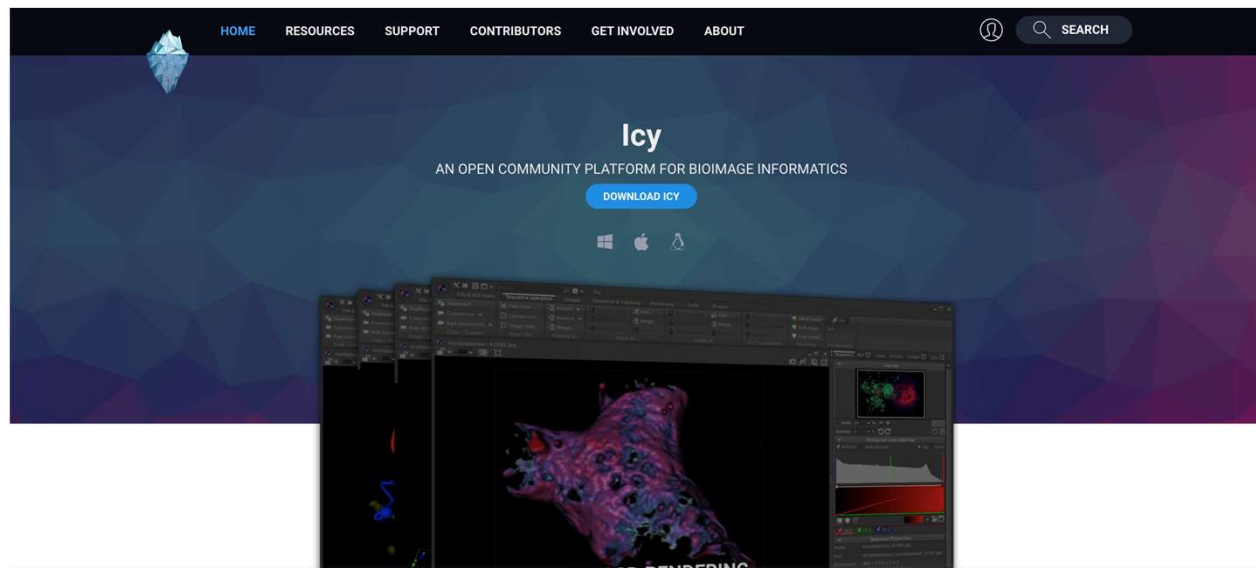
Leonardo Jo

Sept/2023

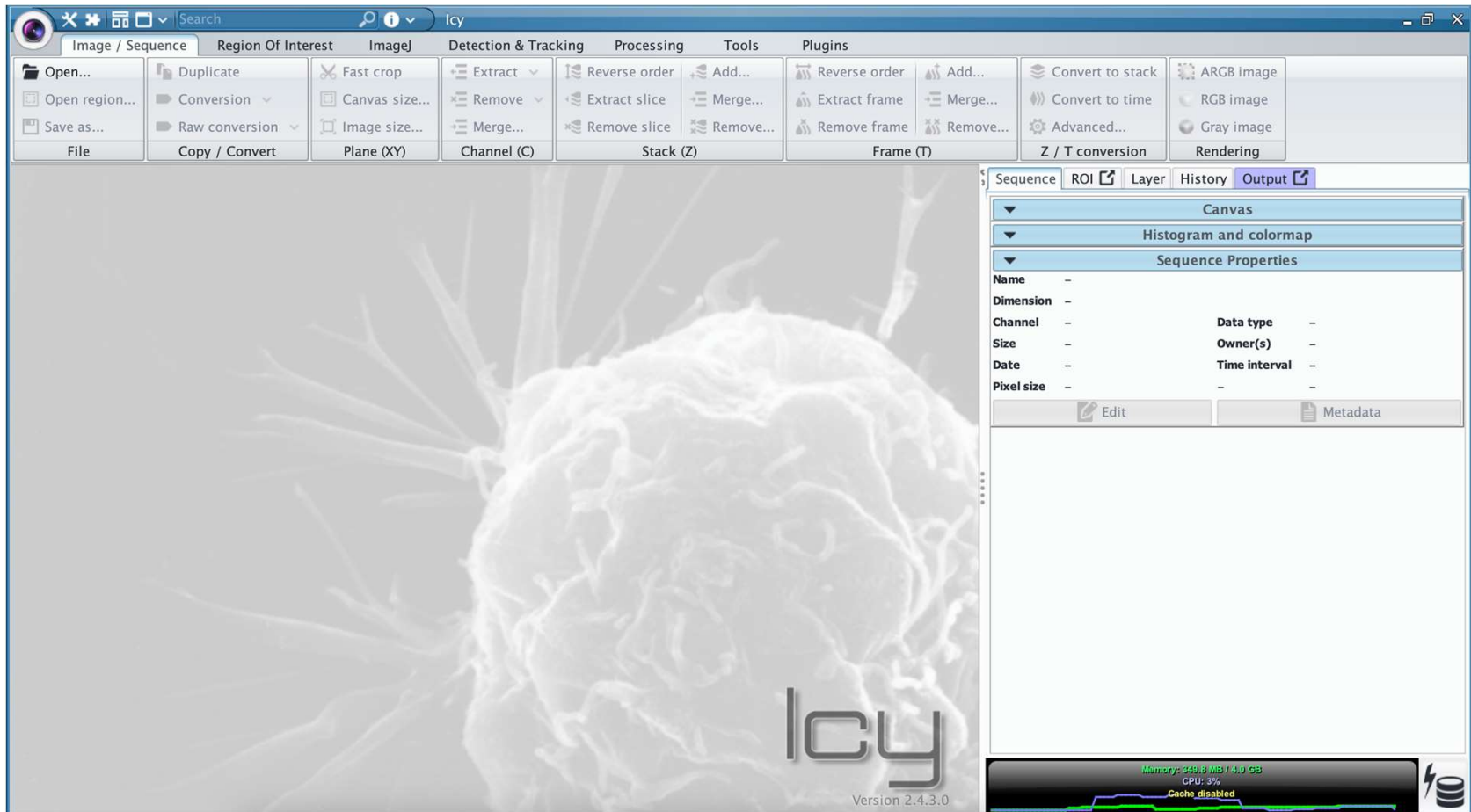


Software

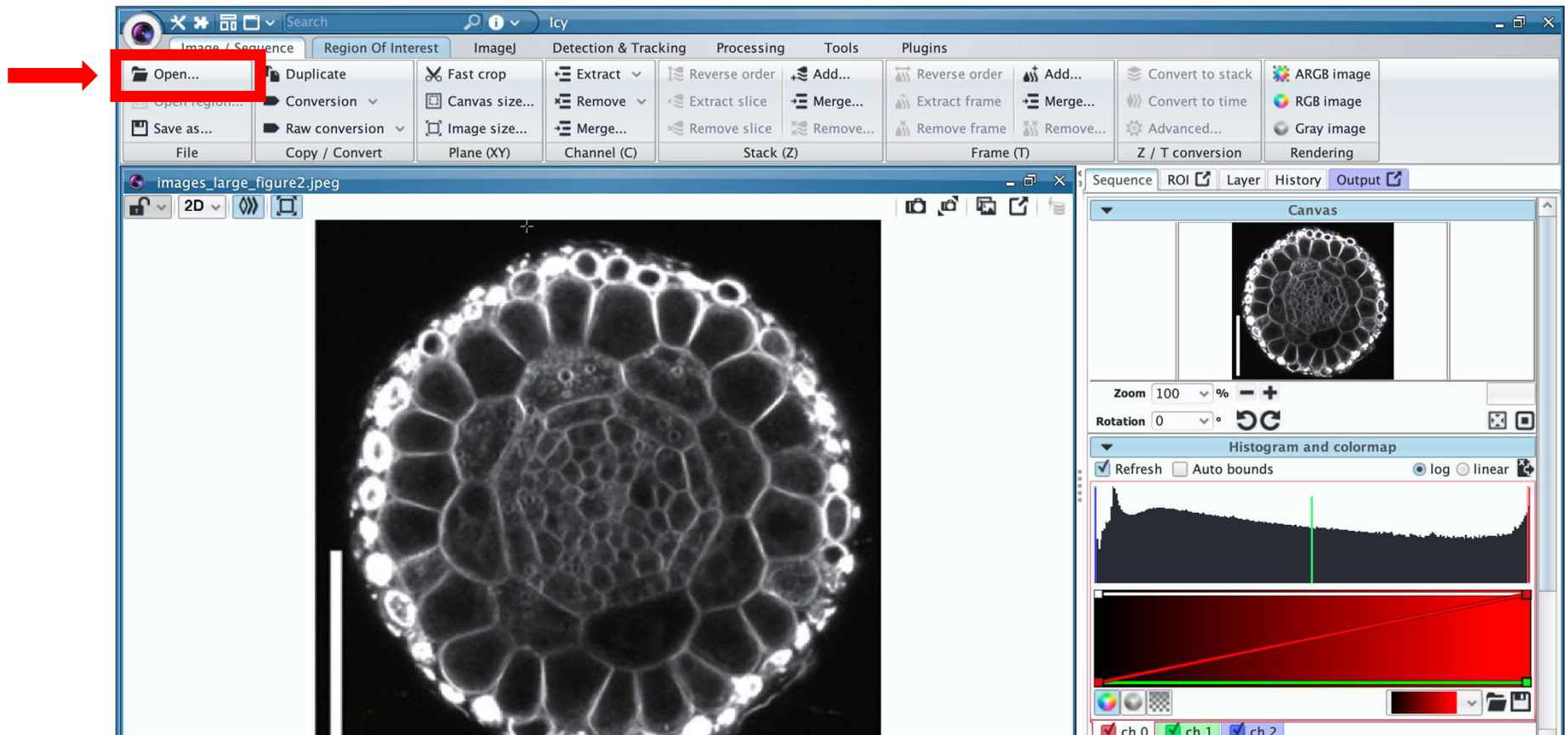
- Icy - Open software for image analysis
- (<https://icy.bioimageanalysis.org/>)



1. Open the software

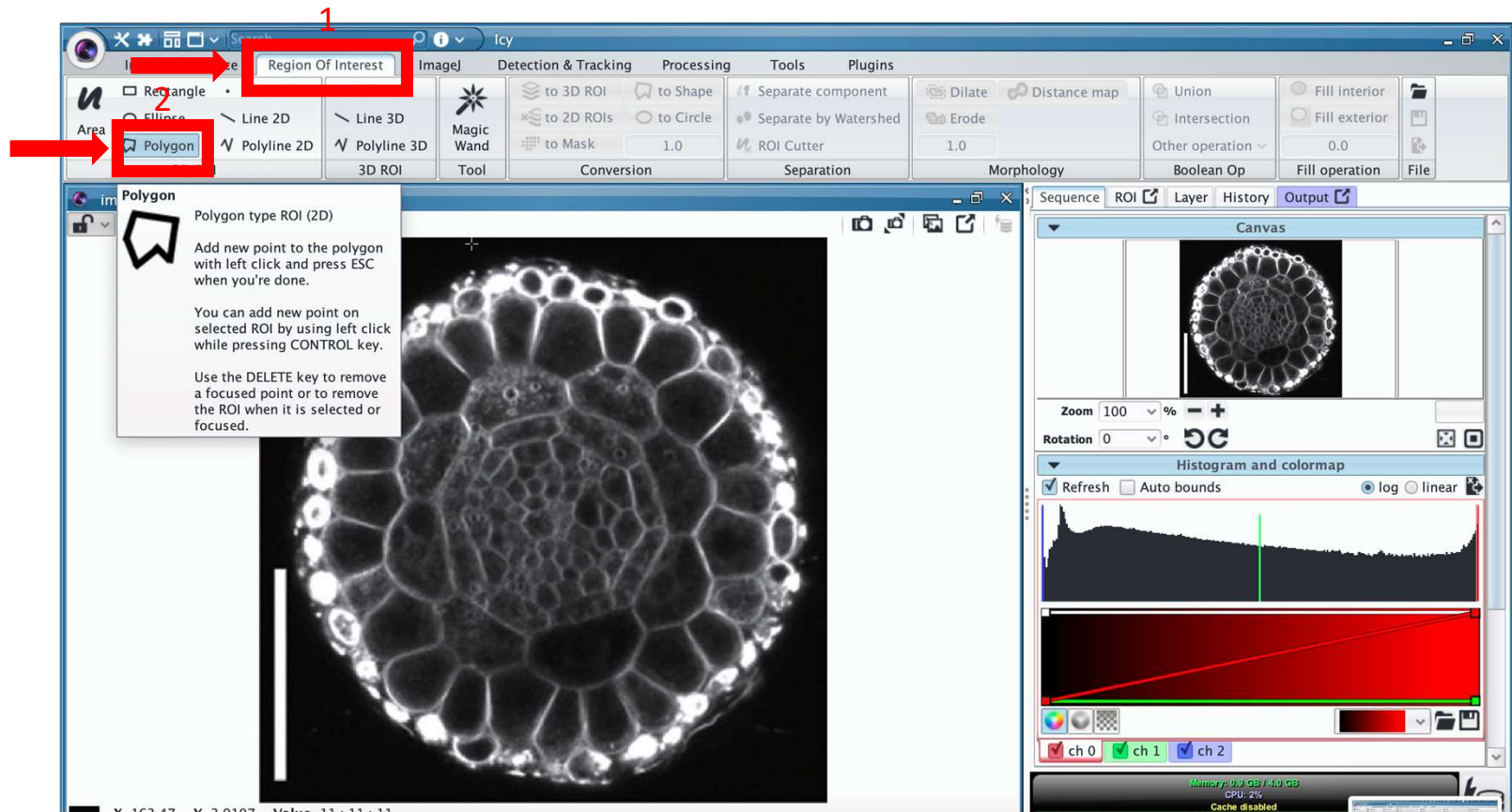


2. Open your image (formats: .png,.jpeg,.tif,.czi)



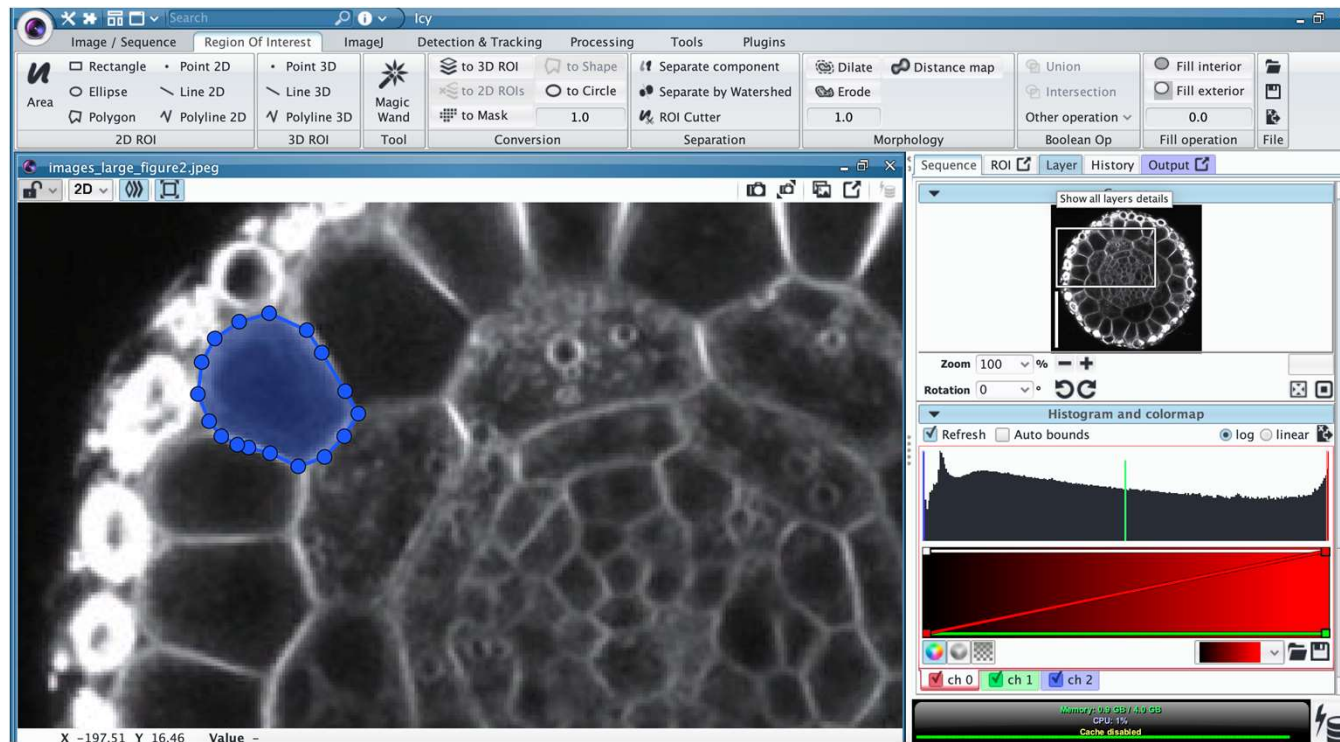
Root image source: <https://www.future-science.com/doi/10.2144/000114621>

3. Click on Region of Interest > Polygon

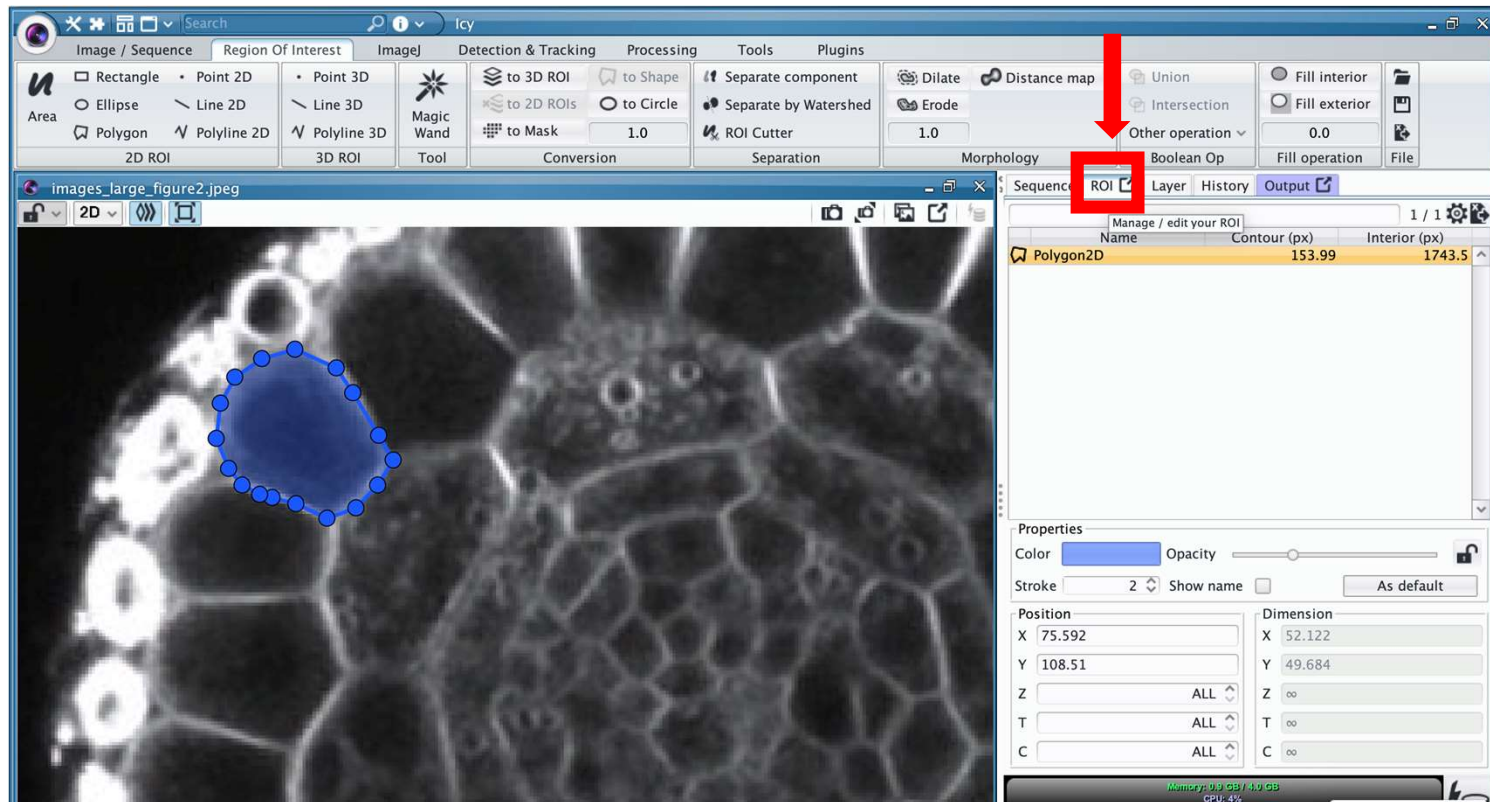


4. Start tracing your object

- Every click will create an edge of your polygon
- It usually takes me around ~1 hour to trace a root image



5. Every polygon you trace is stored in the ROI tab

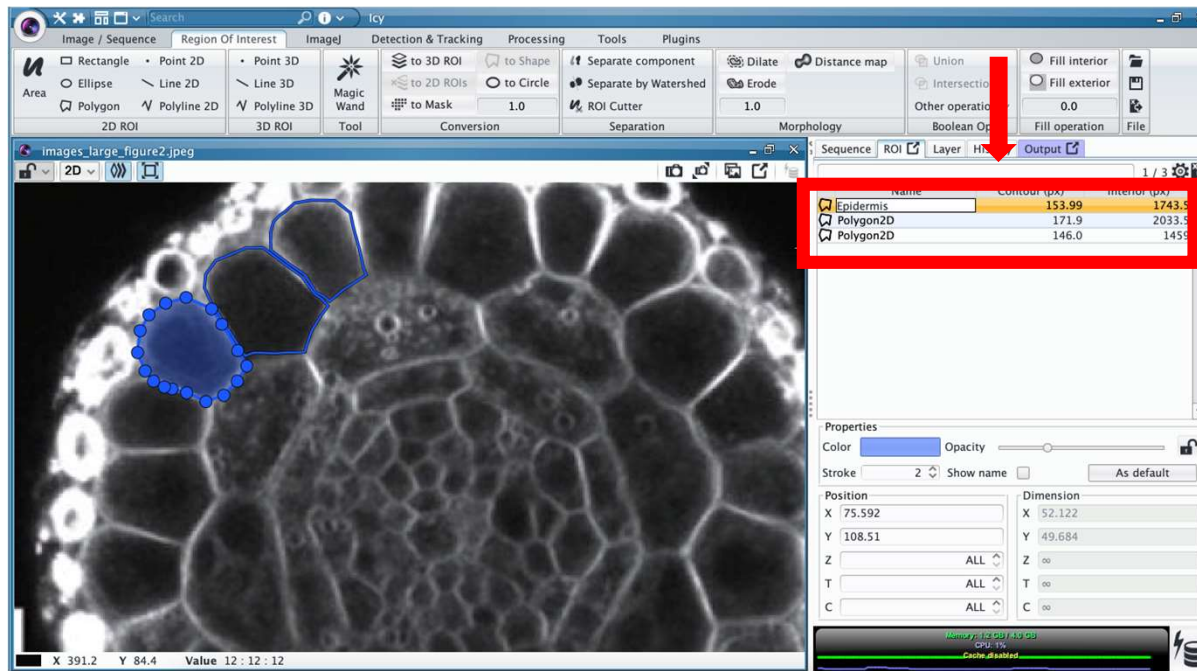


6. Continue tracing and when you are done, rename the ROI with their unique classification

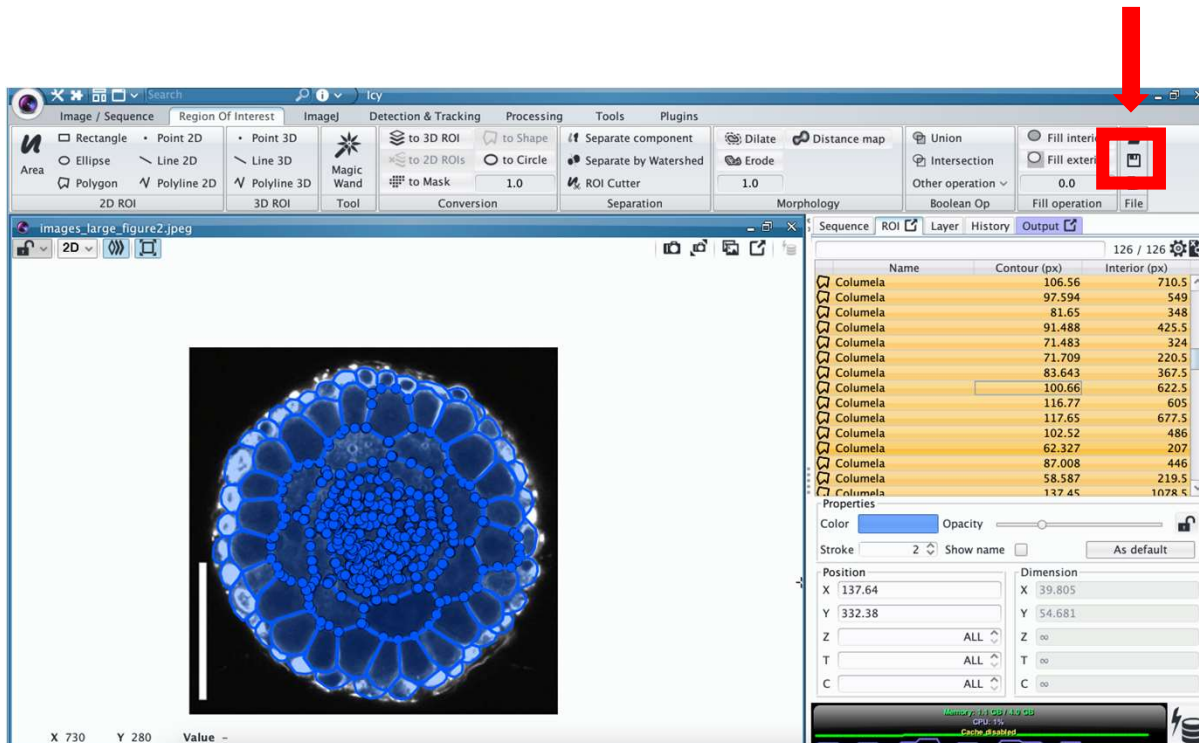
Tip1 : IMO, it is faster if you finish tracing one group and rename this group all at the same time. For example, trace all the epidermal cells first before renaming them.

Tip2: The name of the ROI will be important to classify distinct groups that can be mapped uniquely in the ggplot

Tip3: If multiple levels will be assigned to the same ROI, you can separate them by adding a point(.) in between levels.
Ex: Epidermis.MaturationZone

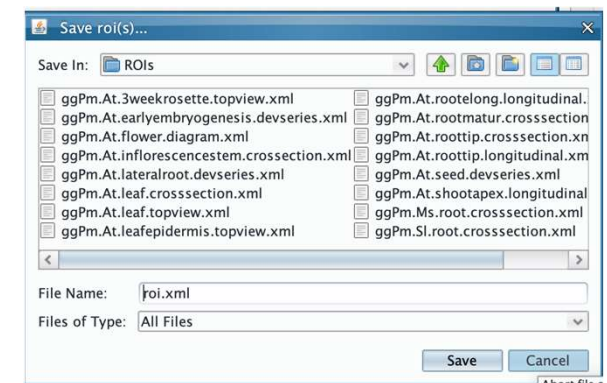


7. After you are done tracing, save your ROIs into a xml file



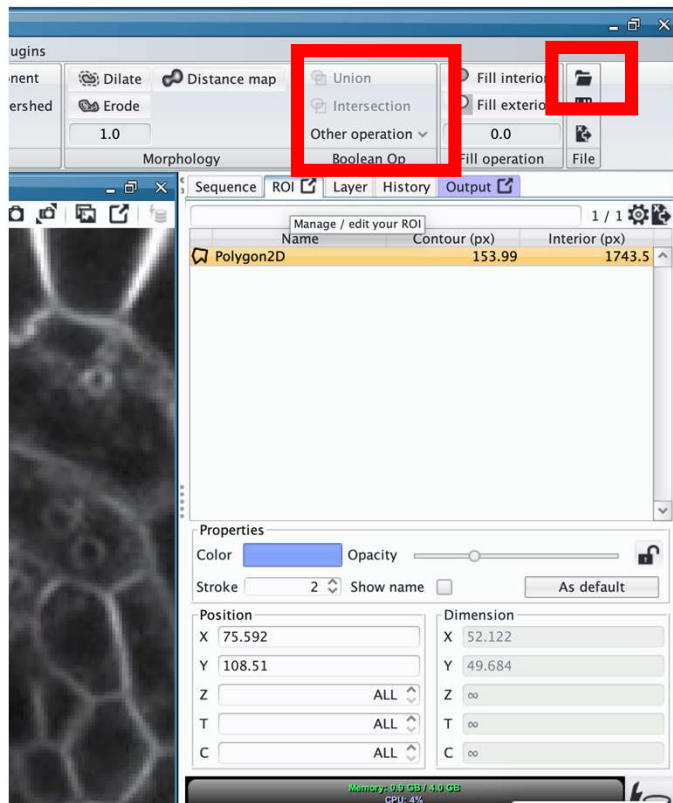
IMPORTANT:

Select all your ROIs before saving. Icy will only save the selected ROIs

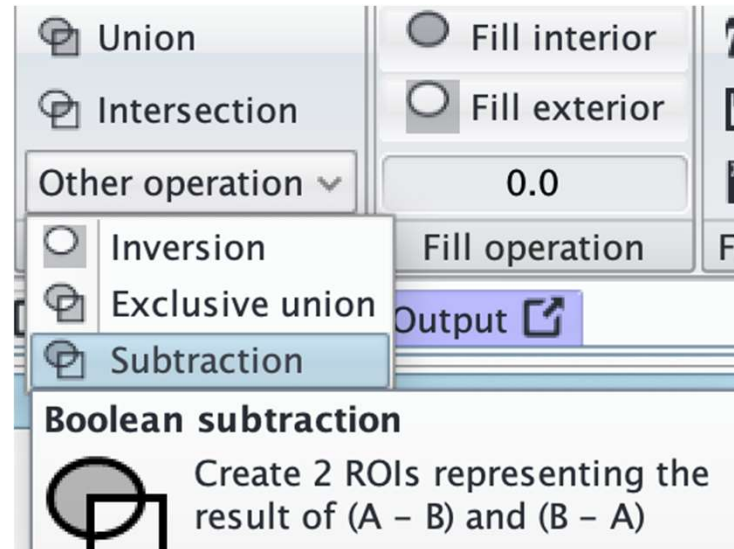


8. This xml file will be used in the XML.to.ggPlantmap() function

Extra tips



Tip1: If you are not satisfied with the ggPlantmap generated by the xml file, you can always load the existing xml file on top of the image and adjust existing ROIs



Tip2: Boolean operations can be extremely helpful. You can use one ROI to shape another ROI using the subtraction operation. I strongly recommend experimenting with it!