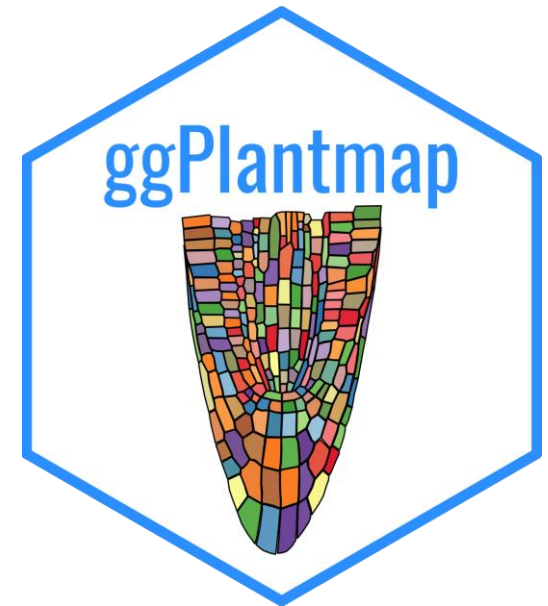


# Tutorial on how to generate xml files for ggPlantmap

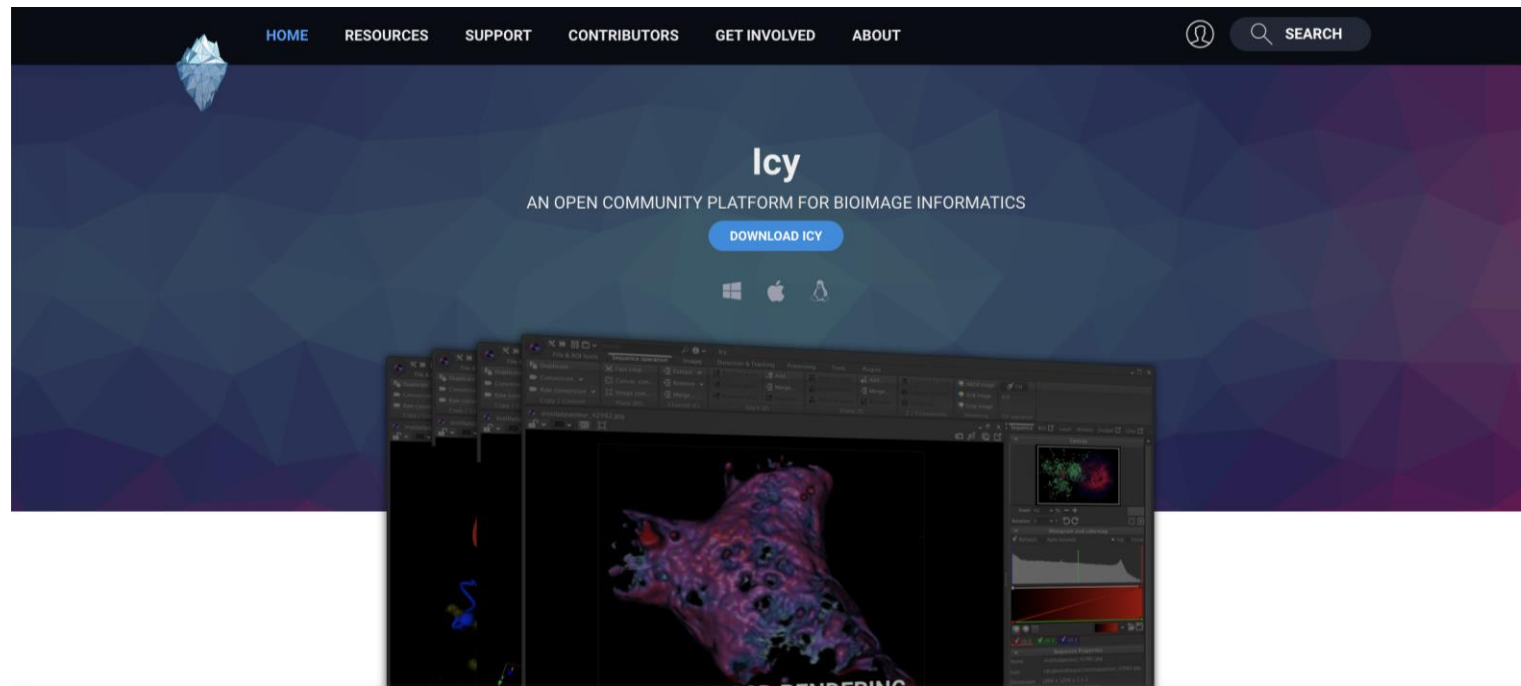
Leonardo Jo

Sept/2023

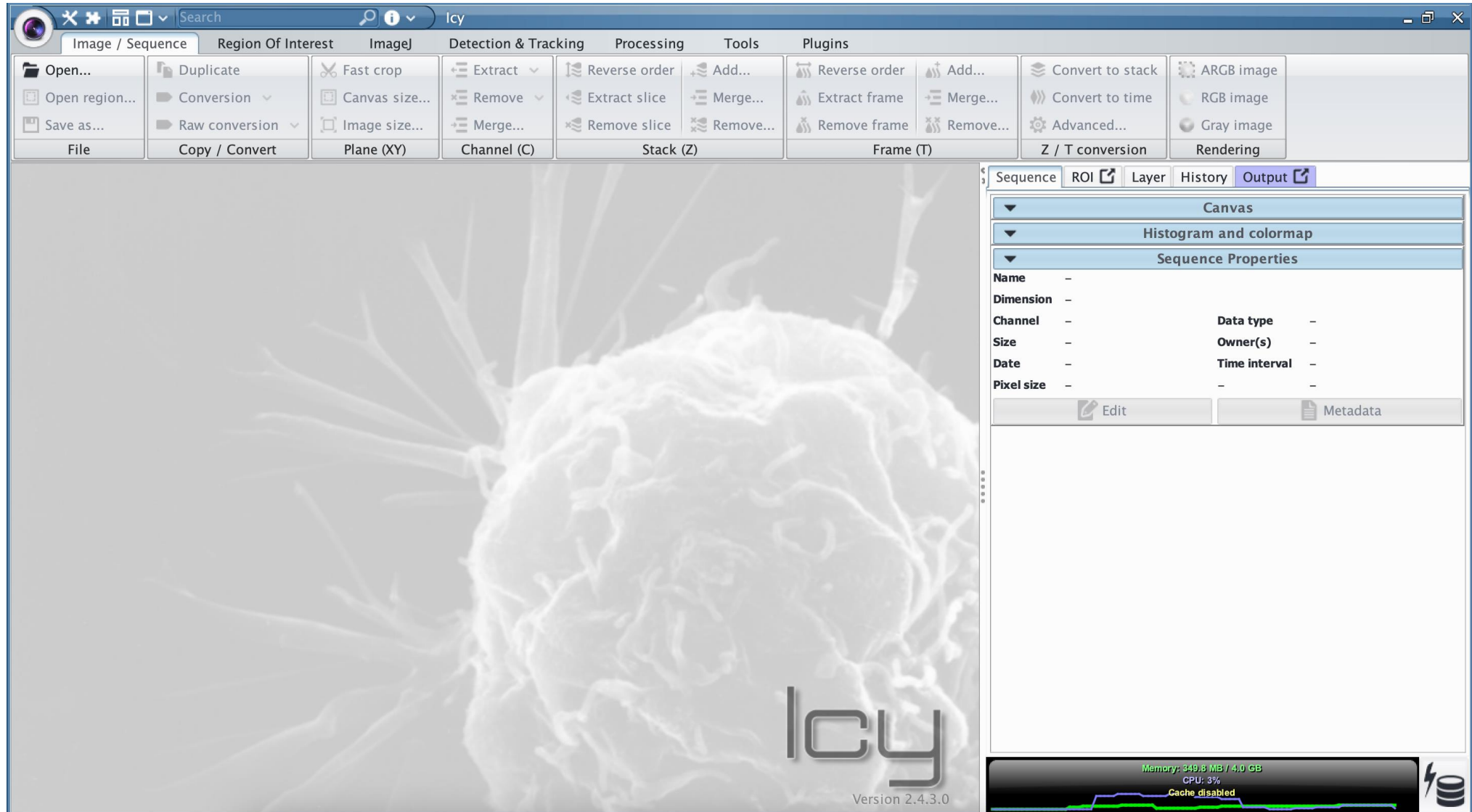


# Software

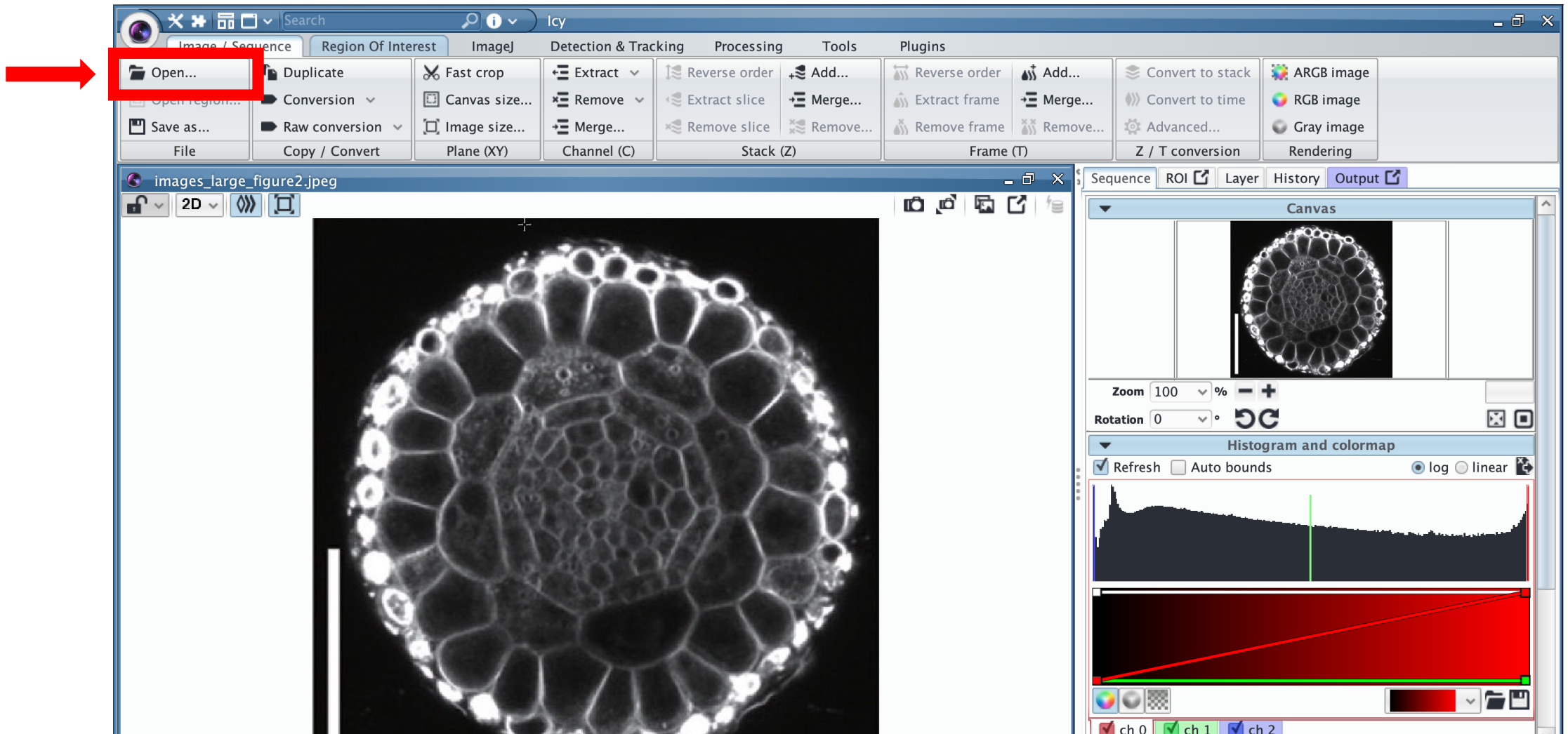
- Icy - Open software for image analysis
- (<https://icy.bioimageanalysis.org/>)



# 1. Open the software

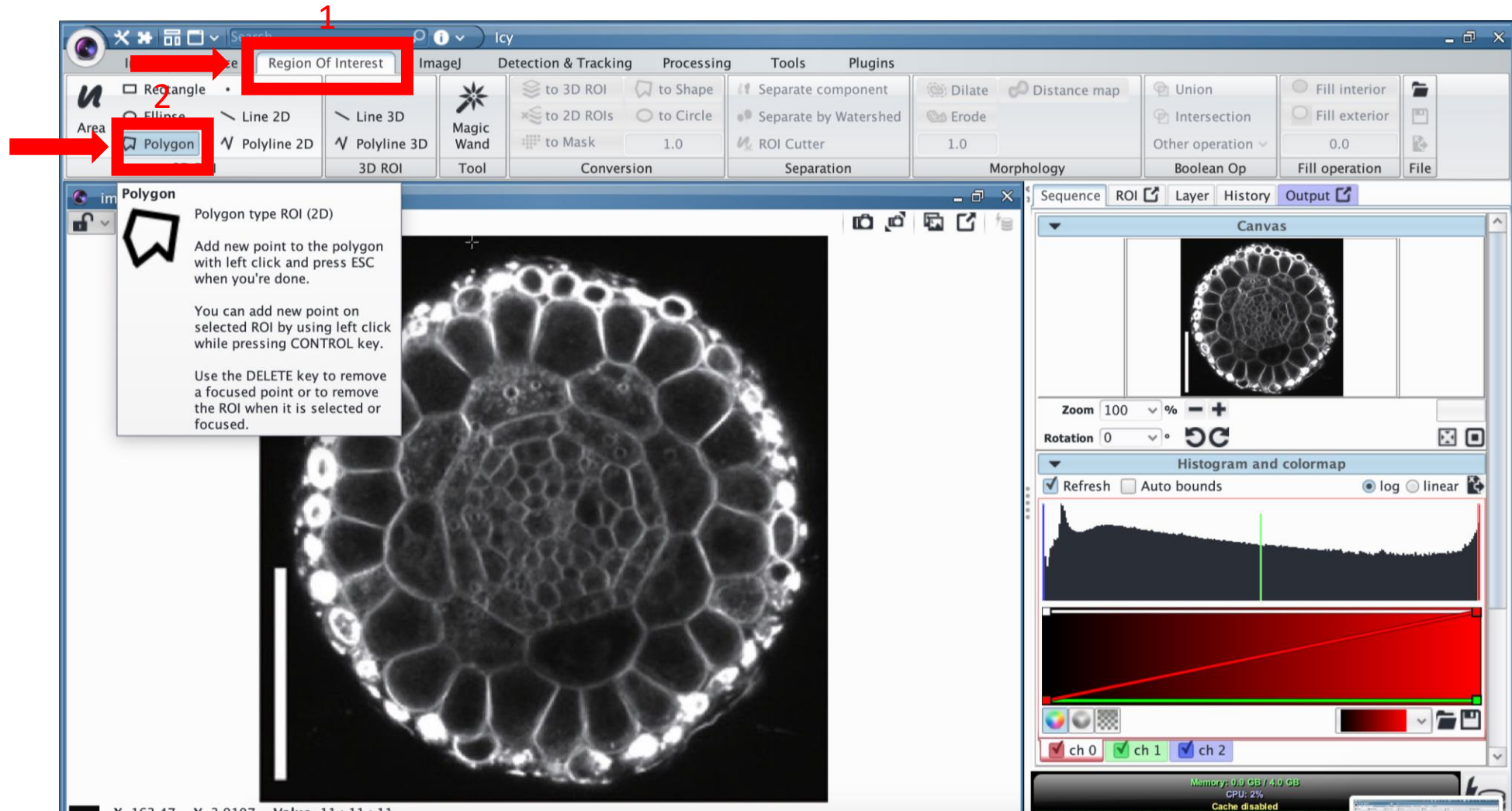


## 2. Open your image (formats: .png,.jpeg,.tif,.czi)



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

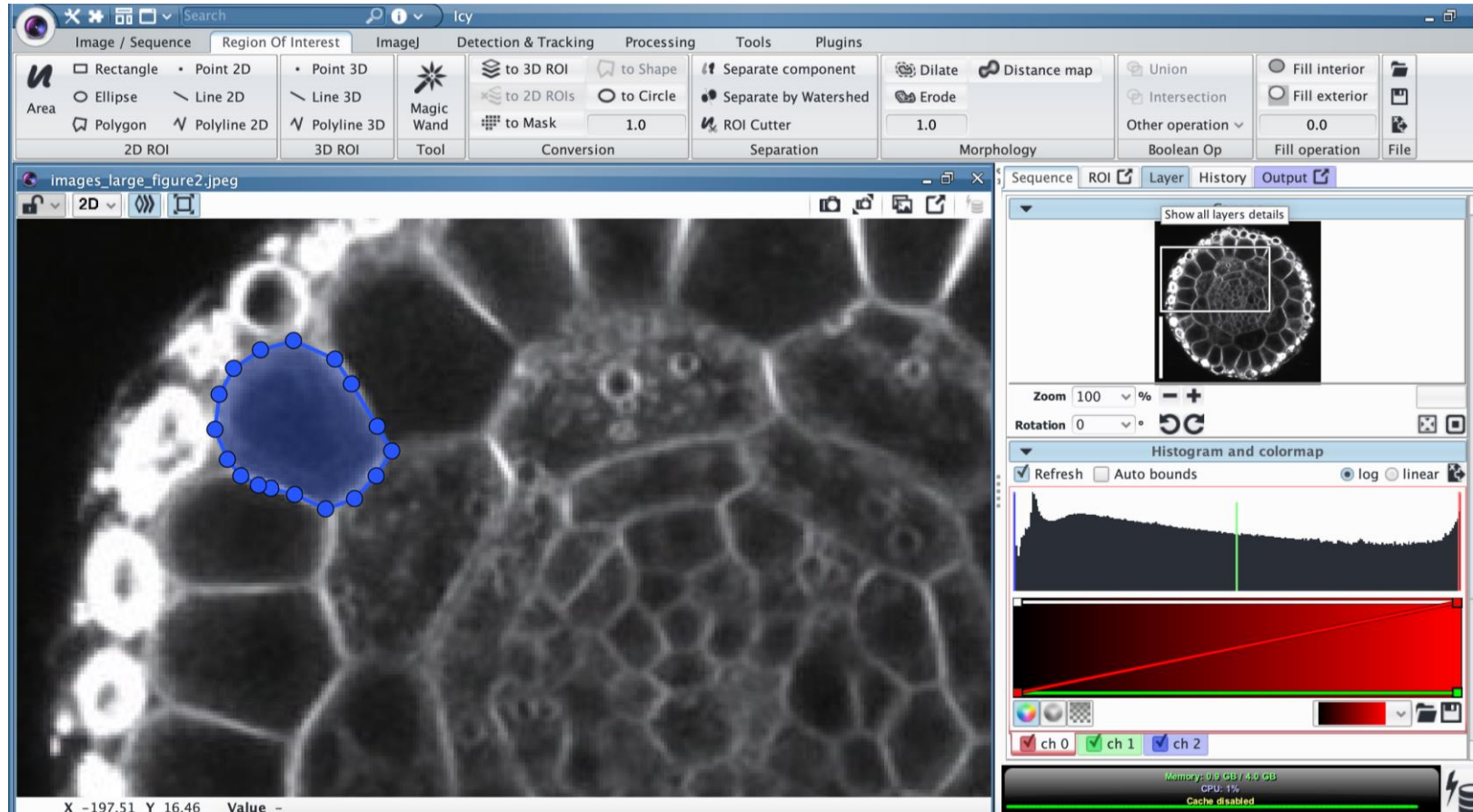
### 3. Click on Region of Interest > Polygon



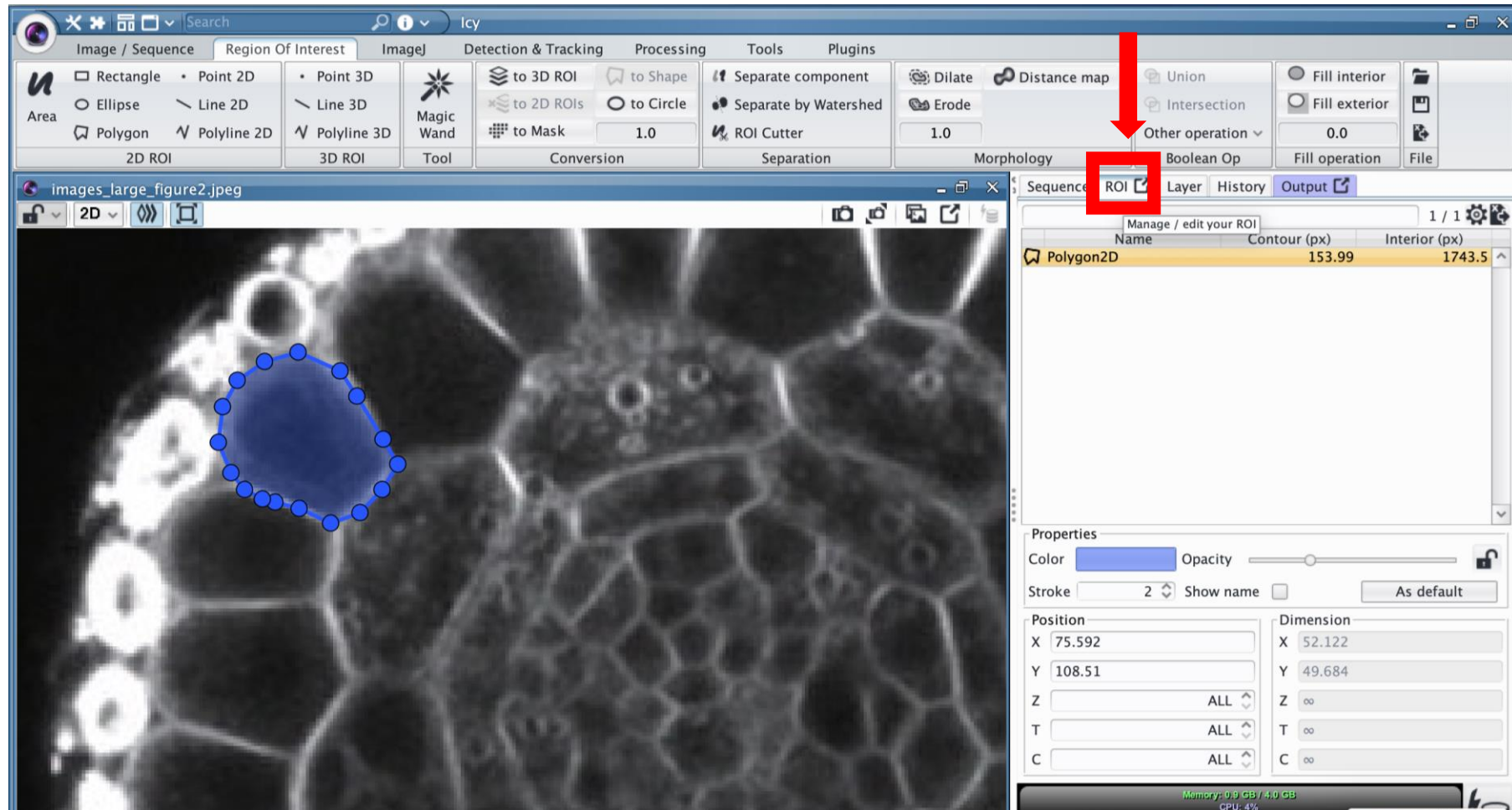


## 4. Start tracing your object

- 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

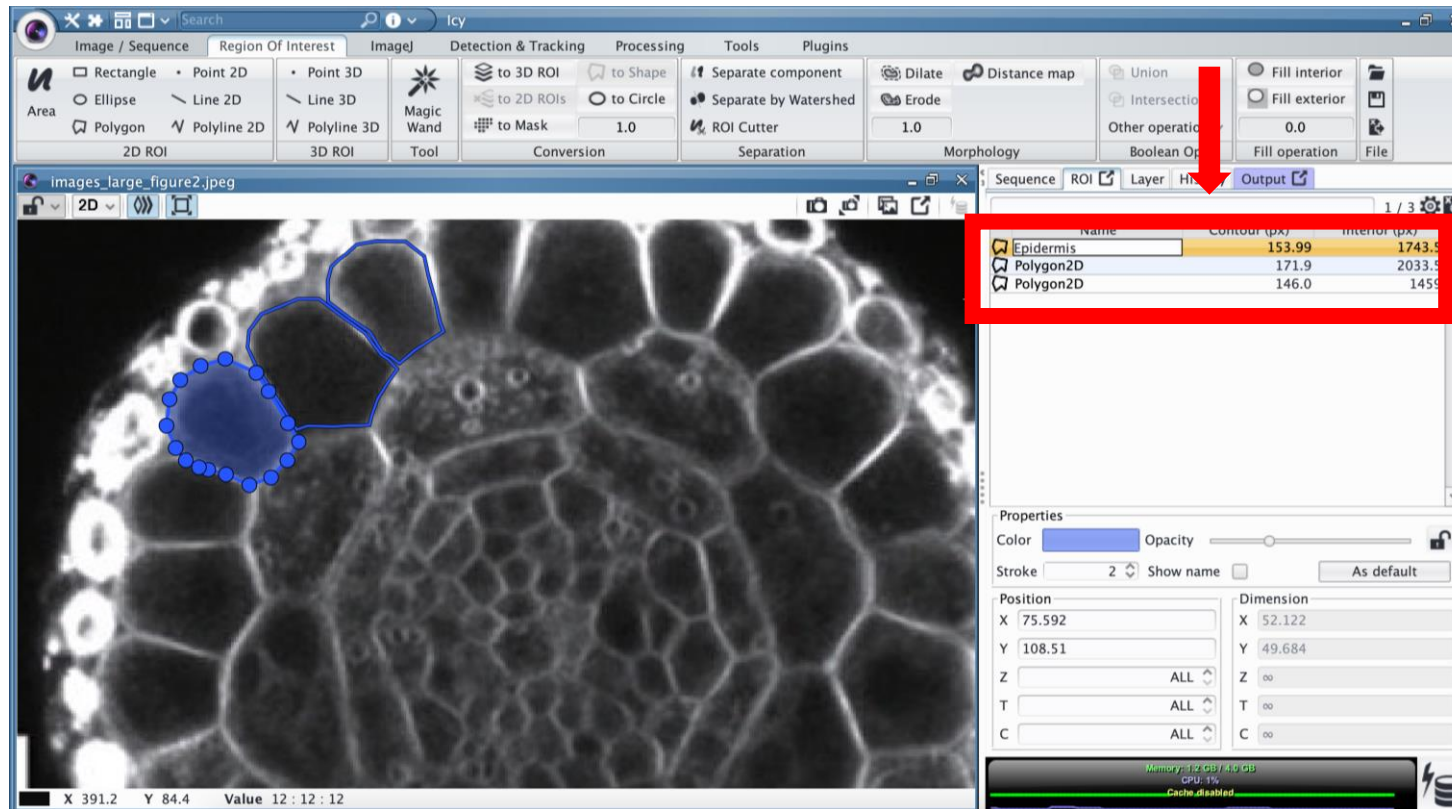


## 6. Continue tracing and when you are done, rename the ROI with their unique classification

**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.

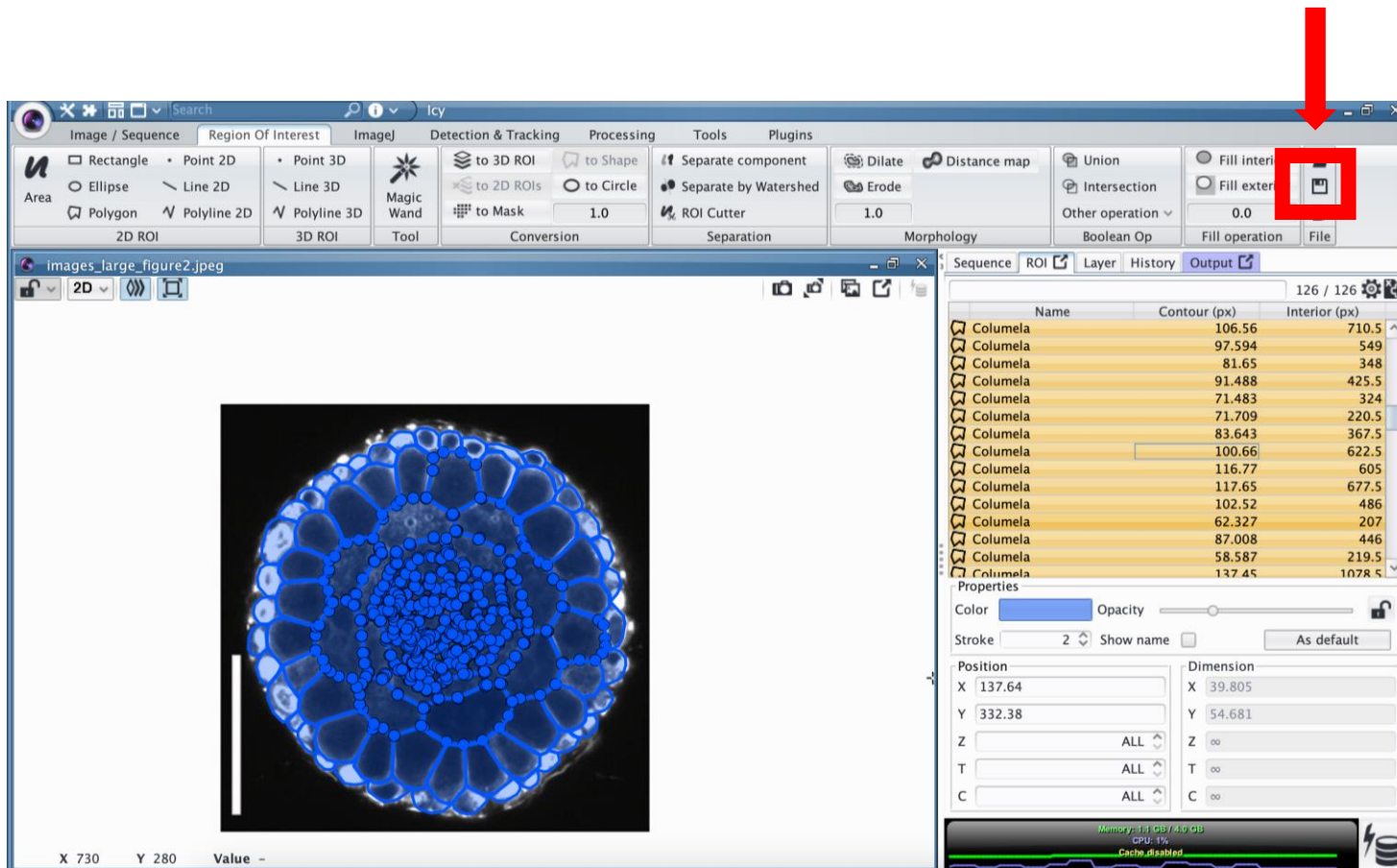
**Tip2**: The name of the ROI will be important to classify distinct groups that can be mapped uniquely in the ggplot

**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



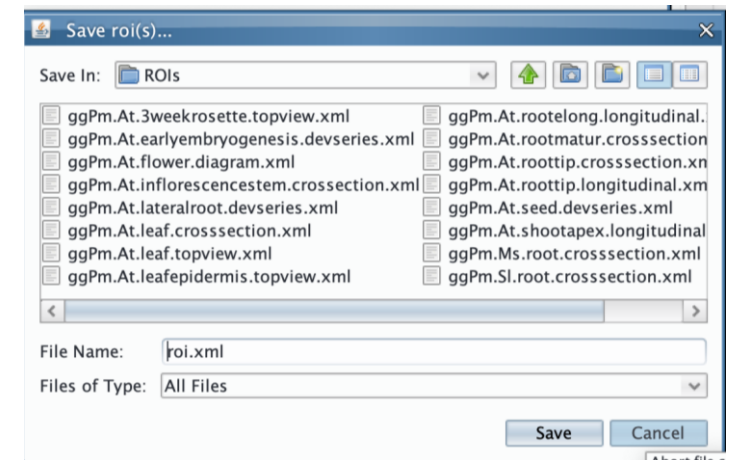


## 7. After you are done tracing, save your ROIs into a xml file



### 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

## 8. Converting a xml file into a ggPlantmap

Once your ROI file is saved (ex: roi.xml)

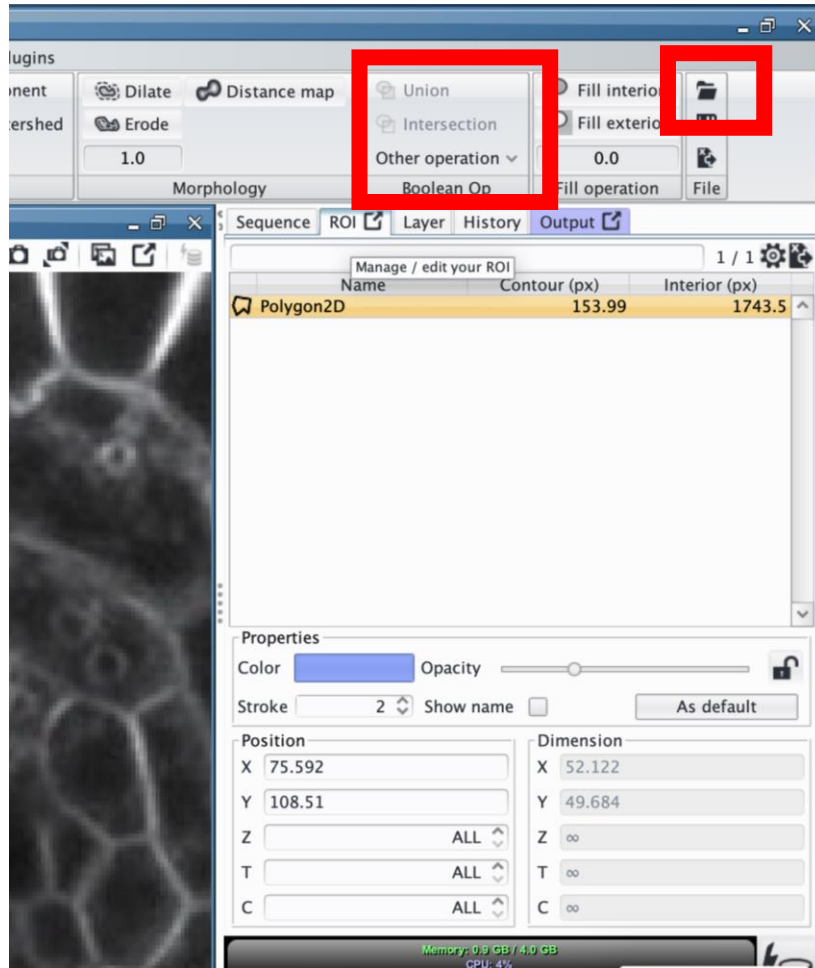
You can transform it into a ggPlantmap using the XML.to.ggPlantmap() function

Example:

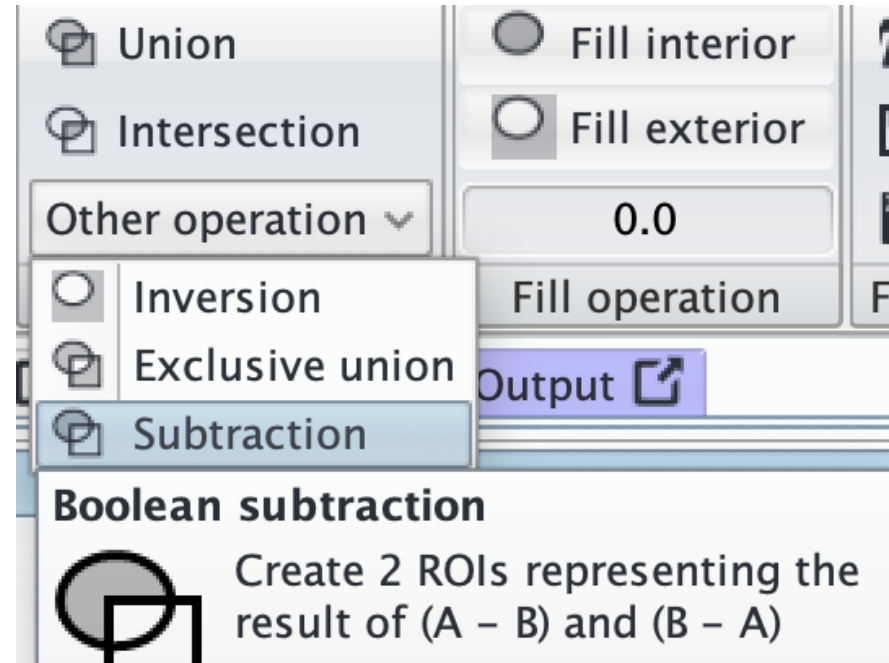
XML.to.ggPlantmap("ggPm.At.inflorescencestem.crossection.xml")

```
# A tibble: 4,446 x 5
  ROI.name ROI.id point    x    y
  <chr>    <int> <int> <dbl> <dbl>
1 Epidermis      1     1  668. -103.
2 Epidermis      1     2  636. -123.
3 Epidermis      1     3  630. -110.
4 Epidermis      1     4  626. -99.9
5 Epidermis      1     5  654. -81.9
6 Epidermis      1     6  663. -90.9
7 Epidermis      2     1  655. -80.2
8 Epidermis      2     2  655. -69.1
9 Epidermis      2     3  678. -54.4
10 Epidermis     2     4  703. -59.0
# i 4,436 more rows
# i Use `print(n = ...)` to see more rows
~ |
```

# 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!