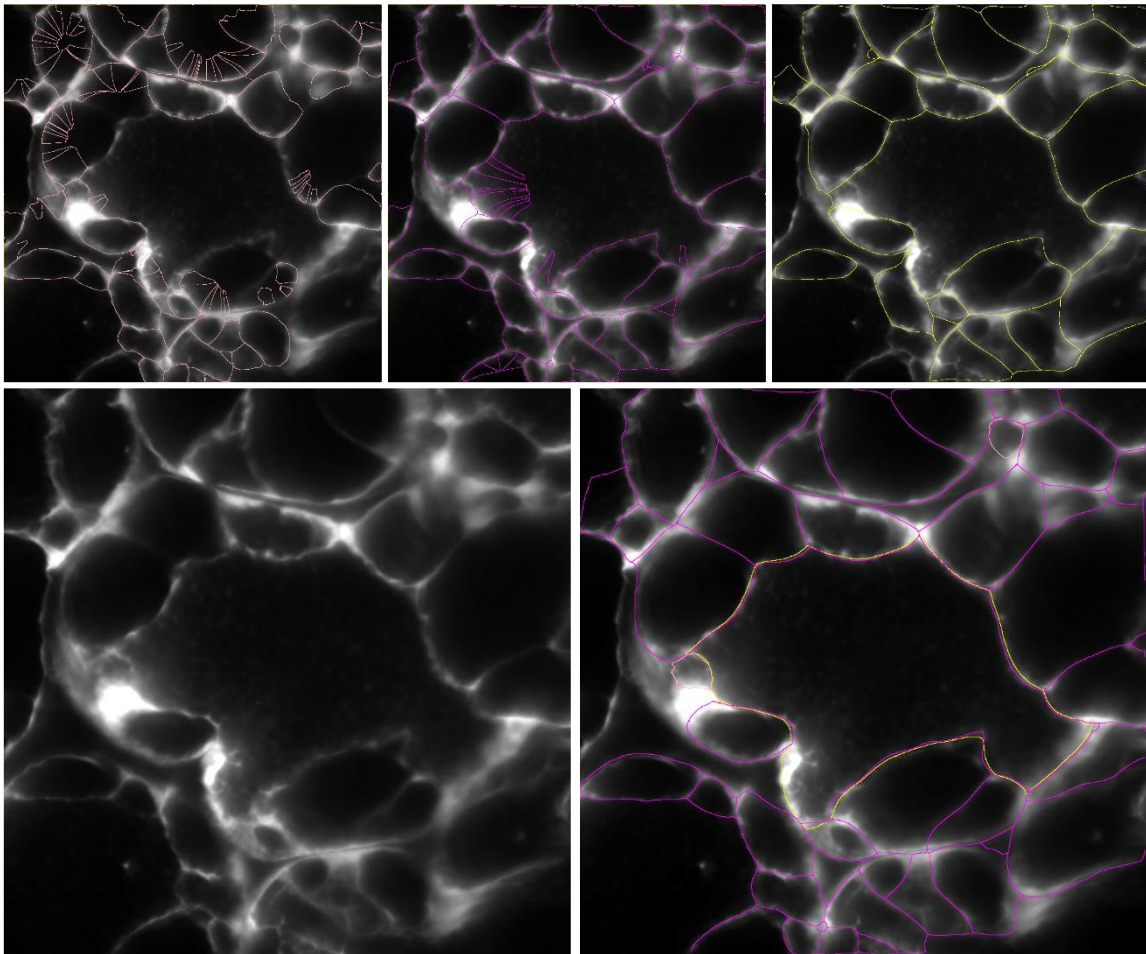


Internship – Combining segmentations obtained at different scales



Graphical abstract. Top left: cellpose segmentation obtained at scale 1. Top middle: cellpose segmentation obtained at scale 2. Top right: cellpose segmentation obtained at scale 3. Bottom left: Original image. Bottom right: combination of segmentations shown at top.

Motivation

The advent of **deep learning methods** revolutionized **image segmentation** in computer vision. It also had a major impact in segmentation of **microscopy images** [1] and it is now possible to routinely **segment individual nuclei** and **cells** with **high accuracy** [2, 3]. The same methods have also been used for segmentation of **other biological objects** such as ovaries [4]. The access of **large amounts of annotated data** in 2D [5] actually allows to train widely **versatile models**. Unfortunately, **scale invariance** remains a major hurdle and objects of different sizes are still difficult to accurately segment. The goal of this internship is to propose a method to **combine segmentation masks** obtained at **different scales** to accurately identify biological objects demonstrating a large range of sizes.

Research program

You will develop a **new method** to **combine** segmentation masks obtained at **different scales** with cellpose for **2D** and **3D** images. Both classical **computer vision** approaches and **machine learning** approaches will be explored. This internship will be a collaboration between **FAIIA** shared facility at Rennes University and **SAIRPICO** research lab at INRIA Rennes.

Requirements

Candidates in the last year of Master in **computer science** or **applied mathematics** are eligible to this internship. Programming skills in **Python** are required. Knowledge in **image processing** will be appreciated.

Application

Please send a **CV**, a **cover letter** and email addresses of two **references** to Thierry.pecot@univ-rennes.fr with the subject line "Application to internship".

References

- [1] Ronneberger, O., Fischer, P., & Brox, T. (2015). U-net: Convolutional networks for biomedical image segmentation. In *Medical Image Computing and Computer-Assisted Intervention–MICCAI 2015: 18th International Conference, Munich, Germany, October 5-9, 2015, Proceedings, Part III 18* (pp. 234-241). Springer International Publishing.
- [2] Schmidt, U., Weigert, M., Broaddus, C. and Myers, G., 2018. Cell detection with star-convex polygons. In *Medical Image Computing and Computer Assisted Intervention–MICCAI 2018: 21st International Conference, Granada, Spain, September 16-20, 2018, Proceedings, Part II 11* (pp. 265-273). Springer International Publishing.
- [3] Stringer, C., Wang, T., Michaelos, M. and Pachitariu, M., 2021. Cellpose: a generalist algorithm for cellular segmentation. *Nature methods*, 18(1), pp.100-106.
- [4] Lesage, M., Thomas, M., Pécot, T., Ly, T.K., Hinfrey, N., Beaudouin, R., Neumann, M., Lovell-Badge, R., Bugeon, J. and Thermes, V., 2023. An end-to-end pipeline based on open source deep learning tools for reliable analysis of complex 3D images of ovaries. *Development*, 150(7), p.dev201185.
- [5] Greenwald, N.F., Miller, G., Moen, E., Kong, A., Kagel, A., Dougherty, T., Fullaway, C.C., McIntosh, B.J., Leow, K.X., Schwartz, M.S. and Pavelchek, C., 2022. Whole-cell segmentation of tissue images with human-level performance using large-scale data annotation and deep learning. *Nature biotechnology*, 40(4), pp.555-565.