OX-UK

Authors: Martin Hailstone, Dominic Waithe

Email: martin.hailstone@bioch.ox.ac.uk

Platform: Windows (x64)

Prerequisites: None

OX-UK: SUMMARY

We use CytoCensus [1] to first detect cells, and follow this by an active contour segmentation method [2], splitting merged cells using marker-based watershed from the CytoCensus centers. CytoCensus is intended to simplify the process analyzing 3D images, requiring only 2D annotations, and has been used successfully with a wide variety of different markers, including more complex ones than are used in this challenge. However, this approach is highly dependent on the quality of the detected centers to determine the number of objects and assumes cells are approximately round. Consequently, it is not well suited to tasks with extended, misshapen objects, for instance in **Fluo-C3DL-MDA231**.

OX-UK: PREPROCESSING

All images were downsampled by a factor of *d* before processing to increase its speed.

OX-UK: DETECTION

We trained CytoCensus as described in [1] on each dataset using the GUI. Four frames were selected (from the training set) to capture the imaging variation within datasets for training. Typically this was the first and last frame of each dataset replicate. We set the object radius to an appropriate size σ_d (a little smaller than the radius of the object of interest), and adjusted the detection threshold d_{thres} if necessary. We trained a specific model for each dataset. We applied each model to the corresponding dataset to generate detections.

OX-UK: SEGMENTATION

Following object detection, we created a crude segmentation: a sphere of specified size o_{size} centered around each object detection, and corrected for the differences in sampling and object size in the axial direction by z_{corr}. We refined this segmentation using a small number of iterations (*iter*) of an active contour segmentation method [2]. We mirror boundaries to minimize edge effects of the segmentation. This was optionally followed by marker-based watershed from the CytoCensus centers in order to separate detected objects.

REFERENCES

1. Hailstone M, Waithe D, Samuels TJ, Yang L, Costello I, Arava Y, Robertson EJ, Parton RM, Davis I. CytoCensus: Mapping cell identity and division in tissues and organs using machine learning. *bioRxiv* 137406 (2019).
2. Márquez-Neila P, Baumela L, Alvarez L. A morphological approach to curvature-based evolution of curves and surfaces. *IEEE Transactions on Pattern Analysis and Machine Intelligence* **36**, 2-17 (2014).