Livecell Segmentation

Minimal Supervision Cell Segmentation for Livecell Microscopy

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In Short

- A new reseach initiative in Göttingen is driving the development of livecell imaging methods.
- Reliable and scalable data analysis methods are required to process the data acquired in this context.
- A particular challenge is cell segmentation; we will develop more robust and generalizable methods for this task.
- Beyond the livecell imaging application we anticipate our methods to impact image analysis for microscopy and self-supervised learning.
- To process the large datasets acquired by the initiative and develop new deep learning method HPC resources, especially GPUs are required.

The "CIDAS/Sartorius Quantitative Cell Analytics Research Initiative" (QuCellAI) is a research initiative that aims to spearhead the development of livecell microscopy, a technique that is widely used to study the dynamics of cell populations. The acquired data is used to investigate various research questions in the life sciences, from cell biology to drug discovery. Answering these questions relies on quantitative and scalable data analysis, one fundamental step being reliable cell segmentation. The state-of-the-art methods for this task are based on fully supervised deep learning. They yield high quality segmentation results given enough annotated training data, but fail to generalize to the various experimental conditions acquired by the research initiative. Figure 1 shows an overview of current state-of-the-art methods trained on the LiveCELL dataset (1) applied to data from QuCellAI, including failure cases. To provide more reliable cell segmentation we aim to develop novel methods based on domain adaptation (2) and self-supervised learning paradigms. While these methods require significantly less annotated training data, they increase the overall need for unlabeled training data and computational resources. This motivates us to collect a large-scale dataset that will enable training generalist cell segmentation models for livecell imaging. It further creates the need for computational resources, especially GPUs, to train and evaluate these models, as well as applying them to data acquired by the initiative. Beyond the direct impact in the research initiative, we anticipate the newly developed methods to be of significant value to microscopy image analysis at large and aim to establish the dataset collected as a new benchmark for self-supervised learning methods.

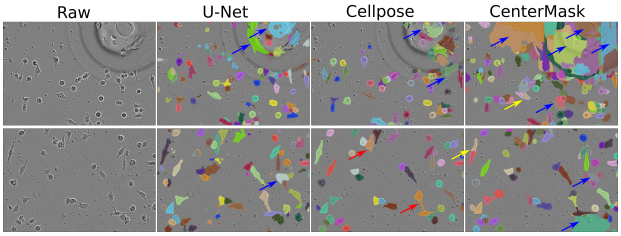

***Figure 1:** State-ofthe-art cell segmentation methods for livecell imaging applied to data acquired within QuCellAI. Three different failure cases are highlighted by arrows: spurious objects (blue), incorrect merges of multiple cells into a single object (red) and incorrect splits of one cell into multiple objects (yellow). Please note that we just show a subset of errors in the field of view. Overall the error rate is too high for advanced analysis, such as tracking cells over time, for all three methods.*

In order to develop these methods and provide capacities to process the data acquired by QuCellAI we apply for computational resources within NHR. Our main requirements will be GPU resources in order to train large neural networks that can reliably and robustly segment cells in livecell imaging data. These methods will provide the basis for answering many research questions pursued by members of the initiative.

WWW

https://www.uni-goettingen.de/en/619480.html

More Information

[1] C. Edlund et al., *Nature Methods* **18**, 1038–1045 (2021). doi:10.1038/s41592-021-01249-6

[2] A. Matskevych, A. Wolny, C. Pape, A. Kreshuk, *Frontiers in Computer Science* doi: 10.3389/fcomp.2022.805166

Project Partners

CIDAS/Sartorius Quantitative Cell Analytics Research Initiative: UMG, CIDAS, MPI for Multidisciplinary Sciences, GWDG, CBDN, Sartorius AG

DFG Subject Area

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