The *TYC Dataset* for Understanding Instance-Level Semantics and Motions of Cells in Microstructures

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Introduction & Motivation

- Many biomedical applications require the segmentation of single cells in microscopy imagery

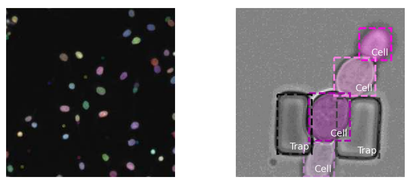


Fig. 1. Existing datasets (DSB2018 [1] left & Reich *et al.* [2] right).

Existing datasets only consider limited scenes (*e.g.*, no microstructures) or only offer limited annotations (*c.f.* Fig. 1)

Dataset Overview

Dataset	# ann. pix. [10^7]	# cells	# traps	Resolution	Annotation type	# trap types
Bakker *et al.* [3]	–	1000	0	512×512	cell outline	1
Reich *et al.* [2]	0.81	914	971	128×128	instance seg.	2
TYC dataset (ours)	46.39	14541	4405	≥2048×2048	instance seg.	6

Tab. 1. Dataset comparison of existing datasets including cells and traps *vs.* our TYC dataset.

We present the largest labeled dataset to include cells & microstructures

Data Acquisition

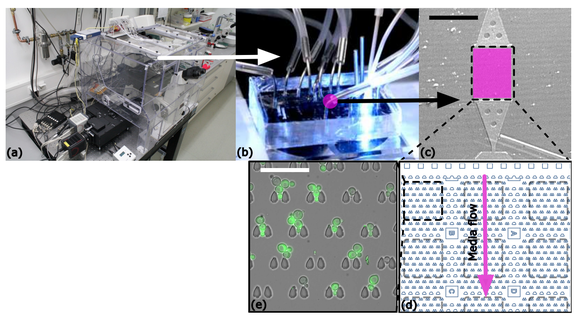


Fig. 2. Overview data acquisition process.

We utilize data from more than a dozen experiments

TYC Labeled Set

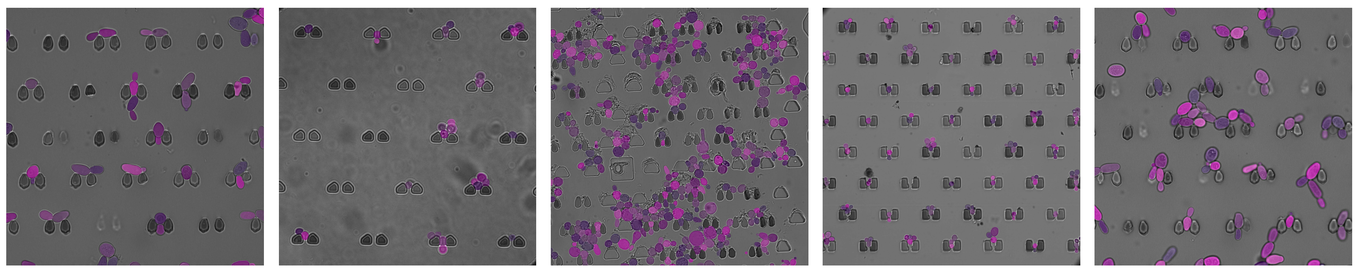


Fig. 3. Labeled sample of our TYC dataset; traps in grey (■■■) and cells in pink (■■■).

We release ∼19k instance masks for both cells and microstructures

TYC Unlabeled Set

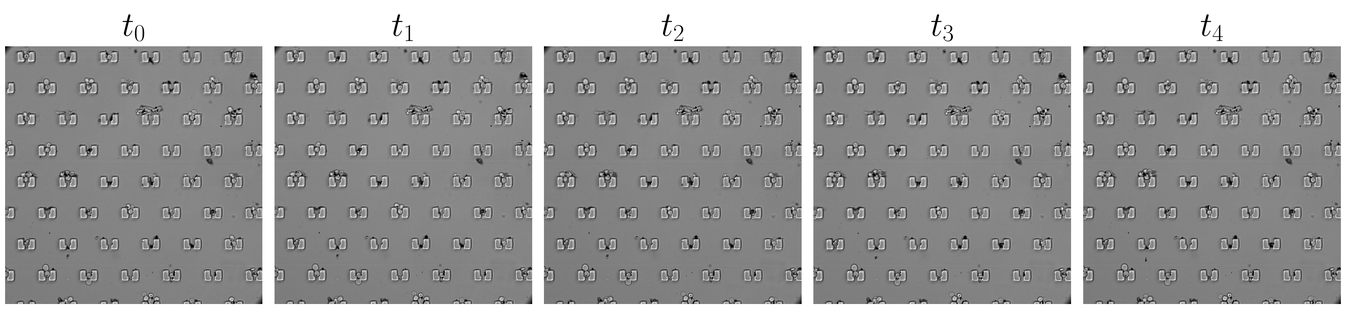


Fig. 4. Unlabeled brightfield microscopy image sequence.

We present 61 curated video clips to facilitate unsupervised learning

Evaluation

Semantic-level evaluation (cell class Intersection-over-Union)

$$\mathrm{IoU} = \frac{|p_c \cap g_c|}{|p_c \cup g_c|},$$

Instance-level evaluation (Panoptic Quality [4])

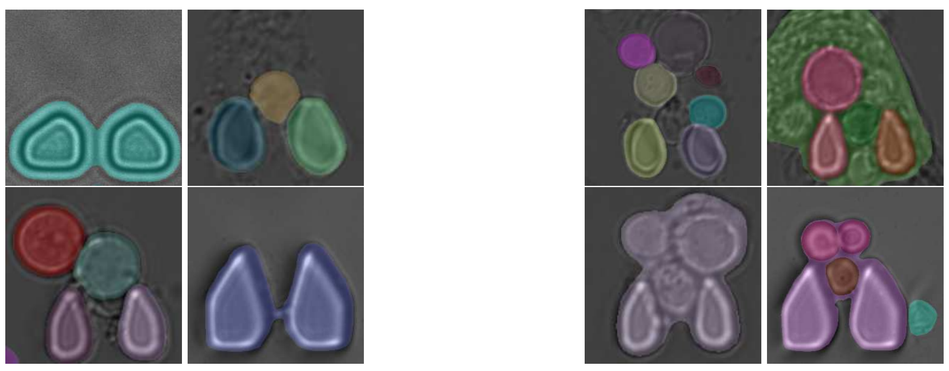
$$\mathrm{PQ} = \underbrace{\frac{\sum_{(p,g)\in \mathrm{TP}} \mathrm{IoU}(p,g)}{|\mathrm{TP}|}}_{\text{Segmentation quality (SQ)}} \underbrace{\frac{|\mathrm{TP}|}{|\mathrm{TP}| + \frac{1}{2}|\mathrm{FP}| + \frac{1}{2}|\mathrm{FN}|}}_{\text{Recognition quality (RQ)}},$$

Dataset Split

Split	# images	# ann. pix. [10^7]	# cells	# traps
Training	81	35.53	12296	3448
Validation	8	3.69	950	310
Test	8	3.59	753	346
OOD Test	8	3.58	542	301

Tab. 2. Split of our labeled set.

Segment Anything Results



(a) Good examples **(b)** Poor examples

Fig. 5. Zero-shot results of SAM [5] on our TYC dataset.

SAM fails to produce accurate segmentations out of the box

References

[1] J. C. Caicedo, A. Goodman *et al.*, "Nucleus segmentation across imaging experiments: the 2018 Data Science Bowl," *Nature Methods*, vol. 16, no. 12, pp. 1247–1253, 2019.
[2] C. Reich, T. Prangemeier, A. O. Françani, and H. Koeppl, "An Instance Segmentation Dataset of Yeast Cells in Microstructures," in *EMBC*, 2023.
[3] E. Bakker, P. S. Swain, and M. M. Crane, "Morphologically constrained and data informed cell segmentation of budding yeast," *Bioinformatics*, vol. 34, no. 1, pp. 88–96, 2018.
[4] A. Kirillov, K. He, R. Girshick, C. Rother, and P. Dollár, "Panoptic Segmentation," in *CVPR*, 2019, pp. 9404–9413.
[5] A. Kirillov, E. Mintun, N. Ravi, H. Mao, C. Rolland, L. Gustafson, T. Xiao, S. Whitehead, A. C. Berg, W.-Y. Lo *et al.*, "Segment Anything," *arXiv preprint arXiv:2304.02643*, 2023.

Paper: `https://arxiv.org/abs/2308.12116`
Dataset: `https://tudatalib.ulb.tu-darmstadt.de/handle/tudatalib/3930`
Project Page: `https://christophreich1996.github.io/tyc_dataset/`
Code: `https://github.com/ChristophReich1996/TYC-Dataset`
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