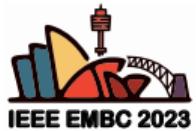


An Instance Segmentation Dataset of Yeast Cells in Microstructures



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[§]Work done at TU Darmstadt

*Christoph Reich & Tim Prangemeier – both authors contributed equally

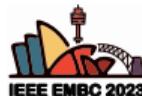
Introduction



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- Many biomedical applications require the segmentation of single-cells in microscopy imagery
- Vast majority of SOTA segmentation algorithms use deep networks (e.g.,[[Stringer et al., 2021](#)])
- For training & **evaluating** deep segmentation model ground truth annotations are required

Introduction



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We propose the first instance segmentation dataset of brightfield microscopy images including both cells and microstructures.

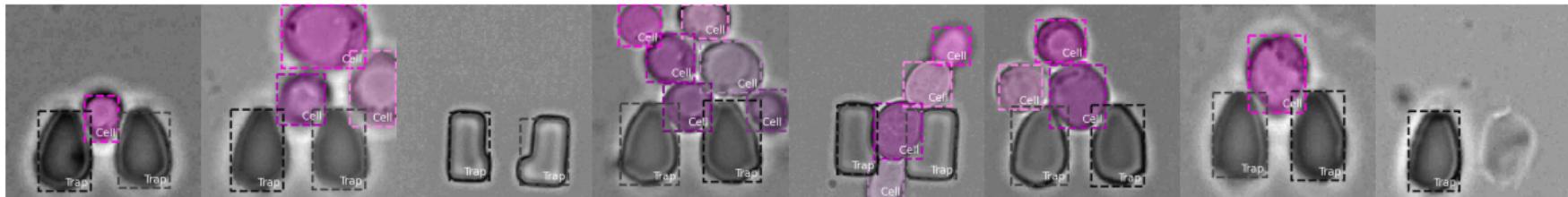
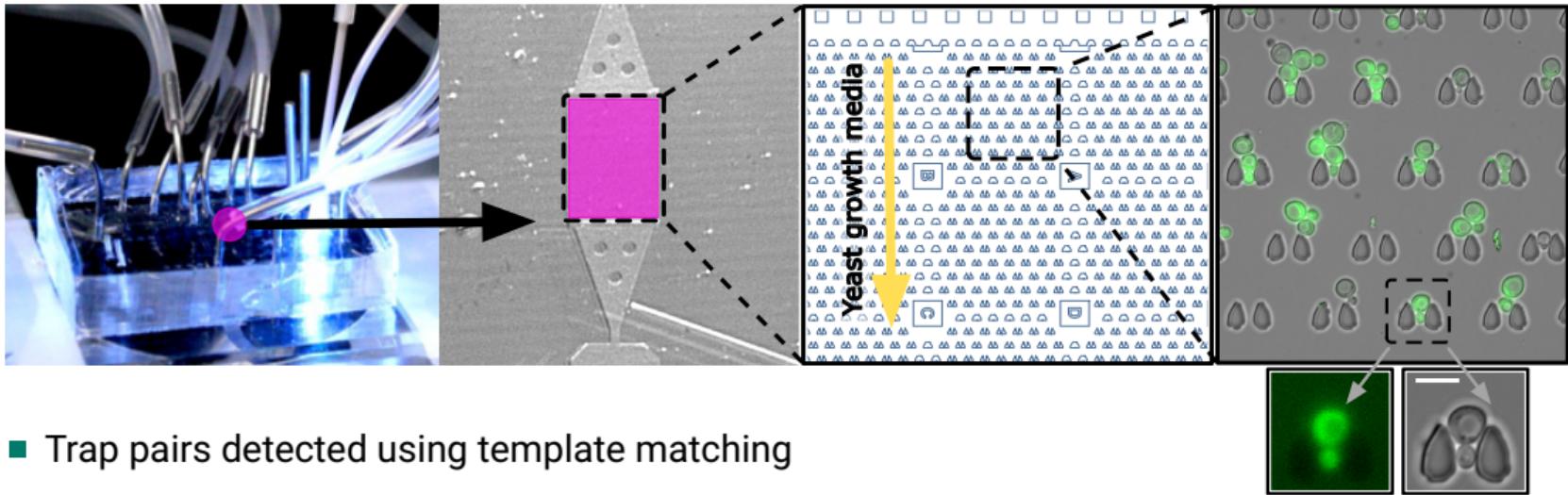


Figure: Samples of our yeast cells (■) in microstructures (■) dataset with instance-level annotations.

Biological Application

Time-Lapse Fluorescence Microscopy



- Trap pairs detected using template matching

Figure: TLFM experiment setup [Prangemeier et al., 2020] for single-cell fluorescence measurement.

Dataset of Yeast Cells in Microstructures



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- We present 493 pixel-wise annotated images, with instance segmentation labels

Dataset of Yeast Cells in Microstructures

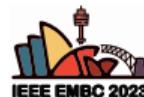


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- We utilize specimen microscopy images of two different experiments

	Trap type	# images	# cells	# traps
Subset 1	Type 1 (<i>regular</i>)	398	702	781
Subset 2	Type 2 (<i>L</i>)	95	212	190
Full dataset	Type 1 & 2	493	914	971

Table: Dataset core features.

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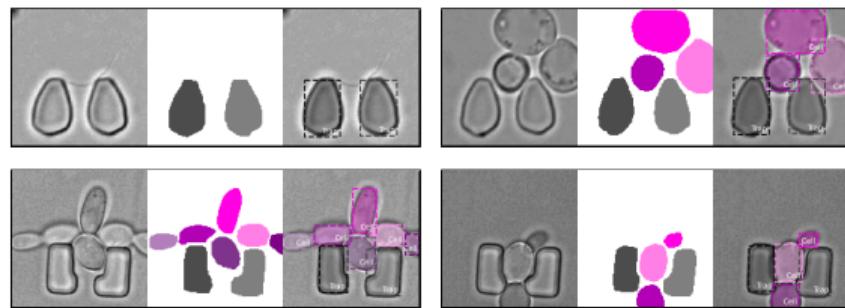


Figure: Brightfield microscopy image (left), instance seg. label (middle), and label-image overlay.

Dataset Split

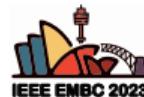


Split	# images	# cells	# traps	Trap type images 1 vs. 2
Training	296	536	582	244/52
Validation	49	108	98	33/16
Test	148	270	291	121/27

Table: Training, validation, and test split.

- We follow the split fraction of the Cityscapes dataset [Cordts et al., 2016] to split our dataset

Dataset Split



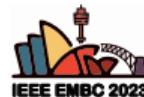
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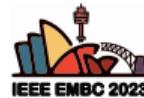


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- We ensure a representative number of both trap types in each set

Performance Evaluation



Semantic-level evaluation

Instance-level evaluation

Semantic-level evaluation

- Cell class intersection-over-union (IoU)

$$\text{IoU}(p_c, g_c) = \frac{|p_c \cap g_c|}{|p_c \cup g_c|}$$

p_c : Segmentation prediction of the cell class

g_c : Segmentation label of the cell class

Instance-level evaluation

Semantic-level evaluation

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Instance-level evaluation

- Panoptic quality (PQ) [Kirillov et al., 2019]

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

IoU: Intersection-over-union

TP: True positives

FP: False positive

FN: False negative

Additional Data

Unlabeled Video Data

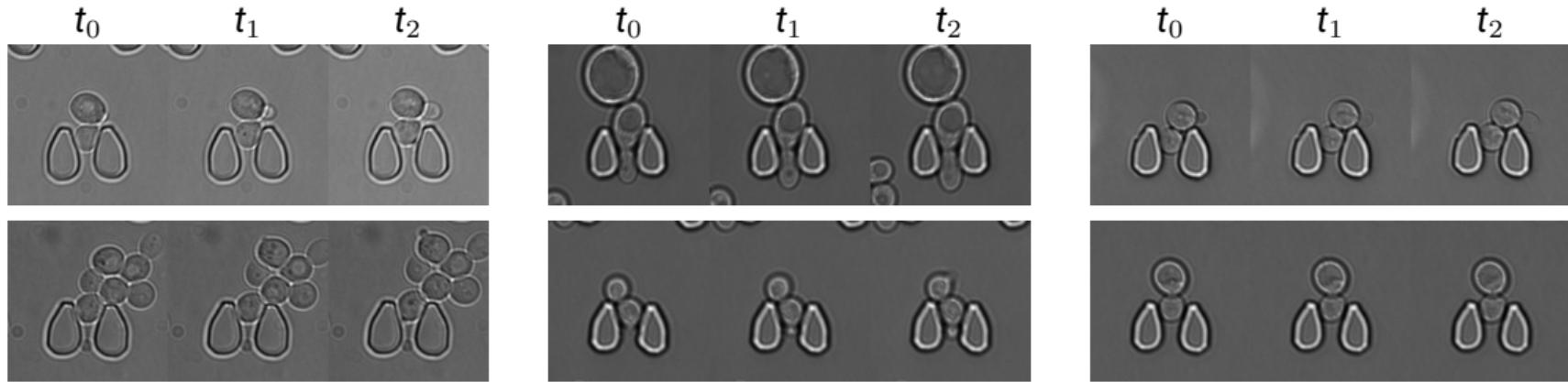


Figure: Unlabeled TLFM video clips with $\Delta t = 10\text{min}$ [Reich et al., 2021].

Ongoing & Future Work



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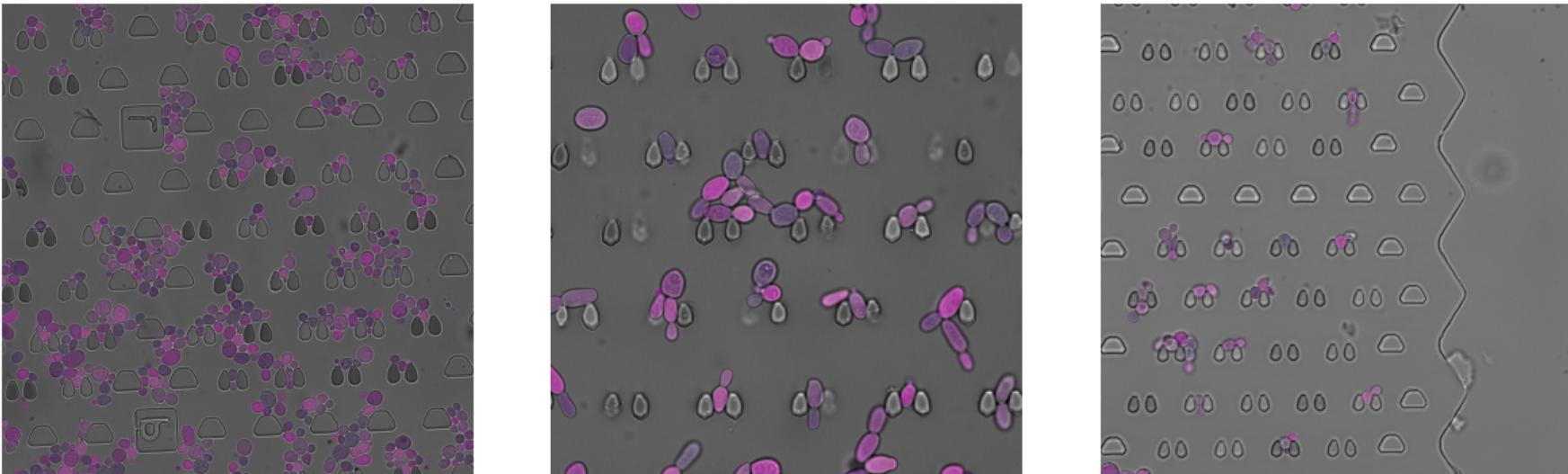


Figure: High-resolution cells in microstructures dataset; currently in preparation.

Ongoing & Future Work

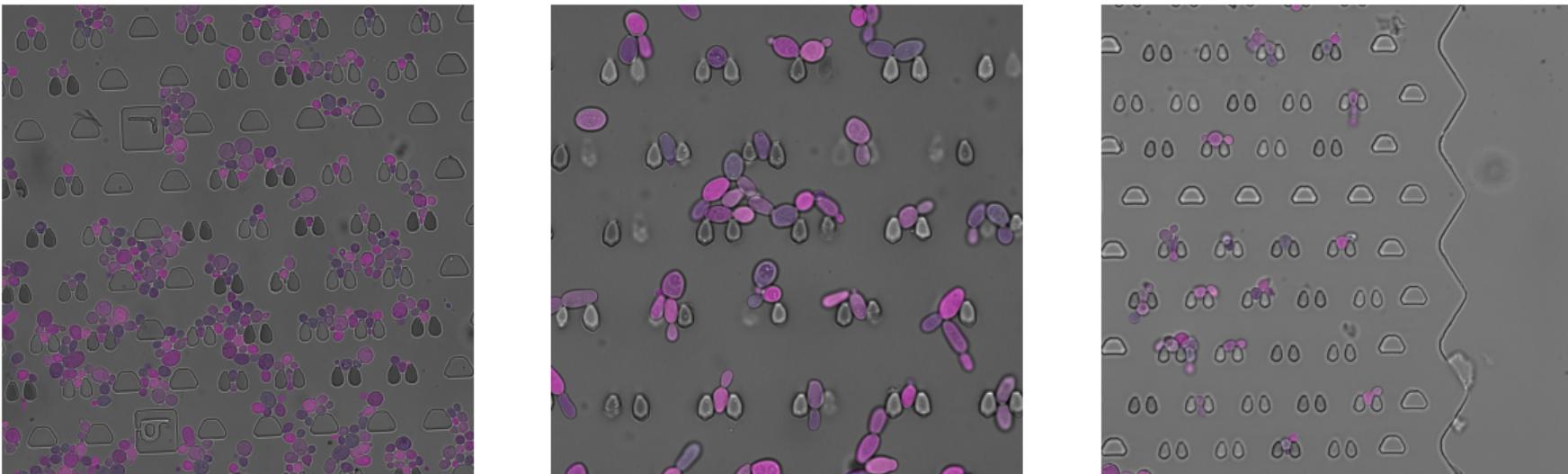
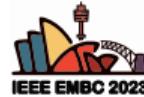


Figure: High-resolution cells in microstructures dataset; currently in preparation.

- **Future work:** Providing temporal labels (video instance segmentation)

Conclusion



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- We proposed the first instance segmentation dataset of cells in microstructures
- We provide a standardized instance and semantic-level evaluation strategy for our dataset

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Project page



Code



Data



Video data



Twitter



https://christophreich1996.github.io/yeast_in_microstructures_dataset/

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