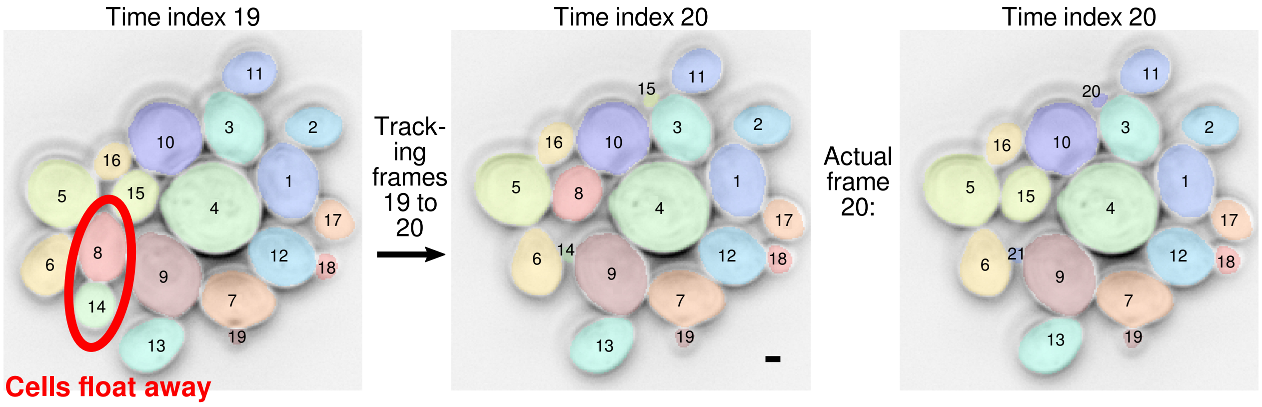
Supplementary Material

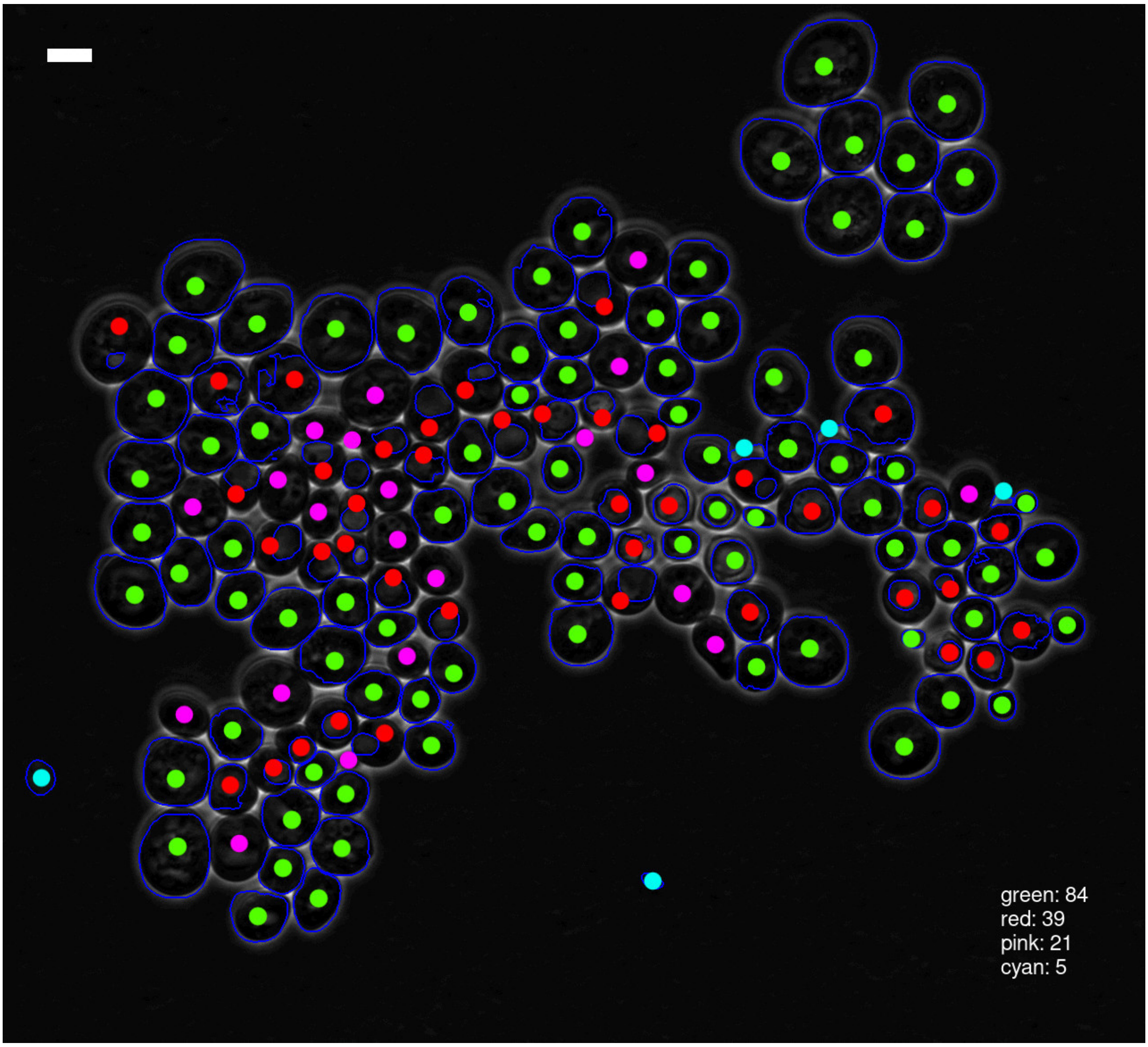
A convolutional neural network segments yeast microscopy images with high accuracy

Dietler et al.

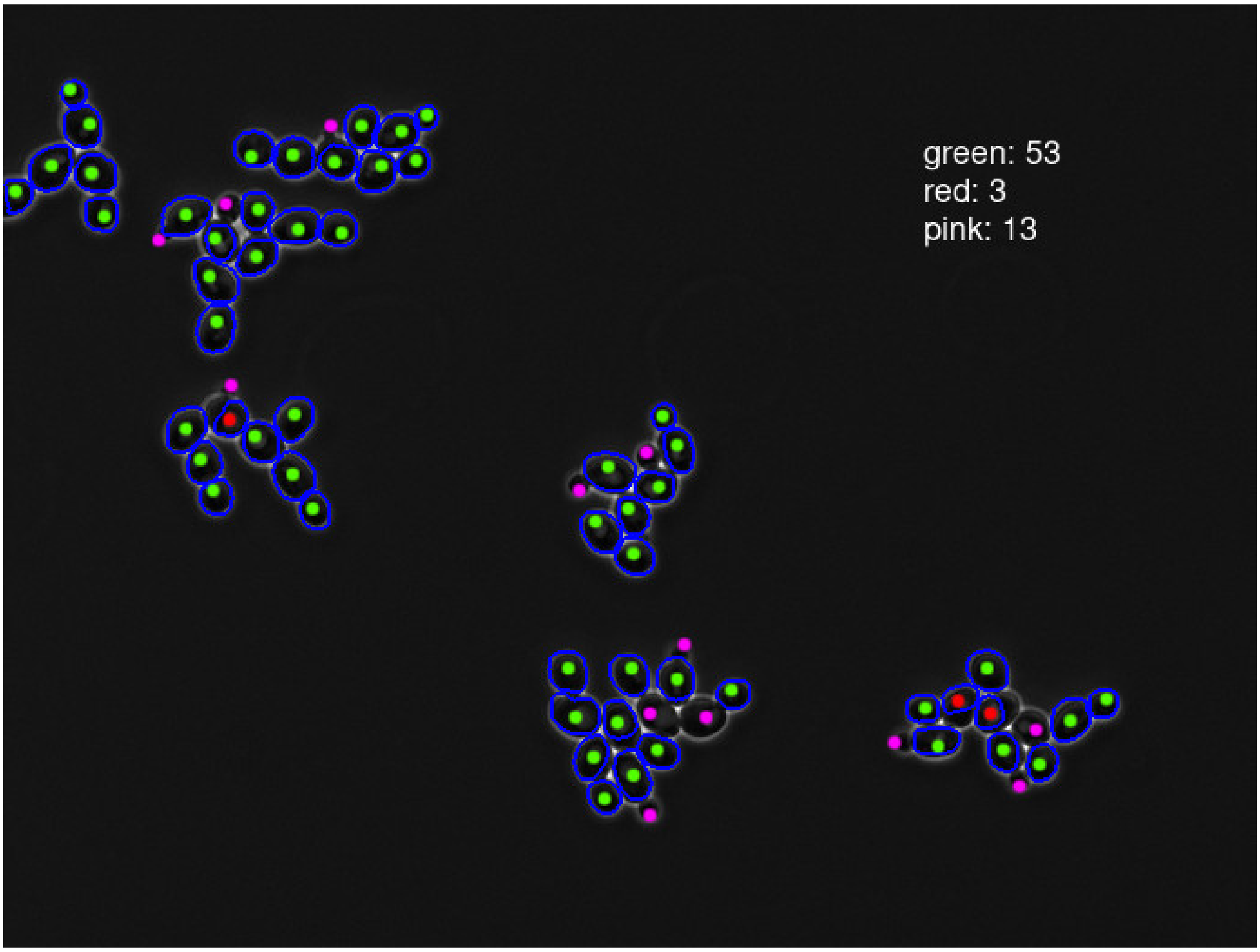
Supplementary Figures



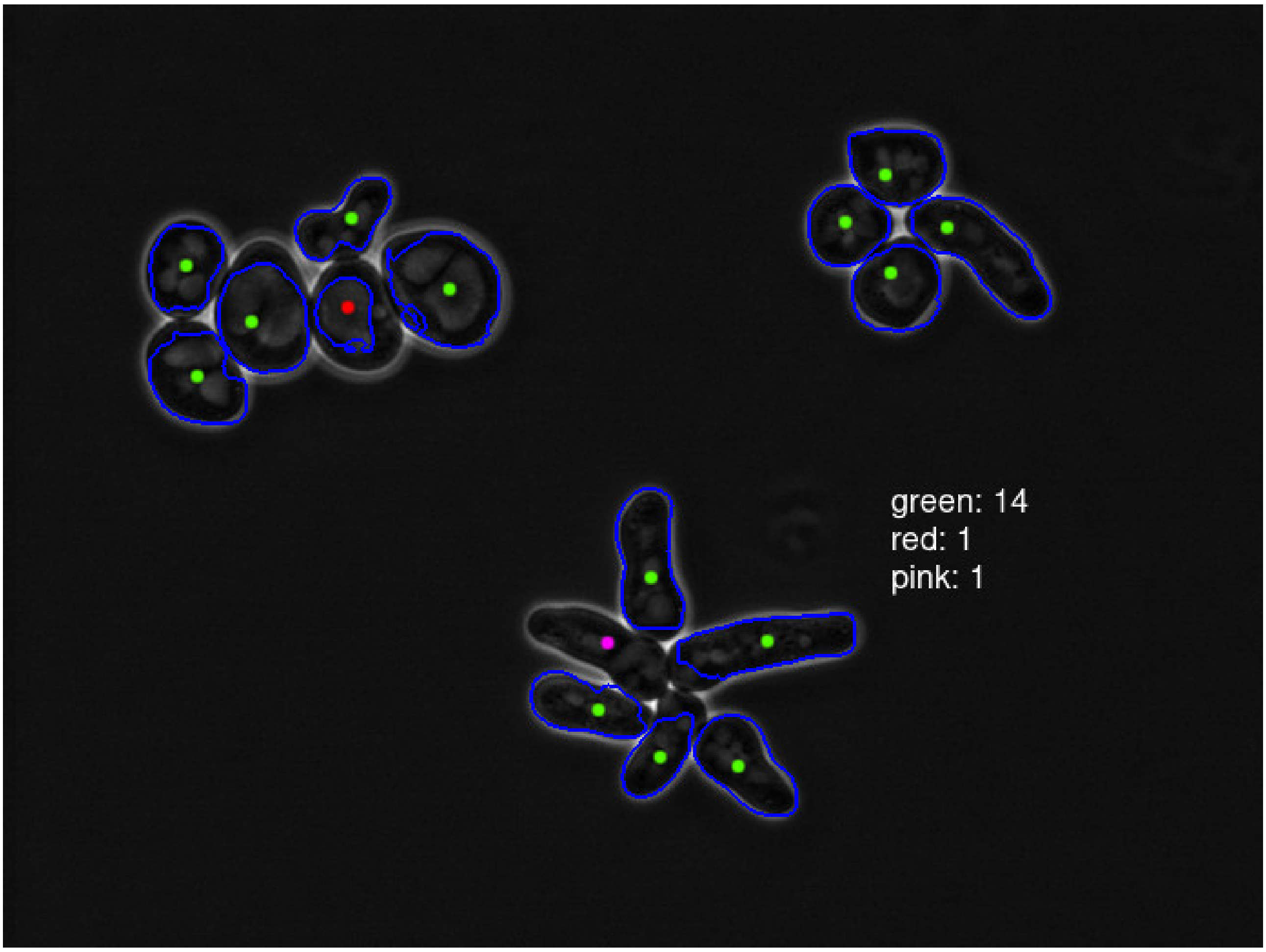
Supplementary Figure 1: Tracking errors caused by two cells floating out of the field of view. Scale bar: 1 μm.



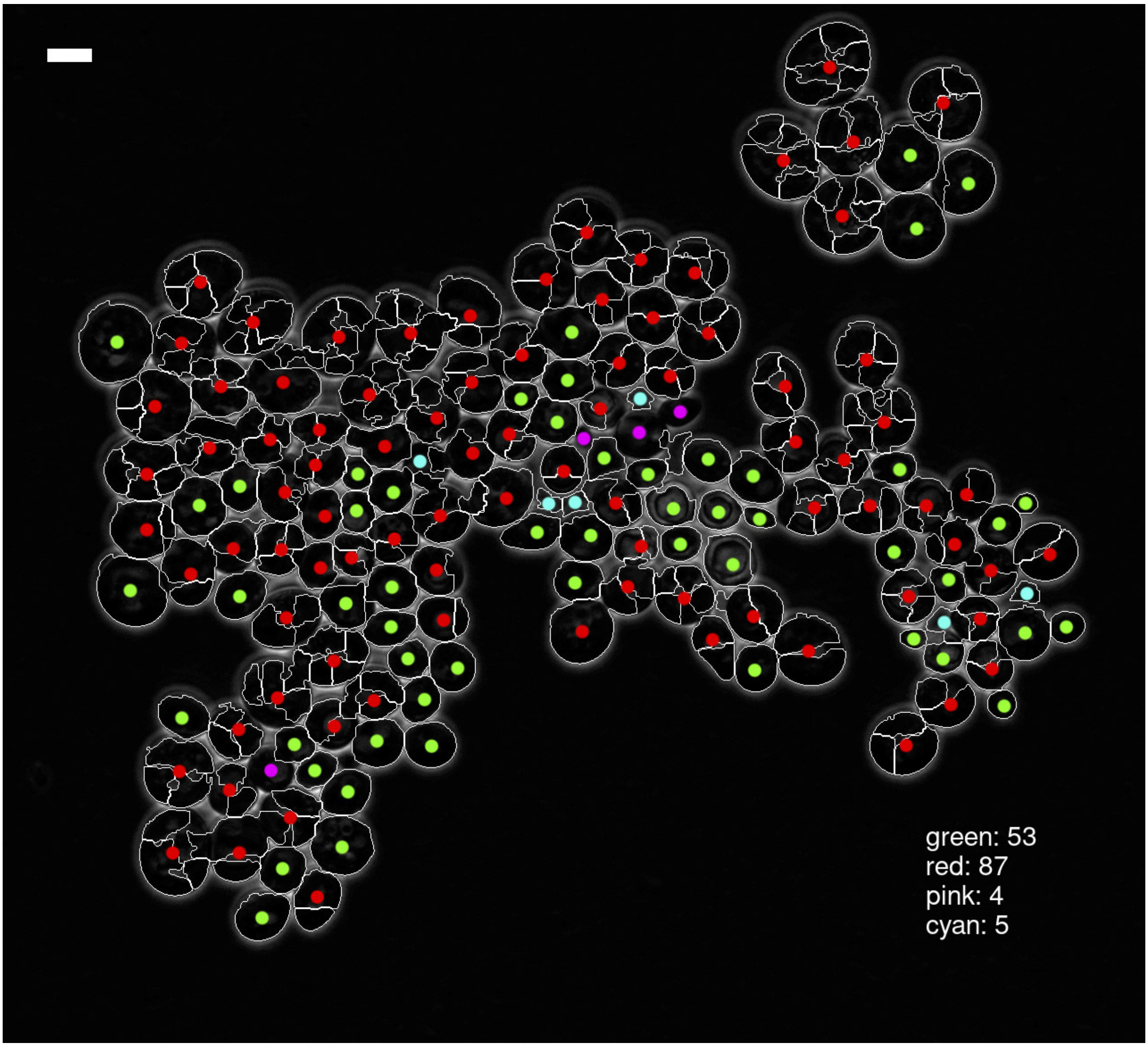
Supplementary Figure 2: Scoring of YeastSpotter results. Green dots: acceptable segmentation, red: bad segmentation, pink: missed cell, cyan: spurious cell. Scale bar: 5 μm.



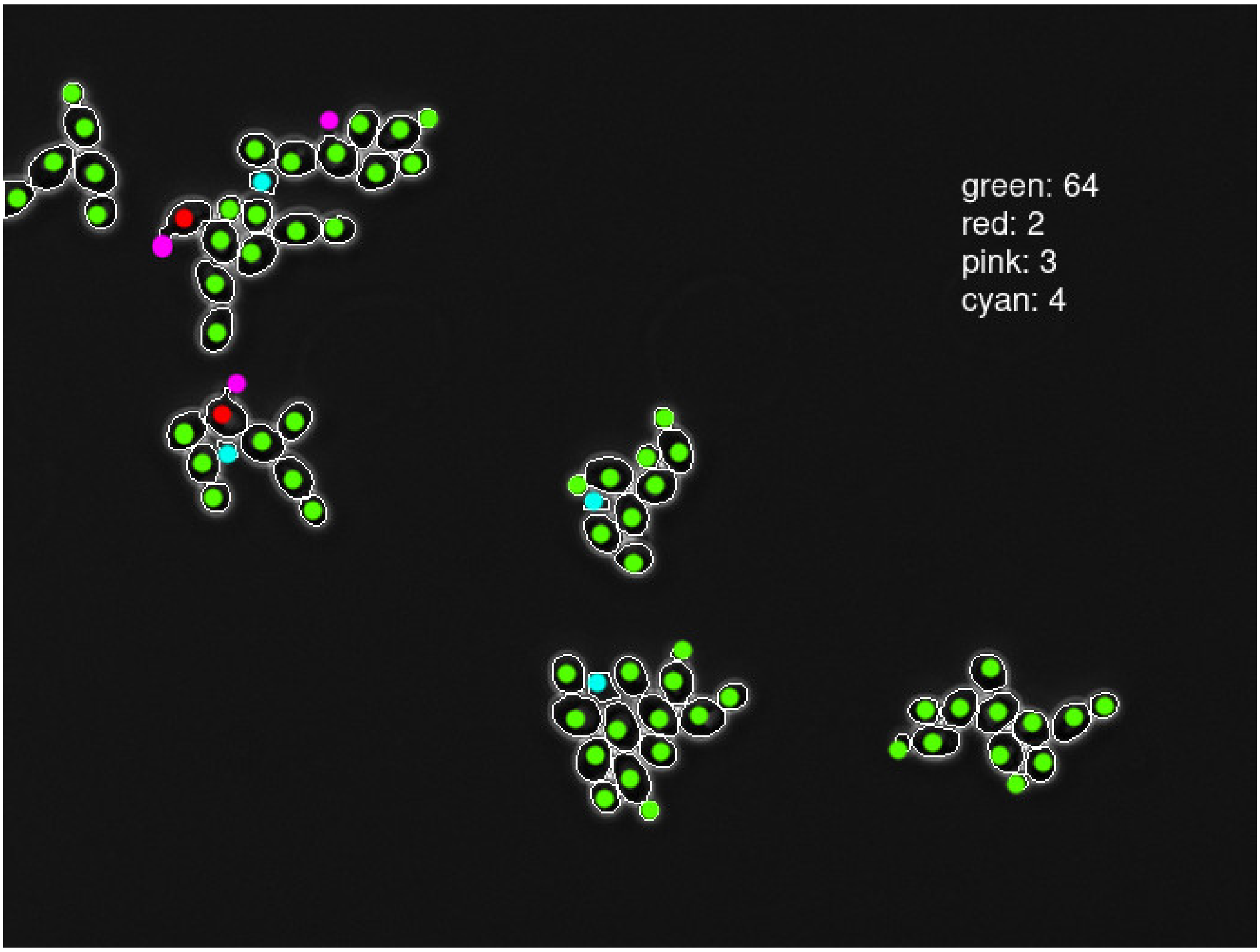
Supplementary Figure 3: Scoring of YeastSpotter results. Green dots: acceptable segmentation, red: bad segmentation, pink: missed cell, cyan: spurious cell. Image from ref. (1), scale bar unknown.



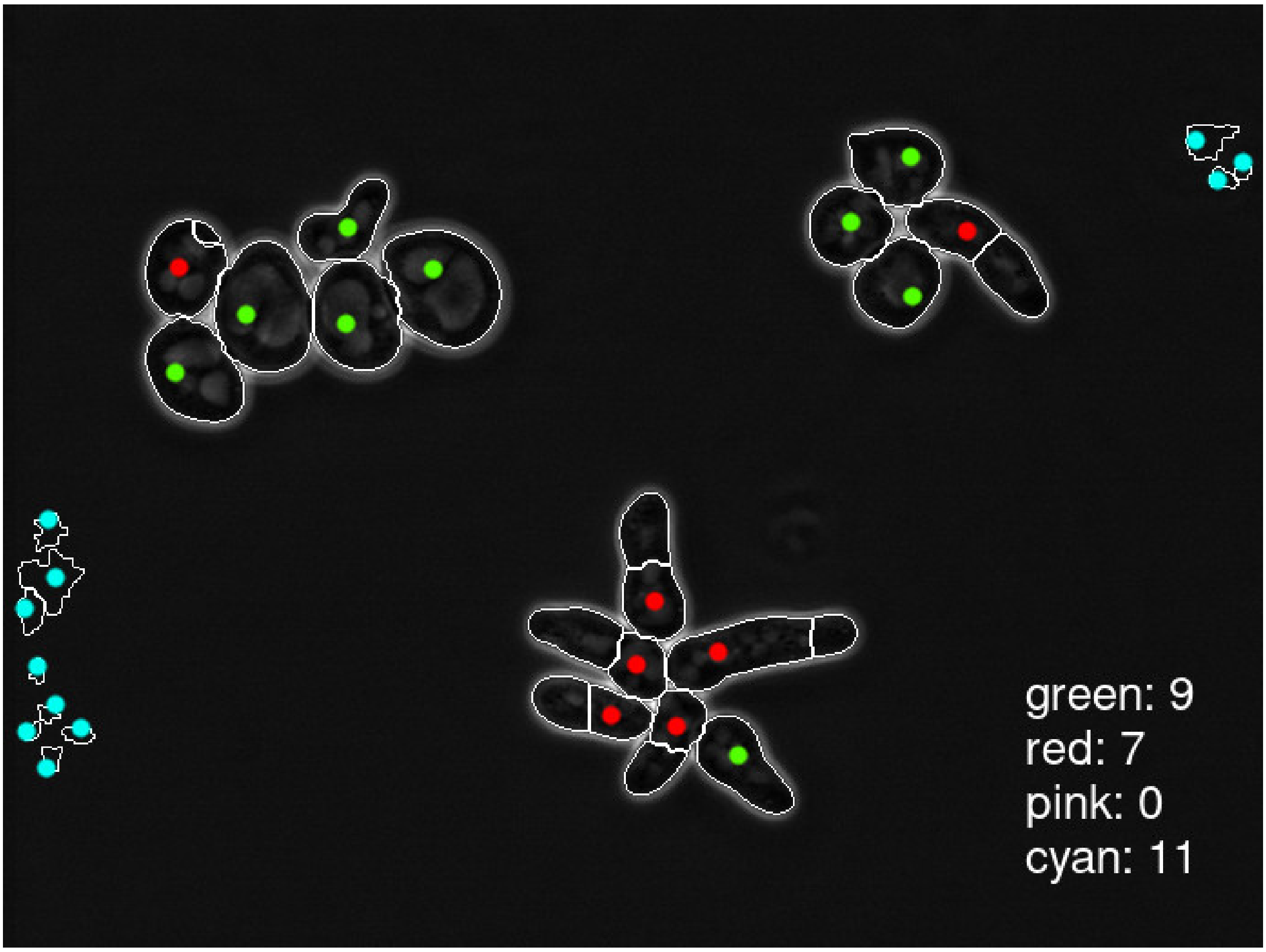
Supplementary Figure 4: Scoring of YeastSpotter results. Green dots: acceptable segmentation, red: bad segmentation, pink: missed cell, cyan: spurious cell. Image from ref. (1), scale bar unknown.



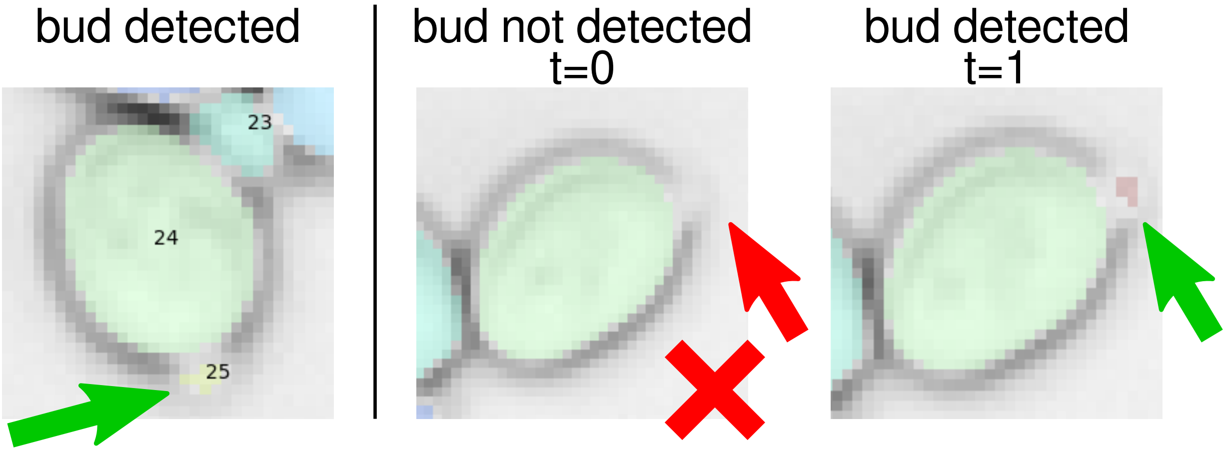
Supplementary Figure 5: Scoring of the results of the method by Wood et al. (2). Green dots: acceptable segmentation, red: bad segmentation, pink: missed cell, cyan: spurious cell. Scale bar: 5 μm.



Supplementary Figure 6: Scoring of the results of the method by Wood et al. (2). Green dots: acceptable segmentation, red: bad segmentation, pink: missed cell, cyan: spurious cell. Image from ref. (1), scale bar unknown.



Supplementary Figure 7: Scoring of the results of the method by Wood et al. (2). Green dots: acceptable segmentation, red: bad segmentation, pink: missed cell, cyan: spurious cell. Image from ref. (1), scale bar unknown.



Supplementary Figure 8: Examples of tiny buds in data set 9 from ref. (1), some only a few pixels in size, that were detected by the YeaZ CNN (left and right) except for four such tiny buds (middle example). The missed bud (middle) was, however, detected at the next time point in the timelapse series (right) when it was slightly bigger. Image from ref. (1), scale bar unknown.

Supplementary Tables

Supplementary Table 1: Training set images

File name	Number of image layers	Number of cells
`a_reexport1_crop_1`	75	1914
`a_reexport2_crop_1`	42	703
`a_reexport3_crop_1`	41	132
`a_reexport3_crop_2`	2	0
`d_reexport1_crop_1`	30	110
`d_reexport1_crop_2`	30	764
`d_reexport1_crop_3`	30	412
`d_reexport1_crop_4`	1	30
`d_reexport2_crop_1`	1	20
`d_reexport2_crop_2`	30	345
`d_reexport2_crop_3`	30	611
`m_reexport1_crop_1`	18	1637
`v_cdc20null_crop_1`	1	171
`v_clnnull_crop_1`	1	107
`Ahmad_frame_16_crop_1`	5	251
`Ahmad_frame_16_crop_2`	5	18
`Ahmad_frame_16_crop_3`	5	10
`Ahmad_frame_16_crop_4`	5	247
`Ahmad_frame_19_crop_1`	5	208
`Ahmad_frame_19_crop_2`	5	158
`Ahmad_frame_19_crop_3`	5	135
`V11032020_p1_crop_1`	1	27
`V11032020_p2_crop_1`	4	200
`V11032020_p3_crop_1`	2	105
`2020_3_24_AS20_1_AS18_Pos11_crop_1`	5	137
`2020_3_24_AS20_1_AS18_Pos11_crop_2`	5	76
Total	384	8528

Supplementary Table 2: Bright-field image segmentations

File name	Number of image layers	Number of cells
`FOV2_1.5p_PhC_absent_crop_1`	1	97
`FOV3_1.5p_PhC_absent_crop_1`	1	83
`FOV4_1.5p_PhC_absent_crop_1`	1	83
`FOV5_1.5p_PhC_absent_crop_1`	1	47
`FOV6_1.5p_PhC_absent_crop_1`	1	107
`FOV7_1.5p_PhC_absent_crop_1`	1	100
`FOV8_1.5p_PhC_absent_crop_1`	1	129
`FOV9_1.5p_PhC_absent_crop_1`	1	58
`FOV9_1.5p_PhC_absent_crop_2`	1	206
`FOV10_1.5p_PhC_absent_crop_1`	1	274
`FOV10_1.5p_PhC_absent_crop_2`	1	62
`FOV11_1.5p_PhC_absent_crop_1`	1	62
`FOV12_1.5p_PhC_absent_crop_1`	1	181
`FOV13_1.5p_PhC_absent_crop_1`	1	74
`FOV14_1.5p_PhC_absent_crop_1`	1	105
`FOV15_1.5p_PhC_absent_crop_1`	1	62
Total	16	1730

Supplementary Table 3: Strains used.

Name	Mating type locus	Genotype
AX42-25A	MATa	wild type W303
JB204-6B	MATa	ADE2 HTB2-mCherry::HIS5
SJR112a12d	MATα	cln1Δ0 cln2Δ0::MET3pr-CLN2 cln3Δ0 HTB2-mCherry::HIS5 ura3Δ0
SJR33h6d		clb2Δ::LEU2 trp1Δ::TRP1::GAL-SIC1(1X) HTB2-mCherry:HIS5 MYO1-GFP::KanMX
SJR36a11b	MATa	cln1Δ cln2Δ:CLN2pr-Venus:TRP1 cln3Δ:LEU2 trp1Δ:TRP1:MET3pr-CLN2 clb5Δ:HIS3 clb6Δ:KanMX HTB2-mCherry:HIS5
CL86-1-11D	MATa	clb1Δ clb2Δ::GALL-CLB2::URA3 clb3Δ::TRP1 clb4Δ::his3Δ::kanMX clb5Δ::kanMX clb6Δ::kanMX swe1Δ::TRP1 ADE2
2147-1C	MATα	cdc20Δ::LEU2 ADE2::GALL-CDC20
AS18	MATαsyn	cln1Δ0 cln2Δ0::MET3pr-CLN2 cln3Δ0::GAL1pr-HO HTB2-mCherry::HIS5 ADH1pr-HOcs-YFP

References

(1) Mróz, F., Kaczmarek, A. & Stoma, S. YIT - Yeast Image Toolkit. *http://yeast-image-toolkit.biosim.eu/pmwiki.php* (accessed: 15.02.2020).

(2) Wood, N. E. & Doncic, A. A fully-automated, robust, and versatile algorithm for long-term budding yeast segmentation and tracking. *PLoS One* **14**, 1–28 (2019).