

Supplementary figures and tables

Supplementary figures

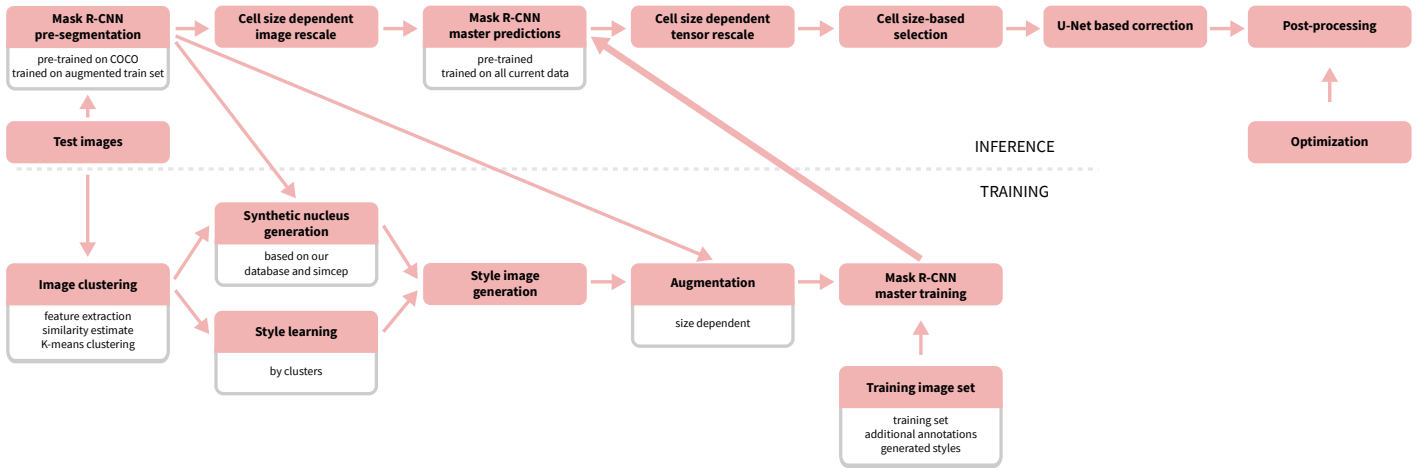


Figure S1. A detailed overview of the proposed pipeline.

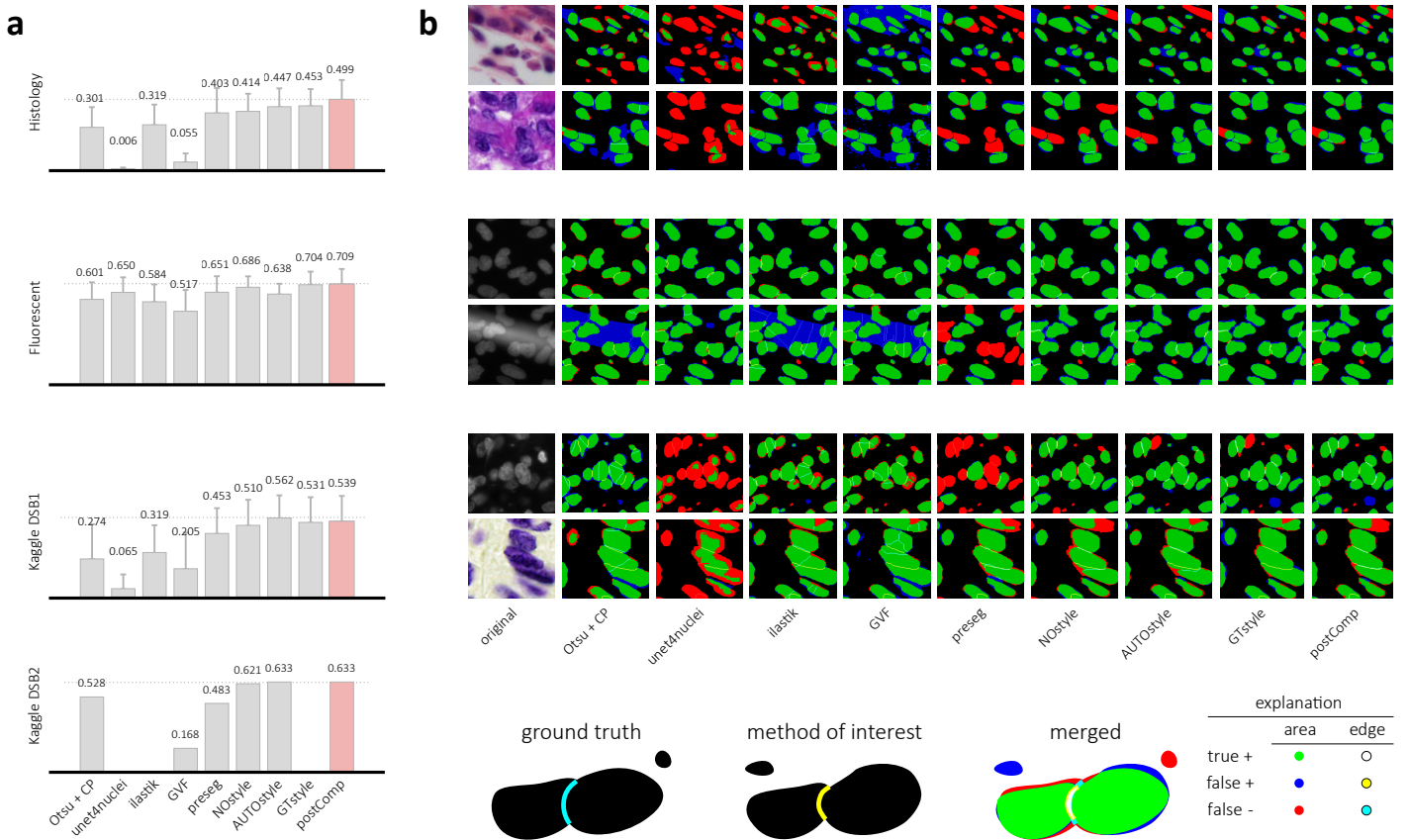


Figure S2. Results from Figure 2 in more detail. a) DSB scores with error bars for the image sets tested. b) Segmentation results for various methods. preseg, NOstyle, AUTOstyle, GTstyle and postComp refer to variations of our approach. See sections 3.2. and 3.4-3.5. for details.

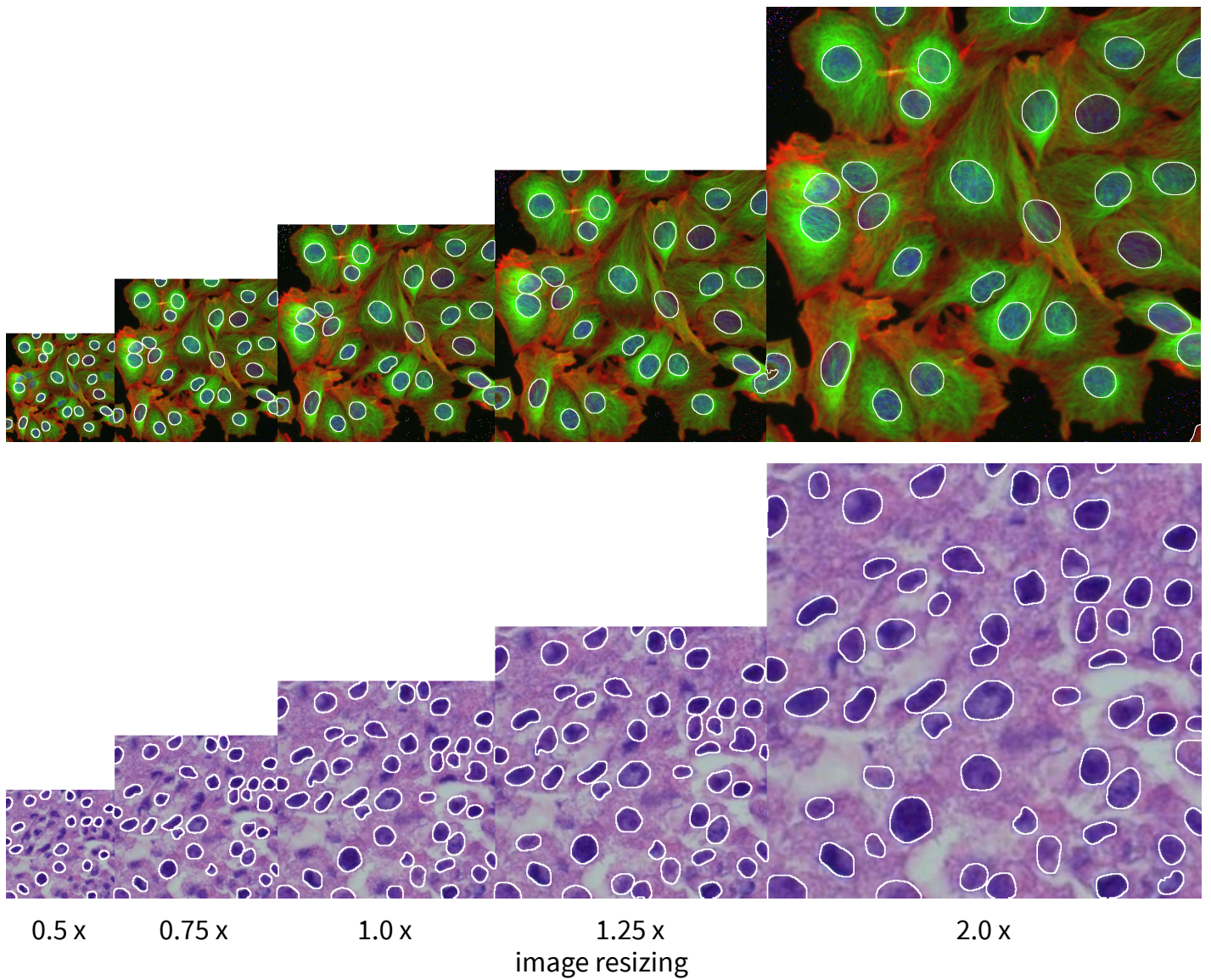


Figure S3. Mask R-CNN nucleus segmentations are reasonably robust to changes in scale, but we found that best performance can be achieved if nucleus size is fixed to 40 pixels diameter (at 1.0x magnification).

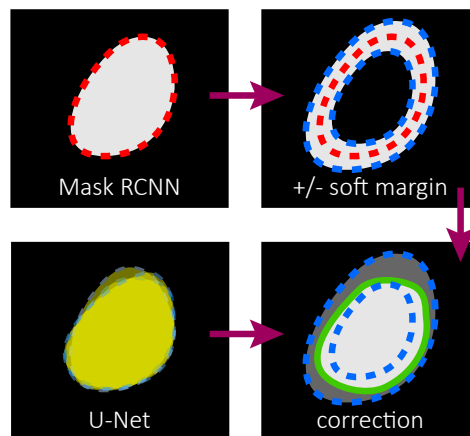


Figure S4. Post-processing contour correction with U-Net. Mask RCNN segmentation contour was refined within a given maximum margin using U-Net segmentation. See Section 2.2.2 for details.

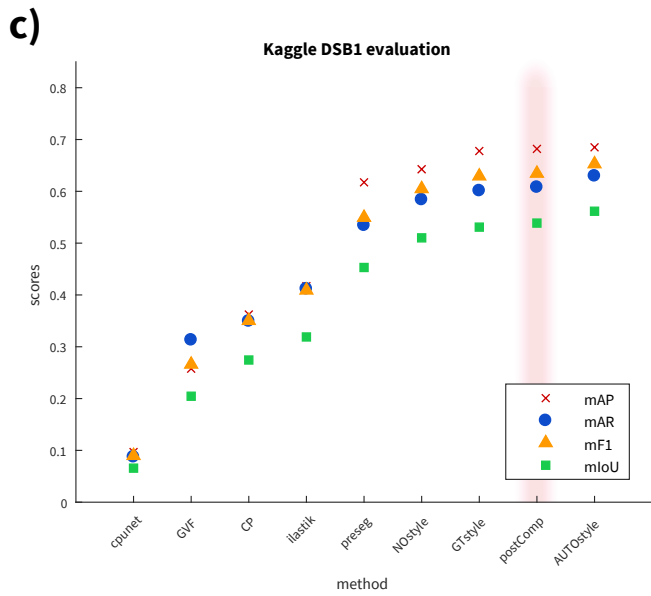
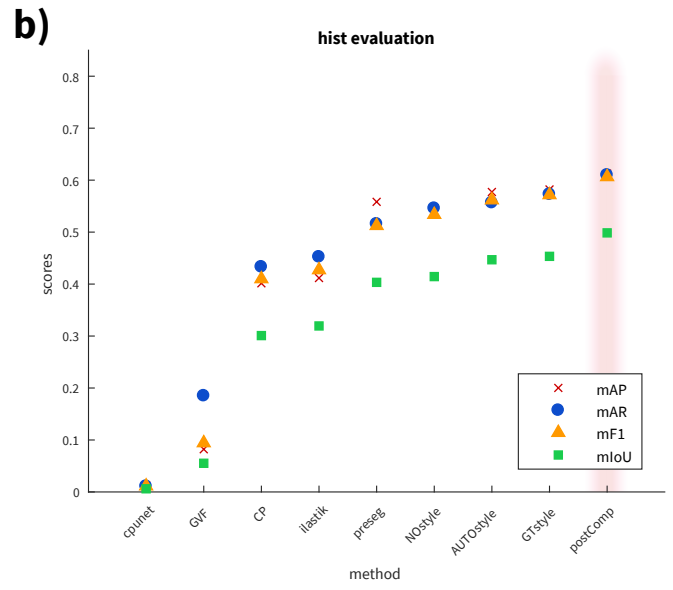
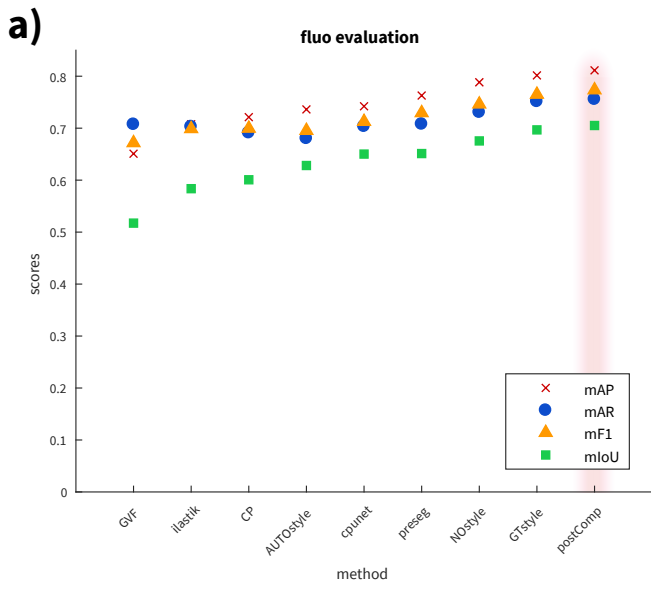


Figure S5. Evaluation of the methods on fluo, hist, and DSB test1 using different metrics: mAP: mean average precision, mAR: mean average recall, mF1: mean average F1-score, mIoU: mean intersection over union. See definitions in 3.3. a) test set fluo, b) test set hist, c) test set DSB test1. postComp is highlighted in light pink shade.

Supplementary tables

Table S1: DSB scores

method	dataset			
	fluo	hist	DSB test1	DSB test2
preseg	0.651	0.403	0.453	0.483
CP	0.600	0.301	0.274	0.528
unet4nuclei	0.650	0.006	0.065	-
GVF	0.517	0.055	0.205	0.168
NOstyle	0.686	0.414	0.510	0.621
AUTOstyle	0.638	0.447	0.562	0.633
GTstyle	0.704	0.453	0.531	-
postComp	0.709	0.499	0.539	0.633
Ilastik	0.584	0.319	0.319	-
Kaggle1	-	-	-	0.631
Kaggle2	-	-	-	0.614

Table S1. DSB scores. We tested the methods described in Section 3.4 on four test datasets: DSB test1, DSB test2, fluo, and hist. Fluo was the BBBC039 9 image set of 200 DAPI-labelled fluorescent images while hist was a randomly selected set of 50 in-house labeled histological images. DSB test1 and test2 are the official test sets of the DSB 2018 competition. The DSB-score is the mean average precision at different intersection-over-union (IoU) thresholds (see Section 3.3). The DSB test2 set has both AUTOstyle and postComp models with the highest score because in this specific case the automated style transfer learning was derived from test2, that was our final competition model. The best performing method’s score is highlighted in bold for each test set.

Table S2: Training dataset statistics

property		subset													
		DSB train	DSB test1	Weebly	TNBC	BBBC021	Internet	biomag 02	biomag 04	biomag 05	biomag 06	jw	ISBI 2009	AS	00733
image type	fluo normal	x	x	-	-	x	x	-	-	-	-	x	x	x	-
	fluo clumped	x	x	-	-	x	x	-	x	x	x	x	-	x	x
	tissue simple	x	x	-	-	-	x	x	-	-	-	-	-	-	-
	tissue complex	x	x	x	x	-	x	-	-	-	x	-	-	-	-
image size	min	256x256	256 256	1000x1000	512x512	1280x1024	213x65	812x828	288x286	256x256	256x340	956x1242	1030x1349	512x512	512x512
	max	1040x1388	520 696	-	-	-	2848x4272	1024x1344	326x327	1024x1360	2048x2048	1040x1388	-	-	-
number of images		670	65	30	50	5	97	11	4	5	32	20	48	11	54
number of nuclei	mean/image	44.27	4152	565.23	81.12	124.40	99.18	94.27	53.25	197.60	67.03	42.30	38.10	110.27	136.15
	total	29662	63.88	16957	4056	622	9620	1037	213	988	2145	846	1829	1213	7352
models trained on		all	all but this	all	all	all	all but hist	all but hist	all	all	all but hist	all	all	all	all
models tested on		-	DSB test1	-	-	-	hist	hist	-	-	hist	-	-	-	-
data source		DSB	DSB	1	2	3, 4	5, 6	7	8	9	10	11	11, 12	11	11

Table S2. Statistics about the training data. Data sources in the last row are as follows.

1: <https://nucleisegmentationbenchmark.weebly.com/dataset.html>

2: Naylor Peter Jack, Walter Thomas, Laé Marick, & Reyal Fabien. (2018). Nuclei Segmentation in Histopathology Images Using Deep Neural Networks (Version 1.0) [Data set]. Zenodo. <http://doi.org/10.5281/zenodo.1174353>

3: <http://mct.aacrjournals.org/content/9/6/1913>

4: <https://www.nature.com/articles/nmeth.2083>

5: https://www.google.hu/search?q=histology+microscope+nucleus&-source=lnms&tbm=isch&sa=X&ved=0ahUKEwiIxb6v_J3aAhXFFJoKHYdzAxUQ_AUICigB&biw=1366&bih=654

6: https://www.google.hu/search?q=dapi+stained+nuclei&client=firefox-b-ab&dcr=0&source=lnms&tbm=isch&sa=X&ved=0ahUKEwik4bK8_Z3aAhXLDZoKHZXTDZkQ_AUICigB&biw=1366&bih=654

7: <https://www.nature.com/articles/nmeth.3323>

8: <https://www.ncbi.nlm.nih.gov/pubmed/28122742>

9: <https://www.nature.com/articles/s41467-017-02628-4>

10: Peter Horvath Laboratory

11: shared by other participating teams of the DSB on the competition website

12: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2901896/>