Towards Low-Cost and Efficient Malaria Detection

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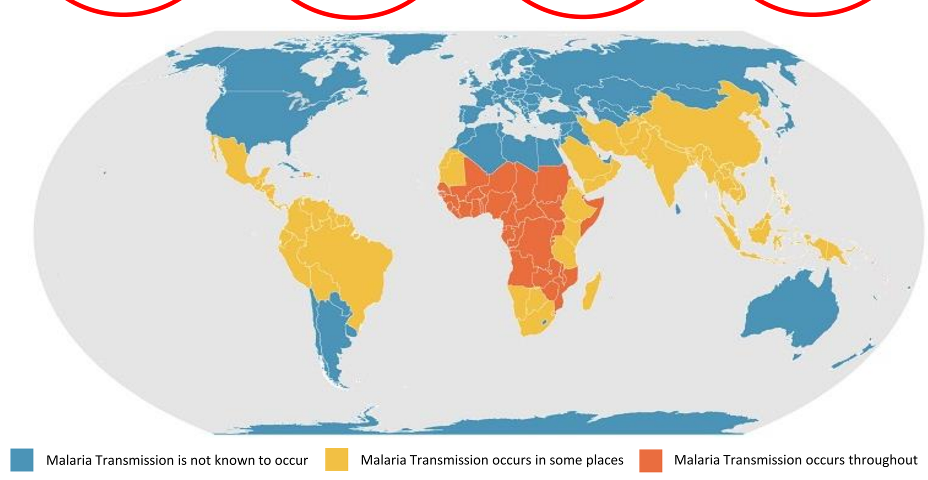
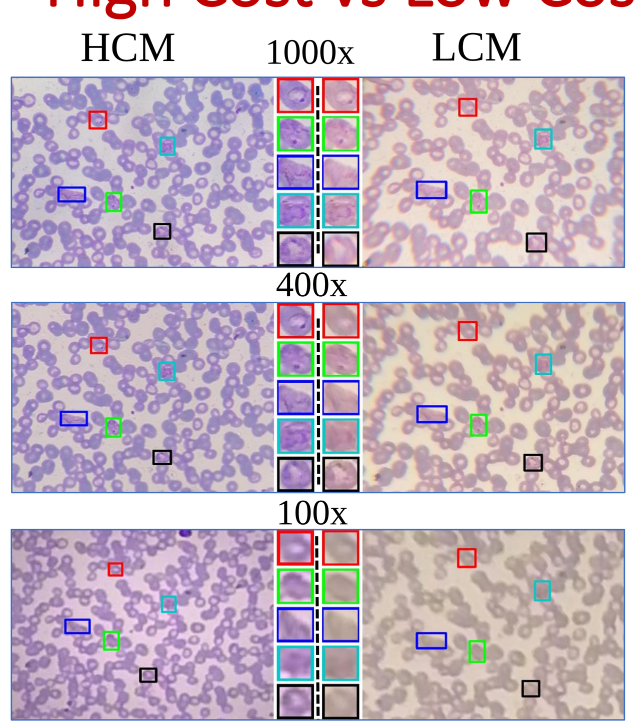
Problem Statement

226M Cases annually | 425K Deaths | 67% Children | Weak Health-care system



- Microscopic investigations are costly and time consuming
- Automatic diagnosis is hampered by lack of sufficient datasets

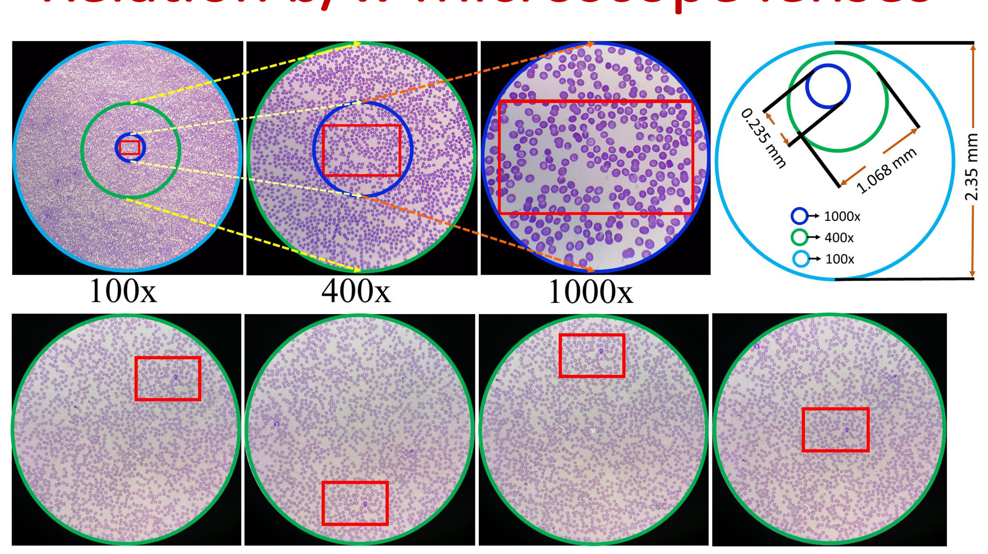
High Cost vs Low Cost Microscope



LCM is 70% cheaper than HCM, However, experts are reluctant to annotate dataset on LCM because it has:

- Smaller FOV
- Blurrier View
- Less Precise Knobs

Relation b/w Microscope lenses



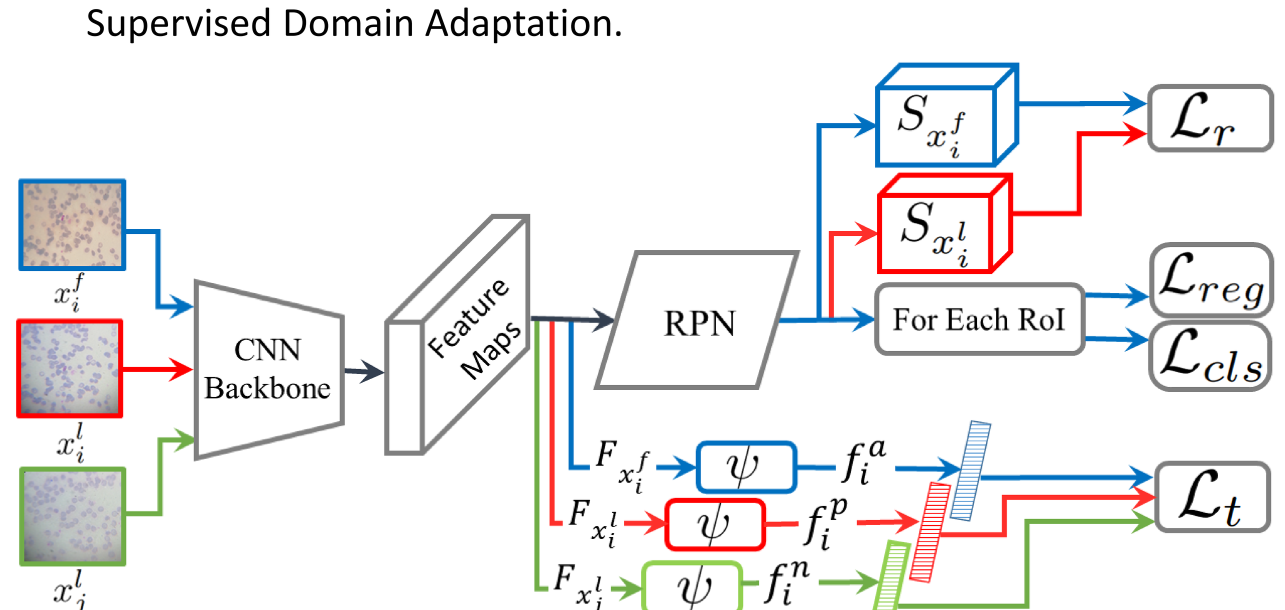
- One FOV of 400x covers around 17 FOVs of 1000x
- Scan a slide 17 times faster with 400x lens

Key contributions

1. Collected the first large-scale multi-microscope multi-magnification malarial image dataset from the thin-blood smear slides
2. Designed an annotation transfer mechanism to transfer annotations across images
3. Computed the baseline results of several object detectors and domain adaptation methods on our dataset
4. Introduced a partially supervised domain adaptation mechanism

Partially Supervised Domain Adaptation

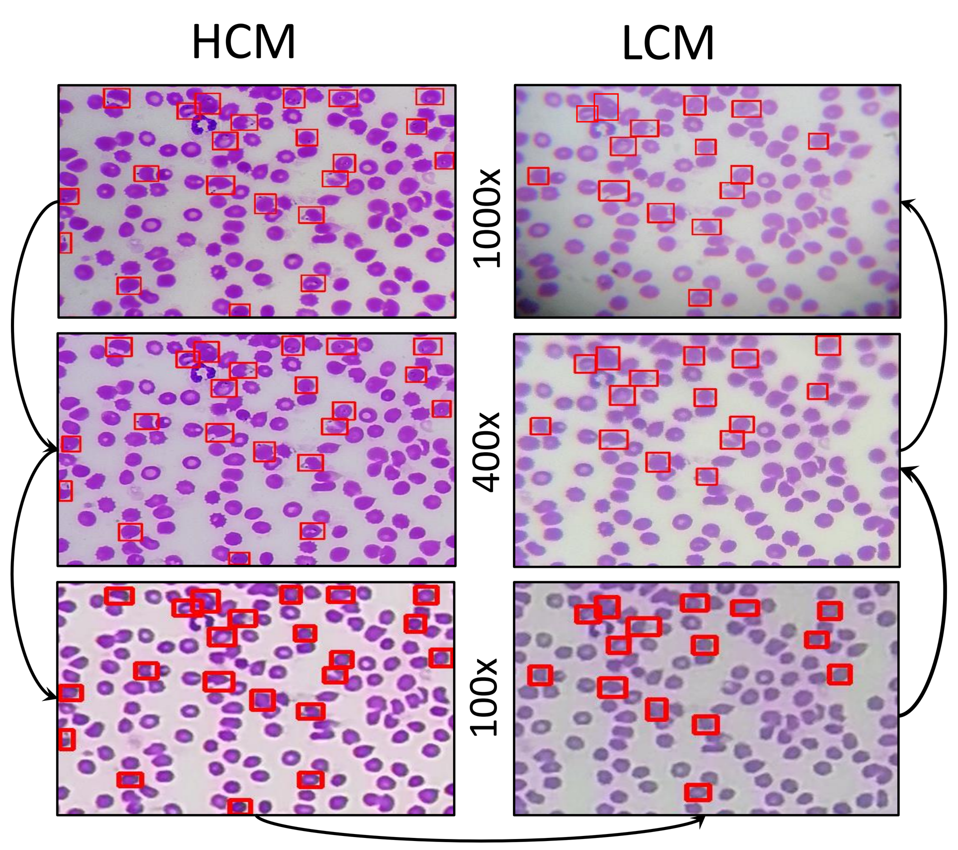
- Every HCM image has a corresponding LCM image.
- Domain shift between HCM and LCM
- The Annotation Transfer is quite good in the location transfer however, the annotations (bounding box) still needs human verification.
- Hence, to overcome this limitation we developed Partially Supervised Domain Adaptation.



$$\mathcal{L}_r(x_i^f, x_i^l) = max(0, avg(S_{x_i^f}) - avg(S_{x_i^l}) - \beta) \quad (1)$$

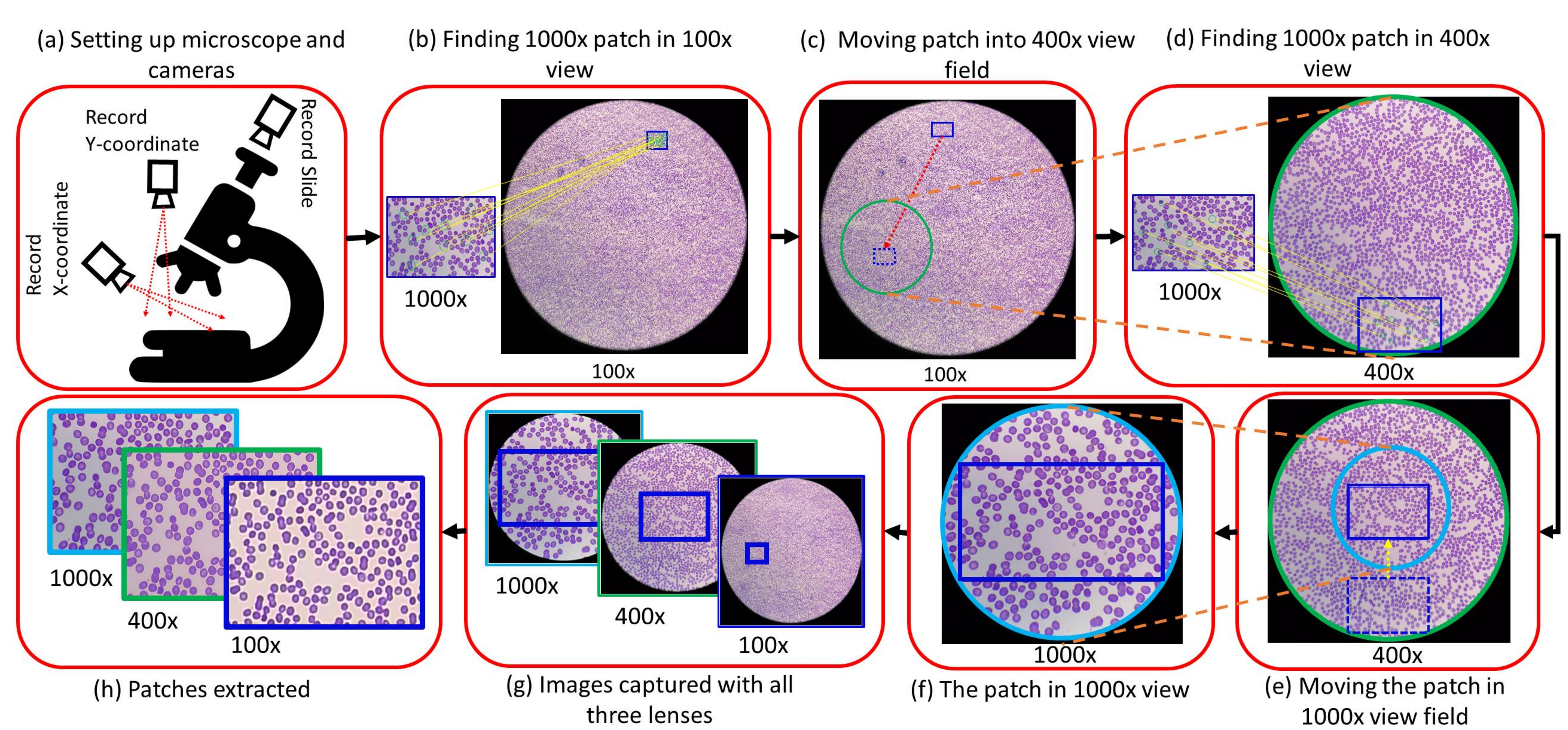
$$\mathcal{L}_t = max(0, \|f_i^p - f_i^a\|_2^2 - \|f_i^a - f_i^n\|_2^2 + \alpha) \quad (2)$$

Annotation Transfer



Since LCM has smaller FOV than HCM, there are fewer number of cell in an image captured by LCM than its corresponding HCM image, nevertheless, they are centered at same region of slide.

Data Collection Process



Comparison with Existing Datasets

Malaria Dataset	Across Microscopes	Multi-Magnification	Malarial Cells Annotated	Bounding Box Annotations	No. of Images
BBBC041 [1]	×	×	2,452	✓	1,364
Malaria655 [38]	×	×	557	×	655
MPIDB [25]	×	×	840	×	229
IML [5]	×	×	529	✓	345
Our Dataset	✓	✓	**20,331**	✓	**7,542**

Project Page

SCAN ME

GitHub

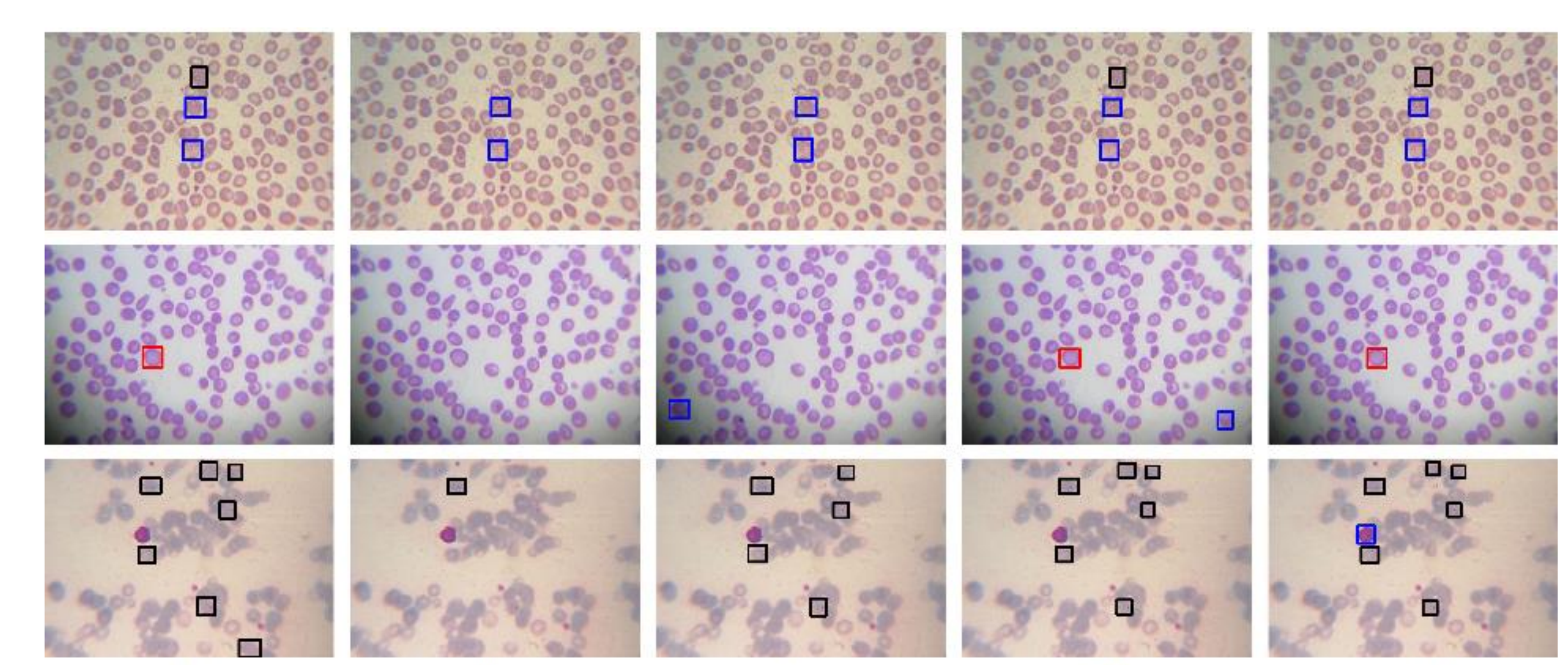
Different Object Detectors' Results in (mAp)

Training Magnification	FCOS			RetinaNet			YOLO			Faster R-CNN		
	Test Magnification											
	1000x	400x	100x	1000x	400x	100x	1000x	400x	100x	1000x	400x	100x
1000x	36.8	13.5	0.0	43.1	29.7	0.0	62.8	36.7	0.0	**66.8**	31.3	0.0
400x	31.4	29.1	1.9	32.9	34.0	1.8	55.2	56.6	4.5	56.9	**61.1**	1.4
100x	9.4	14.8	8.9	10.2	15.4	16.3	10.5	3.9	20.1	25.4	**31.9**	31.5

DA Results in (mAP)

Methods	Source = HCM, Target = LCM	
	1000x → 1000x	400x → 400x
Xu et al. [44]	15.5	**21.6**
Saito et al. [37]	**24.8**	21.4
Chen et al. [9]	17.6	21.5
Source only	17.1	26.7
Fine Tuning on fake-LQM	33.3	31.8
Ranking loss	35.7	32.4
Triplet loss	37.2	32.2
Ranking+Triplet loss	**37.5**	**33.8**

Qualitative Result



(a) Ground truths (b) Source only model (c) Ranking loss (d) Triplet loss (e) Ranking + triplet loss

Conclusion

- ✓ We have attempted making malaria detection low- cost and efficient.
- ✓ We have collected a large-scale multi-magnification, multi-microscope malaria dataset.
- ✓ We benchmark different popular object detectors and domain adaptation methods on our dataset.
- ✓ We have introduced Partially Supervised Domain Adaptation strategy.
- ✓ We believe that this dataset will pave the way for future research in developing algorithms that can work with low-cost microscopes.

Acknowledgements

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