



Data Augmentations for Cell-Type Generalizable Instance Segmentation

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Abstract

Quantifying cell abundance through computer vision approaches in an instance segmentation task can greatly streamline cell-based assays and workflows for researchers in the biological sciences. Instance segmentation of cells in phase microscopy images, a relatively non-disruptive method of imaging live cells, is thus an important and high-demand task in computer vision. Recent work and the generation of a large-scale labeled dataset have greatly expedited progress on this task. However, given the highly heterogenous and diverse array of cell types and growth conditions, there still exists a need for generalizable models that can transfer and perform well on data from a cell type or condition not encountered in the training dataset. In this paper, I explore the usage of data augmentations to improve model performance on test data drawn from previously unseen cell types. In my experiments, I find that improvement in the transfer task following single data augmentation varies greatly depending on the transformation applied and the testing cell type. Pooling together transformations through stacking or random selection can yield augmentation strategies with much more generalizable improvements on the transfer task across all or nearly unseen cell types.

Methods

Model is pre-trained on single cell type image dataset of A172 cell line, fine-tuned on an augmented version of same dataset and then cross-evaluated on all other cell types. Image dataset and pre-trained models are from [1]

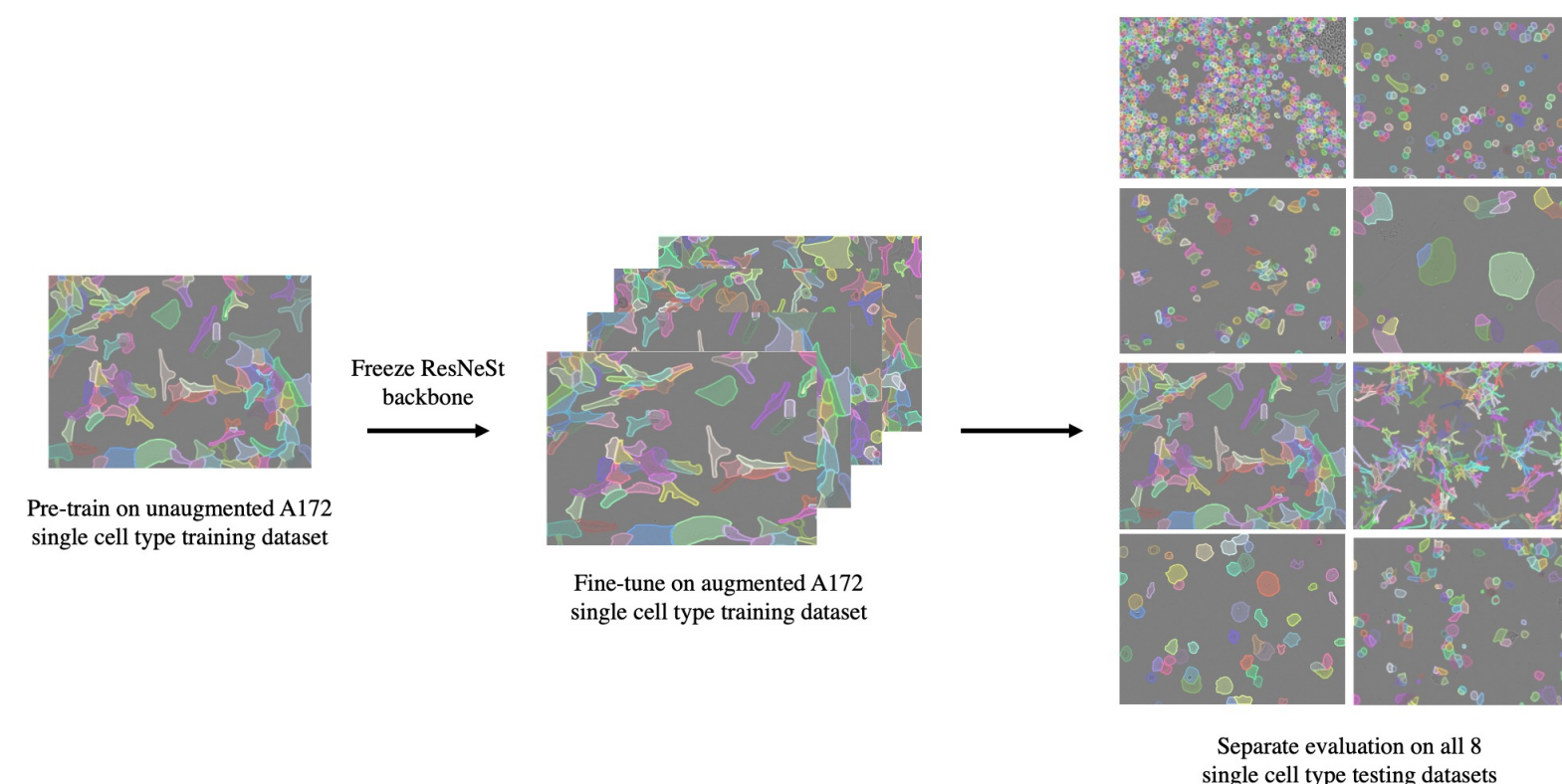
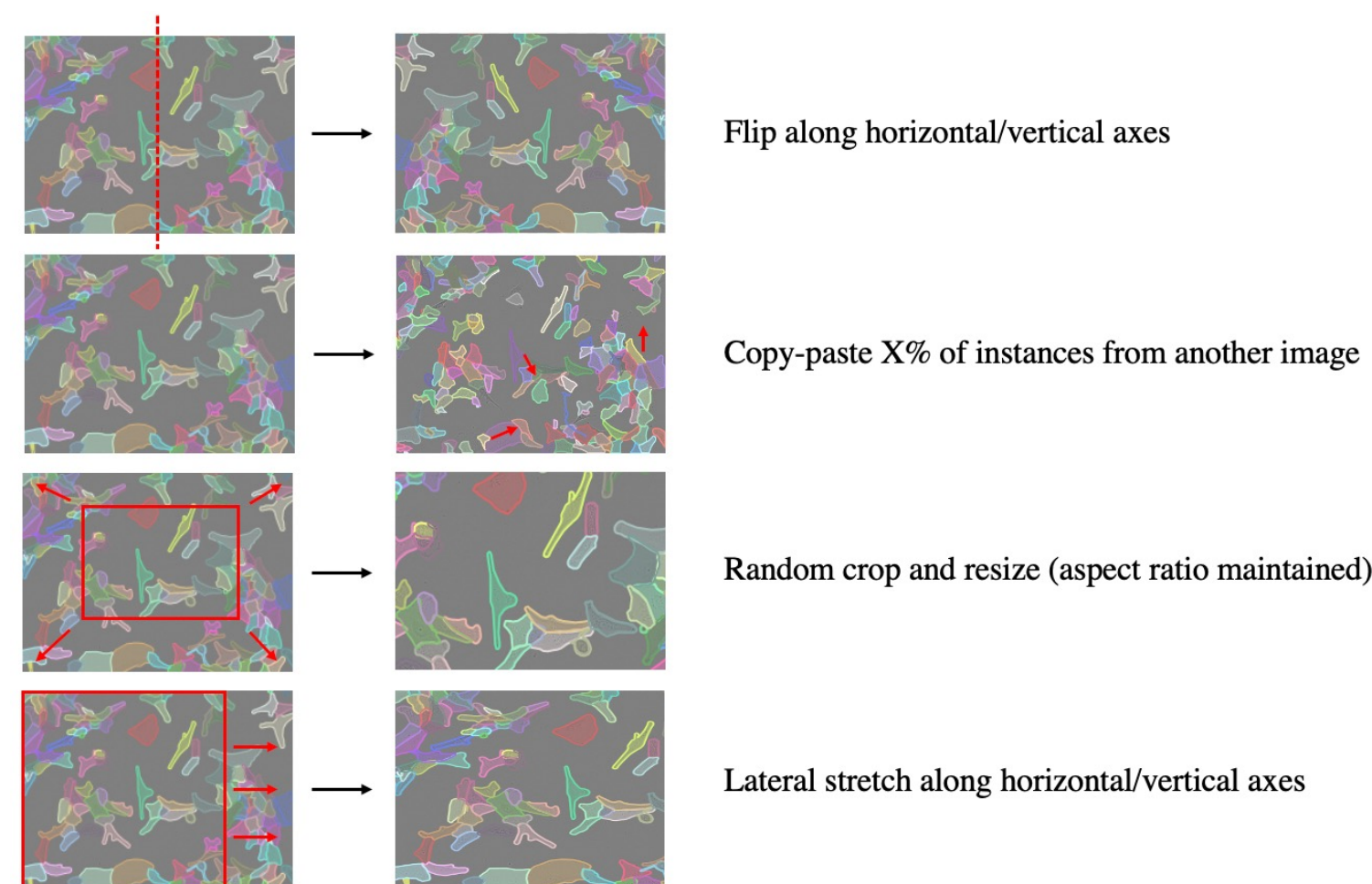
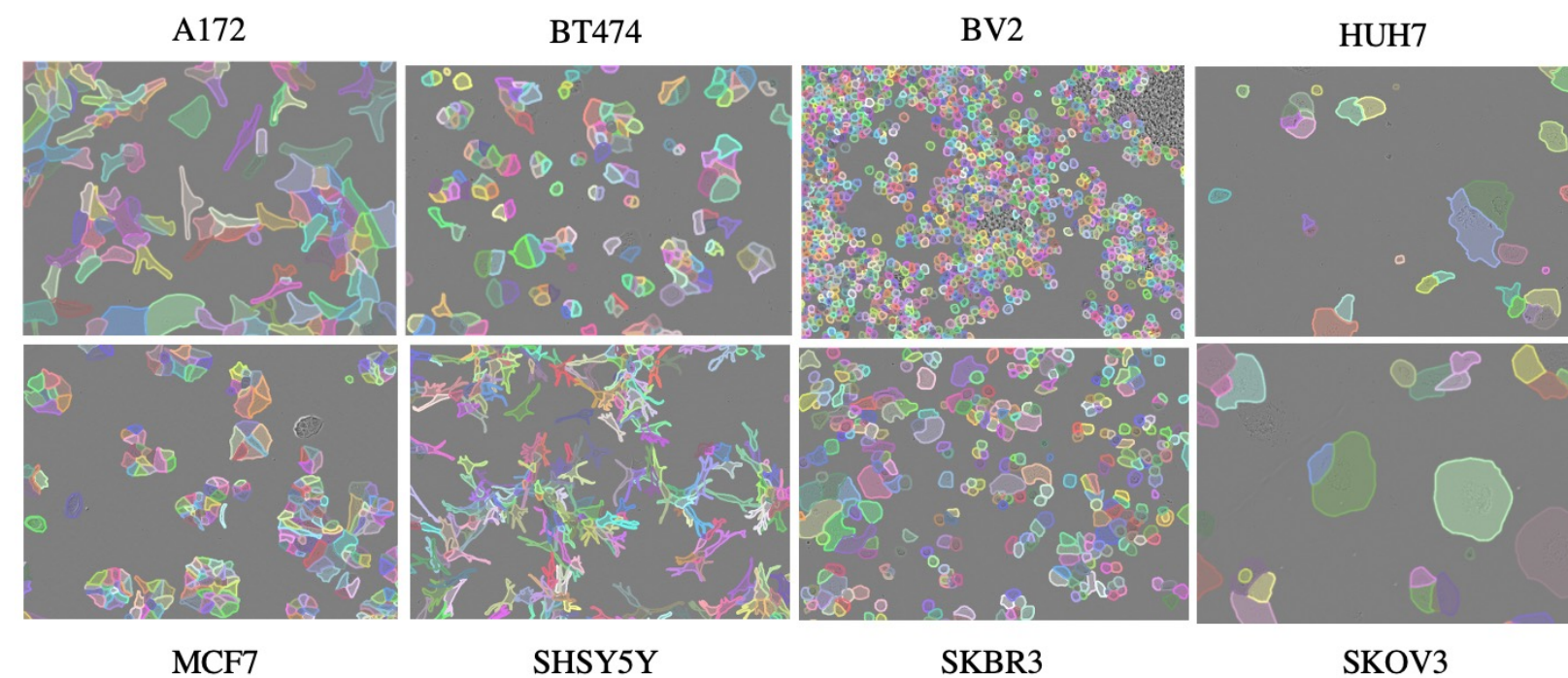
Naïve image transformations

Flipping, random crops, color jitter, simple copy-paste, random scaled copy-paste, lateral stretch

These simple transformations were then stacked and applied sequentially to images with a probability p or one transformation was chosen at random and applied to the image

FasterAutoAugment-based learned augmentation policy

Explore augmentation policies and assign learnable weights to each transformation [2]. Compute loss against difference in augmented image distribution and GT image distribution and backpropagate through model.



Results

AP50 segmentation scores: Naïve single augmentations

Average Precision @IoU=0.5	None	Lateral stretch	Flip	Simple copy paste	Scaled copy paste	Crop	Color jitter
A172	73.76	74.09	73.51	71.94	73.32	73.86	72.54
BT474	47.55	49.9	53.3	54.52	50.41	49.35	55.3
BV2	62.33	62.46	66.70	66.33	60.27	61.23	62.35
HUH7	72.32	73.57	73.49	72.21	73.74	74.73	71.66
MCF7	41.51	48.04	47.49	47.38	45.36	45.32	50.19
SHSY5Y	41.66	45.11	47.03	45.78	43.79	43.74	45.92
SKBR3	87.01	87.15	88.13	88.01	87.65	86.87	88.17
SKOV3	83.51	84.73	82.69	80.51	83.50	84.24	81.29

AP50 segmentation scores: Combined augmentation policies

Average Precision @IoU=0.5	None	Stacked p=0.5	Stacked p=0.8	Random choice	AutoAlbument
A172	73.76	73.78	71.77	73.25	71.61
BT474	47.55	53.93	49.29	51.89	57.62
BV2	62.33	62.36	49.83	63.19	60.25
HUH7	72.32	75.61	72.45	73.33	71.67
MCF7	41.51	47.98	42.79	49.93	48.67
SHSY5Y	41.66	43.36	39.77	46.92	41.47
SKBR3	87.01	88.09	86.54	88.03	87.72
SKOV3	83.51	83.74	81.07	82.95	79.96

Conclusions

- Downstream improvement on the transfer learning task across different cell types varies when only a single transformation is applied
- Combining transformations can produce policies that more consistently improve downstream performance
- Even relatively simple transformations like flipping that preserve the relative size/shape of cell instances are quite effective
- Certain test time cell types are consistently improved by augmentation – possibly due to modest difference in size distribution which is countered by distortion augmentations
- Future work should explore which augmentations are useful when training on a multi-cell-type dataset and evaluating on new cell types
- Another interesting point to investigate would be guided adaptation of FasterAutoAugment or learned policies for instance segmentation task and specifically for the downstream transfer task

References

- [1] C. Edlund, T. R. Jackson, N. Khalid, N. Bevan, T. Dale, A. Dengel, S. Ahmed, J. Trygg, and R. Sjögren. Livecell—a large-scale dataset for label-free live cell segmentation. *Nature Methods*, 18(9):1038–1045, Sep 2021.
- [2] R. Hataya, J. Zdenek, K. Yoshizoe, and H. Nakayama. Faster autoaugment: Learning augmentation strategies using backpropagation, 2019.