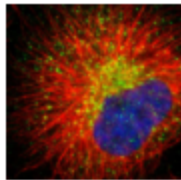


Review my approach for Human Protein Atlas - Single Cell Classification Kaggle Competition



Human Protein Atlas - Single Cell Classification

Find individual human cell differences in microscope images

Featured · Code Competition · 3 days ago



15/757

Top 2%

Summary

1. I used 2 stages approach

1st : image classification for getting CAM

2nd : Semantic segmentation with pseudo label from 1st stage CAM

2. My initial plan SC-CAM x Puzzle CAM did not work.

3. Successfully train 2nd stage semantic segmentation

4. Compared to the TOP 1 solution

- use the same 2 stages pseudo label approach
- but each stage for TOP 1 solution got much better score.

TOP 1 solution was evolving a research result for this cell problem.

Outline

0. Summary
1. Introduction to “Human Protein Atlas - Single Cell Classification”
2. Main Challenges to this competition
3. Public Approaches
 - Cellwise classification approach
 - CAM/Puzzle CAM approach
4. My Plan
5. Results
6. Check top 1 solution

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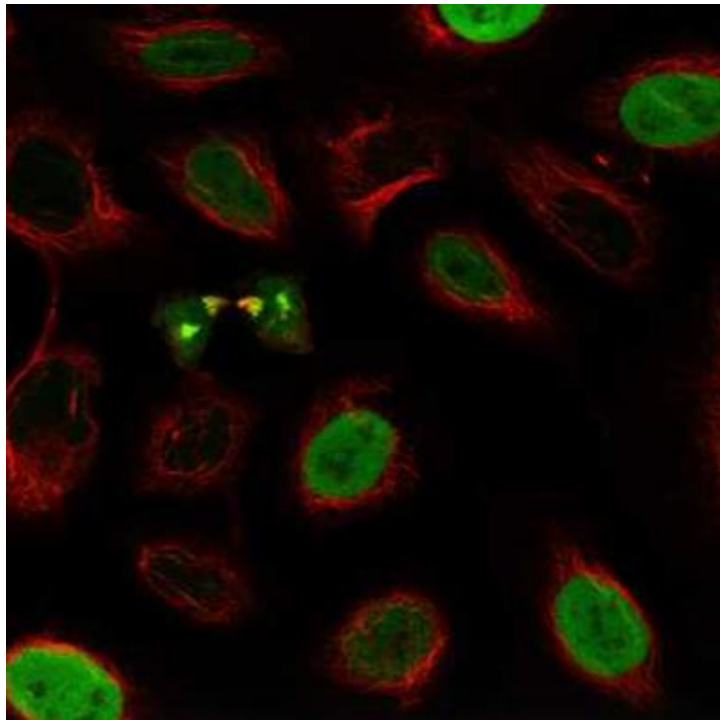
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Human Protein Atlas - Single Cell Classification

Weakly Instance segmentation for proteins
Metric: mAP for 19 proteins

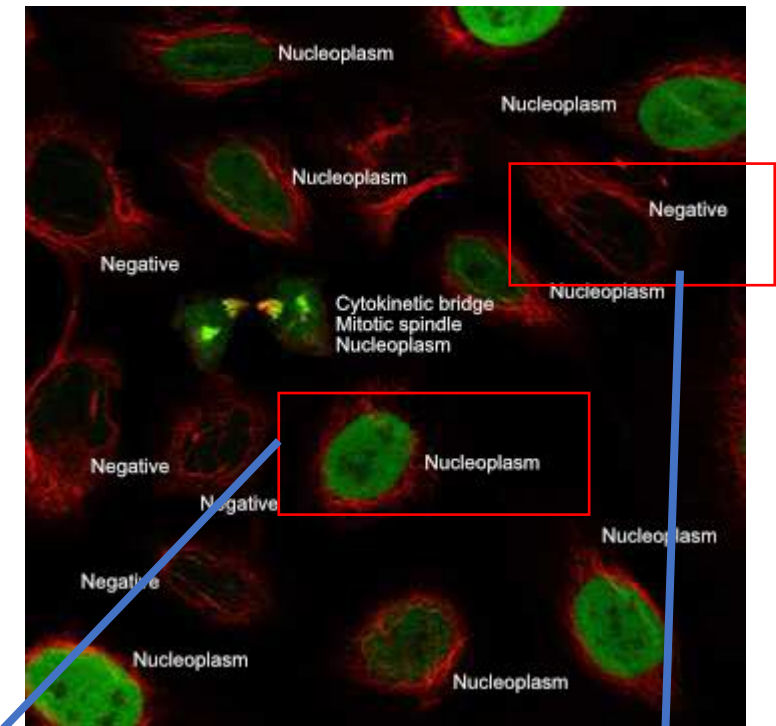
Input:
1728x1728 ~ 3072x3072
4ch cell image



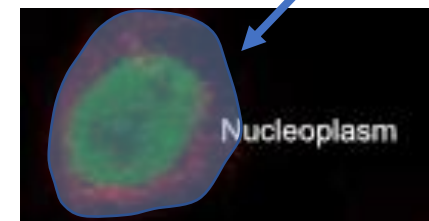
Provided label:
Image level class label

“Nucleoplasm”,
“Cytokinetic bridge”,
“Mitotic spindle”

Required Prediction:
Cell instance mask and its class label



Mask & Label



Mask & Label



Figures from
<https://www.kaggle.com/lnhtrang/single-cell-patterns/notebook>

Human Protein Atlas - Single Cell Classification

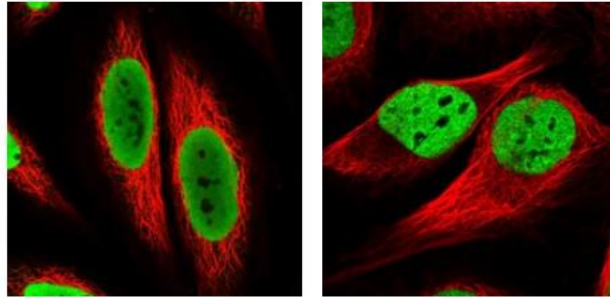
Protein Class: 19 classes

For more details about protein

please check -> <https://www.kaggle.com/lnhtrang/single-cell-patterns/notebook>

0. Nucleoplasm

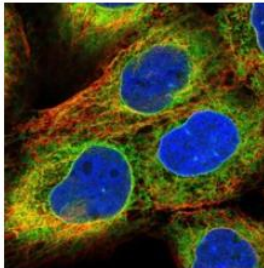
The nucleus is found in the center of cell and can be identified with the help of the signal in the blue nucleus channel. A staining of the nucleoplasm may include the whole nucleus or of the nucleus without the regions known as nucleoli (Class 2).



[More examples](#)

6. Endoplasmic reticulum

The endoplasmic reticulum (ER) is recognized by a network-like staining in the cytosol, which is usually stronger close to the nucleus and weaker close to the edges of the cell. The ER can be identified with the help of the staining in the yellow ER channel.

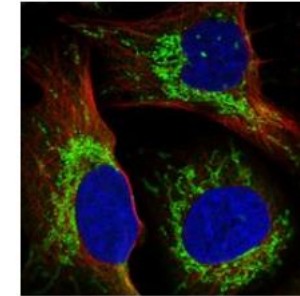


[More examples](#)

Figures from
<https://www.kaggle.com/lnhtrang/single-cell-patterns/notebook>

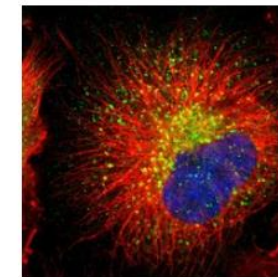
14. Mitochondria

Mitochondria are small rod-like units in the cytosol, which are often distributed in a thread-like pattern along microtubules.



17. Vesicles and punctate cytosolic patterns

This class includes small circular compartments in the cytosol: Vesicles, Peroxisomes (lipid metabolism), Endosomes (sorting compartments), Lysosomes (degradation of molecules or eating up dead molecules), Lipid droplets (fat storage), Cytoplasmic bodies (distinct granules in the cytosol). They are highly dynamic, varying in numbers and size in response to environmental and cellular cues. They can be round or more elongated.



[Vesicles](#) | [Peroxisomes](#) | [Endosomes](#) | [Lysosomes](#) | [Lipid droplets](#) | [Cytoplasmic bodies](#)

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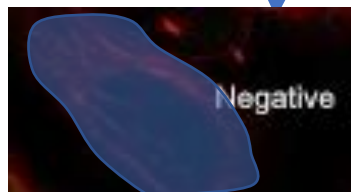
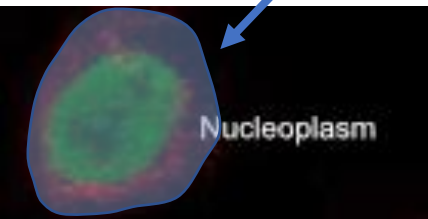
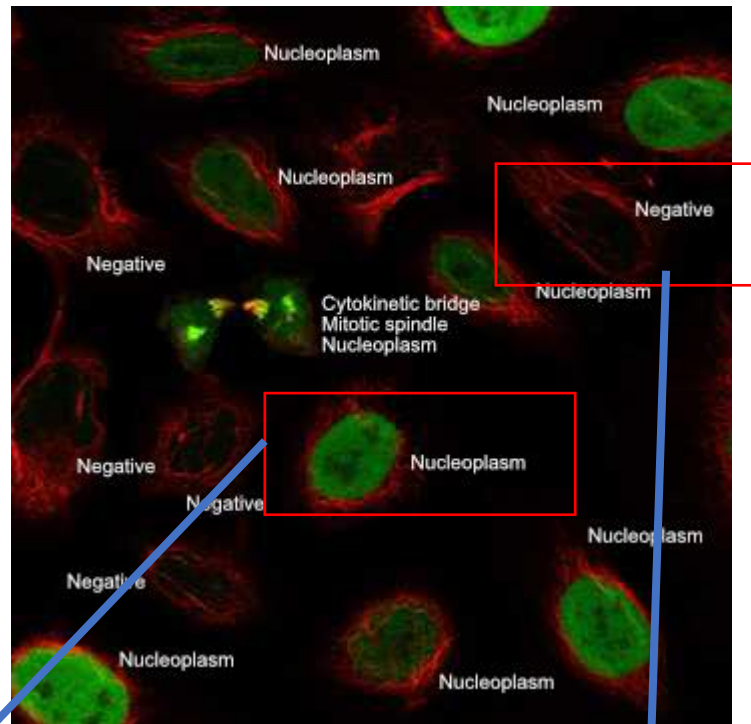
5. Results

6. Check top 1 solution

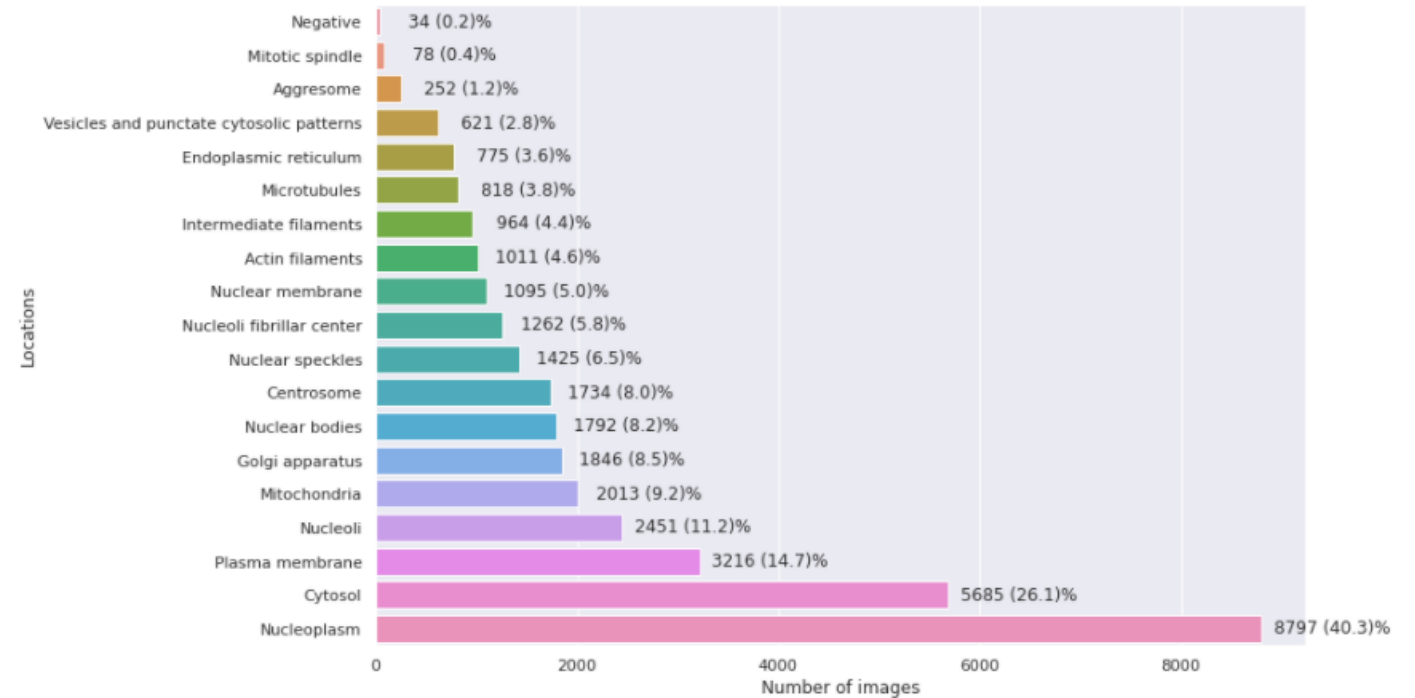
Main challenges

1. Weakly Instance segmentation. Few research papers.
2. Large image size, 1728x1728 ~ 3072x3072
3. Unbalanced class dataset

Required Prediction:
Class for each cell and cell instance mask



Class distribution



From <https://www.kaggle.com/lnhtrang/single-cell-patterns/notebook#Label-distribution-in-the-training-set>

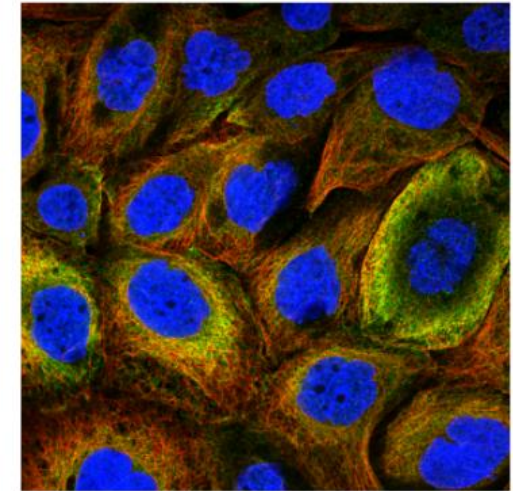
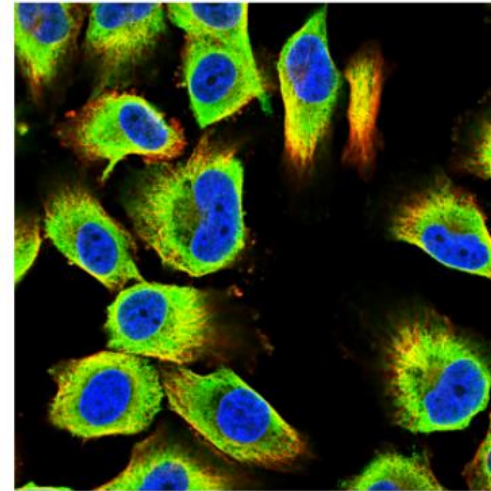
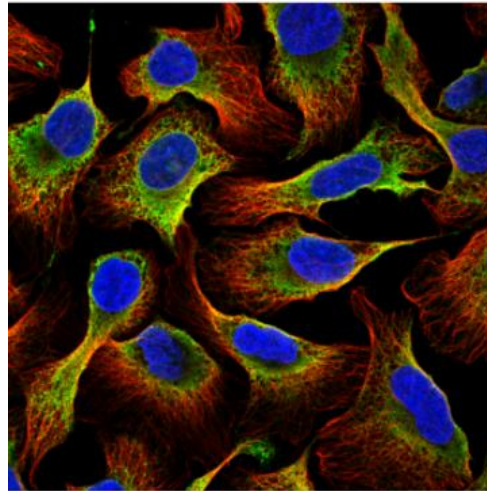
Available Tool : HPA-Cell-Segmentation

Good cell instance segmentation model is available.

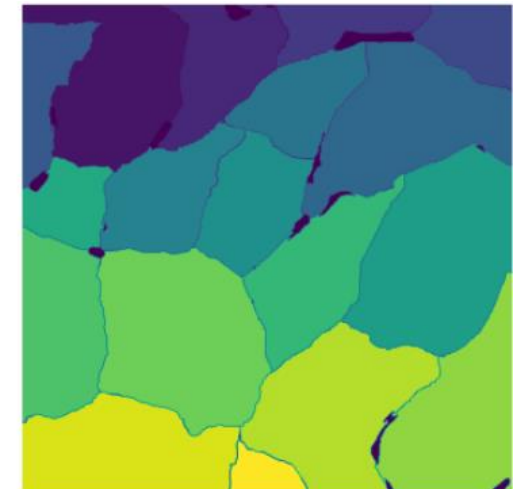
<https://github.com/CellProfiling/HPA-Cell-Segmentation>

-> We can focus on protein classification for each mask from this tool.

Input:



HPA-Cell-Segmentation:



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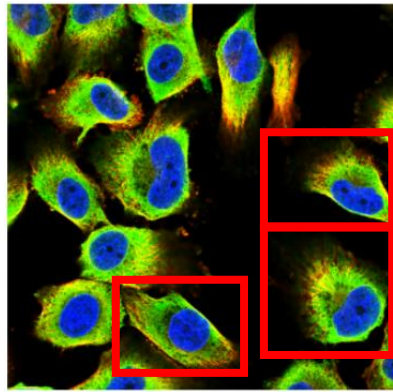
6. Check top 1 solution

Two major approaches at Kaggle

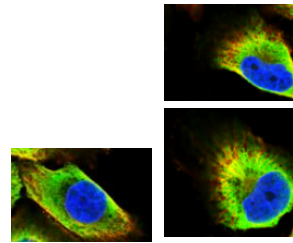
Kaggle public approaches disclosed during this competition.

1. Cellwise Approach, Public score ~ mAP 0.35
2. Class Activation Map, CAM, Public score ~ mAP 0.34

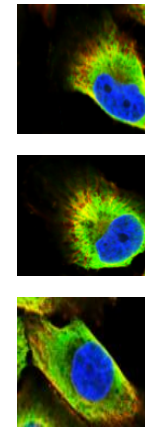
Cellwise Approach



Crop



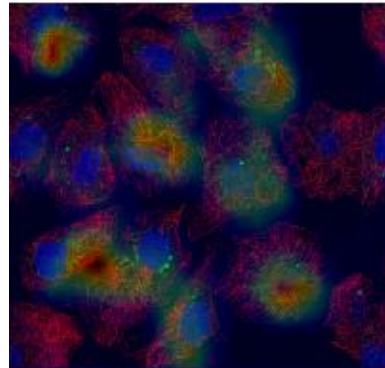
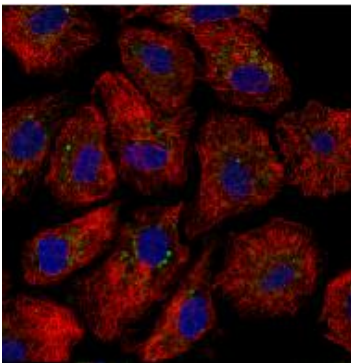
Resize~224x224



Cell Dataset

CNN
classification

Class Activation Mapping, CAM:



1. Cellwise Approach

Pros:

- easy to train
- keep fine resolution with cropping.

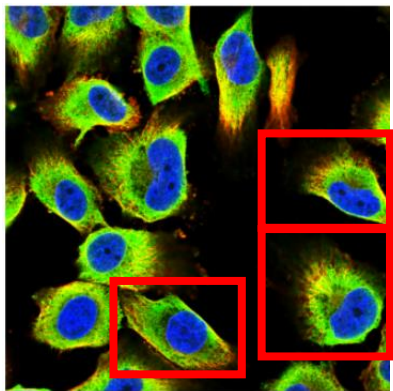
Original input size is $\sim 2048 \times 2048$ and really hard to train as it is.

Cons:

- noisy label assignment for multi labeled image.

We have only image level class label, so after cropping we cannot avoid labeling all crop images with the same image label.

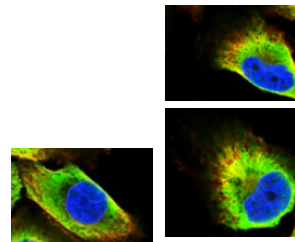
Cellwise Approach



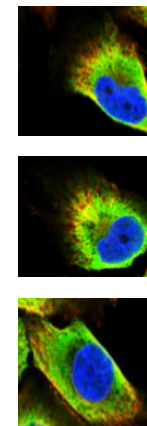
If this image has the label “0”, “13”



Crop



Resize $\sim 224 \times 224$



Cell Dataset

Score ~ 0.35

CNN
classification

“0”, “13” are assigned for all cropped images

2. CAM Approach: CAM?

Class Activation Mapping, CAM

<https://arxiv.org/abs/1512.04150>

Object localization method with image level class label

-> but at this method, only focus discriminative part not whole part

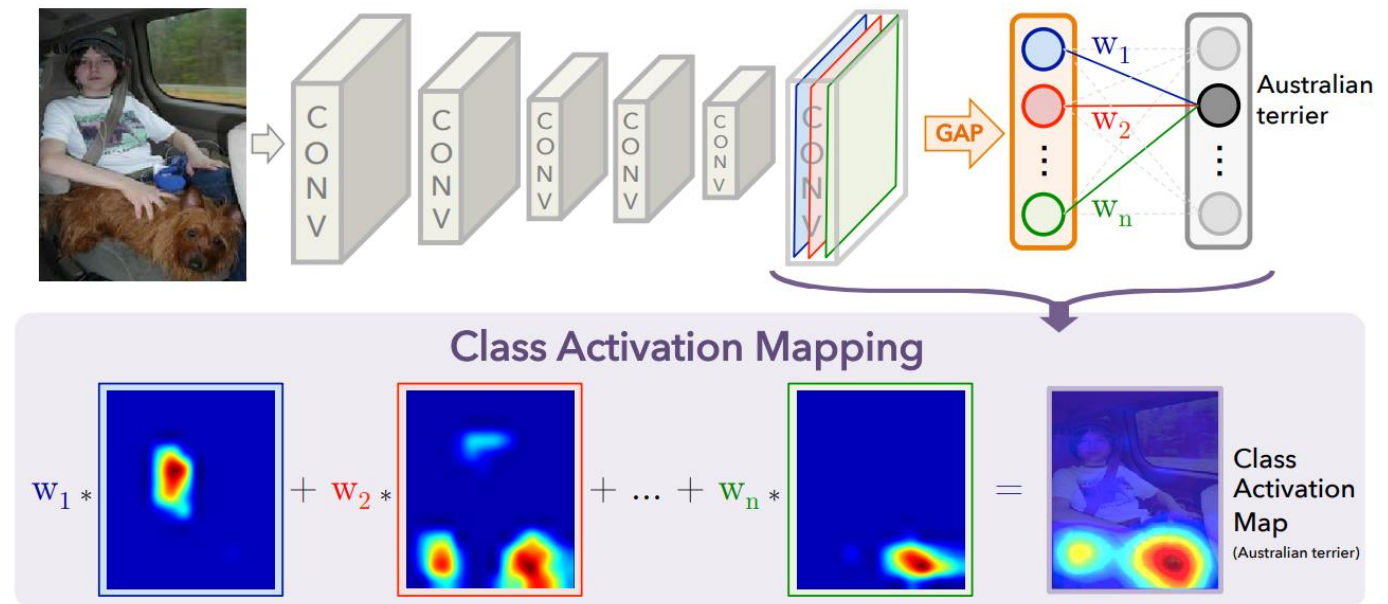


Figure 2. Class Activation Mapping: the predicted class score is mapped back to the previous convolutional layer to generate the class activation maps (CAMs). The CAM highlights the class-specific discriminative regions.

2. CAM Approach: Puzzle CAM

Puzzle-CAM: Improved localization via matching partial and full features

<https://arxiv.org/abs/2101.11253>

Splitting input image like tile, and training each split images and original image with reconstruction loss .

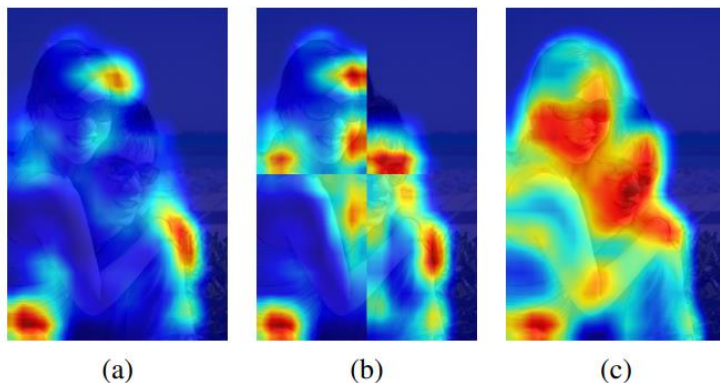


Fig. 1: CAMs generated from tiled and original images: (a) conventional CAMs from the original image, (b) generated CAMs from the tiled images, and (c) predicted CAMs by the proposed Puzzle-CAM.

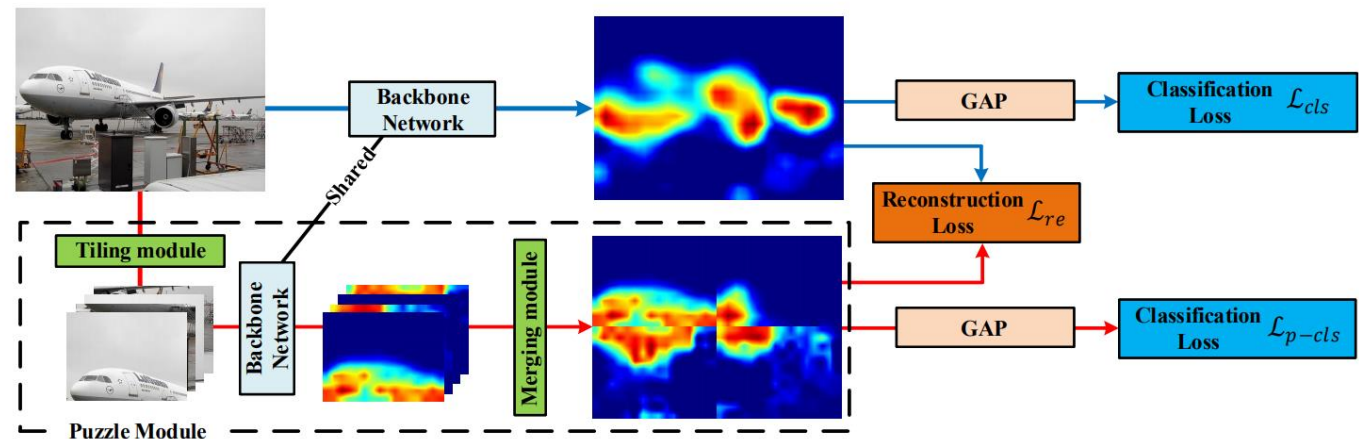


Fig. 2: The overall architecture of the proposed Puzzle-CAM showing the integration of reconstructing regularization and the puzzle module.

[from https://arxiv.org/abs/2101.11253](https://arxiv.org/abs/2101.11253)

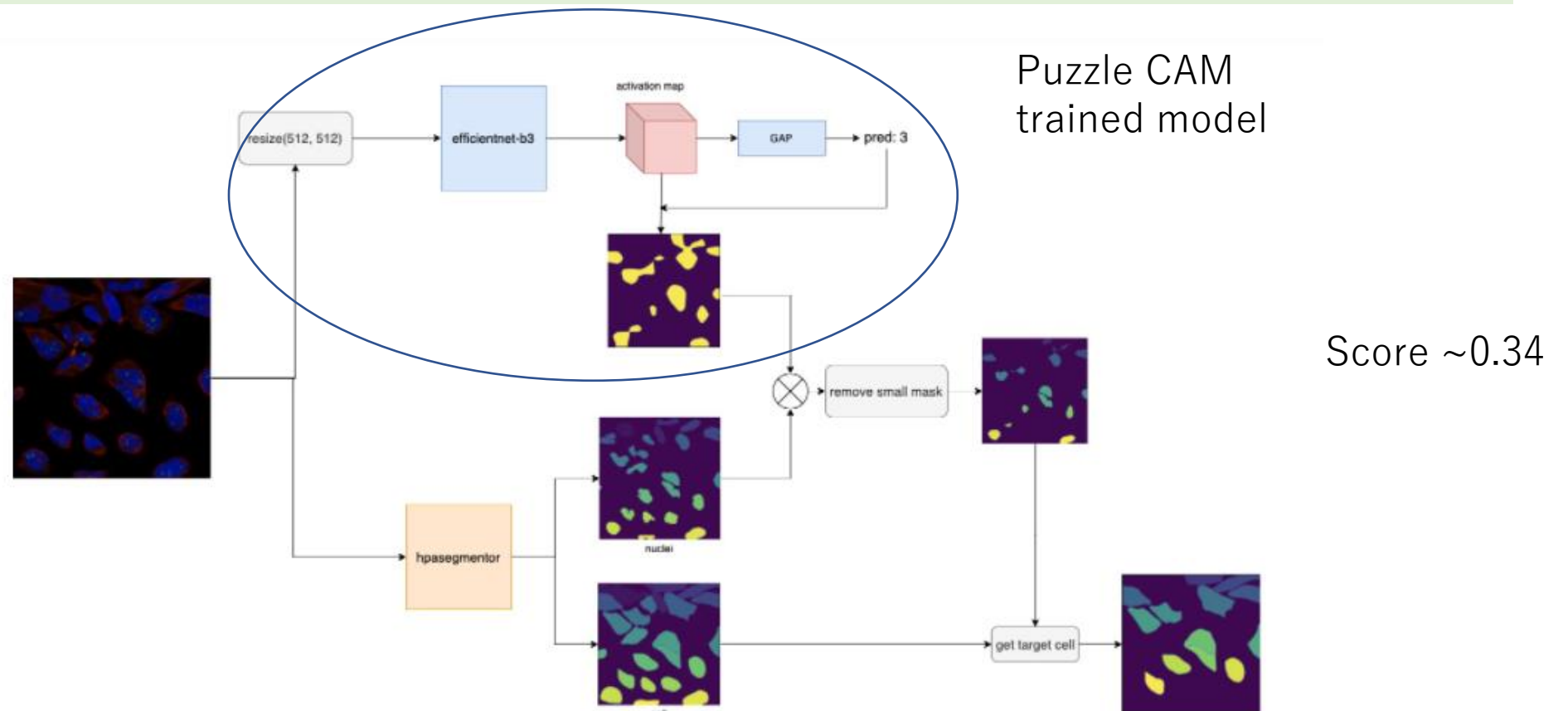
2. CAM Approach: Puzzle CAM

Pros:

- no any noise at training

Cons:

- does not keep original resolution $\sim 2048 \times 2048$
- Puzzle CAM is still not perfect for localization.



From <https://www.kaggle.com/c/hpa-single-cell-image-classification/discussion/217395>

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My plan

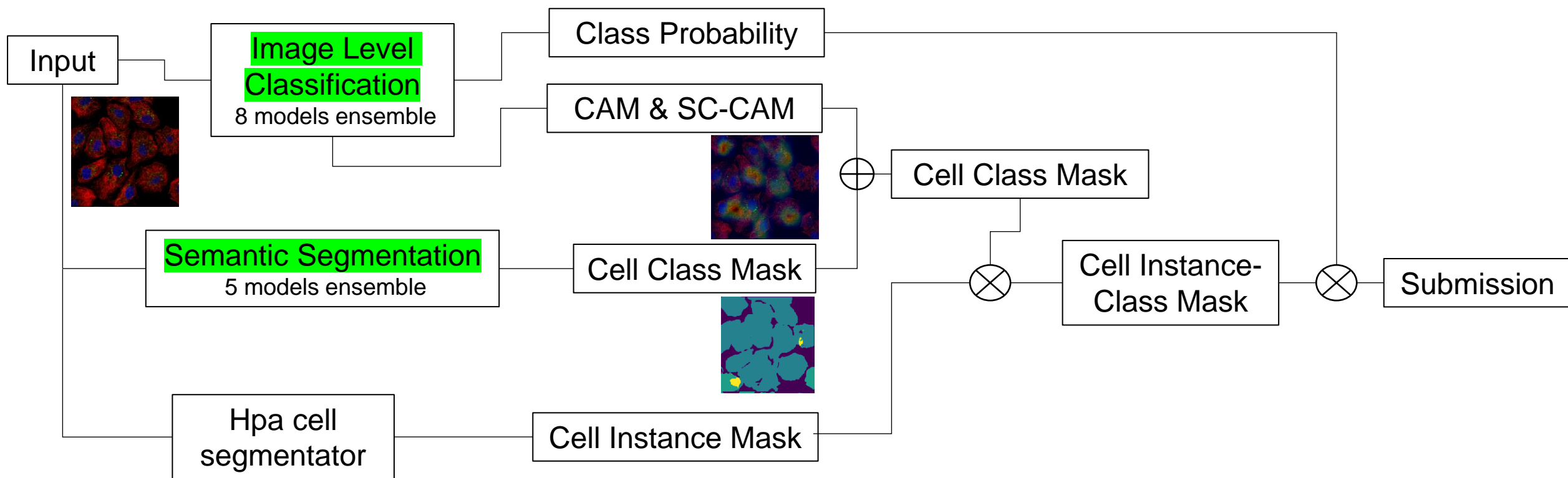
1. CAM, SC-CAM x Puzzle CAM

Puzzle CAM: localization improvement for CAM

Subcenter CAM, SC-CAM: differentiate intra-class. -> expecting additional improvement

<https://arxiv.org/pdf/2008.01183.pdf>

2. Semantic Segmentation with pseudo label by CAM



My plan : SC-CAM

SC-CAM: Sub category CAM

1. Introducing sub category from a clustering of CNN feature.
2. This sub category is contributed to differentiate intra-class variation
 - > extend the area of CAM
3. This improvement may independent from Puzzle CAM which focus on spatial feature.
 - > Puzzle CAM x SC-CAM should be the best ! !

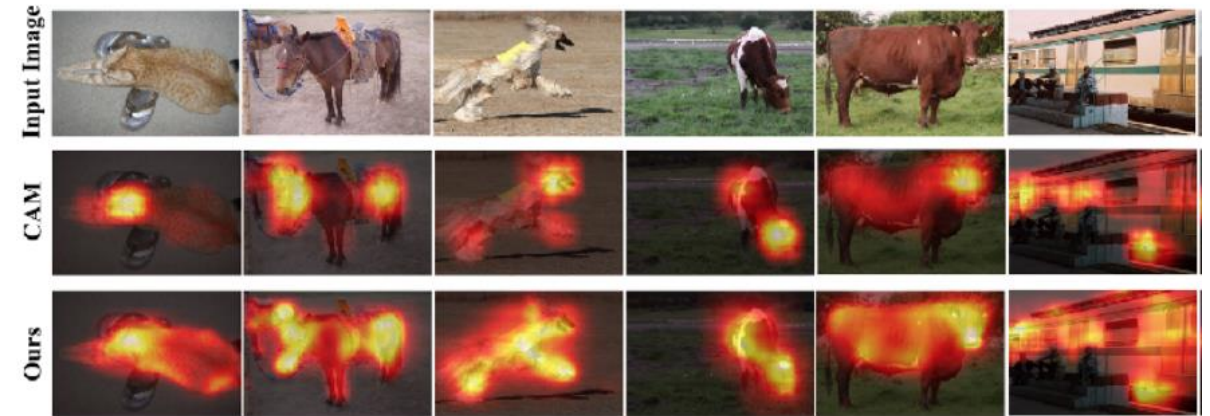
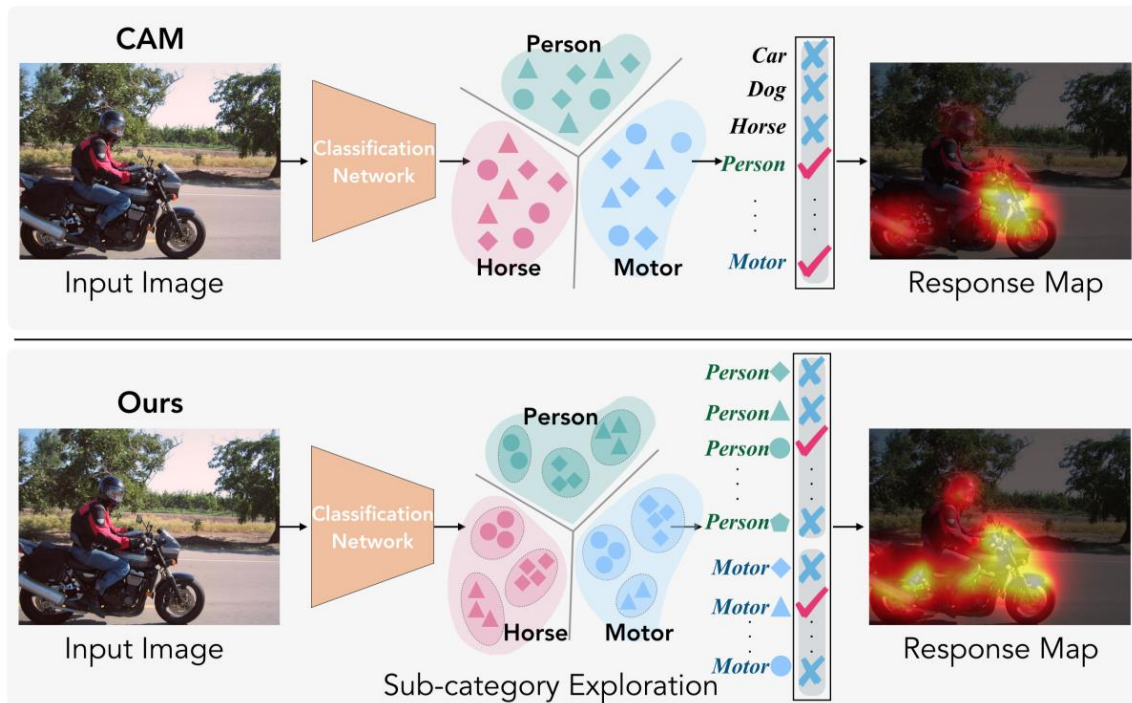


Figure 3: Sample results of initial responses. Our method often generates the response map to object (i.e., attention on the body of the animal), while the response map produced by CAM discriminative parts.

My plan : SC-CAM training procedure

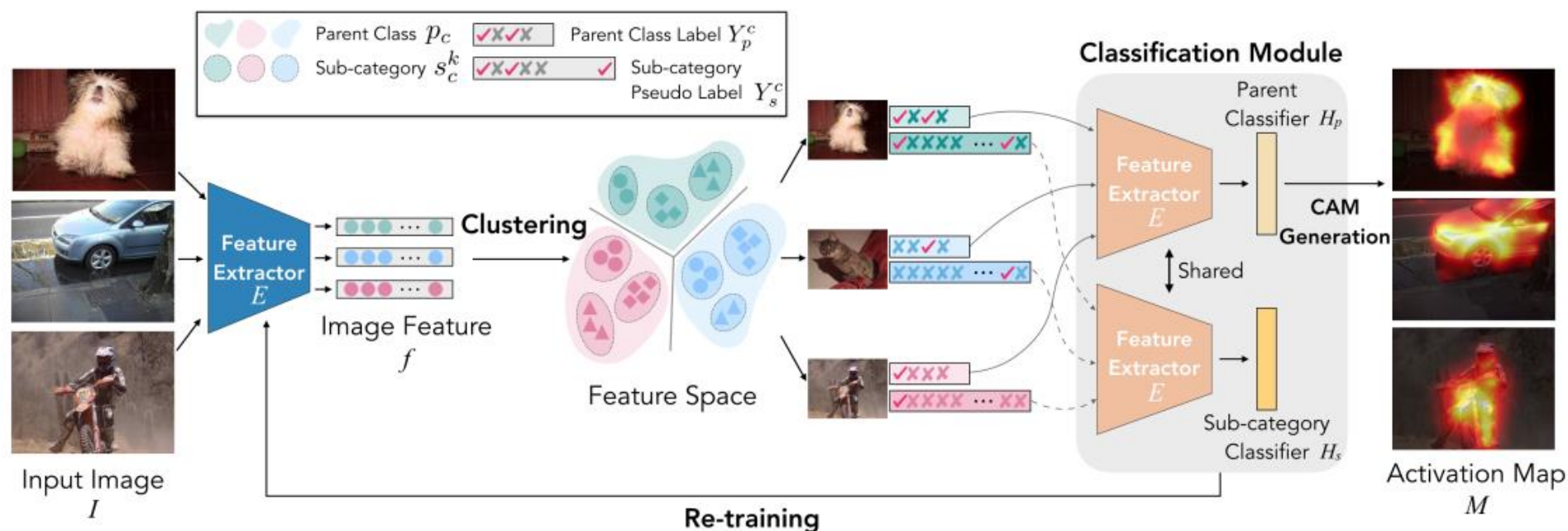
SC-CAM

- multi rounds training.
- original SC-CAM uses 3 rounds but at this task 1 round is enough.

SC-CAM round 0 train
normal label 19 classes

Sub category label generation
CNN feature & k-means

SC-CAM round 1 train
normal label 19 classes
+ sub category label 19x10 classes



From <https://arxiv.org/abs/2008.01183>

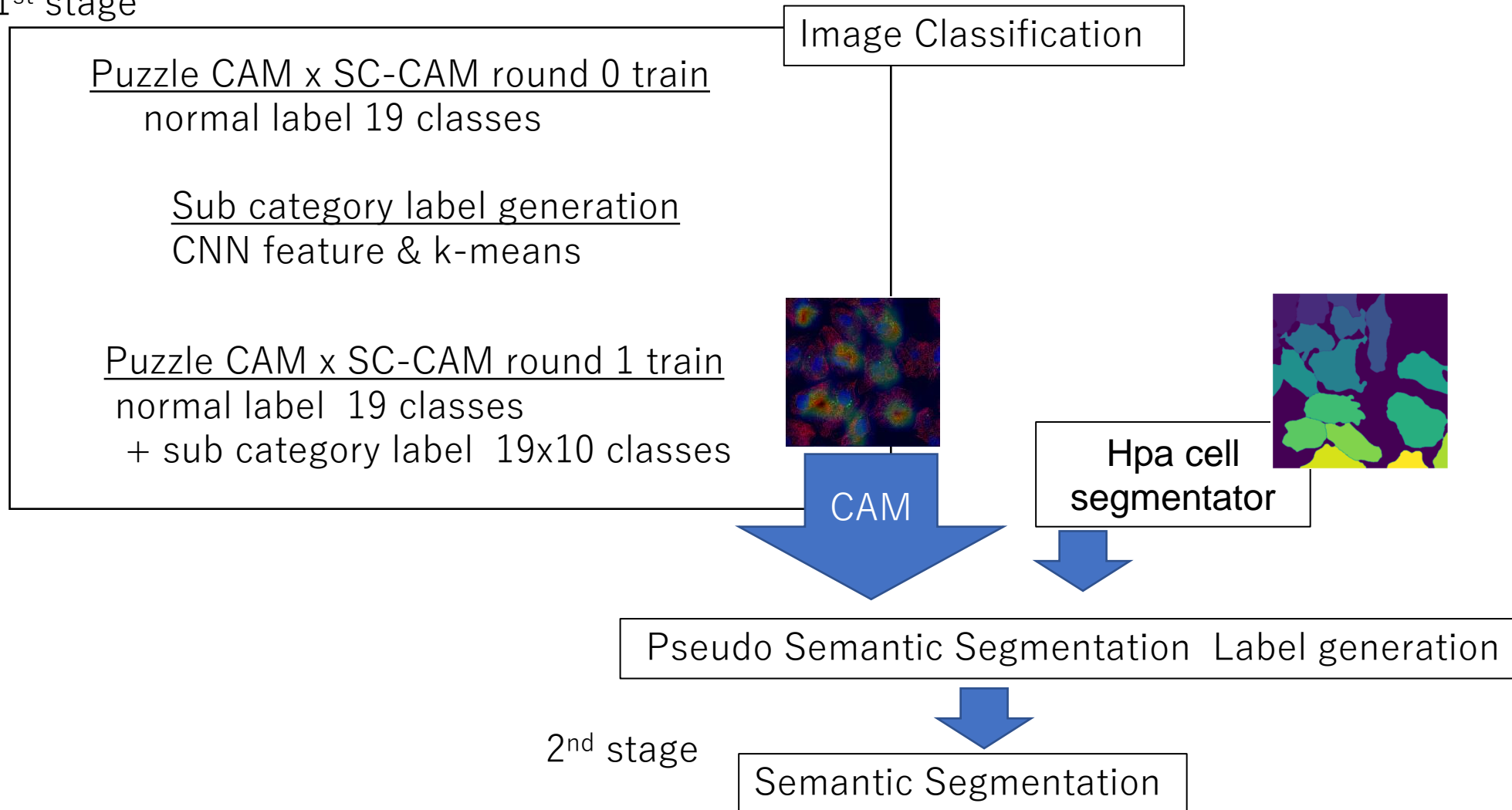
My plan : training procedure

2 stages

1st stage: CAM x SC-CAM generation

2nd stage: Semantic Segmentation with the pseudo label from CAM

1st stage



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Results for image classification part SC-CAM and Puzzle CAM

Sadly SC-CAM x Puzzle CAM does not work.

- separate use is better,
 - SC-CAM is better than Puzzle CAM at my experiment
- SC-CAM worked only for image size 512x512

| Image size | External Data | SC-CAM | Puzzle-CAM | Public mAP |
|------------|---------------|--------|------------|--------------|
| 512 | | | | 0.334 |
| 512 | | ✓ | | 0.373 |
| 512 | | | ✓ | 0.352 |
| 512 | | ✓ | ✓ | 0.360 |
| 512 | ✓ | | | 0.381 |
| 512 | ✓ | ✓ | | 0.404 |
| 768 | ✓ | | | 0.423 |
| 768 | ✓ | ✓ | | 0.399 |
| 1280 | ✓ | | | 0.429 |

Resnet50 is used for all runs

“External data” with dropping frequent class

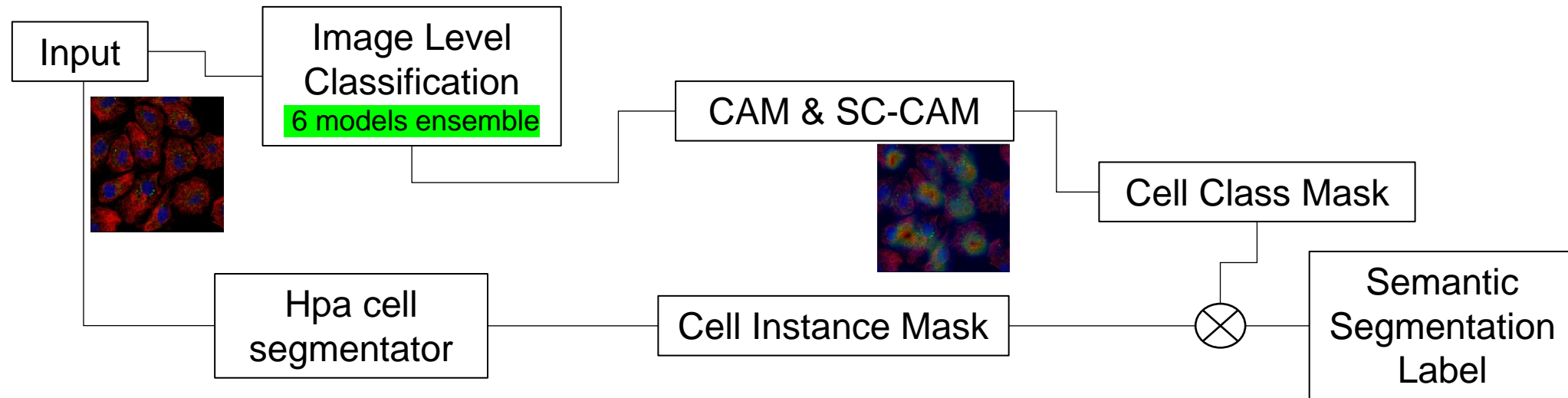
Semantic Segmentation

Heavy ensemble pseudo labeling.

-> 0.02 improvement

Using hard label:

-> but the threshold was really sensitive. I choose 0.225 based on public mAP score.



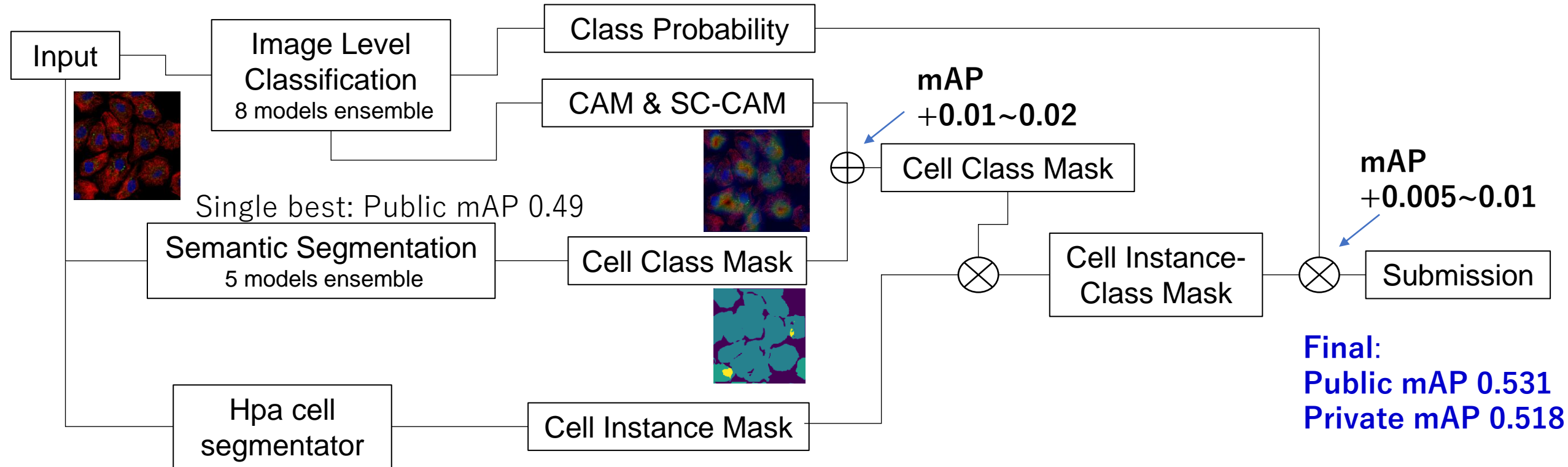
Only one CAM model pseudo label: mAP 0.47

6 different model {resnet, resnest, effcientnet} : mAP 0.49

Final Submission

- + CAM&SC-CAM, Semantic Segmentation and HPA cell segmentator
- + Image Level Classification was trained for pseudo semantic segmentation label, But it contributed to the score, approximately mAP 0.01~0.02.















Single best: Public mAP 0.445



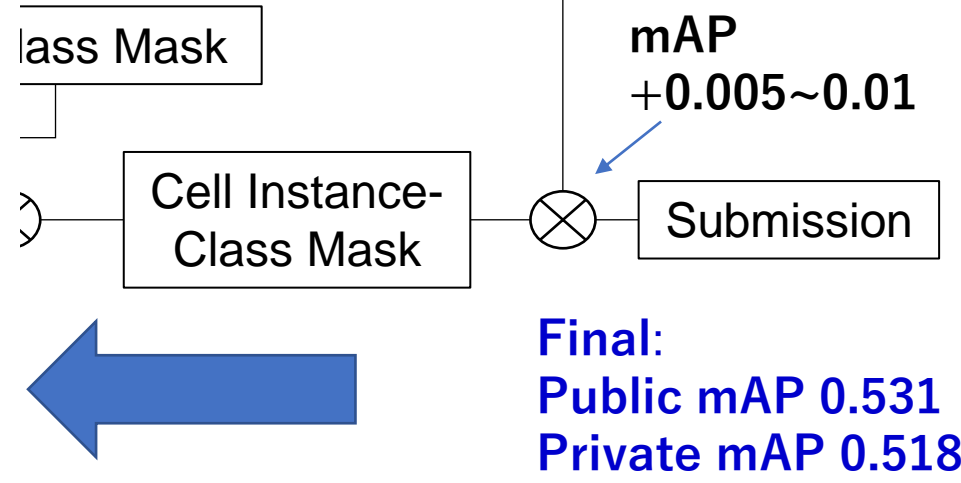
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Single best: Public mAP 0.445

| Input | | Image Level | Class Probability | | | |
|-------|------|---|---|---------|-----|----|
| 7 | ▼ 3 | PFCCell |  | 0.54053 | 162 | 4d |
| 8 | ▲ 9 | Guanshuo Xu |  | 0.53898 | 62 | 4d |
| 9 | ▲ 2 | AllDataAreExt & Galixir |  | 0.53557 | 488 | 4d |
| 10 | ▲ 4 | [RAPIDS.AI] Cell Game [Rist] </> [HPA2021] p all 1st... |  | 0.53503 | 166 | 4d |
| 11 | ▼ 1 | Silvers |  | 0.53287 | 411 | 4d |
| 12 | ▲ 1 | Andrew Tratz |  | 0.53049 | 134 | 4d |
| 13 | ▼ 1 | CVSSP + forecom.ai |  | 0.52717 | 202 | 4d |
| 14 | ▲ 2 | ! |  | 0.52417 | 162 | 4d |
| 15 | ▲ 6 | Fumihiko Kaneko |  | 0.51860 | 144 | 4d |
| 16 | ▼ 1 | Looking for the lost cell |  | 0.51711 | 431 | 4d |
| 17 | ▲ 2 | Tom |  | 0.51688 | 307 | 4d |
| 18 | ▲ 9 | yuvaramsingh |  | 0.51559 | 162 | 4d |
| 19 | ▼ 10 | [Aillis] YujiAriyasu |  | 0.51507 | 185 | 4d |
| 20 | ▲ 13 | Da Yu |  | 0.50626 | 88 | 3d |

1~0.02



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Top solution: “bestfitting”

2 stages approach

1st stage: Extend Puzzle CAM -> Fair Cell Activation Network

2nd stage: Cell wise pseudo leveled label by 1st stage

5 levels label: [1.0, 0.75, 0.5, 0.25, 0.0]

normal label : [1.0, 0.0]

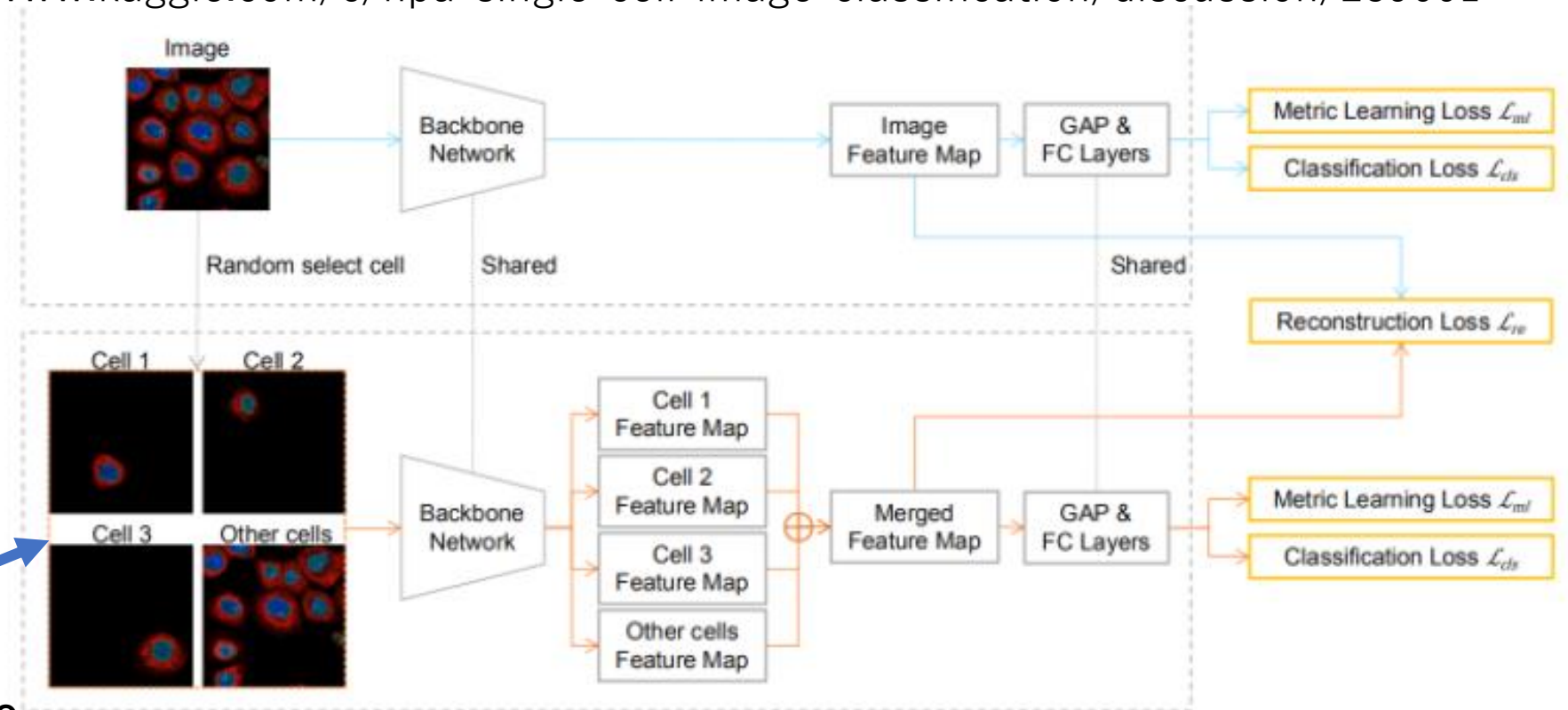
1st stage

<https://www.kaggle.com/c/hpa-single-cell-image-classification/discussion/239001>

Fair Cell Activation Network

Best single model
Public mAP: 0.565
Private mAP: 0.547

Final ensemble 6 models
Public mAP: 0.590
Private mAP: 0.566



Replace the split of the Puzzle CAM with cell mask

Summary

1. I used 2 stages approach

1st : image classification for getting CAM

2nd : Semantic segmentation with pseudo label from 1st stage CAM

2. My initial plan SC-CAM x Puzzle CAM did not work.

3. Successfully train 2nd stage semantic segmentation

4. Compared to the TOP 1 solution

- use the same 2 stages pseudo label approach
- but each stage for TOP 1 solution got much better score.

TOP 1 solution was evolving a research result for this cell problem.

Appendix

Model and other details

Image Level Classification

- model: resnest50, resnet50, resnet200d, effb3
- Input size: 512x512 ~ 1280x1280
- Loss: focal loss
- Learning rate scheduler: Cosine Annealing

Semantic Segmentation

- model: Unet{resnest50, resnet50, resnext50}
- Input size: 512x512 ~ 768x768
- Loss: focal loss
- Learning rate scheduler: Cosine Annealing

Other Tips

- Training speed : NGC container x Channel Last for pytorch memory format
 - + following [the benchmark result at timm](#), my resnet training time reduced by 40% from my initial configuration. Also effb training reduced by 20 or 30%.
- TTA, Test time augmentation
 - h/vflip, image scale { x1.2, x1.4} improve the CAM model score by 0.01~0.03