

## Pseudo-Code for the method presented in “Cell Segmentation in Images Without Structural Fluorescent Labels”

C = number of fluorescent channels

X = training set of images *#shape: (C, N, H, W)*

X\_valid = validation set of images *#shape: (C, N, H, W)*

X\_inf = inference set of images *#shape: (C, N, H, W)*

**finetuning**(model, images, labels) = function to train a model with new examples *# returns model*

**fusion**(flows\_0, ... flows\_c) = function which fuses segmentation flows into an average segmentation map  
*#returns segmentation maps (N, H, W)*

**scoring**(prediction, ground\_truth) = function which assess the quality of a segmentation *# returns score scalar*

### **function Training(organelle):**

organelle: organelle to segment ("cyto" or "nuclei")

y = training set of segmentation labels for organelle *#shape: (N, H, W)*

y\_valid = validation set of segmentation labels for organelle *#shape: (N, H, W)*

M = pretrained cellpose model for organelle

#### *#channel-wise training*

channel\_wise\_models = []

for c in [0, ..., C]:

while not early stopping:

    M\_c <- finetuning(M, X[c], y)

    channel\_wise\_models.add(M\_c)

channel\_wise\_scores = {}

for mc in powerset of [0, ..., C]:

if size(mc)>0:

    pred\_mc = fusion(M\_c(X\_valid[c]) for c in mc)

    score = scoring(pred\_mc, y\_valid)

    channel\_wise\_scores[mc] = score

#### *#multi-channel training:*

multi\_channel\_models = []

for mc in powerset of [0, ..., C]:

if size(mc)>1:

while not early stopping:

    M\_mc <- finetuning(M, concatenate([X[c\_i] for c\_i in mc]), y)

    multi\_channel\_models.add(M\_mc)

multi\_channel\_scores = []

for mc in powerset([0, ..., C]):

if size(mc)>0:

    pred\_mc = fusion(M\_mc(X\_valid[c]) for c in mc)

    score = scoring(pred\_mc, y\_valid)

    multi\_channel\_scores[mc] = score

return channel\_wise\_models, channel\_wise\_scores, multi\_channel\_models, multi\_channel\_scores

### **function Inference(organelle, channel\_wise\_models, channel\_wise\_scores, multi\_channel\_models, multi\_channel\_scores):**

organelle: organelle to segment ("cyto" or "nuclei")

channel\_wise\_models/multi\_channel\_models: list of finetuned channel\_wise\_models

channel\_wise\_scores/multi\_channel\_scores: dictionary of scores associated with finetuned models

y\_inf = inference set of segmentation labels for organelle *#shape: (N, H, W)*

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if max(channel_wise_scores)>max(multi_channel_scores):
    mc = argmax(multi_channel_scores)
    pred = fusion(channel_wise_models[c](X_inf[c]) for c in mc)
else:
    mc = argmax(channel_wise_scores)
    pred = fusion(multi_channel_models[mc](X_inf[c]) for c in mc)

return pred
```