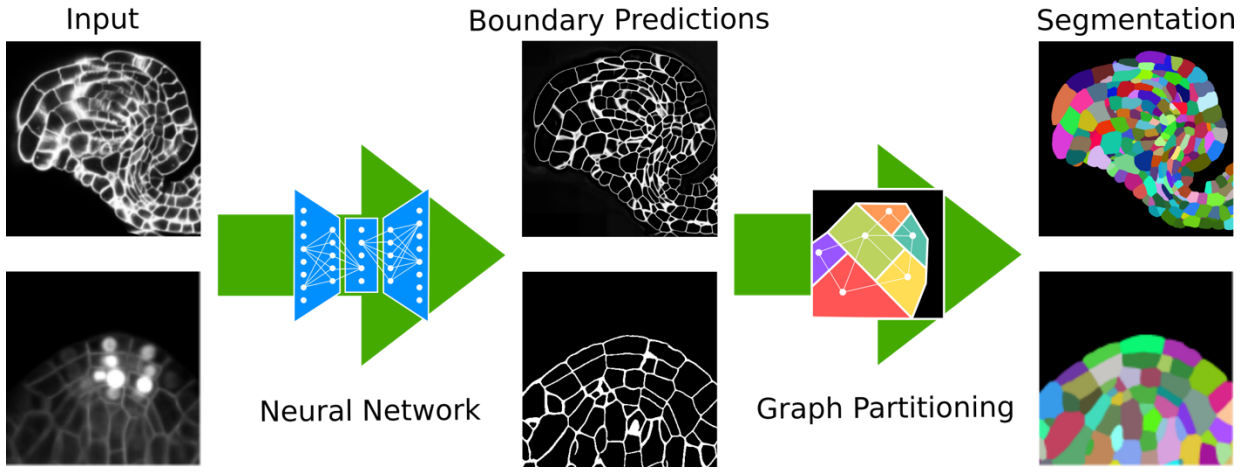
Lab meeting 27.05
Plantseg and new model !?

Adrian Fernandez Lojo

What is plantseg ?

- Tool for 2D and 3D segmentation
  - Unet prediction task
  - Watershed task + clustering task + post processing task
- Different models for different data



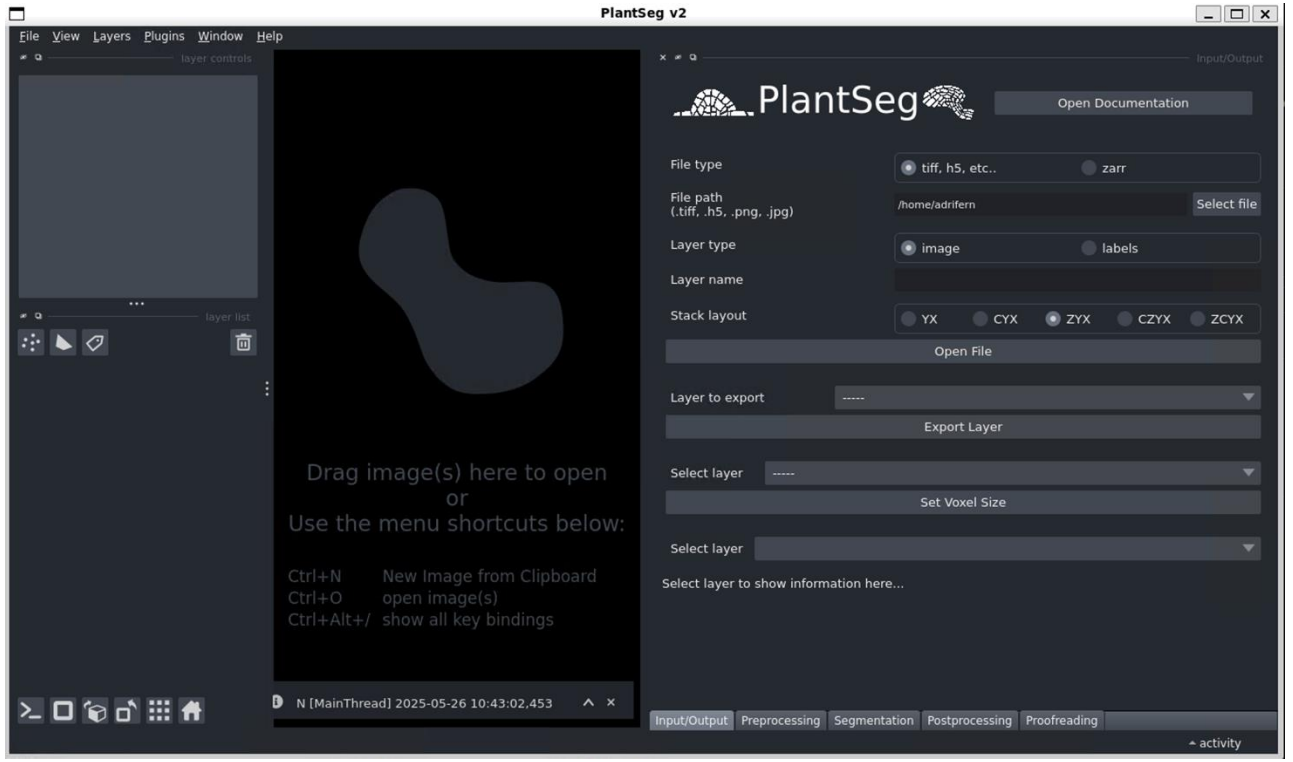
Segmentation of plant tissues into cells using PlantSeg. A.Wolny *et al*, 2020

	Generic unet	Arabidopsis Ovules	Lateral Root Primordia	Arabidopsis thaliana Apical stem cell	Mouse embryo ex vivo
Resolution [µm]	[0.235, 0.150, 0.150] / [0.25, 0.1625, 0.1625]	[0.235, 0.075, 0.075] / [0.235, 0.150, 0.150] / [1., 0.150, 0.150]	[0.25, 0.1625, 0.1625] / [0.25, 0.325, 0.325] / [0.25, 0.4875, 0.4875]	[1., 0.25, 0.25] / [0.25, 0.25, 0.25]	[1.0, 0.2, 0.2]
Dimensionality	3D	3D / 2D	3D / 2D	3D / 2D	3D
Modality	Light-sheet / Confocal	Confocal	Light-sheet	Confocal	Light-sheet / Confocal
Recommended patch size	[80,160,160]	[80,160,160] / [1, 256, 256]	[80, 160, 160] / [1, 256, 256]	[1, 256, 256] / [80, 160, 160]	[80, 160, 160] / [40, 220, 220]
Output type	Boundaries	Boundaries	Boundaries / Nuclei	Boundaries	Boundaries / Nuclei

See more detailed : https://github.com/kreshuklab/plant-seg/blob/master/plantseg/resources/models_zoo.yaml

PlantSeg Graphical User Interface (GUI)

- Very intuitive, but might be overwhelming
  - Install plantseg (https://kreshuklab.github.io/plant-seg/chapters/plantseg_legacy/installation/) Linux :
    conda create -n plant-seg -c pytorch -c nvidia -c conda-forge pytorch pytorch-cuda=12.1 plant-seg=1.8.1 bioimageio.core --no-channel-priority
  - Activate evironment and run:
    plantseg --napari



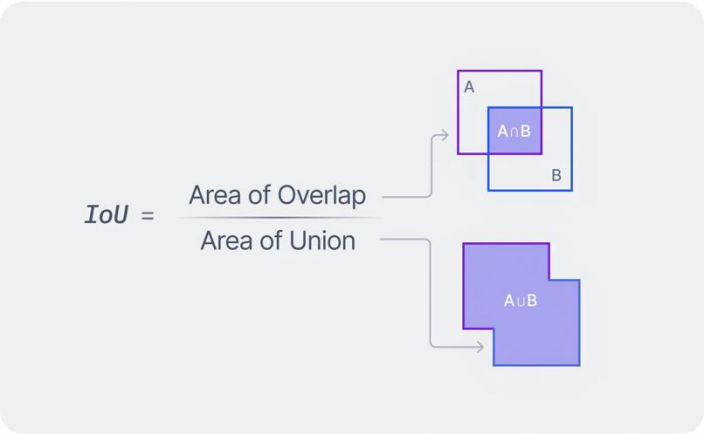
A lot of Options

- GridSearch, Avoid repeating already done computations
  - Pyramidal structure in 3 : Watershed task + clustering task + post processing task
- Metric and Ground Thruth (Jean Yves), StarDist

Metric : Intersection over Union

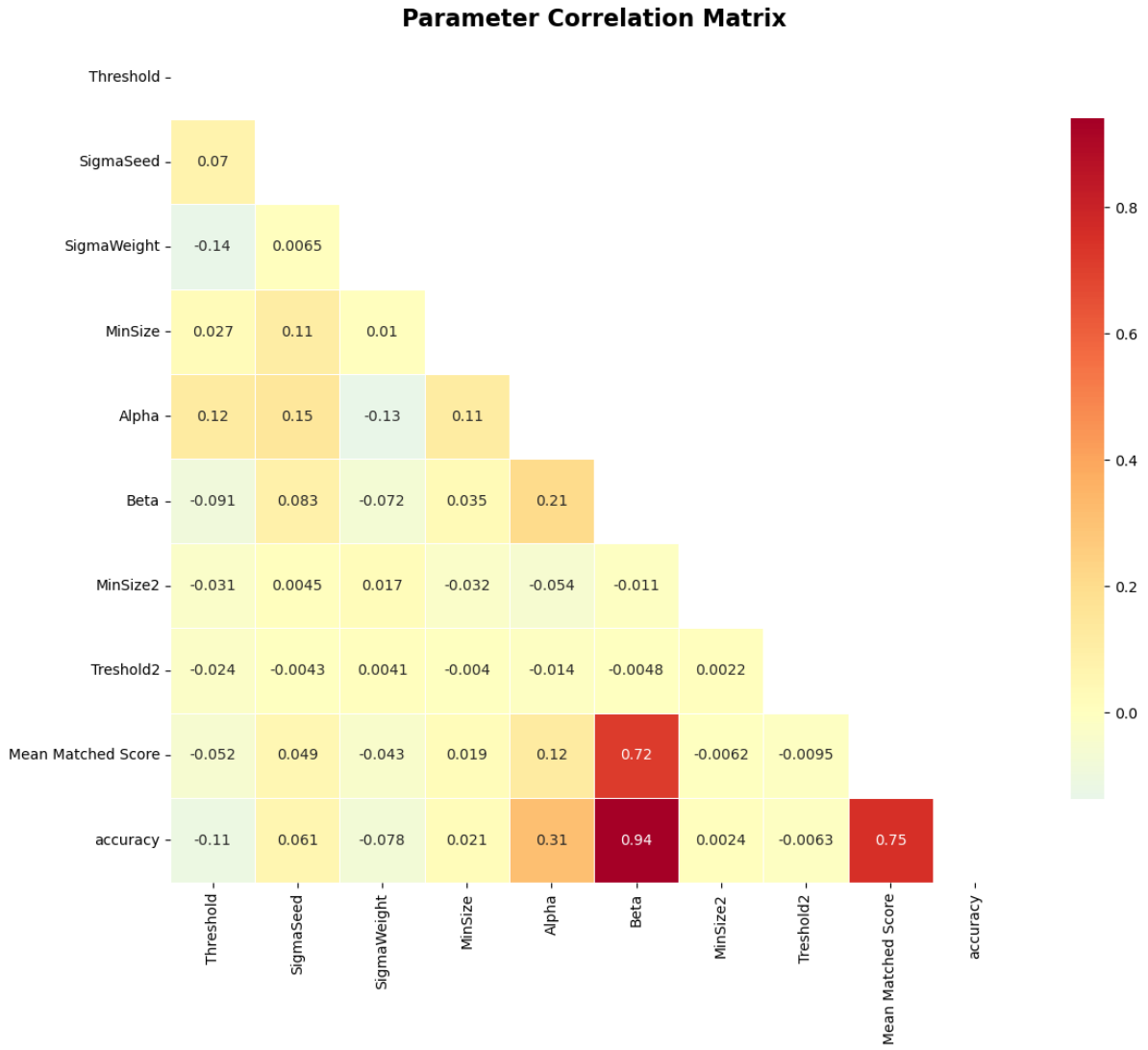
Mean Matched score : is the mean IoUs of matched true positives

Accuracy : Proportion of total predictions that are correct

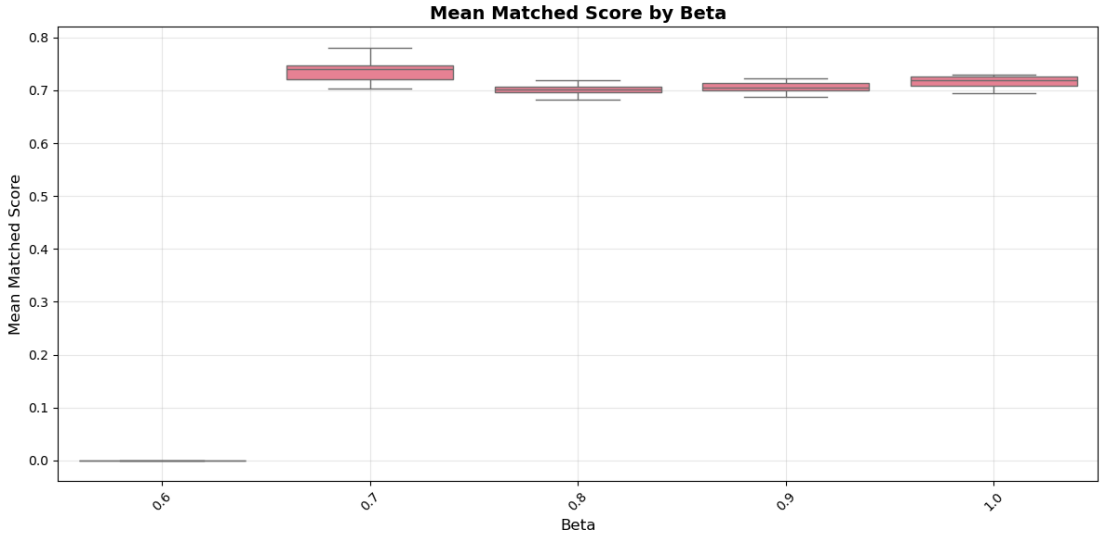


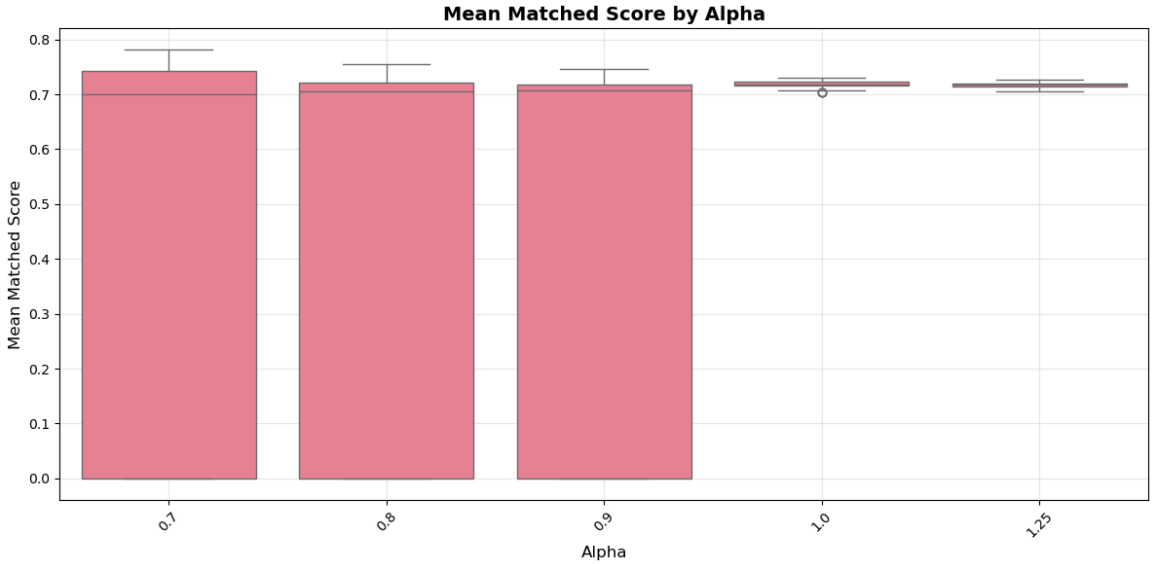
https://www.v7labs.com/blog/intersection-over-union-guide

Closer look to the parameters :

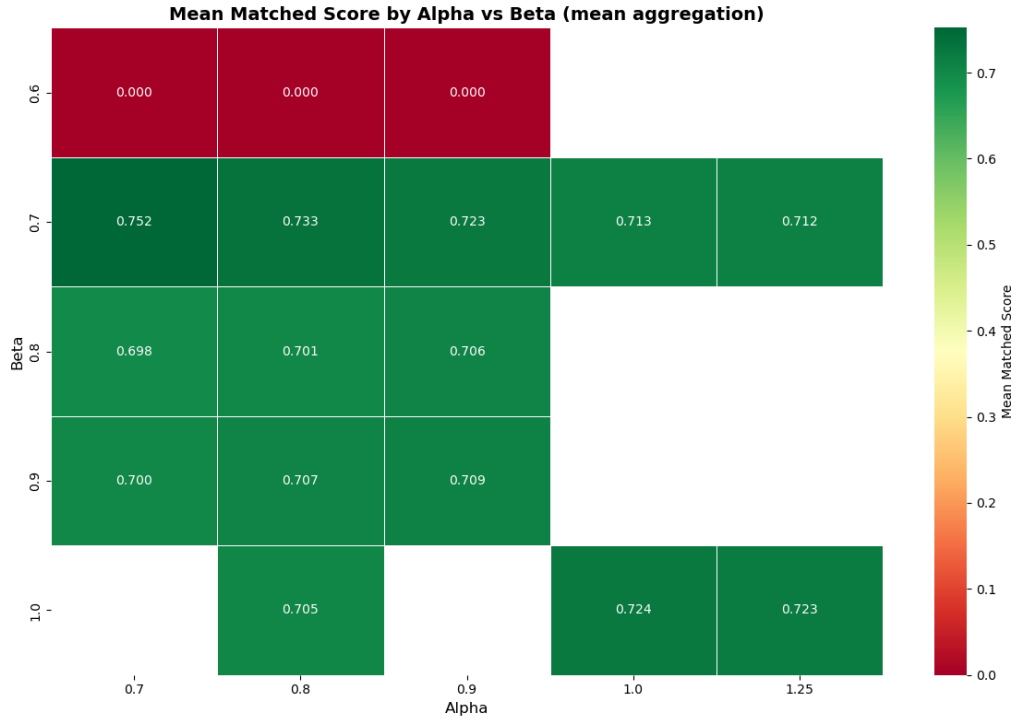


Closer look to the parameters :





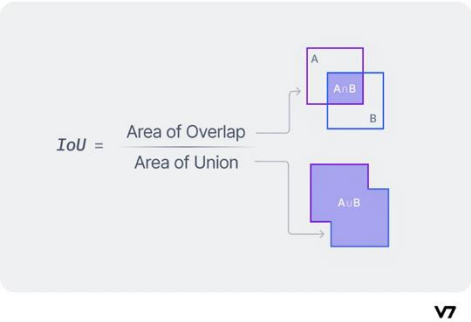
Closer look to the parameters :



Best model

Metric : Intersection over Union

Mean Matched score : is the mean IoUs of matched true positives



https://www.v7labs.com/blog/intersection-over-union-guide

Cellpose : No smoothing, CP_20241007_h2bxncad model, channels = [[1,2]], diameter=30
Mean Matched score : 0.7466

Plantseg 1: gaussian smoothing α=2.5, lightsheet_3D_unet_mouse_embryo_cells model,
Watershed options : Threshold=0.4, SigmaSeed=0.2, SigmaWeight=0, MinSize=90, Alpha=0.7, PixelPitch=(1.441,1,1), Mode=gasp
Clustering options : Beta=0.7, Minsize=100
Post Processing options: Threshold=0.1, Instances= False
Mean Matched score : 0.78103
Accuracy : 0.074743

But result are terrible

Plantseg 2 : gaussian smoothing α=2.5, lightsheet_3D_unet_mouse_embryo_cells model,
Watershed options : Threshold=0.7, SigmaSeed=0.2, SigmaWeight=0, MinSize=100, Alpha=1.25, PixelPitch=(1.441,1,1), Mode=gasp
Clustering options : Beta=1.0, Minsize=75
Post Processing options: Threshold=0.1, Instances= False
Mean Matched score : 0.722506
Accuracy : 0.292969

Training our model

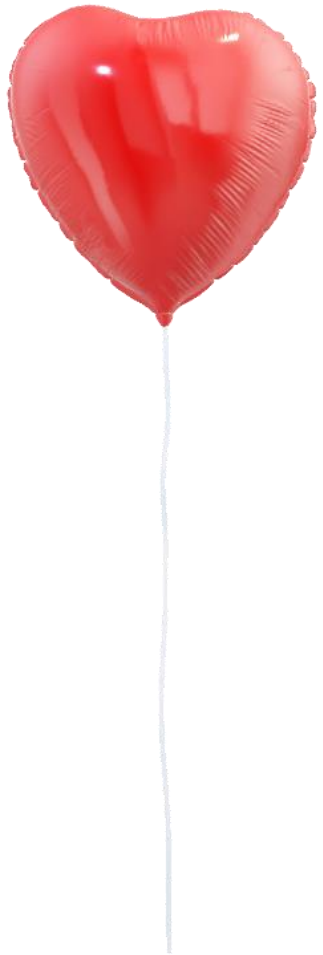
- Retrain lightsheet_3D_unet_mouse_embryo_cells model
  - Took similar parameters that the original one
  - File formats
  - Low training data (3 for train and 5 for validation) converges (25h)
  - High training data (70% for train and 30% for validation) does not converge (not even 1 epoch in 48h)
  - Carfull with memory error

Results (biased because file in validation data)

- Its still running ☹

Future aspects

- Is my metric good/did I understand correclty how it works, tune the thresholds
- Work with general model from plantseg
- Finish correctly the new model, preprocessing training data, early stopping in order to avoid the cons of cellpose ?
- Perhaps making a general classification model could help



Thanks a lot for everything