

Image processing coding contest

Workflow ideas



Contest dates: Oct. 30th – 16 Nov. 2018

Idea 1: Segmentation Workflow

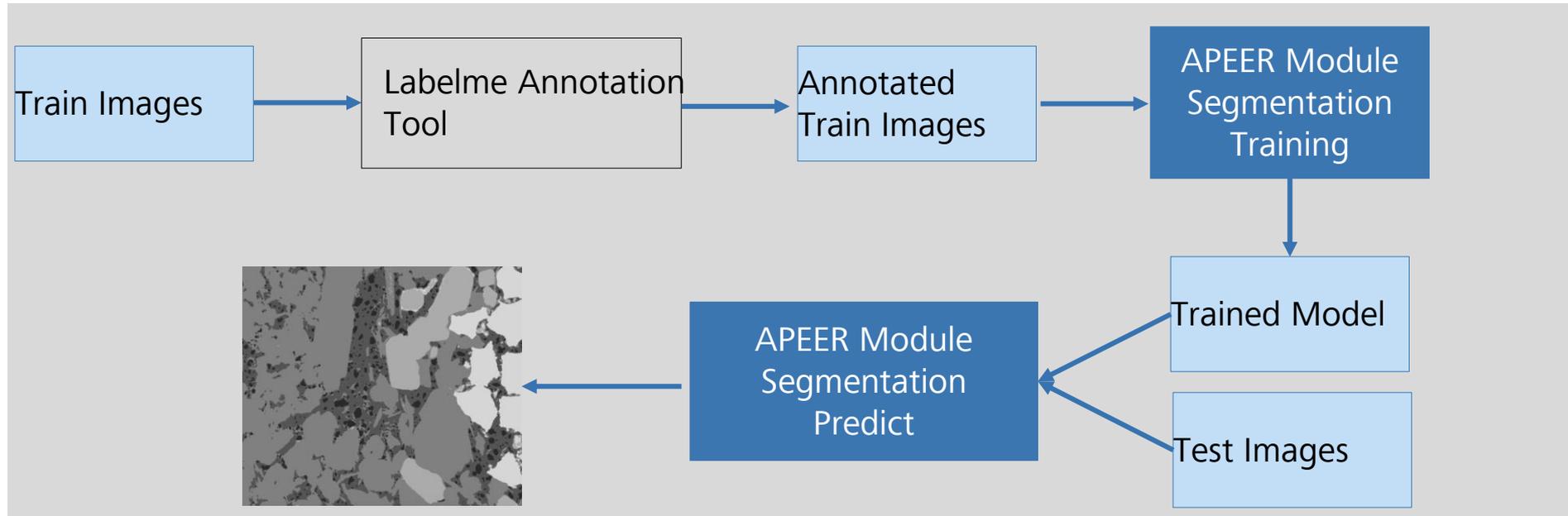


The task is to create two APEER modules:

1. A module that allows to train a segmentation algorithm (e.g. Deeplab) on any kind of image set and that returns the trained model
2. A module that uses the trained model to segment test images

Note: The data annotation can be done with an external open source tool, such as labelme

Example dataset information is given on the following page.



Idea 1: Segmentation Workflow

Example dataset information



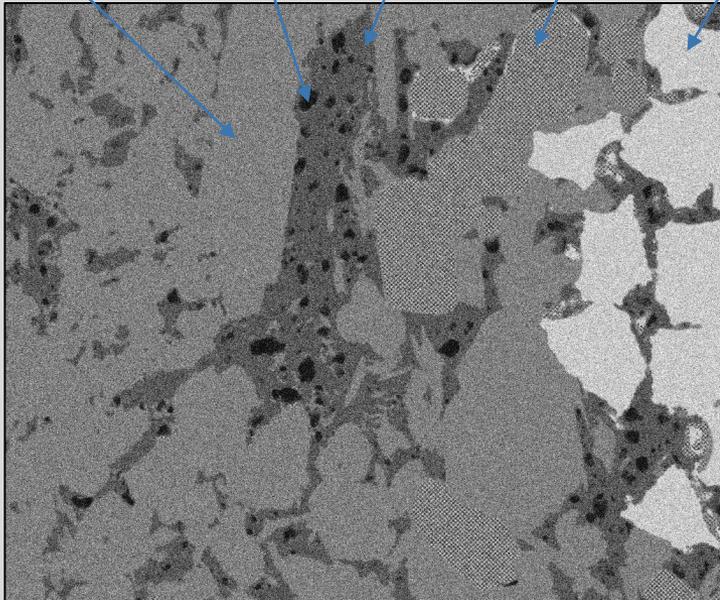
Download the file from: <https://spaces.hightail.com/space/7m0BHiVOqs>

Tiff stack with 606 images in the series (509 MB)

Contains 5 different regions that need to be segmented

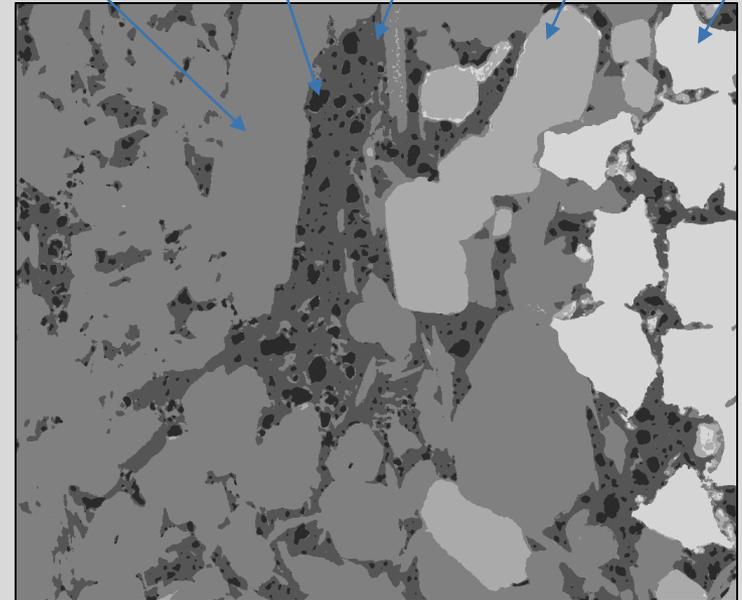
Region 3 has synthetic texture

Region 4 Region 1 Region 2 Region 3 Region 5



Images to be segmented

Region 4 Region 1 Region 2 Region 3 Region 5



Example segmented mage

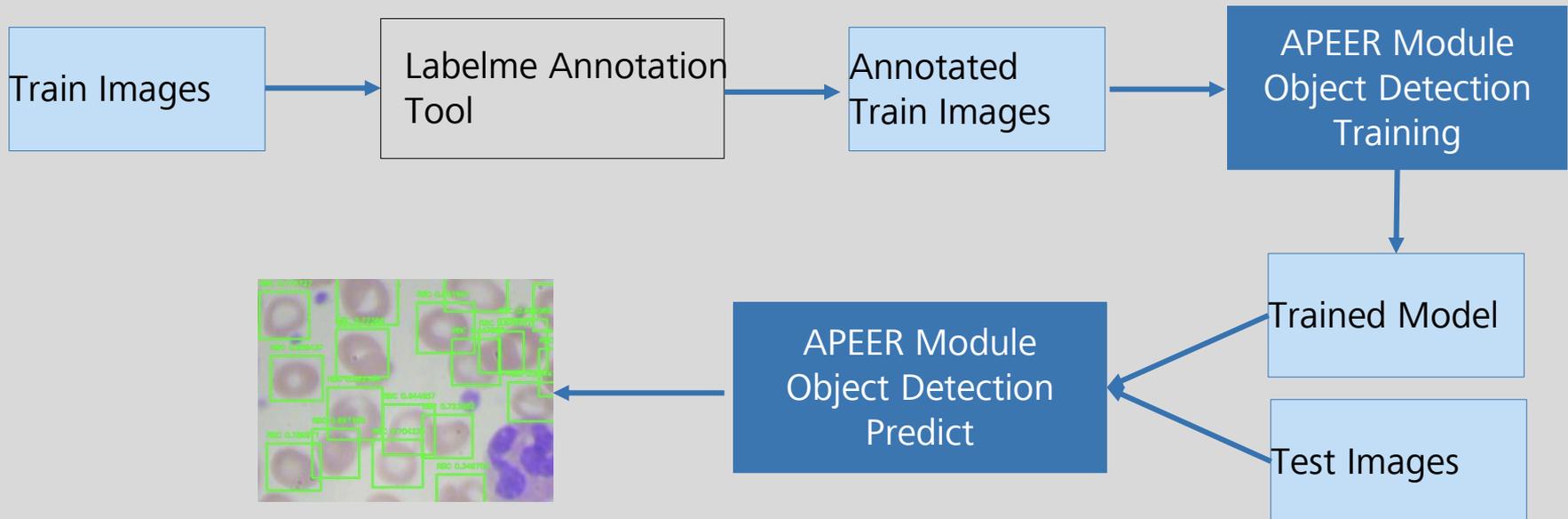
Idea 2: Object Detection Workflow



The task is to create two APEER modules:

1. A module that allows to train an object detection algorithm (e.g. Yolo from Darknet or the Tensorflow Object Detection API) on any kind of image set and that returns the trained model
2. An APEER Module that uses the trained model to detect objects in test images

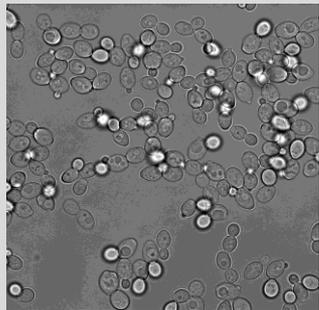
Note: The data annotation can be done with an external open source tool, such as VOTT or labeling



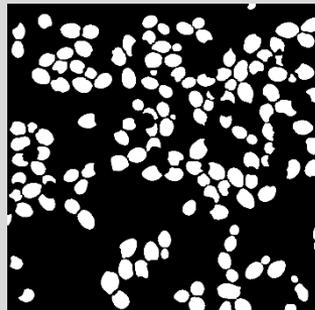
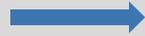
Other Ideas: Any workflow of your choice that automates a current manual workflow



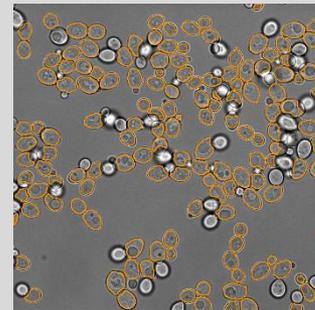
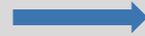
Here is one of the example workflows from APEER. This workflow automates the process of detecting, sizing, and plotting the dimensions of individual yeast cells in a microscope image.



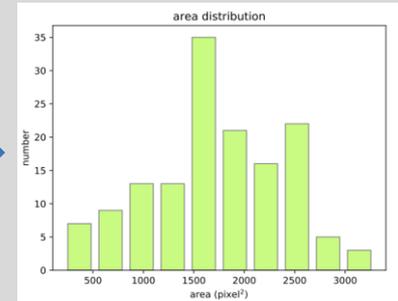
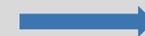
Input image of yeast cells collected on a microscope



Tensorflow based object recognition algorithm to identify individual yeast cells



Python code to measure individual yeast cell dimensions



Plotting of yeast cell dimensions

NOTE: Do not work on this exact workflow as it already exists on APEER. The description is for example purposes only.

Other potential workflow examples include:

- Deep learning based tumor detection
- Mitosis detection in histology images
- Segmentation of pores (or other features) in 3D microscopy images of battery materials, reservoir rocks, 3D printed components, etc.
- Separation of circular vs non-circular features
- Or any other image processing workflow up to your imagination!



"I wish I could build a streamlined workflow for my research challenge."



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Create

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Automate

Automate your Workflows to ensure maximum reproducibility.



Research

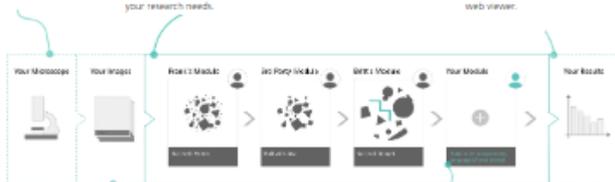
Save valuable research time by not re-inventing code.

This is how your customized solution could look like.

Connector Modules enable direct connection between APEER and your microscope or other hardware

A workflow is an arrangement of Modules put together in a unique order to address your specific job to be done. You can easily create a Workflow from scratch or customize an existing Workflow to fit your research needs.

The results from all your experiments (Workflow runs) are stored under your APEER account and can be accessed by you anytime from anywhere. Visualize your images using the integrated 2D/3D web viewer.



Images and other data input for your Workflow can directly come from your microscope or uploaded to APEER from your local drive or a web location.

A Module is a unit operation with a user interface and is designed to perform a single task. The task could be simple, such as converting a file format, or complex, such as using a deep learning algorithm for feature detection. You can use community shared Modules or create your own using a programming language of your comfort, including Python and ImageJ scripting.

Check out [Workflows](#) and [Modules](#) from the community

Read more about the APEER Initiative on the [blog](#).



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