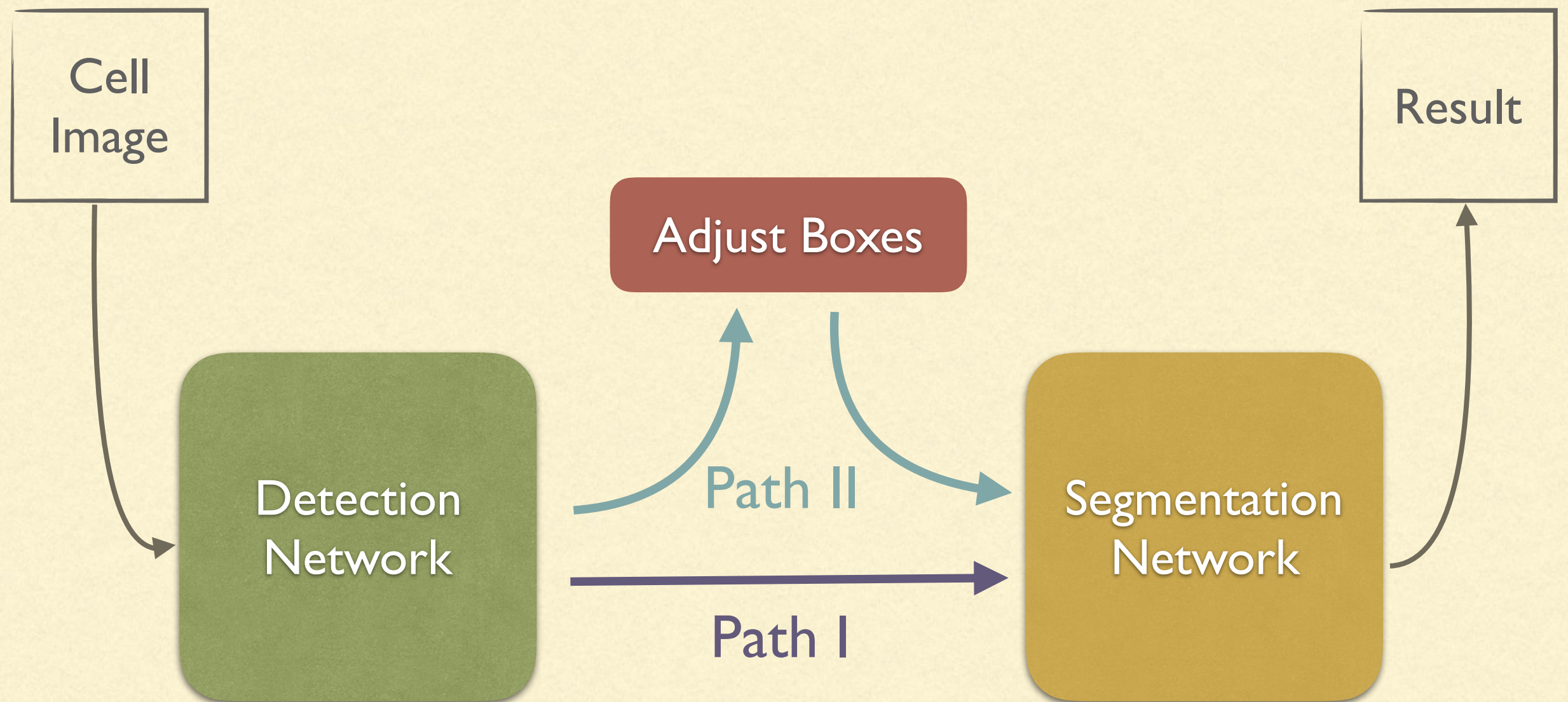

CELL IMAGE PIPELINE

Yu-Hui Wu

Mentor: Ali Selman Aydin

Instructor: Roy Shilkrot

ARCHITECTURE



I/O DETAILS

- **Input:** Folder containing all testing cell images.
 - **Output:** “.mat” files with segmentation results of all cell crops within each image.
 - Run “*ShowSingleImageMask.m*” or “*ShowFolderImageMask.m*” to visualize “.mat” results as images.
-

INTERMEDIATE DETAILS

- **Adjust Boxes:** To fix imperfect results of detection network. Allows 1) adjust & delete 2) add bounding boxes. Overwrites previous results.
 - Run “*ShowSingleImageBox.m*” or “*ShowFolderImageBox.m*” to visualize “.txt” bounding box results on each image.
 - Run “*AdjustSingleImage.m*” or “*AdjustFolderImage.m*” to adjust/delete/add bounding boxes on each image.
-

NETWORK DETAILS

- **Detection Network:** Trained pretrained YOLO network on Yeast cells dataset. Achieve IOU $\sim 50\%$.
 - **Segmentation Network:** Trained CNN segmentation network on Yeast cells dataset. Achieve accuracy $\sim 80\%$.
 - **Dataset:** Sequence Yeast Cells - 20 images per sequence with total 9 sequences. Scattered as 180 individual images in this pipeline. 140 images (7 seq.) as training set; 20 images (1 seq.) as validation and 20 images (1 seq.) as testing.
-

ENVIRONMENT / SOFTWARE

- Tensorflow 1.3.0
 - Keras 2.0.5
 - GPU / CUDA / CUDNN 5.1
 - Matlab
 - Python 3.6.3
-

DEMO

Thank you!

Yu-Hui Wu

yuhwu@cs.stonybrook.edu
