IRISAI SUBMISSION

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We use a simple pipeline with the next steps:

1. Unet segmentation for keeping cellular areas, and discarding areas without many cells.  
   We trained a unet segmentation network in x5 resolution, using annotations we did ourselves (not by pathologists).
2. We created a training dataset with 900,000 256x256 crops, in x40 resolution, using Unet for filtering.
3. We trained a Resnet50 model on this dataset, using 0 as labels for crops from slides without HER2, and 1 as labels for crops from slides with HER2.
4. We trained on the entire dataset, for 4 epochs, with 10%/90% label smoothing.
5. At test time, for every slide, we collect all the tiles that more than 95% of their area is cellular, according to the Segmentation mask.  
   We apply the classifier on them.
6. The slide prediction is the ratio of the tiles that are labeled as positive by the classifier (threshold of 0.5).

To run:

Dependencies:

PyTorch, Torchvision, opencv, tqdm, openslide-python, numpy, pandas

‘ python classify.py --slides\_path <directory with the mrxs files>`