

Evaluation Function

The evaluation code is used to quantitatively assess the segmentation performance. It consists of two functions:

- **evaluateCytoSegmentation.m**: Function to evaluate the result.
- **SegEvaluateJIDiceTPRFPR.m**: Function about the evaluation measurement, called by evaluateCytoSegmentation.m.

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You need to load the cytoplasm annotation of each cell into a Matlab Cell structure before you call the function **evaluateCytoSegmentation.m** to start evaluating. For example, cell **GroundTruth{numImage_i,1}{CellID_j,1}** refers to the j-th cell annotation of image i.

HINT: we generate an example code that uses binary images of cytoplasms and nucleus and we suggest your results of segmentation are organized in the same way, take a look on our example and **use it !!!**

diceevaluation_run.m

The code uses a particular directory tree for files and segmentation result.

\isbi2014_test - main directory of TEST images, **GT** for Ground Truth, **ORIG** for original EDF images and **SEG** for segmented images using YOUR CODE.

\isbi2014_test\GT|SEG\Cyto - ground truth (or segmented) directory for cytoplasms, one directory for each image from original EDF, where each directory has one binary image for each cytoplasm.

\isbi2014_test\GT|SEG\Nucleus - ground truth (or segmented) directory for nucleus, one binary image for all nucleus of each image.