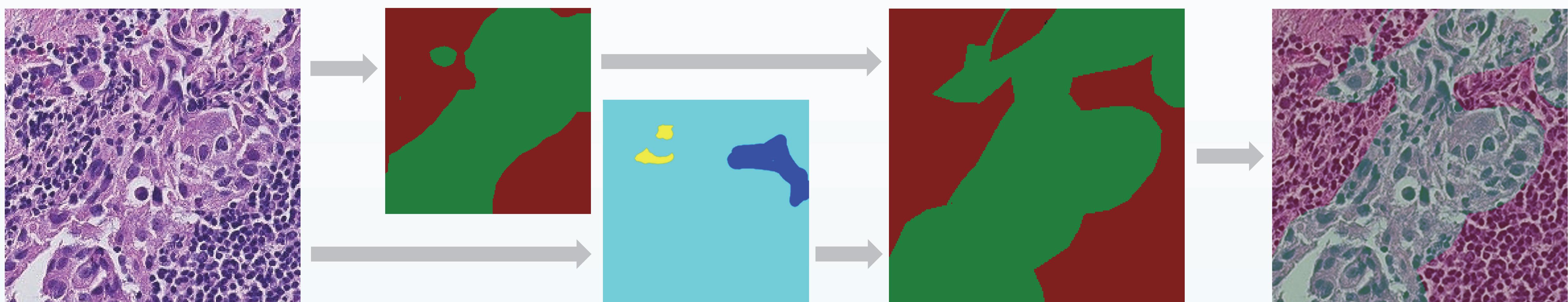


Collaborative slide screening for the diagnosis of breast cancer metastases in lymph nodes

Gianluca Gerard, Patrizia Morbini, Marco Piastra

University of Pavia, Policlinico San Matteo Foundation IRCCS and i-data.tek



Breast cancer is the most common form of cancer among Italian women

The **prognosis** depends on whether the cancer has spread to other organs

Sentinel lymph nodes are the target organs primarily reached by metastasizing cancer cells

The diagnosis is conducted by cutting slices from the sentinel lymph nodes, fixing them on glass slides, staining the tissues and, for a digital diagnostic pipeline, digitalizing the slides, to obtain Whole Slide Images (WSIs)

Research Goal

Our goal is to design an automated segmentation method to support the pathologists in the diagnosis of WSIs

able to **improve its performances based on a limited set of error corrections** (provided by the pathologist)

Automated Segmentation

Automated segmentation of WSI promises to improve the speed and quality of pathologist's work by

- skipping irrelevant regions
- focusing on the highlighted potential regions of interest

However current **segmentation tools suffer from biases introduced by the tool developers and by the training sets.**

To address such limitations, it is necessary to develop and validate in a clinical environment a method that can adapt its behavior to the work practices, digital instrumentation, and patient population of the clinic

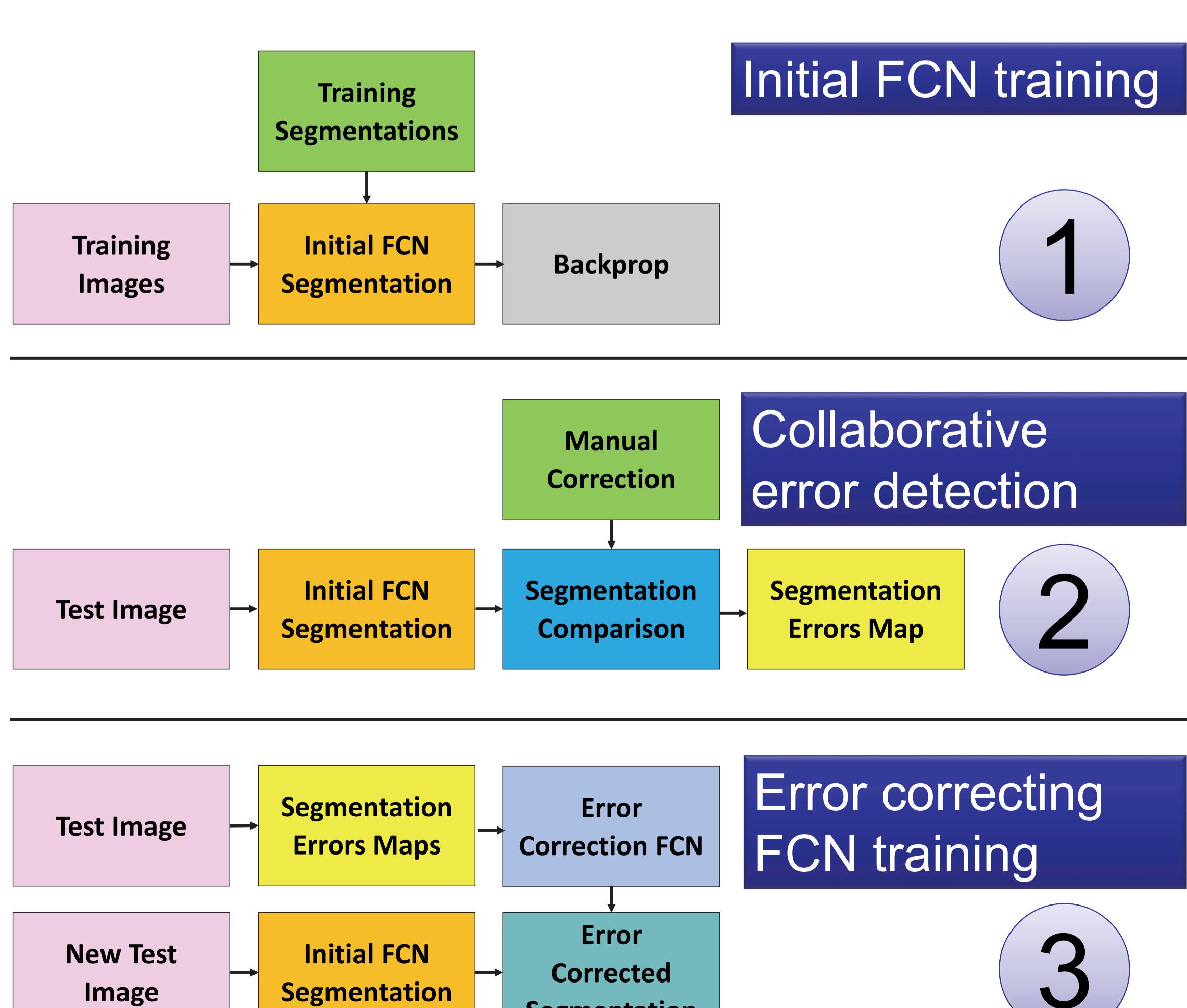
The method must satisfy several requirements:

- It has to be collaborative
- it should achieve state-of-the-art accuracy
- it should require minimal maintenance

We aim at designing such a tool by integrating into a unified pipeline the following two methods:

- *deep fully convolutional networks*
- collaborative segmentation with interactive segmentation

Collaborative FCN Training



Fully Convolutional Networks (FCN)

We use a ResNet50 Dilated FCN [1] as our main network

The classical ResNet50 architecture is modified such that the last three residual blocks have the standard convolutions replaced by dilated convolutions. The last fully connected layer is replaced by a convolution layer followed by bi-linear up-sampling

The training images are derived by segmenting WSIs in a regular grid of patches, each 448x448 pixels. Patches with no tissue are discarded by a filter applied to the HSV channels, and the whole network is trained to classify the images with three labels:

background, normal tissue and lesion

Due to the heavy imbalance of normal patches vs patches with lesion we downsample the normal patches and we only process WSIs that contain at least one lesion

Our interactive pipeline then takes inspiration from [2] as we use a separate path to identify discrepancies between the tool's segmentation (host network) and the manual pathologist segmentation

The error correction network is based on a recently introduced Fully Convolutional Network (FCN) that learns how to segment new categories with very few input examples [3]

This new FCN is called **conditional FCN** and it achieves excellent results even if conditioned on single pixels instead of dense segmentations

The error correction network is the same FCN with a conditional path that learns to recognize, segment and reclassify misclassified regions between the pixels where the automatic segmentations agree with the manual segmentation from the ones that doesn't

The trained conditional FCN is used on the training set to correct the training labels and to correct its parameters

Lesions in lymph-nodes

We devise a new framework for interactive correction of automated segmentation of lesions in lymph-nodes

Our method relies on a recently introduced enhancement to the Fully Convolutional Network [3] that allows to segment regions of new classes starting from very few samples of the new class. In our framework this allows to pass segmented error regions to the segmentation network and use it as an error detector and classifier

Once the error correction is applied to the original training dataset the network can adapt and change its behavior according to the correction provided by the pathologists

Our framework is a novel application of co-FCN in the field of biomedical images

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