Detection of lung cancer cells on Whole Slide Images using Deep Convolutional Neural Networks

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ABSTRACT

AI and computer vision are combined in order to detect cancer cells within whole slide images, using state-of-the-art segmentation models. The Whole Slide Images (WSI) obtained from the Sotiria General Hospital pathology department were digitised as a first step. An algorithm runs all over the image to slice it into several smaller images to reduce processing time and simplify the process. Each slice is passed as input to the model to classify and segment cells as malignant or not. The purpose of the trained model is to detect all malignant cells within a given WSI as input and return suggestions of malignant cells found within the image to the end user. In this way, the model offers efficient workflows, easier collaboration and telepathology and new biological insights into histopathology data through usage of images processing and computer vision algorithms to detect clinopathologic patterns.

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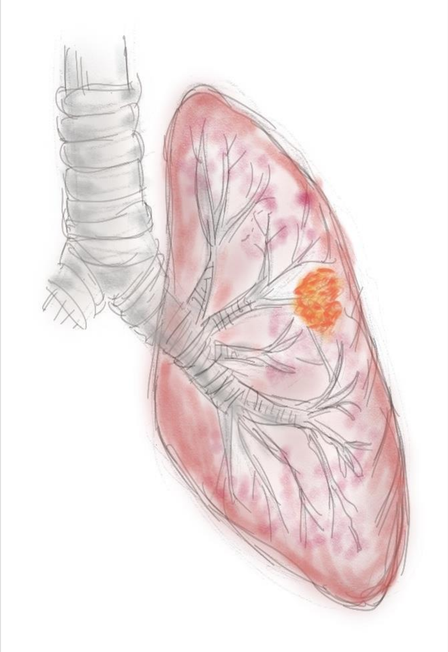
PROBLEM STATEMENT

Goal: Early detection of lung cancer for improved survival & quality of life

Problem: Current process is slow

Tool: AI-based computational pathology [1]

Advantage: Reduce errors in diagnosis & classification



AI can help in:

1) **Detection:**

- Analysis of imaging data for identification of suspicious regions
- Addressing of high false positive rates and over-diagnosis

2) **Characterization**:

- Identification of tumor heterogeneity
- Segmentation using 2D or 3D assessments in order to clarify the extent of abnormality
- Staging: classify tumors based on expected stages and therapeutic strategies
- Diagnosis: classify benign and malignant abnormalities
- Imaging genomics: combine imaging and genomic data

3) **Monitoring**

- Observe temporal tumor changing with respect to treatment

METHOD: Digitization of Images

- Biopsy Lung **specimens** were obtained by the Sotiria General Hospital histopathology department
- Digitization of the WSIs performed using conventional methods in order to reconstruct and augment the quality of the picture by Sotiria General Hospital
- Software to process the whole slide image and divide it into smaller slices. For each slice, nuclei segmentation manual annotation, to label as malignant or not the substructure of the image (Figure 1)

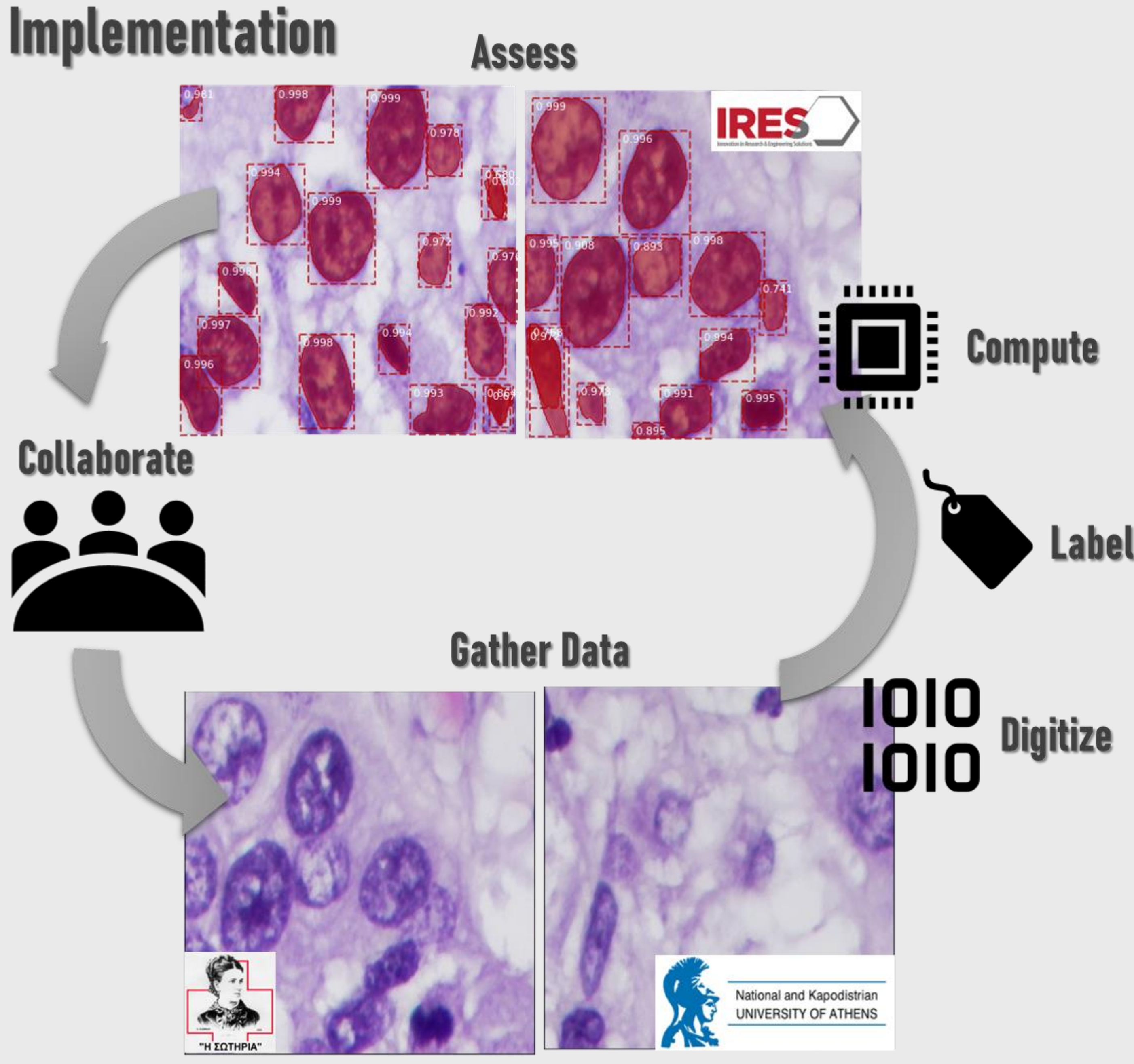


Figure 1. Pipeline Definition.

METHOD: Software Development

- Instance segmentation models (Mask R-CNN) were used for nuclei segmentation within an image (Figures 2 and 3)
- Training using a labelled dataset was performed; performance was used to select the best model from a pool of possible ones
- The selected model was deployed for an interactive application
- A web-based platform was deployed to assist histopathology experts when assessing WSI
- Results are uploaded and saved to a private repository connected to a relational database

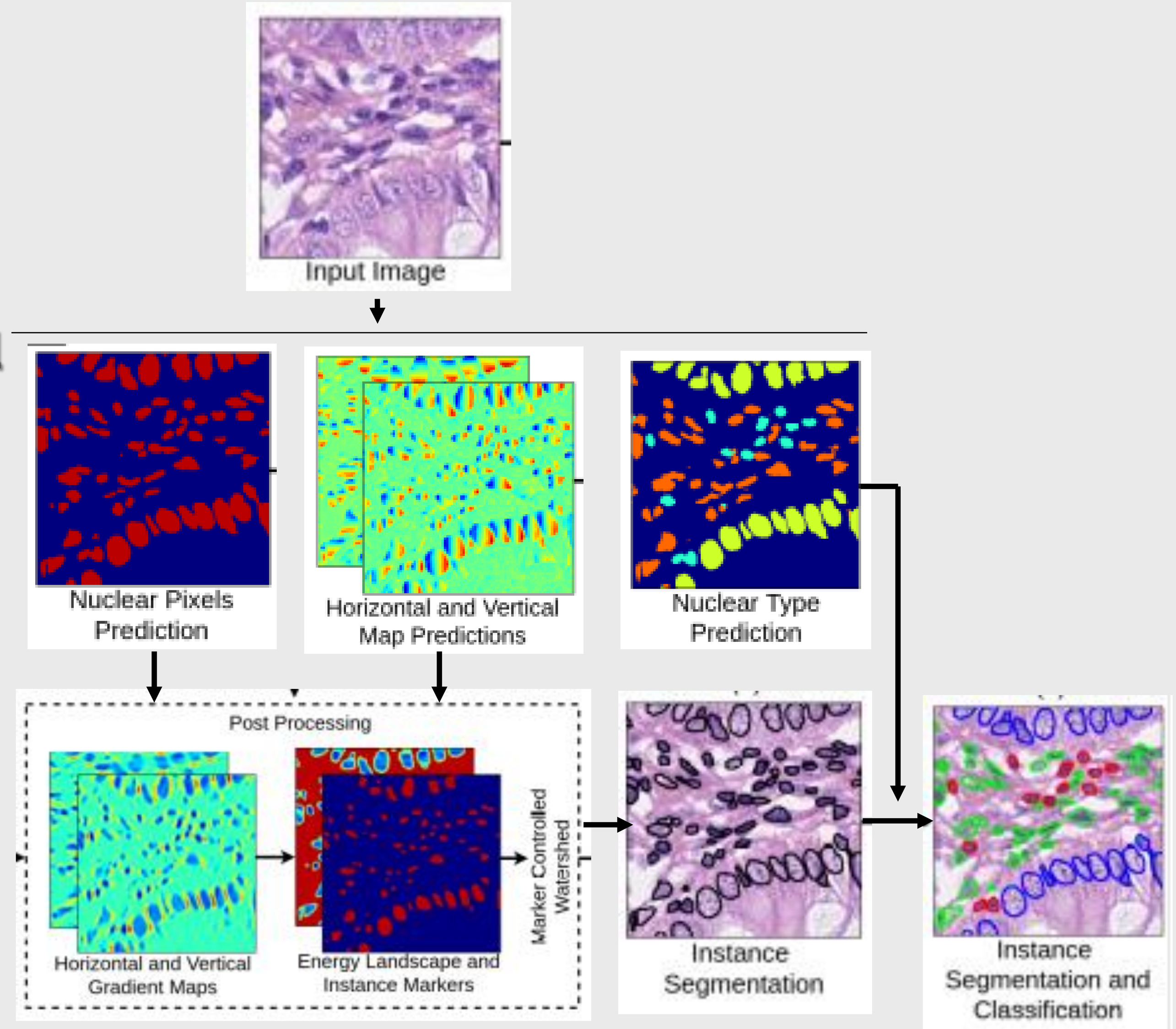


Figure 2. HoVer-Net Model [3].

RESULTS & FUTURE WORK

- Identification, detection and classification of the malignant nuclei
- Creation of a pipeline and web-based platform
- Expand the model by training more cell data (e.g. neoplastic epithelial, inflammatory, non-neoplastic epithelial)

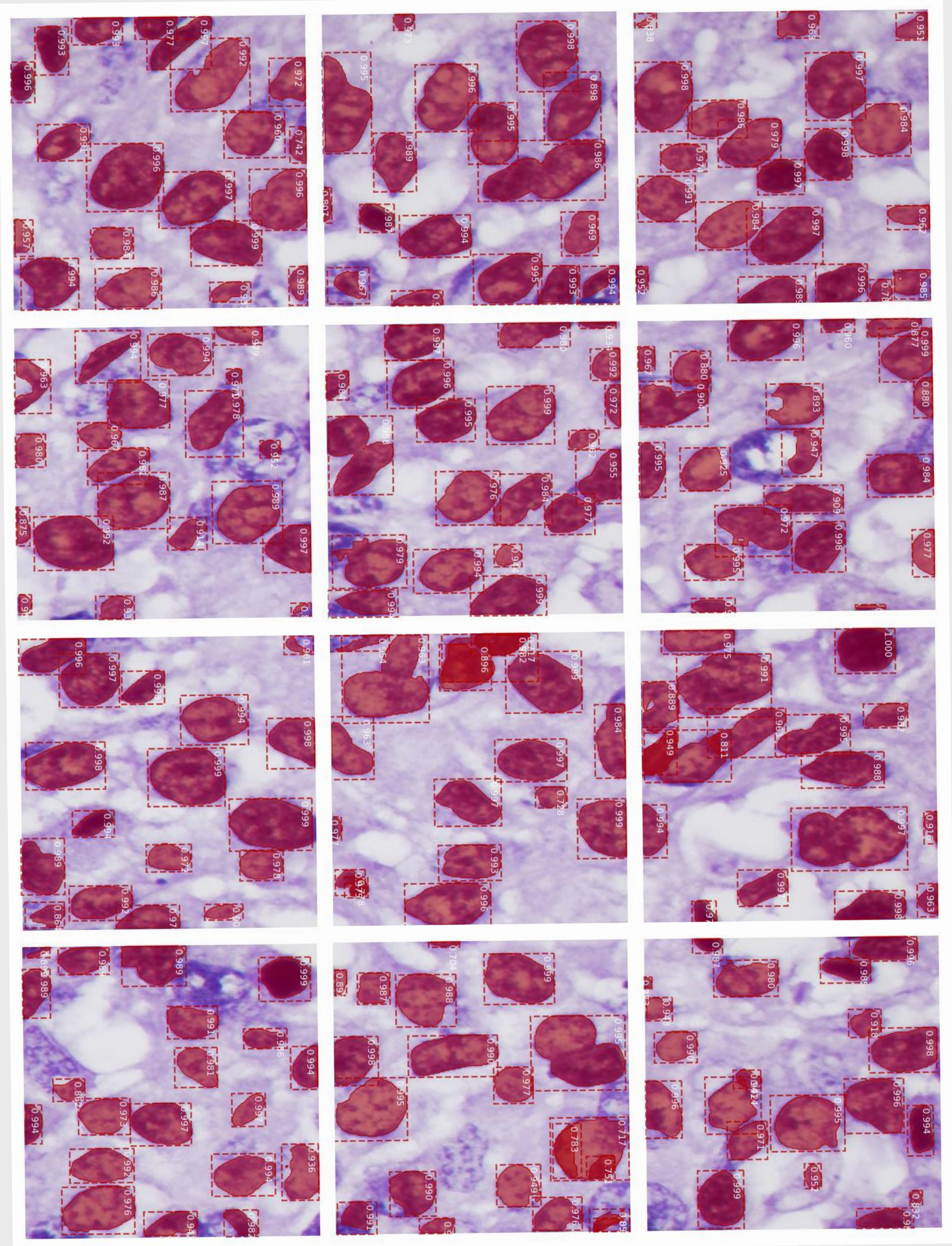


Figure 3. Model Output.

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[3] Graham, S., Vu, Q., Raza, S., Azam, A., Tsang, Y., Kwak, J., & Rajpoot, N.. (2018). HoVer-Net: Simultaneous Segmentation and Classification of Nuclei in Multi-Tissue Histology Images.

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