

CNN-based Approach for Cervical Cancer Classification in Whole-Slide Histopathology Images

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Background

1. According to IARC/WHO, Cervical Cancer (CC) will cause 460 000 deaths per year by 2040 in the absence of decisive actions (~50% over 2018 levels with ~90% of deaths in LMICs, particularly sub-saharan african women).



Figure 1: The Uterine Cervix

2. Histopathological assessment is the cornerstone for non-invasive/invasive cancers diagnosis/treatments and still crucial for cervical cancer screening programs evaluation. (Teixeira and Vasconcelos, 2019; Bulten et al., 2011).

Background

3. *"Numerous publications show the clinical and economic benefits of obtaining a second opinion for Pathology specimens ... In terms of cancer, changes can be from cancer to benign (or vice versa) or from one type of cancer to another, which could have a significant impact on treatment and prognosis ..."*

— Jonathan Epstein, M.D.
Director of Surgical Pathology
Johns Hopkins Hospital

Background

4. The emergence of Whole-Slide Imaging (WSI), i.e. virtual microscopy, has led to an unprecedented synergy between AI and digital pathology to address several issues like misdiagnoses.



Figure 2: Digitization of Pathology Specimens

5. WSIs come with several obstacles that limit AI potentials exploit in computational pathology, e.g. single WSI dimension, clinical features variability, lack of annotated data, etc. (Tizhoosh and Pantanowitz, 2018).

Dataset Acquisition

Formalin-Fixed Paraffin-Embedded (FFPE) Tissue Specimens

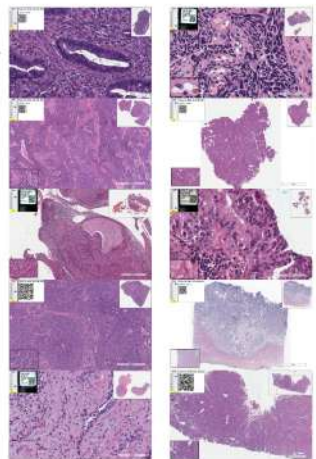
File Properties	
Name	TGSA-5392-112-161-01-0110121819-1940-4789-0040-0110000101001
Accession	W
MD5	2017c31ea480-18ee-6103-57a6a2c3e1e0
Data Format	SVS
Size	6.17 GB
MD5 Checksum	8e76d4176e4b58888011210114880
Archive	-
Project	TGSA-5392

Data Information	
Data Category	BioSpecimen
Data Type	Slide Image
Experimental Strategy	Diagnostic Diagnostic Platform
Platform	-

WSI Batch Effects Artifacts Free

Cervical Squamous Cell Carcinoma (SCC), H&E

Endocervical Adenocarcinoma (AC), H&E

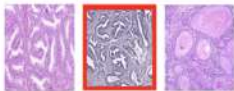
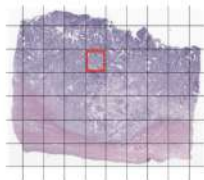


Workflow

1. Import Data

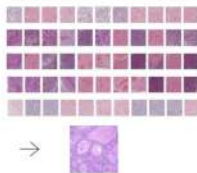


2. WSI Tile - Based Approach



> 12,412 ROIs, 600 selected
 1024 x 1024 ROIs, 226 / 224 x 224 ROIs, 20x
 > 80% of Tissue, one histologic criteria at least

3. Stain Normalization & Data Split



$$\exp \left(\ln RGB_{t,p} \begin{bmatrix} 0.655 & 0.715 & 0.290 \\ 0.083 & 0.985 & 0.115 \end{bmatrix}^T \right) = HE_{t,p}$$

Table 1: Statistics of data split

Train	Validation	Test
216 SCC	24 SCC	60 SCC
216 AC	24 AC	60 AC

4. Augmentation

5. Training

Table 2: VGG-16 network

Layer	Size
conv x2	224 x 224 x 64
pool	112 x 112 x 64
conv x2	112 x 112 x 128
pool	56 x 56 x 128
conv x3	56 x 56 x 256
pool	28 x 28 x 256
conv x3	28 x 28 x 512
pool	28 x 28 x 512
conv x3	14 x 14 x 512
pool	7 x 7 x 512

[Fully-connected]

BNF
 Acc
 97%

Classifier

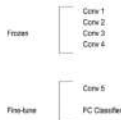


Table 3: Performance (%) on the test set

Accuracy	Precision	Recall	F1
98.26	96.8	99	97.9

Contribution

The major contribution focuses on the potential of a pre-trained CNN approach for an Hematoxylin & Eosin histopathology image analysis of cervical cancer to acquire efficient classification despite the data-poorness and unlabelled problems. Hence, the challenge relied on the non trivial task of WSIs processing and the VGG16-CNN pre-trained model fine tuning from a totally different data on which it was trained on.

Future Work : Integration of proteogenomics, clinical data and WSI to detect cancer patterns.

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